Prague, Czech Republic, January, 7-11, 2024

INTERNATIONAL
BIOGEOGRAPHY
SOCIETY
11th Biennial Conference

11th Biennial Conference

PRAGUE, CZECHIA

POCKET PROGRAM

January 7- 11, 2024

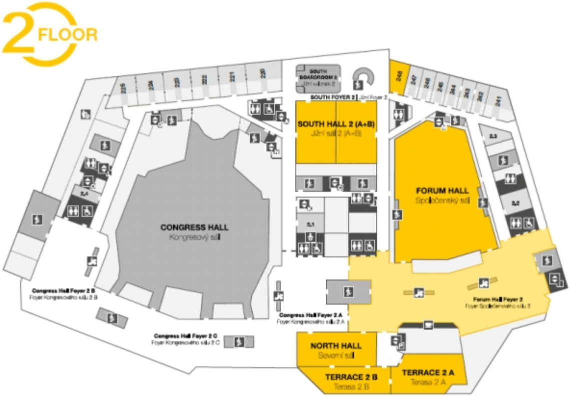
INTERNATIONAL
BIOGEOGRAPHY
SOCIETY

ORGANIZED BY:

INTERNATIONAL
BIOGEOGRAPHY
SOCIETY

Czech
Society
for Ecology

POCKET PROGRAM
January 7- 11, 2024



Wifi name: IBS24
Password: biogeography

ORGANIZING COMMITTEE

- David Storch (Chair)
- Tereza Jezkova
- Seda Akkurt Gumus

2022-2024
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- Samuel Scheiner
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SCHEDULE OVERVIEW

7-JAN	8-JAN	9-JAN	10-JAN	11-JAN
09:00 am WORKSHOPS	08:15 am Welcome Symposium 01 - Island Biogeography (Forum Hall)	08:30 am Symposium 03 Network Biogeography (Forum Hall)	08:30 am Awards - Wallace Award, Wilson and MacArthur Award, Dissertation Award (Forum Hall)	09:00 am FIELD TRIPS & SELF GUIDED TOURS IN PRAGUE - FAREWELL GROUPS
	10:15 am Coffee Break	10:15 am Coffee Break	10:15 am Coffee Break	
	10:45 am Symposium 02 - The Biogeography of Cities (Forum Hall)	10:45 am Symposium 04 - Ecosystem Engineering (Forum Hall)	10:45 am 5 Concurrent Sessions	
	12:30 pm Lunch Break	12:30 pm Lunch Break	12:30 pm Lunch Break	
	02:00 pm 5 Concurrent Sessions	02:00 pm 5 Concurrent Sessions	02:00 pm 5 Concurrent Sessions	
	04:00 pm Poster Session 1 (Forum Hall Foyer, 2nd Floor)	04:00 pm Poster Session 2 (Forum Hall Foyer, 2nd Floor)	04:00 pm - 04:15 pm Coffee Break	
			04:15 - 05:00 pm Business Meeting/ Closing/Awards	
06:00 pm REGISTRATION & WELCOME RECEPTION (Forum Hall Foyer 2)			05:00 pm - 7:00 pm Early Career Mixer (Restaurace U Šumavy*)	
			7:30 pm - 10:30 pm Banquet (Municipal House Brewery**)	

*Štěpánská 3, Praha 2
**Pivnice Obecní dům nám. Republiky 1090/5110 00 Praha 1

SYMPOSIA
Forum Hall

8-JAN	9-JAN	10-JAN
08:15 am Welcome: Felisa Smith **Symposium 01 - Island Biogeography** 8:30 am Sandra Nogué: Introduction	08:30 am **Symposium 03 - Network Biogeography** 08:30 am Laura Pollock: Introduction	08:30 am **Awards - Wallace Award, Wilson and MacArthur Award, Dissertation Award**
08:35 am 4. Martha Paola Barajas Barbosa: "A picture of plant functional diversity on an oceanic island (Tenerife, Canary Islands)" Martha Paola Barajas	08:35 am 14. Dominique Gravel: "Past, present and future of network biogeography"	1. Robert Whittaker: "Patterns and Processes of Island Assembly" 2. Tom Matthews: "Assessing the wider implications of species extinctions: island birds and beyond" 3. Benjamin Shipler: " The Geography, Ecology, and Evolution of Mammalian Endemism"
08:55 am 5. Manuel Steinbauer: "Biodiversity dynamics: from the fossil record to human dominated systems"	08:55 am 15. Wilfred Thuiller: "Understanding and predicting trophic webs in space and time"	
09:15 am 6. Roberto Rozzi: "The demise of dwarfs and giants: body size shifts predispose insular mammals to anthropogenic extinctions"	09:15 am 16. Núria Galiana: "Climate or diet? The importance of biotic interactions in determining species range size"	
09:35 am 7. Sonya Clegg: "The island syndrome in a great speciator: the silvereye in the south Pacific"	09:35 am 17. Louise M. J. O'Connor: "An overview of emerging approaches for conserving food webs across space"	
09:55 am 8. Keonhak Lee & Daehyun Kim: "An island biogeographical analysis of the uninhabited islands in the Shinan Province, South Korea"	09:55 am 18. Miguel Bastos Araújo: "Emerging patterns in trophic network biogeography"	
10:15 am Coffee Break	10:15 am Coffee Break	

SYMPOSIA

Forum Hall

8-JAN

10:45 am

Symposium 02 -
The Biogeography of Cities
Susanne Renner: Introduction

10:50 am

9. Elizabeth J. Carlen: "Linking the past to the present: How human history has shaped the distribution and evolution of urban wildlife"

11:10 am

10. Manuel Esperon-Rodriguez: "Will climate niche and functional traits facilitate the expansion of urban tree species in cities worldwide?"

11:30 am

11. Federico Morelli: "The global decline of evolutionary uniqueness of avian communities within cities: conservation implications"

11:50 am

12. Jens-Christian Svenning: "Urban greenspaces to benefit people and biodiversity – a biogeographic-macroecological perspective"

12:10 pm

13. Sarel Cilliers and Marie du Toit: "Socioeconomics and culture as drivers of urban biodiversity patterns in the Global South"

9-JAN

10:45 am

Symposium 04
Ecosystem Engineering
Kate Lyons: Introduction

10:50 am

19. Simon Darroch: "Ecosystem engineering, 'Earth systems engineers', and the lasting impact of organisms in deep time"

11:10 am

20. Katherine Turk: "Elucidating the effects of Ediacaran-Cambrian ecosystem engineering: A neoichnological case study"

11:30 am

21. William Matthaeus: "Bridges to Pangaea: Paleo-trait ecology connects us to deep-time Earth systems"

11:50 am

22. Torben Rick: "Offshore Ecosystem Engineering: Origins and Evolution of Pelagic Fisheries in the Northeastern Pacific"

12:10 pm

23. Liesbeth Bakker: "Restoring natural processes through rewilding with ecosystem engineers"

8 JANUARY
CONCURRENT SESSIONS

CATEGORY TITLE

Session 1
Biogeography of Anthropocene
South Hall 2A
Moderator - Christine Meynard

15min talks	TITLE	SPEAKER
02:00	24.The rising novelty of the biosphere: a macroecology-biogeography perspective	Matthew Kerr
02:15	25. Pre-Columbian forest recovery in Amazonia	Mark Bush
02:30	26. Undiscovered bird extinctions obscure the true magnitude of human-driven extinction waves	Søren Faurby
02:45	27. Effects of climate change and agricultural practices on plant communities: synthesis from a long-term, large scale monitoring effort in France	Christine Meynard
03:00	28. Urbanization dampens the latitudinal diversity gradient in birds	Jory Griffith
03:15	29. The Impact of European Colonialism on Global Plant Redistribution	Bernd Lenzner
03:30	30. GEDI predicts less than expected aboveground forest biomass in Ghana: implications for modelling carbon storage and forest restoration	David Shen
03:45	31. Gulls in the Urban Archipelago: Reconsidering the Island Syndrome	Yuval Itescu

CATEGORY TITLE

Session 2
Island Biogeography
South Hall 2B
Moderator - Julia Heinen

15min talks	TITLE	SPEAKER
02:00	32. Beyond Endpoints: Islands drive radiation of passerine birds in the Indo-Australian Archipelago	Audrey Prasetya
02:15	33. Neutral and Selective Processes Across Scales Identify Marine Islands	Michael Dawson
02:30	34. Introductions outweigh extinctions in shifting seed dispersal potential across 118 island plant–frugivore communities worldwide	Julia Heinen
02:45	35. Spatial variation of phenotypic traits is higher between islands than between mainland populations, but spatial variation of genetic diversity is rather similar across the two systems	Anna Csergő
03:00	36. Non-uniform change of ecosystem functioning on oceanic islands during the last 10,000 years	Franka Gaiser
03:15	37. Accessing islands' vulnerability to climate change	André Menegotto
03:30	38. Exploring mechanisms behind species-area relationship on habitat patches of acidophilous grasslands: a case study from the Czech Republic	David Zelený
03:45	39. Floristic homogenisation on South Pacific islands during the last 5000 years	Sandra Nogué

8 JANUARY
CONCURRENT SESSIONS

Session 3
Climate Change Biogeography
North Hall
Moderator - Josep Padullés Cubino

CATEGORY TITLE

15 min talks

	TITLE	SPEAKER
02:00	40. Variation and temporal trends of climate matching in birds	Duarte Viana
02:15	41. Climate-induced range and niche shifts in European and North American breeding birds	Damaris Zurell
02:30	42. Towards a Novel Biosphere in 2300: rapid and Extensive Global and Biome-wide Cli-matic Novelty in the Anthropocene	Alejandro Ordonez
02:45	43. Plant lineage gains and losses in temperate forest understories in response to global change drivers	Josep Padullés Cubino
03:00	44. Global records of soil fungi show climatic constraints of distribution and common cosmopolitanism	Petr Baldrian
03:15	45. Attributing biodiversity change to processes and drivers in the Alps - a dynamic modelling perspective	Anne Thomas
03:30	46. A climate-induced tree species bottleneck for forest management in Europe	Johannes Wessely
03:45	47. Range lags in European alpine plants under climate change	Christopher Johnson

Session 4
Phylogeography
Terrace 2A
Moderator - David Nogues Bravo

CATEGORY TITLE

15 min talks

	TITLE	SPEAKER
02:00	48. SPA: A predictive biogeographical framework to explain population differentiation through the prevalence of environmental suitability	Angel Robles Fernandez
02:15	49. Incorporating life history strategies in genetic models of demographic history	Rilquer Mascarenhas
02:30	50. A database and web application for sharing the entire alpine flora genomic data	Julien Renaud
02:45	51. Pleistocene climate oscillations, not orogeny, drove the assembly of the European Alpine sky island flora	Lara Wootton
03:00	52. Genomic evidence from forest understorey species suggests unexpected prevalence of cryptic temperate forest refugia in Europe	Philipp Kirschner
03:15	53. Genomic adaptation and future responses of an alpine Rhododendron species at eastern Hengduan Mountains	Qin Li
03:30	54. Repeated upslope biome shifting during late-Cenozoic climate cooling in a diverse alpine plant clade	Wolf Eiserhardt
03:45	55. Gaps in the global protection of terrestrial genetic diversity	David Nogues Bravo

8 JANUARY
CONCURRENT SESSIONS

Session 5
Biodiversity Patterns and Maintenance
Terrace 2B
Moderator - Milan Chytrý

CATEGORY TITLE

15 min talks	TITLE	SPEAKER
02:00	56. The ecology and biogeography of endemic mammal species	Benjamin Shipley
02:15	57. Niche Trackers Don't Play by the Rules: Consequences of Niche Tracking on Seasonal North American Bird Biogeography	Dominique Caron
02:30	58. Seasonal variation in dragonfly assemblage colouration suggests a link between thermal melanism and phenology	Roberto Novella Fernandez
02:45	59. Multiple dimensions of 3D habitat structure drives multiple dimensions of avian community diversity in North America	Colin Sweeney
03:00	60. Fine-scale patterns of plant community diversity across Europe	Milan Chytrý
03:15	61. Multifaceted biodiversity-stability relationships in boreal to subarctic ecosystems	Tuuli Rissanen
03:30	62. Taxon and area invariance of macroecological biodiversity patterns	Arnost Sizling
03:45	63. Idiosyncratic patterns of local species richness and turnover define global biodiversity hotspots	Jesper Sonne

9 JANUARY
CONCURRENT SESSIONS

Session 6
Functional Macroecology
South Hall 2A
Moderator - Lauri Laanisto

CATEGORY TITLE

15 min talks	TITLE	SPEAKER
02:00	64. Mammal life history strategies are strongly associated with environmental realms	Eleonora Beccari
02:15	65. Integrating functional and phylogenetic diversity in conservation science	Sonia Llorente-Culebras
02:30	66. Fine-scale alpine plant community assembly: Relative roles of environmental sorting, dispersal processes and species interactions	Norbert Helm
02:45	67. The ultimate guide of mycorrhiza and abiotic stress polytolerance in woody plants	Lauri Laanisto
03:00	68. Functional diversity promotes community stability over time across taxonomic groups	Enrico Tordoni
03:15	69. Evolutionary history and environmental variability shape resource specialization in tropical mammals	Chia Hsieh
03:30	70. Evolutionary and ecological determinants of decoupled phylogenetic and functional diversity in European grasslands	Martin Večeřa
03:45	71. The global evolution and distribution of plant defense traits is shaped by mammalian herbivores	Rachel Souza Ferreira

Session 7
Models and Methods
South Hall 2B
Moderator - Alfredo Ascanio

CATEGORY TITLE

15 min talks	TITLE	SPEAKER
02:00	72. Niche Divergence Plane: New conceptual framework to classifying and quantifying ecological niche divergence between taxa	Alfredo Ascanio
02:15	73. Harnessing AI and Remote Sensing to foster high resolution habitat mapping	Wilfried Thuiller
02:30	74. FOSSILPOL: The workflow to process global palaeoecological data of fossil pollen for vegetation-based macroecological synthesis	Ondřej Mottl
02:45	75. Predicting spatiotemporal community shifts in the Australian Wet Tropics	Seamus Doherty
03:00	76. Large-scale monitoring of biodiversity: a Human-Assisted Molecular Identification (HAMI) method using metabarcoding while accounting for abundances and systemic errors	Benoit Penel
03:15	77. Reliability of presence-only data for assessing plant community responses to climate warming	Laura Pacheco Riaño
03:30	78. A scalable machine learning approach to assess the combined effect of habitat loss and climate change on biodiversity	Victor Boussange
03:45	79. Unveiling Climate-Biodiversity Interactions: The influence of nature futures biodiversity scenarios on regional climate	Dirk Nikolaus Karger

9 JANUARY
CONCURRENT SESSIONS

CATEGORY TITLE

Session 8
Functional Biogeography
North Hall
Moderator - Ana Santos

15 min talks	TITLE	SPEAKER
02:00	80. Rewiring potential of plant-bird pollination networks in the Americas	Emma-Liina Marjakangas
02:15	81. Effect of grazing intensification on dung beetle biodiversity-ecosystem functioning relationship in a biogeographical context	Ana Santos
02:30	82. Orphans of the past: the global distribution, dispersal and extinction risk of plants with megafaunal fruits	Renske Onstein
02:45	83. Low redundancy drives functional diversity and vulnerability in Arctic ecosystems	Isaac Eckert
03:00	84. Climate influences the spatiotemporal variation of bird functional diversity in a global biodiversity hotspot	Jan Kalusche
03:15	85. Mutualistic interactions with seed-dispersing vertebrates is linked to global and regional variation in plant dispersal trait syndromes	Andressa Cabral
03:30	86. Predicting plant communities: a matter of species and traits!	Gabrielle Deschamps
03:45	87. Spatiotemporal variation in dietary strategies in birds	Marta Jarzyna

CATEGORY TITLE

Session 9
Historical Biogeography
Terrace 2A
Moderator - Luis Valente

15 min talks	TITLE	SPEAKER
02:00	88. Pantropical plant dispersal out of Madagascar's forests	Jan Hackel
02:15	89. The legacy of ecological and evolutionary processes in phylogenetic tree shape	Wilhelmine Bach
02:30	90. Africa as an evolutionary arena for large fruits	Friederike Wölke
02:45	91. Two debates in one go: the role of dispersal vs vicariance and of equilibrium vs non-equilibrium in Madagascar	Luis Valente
03:00	92. Do the species with large geographic ranges diversify faster?	Jan Smycka
03:15	93. Historical biogeography and patterns of diversification in African freshwater fishes of the genus Bryconaethiops revealed by phylogenomics (Teleostei: Alestidae)	Bruno Melo
03:30	94. Habitat specialization predicts demographic response and vulnerability of floodplains birds in Amazonia	Eduardo Schultz
03:45	95. Phylogenetic Lévy models reveal pulsed niche evolution underlying alpine biome shifts	Jurriaan de Vos

9 JANUARY
CONCURRENT SESSIONS

Session 10
Species Distributions
Terrace 2B
Moderator - Dan Warren

CATEGORY TITLE

15 min talks	TITLE	SPEAKER
02:00	96. A general framework for randomization analyses in SDM	Dan Warren
02:15	97. The impact of taxonomy on species distribution modelling: the overlooked pitfall of online biodiversity databases	Bryony Blades
02:30	98. Watch out for niche truncation: towards hierarchical species distribution models ?	Antoine Guisan
02:45	99. Projecting the untruncated response of biodiversity to climate change in Switzerland	Antoine Adde
03:00	100. What can the analysis of trait coordination tell us about plant functional responses to insularity?	Gianluigi Ottaviani
03:15	101. Assessing the global connectivity of a local community through seasonal migration: a tale from the High-Arctic	Louis Moisan
03:30	102. Mechanistic modelling of medically important snails: challenges and opportunities	Tiem van der Deure
03:45	103. Mountain plants survived the ice ages in a network of glacial refugia in the southeastern Alps, although with disparate demographic dynamics	Pau Carnicero

10 JANUARY
CONCURRENT SESSIONS

CATEGORY TITLE

Session 11
Marine Biogeography
South Hall 2A
Moderator - Hannah Owens

15 min talks	TITLE	SPEAKER
10:45 am	104. Historical biogeography of New World Killifishes recapitulates geographical history in the Gulf of México watershed	Christopher Hoagstrom
11:00 am	105. A New View of Marine Biodiversity	Hannah Owens
11:15 am	106. The biogeography of marine vertebrate trophic structures	Juan González Trujillo
11:30 am	107. Deep Time Historical Biogeography of Mytilid Bivalves	Alejandro Prieto
11:45 am	108. Biogeographical-scale impacts of future climate change in the aboveground biomass of seagrasses	Lidiane Gouvêa
12:00 pm	109. Ancient Indigenous fisheries catches document latitudinal temperature gradients across the Eastern Pacific over millennia	Jasmin Schuster
12:15 pm	110. Projecting changes in marine biota distribution to support climate-resilient marine spatial plans in Portugal	Elisabeth Julien

CATEGORY TITLE

Session 12
Macroecology: disturbance and humans
South Hall 2B
Moderator - Ole Vetaas

15 min talks	TITLE	SPEAKER
10:45 am	111. Convergent climate trait evolution provides a similar rank order of polyphyletic woody plant genera in the Himalayas and Andes.	Ole Vetaas
11:00 am	112. Global trends of aquatic food webs in the Anthropocene	Juan Carvajal-Quintero
11:15 am	113. Niche of plant species native to the temperate forest biome in Europe matches heterogenous natural vegetation shaped by large herbivores	Szymon Czyżewski
11:30 am	114. Evolutionary assembly of tropical rainforests	Melanie Tietje
11:45 am	115. Trait filtering and selection may explain the island rule in mammals	Kimberly Cook
12:00 pm	116. Spatial and macroecological patterns of hummingbird pollination syndrome in the Americas	Elisa Barreto
12:15 pm	117. From α- to β-diversity: Understanding the past, present, and future diversity patterns of Fagaceae in Southwestern China	Bikram Pandey

10 JANUARY
CONCURRENT SESSIONS

CATEGORY TITLE

Session 13
Invasion Biogeography
North Hall
Moderator - Franz Essl

15 min talks	TITLE	SPEAKER
10:45 am	118. A new perspective on the biogeography, macroecology and conservation impacts of biological invasions in the Anthropocene	Franz Essl
11:00 am	119. Megaherbivores as nature-based solution for resisting invasion dominance	Ninad Mungi
11:15 am	120. Do human impacts explain the prevalence of threatened bird species on islands?	Maira Cardoso
11:30 am	121. Distinguishing among alternative vectors for marine invasive species: Shipping versus Oyster transport	Allan Strand
11:45 am	122. Biotic resistance in highly diverse Ecosystems: Plant invasions in the tropics - Packed niche space or historic legacies	Marten Winter
12:00 pm	123. Biogeography and global flows of 100 major alien fungal and fungal-like oomycete pathogens	Anna Schertler
12:15 pm	124. Alien species and the shape of commonness and rarity in the European flora	Trevor Fristoe

CATEGORY TITLE

Session 14
Species Distributions
Terrace 2A
Moderator - Andrea Chiocchio

15 min talks	TITLE	SPEAKER
10:45 am	125. Mountains of Data: An Integrated Workflow for an Alpine Biodiversity Inventory Across Multiple Taxa	Lotta Schultz
11:00 am	126. From the Mountains to the Sea: mobile glacial refugia for terrestrial vertebrates in the Italian peninsula	Andrea Chiocchio
11:15 am	127. Applying invasive ecology to test how biotic interactions affect range shifts across large gradients	Namfon Booncharoen
11:30 am	128. The effect of biotic interactions on modelling responses to climate change in an alpine ecosystem	Alke Voskamp
11:45 am	129. Conserving Southeast Asian tree distributions requires a sustainable pathway mitigating both climate and land-use change	Sean Pang
12:00 pm	130. Multi-temporal species distribution models to characterize ecological niche	Elham Ebrahimi
12:15 pm	131. What defines the range limits of alpine plants?	Sophie Weides

10 JANUARY
CONCURRENT SESSIONS

CATEGORY TITLE

Session 15
Biodiversity Patterns and Maintenance
Terrace 2B
Moderator - Antonin Machac

15 min talks	TITLE	SPEAKER
10:45 am	132. Worldwide Late Pleistocene and Early Holocene population declines in extant megafauna are due to Homo sapiens rather than climate	Juraj Bergman
11:00 am	133. Species richness gradients are not universal, but change systematically across the phylogeny	Antonin Machac
11:15 am	134. Stochastic process, environmental filtering and species association jointly shape community assemblages along elevational gradients in Qinling mountain, China	Erhan Huang
11:30 am	135. Connecting spatial scaling of biodiversity change to per-individual ecological processes	Petr Keil
11:45 am	136. Land-use management impacts on species habitat suitability and functional diversity	João Campos
12:00 pm	137. Mammal food web susceptibility to extinction cascades	Lydia Beaudrot

CATEGORY TITLE

Session 16
Gradients, Range Limits, Beta Diversity
South Hall 2A
Moderator - Pilar Rodrïguez

15 min talks	TITLE	SPEAKER
2:00 pm	138. Prioritizing areas to monitor genetic diversity during climate change: an approach based on niche marginality	Olivier Broennimann
2:15 pm	139. BIOREALM: an ontology for biogeographic areas	Visotheary Ung
2:30 pm	140. Taxonomic, functional and phylogenetic dynamics and divergence during primary succession on lava flows	Severin Irl
2:45 pm	141. Geometric causes of species rarity	Anna Tószögyová
3:00 pm	142. Nutrient use by tropical ant communities varies among three extensive elevational gradients: a cross-continental comparison	Petr Klimeš
3:15 pm	143. The fungi among us: Contrasting turnover between rare and common fungal endophytes across the global distribution of two widespread C4 grass genera	Mathew Harris
3:30 pm	144. Predicting functional trait variation across climatic gradients with mechanistic models	Juan Rubalcaba
3:45 pm	145. Temperature attributes responsible for local distributions of alpine plants	Kryštof Chytrý

10 JANUARY
CONCURRENT SESSIONS

Session 17
Climate Change Biogeography
South Hall 2B
Moderator - Frédérik Saltré

CATEGORY TITLE

15 min talks	TITLE	SPEAKER
2:00 pm	146. Global spatial potential for implementing land-based climate solutions	Evelyn Beaury
2:15 pm	147. The opportunities and challenges of using genomic offset metrics to integrate local adaptation to climate into forecasts of future habitat suitability	Matt Fitzpatrick
2:30 pm	148. Increasing landscape connectivity can allow megaherbivores to maintain ecological function	Jenny McGuire
2:45 pm	149. Legacy of climate change in the global relationship between mammal trait variation and ecosystem stability	Frédérik Saltré
3:00 pm	150. myClim: Microclimate data handling and standardised analyses in R	Matej Man
3:15 pm	151. Lagged plant species responses to recent climate change and their associated traits	Sean Pang
3:30 pm	152. Predicting range dynamics of butterfly species and their host plants with CATS during the 21st century: species interactions matter	Andreas Gattringer
3:45 pm	153. Understanding the leading drivers of tree decline in semi-arid Zagros forests	Elham Shafeian

Session 18
Models and Methods
North Hall
Moderator - Damien Fordham

CATEGORY TITLE

15 min talks	TITLE	SPEAKER
2:00 pm	154. Occupancy modelling based on automatically identified species data: tackling false positives	Ryo Ogawa
2:15 pm	155. TABS: R package for reconstructing altitudinal shifts in biogeographical systems over time	Johannes De Groeve
2:30 pm	156. Unveiling the effects of climate databases on ecological niche models of forest species across scales	Salvador Arenas-Castro
2:45 pm	157. Novel model opens up new opportunities to analyse geographic patterns in animal demography	Tomáš Telenský
3:00 pm	158. eMaxent: an extended and improved maximum entropy algorithm for species distribution modelling	Babak Naimi
3:15 pm	159. Global patterns of taxonomic concept uncertainty in biodiversity databases	Richard Li
3:30 pm	160. Mapping more of biodiversity - modeling advances to improve data-deficient species distribution estimates	Shubhi Sharma
3:45 pm	161. Predicting vulnerability to future climate change with models and paleo-archives	Damien Fordham

10 JANUARY
CONCURRENT SESSIONS

Session 19
Paleobiogeography
Terrace 2A
Moderator - Carina Hoorn

CATEGORY TITLE

15 min talks	TITLE	SPEAKER
2:00 pm	162. Substantial light woodland and open vegetation characterised the temperate forest biome before Homo sapiens	Elena Pearce
2:15 pm	163. The Transformative Holocene: Evaluating the influence of environmental and genetic factors in the expansion of domesticates in West Eurasia	Elisabetta Canteri
2:30 pm	164. Functional Diversity Patterns Across the Ediacaran	Matthew Craffey
2:45 pm	165. The biogeography of the Great American Biotic Interchange	Juan Carrillo
3:00 pm	166. I estimate the rains down in Africa: Building ecometric models using small mammal hypsodonty to estimate paleoprecipitation across eastern Africa	Julia Schap
3:15 pm	167. The effects of climate change on fossil diversity of Asian mammals through the Paleogene: regional aridification vs. global cooling	Susanne Fritz
3:30 pm	168. Warming worlds of the past: paleobiogeographic changes in the Asian continental interior during early Eocene hyperthemals	Carina Hoorn
3:45 pm	169. Late-Quaternary megafauna extinctions have greatly reduced mammalian vegetation consumption	Rasmus Pedersen

Session 20
Macroecology patterns
Terrace 2B
Moderator - Kathy Willis

CATEGORY TITLE

15 min talks	TITLE	SPEAKER
2:00 pm	170. Environmental filtering, not dispersal history drives global patterns of phylogenetic turnover in seed plants at deep phylogenetic timescales	Lirong Cai
2:15 pm	171. Equilibrium Theory of Biodiversity Dynamics: Identifying patterns, parameters, and predictions using simulations	Grace Ridder
2:30 pm	172. The Potential for Re-evaluating Biodiversity Patterns in Environmental Space	Catherine Graham
2:45 pm	173. Environmental space and species turnover explain the land-sea biodiversity paradox	Ian McFadden
3:00 pm	174. Reclassifying biomes: a new climatic R function	Emilia Galli
3:15 pm	175. Range overlap, clade density and the evolution of diversity-dependent diversification	Marcio Pie
3:30 pm	176. Biogeographical cradles and museums segregating within Andean hotspots of endemism	Carsten Rahbek
3:45 pm	177. Genetic diversity and habitat stability in Sahara-Sahel vertebrates	Duarte Gonçalves

8 JANUARY
POSTER SESSION 1

8 - JANUARY (4:00 pm - 6:00 pm)
Forum Hall Foyer, 2nd Floor

Biogeography of the Anthropocene

TITLE	PRESENTER
178. Spatial patterns in vertebrate attractiveness reveal hotspots of untapped flagship potential	Tom Smart
179. Using Ecological Niche Modeling and Biogeography as a Model for Preventing Bat Borne Rabies	Paige Van de Vuurst
180. Drivers of long-term occupancy trends in three insect taxa in Central Europe	Eva Katharina Engelhardt
181. A global model of changes in human terrestrial impacts over five decades	Michelle Bardales Cruz
182. Priorities in spatial nature protection: case of Czechia	Tomáš Janík
183. Differential ecological impacts of feral cats among continents	Philippe-Lesaffre Martin
184. The biogeographies of Anthropocene Biogeography	Yuri Rocha
185. Forest legacies of the pre-contact Maya	Sara Eshleman
186. Sample coverage-based standardization of species diversity improves description and prediction of biogeographic patterns	Buntarou Kusumoto
187. Effect of past megafauna on genetic structure and demographic histories of megafruit plants in mainland Africa and Madagascar	Yuanshu Pu
188. Environmental Change Through Time and Its Relation to Biotic Homogenization/Differentiation of North American Birds	Martha Paola Barajas Barbosa
189. Naturally occurring and anthropogenic-driven gene flow in Carpathian ox-eye daisies (Leucanthemum, Asteraceae)	Kamil Konowalik
190. Integrating biogeography and behavioral ecology to rapidly address biodiversity loss	Katharine Marske
191. Threatened at home but naturalized elsewhere: conservation conflict or opportunity?	Weihan Zhao
192. Large-scale dietary changes over the past 30 years in African forest elephants (Loxodonta cyclotis) in Lopé National Park, Gabon.	William Tejler
193. Hotspots of human pressure on the threatened European gastropods	Panayiota Kotsakiozi
194. Evidence of Neotropical carnivores' continental geographic range contractions over the last two decades	Petr Keil
195. Microclimate buffering and plant biogeography in temperate forests	Martin Kopecký
196. Palaeoecological trajectories of non-native vegetation and plant homogenization on islands globally	Anna Walentowitz

Climate Change Biogeography

TITLE	PRESENTER
197. Biological Consequences of Global Change	Wenhua Xiong
198. Travelling on the Silk Road: grassland degradation in the high mountains of Kyrgyzstan	Sherry Young
199. Lags in the response of plant assemblages to global warming depends on temperature-change velocity	Laura Pacheco Riaño
200. Ecologist in a tough spot: Communicating plant shifts responses to a young audience	Laura Pacheco Riaño
201. A multifaceted and multi-taxa approach for Mediterranean forests conservation	Camille Magneville
202. Microclimate, an inseparable part of ecology and biogeography	Julia Kemppinen
203. A novel evaluation of alternative species distribution models using population genomics	Allan Strand
204. Microrefugia for Alpine Plant Life (MAPLe)	Jonathan von Oppen
205. Predicting the distribution and potential range shifts of northern pikas incorporating microclimates	Tomoki Sakiyama
206. Is averaging the answer?: Uncertainty in consensus predictions of plant species' vulnerability to climate change	Brooke Rose
207. Using museum collections and species distribution modelling to understand the potential impacts of environmental change on Neolindus rove beetles	Yoan Guzman
208. Has butterfly wing colour lightness changed over recent decades in Canada?	Sarah Dolson
209. Predicting the Spatial Distributions of Korean Endemic Plants under the Recent and Future Climate Change	Mincheol Lee
210. Is there stability across time between bioclimatic variables and topographic complexity in the Atlantic Forest?	Marcela Brasil de Godinho
211. An alpine bird is reducing its distribution and moving to higher altitudes in its southernmost European distribution	Antonio Román Muñoz Gallego
212. Impact of climate change on the distribution and phenotypic diversity of a widespread Palearctic snake species using experimentally informed species distribution models	Iulian Gherghel

TITLE	PRESENTER
Freshwater Biogeography	
213. Freshwater megafauna shape ecosystems and facilitate restoration	Fengzhi He
214. Beneath the surface: systematic and large-scale modeling of groundwater amphipod diversity	Mara Knüsel
215. Species Distribution Models in freshwater restoration contexts - an integrative framework	Graciela Medina Madariaga
216. Cryptic biodiversity in Amazonian freshwater fishes of the genera Cyphocharax and Curimatella revealed by mitochondrial DNA (Teleostei: Curimatidae)	Bruno Melo
Functional Biogeography	
217. Functional reorganization of North American wintering bird communities	Juan Pablo Quimbayo
218. Plant functional traits couple with range size and shape in European trees	Gabriele Midolo
219. Flap or Fail: Exploring the Role of Native Functional Richness on the Establishment Success of Non-Native Birds on Oceanic Islands	Maria Jørgensen
220. Cranial morphological disparity in flying squirrels across tropical and temperate biomes	Álvaro Quesada
221. How does plant functional diversity change along environmental gradients?	Sisimac Duchicela
222. Elevation and aspect interactively shape the functional diversity of forest plant communities	Joshua Erkelenz
223. Functional Distinctiveness of the World's Resident and Migratory Avifauna.	Reymond Miyajima
224. Revealing biogeographic patterns of northern European flora through functional traits	Pekka Niittynen
225. Functional traits of habitat-specialized (succulent) plants on edaphic quartz islands	Pia Eibes
226. Heterogeneous trait responses of Paramo plant species and communities to experimental warming	Carolina Tovar
227. Broadening Participation in Ecometrics Research: An Initiative to Expand the Collection of Functional Trait Data	Michelle Lawing
228. Thepparatia, the evolution of dioecy and the lianescent habit in Hibisceae clade Trionum (Malvaceae, Malvoideae)	Shook Ling Low

TITLE	PRESENTER
Gradients, Range-limits, and Beta-diversity	
229. The cold range limit of prominent alpine graminoid species	Raphael von Büren
230. Spatial scaling of beta diversity is broadly consistent and repeatable among ants, birds, diatoms, and trees	David Jenkins
231. Bioclimatic niche similarity and species relatedness shift their influence on forest bryophyte co-occurrence across scales	Joaquin Hortal
232. Understanding elevational gradients in species richness, range size and niche asymmetry with ecological null models	Martin Macek
233. Does the thermal niche explain the distinctness of alpine assemblages? Insights from water beetles	Pedro Abellán
234. Biogeography and diversity patterns of insects along an elevational gradient in a tropical-temperate transitional zone	Milan Janda
235. Climate extremes and climate means importance in delimiting species ranges	Eduardo Arlé
Historical Biogeography	
236. The tangled biogeographic history of tarantulas: An African centre of origin rules out the centrifugal model of speciation	Aritra Biswas
237. Ecological legacies of past fire and human activity in a Panamanian forest	Crystal McMichael
238. Biogeography of the Early/Middle Pleistocene Transition in Central Europe.	Ivan Horacek
239. Molecular dating reveals multiple Pleistocene to Holocene faunal connectivity episodes between the Black and Caspian Sea basins	Denis Copilas-Ciocianu
240. Once upon a fly: the biogeographical odyssey of Labrundinia (Chironomidae, Tanypodinae), an aquatic non-biting midge towards diversification.	Fabio Laurindo da Silva
241. Geodiversity in the Amazon Drainage Basin as a Corner Stone for Biodiversity?	Cécile Alsbach
242. Assessing temporal variations in macroevolutionary rates: the reliability of the time-bin approach with an example of intercontinental dispersal during the Cenozoic	Octavio Jiménez Robles
243. Do biome shifts promote sexual system transitions? Evolution of reproductive traits in Veronica with shifts into the New Zealand alpine zone	Esther Dale
244. Rethinking spatial history: Envisioning a mechanistic historical biogeography	Eduardo Schultz

TITLE	PRESENTER
Invasion Biogeography	
245. Alien ants break down biogeographic boundaries and homogenize community assemblages in the Anthropocene	Lucie Aulus
246. Niche dynamics of non-native plants vary between regions.	Anna Rönnfeldt
247. Plants that have recently become more common in their native range are also more likely to be successful as naturalized aliens elsewhere	Rashmi Paudel
248. Reconstructing invasion spatial dynamics and life history traits from heterogeneous occurrence data	Christophe Botella
249. The importance of variable selection when modelling alien species under non-analog conditions	Tom Vorstenbosch
250. Trees from Australia in the Mediterranean basin	Giuseppe Brundu
251. Functional trait differences between native and alien plant species in local communities of different habitat types	Jan Divíšek
252. Marsh frog invasions in Western Europe: multiple biogeographical origins, opportunism and effects on native pond communities	Mathieu Denoël
253. Anticipating the Global Expansion of the Monk Parakeet Invasion	Antonio Román Muñoz Gallego
Island Biogeography	
254. Spatial resolution impacts projected plant responses to climate change on topographically complex islands	Flavien Collart
255. PleistoDist: A toolbox for visualising and quantifying the effects of Pleistocene sea-level change on island archipelagos	David Tan
256. Trait-dependent diversification and biogeography of Canary Island angiosperms: a community-wide approach	Ryan Brewer
257. MEDIS - A Comprehensive Spatial Dataset on Mediterranean Islands for Biogeographical and Evolutionary Research	Michele Di Musciano
258. Diversification dynamics in a highly successful insular plant taxon are consistent with the general dynamic theory of oceanic island biogeography	Alexandra Muellner-Riehl
259. Great speciators of the plant world: Island biogeography of Hawaiian Asteraceae	Lizzie Roeble
260. Combining in-situ monitoring and remote sensing to detect impacts of volcanic sulfur in the Canary Pine forests of La Palma, Spain.	Frank Weiser
Paleoecology	
261. Tropical Wetlands: Landscapes of Change	Ian Lawson
262. Missing Lynx: Dietary variability of Lynx rufus across space and time as inferred from dental microwear texture analysis	Larisa DeSantis

TITLE	PRESENTER
Other	
263. Effects of urbanization on social spiders: the costs of urban living	Jennifer Guevara
264. “Flower power”: how flowering affects spectral diversity metrics and their relationship with plant diversity	Michela Perrone
265. Macroecological analysis of sustainability of cashmere production at the continental- and regional level: impact of climate change and land use on biodiversity of grassland ecosystem	Yasuhiro Kubota
266. Dispersion of dragonflies in cities: experimental study	Bohumil Fiala
267. How detrital food webs differ from grazing food webs and how can food web models be linked to biogeochemical models	Olga Vindušková
268. From plant-soil feedback to soil biota engineering and soil formation and back: a continuum of soil and biota interactions at various spatiotemporal scales	Olga Vindušková
269. When cheating turns into a stabilizing mechanism of mutualistic networks	François Duchenne
Marine biogeography	
270. Combining natural history archives with models to quantify the resilience of bowhead whales to past, present, and future threats	Nicholas Freymueller
271. Bipolar, Antitropical, or Cosmopolitan? Untangling the presence and extent of true bipolarity in marine taxa	Emily Chen
272. Unveiling Bergmann’s Rule in Ectotherms: Processes associated with geographic gradient in body size in North Atlantic Reef Fish	Sabrina Jorge
273. Expanding the known distribution range of existing species and the new North Pacific deep-sea coral species (Paracis, Paramuriceidae, Octocorallia, Anthozoa).	Asako Matsumoto
274. Latitudinal variation in the geographical range of North Atlantic reef fishes is not driven by temperature	Sabrina Jorge
Paleobiogeography	
275. Exploring 5 Million Years of Climate-Induced Fragmentation	Sara Gamboa
276. Comparative analysis of palaeoclimate models' estimations of treelines and alpine biomes in mountains worldwide	Eline Rentier
277. Climate and human land use as drivers of disequilibrium in post-glacial European tree distribution dynamics	Andreas Schweiger
278. Holocene climate and the first farmers of Europe	Wolfgang Traylor
279. Virtual Taphonomy: Simulating taphonomy and its influence on ecological niche reconstruction	André Bellvé
280. Do mammals track climate better than plants?	Corentin Gibert Bret

9 JANUARY
POSTER SESSION 2

9 - JANUARY (4:00 pm - 6:00 pm)
Forum Hall Foyer, 2nd Floor

Biodiversity Patterns and Maintainance

TITLE	PRESENTER
281. Unveiling Cryptic Species of Aquatic Macroinvertebrates through DNA Barcoding in Narupa Reserve, Napo, Ecuador	Sofía Cristina Barros Hurtado
282. All about being old and shooting hairs: Clade age and Urticating hair explain the patterns of diversification in tarantulas	Aritra Biswas
283. Scaling laws reveal a unified energy theory for mountain biodiversity patterns	Zihan Jiang
284. Historical land use determines arbuscular mycorrhizal diversity in agricultural landscapes	Oscar Zarate
285. Revisiting the spatial phylogenetics of North American seed plants	Israel Borokini
286. Novel ecological and environmental data enhance our comprehension of tree species composition changes across Amazonia	Bruno Luize
287. Bat communities of savanna biome: a case study in Kruger NP.	Ivan Horacek
288. Dark diversity reveals human impacts on biodiversity in natural vegetation worldwide	Meelis Pärtel
289. Correlates of zoogeographical boundaries among terrestrial vertebrates in Atlantic Forest hotspot	Fernando Da Silva
290. Global patterns and drivers of taxonomic, phylogenetic and functional diversity in specialist river birds	Ankita Sinha
291. Heterogeneous dispersal networks to improve biodiversity analyses: relevance and methods	Paul Savary
292. Global and regional interaction between threats to bird species: Wind farms and other human activities	Antonella Gorosábel
293. How species, functional and phylogenetic diversity accumulate in vertebrates across regions, clades and scales	Inigo Rubio Lopez
294. A Global database of habitat specific abundances for birds	Heléne Aronsson
295. Diversification patterns and their underlying mechanisms across phylogenetic scales	Maxime Quétin
296. Missing links: predicting unknown associations of host plants with fungal endophytes and pathogens	Nick Bard
297. Distribution and effects of trash-basket epiphytes and tank-bromeliads on canopy biodiversity and ecosystem functions	Gabriel Ortega
298. The use of mineral sources by the African forest elephant.	Claire Herlihy
299. A signature from the sky: using remote sensing to assess the effects of rewilding on the ecology of vegetation	Alessandro Mereghetti

TITLE	PRESENTER
300. GetDiv - Global experiment on trail diversity: a call for participation	Piia Jaksi
301. Analyzing changes in structural diversity of the agricultural landscape of Saxony using historic and modern remote sensing data	Eric Kosczor
302. Environmental drivers of local bats species richness in Czech Republic: the role of hibernacula caves	Rafael Fortes
303. Species abundance distributions and complex relationship between diversity and extinction rates in North American birds	Eliska Bohdalkova
304. Effects of conservation measures on plant diversity in grasslands in Southern Germany	Esther Baumann
305. Modelling the future distribution and biodiversity of European fen habitats under global change	Patrícia Singh
306. Underlying linkage rules of pollination networks reveal their fragility	François Duchenne
307. Integrating the Equilibrium Theory of Biodiversity with the Metabolic Theory of Ecology to predict the effects of temperature and body mass on biodiversity	Jordan Okie
308. Restoring degraded ecosystems to improve and enhance biodiversity and ecological connectivity in the Central European Green Belt	Hana Skokanova
309. Global Insights on Mountain Regions as Hotspots of Fungal Diversity	Petr Kohout
310. Conserving evolutionary processes of endemic amphibians in the megadiverse Atlantic Forest	Ricardo Sawaya
311. Parasitic plants in Europe. Are they associated with high community diversity?	Jakub Těšitel
312. Number of species of Coccinellidae in individual European countries and Iranian provinces – correlates and needs for more surveys	Oldřich Nedvěd
313. Global diversity patterns of vascular plants – occurrence point data versus checklists	Pierre Denelle
314. Understanding Carbon Storage Dynamics in Ayeyarwady Delta's Mangrove Ecosystem in Myanmar: Insights for Restoration Efforts	Bikram Pandey

Macroecology

TITLE	PRESENTER
315. Decomposing abundance change to recruitment and loss: analysis of the North-American avifauna	François Leroy
316. Deep biogeographic barriers explain divergent global vertebrate communities	Peter Williams
317. Testing the latitudinal gradient in plant range size and environmental breadth	Marco Barandun
318. Conservation planning in Switzerland is central to preserve natural resources in Europe	Yohann Chauvier-Mendes
319. Factors and mechanisms driving functional variations in urban bird assemblages between developed and developing countries	Mao-Ning Mao-Ning
320. Rhizome or rootstock: variation in definitions of plant clonal growth organs, with implications for macroecology	Timothy Harris
321. Rodents show darker and redder coloration in warm and rainy environments	Felipe Cerezer
322. Locally evolutionarily distinct species in frugivore networks have fewer links and more specialized partners	Avery Kruger
323. Secondary sympatry and syntopy in birds: methods, patterns, and processes	Vladimir Remes
324. Revealing macroecological dynamics to understand biodiversity shifts in the Anthropocene	Pierre Gauzere
325. The Seed Dispersal Database for the European flora	Zdeňka Lososová
326. Fuzzy competitive exclusion explains parapatric distributions and highlights areas of concern for native species due to biological invasions	Raimundo Real
327. Climatic stability predicts the congruence between species abundance and genetic diversity	Victoria Formoso Freire
328. Priority areas based on the spatial structure of evolutionary uniqueness at a global scale	Andrés Baselga
329. Spatial and temporal patterns of shrew diversification	Lucie Farková
330. The role of niche conservatism and niche divergence in driving in situ speciation in the Alps	Luiz Jardim de Queiroz
331. Cocos: effects of climatic extremes on ecosystem stability	Manuele Bazzichetto
332. Spatial patterns in farmland bird population trends across Europe	Jiři Reif
333. The influence of niche partitioning and evolutionary dynamics on reef fish diversity	Melina Maxwell
334. Using the Global Inventory of Floras and Traits (GIFT) for plant biogeography and macroecology	Patrick Weigelt

TITLE	PRESENTER
335. The global distribution of ferns with chlorophyllous spores	Daniela Mellado
336. Floral traits predict hummingbird visitation rates better than conspecific and heterospecific flower abundance	Elisa Barreto
337. Diversity Unveiled: Exploring Evolutionary Diversification Patterns in Clonal and Non-Clonal Plants	Sonia Kadyan
338. Beyond climate control: soil pH and phylogenetic composition medi ate drought-deciduousness in the species-rich Latin American tree flora	Cibele Cássia-Silva
339. Patterns of spatial and temporal autocorrelation of species richness and distributions across scales	Carmen Soria
340. The dynamics of the diversity-energy relationship during the last 21,000 years differs for woody and herbaceous species	Irena Simova
341. A macroevolutionary perspective on how dispersal can affect biodiversity and vice versa	Oskar Hagen
342. Macrobehaviour - do you want to join the challenge?	Sally Keith

Models and Methods

TITLE	PRESENTER
343. Mismatched environmental variable scale in SDM cause misspecified inference	Cheongok Jeon
344. bamm: An R package for estimating the dynamics of species distributions using the concepts of the BAM diagram	Luis Osorio-Olvera
345. voluModel: Modelling species distributions in three-dimensional space	Hannah Owens
346. #modelevaluation – generating spatial splits for ecological models using a hashtag sampling method	Peder Engelstad
347. Spatial patterns of marine litter accumulation on the remote island of Santa Luzia (Cabo Verde)	Diana Sousa-Guedes
348. The Botanical Information and Ecology Network Database: a tool for plant biogeography	Brian Maitner
349. Identifying Marine Food Web Homogenization Patterns	Yan Xu
350. To clamp or not to clamp? That is the extrapolation question.	Gonzalo Pinilla Buitrago
351. Stability in ecological niche models measured with the standard deviation	Neftalí Sillero
352. SPARSE 1.0: a template for databases of species inventories, with an open example of Czech birds	Petr Keil
353. Using Google Earth Engine as a framework for Ecological Niche Modelling in northeastern Portugal	Daniel Silva

TITLE	PRESENTER
354. Testing Assumptions of Historical Occurrence Use in Species Distribution Models	Jason Bracken
355. Inferring land use legacies for Denmark using historical aerial photography	Oliver Baines
356. Apparent effect of range size and fruit colour on palm diversification may be spurious	Adrian Hill
357. hsbm: A novel R-package for ecological network analysis and reconstruction	Rubén Mateo

Species Distributions

TITLE	PRESENTER
358. Can we accurately predict the distribution of soil microorganisms occurences and relative abundances? A case study in the Western Swiss Alps	Valentin Verdon
359. How sensitive are species distribution models to the selection of background points?	Bart Steen
360. Is the distribution of non-native species predicted from the same environmental descriptors as native species?	Bart Steen
361. Improving Local-scale Species Distribution Models through Interpretable Machine Learning: A case of Cormorants in South Korean Rivers	Junbeom Bahk
362. Estimating ungulate distributions and relative abundance at a continental scale	Ming Ni
363. Do SDM performance scores tell us anything about reality? A test with virtual species	Hannah Bevan
364. Diversity of fishes of the Napo and Arajuno rivers, with potential of handling,in the Parish Ahuano, Canton Tena, Napo Province	Ivan Morillo
365. Unveiling niche-based responses and patterns of local occupancy of dryland species	Alejandra Zarzo-Arias
366. Predicting spatial distribution of nature's contributions to people from individual species	pierre-louis Rey
367. Contrasting elevational zonation patterns of forest birds on Mt. Cameroon, west-central Africa, and Mt. Wilhelm, Papua New Guinea	Riccardo Pernice
368. Global biodiversity map: its completeness assessment based on temporal pattern of species occurrence records	Shogo Ikari
369. Spatial patterns and quantifications of habitat loss differ between remotely sensed resolutions and those required for IUCN Redlisting	Bethany Johnson
370. A sky island perspective: New England alpine plant distributions across the region	Andrea Tirrell
371. Modeling the relationship between climate, habitat, fire, and small mammal richness across the Sierra Nevada	Reina Warnert
372. Plant functional groups as an input for dynamic vegetation modelling	Irena Axmanová

TITLE	PRESENTER
373. The Botanical Frontier: Anticipating the Revelation of over 1000 New Plant Species in Nigeria	Alexandra Muellner-Riehl
374. Oh, the places they'll grow: Do trees' climate tolerances differ across life-history?	Bailey McLaughlin
375. Ecology and Evolution of Clonal Growth Forms in the Lamiaceae Family Across Iranian Plateu	Chonour Mahmoudi
376. Unravelling the impact of soil data quality and resolution on species distribution models of temperate forest woody plants	Francesco Rota
377. A critically endangered African vulture starts breeding in Europe: escaping from extinction or entering a genetic amalgamation trap?	Antonio Román Muñoz Gallego
378. Biogeographic Implications of Saharan Refugia for Herpetofauna Diversity of Northern Africa	Calvin Schaefer
379. Modelling the potential biodiversity distribution - a tool for prioritisation in nature conservation	Dušan Romportl
380. 3D canopy structure as an indicator of grassland diversity	Robert Pazúr
381. Standardized data collection across continents in ecology, behaviour and conservation: Lessons learned from ÉLVONAL Shorebird Science project	Vojtech Kubelka

Phylogeography

TITLE	PRESENTER
382. Survival under the ice - Pleistocene glaciation imprints contemporary population genetic structure of five peri-alpine groundwater amphipods species	Marjorie Couton
383. C4 photosynthesis provided an immediate demographic advantage to populations of the grass Alloteropsis semialata	Graciela Sotelo
384. Host-Virus Cophylogeny Trajectories: Investigating Molecular Relationships between Coronaviruses and Bat Hosts	Nadia Tahiri
385. Molecular diversity of spring fen macrozoobenthos from two geomorphological regions	Magdalena Gajdošová

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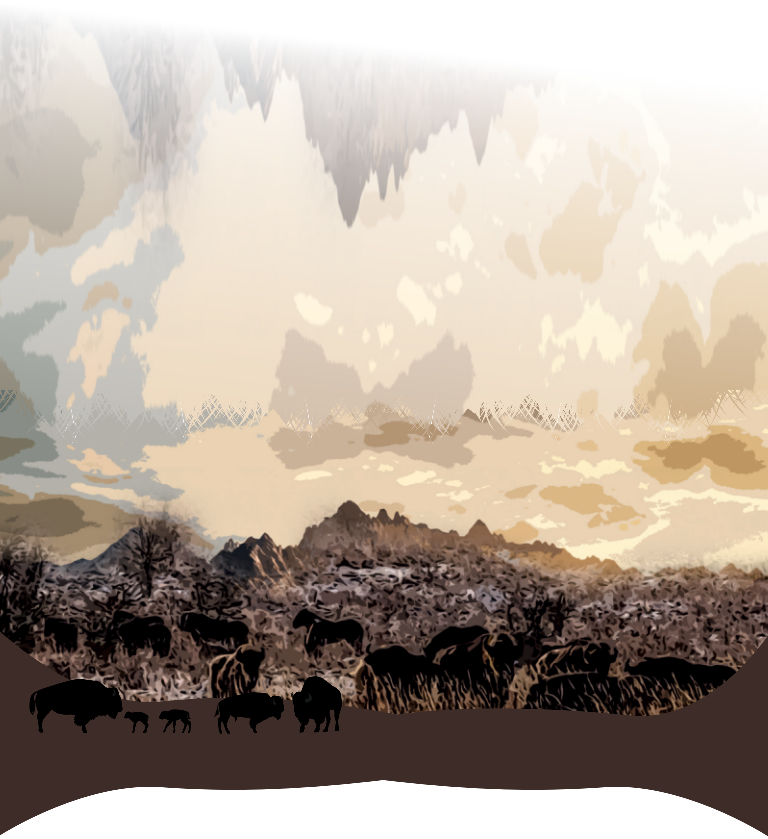

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AWARDS ABSTRACTS

1. Patterns and Processes of Island Assembly

Robert J. Whittaker, Oxford University, Oxford, United Kingdom

It is half a century since Jared Diamond introduced his analyses of sedentary, tramp and supertramp bird species on islands near New Guinea, laying the foundations of island assembly theory, focussed on describing and understanding non-random patterns in the composition of island avifaunas. Yet, a settled general theory of island meta-community assembly applicable to multiple taxa is still lacking. I review progress in this area, focusing particularly on research that I and my collaborators have been involved in, initially working on the Krakatau Islands and subsequently expanding to analyses of community compositional attributes of biotas from multiple archipelagos around the world's oceans.

2. Assessing the wider implications of species extinctions: island birds and beyond

Tom Matthews, University of Birmingham, United Kingdom

Humans, through a range of drivers, are known to have increased species extinction rates by orders of magnitude compared to the background extinction rate. Island birds have been particularly impacted, with hundreds of known extinctions. Given the increasing availability of data relating to extinct species and their functional traits, including a novel database on extinct birds that I present here, it is now possible to evaluate many of the wider impacts of anthropogenic extinctions. Focusing primarily on island birds as a case study, I review three such impacts, namely the effect of species loss on: (i) functional and phylogenetic diversity, (ii) island ecosystem functioning, and (iii) our understanding of biogeographic patterns, and the natural world more broadly.

3. The Geography, Ecology, and Evolution of Mammalian Endemism

Benjamin R. Shipley[1], Jenny McGuire[1]

[1]*Georgia Institute of Technology, Atlanta, GA*

Endemic species, species with restricted range sizes, are vulnerable to extinction and often ecologically and evolutionarily unique. Because of their ecological and conservation importance, understanding how abiotic factors, species traits, and community composition influence endemism is a defining question in biogeography. In my dissertation, I examined drivers of mammalian endemism from multiple angles. First, I evaluated how patterns in global mammalian endemism are driven by landscape factors like topography and long-term climate stability, trends in species richness, and the climatic specialization (niche breadth) of the species. I developed a novel null-model technique that employs spatial randomization to isolate the abiotic effects on endemism patterns. Next, I expanded my analyses from the abiotic to the biotic factors influencing endemism, evaluating the ecological and evolutionary distinctiveness of highly-endemic mammalian communities. Overall, although areas of high mammalian endemism mirror those of high richness, endemism is even more prevalent in topographically diverse regions that have had stable climates through time. Species that live in areas of high endemism tend to have small body sizes, short lifespans, and few offspring per year, indicating they may have been unable to expand their ranges after habitat fluctuations. However, I found little evidence that climatic niche breadth structures continental patterns of small-ranged species. To explore this result further, I narrowed my focus from global endemism to island-endemic mammals, using the controlled situation of island biogeography to determine that geography, rather than relatedness or phenotype, influenced climatic niche evolution in island endemics. Overall, my results suggest that suggesting that geography is the primary driver of restricted-range species distributions, demonstrating that understanding geographical patterns is vital for preserving unique species, communities, and ecosystems.

4. A picture of plant functional diversity on an oceanic island

Martha Paola Barajas Barbosa[1], Dylan Craven[1], Patrick Weigelt[2], Pierre Denelle[3], Rüdiger Otto[3], Sandra Díaz[3], Jonathan Price[3], José María Fernández-Palacios[3], Holger Kreft[4]
[1]iDiv, Leipzig, Germany, [2]University of Goettingen; Macroecology, Biodiversity and Conservation Biogeography Group, Goettingen, Germany, [3]University of Göttingen, Germany, [4]University of Goettingen

Oceanic islands have served as valuable natural laboratories to test fundamental ideas about biodiversity for centuries. Oceanic islands often possess a distinctive geology and are highly isolated. In theory, these characteristics would make their plants functionally distinct from flora in other locations. However, until now, research into the characteristics of island floras has been impeded by a lack of empirical data on fundamental plant traits such as leaf area, plant height and stem density. We addressed this gap by collecting plant-trait data from Tenerife (Canary Islands, Spain), a charismatic oceanic island situated off the coast of North Africa in the Atlantic Ocean, and comparing them against the widely accepted global spectrum of plant form and function data set. We found that environmental conditions have selected for adaptations in plant size and shape, as well as for those linked to a plant's persistence on the island. Tenerife's mostly semi-arid conditions favour a dominance of shrubs. The dominance of woody shrubs might also relate to a frequently observed island phenomenon called insular woodiness, whereby small herbaceous plants develop stems and evolve to become woody over time. We further found that much of the oceanic island's functional diversity came from a species colonizing its habitats through longdistance dispersal. By contrast, we found that the evolution of new species on Tenerife contributed little to the overall functional diversity of the island. This is because many recently evolved plant species on Tenerife had not adapted to different ecological niches, but rather inhabited similar habitats to those of their ancestors. This results in the evolution of species that are functionally similar to their ancestors and thus share similar traits.

5. Biodiversity dynamics: from the fossil record to human dominated systems

Manuel J. Steinbauer, Bayreuth University, Bayreuth, Germany

The fundamental processes that generate and maintain the complex patterns of life on Earth are not only human dominated but also strongly influenced by interactions across time. Understanding the effect of human behaviour and decision-making as well as the legacy of past processes is thus central for society, which critically depends on the many vital ecosystem services provided by biodiversity and ecosystem functioning.

Using oceanic islands as model systems, the talk will first explore how biodiversity dynamics are interacting with the earth system and how the effects of climate change today are influenced by environmental processes from the deep-time past. I will then show how human induced dynamics in ecological systems have intensified from the first arrival of our ancestors to a situation where human induced effects are an integral part of modern ecosystems.

The talk not only aims in presenting different case studies, many of which come from island biogeography. It also aims in discussing the potential and limitations of data available for studying biodiversity dynamics and their interaction with humans and environment on very different timescales from decades (historic vegetation surveys) over millennia (pollen record) to the deep time fossil record.

6. The demise of dwarfs and giants: body size shifts predispose insular mammals to anthropogenic extinctions

Roberto Rozzi, Zentralmagazin Naturwissenschaftlicher Sammlungen, Martin-Luther-University Halle-Wittenberg, Halle (Saale), Germany

Islands have long been recognized as laboratories for the study of the generation and maintenance of biodiversity. These isolated evolutionary arenas often lead to morphologically unique species, such as insular dwarfs and giants, which are well-documented in the fossil record. Yet, many of these peculiar biotas have been driven extinct in historic or prehistoric times, and those remaining are often threatened, hinting at a possible link between body size changes and increased vulnerability to extinctions. In this talk, I will discuss how body size evolution in island mammals has exacerbated their fragility, and how human arrival has contributed to their past and ongoing extinctions. Based on a newly compiled dataset including 1,231 extant and 350 extinct insular species from islands and paleo-islands worldwide spanning the past 23 million years, we found that the likelihood of extinction and of endangerment are highest in those insular species that exhibit the most extreme body size shifts towards dwarfism or gigantism. Furthermore, our results reveal a series of extinction pulses on islands starting more than 100,000 years ago, and a marked temporal association between island extinctions at a global level and the arrival of modern humans. Extinction rates of mammals on islands accelerated by over 10-fold following human colonization, resulting in the almost complete demise of iconic giants and dwarfs. These findings highlight the importance of morphological adaptations associated with the island syndrome in predisposing island biotas to extinction.

7. The island syndrome in a great speciator: the silvereye in the south Pacific

Sonya Clegg[1], Ashley Sendell-Price[1], Andrea Estandia[1]
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The island syndrome refers to the phenomenon where sets of morphological, physiological, and behavioural traits evolve in a predictable way when organisms colonise islands. Changes include body size shifts (the ‘island rule’ of tendency toward medium body size), and reductions in dispersal capacity among many other patterns. The island syndrome is linked with a second phenomenon, that of the evolution of great speciators, those forms that exhibit multiple phenotypes distributed across many islands. The existence of great speciators has been presented as a paradox because their wide distributions imply high dispersal ability, but their high levels of phenotypic divergence imply dispersal is limited. Silvereyes (*Zosterops lateralis*) have colonised numerous islands and archipelagos of the southwest Pacific and exhibit aspects of the island syndrome, most notably a repeated pattern of body size increase in island populations. Despite the impressive dispersal capacity, 11 exclusively insular morphological subspecies are recognised, and they are classified as a great speciator. Using the well understood colonisation history of the silvereye, I present results on the genetic impacts of island colonisation, and the genomic basis of repeated body size evolution and changes in dispersal propensity.

8. An island biogeographical analysis of the uninhabited islands in the Shinan Province, South Korea

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Theories of island biogeography have generally been developed and evaluated at broad spatial scales. Large, remote, and linearly distributed archipelagos are excellent natural laboratories and typical geological settings to study species-area relationship (SAR), distance effect, and community dynamics of island biogeography. However, it remains elusive whether traditional theories of island biogeography would still be valid at sub-regional scales, in which many islands tend to be more or less similarly small-sized and spatially aggregated, not necessarily perpendicular to the mainland. In this study, we took advantage of having a detailed dataset, in which 175 uninhabited islands of the Shinan Province in South Korea (all within 50 km from the mainland) were intensively surveyed for, among others, the presence of vascular plant species. Using logistic regression and partial correlation analysis, we found that island size and distance to the species source (mainland) significantly explained the plant species richness of the islands. Furthermore, a Mantel bearing correlogram revealed that not only the mainland but also the neighbouring islands functioned as species sources, indicating a significant level of species exchange effect among the islands. We propose that the traditional island biogeographical theories (i.e., SAR and distance effect) are not restricted to broad spatial scales but might also work at sub-regional scales. In addition, the species exchange effect between nearby islands seems to be another significant biogeographical mechanism for densely distributed islands in southwestern Korea.

9. Linking the past to the present: How human history has shaped the distribution and evolution of urban wildlife

Elizabeth Carlen, Washington University in St. Louis

We are in the Anthropocene, characterised by a plethora of human-driven environmental changes that impact ecosystems. While most people now live in cities, these cities are also home to numerous native wildlife. Reconciling cities for use by humans and wildlife requires careful consideration of how features of our socio-political decision-making drive evolutionary processes. Genetic evolution has been considered a slow process, yet it can also happen rapidly, especially when evolutionary forces are strong. Some of the textbook examples of evolutionary change, such as melanism in the peppered moth (Biston betularia), have happened rapidly and are linked to urbanisation. However, the extent to which past human behaviour has shaped the biogeography of cities requires special consideration. I will explore how human actions have influenced the evolution of wild species in cities and present data from case studies on multiple urban taxa.

10. Will climate niche and functional traits facilitate the expansion of urban tree species in cities worldwide?

Manuel Esperon-Rodriguez[1], Mark G. Tjoelker[2], Jonathan Lenoir[3], Bree Laugier[2], Rachael V. Gallagher[2]
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Climate plays a key role in determining the geographic space that a species can occupy across the landscape, where range limits are established by the species' intrinsic tolerance. Cities, however, are unique environments where human preferences and management define the species composition. Therefore, cities often harbour species outside the limits of their climatic tolerance inferred from their native range. Eucalypts are popular urban tree species worldwide, but little is known about which aspects of their climatic niche and which functional traits predict their success, and vulnerability, to current climate change. We assessed the relationship between the climatic tolerance limits of 50 eucalypt species and key plant functional traits to classify species resilience and vulnerability in 67 cities in 21 countries. We used the concept of species safety margin — an index of potential climatic tolerance, to determine the cities where eucalypt species are planted outside their native climatic tolerance. Then, we assessed which functional traits (leaf δ13C, leaf dry mass, leaf length, leaf N per dry mass, wood density) were correlated with species' safety margins. Forty-two species planted in 40 cities exceeded their thermal safety margins for temperature, while 43 species in 38 cities exceeded their hydraulic safety margins for precipitation. In general, species with small leaves, high δ13C, high leaf N per dry mass and high wood density are more likely to be planted in cities outside their native climate tolerance. Eucalypts exhibit broad adaptability in terms of occurrence in cities outside their native climatic ranges displaying functional trait characteristics of heat and drought tolerance.

11. The global decline of evolutionary uniqueness of avian communities within cities: conservation implications

Federico Morelli, Czech University of Life Sciences Prague, Prague, Czech Republic

Urbanization represents the hugest anthropogenic impact on our planet, modifying landscapes and increasing habitat fragmentation globally. The main effects of urbanization on biodiversity are negative and mainly related to an overall decrease in the number of species. However, such effects depend on the group of animals we are focusing on. Urbanization filters some bird species, altering the composition of avian communities in different ways. For example, a continuous replacement of specialists by alien or invasive species, often more generalist ones, can increase the functional relatedness among birds within the assemblage, leading to biotic homogenization. Through the results of three recent large spatial-scale studies (two continental and one global), we found evidence of a significant decline in the evolutionary uniqueness of avian communities associated with the urbanization process. A first study showed a lower evolutionary uniqueness for avian communities from urban areas when compared to rural areas, in Europe. A similar pattern was found when comparing urban vs. natural areas at the global scale. Finally, performing a study focusing on a gradient of urbanization, we found that, overall, urban bird assemblages from dense areas (e.g., city centres) supported one million years less of evolutionary history than communities from low-dense urban areas (e.g., residential areas). Such evolutionary homogenization is due to a filtering process of the highest phylogenetic diverse birds. Metrics related to the evolutionary uniqueness of communities have to play a role in assessing the effects of urbanization on wildlife.

12. Urban greenspaces to benefit people and biodiversity – a biogeographic-macroecological perspective

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Urbanization is one of the global megatrends. While it comes with challenges, it also offers opportunities for sustainable development worldwide. In terms of living conditions for people and biodiversity, the high densities of people and their activities have direct impacts. However, there are also important derived impacts that need consideration, e.g., urban heat-island effects and elevated rates of alien species introductions. Rewilding principles offer a useful framework for designing urban greenspaces to benefit people and biodiversity, notably via focus on area, connectivity, disturbance regimes, and trophic complexity. Here, I first outline lessons from biogeographic-macroecological inspired studies of urban greenspace, e.g., showing how greenspace area positively affects biodiversity, human mental health as well as ecosystem services such as cooling to alleviate heat stress. I then show how greenspace planning can be implemented to strategically benefit biodiversity and people, with an example from the Global South. Finally, I exemplify how trophic rewilding with megafauna can be implemented in a peri-urban setting and discuss its biodiversity outcomes. Overall, the existing evidence suggest that if substantial amounts of greenspaces is implemented into urban areas using pragmatic rewilding principles, there is strong potential to enhance living conditions in cities for both people and biodiversity, something that needs particular attention given the expected rising stress from global warming. If this becomes a common approach, there is hope to realize urbanization's positive potential.

13. Socioeconomics and culture as drivers of urban biodiversity patterns in the Global South

Sarel S. Cilliers, North-West University, Potchefstroom, South Africa

Socioeconomics and culture as drivers of urban biodiversity patterns in the Global South

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The Global South (GS) is urbanizing at a much faster pace than its northern counterpart, with more than 75% of the global urban population living there. Urbanization has major impacts on the local environment with several filters operating simultaneously to determine urban biodiversity assemblages. Several frameworks and models have been proposed to describe the relationship between humans and their natural environment in urban areas. The multi-scalar framework is one attempt to explain how biodiversity is spatially structured within urban landscapes, with varying effects of social, biophysical, and spatio-temporal filters from local, to neighbourhood-level, to regional scales. However, much of the focus has been on cities of the Global North (GN). Through legacies of the past, current stark socioeconomic realities, and diverse cultural backgrounds, we will show that context matters in explaining biodiversity patterns of specific urban areas in the GS. The mechanisms which are often used to explain positive relationships between socio-economic status and urban biodiversity include the luxury effect, ecology of prestige and a hierarchy of needs. Other mechanisms, such as the legacy effect, could, however, lead to different current relationships. We will use case studies to show the impact of socioeconomic factors and cultural differences on urban species assemblages. We will further discuss unique patterns and similarities in comparing the GS with the GN and highlight what relevant lessons and insights the rest of the world could gain from the GS.

14. Past, present and future of network biogeography

Dominique Gravel, Université de Sherbrooke

Biogeography has traditionally focused on the spatial distribution and abundance of species. Both are driven by the way species interact with one another, but only recently community ecologists realized the need to document their spatial and temporal variation. Network approaches offer a convenient representation of communities because they simultaneously account for species composition and their interactions. At the intersection of biogeography and community ecology, the field of network biogeography is rapidly raising with proposition of new concepts, methods, data and observations. The objective of this talk is to synthesize ten years of research on spatial variation of ecological networks and discuss the most promising directions for the future. I will first rigorously formalize the object of study and develop theory to explain spatial variation in network structure. I will explore predictions, in particular about the variation of network structure along environmental gradients. Second, I will assess the current empirical support for these predictions. We will find significant constraints on data collection limiting our current ability to test these predictions. Finally, I will turn to a new concept, the ecological coherence, to explore the joint response of network elements to environmental changes. Quantifying ecological coherence of a network facilitates the analysis of network variation over biogeographical gradients and predictions of their response to environmental changes. I expect the notion of coherence will offer a theoretically sound, reliable, measurable and communicable tool to monitor complex biodiversity changes.

15. Understanding and predicting trophic webs in space and time

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Spatial network ecology has recently come up as a new vibrant research area. Understanding how ecological networks are distributed, how do they respond to anthropogenic and environmental changes and, most importantly, how to predict them in unobserved locations are crucial questions to address. Here, using a large and innovative species interaction dataset for all European terrestrial vertebrates, alongside species distribution information, we explore the spatial distribution of the European terrestrial vertebrate food webs.

- First, we analyze their spatial coherence with traditional functional and phylogenetic diversity and show why interaction diversity should be considered as another important biodiversity facet.
- Then, through the use of spatial-distance decay analyses, we contrast the uniqueness of trophic networks with their vulnerability to human footprint and climate change, and measured their coverage within protected areas. We revealed that unique networks situated in southern Europe were particularly exposed to human footprint, and that unique networks in the Arctic might be at risk from future climate change. However, considering interaction networks at the level of trophic groups, rather than species, revealed that the general structure of trophic networks was redundant across the continent, in contrast to species' interactions.
- Finally, we introduce a novel framework that combines knowledge of trophic interactions with Bayesian structural equation models to model each species as a function of its prey or

predators and environmental conditions. This framework stands out as a novel solution for modeling multitrophic community distributions when trophic interactions are known or assumed.

16. Climate or diet? The importance of biotic interactions in determining species range size

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Species geographical range sizes play a crucial role in determining species vulnerability to extinction. Although several mechanisms affect range sizes, the number of biotic interactions and species climatic tolerance are often thought to play discernible roles, defining two dimensions of the Hutchinsonian niche. Yet, the relative importance of the trophic and the climatic niche for determining species range sizes is largely unknown. We use data documenting the spatial distributions and biotic interactions of 96 herbivore species, and their 125 parasitoids, across Europe and analyse the relationship between species range size and the climatic and trophic dimensions of the niche. We then compare the observed relationships with null expectations based on species occupancy to understand whether the relationships observed are an inevitable consequence of species range size or if they contain information about the importance of each dimension of the niche on species range size. We find that both niche dimensions are positively correlated with species range size, with larger ranges being associated with wider climatic tolerances and larger numbers of interactions. However, diet breadth appears to more strongly limit species range size. Species with larger ranges have more interactions locally and they are also able to interact with a larger diversity of species across sites, resulting in a larger number of interactions at continental scales. Our study offers new insight into the importance of biotic interactions in determining species spatial distributions, which is critical for improving understanding and predictions of species vulnerability under the current rates of global environmental change.

17. An overview of emerging approaches for conserving food webs across space

Louise O'Connor, Laboratoire d'Ecologie Alpine, Université de Grenoble Alpes, Grenoble, France

Species are embedded in food webs, and need to be protected within diverse, functional, and resilient communities. Food webs can help identify the species and areas in need of conservation, as well as mitigate threats to biodiversity. Despite their potential, food webs are rarely used in biogeography and spatial conservation, leaving best practices uncertain. Here, we explore ways in which we can use food web data in conservation. We combined trophic interaction data for over 800 European terrestrial vertebrates with their spatial distributions and the threats they face. We found that agricultural intensification and direct exploitation were two major threats to terrestrial vertebrate food webs in Europe. Furthermore, incorporating trophic information reshapes conservation priorities, enhancing the representation of predators, prey, and threatened species. While challenges remain to effectively integrate food webs in conservation, our work highlights the need for a more holistic paradigm in conservation that considers biodiversity as an interconnected system.

18. Emerging patterns in trophic network biogeography

Miguel Araujo, Museo Nacional de Ciencias Naturales, CSIC, Madrid, Spain

Recent research has provided evidence for striking regularities in the behaviour of consumer-resource interaction networks from local to global scales, both driven by disturbances and energy availability. I will show that departures from expected network topologies are related to strong human disturbances, and that the local configuration of network topologies predictably change to maximise ecosystem resilience to these disturbances. I will also show that climate acts as the main control parameter modulating consumer-resource networks, and that changes in climate trigger abrupt changes in energy flows resulting from phase transitions between different dynamical consumer-resource states. I argue that ongoing research will provide a baseline expectation to predict the consequences of human pressures, including climate change, on the dynamics of ecosystems at biogeographical scales.

19. Ecosystem engineering, 'Earth systems engineers', and the lasting impact of organisms in deep time

Simon A. Darroch, Senckenberg Research Institute and Natural History Museum, Frankfurt am Main, Germany

All species interact with their environments, but 'ecosystem engineers' modify resource flows in a way that changes, maintains, creates/destroys habitats, and thus control the ecological structure of communities. The study of ecosystem engineering has consequently become crucial to understanding the structure and function of the biosphere. Despite this, extending the concept of ecosystem engineering into a deep-time and evolutionary context has been difficult; two related concepts – 'niche construction' and 'legacy effects' – explicitly incorporate time, but arguably do not provide a single framework that allows us to consider ecosystem engineering-type effects through the history of life.

Here, we propose a conceptual framework for ecosystem engineering-type effects that combines both modern and deep-time biotic processes, and thus will be of broad use to ecologists, paleoecologists, and evolutionary biologists. First, we argue that a new term is required to describe organisms that not only modulate the availability of biologically-important resources, but which also alter the structure, function, and/or interactions between planetary spheres. To distinguish these organisms, we propose the term 'Earth systems engineers' ('ESEs'). Second, we describe a spectrum of possible scenarios surrounding the evolution of new EEs and ESEs, including a discussion of processes vs. consequences, macroevolutionary lags, legacy effects, and putative thresholds controlled by abundance or interactions between organismal groups. Lastly, we use case studies drawn from the fossil record to show how these can be broadly applied both across the tree of life, and throughout the span of Earth history.

20. Elucidating the effects of Ediacaran-Cambrian ecosystem engineering: A neoichnological case study

Katherine Turk, Vanderbilt University, Herndon, Virginia

Bioturbation, or the physical movement of sediment by organisms, represents a powerful form of ecosystem engineering through which animals can influence the characteristics of seafloor sediments and control the distribution of habitable ecospace. The emergence and proliferation of these behaviors – amid a general rise in the diversity and intensity of metazoan ecosystem engineering – during the Ediacaran-Cambrian transition ('ECT'; ~550-538 Ma) is coincident with the establishment of animal-dominated ecosystems. Consequently, understanding the deep-time evolution of ecosystem engineering is key to understanding the biotic drivers of this unique interval in Earth history. Bioturbation over the ECT is thought to have resulted in several critical downstream effects, including downwards transport of surficial materials, porewater chemistry changes, and increased subsurface oxygenation. However, there remains a dearth of empirical data illustrating exactly how and at what magnitude these behaviors alter environments. The study of modern organisms and behaviors in analogous environments (‘neoichnology’) thus represents a promising avenue through which to explore these questions long shrouded by the vagaries of deep time. Here I provide an overview of the evolution of these key ecosystem engineering behaviors across the ECT, and present the early results from experiments designed to quantify the impacts of bioturbative taxa thought to have evolved during this interval. I use these experiments to highlight several instances in which neoichnology can be used as a basis for understanding and reinterpreting ECT tracemaker behaviors, with important implications for understanding their role in ecosystem engineering and the emergence of the modern marine biosphere.

21. Bridges to Pangaea: Paleo-trait ecology connects us to deep time Earth systems

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Plants are the primary source of organic carbon for terrestrial ecosystems, interact with nutrient and water cycles, and create unique niches like forest canopy. Plants have likely served as the foundation of terrestrial ecosystems for hundreds of millions of years. However, the earliest plants were little more than ‘green slime:’ small, prostrate organisms that were limited to wet environments. Over the course of the evolutionary transformations that led from green slime to boreal forests and savannahs, plants acquired considerable environmental tolerances. The appearance of evolutionary innovations like cuticle, wood, and seeds, and variation in measurable aspects of these structures (functional traits). Ecosystems based on non-analog plants, which are extinct and radically different than contemporary plants, may have functioned differently. Further, because the fossil record is patchy in time and space, even deep-time vegetation cover is unknown. Functional traits can be measured from plant fossils (paleo traits), and present the opportunity to infer ecosystem function and distribution where no direct information is available. Recently, synthesis of multiple paleo traits in the context of an ecosystem model forced by global climate model data suggests that ecosystems more than 300 million years old may have exceeded the productivity and water transport capacity of modern angiosperm-based ecosystems, and covered much of Pangea. I will use examples to support the considerable potential for insight into deep time ecosystem function based on paleo traits, discuss limitations and biases, and present strategies for improving uncertainty, in particular by promoting synergy between the relevant fields.

22. Offshore Ecosystem Engineering: Origins and Evolution of Pelagic Fisheries in the Northeastern Pacific

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People have been ecosystem engineers in nearshore marine environments of the northeastern Pacific for over 10,000 years. However, questions persist about the antiquity and evolution of people’s influence on offshore, pelagic ecosystems and organisms. We explore the deep history of human interactions with northeastern Pacific offshore marine ecosystems, focussing on the origins and expansion of fisheries for apex pelagic fishes, *Thunnus* spp., in southern California. We synthesize the archaeology of tuna fishing during the Holocene, explore commercial and recreational catch records since the early 1900s, and document museum specimen data from the past 100 years. These data demonstrate that Indigenous people in southern California fished for tuna beginning over 5000 years ago but, with few exceptions, tuna were not a focus of Indigenous fisheries which largely targeted nearshore kelp forest, rocky reef, and estuary habitats. Beginning in the early 1900s, capitalist commercial fisheries for tuna commenced and rapidly accelerated during the 1930s to 60s, resulting in significant impacts on pelagic fishes and ecosystems. Despite millennia of tuna fishing by Indigenous people, significant human degradation of offshore marine ecosystems in southern California correlates with the mid-20th century Great Acceleration and the relatively recent proposed onset of the Anthropocene. These data illustrate the important role of humans as ecosystem engineers in marine habitats around the world, but document significant variability in the timing of anthropogenic influence on nearshore coastal compared to offshore pelagic ecosystems.

23. Restoring natural processes through rewilding with ecosystem engineers

Liesbeth Bakker, Netherlands Institute of Ecology, Netherlands

Large herbivores have strong effects on ecosystems through consumptive and engineering effects. This role of large herbivores in landscapes has diminished over time due to long-term and ongoing defaunation globally. The loss of large herbivores is part of the wider biodiversity decline, which calls for solutions to bend the curve of biodiversity decline through conservation and restoration. Rewilding has emerged as an approach to ecosystem restoration, which aims to restore natural processes. Restoring the role of large herbivores as a natural process in landscapes may benefit biodiversity. Here, we look at the role of different large herbivores in rewilding projects through ecosystem engineering and see how this affects the landscape structure and species diversity. Furthermore, we look at the role of different functional groups of herbivores, comparing bioturbation versus non-bioturbating animals. Bioturbating wild boar in fact create very herb rich grasslands, which is an interesting analogy to the observation of herb-rich plant communities in the paleo record, in the presence of megafauna assemblages, which may also have had important bioturbation effects. Therefore, present-day rewilding studies may also yield useful information about the roles of herbivores in the past and vice versa.

24. The rising novelty of the biosphere: a macroecology-biogeography perspective

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The concept of novel ecosystems has been discussed for more than a decade to describe ecosystems that have an altered species composition and function, such that the community has crossed a threshold forbidding a return to its historical state. While spatial and temporal community compositional change has been well studied in biogeography, studies on modern novel ecosystems tend towards classifying novelty based on an arbitrary baseline. Given that the abiotic and biotic drivers of novelty are in a state of rapid change, reaching levels unprecedented within the last hundred thousand to million years, defining such a threshold requires additional thought. In this talk we will explore how novelty can be defined in an environment undergoing progressive global change. We map the variation in the key drivers and indicators of novelty, measuring the natural variation experienced by a site over the last 800,000 years to modern and future conditions. By comparing these temporal maps to maps of biotic novelty, we can examine how novelty indication is affected by both the environmental history of an area and the choice of temporal baseline. Finally, we suggest macroecological and biogeographical pathways through which the emergence and spread of novelty can be further explored, understood, and managed beyond the perspective we offer here.

25. Pre-Columbian forest recovery in Amazonia

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European contact (around 1550-1600 CE) is said to have caused a c. 90% decline in the human population of Amazonia precipitating widespread abandonment of the land. The Orbis Spike, a c. 10 ppm decline in global atmospheric CO_2 concentrations at c. 1620 CE has been attributed to the resulting forest regrowth and carbon sequestration in lands that were deforested prior to European contact. Paleoecological analysis of Amazonian lake records showed that there was no such abandonment between 1550 and 1750 CE, but there was an earlier abandonment followed by a strong forest recovery between c. 950-1150 CE. These data suggest that the phase of site abandonment occurred long before European arrival, contra to the hypothesis that the Orbis Spike was caused by forest regrowth. The study of two Amazonian lakes, Ayauchi and Kumpaka, which lie within 25 km of each other, highlights the heterogeneity of indigenous land use. Applying a new transfer function for forest openness, fossil pollen projects that these settings never lost more than 50% of forest within 1 km of the lake during the last 2000 years, even at the peak of deforestation. Our data indicate that the period between c. 950 - 1150 CE is critically important in Amazonian pre-history with greater ecological impact than the period of initial European contact (1550-1750). Our data do not reveal any forest signature connected to a major population collapse or forest recovery that could account for the Orbis Spike.

26. Undiscovered bird extinctions obscure the true magnitude of human-driven extinction waves

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Birds are among the best-studied animal groups, but their prehistoric diversity is poorly known due to low fossilization potential. Hence, while many human-driven bird extinctions have been recorded, the true number is much larger. Here, by combining recorded extinctions with model estimates based on the completeness of the fossil record, we estimate that ~1,300 – 1,500 bird species (~12% of the total) have gone extinct since the Late Pleistocene, with 55% of these extinctions ‘undiscovered’ (not yet discovered or left no trace). We estimate that islands in the Pacific accounts for ~60% of total bird extinctions, with the majority of the other extinctions occurring on other islands. Bird extinction rate varied substantially through time with the largest peak ~1300 CE associated with the arrival of humans to islands in the eastern Pacific. This time period saw an extinction rate substantially above what is currently seen and likely represents the largest human-driven vertebrate extinction wave ever. Thus, humans have already driven more than one in nine bird species to extinction, with likely severe, and potentially irreversible, ecological and evolutionary consequences. □

27. Effects of climate change and agricultural practices on plant communities: synthesis from a long-term, large scale monitoring effort in France

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Agriculture has been one of the major drivers of global change. Keeping food production for a growing human population while minimizing agricultural impacts on the environment has therefore become a major challenge that needs empirical ecological solutions at large scales. Here we synthesize results from a national yearly monitoring effort in field margin plant communities in 500+ sites across continental France between 2012 and 2022. We show trends in temperature, soil moisture, and pesticide use at the national level, as well as plant community changes over time. We interpret these large-scale community changes in light of their functional consequences and Grime's CSR (Competitive, Stress-tolerant and Ruderal species) theory. Results show that while climate change is clear in the temporal time-series, agricultural management does not show a consistent de-intensification trend over time. Associated changes in plant functional traits reveal some important trade-offs. In Grime's CSR theory, climate change translate into a selection towards more stress-tolerant and less ruderal species over time. Agricultural management practices have noticeable impacts in spatial patterns, with the selection of ruderal species, i.e. those that can grow quickly in a highly disturbed environment. Put together, these results suggest that plant communities are receiving opposing selective pressures from climate change and agricultural intensification. We suggest Grime's CSR theory provides for a useful simplified vision of plant trait composition that allows understanding and anticipating future changes in plant diversity in agroecosystems. We put forward further areas to relate macroecological theory to practical management scenarios in these highly anthropized environments.

28. Urbanization dampens the latitudinal diversity gradient in birds

Jory Griffith, McGill University

Urbanized areas are rapidly expanding, causing the rise of a brand new biome that is globally distributed. The large-scale habitat transformation caused by urbanization often leads to a local decline in species diversity. However, little is known about how urbanization affects biodiversity patterns on global scales. The oldest and most well-known biodiversity pattern is the latitudinal diversity gradient, where species richness declines from the equator to polar regions. Urbanization has the potential to alter this pattern by filtering for generalist species that are tolerant of high disturbance, however, few studies have examined this, and none at a global scale. Using the citizen science database eBird and the European Commission Global Human Settlement data, I examined how urbanization affects the latitudinal diversity gradient in birds by comparing the relationship between species richness and latitude in urban, suburban, and rural areas globally. I found that urbanization has a dampening effect on the latitudinal diversity gradient, and that this dampening effect is strongest in summer, erasing the latitudinal gradient entirely. Furthermore, I found evidence that this dampening is largely driven by the disproportionate loss of specialist species at lower latitudes, where there is a higher porportion of specalists that are maladapted to urban environments. These results demonstrate how urbanization has disrupted biodiveristy patterns at global scales, leading to the formation of novel ecosystems governed by spatially independent novel assembly rules.

29. **The Impact of European Colonialism on Global Plant Redistribution**

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The redistribution of alien species across the globe accelerated with the start of European colonialism. European powers were responsible for the deliberate and accidental transportation, introduction and establishment of alien species throughout their occupied territories and the metropolitan state. Here, we show that these activities left a lasting imprint on the global distribu- tion of alien plants. Specifically, we investigated how four European empires (British, Spanish, Portuguese and Dutch) structured current alien floras worldwide. We found that compositional similarity is higher than expected among regions that once were occupied by the same empire. Further, we provide strong evidence that floristic similarity between regions occupied by the same empire increases with the time a region was occupied. Network analysis suggests that historically more economically or strategically important regions have more similar alien floras across regions occupied by an empire. Overall, we find that European colonial history is still detectable in alien floras worldwide.

30. **GEDI predicts less than expected aboveground forest biomass in Ghana: implications for modelling carbon storage and forest restoration.**

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Aboveground forest biomass is an important store of carbon and aids in the regulation of greenhouse gases. This vital role of forests also makes them ideal targets for restoration projects, and as such, they are increasingly targeted for carbon credit projects. To maximise the benefit of this restoration and effectively contribute to climate change mitigation, it is crucial to understand where carbon is being stored, and what the storage potential for a particular area could be for a restoration project. The Global Ecosystem Dynamics Investigation (GEDI) provides a unique source of point data for forest biomass for the entire planet. We modelled the distribution of aboveground forest biomass using GEDI data to estimate the current and carbon storage potential of forests in Ghana. By interpolating the GEDI biomass data with a suite of environmental and remotely sensed variables, we constructed a random forest model of forest carbon. Results showed the majority of forest biomass is found in the wetter south, with higher carbon storage potential, compared to the more arid north. Therefore, the south of the country has higher carbon storage potential for a given restoration project, than an equivalent sized site further north. Crucially, our models for forest carbon were significantly lower than previous estimations for forests in similar ecoregions, derived from direct sample plots. This analysis highlighted the uncertainty in using remotely sensed biomass values, at best leading to underestimates of carbon storage potential, at worst leading to overprediction and overstating the benefit of a restoration project.

31. Gulls in the Urban Archipelago: Reconsidering the Island Syndrome

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The island syndrome hypothesis, which suggests that insular populations exhibit distinct life-history traits due to ecological differences, has long intrigued ecologists. Recently, urban environments have emerged as potential analogs to islands due to their isolation and unique conditions. Our study investigates the island syndrome in urban gull populations and how it relates to anthropogenic drivers using a global dataset for seven gull species. We compared mainland vs. island and urban vs. rural populations, focusing on four life-history traits and their isolation effects. Surprisingly, we found that mainland populations had higher reproductive success primarily in the number of fledglings per nest. Similarly, urban populations exhibited greater reproductive success during the fledgling stage compared to rural populations, with isolation having a weak influence.

Our investigation into the relationship between reproductive success and anthropogenic food consumption revealed urban gulls feeding on human waste twice as often, a contrast not seen on true islands where diet and breeding success remained similar.

In conclusion, our study challenges conventional island syndrome predictions, suggesting that urban gulls resemble mainland populations in reproductive success. Predation pressure, resource availability, and access to anthropogenic food sources likely drive these patterns. This research advances our understanding of urban biodiversity, highlighting the potential of applying an island biology framework to urban areas, providing insights into wildlife dynamics and biodiversity conservation in our increasingly urbanized world.

32. Beyond Endpoints: Islands drive radiation of passerine birds in the Indo-Australian Archipelago

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Islands are often perceived as endpoints of colonization. However, recent research has highlighted the pivotal role of islands as sources of both speciation and dispersal. In regions of high species turnover such as the Indo-Australian Archipelago, dispersals have typically been treated as a dichotomy between the main continental shelves of Sunda and Sahul. This undermines the role of intervening islands to act not only as sites of insular diversification but also as sources of radiation following upstream colonization events. We aim to explore the substantial role of islands using large-scale ancestral state estimations on passerine birds of the Indo-Australian Archipelago. We tested the effects of historical changes in connectivity, compared within-area diversifications along with inwards and outwards dispersal between areas, and investigated speciation events occurring post-upstream dispersal. We show that islands such as Wallacea, New Guinea, and the East Melanesian arc disproportionately influence the generation of lineages that further diversify into major clades of the passerine super radiation. These findings support recent perspectives that position islands as catalysts for colonization. Our study underscores the important biogeographical role of islands, highlighting their dual capacity as both sources and sinks. By shedding light on the ability of islands to drive radiations across a region, our research offers insights with broad implications for understanding the dynamics of species diversification and biogeography.

33. Neutral and Selective Processes Across Scales Identify Marine Islands

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In recent years, a previously anethematic idea—that marine systems include places with island-like properties—has become more widely accepted. However, much confusion exists about when and where marine islands occur. It is essential that the current largely phenomenological and qualitative approach to identifying and classifying island-like marine habitats become more theoretically grounded and quantitative. We explore the prototypical class of marine island — marine lakes — from the perspectives of community genetics, species composition, and traits. We use surveys of microbial taxa, macroinvertebrates, macrophytes, and fishes. We consider evidence from species-level alpha and beta diversity, genetic diversity and differentiation, species abundance distributions (SADs), and traits that are enriched within communities in relation to the range of physical environments. Species-level data, including genetically barcoded microbial and invertebrate OTUs, reveal pairwise dissimilarities in community composition among lakes that are positively correlated between microbes and macro-invertebrates, and influenced to a similar degree by marked gradients in oxygen concentration and salinity. More isolated locations distinguished by low oxygen concentration and salinity also are characterized by non-neutral SADs. Fish in these more extreme environments have a biased subset of traits linked to dispersal, parental investment, body size, and diet. Whole genome sequencing of a jellyfish indicates shared genotypes across highly insular habitats indicating environmentally mediated selection. These kinds of quantitative estimates of marine lake communities are directly comparable with similar data from other marine, freshwater, and terrestrial systems, providing a more quantitative and synthetic perspective on islands and island-like locations.

34. Introductions outweigh extinctions in shifting seed dispersal potential across 118 island plant–frugivore communities worldwide

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Oceanic islands are hotspots of both anthropogenic extinctions and introductions of non-native species, leading to marked functional shifts in island communities. Functional shifts threaten to disrupt key species interactions, such as animal-mediated seed dispersal, with potential long-term impacts on the integrity of island plant communities and vegetation structure. Though some recent studies of individual taxa and islands have confirmed such shifts, it remains unknown whether animal community trait shifts actually translate to ecologically relevant mismatches with native plant species, and whether these mismatches are globally uniform in intensity and effect. Here, we document extensive functional remodelling of 118 island frugivore communities within 20 archipelagos worldwide, based on seed dispersal-specific traits from all native, extinct and introduced vertebrate frugivores (birds, mammals and reptiles), and relate them to seed traits of the native plant communities. There is an overall pattern of taxonomic and functional substitution, mainly of large-gaped flying seed dispersers, by mostly terrestrial mammalian omnivores, which has caused a mismatch between frugivore gape sizes (e.g. bill width) and seed sizes. This shift in seed dispersal potential would be underestimated in single-taxon studies. However, the general pattern is modulated by substantial spatial variation and idiosyncratic functional shifts for individual island systems. Together with variation in plant seed size distributions this means that the realized functional mismatch varies substantially among island systems. A story of similar functional homogenization across the world's archipelagos is thus oversimplified.

35. Spatial variation of phenotypic traits is higher between islands than between mainland populations, but spatial variation of genetic diversity is rather similar across the two systems

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A recent realization in ecological biogeography is that reconciling island biogeography theory with ecological and evolutionary theories developed in parallel could open up new avenues in isolation research and refine current global biodiversity models. We addressed this challenge and we hypothesized that marine island systems exhibit higher between-site variation than mainland systems. We performed a meta-analysis to test the strength of isolation due to geographic- and macroclimatic distances for paired marine island and paired mainland populations within the same species, comparing published measurements of phenotypic traits and neutral genetic diversity for 1608 georeferenced populations of 108 plants and animals worldwide. Variation in phenotypic traits was higher between marine islands than between populations on the mainland, but we found no consistent signal for differences in spatial patterns of neutral genetic diversity between the two systems. These results

suggest that spatial patterns of phenotypic variation are determined by eco-evolutionary pressures that differ more between islands than between mainland populations, while the spatial variation of neutral genetic diversity might be shaped by rather similar processes in the two systems. These findings have implications for future models of population variability at biogeographic scales, which we show can be improved by considering the spatial structure of populations in addition to the commonly employed predictors of environmental conditions or geographic distances between populations. Our findings may also be useful guides in conservation decisions. Larger areas may be necessary to preserve similar levels of phenotypic variability in homogeneous than in spatially more structured habitats.

36. Non-uniform change of ecosystem functioning on oceanic islands during the last 10,000 years

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Plant Functional Traits (PFTs) are informative indicators of ecosystem functioning. The integration of PFTs in palynological analyses enables us to reconstruct the response of ecosystem functioning to environmental change in the absence and presence of human activity over millennia. On islands, assigning PFTs to fossil pollen taxa is not only challenging because pollen taxa are usually identified on higher taxonomic levels such as genera or families, but also because plant species on islands may have evolved very different PFTs than on the mainland. We assigned the binary traits survival strategy (above-ground or below-ground survival) and pubescence (hairy or not hairy leaves) to fossil pollen taxa of 14 sedimentary cores spanning three archipelagos of Macaronesia (i.e., Azores, Canary Islands, and Cabo Verde). We reconstructed temporal trajectories of the community weighted means of both traits across each sediment record and archipelago. This allowed us to correlate traits trajectories with drivers of vegetation change on islands, such as climate and human colonization. Our findings reveal an increase in the proportion of plant species that make use of below-ground survival strategies, from past to contemporary communities. The correlations between temporal trait trajectories and climatic variables, such as temperature and precipitation, were weak, but trait trajectories changed around human colonisation in the Canary and Azores archipelagos. All in all, we did not observe a coherent systematic change of survival strategy and pubescence across all archipelagos, but tracking ecosystem functioning from a natural system into a human dominated world was possible by using fossil pollen.

37. Assessing islands’ vulnerability to climate change

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Climate change is one of the greatest threats to biodiversity. With a 1.5 ºC rise in the global average temperature almost certain, the current rate of greenhouse gas emissions may lead to a global warming

of 3 ºC above pre-industrial levels by the end of the century. This change is already causing shifts in species' geographical distribution to meet the environmental conditions required for their survival. For most species living on islands, though, such shifts are simply not possible. Here, we evaluate how climate change will affect islands' climatic space in the near future by quantifying the mismatch between current and projected climate conditions. Our analysis includes more than 22,000 islands under global warming scenarios of 1.5, 2, 3 and 4 ºC. Our results show that an increase of one degree leads to an average 10% reduction in the similarity of the environmental space of islands worldwide. This decrease in similarity is characterized mainly by a shift of the environmental space rather than a change in the size of the environmental envelope, indicating that islands will be exposed to non-analogue climates as global temperature rises. However, these changes will not affect all islands equally. While a high similarity in climate conditions predominates on islands located at latitudes above 25º, islands below this latitude may experience a total climate mismatch as temperature increases. Our study reveals that though climate change is a global threat, tropical islands are the most exposed to potential climate-driven extinctions.

38. Exploring mechanisms behind species-area relationship on habitat patches of acidophilous grasslands: a case study from the Czech Republic

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Three mechanisms are hypothesized to affect the species-area relationship on island-type habitats: passive sampling, habitat heterogeneity and "area per se". We aimed to test these mechanisms in patches of dry acidophilous grasslands scattered across Czechia's agricultural landscape near the city of Třebíč, which host a number of threatened vascular plant species. In a subset of 44 grassland patches (area 100–8600 m^2), we sampled vascular plants and their cover in four randomly located 0.5 × 0.5 m plots and recorded all plant species in the patch. We used the analytical framework proposed by Chase et al. (2019, Front Biogeogr) to disentangle the effect of the three mechanisms. The framework uses data on multiple scales (alpha: species within each plot; gamma: species in a set of plots within the same patch; beta: calculated from alpha and gamma; and island: all species in the habitat patch) and also two diversity metrics (richness and Simpson's diversity index). We considered only habitat specialists of acidophilous grasslands. We found that alpha and gamma diversity decreased with decreasing patch area, indicating that in addition to passive sampling, the "area per se" plays a role in the species-area relationship. Since only the species richness, but not Simpson's diversity, changed with the island area, we suggest that these disproportionate effects are related to the extinction of rare plant species in smaller patches, possibly due to random drift. We demonstrate that empirical data from grassland habitat patches can provide insights into the mechanisms behind the assembly of their plant communities.

39. Floristic homogenisation on South Pacific islands during the last 5000 years

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There is a relevant body of work stemming from island palaeoecological research that contributes greatly to the global understanding of ecosystem changes, including the increasing similarity of plant species, globally. Here, we will present results from a collaborative effort that aims to understand floristic trends during the past 5000 years across the tropical, sub-tropical, and the warm temperate South Pacific. While floristic homogenisation is often referred to as a contemporary issue, we have identified a much earlier trend, likely driven by human actions. First, the site comparisons show and increasing trend of floristic homogenisation over the last 5000 years. Second, pairwise Bray-Curtis similarity results show that when two islands were settled in a given time interval, their similarity was greater than when one or neither of the islands were settled. Finally, future trends of biotic similarity will depend on the levels of continued human ecosystem modification, rates of non-native introductions, and rates of extinctions and extirpations.

40. Variation and temporal trends of climate matching in birds

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Climate is an important driver of species abundances and distributions. However, some species are more closely matched to variations in climate than others; and the magnitude of climate matching might also change through time under fast global change. Using long-term data on North American birds, we found that variation in climate matching was associated to species traits. Intermediate-sized species were more well matched to climate than smaller or larger species, as were species that lived primarily in forested compared with open habitats, species that were locally more abundant and species that were more territorial. Alternatively, species that were more specialized or had high variability in abundance among sites were less well matched to climate. We also found that species abundances and distributions are becoming more decoupled from climate as it changes through time. Climatic decoupling through time was particularly prominent for birds that were declining in abundance and occupancy, which could lead to a feedback as birds experience increasing exposure to suboptimal climatic conditions. Temporal trends in climate matching were related to species traits, particularly habitat specialization, but not to average rates of climate and land use change within the species' ranges. Our findings provide an ecological basis for understanding the extent to which species abundances and distributions match broad climatic gradients, and how it changes through time.

41. Climate-induced range and niche shifts in European and North American breeding birds

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Species respond dynamically to climate change leading to transient dynamics and time lagged range shifts. In consequence, species may not occupy their full climatic niche during range shifting. Here, we aim to assess niche tracking during recent range shifts of European and US birds. Using data from two European bird atlases and from the North American Breeding Bird Survey between 1980s-2010s, we analyse range overlap and climate niche overlap based on kernel density estimation and null model analyses. Phylogenetic multiple regression was used to assess the effect of species morphological, ecological and biogeographic traits on range and niche metrics. European birds shifted their ranges north and north-eastwards, US birds westwards. Trailing range edges were more inert than leading range edges in both regions. Although transient dynamics were more pronounced in US, we found niche expansion was more common than niche unfilling in both regions. Trait analyses revealed some commonalities but also important differences between the two regions. Overall, dispersal limitations were minor in both regions while severe lagging of trailing range edges could be indicative of extinction debts. Differences between regions suggest different underlying mechanisms, for example related to land use history, that should be further investigated.

42. **Towards a Novel Biosphere in 2300: rapid and Extensive Global and Biome-wide Cli-matic Novelty in the Anthropocene**

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The climatic changes that characterize the incipient Anthropocene indicate a rewinding of the climate clock by approximately 120,000 years. Such drastic climatic changes would inevitably change species distributions, reshuffle their spatial configurations, and result in the emergence of new ecosystems due to different responses to climatic changes. This work addresses two critical questions: *Where is anthropogenic climate change likely to result in the emergence of novel ecosystems by 2300? To what extent biomes, at their current distribution, will experience rising climatic novelty?* To answer this question, we combined three perspectives on how climate novelty could result in novel ecosystems: defining where local climate changes are expected to be fast, in divergent directions, and resulting in climatic combinations that differ from the 1980-2010 climate normal of variability. Based on these metrics, we then establish the exposure to novel climates of different biomes in the near (2100) and long term (2300). Establishing the links between different ways climate change can rearrange the biosphere is essential to assess the likely changes in the exchange of energy, moisture, aerosols, and trace gases between the land surface and the atmosphere. We find rapidly increasing coverage of climatic novelty after 2100 without rapid mitigation, with over 50% of the biomes experiencing climate changes that would lead to novel ecosystems by 2300 under all evaluated scenarios. Our results show the diverse mosaic of climate change vulnerability and how the three evaluated factors contribute to this heterogeneity while considering the long-term temporal dynamics in climate-driven ecological novelty.

43. **Plant lineage gains and losses in temperate forest understories in response to global change drivers**

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Environmental changes leading to species extinction and colonization have resulted in the loss and gain of unique evolutionary lineages. Our research investigated whether these changes are random across the evolutionary tree. We examined alterations in the phylogenetic diversity structure of plant species lost and gained in European temperate forest understories over an average of 40 years. We also explored the influence of macroclimate variations and nitrogen deposition on these changes. Our findings indicate that losses and gains of species were clustered within specific lineages, with certain families consistently experiencing either losses or gains. For instance, the Fabaceae, Orchidaceae, and Rubiaceae families consistently showed losses, while the Fagaceae, Betulaceae, and Rosaceae families exhibited consistent gains. Areas with reduced annual precipitation but consistent minimum winter temperatures demonstrated greater losses in phylogenetic diversity. Conversely, communities in regions with low nitrogen deposition and warmer summers experienced an increase in phylogenetic diversity. The lost and gained species were not closely related, suggesting that specific traits did not significantly influence their ability to adapt to new environments or their susceptibility to extinction. Additionally, our analysis revealed that environmental shifts did not appear to affect the phylogenetic structure of the lost and gained species. In summary, our findings underscore the impact of recent environmental changes on phylogenetic diversity patterns in temperate forests, shedding light on which branches of the evolutionary tree and ecological strategies may be influenced by global shifts.

44. **Global records of soil fungi show climatic constraints of distribution and common cosmopolitanism**

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Soil fungi are an important group of microorganisms that are important for ecosystem processes including plant nutrition and decomposition. These organisms of which the majority has a cryptic lifestyle, largely evaded the attention of biogeographers in the past. The advance of high-throughput sequencing methods in microbial ecology represented a breakpoint in the ability to track fungi across global soils since it led to the accumulation of vast amounts of observations of fungi based on environmental DNA metabarcoding. When compiled, validated and linked to environmental metadata, such as in the GlobalFungi database (https://globalfungi.com) for general fungi and GlobalAMFungi database (https://globalamfungi.com) for plant-symbiotic fungi, forming arbuscular mycorrhiza, these large observatory data are useful to explore global distribution of fungal taxa. Here, we show that climatic constraints are important drivers of global biogeography of fungal species, although climate does not affect all fungal species equally and smaller-scale distribution is driven by other factors. Importantly, climatic niches are narrower in ectomycorrhizal fungi than in plant pathogens or saprotrophs which can have important consequences if we consider the ongoing change of global climate. High share of fungal species, including soil saprotrophs, yeasts and arbuscular mycorrhizal plant symbionts exhibit cosmopolitan distribution or distribution across multiple continents with suitable climatic conditions, indicating efficient dispersal. Our study also shows the utility of public data sharing and FAIRification for the advance in the fields of microbial biogeography and ecology.

45. Attributing biodiversity change to processes and drivers in the Alps - a dynamic modelling perspective

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Understanding and projecting biodiversity responses to land use and climate change is an urgent priority in global and European conservation, especially in sensitive, species-rich mountain environments. Recent calls for standard empirical frameworks for detection and attribution of biodiversity change such as Gonzalez et al. (2023) reflect this priority. However, these approaches emphasize identifying drivers of change such as climate patterns, neglecting the underlying ecological processes and interactions that link drivers to biodiversity shifts. Process-based models of biodiversity dynamics are poised to fill this gap, integrating observed biodiversity patterns, climate and land use drivers, and ecological processes such as biotic interactions and demography. Importantly, models also allow projection of biodiversity shifts under future scenarios of climate and land use change, including adaptive scenarios that represent constructive societal responses to climate change. Our study uses a process-based vegetation model, FATE-HD, to disentangle the effect of anthropogenic drivers and biotic interactions on biodiversity change in the Alps under a range of future climate and land use conditions. Building our analyses on novel land use scenarios that implement the IPBES Nature Futures Framework, we demonstrate that while climate change is a determinant driver of vegetation dynamics across the Alps, its effects are long-term and slower than those of land use changes that act regionally and immediately. Plant-plant interactions combined with land uses limit the tree-line shift and have marked effects on the Essential Biodiversity Variables monitored. We conclude by advocating better uptake of process-based models together with adaptive land use scenarios to safe-guard biodiversity.

46. A climate-induced tree species bottleneck for forest management in Europe

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Large pulses of tree mortality have ushered in a major reorganization of Europe's forest ecosystems. For initiating a robust next generation of trees, the species that are planted today need to be climatically suitable throughout the entire 21st century. Here, we developed species distribution models for 69 European tree species based on occurrence data from 238,080 plot locations to investigate the options space for forest management in Europe. We show that if the need for a continuous climate suitability throughout the century is considered, the average tree species pool decreases by between 33.1% and 49.2% compared to current values, even if these pools would be larger by 85.5% under the climate of the late century. This bottleneck could have strong negative impacts on timber production, carbon storage and biodiversity conservation, as only three species of high potential for providing these functions remain suitable on average per square kilometre. Our results indicate that the option space for silviculture is narrowing substantially because of climate change, and that an important adaptation strategy to increasing uncertainty – creating mixed forests – might be curtailed by widespread losses of climatically suitable tree species.

47. Range lags in European alpine plants under climate change

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Many alpine plant species are shifting their geographical ranges in response to global climate change. These range shifts, however, often occur more slowly than the rate of climate warming, leading to growing lags between species' expected and observed ranges – lags that can potentially drive species to extinction. With accelerating climate change, it is important to better understand how lags in the colonization of newly-suitable habitats (colonization credits) and lags in extinction of formerly-suitable habitats (extinction debts) accrue over time. What are the consequences of accrued lags in colonization credits and extinction debts for species' ranges under climate change? To investigate this issue, we are using Europe-wide alpine vegetation re-survey data to inform species distribution models in order to quantify range lags in alpine plants over the last several decades of climate change. We find that very few species are able to fully track their expected niche with climate change, such that colonization credits and extinction debts generally increased over time. Our modeling analyses reveal complex relationships between key environmental variables and the dynamics of alpine plant range shifts. By disentangling the temporal dynamics of range lags in alpine plants across Europe, we aim to better understand the impact of climate change on alpine plant communities as well as lay a foundation for forecasting the future range dynamics of alpine plants under ongoing climate change.

48. SPA: A predictive biogeographical framework to explain population differentiation through the prevalence of environmental suitability

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Genetic variation among populations is known to exhibit biogeographic patterns in many species, but there is still no consensus on the general rules of spatial genetic variation. We establish a theoretical framework based on the backward projection of Grinelian environmental niches to relate the current geographic distribution of population genetic structure to the historical evolutionary context of a given species.

We test this idea in the Tassel-eared Squirrel (*Sciurus aberti*) to jointly analyze spatial, environmental, and genetic data to predict the historical endemic area of this species. Our results reveal that in cases of genetic isolation by geographic distance, the prevalence of environmental suitability over time corresponds to the genetic fixation index of populations with respect to a source population. Populations closer to the historical endemic area present a higher genetic diversity and lower fixation index values. This empirical example allows us three further advances:

1. Propose an index to delimit historical endemic areas through environmental suitability prevalence.
2. Explain results obtained from population genetic methods from biogeographic patterns.

3. Generate maps of this genetic structure as a predictive tool supporting biodiversity conservation efforts.

This work advances a perspective that integrates population genetics with historical species distribution patterns.

49. Incorporating life history strategies in genetic models of demographic history

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Ecological differences across species have long been recognized as important to explain the biogeographic distribution of intraspecific genetic diversity. Specifically, individual dispersal capacity has been linked to levels of genetic differentiation across space, whereas life history strategies, such as different fecundity and survival rates, may explain both present and past estimates of effective population size. Therefore, genetic models that explicitly incorporate this ecological information are promising approaches to accurately estimate demographic history. Although attempts have been made to incorporate environmental niche as a proxy for dispersal capacities, less progress has been made in incorporating life history strategies. Here, we utilized individual-based forward simulations to assess the effect of such strategies on observed genetic variation. Our goal is to investigate whether incorporating life history variation aids in estimating historical demographic parameters, such as population size through time and intensity of demographic changes. In a simulation exercise for a single population, we explored varying values of the following parameters: generation time, adult longevity, adult annual mortality and number of mates per reproduction event. Generation time and number of mates had a strong negative correlation with levels of genetic diversity, whereas mortality had a moderate negative correlation. In ongoing work, we are applying this approach to a mitochondrial DNA dataset from two Neotropical passerines to show how ecologically informed simulations can be used for inference of population demographic history. The results reinforce the importance of life history strategies and introduce an approach to incorporating them when estimating biogeographic history from genetic data.

50. A database and web application for sharing the entire alpine flora genomic data

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Due to their isolation and intricate terrain, high mountain regions are renowned for being incredible biodiversity hotspots. Major challenges in the study of these hotspots resides in understanding the evolutionary scenarios and species coexistence mechanisms that have shaped biodiversity patterns. These endeavors require high-quality genomic data on a large number of species, a field often termed "biodiversity genomics". In 2009, the Phyloalps consortium initiated the collection of the entire Alpine flora and sisters species in the Pyrenean and Carpathians. They subsequently sequenced approximately 6000 species, among which 4000 alpine species, covering 95% of the entire flora of the European Alps. This endeavor required building a common database for systematic archiving and data sharing. This presentation will highlight the major accomplishments of this initiative, encompassing an outline of the database's structure and a focused examination of key functionalities such as synonymy management according to international taxonomies and data interoperability with existing databases. Additionally, we will introduce an online application that will serve as a user-friendly interface for exploring, downloading, and analyzing the information.

51. Pleistocene climate oscillations, not orogeny, drove the assembly of the European Alpine sky island flora

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The relative impact of orogeny and paleoclimate on the evolutionary assembly of species-rich mountain floras remains debated. Here, we aim to uncover how the physical history of the European Alps drove the assembly of the European Alpine sky island (ASI) flora. Using whole chloroplast genomes for 96% of the ASI flora (1320 species), we reconstruct a time-calibrated phylogenetic tree to infer temporal changes in the rates of two key assembly processes, namely colonisation and diversification. By including species-poor lineages that are generally excluded from macroevolutionary studies, we were able to show that the majority of the flora assembled via colonisation or individual speciation events into the sky islands, rather than the *in situ* diversification of large clades. The accumulation of extant lineages was decoupled from major orogenic events, such as the initial uplift of the Alps. Instead, the Quaternary climate oscillations had the strongest impact on colonisation and diversification rates, which increased substantially during the Pleistocene glacial period. Many ASI lineages originated in Europe, rather than through long distance dispersal from temperate Asian mountain ranges. We conclude that the ASI flora consists of a continuous subset of the European flora, filtered by the ability to disperse into the sky islands during and after the profound landscape transformation of the Pleistocene glacial cycles.

52. Genomic evidence from forest understorey species suggests unexpected prevalence of cryptic temperate forest refugia in Europe

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Temperate forests are the dominant natural vegetation of Europe today. During Pleistocene cold stages, these forests underwent large-scale and continent-wide range losses, and were repeatedly forced to retreat into comparably small refugia in southern and central Europe. In recent years, genetic studies added conclusive evidence supporting the location of these long-hypothesized refugia, and further hinted the existence of previously unknown, cryptic refugia. However, the evidence in support of cryptic refugia remained ambiguous, as it mostly consisted of low-resolution markers from anemophilous trees with shallow genetic structures. To understand the prevalence and the importance of cryptic refugia, we pursue an indirect approach that focused on five forest understorey herbs that we cautiously interpret as proxies for temperate forests (*Aposeris foetida*, *Cardamine trifolia*, *Euphorbia carniolica*, *Helleborus niger* and *Hacquetia epipactis*). For each species, we inferred population structure and tested explicit demographic scenarios based on range wide samplings and genomic SNPs. This was further complemented by ecological niche models projected to late Pleistocene conditions. Our findings suggest that forest understorey species have survived at least the last cold

stage in multiple cryptic forest refugia (e.g. in the Southern Alps). Deep phylogenetic splits between refugial areas, sometimes even predating the Pleistocene, supported long-term stability of many cryptic refugia. We hypothesize that the prevalence of cryptic refugia enabled tree species such as beech (*Fagus sylvatica*) to expand rapidly after the Last Glacial Maximum, which might even clarify Reid's paradox of an unrealistically fast migration of tree species in Europe.

53. **Genomic adaptation and future responses of an alpine Rhododendron species at eastern Hengduan Mountains**

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Plant species at high altitudes have shown local adaptations to particular environments, such as low temperature, drought, ultraviolet radiation, and a short growing season. In the face of climate change, alpine specialists are more likely to experience range contractions and evolutionary risks. To quantify such vulnerability, we sampled 15 populations of an alpine Rhododendron (*R. intricatum*) spanning with a large elevational range (3000 m - 4500 m) at the Mt. Gongga region of eastern Hengduan Mountains in southwestern China. With a whole-genome re-sequencing dataset, we performed genotype-environment association (GEA) and gene ontology (GO) enrichment analyses to explore its adaptation signature along elevation. Using inferred outlier SNPs (single nucleotide polymorphisms), we then modelled the genetic turnover in a multidimensional climate space and estimated genetic offsets under climate change. The genomic data showed no significant geographic structure, while GAE tests returned a large number of outlier SNPs being associated with altitude. Among inferred significant SNPs, the GO enrichment analysis obtained a strong functional tendency associated with reproductive processes, such as pollination and signalling. The current genetic turnover shows strong signals along climatic variables related to precipitation seasonality and extremes, which matches a northeastern-southwestern geographical separation among population. Meanwhile, such turnover signals would lead to remarkable risks at high elevation with intense precipitation changes in the future. Together, we highlight the genomic mechanisms underpinning local adaptation at high altitudes. More importantly, we show that predicting climatic vulnerability from both evolutionary and ecological factors reveals population-level risks to climate change in a mountainous region.

54. **Repeated upslope biome shifting during late-Cenozoic climate cooling in a diverse alpine plant clade**

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Mountainous regions are renowned for their high biodiversity, not least due to their steep environmental gradients that culminate in the alpine zone, an exposed and stressful habitat beyond the climatic treeline. Although many mountain ranges are ancient, the extant biodiversity of their alpine zones may be surprisingly young. To shed light on the historical assembly of alpine biota, we built a densely sampled genomic phylogeny of the flowering plant genus *Saxifraga* Tourn. ex L. (Saxifragaceae, ca. 557 species), an important element of alpine floras across the Northern Hemisphere. Using a customized probe set for targeted sequence capture, we generated DNA sequence data for 329 low-copy nuclear loci in 407 species, and used coalescent-based methods to reconstruct the species tree of the genus. We then gathered a comprehensive dataset on the geographic occurrence and biome associations of species. Based on these data, we modelled the rate at which lowland lineages have transitioned into the alpine zone over time, and the rates at which alpine-adapted lineages have speciated and dispersed among regions. Our results suggest that *Saxifraga* has colonized the alpine zone frequently from lowland ancestors, with most colonisations occurring in the last five million years. In contrast, dispersal of alpine-adapted lineages among regions is rare, and speciation in alpine-adapted lineages is relatively slow. Taken together, these results suggest that the large number of saxifrage species in many alpine regions is mostly the product of recent rampant upslope biome-shifting, presumably driven by repeated climate-driven expansions of the alpine zone during the Quaternary.

55. Gaps in the global protection of terrestrial genetic diversity

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In recent decades, increased anthropogenic impact has led to a global decline in genetic diversity. Before the Kunming-Montreal Global Biodiversity Framework (2022), the absence of international consensus on how to directly assess and monitor genetic diversity, hampered large-scale conservation efforts. Scarcity of assessable genetic data has hindered the evaluation of conservation policies in safeguarding genetic diversity. This study presents the first global approach for evaluating the protection of genetic diversity. By examining the global distribution of mammalian intraspecific mitochondrial DNA and protected area coverage, we identify regions with high genetic diversity and insufficient protection coverage, e.g. regions of critical importance for biodiversity in the Brazilian Atlantic Forest. Additionally, we estimate the impact of global change scenarios on genetically diverse regions with a low degree of protection, revealing high vulnerability of areas in Central Africa. Nonetheless, integrating robust analysis into conservation planning remains challenging. Incorporating Macrogenetics into conservation planning holds the potential to reverse biodiversity decline.

56. The ecology and biogeography of endemic mammal species

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Endemic species, species with restricted range sizes, are vulnerable to extinction and often ecologically and evolutionarily unique. Because of their ecological and conservation importance, understanding how abiotic factors, species traits, and community composition influence endemism is a defining question in mammalogy. We examine drivers of mammalian endemism from multiple angles. First, we use a novel null-model technique, employing spatial randomization that removes ecological factors, to explore the long-term effects of climate stability, topography and species richness on endemism patterns. Next, we reincorporate ecological factors, evaluating the traits characteristic to endemic mammals and the functional diversity of highly-endemic mammalian assemblages. Finally, we narrow our focus to island-endemic species, exploring how differences in climate, geography, and traits influence the evolution of these species' climatic niches. Overall, although areas of high mammalian endemism mirror those of

high richness, endemism is even more prevalent in topographically diverse regions that have had stable climates through time. Species that live in areas of high endemism tend to have small body sizes, short lifespans, and few offspring per year, indicating they may have been unable to expand their ranges after habitat fluctuations. However, we also find little support for the influence of climatic niche shifts on broad-scale continental or island endemism patterns, suggesting that geography is the primary driver of restricted-range species distributions. Thus, conservation efforts should focus on rugged, climatically stable areas, often characteristic of coastal montane regions.

57. Niche Trackers Don't Play by the Rules: Consequences of Niche Tracking on Seasonal North American Bird Biogeography

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Each year, nearly 20% of the world's bird species migrate in response to seasonal environmental changes. This predictable redistribution of bird diversity plays a pivotal role in ecological processes and the shaping of biogeographic patterns. However, our understanding of how seasonal variation, species traits, and their consequences for biogeography are interconnected remains fragmented. Our study addresses two fundamental questions: 1) How do species traits influence their degree of climatic niche tracking? 2) What is the impact of these trait-niche tracking relationships on seasonal bird biogeography? To answer these questions, we integrate daily climate data, bird traits, and weekly distribution estimates of over 600 species across Canada and the United States. We identify species that favour minimizing movement in geographic space (niche switchers) over climatic space (niche trackers).

Our results support the hypothesis that larger species can tolerate a broader range of climatic conditions, making them more likely to switch their climatic niche throughout the year. In contrast, efficient dispersers tend to favor niche tracking. This trade-off leads to varying migration patterns among species guilds, with significant implications for ecosystem functioning. We also demonstrate that species tending to track their climatic niche induce critical shifts in two well-accepted ecogeographical rules across seasons: the Latitudinal Diversity Gradient and Bergmann's rule.

These insights enhance our understanding of how niches interact with bird migratory behaviour, underscoring the importance of integrating seasonality into large-scale predictive models, especially in the current context when climate and seasonal regimes are changing.

58. Seasonal variation in dragonfly assemblage colouration suggests a link between thermal melanism and phenology

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Phenology, the seasonal timing of life events, is an essential component of diversity patterns. However, the mechanisms involved are complex and understudied. Body colour may be an important factor, because dark-bodied species absorb more solar radiation, which is predicted by the Thermal Melanism

Hypothesis to enable them to thermoregulate successfully in cooler temperatures. Here we show that colour lightness of dragonfly assemblages varies in response to seasonal changes in solar radiation, with darker early- and late-season assemblages and lighter mid-season assemblages. This finding suggests a link between colour-based thermoregulation and insect phenology. We also show that the phenological pattern of dragonfly colour lightness advanced over the last decades due to global warming, which together with the static nature of solar radiation, may drive flight periods to suboptimal seasonal conditions. Our findings open a research avenue for a more mechanistic understanding of phenology and spatio-phenological impacts of climate warming on insects.

59. Multiple dimensions of 3D habitat structure drives multiple dimensions of avian community diversity in North America

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Habitat loss is the leading cause of terrestrial species declines globally, yet how existing habitats shape community composition remains unclear. In particular, the role that 3D habitat structure, the combination of 3D habitat composition (volume) and 3D habitat configuration (horizontal and vertical arrangement), has on avian diversity is not yet elucidated. Most studies of 3D habitat structure rely on simplistic metrics of habitat structure (i.e. canopy height) and often single measures of diversity (i.e. species richness). Thus, there is a gap in the research to examine the independent influence of both 3D habitat composition and configuration on avian taxonomic, functional, and phylogenetic diversity, as well as on individual traits. We used LiDAR data and abundance-corrected avian data from across the National Ecological Observatory Network (NEON) to calculate eight different biodiversity indices and eleven different measures of habitat structure. Using Bayesian models, we tested different model hypotheses, comprised of different combinations of compositional, configurational, and climatic covariates. We found 3D habitat structure best predicted measures of functional diversity and trait-based PC axes, with little effect on phylogenetic or taxonomic diversity indices. Habitat composition and configuration varied in effect across different vertical height strata (understory, midstory, subcanopy, canopy) and across trait-based indices. Additionally, we found plots with lower vegetation amounts had communities with different dietary, foraging, and morphological traits compared to high vegetation plots. Our findings suggest that studies of 3D habitat structure should focus on functional and trait-based measures of diversity and use both compositional and configurational measures of habitat structure.

60. Fine-scale patterns of plant community diversity across Europe

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Recent compilations of large databases of vegetation-plot data have paved the way for mapping and analyzing plant biodiversity patterns at fine spatial resolution over large areas. The European Vegetation Archive (EVA), which contains ~2 million vegetation plots, is by far the largest regional vegetation-plot database in the world. We used this database to examine patterns of taxonomic, phylogenetic and functional alpha diversity of vascular plant communities across Europe, and here we synthesize the results of our recent studies. For taxonomic alpha diversity, we showed that the richest plant communities occur in mountainous areas of southern Central Europe and submediterranean Europe, particularly on calcareous substrates, whereas Northwestern Europe is generally characterized by species-poor plant communities. For phylogenetic alpha diversity, we identified high values in areas that were historically exposed to less dramatic environmental changes or have mountainous topography that provides refugia in times of climate change. Similar to taxonomic alpha diversity, phylogenetic alpha diversity also tends to be low in Northwestern Europe. Functional alpha diversity depends on the traits selected to quantify it, but considering a simple measure of the number of life forms, it tends to increase from Northwestern to Southeastern Europe. Nevertheless, there is a strong, symmetrical north-south geographical pattern in functional diversity, with trait syndromes associated with slow nutrient economies prevailing both in the north (reflecting cold stress) and the south (reflecting drought stress) and syndromes associated with fast nutrient economies predominating in the European cool-temperate zone.

61. Multifaceted biodiversity-stability relationships in boreal to subarctic ecosystems

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The biodiversity – ecosystem functioning relationship predicts that increasing biodiversity promotes stability in ecological communities. Climate change and human-caused habitat disturbance are altering biodiversity at unprecedented rates, threatening the stability of the ecosystem services on which humans depend. However, most of what is known about biodiversity-stability relationships comes from experimental studies making extrapolation to real ecosystems difficult. Here, we utilize terrestrial and aquatic long-term monitoring datasets encompassing entire assemblages at hundreds of georeferenced sites covering the boreal to subarctic ecosystems of Finland, to test how the shape of the biodiversity-stability relationship varies among taxa. Specifically, we explore the pathways via which species richness and the degree of asynchrony in species' population dynamics, contribute to community stability on decadal timescales. Furthermore, we account for the effects of environmental drivers, species traits describing key ecological strategies, and phylogenetic relatedness on variation in temporal stability. The biodiversity-stability relationship is studied using structural equation models fitted to each taxon group: birds, butterflies, mammals, moths, phytoplankton, and rodents. Each dataset represents species abundances, and the monitoring was established in the 1960-1990s. According to the first results, there is a positive relationship between community stability, species richness and population asynchrony, but this relationship may vary among taxa, and is modulated by inter-specific ecological trait similarity, phylogenetic relatedness, and underlying environmental gradients. Our results suggest that considering multiple taxa and their functional properties is essential for a comprehensive analysis of this classic yet timely hypothesis to understand and maintain the functioning of the ecosystems.

62. Taxon and area invariance of macroecological biodiversity patterns

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Diversity patterns cannot be properly interpreted without a theory providing criteria for their evaluation. Most biodiversity patterns comprise assemblages of species of given higher taxon (e.g. class) that differ in their location and size. This requires either (i) a strict specification of the taxonomic clade and assemblage for which the pattern is observable (more specifically, particular phylogenetic and spatial scales at which the patterns should be observed), or (ii) an asumption that the patterns are invariant against the change of the clade or site area. As these two alternatives cover all possible scenarios and can be tested for mutual exclusivity, the criterion of taxon and area invariance is a powerful tool to examine theories concerning the

form of macroecological patterns. We propose that truly universal patterns should not change when we change taxonomic scope by focusing on subtaxa or when we merge several sister taxa together. We show how to use the principle to derive and test truly universal patterns and refer to the findings that have already been achieved using this principle. We will focus mainly on two master macroecological patterns, namely species-sbundance distribution (SAD) and species –area relationship (SAR), and show that the functional form of both these patterns can be derived by assuming their taxon and area invariance.

63. Idiosyncratic patterns of local species richness and turnover define global biodiversity hotspots

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Tropical mountains are global biodiversity hotspots, owing to a combination of high local species richness and turnover in species composition. As the patterns of local species richness and turnover explain why tropical mountain regions are more species-rich than the lowlands, the same patterns explain why some mountain regions are disproportional more species-rich than others, even within the tropical zone. Thus, high levels of local richness and turnover are also implicitly assumed to converge among the World's most species-rich tropical mountain regions. We investigated this untested assumption using high-resolution distribution data for all bird species found in the World's mountain regions. Contrary to expectations, the mountain regions with the highest local richness differed from those with the highest species turnover and were associated with distinct climates and habitat types. Forest habitats and humid tropical climates characterise the mountain regions with the highest local richness. In contrast, the mountain regions with the highest turnover are generally colder with drier climates and have mostly open habitat types. The highest local species richness and turnover levels globally converge in only a few mountain regions with the greatest climate volumes and topographic heterogeneity, resulting in the most prominent global hotspots for avian biodiversity. These results underline that species-richness hotspots in tropical mountains arise from idiosyncratic levels of local species richness and turnover, a pattern that traditional analyses of overall regional species richness do not detect.

64. Mammal life history strategies are strongly associated with environmental realms

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Mammalian investments in survival, development, and reproduction are constrained by physiological and evolutionary factors. Mammalian life history strategies can be characterized by a few axes of variation, which conform a space where species are positioned according to which life history strategies are favoured in the environment they exploit. Yet, we still lack global descriptions of the diversity of realized mammalian life history and of how this diversity is shaped by the environment. We used six life history traits to build a global life history space and explored how major environmental realms (land, air, water) influence mammalian life history strategies. We demonstrate that realms are tightly linked to distinct life history strategies. Predominantly, aquatic and aerial species adhere to slower life history strategies, while terrestrial species tend to exhibit faster life histories. Highly encephalized terrestrial species, like primates, are a notable exception to these patterns. In addition, species transitioning between the terrestrial and aquatic realms, such as seals and otters, show intermediate life history strategies. Further, different behaviours may play a significant role in allowing to expand the set of strategies exploitable in the terrestrial realm. Our results provide compelling evidence linking environmental realms to the diversity of life history strategies among mammals, potentially informing assessments of species viability.

65. Integrating functional and phylogenetic diversity in conservation science

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In an effort to halt the alarming loss of biodiversity, nearly all countries have implemented networks of protected areas designed to safeguard biologically valuable regions. Here we will give an overview of how functional and phylogenetic diversity have been incorporated in the planning of protected areas. Based on a systematic literature review, we found that studies on protected areas have focused mainly on species richness and diversity, while functional and phylogenetic diversity have received considerably less attention. Exclusive emphasis on taxonomic diversity assumes equal contributions from all species to biodiversity, disregarding their unique roles in ecosystems and their distinct evolutionary histories, which hinders a comprehensive evaluation of protected area effectiveness. We present two examples which illustrate how functional and phylogenetic diversity can be incorporated into conservation science. The first study assesses whether protected areas adequately represent regional diversity. This research focuses on the taxonomic, functional, and phylogenetic diversity of terrestrial tetrapods of the Iberian Peninsula, and shows that protected areas generally capture the regional diversity of amphibians, reptiles, and mammals, but not birds. The second study predicts changes in functional diversity if current endangered mammal species became extinct. This study focuses on islands, which are highly vulnerable regions, and identifies islands that are more vulnerable to future functional diversity loss. Such losses (through extinction) often do not immediately lead to a drastic reduction in functional diversity, though the long-term ecological consequences of even minor losses remain uncertain.

66. Fine-scale alpine plant community assembly: Relative roles of environmental sorting, dispersal processes and species interactions

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In a warming macroclimate the rugged alpine terrain might offer microrefugia for cold-adapted plant species. However, the efficiency of these refugia will depend on fine-scale population and community dynamics, and how these processes are affected by dispersal and biotic interactions as

compared to environmental sorting. We analyzed data from 660 permanent 1-m² plots in the alpine-nivale ecotone of Mt. Schrankogel, Austrian Alps. We combined these data with species lists from 899 additional plots newly sampled across a larger landscape which we used for fine-scale habitat suitability modeling. We assessed the relative effects of projected habitat suitability, propagule pressure from surrounding populations and vegetation density on 1530 colonization and 372 extinction events of 31 species observed between 1994 and 2014.

We found that all three predictors are related to both colonizations and extinctions, with habitat suitability having the strongest, propagule pressure a slightly weaker, and vegetation density the weakest effect. Colonizations can be significantly better explained by the three process-proxies than extinctions.

The results indicate that, besides environmental filtering, neutral processes, especially dispersal limitation, have a strong, yet underestimated impact on alpine plant community (re-)assembly and may compromise the efficiency of scattered cold microrefugia in rescuing the alpine flora from climate warming.

67. The ultimate guide of mycorrhiza and abiotic stress polytolerance in woody plants

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Mycorrhizal symbiosis is an ancient association between plants and fungi, crucially important especially for woody plants, as they have to maintain aboveground structures. Our current understandings of how woody plants respond to abiotic stress and how mycorrhiza mitigates this stress is very limited and considers almost exclusively just a single stress factor at a time. Functional diversity of both woody plants and mycorrhizal fungi interacting with them, variability of the strength and composition of multiple stress conditions in different regions of the world – all this makes it difficult to predict the patterns of these interactions from both the adaptational and mitigational point of view. In this study we used top-down approach, where known interactions are partitioned into functional and biogeographical groups, and then the stress tolerances and interactions are mapped into overlapping heatmaps to provide us large-scale patterns of these associations. We compiled a concordant dataset of 621 woody species stress polytolerance (including shade, drought, waterlogging, cold stress) and their known species-specific mycorrhizal interactions. We tested how stress polytolerance correlates with different mycorrhiza functional types. Our results confirmed contrasting patterns between single vs. multiple type, arbuscular vs. ectomycorrhiza, and obligate vs. facultative mycorrhizal interaction. Functionally different symbionts form significantly polarizing abiotic stress mitigation patterns with woody species with different life forms, growth forms, and biogeographical origin. These results provide insight into both evolutionary and biogeographic patterns related to the development of plant-mycorrhiza interactions.

68. Functional diversity promotes community stability over time across taxonomic groups

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Global change (e.g., climate change, land use change) is threatening worldwide biodiversity, potentially causing drastic ecological disruptions. To anticipate the trajectories of biodiversity change, it is fundamental to assess their temporal trends. Recent studies investigated temporal trends of different taxa across biomes finding no net change in global species richness patterns, lacking evidence of a systematic biodiversity loss. However, most of the studies performed so far considered only the taxonomic dimension, lacking information about temporal trends in functional diversity (i.e., trait differences among species). In this study, we examined spatio-temporal dynamics of the functional structure of tetrapods and vascular plants (87 studies and 2906 plots across the globe) using the BioTIME database, quantifying patterns of temporal α diversity (change in functional richness, α-FD), and temporal β diversity (β-FD, functional turnover reflecting how the occupation of the functional space of an assemblage vary through time). We found no net effect of changes in α-FD across the time series, even though the temporal divergence in functional structure is faster than expected by chance suggesting consistent significant functional differentiation over time since the first year of sampling. We also demonstrated that functionally redundant assemblages tend to be more stable through time. Investigating change of multifaceted diversity is of utmost importance toα have a holistic perspective on the effects of global change.

69. Evolutionary history and environmental variability shape resource specialization in tropical mammals

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Tropical regions harbor the most diverse terrestrial mammal communities on the planet. The coexistence of tropical mammal species may result from the evolution of narrower niches, including specialized resource niches, through niche-filling in stable, productive, and biodiverse environments. Yet how evolutionary history, paleoenvironmental changes, and human impacts have shaped consumer-resource interactions in tropical mammal food webs worldwide is unknown. We compiled the first predator-prey interaction metaweb for tropical mammal species in 391 communities throughout the Americas, Africa, and Southeast Asia. The degree of resource specialization in each community was estimated by two food web-level metrics: linkage density and the mean hypervolume of resource species among consumer species, given species richness. Using spatial regression models, we tested the relative effects of evolutionary history of tip speciation rates, environmental variability in climate and productivity over geological time, and human impacts on mammal resource specialization. Our results documented regional-specific evolutionary and environmental drivers of resource specialization. In the Americas, the slower speciation rate was the only significant predictor of resource specialization. In Africa, contemporary climate and productivity stability were significantly predictive of resource specialization. In Southeast Asia, slower speciation rates, lower elevation variability, and greater climatic variability over geological time were significantly associated with resource specialization. Our findings provide insight into the formation of trophic interactions among tropical mammals, along with their biogeographic evolutionary histories and the potential impacts of environmental changes on altering mammal trophic structures in a changing world.

70. Evolutionary and ecological determinants of decoupled phylogenetic and functional diversity in European grasslands

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The relationship between phylogenetic diversity (PD) and functional diversity (FD) plays a key role in understanding the underlying mechanisms of community assembly. Traditionally, it is expected that these measures are coupled, shaped by competitive exclusion and environmental filtering. Recent findings have challenged this view, revealing patterns of decoupled PD (phylogenetic over-dispersion linked with trait convergence) and decoupled FD (functional over-dispersion linked with phylogenetic clustering). Yet, the prevalence of these patterns in plant communities across broad geographic regions and diverse contexts remains understudied. We explored the PD-FD relationship within vascular-plant communities in European grasslands, focusing on decoupled patterns. We hypothesised that patterns of decoupled diversity are tied to historical environmental shifts and occur less frequently than coupled patterns.

We examined 81,484 plots from European dry, mesic, wet and alpine grasslands, comprising 4,119 angiosperm species, and used information on six key functional traits. Our results reveal diverse PD-FD patterns across habitats, traits and regions, with coupled patterns widespread but not universal. Many communities exhibit decoupled PD, particularly in dry grasslands, suggesting environmental filtering of phylogenetically diverse species pools. We also observed decoupled FD in mesic and wet grasslands, linked to specific traits and competitive interactions influenced by recolonization history. Decoupled PD is notably common in mountainous regions, likely due to refugial effects that preserve distinct lineages while species share similar functions due to environmental filters.

Our study highlights the diverse insights PD and FD offer into community structure and assembly, emphasizing the need for further research on decoupled PD and FD.

71. The global evolution and distribution of plant defense traits is shaped by mammalian herbivores

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The evolutionary arms race between plants and herbivores has led to many adaptations and counter-adaptations in both organismic groups. Plants possess numerous analogous morphological structures, such as prickles, thorns, and spines, that deter predation from herbivores, especially large mammals. The debate is whether these traits evolved in response to herbivory or other environmental factors like temperature and aridity. Here, we used a macroecological approach and hypothesized that the evolution and distribution of plant defense traits is convergent and has been shaped by the interaction with medium- to large-sized mammalian herbivores (i.e., more than 10kg). We focus on 2338 species of mimosoid legumes (69% of total species), a pantropical lineage that shows a wide diversity of herbivory defense traits. We integrated these with morphological, phylogenetic, and geographical data on 235 extant and 185 extinct species of mammalian herbivores, fire regimes, and climate, and applied phylogenetic and structural equation models at global and continental scales. Results illustrate the repeated evolution of defense traits, and that, the global proportion of armed species is strongly associated with herbivore richness and extended drought periods. Furthermore, we detected extinct herbivore richness as the primary driver in African assemblages of plant defense, whereas extant herbivores dominated in the Americas. Our findings suggest that environmental correlates of plant defense traits are scale-dependent, and ecosystems cannot be properly understood without considering interactions with extinct species. The complex interplay of fire, drought, temperature, the expansion of savanna habitats, and mammalian herbivore evolution have influenced the evolution and distribution of plant defense adaptations.

72. Niche Divergence Plane: New conceptual framework to classifying and quantifying ecological niche divergence between taxa

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Comparisons between a pair of ecological niches are often performed by contrasting hypervolumes generated using ecologically relevant variables. Currently, most comparisons test the null hypothesis of niche conservatism or equivalency, with niche divergence representing the departure from the former. However, niches can shift, expand, shrink, or tilt, and individual environmental axes might diverge in different ways and magnitudes. We introduce a new framework that allows quantification and classification of niche divergence between two taxa along a niche axis. This framework, the Niche Divergence Plane, relies on two indices: niche exclusivity and niche dissimilarity, representing the range of values along the axis that is exclusive to each taxon and the area under response curves not shared between the taxa, respectively. Based on the position of the indices on a plane, we can distinguish niche conservatism from four general types of niche divergence: hard, soft, weighted, and nested. We compare the niche divergence plane with other measurements of niche dissimilarity (such as Hellinger's I or Schoener's D), and further demonstrate its utility by exploring inter-specific ecological niche divergence using virtual species and empirical occurrence records from two species of sympatric salamanders, *Ambystoma opacum* and *A. maculatum*.

73. Harnessing AI and Remote Sensing to foster high resolution habitat mapping

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Si-Moussi S., Hennekens S., Mucher S. and Thuiller W. Habitats are crucial for conservation targets and for ecosystem accounting and valuation. Despite limited predictive efforts at a resolution (<1km2) suitable for decision-making, accurate habitat mapping is essential, especially with refined thematic definitions that can distinguish specific habitats. In this study, we leverage recent remote sensing products and advanced machine and deep-learning techniques to predict habitats at high resolution in Europe. Our approach involved over two million vegetation communities from the European Vegetation Archive, translated into EUNIS classes,' to 'Our approach involved **1.6** million vegetation **plots** from the European Vegetation Archive, translated into EUNIS classes **level 3**, which offer a comprehensive and hierarchical habitat identification system for Europe. We modeled habitat classes based on climate, terrain, hydrology, soil predictors, and incorporated ecosystem descriptors from high-resolution remote sensing products. Using deep learning algorithms, we explored the extraction of additional features from raw multi-spectral images. We evaluated various classification strategies, including binary, multi-class, and hierarchical approaches, each varying in their constraints on habitat co-occurrence. Our ensemble of state-of-the-art algorithms, including neural networks, boosting, and bagging, was utilized for habitat modeling. Ultimately, we generated high-resolution European habitat maps at 100m resolution (Figure 1), which we validated at regional scales against independent EUNIS datasets from the Netherlands, and against local reference EUNIS maps of Austria and Southern Portugal. Our results revealed distinct recall and precision trade-offs with different classification strategies. The integration of remote sensing-based predictors significantly improved the overall predictability of habitat models, with varying impacts across habitat classes. Additionally, the inclusion of multi-spectral images enhanced the recall of most habitats, emphasizing the importance of spatial landscape structure for habitat suitability.

74. **FOSSILPOL: The workflow to process global palaeoecological data of fossil pollen for vegetation-based macroecological synthesis**

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In macroecology and biogeography, studies on past vegetation dynamics are a key factor in the exploration of biodiversity and ecosystem dynamics across time and space. This requires synthesising extensive palaeoecological data such as fossil pollen datasets. Though an increasing number of datasets are open access (e.g. Neotoma), there is a lack of guidelines for interdisciplinary data analysts to process and standardise large dataset compilation of palaeoecological records. This jeopardises the appropriate use of the data and undermines follow-up analyses. In response to this, we introduce FOSSILPOL, a workflow that facilitates the processing, harmonisation and standardisation of global fossil pollen datasets. FOSSILPOL enables the preparation of reproducible palaeoecological compilations for synthetic and cross-disciplinary analyses with macroecological, biogeographical, and palaeoecological perspectives. Our workflow documentation and website (bit.ly/FOSSILPOL) outline the most crucial decisions needed to standardise palaeoecological data, specifically using fossil pollen data. Researchers can define project-specific criteria tailored to their research questions, consolidating them into a single, readily reviewable file to enhance transparency and reproducibility. Therefore, FOSSILPOL offers an easy and transparent way to prepare for analyses that require large-scale syntheses of past vegetation dynamics.

By leveraging palaeoecological data while acknowledging its inherent strengths and limitations, researchers in any field can address pivotal research questions about past vegetation patterns. These insights, in turn, contribute to a deeper understanding of biodiversity and ecological processes, benefiting decision-makers, conservation organizations, and governmental bodies.

75. Predicting spatiotemporal community shifts in the Australian Wet Tropics

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Ecological communities across the globe are changing rapidly due to a wide range of anthropogenic threats. Because ecological communities consist of networks of interacting species, threats that directly affect some species within a community usually have indirect effects on others. While most studies have focused on the direct impact of anthropogenic threats on species, indirect effects and the influence interactions have on species' extinction risks are much less documented because of an absence of a framework to quantify the extinction risk of species to trophic cascades and co-extinctions. Using the vertebrate communities found in the tropical rainforests of Far North Australia as a case study, I will present a new framework to better evaluate extinction risks by applying a range of novel modelling techniques to (*i*) identify communities, (*ii*) infer species trophic interactions, (*iii*) construct ecological network models, and (*iv*) evaluate extinction vulnerabilities from bottom-up cascades. By subjecting these models to co-extinction simulations triggered by probable future environmental perturbations, I will show how this framework can reveal community responses to global warming via trophic interactions in terrestrial ecosystems, as well as can assist current environmental and conservation management to reduce the likelihood of co-extinction cascades in the future.

76. Large-scale monitoring of biodiversity: a Human-Assisted Molecular Identification (HAMI) method using metabarcoding while accounting for abundances and systemic errors

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Evidence of a sharp decline in insect biodiversity continues to accumulate. However, our ability to precisely monitor their decline is affected by observation scale bias and approximative species identifications, due to a lack of resources. DNA-based identification methods have been proposed as an efficient alternative to conduct large-scale biomonitoring. Metabarcoding approaches have an immense potential for large-scale biodiversity assessment, but they cannot provide estimates of abundance. In addition, rates of systemic errors (*i.e.,* false positives and negatives) are rarely considered. To overcome these obstacles, we introduce a Human-Assisted Molecular Identification (HAMI) method, a semi-automated, rapid and reliable molecular identification methodology. It relies on a combination of bioinformatic processes and para-taxonomic expertise. It was developed and tested on a highly diverse group (Coleoptera) within the 500ENI-network, a French national

biodiversity monitoring initiative covering more than 500 agricultural parcels. We assess the advantages of HAMI compared to relying exclusively on molecular identification by examining 132 communities. When relying exclusively on molecular approaches, species richness is largely overestimated due to contamination (avg. 22.4%) and to false-negatives identification associated with primer biases occur (avg. 18.62%). Metabarcoding has the potential to achieve large-scale monitoring and reduce knowledge gaps about communities composition, species distribution and the anthropic factors driving biodiversity change, but our results underline that their use alone is insufficient. The combination of molecular methodologies and para-taxonomists expertise in HAMI considerably reduces metabarcoding biases, identifies specimens requiring further investigation (e.g., species without barcodes), streamlines the time-consuming taxonomist expertise step and provides information on relative abundance.

77. **Reliability of presence-only data for assessing plant community responses to climate warming**

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Climate warming has triggered shifts in plant distributions, resulting in changes within communities, characterized by an increase in warm-demanding species and a decrease in cold-adapted species - referred to as thermophilization. Researchers conventionally rely on co-occurrence data from vegetation assemblages to examine these community dynamics. Despite the increasing availability of presence-only data in recent decades, their potential has largely remained unexplored due to concerns about their reliability. Our study aimed to determine whether climate-induced changes in community dynamics, as inferred from presence-only data from the Global Biodiversity Information Facility (GBIF), corresponded with those derived from co-occurrence plot data in Norway. To assess the differences between these datasets, we used the Community Temperature Index (CTI) and the thermophilization index and assessed how different the indices were when derived from each of the datasets. We assessed the interchangeability of these two datasets, either used alone or together, for model calibration and CTI prediction. Preliminary findings favored transfer functions involving both datasets. Subsequently, we compared CTI and thermophilization index values from the pseudo-plots to a spatially and temporally paired dataset of co-occurrence plots. Results showed similar values for the CTI and thermophilization index between the two datasets. Our assessment demonstrated the potential of employing presence-only data for evaluating community responses to climate warming, specifically by quantifying the Community Temperature Index (CTI) and thermophilization and we propose an outline that can be applied to global change research.

78. **A scalable machine learning approach to assess the combined effect of habitat loss and climate change on biodiversity**

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Climate change and habitat loss are major threats to biodiversity, which combined effects at local and global scales are not clearly understood. To improve our understanding of the complete response of biodiversity to these intertwined drivers, we propose a novel machine-learning approach that builds upon two fundamental generalisation in ecology, namely species-area relationships (SAR) and environmental niche. Focusing on European plant species within six distinct vegetation groups, we draw from an extensive dataset of 11,681 vegetation plots from the European Vegetation Archive to construct group-specific SAR curves, that we combine with plant-relevant environmental predictors derived from CLM5 simulations to train a neural-network-based model that predicts local species richness. Validation against independent datasets demonstrates the model's capability to reasonably predict species richness across the vegetation groups. Furthermore, through the application of explainable AI techniques based on Shapley values, we dissect the underlying processes guiding the model's predictions, allowing to disentangle vegetation group-specific drivers of species richness at a global scale. The scalability of our approach makes it highly relevant for use in attribution studies, offering the means to map species richness under diverse climate and land-use scenarios. In prospect, we intend to employ our approach to conduct comprehensive biodiversity change attribution studies.

79. **Unveiling Climate-Biodiversity Interactions: The influence of nature futures biodiversity scenarios on regional climate**

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Optimizing climate change mitigation efforts without compromising biodiversity conservation poses a significant challenge in addressing global change. A key aspect of meeting this challenge involves enhancing our understanding of the intricate relationship between biodiversity and the climate system. While substantial progress has been made in predicting how biodiversity responds to a shifting climate, uncertainties persist regarding the consequences of these changes on the climate system. A major impediment lies in the incorporation of biodiversity within climate models, necessitating a bridge between two distinct disciplines: biodiversity modeling and climate modeling, each characterized by their unique paradigms and methodologies. In this context, we present an initial overview of the obstacles and prospects associated with the integration of biodiversity scenarios into the coupled biosphere-atmosphere regional climate model, COSMO-CLM^2. We elucidate how the incorporation of different biodiversity scenarios can have feedback effects on regional climates. Our approach involved running COSMO-CLM^2 simulations for Europe utilizing spatial land cover scenarios derived from the Nature's Futures Framework, which were further enriched with data from biodiversity inventories and habitat distributions sourced from EUNIS (European nature information system) and EVA (European Vegetation Archive). By furnishing a comprehensive examination of how the implementation of specific Nature's Futures scenarios can influence regional climate evolution, we lay the groundwork for future collaboration between Earth system modeling and biodiversity modeling. This collaboration will be instrumental in the development of effective mitigation strategies to combat the impacts of global change.

80. Rewiring potential of plant-bird pollination networks in the Americas

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Global change leads to reorganization of species interactions across ecological networks. This ‘interaction rewiring’ can occur both via the establishment of new or disappearance of existing interactions and the changes in interaction strengths between species. As rewiring can drastically alter nature’s functions, determining the likelihood of interaction rewiring and predicting the future structure, functioning, and stability of ecosystems is paramount. The potential of a species to rewire its interactions can be quantified as the interaction niche breadth, which is defined as the trait value range of interaction partners. Here, we quantified the interaction niche breadths in mutualistic plant-bird pollination networks in the Americas, including 867 plant and 318 bird species to understand the large-scale variation in rewiring potential. We used trait-based machine learning models to predict interaction probabilities across the metanetwork that includes all 275,706 possible plant-bird-pairs. We quantified the fundamental interaction niche breadth of each species in the metanetwork by calculating the functional richness across each species’ predicted interaction partners. To understand the spatial variation in rewiring potential, we averaged the fundamental niche breadths within plants and birds separately in 78 empirical pollination networks. The interaction niche breadths of plants tended to be narrower than those of birds, and the rewiring potentials at these trophic levels did not covary. Moreover, the average interaction niche breadths of plants, but not birds, increased with absolute latitude. In the future, the networks with high interaction rewiring potential will likely have a better ability to adapt to the intensifying global change effects.

81. Effect of grazing intensification on dung beetle biodiversity-ecosystem functioning relationship in a biogeographical context

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Rebolledo[48], Angela Roggero[15], Ada Sánchez-Mercado[49], László Somay[19], Jutta Stadler[50], Pejman Tahmasebi[46], José Darwin Triana Céspedes[32], **Ana M. Santos[51]**

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Landscape modification and intensification of farming practices generally reduce species richness and functional diversity, although with some exceptions and regional differences. We assessed the relationship between grazing intensity, climate, biodiversity, and ecosystem functioning on global pasturelands, a human-modified ecosystem distributed worldwide. Specifically, we studied the determinants of several aspects of dung beetle (Coleoptera: Scarabaeoidea) diversity (abundance, species richness, and functional diversity) and their consequences on the provision of dung removal, a key ecological function associated with several ecosystem services, including nutrient cycling, bioturbation, and secondary seed dispersal. To do this, we performed paired field experiments using a standardized protocol in pasturelands of 38 localities scattered worldwide, albeit with better coverage of the Americas and Europe. These experiments compared the variation in dung beetle diversity and dung removal rates between pastures subject to low and high cattle stocking rates as a measure of management intensity. Species richness was significantly higher in low-intensity pastures, but abundance, dung removal and functional diversity showed no overall differences between low- or high-intensity pastures. However, dung removal increased with species richness across sites, while functional diversity consistently enhanced the provision of this ecosystem service in low-intensity pastures. This implies that, despite intensified cattle stocking rates, ecosystem services related to decomposition and nutrient cycling can be maintained when a diverse dung beetle assemblage inhabits human-modified landscapes. Therefore, actions to maintain functional diversity and fragments managed extensively at the landscape level will improve biodiversity conservation, enhance matter and energy cycles, and maximize ecosystem service delivery in pasturelands.

82. Orphans of the past: the global distribution, dispersal and extinction risk of plants with megafaunal fruits

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Plants with megafaunal fruits (>4 cm) have relied on dispersal by megafauna and other large-bodied vertebrates (> 40 kg) throughout their million-year evolutionary history. How megafruit plants have persisted in contemporary ecosystems after the Pleistocene extinction of most megafauna remains an evolutionary enigma. By integrating global data on traits, seed dispersal interactions, phylogenies and geographical occurrences for >1500 megafruit plants, we show that many megafruit species (613 species, 40%) interact with contemporary dispersers, including humans, megafauna (e.g.,

elephants), secondary dispersers (e.g., rodents), or water, providing an explanation for their persistence. These megafruit species often have large geographical range sizes, strongly contrasting the 128 (up to 300) megafruit species that are currently threatened with extinction, suffer from small range sizes, and lack suitable co-occurring dispersers, primarily on isolated islands in Australasia, IndoMalay and Madagascar. Our results illustrate how the Pleistocene extinctions and ongoing defaunation limit seed dispersal of many plant populations with megafaunal fruit, but humans may have replaced megafaunal dispersal functions for s subset of taxa.

83. Low redundancy drives functional diversity and vulnerability in Arctic ecosystems

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Accelerating species loss due to rapid environmental change caused by humans threatens the functioning and stability of ecosystems around the world. Understanding how variation in the diversity of species and their functional traits influences the resiliency of ecosystem functioning and structure can help us better predict the future and inform conservation action to protect our most vulnerable ecosystems. In general, species richness is thought to drive high functional diversity and redundancy, which increases ecosystem resiliency to species loss. However, at high latitudes, low species richness and extreme adaptations to harsh environments has the potential to give rise to high functional diversity but low redundancy, where even the loss of a few species may threaten the functioning and structure of the entire assemblage. To test this idea, we modelled the distribution of all Canadian vertebrates, plants, and butterflies to understand spatial variation in functional diversity, redundancy, and resiliency to species loss. We found that while plant and butterfly functional diversity decreases towards higher latitudes, vertebrate functional diversity increases dramatically, driven by dissimilarity between bird and mammal assemblages in Arctic ecosystems. This decreased functional redundancy in the Arctic results in high vulnerability of those ecosystems to species loss. The loss of imperilled species or megafauna from high-latitude ecosystems results in the loss of up to 40% of functional diversity, likely collapsing terrestrial food webs. Therefore, rapid conservation action such as the establishment of protected areas and monitoring networks may be necessary to ensure the persistence of these vulnerable communities.

84. Climate influences the spatiotemporal variation of bird functional diversity in a global biodiversity hotspot

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Climate change significantly impacts bird populations, affecting various aspects such as range shifts and breeding behaviour. As a result, the functional diversity of bird communities changes. Since information on abundance is usually unavailable, previous studies assessing functional diversity are based on the presence and absence of species alone, limiting inferences. We use an extensive dataset from the global biodiversity hotspot, national park and World Heritage Site, Wadden Sea, which provides detailed population data of breeding and migratory birds on the East Frisian Islands over 25 years. We assess the impact of climate trends on the functional richness and functional dispersion of bird communities in relation to island characteristics and potential functional diversity corrected for species richness.

We show that the development of Functional Diversity over time differs between breeding and migratory birds and between islands. Generally, bird species diversity increased between 1996 and 2021 while corrected Functional Diversity decreased. Rising air temperatures lead to a lower functional dispersion than expected based on the diversity of breeding birds. For migratory birds, functional richness increased at the upper part of the range due to rising temperatures, while decreasing precipitation led to a decrease in functional dispersion.

Overall, the species diversity of breeding and migrating birds is increasing, but the functional richness and functional dispersion are lower than expected based on species richness. This can be attributed to climate change and island characteristics as additional factors for species and functional diversity on islands.

85. Mutualistic interactions with seed-dispersing vertebrates is linked to global and regional variation in plant dispersal trait syndromes

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Mutualistic interactions between fruits and frugivores (i.e., fruit-eating and seed-dispersing animals) are prominent in tropical rainforests, and may influence diversification and diversity. These interactions are facilitated by the evolution of functional trait matching between plants and frugivores, and may explain the evolution of 'fruit dispersal syndromes' as the result of co-evolutionary selective pressures from interacting partners. Here, we integrate global occurrence and novel trait data for a tropical plant lineage (Annonaceae) with data for frugivorous birds and mammals and applied functional diversity metrics, structural equation models and fourth corner analysis to evaluate whether there is a match in the global distribution of plant and frugivore taxonomic richness and dispersal syndromes. We hypothesize that co-diversification and selection on co-evolving traits has shaped plant-frugivore interactions and co-occurrence across broad-scale assemblages. We show that global variation in Annonaceae species and functional diversity was strongly influenced by the diversity and trait matching of co-occurring frugivorous mammals, whereas frugivorous birds affected

Annonaceae diversity in the Asia-Pacific and Afrotropic regions. Additional direct and indirect effects of climate, elevation, and net primary productivity on plant and animal diversity were found. Our results suggest that frugivorous mammals have shaped pantropical variation in Annonaceae species richness and traits on a global scale, possibly through mutualistic co-evolutionary dynamics. However, frugivorous birds have influenced the species and trait composition of Annonaceae assemblages at more regional scales, i.e., within Asia-Pacific and the Afrotropics. This suggests that biogeography and scale-dependence modulate how mutualistic interactions promote diversity.

86. Predicting plant communities: a matter of species and traits!

Gabrielle Deschamps, Laboratoire d'Ecologie Alpine LECA - Université Grenoble Alpes UGA, Gières, France

Predicting species distributions, and the community structure they belong to, in response to environmental change is a burgeoning field. Notably, considering that communities are not only the mere sum of species but also are diverse in terms of traits and functions is now seen as crucial. Yet, this is not clear how to model these diversity facets like community-trait mean and variance. Some prefer to model species distributions first and then rebuild community-trait mean and variance through stacking of predictions, others directly model community metrics in function of environmental covariates. While these two approaches have pros and cons, they were neither systematically compared nor were they combined into a unified and optimized framework. In this talk, we first introduce a comparative analysis carried out using a large plant community data in the French Alps, where we show that directly modeling community metrics like trait mean and variance is safer and reach better performance that going through species modeling first. The performance gap even gets sharper when extrapolating to unknown conditions.

We then introduce a machine learning model that combine these two approaches by optimizing both objectives (in terms of community composition and community-trait values). We show that this approach leads to improved community composition as measured by their Jaccard indices, and also improves community-trait predictions

This approach holds great promise to enhance community predictions, using predicted or directly observed functional indices, potentially through satellite data. Looking ahead, it offers exciting prospects for refining our comprehension and predictions of plant communities.

87. Spatiotemporal variation in dietary strategies in birds

Marta A. Jarzyna, The Ohio State University

Seasonal variation in avian trait characteristics, such as foraging behavior, digestive physiology, and dietary preferences, is well-documented in the scientific literature. For instance, resident bird species often display plasticity in their feeding habits, transitioning from arboreal feeders during the breeding season to ground foragers in the wintering season. Additionally, birds can shift their diets from granivorous or frugivorous preferences in winter to insect-based diets during the breeding season. Furthermore, species' associations with different land covers vary across seasons and are influenced by resource availability, affecting their dietary niches. Despite the widespread recognition of seasonality in avian dietary traits, there has been a notable absence of comprehensive quantification of temporal variability in dietary characteristics across the globe. Here, we use SAviTraits 1.0—a compilation of species-specific dietary preferences and their known intra-annual variation for over 10,000 of the world's extant bird species—to quantify temporal variation in dietary strategies of birds across the globe. Our analysis corrects all estimates of dietary variation for the level of effort expanded. Our findings reveal that temporal variability in avian diet, both in its raw form and when corrected for effort, is most pronounced in avian assemblages in North America, Europe, and Asia. Notably, other regions, such as parts of northern Africa and New Zealand, also host bird species with highly variable diets. Our results shed light on the global spatiotemporal dynamics of avian dietary strategies and provide valuable insights into the ecological adaptations and plasticity of birds in response to changing environmental conditions.

88. Pantropical plant dispersal out of Madagascar's forests

Jan Hackel, Universität Marburg, Germany

Madagascar is renowned for its highly diverse and unique biota. Repeated immigration from other areas and diversification in isolation are thought to have generated its outstanding levels of endemism. We show that, conversely, a clade of c. 120 grass species has spread across the tropics from its Malagasy origin. Out of its ancestral forest understory habitat, the group has radiated into diverse niches and colonised areas as distant as the Neotropics. Timing as well as patterns of diversification on the island suggest a driving role of Miocene mountain uplift. This challenges the simplifying notion of Madagascar as a sink of immigrant lineages. Instead, our results suggest that its dynamic geological history also made it a source and laboratory of diversification, contributing species across the tropics. They also emphasise the highly threatened Malagasy forests as evolutionary cradles of diversity.

89. The legacy of ecological and evolutionary processes in phylogenetic tree shape

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Phylogenies are important representations of evolutionary history. Their branching patterns reflect processes which shape global patterns of biodiversity over millions of years. Processes shaping diversity act directly on diversification, with speciation and extinction depending on either diversity, environment, or traits. However, until now, phylogenies simulated in birth-death models that account for diversity dependence, environment dependence or trait dependence show a different shape and are more balanced when compared to empirical phylogenies. Here, we use a biogeographic simulation model to understand which processes drive global biodiversity and how they are reflected in the phylogenetic tree shape. We simulated the emergence of clades in a spatially explicit, process-based model under five different diversification models: a base model, a simple competition model, an environmental diversification model, a trait-based diversification model and a trait-based competition model. Surprisingly, we find that competition models produced phylogenetic tree shapes much closer to observed phylogenetic tree shapes in tetrapods. Since competition increases extinction, this suggests that extinction plays an important role in driving biodiversity and is reflected in the phylogenetic tree shape. Additionally, different empirical clades support different diversification modes, suggesting that different processes act strongly on different clades. These results highlight the importance of studying extinction to understand how biodiversity has been shaped globally over millions of years.

90. Africa as an evolutionary arena for large fruits

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Strong paleoclimatic change and few Late Quaternary megafauna extinctions make mainland Africa unique among continents. Here, we hypothesize that, compared with elsewhere, these conditions created the ecological opportunity for the macroevolution and geographic distribution of large fruits. We assembled global phylogenetic, distribution and fruit size data for palms (Arecaceae), a pantropical, vertebrate-dispersed family with >2600 species, and integrated these with data on extinction-driven body size reduction in mammalian frugivore assemblages since the Late Quaternary. We applied evolutionary trait, linear and null models to identify the selective pressures that have shaped fruit sizes. We show that African palm lineages have evolved towards larger fruit sizes and exhibited faster trait evolutionary rates than lineages elsewhere. Furthermore, the global distribution of the largest palm fruits across species assemblages was explained by occurrence in Africa, especially under low canopies, and extant megafauna, but not by mammalian downsizing. These patterns strongly deviated from expectations under a null model of stochastic (Brownian motion) evolution. Our results suggest that Africa provided a distinct evolutionary arena for palm fruit size evolution. We argue that megafaunal abundance and the expansion of savanna habitat since the Miocene provided selective advantages for the persistence of African plants with large fruits.

91. Two debates in one go: the role of dispersal vs vicariance and of equilibrium vs non-equilibrium in Madagascar

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Madagascar is a central protagonist in two classic discussions in biogeography: the debate on vicariant versus dispersal origins of species assemblages; and the debate on equilibrium versus non-equilibrium explanations for diversity patterns. Here we addressed these two topics simultaneously by employing a whole community species-level phylogenetic approach to study the biogeographical history and diversification dynamics of the four major tetrapod groups on Madagascar: amphibians, birds, mammals, and squamates. We compiled phylogenetic data for the complete native assemblage of Madagascar for these four groups, including recently extinct species and newly discovered taxa. We developed a novel phylogenetic method for continental island biogeography that can quantify the probability that communities were the result of vicariance or over-water dispersal. We find strong evidence that the extant tetrapod fauna of Madagascar did not arise through vicariance at the island's origin. Phylogenetic data show in situ diversification across all taxonomic groups, with between 39-54 in-situ Malagasy tetrapod radiations identified. Speciation and extinction rates are disparate between endo- and ectothermic species, with equilibrium dynamics, although not saturation, detected in the latter. Overall, we present a unified continental island framework that elucidates the absence of vicariance, prevalence of insular radiations, and mixed signals of equilibrium dynamics in one of the world's most biodiverse islands.

92. Do the species with large geographic ranges diversify faster?

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Range size is a universal characteristic of every biological species, and is often assumed to influence diversification rate. However, the relationship between range size and past and future diversification of species remains elusive. On one hand, there are strong theoretical arguments that large-ranged species should have higher rates of diversification. This theoretical view is challenged by observations that small-ranged species are often phylogenetically clustered and form spatially localized hotspots, claimed to be the cradles of biodiversity. The research of range-size evolution is a notoriously complex task, because the range sizes evolve not only anagenetically (range expansion or contraction), but also cladogenenetically (range size change between mother and daughter species during speciation). Here use a state-dependent diversification model covering both anagenetic and cladogenetic changes in range size, and apply it to the phylogenies and range size data of various tetrapod groups. We show that in general, large-ranged species diversify faster, as theoretically expected, and that the phylogenetic clusters of small-ranged species typically reflect past fragmentation of large-ranged species, rather than ongoing radiations. However, the analysis of residual (concealed) variability of our models suggests that there are multiple taxa where this general pattern is reverted and small-ranged species indeed diversify faster. These ongoing radiations of small-ranged species typically take place in volant taxa inhabiting insular landscapes, such as oceanic archipelagos. Our results suggest that, while range size is an important factor influencing species diversification, its effect in real-world systems is often locally modified or even inverted by idiosyncratic geographic context.

93. Historical biogeography and patterns of diversification in African freshwater fishes of the genus Bryconaethiops revealed by phylogenomics (Teleostei: Alestidae)

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Five species of the African alestid genus *Bryconaethiops* are found in freshwater environments ranging from the coastal rivers of southern Nigeria to the Chambezi river in northeast Zambia, with a majority in the Congo basin. No study has investigated interspecific phylogenetic relationships, molecular diversity, or biogeography across their distribution range. We used 1,436 ultraconserved element loci (202,478 bp) and mitochondrial genomes containing 13 protein-coding genes (16,764 bp) from 29 specimens of the five species of *Bryconaethiops* and other alestids as outgroups. The resulting phylogeny reveals that *B. quinquesquamae* (Nigeria) is sister to all species, followed by *B. mocquardianus* (Gabon and Equatorial Guinea), and the clades *B. macrops* (Congo uplands) + *B. yseuxi* (lower Congo) and *B. boulengeri* (Congo) + *B. microstoma* (Congo lowlands). Mitogenome polymorphisms indicate that *B. macrops* is subdivided into the subclades Lulua/Mpozo of the middle Congo and Dja/Malagarasi of Cameroon and Tanzania. Relationships reveal patterns of sympatric occurrence for the sister species *B. boulengeri* and *B. microstoma* in the middle Congo basin. The separate and strongly supported Gabonese lineage requires the taxonomic revalidation of *B. mocquardianus* for the Ogooué basin of Gabon and Equatorial Guinea. The effects of allopatric speciation followed by secondary contact determined by geomorphological processes and

elevational gradients are identified as promoters of species diversification in Central Africa. Findings provide evidence for a higher species diversity in *Bryconaethiops* and open up new paths for studying the historical biogeography of African freshwater fishes.

94. Habitat specialization predicts demographic response and vulnerability of floodplains birds in Amazonia

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The annual flooding cycle of Amazonian rivers sustains the largest floodplains on Earth, which harbor a unique bird community. Recent studies suggest that habitat specialization drove different patterns of population structure and gene flow in floodplains birds. However, the lack of a direct estimate of habitat affinity prevents a proper test of its effects on population histories. In this work, we used occurrence data, satellite images and genomic data (Ultra-Conserved Elements) from 24 bird species specialized on a variety of seasonally flooded environments to classify habitat affinities and test its influence on evolutionary histories of Amazonian floodplain birds. We demonstrate that birds with higher specialization in river islands and dynamic environments have gone through more recent demographic expansion and currently have less genetic diversity than floodplain generalist birds. Our results indicate that there is an intrinsic relationship between habitat affinity and environmental dynamics, influencing patterns of population structure, demographic history and genetic diversity. Within the floodplains, historical landscape changes have had more severe impacts on island specialists, making them more vulnerable to current and future anthropogenic changes, as those imposed by hydroelectric dams in the Amazon Basin.

95. Phylogenetic Lévy models reveal pulsed niche evolution underlying alpine biome shifts

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That flowering plants dominate the worlds terrestrial biomes ultimately results from niche evolution within phylogenetic lineages. Comparative approaches have typically addressed transitions between discrete biomes, but the mode of evolution of the underlying niches, which are of an inherently continuous nature, remains poorly understood. In particular, so far approximately all studies have only considered models of gradual evolution (e.g. Brownian Motion or Ohrnstein-Uhlenbeck models), rather than models that include episodes of rapid "jump-like", pulsed evolution, known as Lévy processes. Clades of species that diversified across mountain ranges are particularly suited to investigate the mode of niche evolution, because of great niche diversity in close geographic proximity and evidence for recurrent biome shifts. Here we present recent results that consider Lévy models alongside models of gradual evolution to better understand the nature of phylogenetic niche evolution underlying biome shifts into and out of alpine areas. We first describe a

new, continuous climatic niche proxy (based on spatial points' vertical distance to the theoretical local climatic tree line), and test whether its mode of evolution differs across three clades of mountain plants (*Primula, Ranunculus, Lupinus*). We find strong evidence for Lévy processes (i.e., pulsed niche evolution) in some, but not all clades. We then explore whether morphological traits typically associated with alpine areas also evolve in a pulsed, rather than gradual fashion. Here we find a striking contrast between tropical and temperate mountain ranges. Overall, these results emphasize the need to re-consider phylogenetic models of pulsed, rather than gradual evolution.

96. **A general framework for randomization analyses in SDM**

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In the field of niche and distribution modeling, data are often subject to multiple interacting sources of uncertainty, bias, and autocorrelation that make them difficult to analyze using traditional statistical approaches. Randomization is often used in statistical tests in order to estimate distributions that are difficult to specify analytically. Decades of development in the niche modeling literature have resulted in randomization tests that allow us to study phenomena as disparate as variable importance, methodological bias, and patterns of niche evolution. Here we present a novel conceptual framework that allows us to both take a synthetic view of existing tests and highlight potentially fruitful avenues for future methodological exploration. We also discuss some interesting patterns that appear when you start to consider this literature as a whole.

97. **The impact of taxonomy on species distribution modelling: the overlooked pitfall of online biodiversity databases**

Bryony Blades, University of Oxford

Over the last two decades, digitization of natural history collections has increased exponentially, allowing research to tackle questions on a previously impossible scale. However, despite the proliferation of studies using these resources, both geographic and taxonomic biases are well-understood to affect data quality and availability, and efforts have been made to develop methods that mediate their effect. Here, I show that taxonomic accuracy of the study taxa is a further, and oft overlooked, concern around data quality, which is particularly concerning given the general decline in taxonomic studies. Using a recently revised genus of dung beetles, *Catharsius*, and multiple species distribution modelling algorithms, I show how outputs of SDMs vary when using occurrence points representing both revised and unrevised taxonomy. With the latter, maps of habitat suitability and response curves are unable to identify highly suitable areas or conditions, with implications for conservation planning in the face of climate change. Additionally, whilst commonly used evaluation metrics of SDMs show models using unrevised taxonomy to perform poorly, they do not perform the worst, underlining that they cannot be relied upon to flag problems with taxonomic accuracy post-factum. Akin to the rare species modelling paradox, it is likely those species that are difficult to identify and classify that would benefit most from predictive models, and yet whose uncertain taxonomy presents the greatest impediment to success. I suggest ways to overcome this pitfall in order to maximise usefulness of growing online repositories in combatting both Linnean and Wallacean shortfalls and, subsequently, biodiversity loss.

98. **Watch out for niche truncation: towards hierarchical species distribution models ?**

Antoine Guisan, University of Lausanne, Lausanne, Switzerland

Species distribution models (SDMs) have become a major tool in biogeography, especially in the context of global change assessments. A key application of SDMs is to derive projections in time, e.g. under climate change. SDMs are also based on several assumptions, one being that to make such temporal projection, the full realized environmental niche must be captured. Yet, the niche has a high risk to be truncated if the geographic – and associated environmental – range used to fit the model is smaller than the range occupied by the species, leading to potential mistakes when making temporal projections. A solution to avoid such niche truncation is to build SDMs in a hierarchical nested way, from global to local. Such approaches have already been applied to SDMs, to model invasive species, to downscale large scale models, to support species conservation, or to improve climate change projections. They were recently implemented in the new N-SDM pipeline in R to derive predictions for large numbers of species. However, the importance of using such hierarchically-nested approach has remained rather hidden and confidential so far in the SDM literature. The aim of this talk is to present a review and synthesis of the developments up to now, and to identify solutions and remaining challenges.

99. **Projecting the untruncated response of biodiversity to climate change in Switzerland**

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Climate projections for Switzerland indicate that the country can expect drier summers, increased precipitation, and less snowy winters. One consequence of these changes for biodiversity is shifts in species' distributions. Species distribution models that incorporate climate data are valuable tools for projecting and mapping prospective species distributions under climate change scenarios. To accurately model species' responses to climate and project potential future distributions, the modeling data should encompass the full spectrum of environmental conditions in which the species occurs globally. Currently, Switzerland lacks comprehensive climate-driven biodiversity projections, posing a challenge for guiding effective conservation efforts. Our study aimed to address this gap by evaluating the potential impact of climate change on Switzerland's biodiversity using a climate envelope modeling approach and species occurrence data that covered the climatic conditions encountered across the full species' ranges. We quantified the relationship between the baseline climate and the spatial distribution of 7,291 species. We projected future climate suitability for three 30-year periods using climate projections based on two concentration scenarios. We evaluated percentage changes in projected climate-suitable areas, examined geographical shifts, and presented illustrative maps for main taxonomical groups. Overall, our results indicated that projected climate changes could decrease the suitable area of 41% of the species evaluated, whereas 53% would experience increases. The most consistent geographical shifts were upward, southward, and eastward displacements of the areas of high climate suitability. Our models and maps provide guidance for spatial planning by identifying future climate-suitable areas for biodiversity conservation.

100. What can the analysis of trait coordination tell us about plant functional responses to insularity?

Gianluigi Ottaviani, Research Institute on Terrestrial Ecosystems (IRET), National Research Council (CNR), Porano, Italy

Plant functional traits are increasingly examined in insular systems because trait-based studies can shed light on which eco-evolutionary drivers contribute to shape island species' persistence and distribution. So far, this effort has concentrated on patterns of trait values (average, functional diversity), whereas coordination between pairs of traits remains unexplored – especially whether trait coordination varies predictably along insularity gradients. This constitutes a relevant lack because bivariate trait coordination analysis can identify fundamental plant functional spectra and strategies, and helps assessing plant responses to changing abiotic conditions. To start bridging this gap, I provide a conceptual and analytical framework that facilitates the inclusion of trait coordination in functional island biogeography. I illustrate – with a case study focused on persistence traits of edaphic island plant specialists – what type of insights can be gained by investigating the response of trait coordination (integrating trait co-variation at the intra- and interspecific level) to insularity. I asked two questions, namely whether the strength of the relationship (R^2) increases (Q1), and the direction of the relationship (slope) decreases (Q2) with increasing insularity. Results tended to positively answer both questions. Multiple lines of evidence suggest a selective forcing towards tighter and better/more strongly coordinated strategies (Q1), and a tendency to functional trade-offs (Q2) with stronger insularity. I discuss ecological and biogeographic implications linked to the observed shifts in trait coordination. I conclude by spotlighting a few take–home messages and possible future research avenues that would benefit from including trait coordination in functional and conservation island biogeography.

101. Assessing the global connectivity of a local community through seasonal migration: a tale from the High-Arctic

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Millions of migratory animals travel the globe seasonally between their breeding and non-breeding grounds. In doing so, they create ecological links between their breeding and non-breeding grounds and maintain meta-ecosystems. Since communities often host several migratory species, migrations can generate vast networks of ecological connections between a community and different regions of the globe. A better understanding of these networks would help us to understand the effects of external stressors on communities and ecosystems. However, we currently lack conceptual, theoretical and empirical developments in this direction. We provide a conceptual framework adapted from a basic network approach to characterize migration patterns at the community level, and present empirical applications with a case study in the terrestrial High Arctic. We focus on Bylot Island, a community used by 30 migratory species to breed, we found that species breeding in the same community during summer can disperse to hundreds of ecoregions during winter with little spatial overlap. We observe that the network is not randomly structured, and presents subgroups of species wintering in common regions of the world (modules). If we consider species abundance and biomass, we see a finer resolution of modules and a more asymmetric connectivity with only a few ecoregions of the world hosting the majority of the community's biomass and abundance during the wintering period. Highlighting the structure of migratory connections in communities provides a better understanding of how environmental changes occurring worldwide can propagate spatially via migratory species, affecting distant but connected communities and ecosystems.

102. Mechanistic modelling of medically important snails: challenges and opportunities

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Climate change has profound consequences on infectious disease, including on schistosomiasis, a snail-borne parasitic disease that affects over 150 million people, chiefly in Africa. Even though many studies have investigated the relationship between environmental conditions and snail-borne disease, the effect of climate change on schistosomiasis is still highly uncertain. Here, using the schistosomiasis vector *Bulinus truncatus* as an example, we demonstrate the potential of mechanistic modelling to predict the impacts of climate change on vector snail distributions and highlight several challenges. The current and future distribution of *B. truncatus* was estimated using a mechanistic model based on thermal performance curves estimated from lab-based experiments. For comparison, the distribution of the same species was estimated using an ensemble of correlative species distribution models (SDMs). Both models were able to reproduce the outer range limits of *B. truncatus*, while the SDMs had higher accuracy. Both models predicted increased suitability in Europe with climate change, possibly indicating increased future schistosomiasis risk. However, in the Sahel region, the mechanistic model showed that climate change will push temperatures to well outside the suitable range for *B. truncatus*, while the SDMs relied on extrapolation and predicted that suitability increased. This demonstrates a key strength of mechanistic models, which is that their outputs are directly rooted in observed environmental responses of fitness traits. The main challenges to continental-scale mechanistic modelling of freshwater snail distributions are the lack of experimental data and the identification and characterisation of habitats, which can have wildly different sizes and microclimates.

103. Mountain plants survived the ice ages in a network of glacial refugia in the southeastern Alps, although with disparate demographic dynamics

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The Pleistocene glaciation was the major event shaping the survival, distribution and demography of biota in the temperate zones since ca. 2.5 million years until the onset of human civilization. Growing glaciers forced shifts in the distributions of mountain plants to climatically suitable refugia, most often weakly glaciated peripheral mountain ranges. Although peripheral refugia in the European Alps are well known, we lack a deeper understanding on their internal structure and population dynamics. Here we studied nine species from the Southern Limestone Alps, an area hypothesized to comprise multiple glacial refugia, to gain understanding of the population structure and demography within and among refugia. Genetic structure analyses based on RADseq and 3RAD sequences revealed significant structure, an indirect indication for survival of multiple populations. Although lack of perfect congruence among their borders, we hypothesize western, central and eastern refugia in the Southern Limestone Alps, which roughly correspond to previous hypotheses. A deeper exploration of the central refugium using a demographic modelling approach revealed two further peripheral refugia and survival on ice-free peaks within ice-sheets in the northern Dolomites. However, ecologically segregated species responded differently to glaciation. While subalpine species showed reduced population sizes during the Pleistocene glaciation and a population expansion towards the present, nival to alpine species often had bigger population sizes during the last glacial than at present. Our results support a complex scenario of multiple interconnected refugia, which contributes to our understanding how glacial refugia preserved not only species, but also high levels of intraspecific genetic diversity.

104. Historical biogeography of New World Killifishes recapitulates geographical history in the Gulf of México watershed

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We reconstructed phylogenetic relationships of New World killifish (Funduloidea) and synthesized their biogeographic history, using two nuclear and three mitochondrial genes for 135 species, with four fossil calibrations, to generate a time-calibrated phylogeny. We estimated diversification rates, ancestral areas (Nearctic or Neotropical), and ancestral habitat (coastal or upland) for each node, melding this information with detailed literature review. Funduloidea originated in the Late Cretaceous and diversified from Late Paleocene to present. Only Cyprinodontidae expressed an accelerated rate of speciation, beginning ~11.02 Ma. Neither viviparity, marine-to-freshwater transition, nor adaptive radiation consistently accelerated speciation, but the latter two occurred within Cyprinodontidae, contributing to its accelerated speciation rate. Funduloidea is largely Nearctic, but invaded the Neotropics repeatedly. The group has a coastal origin, but invaded inland many times. Diversification patterns suggest (1) sea-level falls isolate coastal populations, but increase island accessibility and (2) climatic cooling facilitates invasions of temperate species into the tropics. For continental lineages, courses of ancient river drainages explain lineage distributions, including enigmatic disjunctions in Goodeidae and Fundulus. Antiquity, adaptability, and dynamic geography in the Gulf of México watershed explain the living diversity of Funduloidea. Phylogenetic branching suggests some diversification occurred via barrier displacement and a coastal speciation pump, but overall, it appears a suite of speciation ‘tools’ contributed to total diversification, including time for speciation, transitions to freshwater, dispersal, vicariance, adaptive radiation, and viviparity.

105. A New View of Marine Biodiversity

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Manifold studies exist to determine species richness drivers in terrestrial systems, but corresponding work is comparatively rare in the marine realm. However, marine biodiversity studies may be key to understanding broad scale biodiversity patterns. Temperature and primary productivity, commonly invoked explanatory variables for biodiversity despite being tightly correlated on land, are decoupled in the open ocean. The discriminatory power of such an analysis further increases when considering depth, an oft-neglected axis along which species richness varies. Here, we present a first look at

depth-structured biodiversity patterns of three families of fishes (i.e., Beloniformes, Scombriformes, and Gadiformes) in the Atlantic Ocean. We collected occurrence data for over 280 species of fishes, generated 3D correlative ecological niche models (ENMs) for each and projected the ENMs back into geographic space. Finally, we combined resulting distributions to map species richness of each family as a continuous volume in the Atlantic. This analysis was all done using a recently established workflow facilitated by the R package voluModel. To better visualize species richness volumes, we created a new tool to map transects of species richness by depth within a given volume. The resulting plots emphasize that while horizontal diversity patterns differ among the three groups, strikingly concordant patterns emerge when considering vertical biodiversity patterns. Finally, we suggest how oceanographic processes beyond temperature and primary productivity may be shaping broad-scale species richness patterns in the open ocean.

106. The biogeography of marine vertebrate trophic structures

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Biogeographic regions arise due to constraints on species ranges, fostering lineage divergence as a result. Yet convergent evolution means that evolutionary distinct lineages can share similar characteristics when subjected to similar environmental conditions. The ecological convergence of distinct regions has been demonstrated in terrestrial communities, but it remains uncertain if marine systems exhibit similar patterns given the potential greater ease of dispersal in the ocean. Using information on the dietary preferences of marine vertebrates, we develop a new regionalisation of the ocean that groups regions with similar trophic community structures. Six distinct trophic structures emerge, largely explained by temperature, productivity and depth, and regions with analogous environments support comparable numbers of species with similar feeding strategies. These findings support the notion that independently evolving sets of marine species can converge into functionally analogous communities when exposed to similar environmental conditions. They also establish a benchmark for examining how climate change will affect the functioning of marine trophic assemblages.

107. Deep Time Historical Biogeography of Mytilid Bivalves

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Present-day patterns of biodiversity are heavily influenced by processes operating on million-year timescales, including evolution, extinction, and tectonics. A fundamental unit of biogeography is geographic range, or the physical representation of the spatial area a species inhabits. By reconstructing historic geographic ranges of taxa through deep time, we can understand how various processes have influenced the modern abundance and distribution of species. Here, I use Mytilid

(Family Mytilidae) bivalves – a clade with high preservation potential and an excellent fossil record – as a case study for reconstructing the historical biogeography of a clade in a phylogenetic context. I digitize the known native geographic ranges of 30 extant bivalve species to create authentic geodesic data, and analyze these using ancestral state reconstruction. I leverage this approach to address the following questions: where did the clade originate, and what are the characteristics of its ancestral range? As the clade diversified, were there predictable biogeographic correlates for taxa prone to speciation or extinction? Lastly, are specific lifestyles (e.g., epifaunal, semi-infaunal or boring) geographically constrained, and is this pattern consistent through evolutionary time? With an expanded dataset of extant and fossil taxa, this work will help address longstanding questions in macroecology and macroevolution; specifically the role of biogeography in determining speciation and extinction risk, and to what extent different environmental perturbations (e.g., warming vs. cooling) produce differing effects on biogeographic patterns. Lastly, this may help form a predictive ‘roadmap’ for how we expect species to respond to a variety of future global change scenarios.

108. Biogeographical-scale impacts of future climate change in the aboveground biomass of seagrasses

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Seagrasses are essential marine ecosystems that have experienced accelerating degradation due to anthropogenic and climate change impacts. The magnitude of projected future climate change suggests further seagrass declines, but no biogeographical scale estimates are currently available on the potential changes in aboveground seagrass biomass. Here, we model and quantify the current aboveground biomass (AGB) of seagrasses at the global scale and predict future AGB for the end of the 21st century under contrasting Shared Socioeconomic Pathway (SSP) scenariosfrom low emissions (SSP1-1.9), in line with the Paris Agreement expectations, to higher emissions (SSP3-7.0 and SSP5-8.5). A machine learning algorithm (Boosted Regression Trees) fitted a comprehensive AGB dataset against biologically meaningful predictors. The model performed with high accuracy (deviance explained: 0.69), highlighting the role of genus-specific traits and temperature conditions in defining global AGB patterns and estimating a present-day average and overall AGB of 113.88±88.80 $gDW \cdot m^2$ and 0.10 Pg DW, respectively. Future projections were highly dependent on the emission scenario, with losses in average AGB ranging between 7.49% and 13.25% and in total AGB between 13.90% and 15.53%. Particularly, the higher emission scenario projected severe regional losses along the coastlines of the Tropical Eastern Pacific, the Eastern Indo-Pacific, the Temperate Northern Pacific and the Tropical Atlantic, and gains along the Temperate Southern Africa and the Arctic regions. Our global estimates underline the substantial benefits of the Paris Agreement and serve as new baselines at biogeographical scales to inform conservation and management actions focused on multiple ecosystem services of seagrasses.

109. Ancient Indigenous fisheries catches document latitudinal temperature gradients across the Eastern Pacific over millennia

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Contemporary climate change is altering the dynamics and distribution of species globally. In the ocean, contemporary fish populations are tracking poleward in response to warming, in line with their temperature preferences, shifting the thermal composition of fish assemblages in a given location. These shifts can be tracked in space and time using metrics like the Community Temperature Index (CTI). However, such metrics typically rely on quantitative ecological and fisheries surveys, which have limited temporal scope. Here, we show that pre-industrial fishery landings data from Indigenous archaeological sites can be leveraged to track fish thermal compositions in space and time over several thousand years. We compare ancient and modern fish assemblages in terms of their thermal composition (CTI) at four locations in the eastern Pacific. We find the thermal composition of Indigenous fisheries data varies along a 30° latitudinal temperature gradient, with estimates of ancient CTI ranging from 18.30°C in Southern California to 10.72°C in the Bering Sea. Comparisons of ancient CTI and modern CTI indicate that the average thermal composition of fishes has remained remarkably consistent over the last 1,000-6,000 years, but also exhibit a slight warming signal (0.26-0.43°C increase in CTI from ancient to modern periods). To explore this novel climate signal further, we explore four approaches for integrating zooarchaeological data with CTI and discuss advantages and limitations of each. Given that Indigenous fisheries data from coastal archaeological sites are globally distributed, we believe this approach can extend the temporal scale of our understanding of fish thermal composition globally.

110. Projecting changes in marine biota distribution to support climate-resilient marine spatial plans in Portugal

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Increasing climate change impacts in the oceans include shifts in the distribution of marine species, ecosystem composition and productivity, with strong consequences for human activities, such as fisheries or conservation. Addressing and integrating climate effects in marine planning and management processes is fundamental to supporting ocean sustainability and decreasing climate-related vulnerability and risk. This study aims to project the impacts of climate change on the distribution of main human uses and activities that take place in the Portuguese exclusive economic zone under different climate scenarios (Representative Concentration Pathways, RCP). Results are intended to support the development of climate-smart marine spatial planning in Portugal. Species distribution models (SDMs) were developed for a total of 100 marine species relevant for fisheries, aquaculture, tourism and conservation, and projected in 10-year gaps until the end of the century (for RCP 2.6 and RCP 8.5 scenarios). Obtained results provided invaluable insights about expected changes in the spatial distribution of such species, as well as on potential consequences for dependent maritime uses and activities. The resulting maps were used to build scenarios and to identify spatial opportunities to support social and ecological resilience to climate change effects within the Portuguese maritime space.

111. Convergent climate trait evolution provides a similar rank order of polyphyletic woody plant genera in the Himalayas and Andes.

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Niche conservatism predicts that closely related species will have similar distributions along major environmental gradients, e.g. temperature. This is based on the tenet that environmental filtering facilitates certain monophyletic genera with shared traits to occupy a given climate niche. However, species in polyphyletic genera may also obtain similar traits through convergent evolution. Hence, genera from different continents consisting of morpho-species with polyphyletic origin may occupy similar climate niches. Polyphyletic woody genera (25) common for the Andes and Himalayas were used to assess this hypothesis by comparing the central tendencies of temperature optima and if these genera have a similar rank order (sequence) across continents and hemispheres. A strong rank correlation may indicate that the convergent evolutionary development of traits is a significant driver of temperature tolerance within genera.

Elevation and temperature ranges for all species belonging to 25 disjunct polyphyletic genera of woody plants were compiled (almost no shared species). Temperature optima were established using reciprocal averaging and weighted average temperature. Most genera exhibit a bell-shaped or curvilinear pattern with the maximum number of congeneric species in the centre of the temperature range. The order of generic optima along the temperature gradient in each region was highly correlated between the mountain ranges.

The analyses verify the conjecture that the maximum number of congeneric species is found towards the centre of the temperature range of the genus. Convergent evolutionary processes may cause this, and promote that certain temperature tolerances are related to morphological traits within genera of polyphyletic origin.

112. Global trends of aquatic food webs in the Anthropocene

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Human activities are reshaping biodiversity in unprecedented ways. This reorganization has profound consequences on species interaction networks, like food webs that support ecological and evolutionary processes essential for life on Earth. Yet, we still know little about the direction and magnitude of food web changes, especially at large spatial scales. Early work predicted that global environmental change would cause systematic loss of species and an overall homogenization of biological communities, leading to simplified food webs dominated by generalist species and their interactions. However, recent studies have shown that biodiversity responses in the Anthropocene are complex and suggested that different regions of the globe will experience greater or lower rates of change depending on the biogeographical context and the strength of human pressures. Combining extensive datasets of assemblage time-series, trophic interactions, and species traits, we reconstructed a global database of food web time-series in aquatic ecosystems to identify temporal and spatial patterns of changes in the structure and functioning of food webs. We inferred more than 15,000 food web time-series distributed in both freshwater and marine environments. Our analysis showed that Global Environmental Change also affects other facets of biodiversity beyond population and community diversity changes. Despite the high variability we observed in the global trends, the response of food webs is spatially structured, with different rates of changes according to the biogeographic regions and environmental realms. Our results highlight that exploring other facets of biodiversity, like species interaction networks, is crucial to better understanding the current reshaping of biodiversity.

113. Niche of plant species native to the temperate forest biome in Europe matches heterogenous natural vegetation shaped by large herbivores

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Traditionally the natural vegetation of the temperate forest biome has been characterized as closed-canopy forest. However, recent studies show it to be more heterogenous including open and semi-open canopy, likely maintained by now extirpated megaherbivores. We examined which of these two models of natural vegetation does the niche of vascular plant species native to the temperate forest biome match.
First, we selected all species considered native in temperate Europe (Poland and Germany), subsequently subsetting forest species (after Heinken et al. 2022). Next, for each species, we summarized published niche information for canopy openness and grazing mammal densities. Finally, we explored patterns in these niche gradients across the native species pool.
We found that 74.4% of all plant species and 51.9% of forest species prefer half-light or more open canopy. Only 16.6% of forest species prefer shade. 53.7% of all plants, and 48.1% of forest species prefer grazer densities higher than 7000 kg/km². Species preferring grazer densities from 6000 to 7000 kg/km² made up 24.6% of all plant species, 37.6% of all forest species, and 77.4% of closed-canopy forest species. The degree of open canopy preference was negatively correlated ($p < 0.001$, $R2 = 0.243$) with niche width among native species, meaning that specialists are mostly found in open and semi-open habitats.
These patterns provide support for heterogeneous natural vegetation in the temperate forest biome and show that trophic rewilding through the reintroduction of large herbivores offers a solution to maintain Europe’s rich plant diversity hereunder species associated to woodlands.

114. Evolutionary assembly of tropical rainforests

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Tropical rainforests are among the most complex and diverse ecosystems on Earth, and understanding their evolution has long been of great interest. They are remarkably rich in species, but much remains unknown about the origins of this striking diversity pattern. Recent studies have shown surprisingly low diversification rates within tropical rainforests, leaving other factors such as biome age or high immigration rates as possible causes of rainforest hyperdiversity. Our ongoing work aims to provide new insights into the evolutionary assembly of tropical rainforests. Taking advantage of ongoing advances in computational techniques and available information on phylogeny and species distribution data, we use a dataset of 300,000 seed plant species. We use state-dependent speciation and extinction models (secSSE) to quantify transition patterns in plant lineages between biome types. As a first result, we observe that among the transition patterns between biomes, migrations between tropical rainforest and dry tropical climates seem to be the most prominent.

Authors:

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115. Trait filtering and selection may explain the island rule in mammals

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Island biodiversity has been studied for more than a century, yet a predictable framework for the traits of species inhabiting islands is still unresolved. Here, we develop a conceptual model to explain two primary factors that contribute to island trait diversity: i) interspecific trait-filtering during island formation and ii) intraspecific trait evolution on the island. The model integrates classical life history theory, metabolic ecology and species interactions to predict biogeographic patterns. At the interspecific-level (i), the model predicts trait-filtering based on the extinction bias of the smallest and largest body size species on islands as expected from standard allometric constraints. In contrast, at the intraspecific-level (ii), the model predicts directional selection toward slow life histories, irrespective of initial body size, due to relaxed predation and/or competition. Together, these processes predict mid-sized mammals at small geographic scales emerging as a right-skewed body size distribution at large geographic scales, consistent with empirical patterns. We conclude with applications of this model to a variety of island and island-like systems.

116. Spatial and macroecological patterns of hummingbird pollination syndrome in the Americas

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Pollination syndromes, sets of floral traits that attract specific pollinator groups, have been essential for classifying angiosperms from a functional-ecological perspective. They have proven valuable when developing conservation plans and studying competition, species distribution, and macroevolution. However, little is known about the biogeographic patterns of these syndromes and

their underlying processes. We examined the distribution of hummingbird syndrome in the Americas and the ecological factors explaining them. Hummingbird syndrome consists of flowers with vivid colors, tubular corolla, nectar presence, and diurnal anthesis. Records of hummingbird visitation to 2,674 plant species native to Americas were collected from literature, covering 725 genera and 104 families. We scored all 44,241 species in these genera based on flower morphology and found 9,271 species with hummingbird syndrome. With plant distribution from the Global Inventory of Floras and Traits, we found a greater proportion of plants with the syndrome in the Northern Andes, the Amazon, and the Atlantic Forest of Brazil. GLM models revealed a greater proportion of hummingbird syndrome where these birds are more species-rich (standardized slope coefficient = 0.55) and functionally diverse (0.15), expected given the greater possibilities of niche partitioning, coexistence, and diversification. Hummingbird syndrome is positively associated with higher elevation (0.08), where physiological constraints limit insect pollinators. While no clear association with climate was found, associations were noted with the prevalence of shrubs (0.02), trees (0.04), and herbs (-0.02). These effects are consistent across major plant groups. Understanding the spatial patterns in pollination syndrome is key for comprehending co-evolution among interacting partners.

117. From α- to β- diversity: Understanding the past, present, and future diversity patterns of Fagaceae in Southwestern China

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Macroecological research seeks to elucidate the factors driving variations in species composition and diversity. However, limited effort has been made to clarify the diversity pattern on different geographical and temporal scales. Our understanding of alpha (α) and beta (β) diversity facets and their determinants remains limited in a key biodiversity hotspot. The aim of this study is to fill this gap by investigating the two different facets of the diversity of Fagaceae across past, present, and future timelines in Southwestern China. We used over 11,000 geographical observations to predict the spatial patterns of the α- and β-diversity of 120 species. We calculated the α-diversity and used pairwise Sørensen dissimilarity as a measure for the total β-diversity and partitioned it into turnover (βSIM) and nestedness (βNES) components. We integrated climate variables along with topographic and edaphic related predictors to understand the species diversity across the study sites. We then applied a simultaneous autoregression (SAR) model to evaluate the effects of predictor variables on the α- and β- diversity patterns. Our results indicate a temporal decline in the α-diversity from 120 during the past to 49 in the future. However, the area of the species occurrence increased from the past to the present, concurrently fostering an increase in the β-diversity, and it may potentially continue to increase in the future. In the future, climatic variables will play a significant role in determining the diversity patterns. Comprehending the *α*- and *β*- diversity is crucial for conservation planning of regional biodiversity.

118. A new perspective on the biogeography, macroecology and conservation impacts of biological invasions in the Anthropocene

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Biological invasions have become a defining feature of global environmental change (IPBES 2023). However, the global patterns and underlying factors that determine variation in invasions world-wide are still insufficiently understood. Similarly, future trajectories of biological invasions and the consequences for biodiversity conservation are not fully appreciated. Progress in data coverage and availability, supplemented by new tools for data integration and analyses have facilitated the compilation of comprehensive databases of world-wide alien species distributions such as GloNAF (https://glonaf.org/) for vascular plants (van Kleunen et al. 2015). Similarly, the compilation of the Alien Species First Record-database provides a backbone for analysing spatio-temporal patterns of alien plant species accumulation (Seebens et al. 2017). Further, data on human pressures, on the exchange routes of goods and people, and on a large range of environmental factors have increasingly become available. Combined, these novel data sources have substantially advanced the understanding of the macroecology and biogeography of biological invasions. Here, we will synthesize new key insights into global patterns and drivers of biological invasions. We will highlight likely future trajectories of biological invasions, discuss main gaps of scientific knowledge, and identify new avenues to improve the understanding of alien species spread and impacts. Finally, we will provide a perspective on priority questions for biogeography and biodiversity conservation related to biological invasions.

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119. Megaherbivores as nature-based solution for resisting invasion dominance

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Megaherbivores are known to promote biodiversity and ecosystem resilience, but their relevance in modern ecosystems is diminished by unabated defaunation, human impacts and biological invasions. Understanding their relevance for restoring degraded and invaded ecosystems could be vital but remains unexplored. Addressing this knowledge gap, we used bigdata from a large-scale sampling (~121,330 km^2) to assess the relationship between megaherbivores, native plants and invasive plants across 12 biomes in India. We found a strong positive relationship between megaherbivore abundance and native plants, and a concomitant reduction in invasive plants. This relationship was strongest in protected areas with mid-productive systems, and was seen diminishing as woody invasive plants exceeded 40% cover. To test the global parity of our findings, we conducted a meta-analysis and found the average impacts of megaherbivores comparable to our estimates (56%). Our global projection revealed 89% of areas are now largely devoid of this ecological function due to extinctions and extirpations of megaherbivores. The study shows great potential for megafauna-based trophic rewilding as a nature-based solution to counteract dominance of plant invasions, particularly considering the importance of restoring resilient ecosystems in our increasingly invaded world.

120. Do human impacts explain the prevalence of threatened bird species on islands?

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Approximately 30% of Earth's species are threatened by extinction, but these threatened species are not evenly distributed in space. Islands are among the most threatened ecosystems in the world, and are considered model systems for understanding ecological processes shaping species communities. Yet, no global study has investigated the spatial distribution of threatened species across islands and how island characteristics influence this. Our study aimed to address two main questions: i) do human impacts or environmental variables better explain the presence of threatened species on islands worldwide? ii) which specific human impacts contribute significantly to this pattern? Analysing data from 1254 islands on both total species richness and richness of threatened species, we found human impacts are pivotal in explaining the prevalence of threatened species. Models including human impacts performed significantly better than models with only environmental predictors. When controlling for other environmental factors, human impacts accounted for ~25% of the variance in threatened species prevalence across islands, with only island isolation and net primary production (NPP) showing higher variable importance. Whilst our analysis was not conclusive to identify the particular human impact, our models strongly suggest that the extent of urbanization, especially on oceanic islands, is a key factor. Urban expansion not only exacerbates the negative effects of other land uses like agriculture, but according to our models, it also neutralizes the biodiversity rescue effect associated with higher island NPP. Our research disentangles interaction effects of anthropogenic change and ecosystem properties, highlighting novel implications for directing conservation efforts.

121. Distinguishing among alternative vectors for marine invasive species: Shipping versus Oyster transport

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Non-native species homogenize the Earth's biodiversity and alter ecosystem function. In marine environments, shipping is a critical vector responsible for these invasions. However, vectors other than shipping are also important; one such example is the deliberate worldwide transportation of the Pacific oyster *Crassostrea* (*Magallana*) *gigas* from the northeastern Pacific to North and South America, Europe, Africa, and New Zealand. Here we develop a statistical framework that delineates models of invasive species movement based on shipping and oyster introductions. Shipping vector models are based on International Comprehensive Ocean-Atmosphere Data Set (ICOADS) ship log information from 1950-2015. Oyster vector models are based on our novel population genomic assessment of the global distribution of C. gigas. We weighed the relative support of these models for describing genetic data available in the literature for 14 diverse marine invaders, including algae, annelids, arthropods, tunicates, and vertebrates. This approach uses Approximate Bayesian Computation (ABC) to simulate the history of invaders under each of the alternative vector models and compares simulation results to empirically observed genetic data for each invader. While some results are consistent with prior information and the biology of the invader, we also found that species previously associated with oyster movement likely moved via shipping. Though the ABC approach has been used to distinguish among historical biogeography models and to describe invasion events, this work represents a first effort to use this technology to formally distinguish among alternative vectors.

122. Biotic resistance in highly diverse Ecosystems: Plant invasions in the tropics - Packed niche space or historic legacies

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For decades researchers have seen less successful plant invasions in the Tropics. Several studies using only recently available large scale data on plant invasions showed lower numbers of plant invaders in tropical regions and ecosystems. A long standing invasion hypothesis as part of the diversity-stability hypothesis states that tropical systems might be more resilient against invasions due to their higher functional diversity or densely packed niche space. Species interactions happening at small scales and the process of plant invasions is a complex combination of e.g. resource availability, climatic matching, competition and propagule pressure. However a formal test of this Tropical resistance hypothesis and more generally an in-depth analysis of patterns of plant invasions and their drivers in the Tropics is still missing. This is still mainly due to a lack of robust plant distribution data with large extent (covering different tropical regions) and small grain size (plant communities at a plot level) as well as comprehensive temporal information on plant. This study is the first attempt to analyse large scale plant invasions across all Tropical ecosystems and

regions worldwide using comprehensive plant co-occurrence information. Here we combined the largest compilation of plant plot level data (sPlot, www.idiv.de/splot) with global plant trait data (e.g. TRY) to test and explore to what extent different complex measures of functional diversity (e.g. hypervolumes) might explain different gradients of non-native species richness. We account for different histories of land use and connectivity measures as well as clearly different ecological plant community stratification in the Tropics.

123. Biogeography and global flows of 100 major alien fungal and fungal-like oomycete pathogens

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Spreading infectious diseases associated with introduced pathogens can have devastating effects on native biota and human livelihoods. In this study, we analyse the global distribution of 100 major alien fungal and oomycete pathogens of plants or animals, with substantial socio-economic and environmental impacts. We examine their taxonomy, ecological characteristics, temporal accumulation of first records and taxon flows between continents. Furthermore, we identify regional hot/coldspots, by correcting taxon richness for region area and sampling effort.
We found that Peronosporomycetes (Oomycota) were overrepresented among taxa. Regional first records have increased steeply in recent decades and while Europe and Northern America were major recipients, about half of the taxa originate from Asia. While no island effect was found, likely due to host limitation, regional hotspots were correlated with human modification of terrestrial land, per capita gross domestic product, temperate and tropical forest biomes, and orobiomes.
Therefore, we highlight the putative importance of anthropogenic drivers, such as land use providing a conducive environment, contact opportunities and susceptible hosts, as well as economic wealth likely increasing colonization pressure. Importantly, while most taxa were associated with socio-economic impacts, possibly partly due to a bias in research focus, about a third show substantial impacts to both, socio-economy and the environment, underscoring the importance of maintaining a wholescale perspective across natural and managed systems.

124. Alien species and the shape of commonness and rarity in the European flora

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Bridging natural dispersal barriers and introducing species into new regions, human activities are driving profound changes in the global distribution of biodiversity. While many introduced aliens remain scarce and restricted after establishment, some become abundant and widespread. Combining data from over 1 million vegetation plots covering the extent of Europe and its diversity of habitats with databases on species' distributions and introduction histories, we investigate how aliens are altering the shape of commonness and rarity within a continental flora. Specifically, we apply the dimensions of rarity and commonness framework, measuring and comparing local abundance, geographic extent, and habitat breadth across native and alien species. We find these three dimensions are linked for both groups: locally dominant species also occur over large areas and in diverse habitats. Introductions are driving 'rich get richer' dynamics, with the most abundant, widespread, habitat generalist natives also most likely to invade new regions in the continent. Aliens from abroad comprise a small portion of the total European flora but are overrepresented among the most abundant species - shifting dominance hierarchies and reducing species evenness at local scales. Despite being relatively restricted in habitat use, such extracontinental aliens reach range sizes comparable to those of native species. We further project how these patterns are likely to shift or intensify in the future as aliens are given time to expand their distributions and spread from anthropogenic into less disturbed habitats.

125. Mountains of Data: An Integrated Workflow for an Alpine Biodiversity Inventory Across Multiple Taxa

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Mountains are remarkable in many ways. They shape global and regional climates, ensure the survival and sustainability of many human societies and act as cradles, barriers, and bridges for many species. The complexity of mountains is directly linked to an exceptionally high biodiversity, which is particularly concentrated in the alpine zone, the ecosystem above the treeline. However, alpine biodiversity patterns differ across individual mountain regions resulting from the dynamic interplay between evolutionary processes and the unique biogeographic history of each mountain

range. Yet, the limited availability of alpine biodiversity data still hinders a thorough understanding of alpine biodiversity patterns and the underlying processes shaping them. Current global datasets typically focus on specific taxa and lack information on species elevational distribution or their alpine status. In contrast, regional datasets, though detailed, provide only insights in particular mountain regions and vary in their data formats. A comprehensive, open-source and truly global inventory of alpine species comprising various taxonomic groups remains notably absent. To address this gap, we introduce an R-based workflow equipped with data-specific pipelines, leading to a comprehensive Global Alpine Biodiversity Dataset encompassing plants, mammals, birds, and reptiles. This workflow processes and harmonizes regional and global datasets across multiple taxonomic groups and identifies those species occurring above the treeline in different mountains around the world. Though work in progress, this global checklist of alpine species paves the way for a more profound understanding of biodiversity patterns in mountains and provides a tool to study their underlying drivers.

126. From the Mountains to the Sea: mobile glacial refugia for terrestrial vertebrates in the Italian peninsula

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Glacial refugia are areas of primary importance for the evolution and conservation of biodiversity. Yet, their geographic location remains loosely defined even in intensively studied areas, preventing a thorough understanding of their role in the spatiotemporal biodiversity dynamics. Here, we aim to locate the major glacial refugia within the biodiversity hotspot of the Italian peninsula, to understand the processes that warranted the long-term persistence of biodiversity in the face of climate changes. We i) calibrated species distribution models (SDM) for 22 lineages of terrestrial vertebrates endemic to the Italian peninsula, ii) projected the SDMs to the last-glacial maximum conditions, iii) combined single-lineage projections to investigate the location and spatio-temporal dynamics of multi-species glacial refugia. We found multi-species refugia mostly in coastal areas that have been flooded by the post-glacial marine transgressions, and that are currently below the sea level. Indeed, we identified six major areas acting as glacial refugia, mainly located outside the current coastline in the southern part of the peninsula and along the western coast. These areas were close to previously inferred locations of glacial refugia and genetic diversity hotspots, but none coincided with them. Results from this study outline glacial refugia as highly dynamic units. Indeed, most of the identified refugial areas have been lost by the post-glacial sea-level rise. Accordingly, species persistence through the Late Pleistocene was not granted by long-term environmental stability, but by the opportunity to shift species' distributions along altitudinal gradients, following changes in climate and habitat suitability.

127. Applying invasive ecology to test how biotic interactions affect range shifts across large gradients

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Warming-induced range shifts have been widely discussed in a climatic context without being able to consider biotic interactions at large scales. Here, we apply invasive ecology to tackle this knowledge gap. The biotic resistance hypothesis and Darwin's naturalization hypothesis predict high species richness or close relationships with native species, respectively, making it more difficult for new-coming species to join the recipient communities. We tested these hypotheses using data from the Taiwan Breeding Bird Survey, where more than 300 communities with nearly 300 species have been surveyed yearly since 2009. We investigated the climate niches for each species and analyzed their suitable climate space every year. We compared the characteristics of the recipient communities with/without colonizing events in the newly available climate space, including the phylogenetic distances to the species of concern, richness, and diversity at the phylogenetic, functional, and taxonomic levels. Our preliminary results presented several challenges: (1) SDM indicated that new climatic spaces varied among species and primarily decreased. (2) Source distance affected colonization events. (3) Characteristics of random colonization events and donating communities must be considered. (4) appropriate hypotheses are yet available for testing the contraction at the trailing edges. This framework provides us with testable hypotheses on how biotic interactions affect the warming-induced range shifts, particularly the expansion process. Based on the results, we can further infer that along the latitudinal and altitudinal gradients, where the community composition changes at significantly different rates, may constrain or facilitate biodiversity redistribution.

128. The effect of biotic interactions on modelling responses to climate change in an alpine ecosystem

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Species distribution models (SDMs) are widely used to project species geographic distribution under climate change. These correlative models are designed to capture realised ecological niches, but are often fitted with exclusively climatic data to capture a species' environment. Therefore, SDMs usually ignore biotic interactions, which are known to shape ecological niches of species and affect their distribution. Here, we fitted climate-based SDMs with and without biotic interaction effects for an alpine study system with strong interdependencies of species, using a combination of very finely resolved spatial data across Switzerland and of less resolved data across the rest of Europe. We focussed on the Swiss stone pine (*Pinus cembra*), which forms the tree line in the European Alps, and its primary seed disperser, the spotted nutcracker (*Nucifraga caryocatactes*). Additionally, we developed SDMs for the Norway spruce (*Picea abies*) as the main competitor of the focal tree, and the common hazel (*Corylus avellana*) as an additional important food source for the bird. Our model comparison showed different results for the two focal species regarding the inclusion of biotic interactions. Whilst including occurrence probabilities for the bird's food sources (Swiss stone pine and hazelnut) significantly improved quality and fit of the SDMs for the nutcracker, including occurrence probabilities for spruce (competitor) and nutcracker (seed disperser) in the Swiss stone pine SDM did not improve the model. Our results imply that accounting for food plants is helpful to model herbivore distributions, but that the signature of biotic interactions such as competition and seed dispersal might be more challenging to capture.

129. Conserving Southeast Asian tree distributions requires a sustainable pathway mitigating both climate and land-use change

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Both climate and land-use change threaten Southeast Asia's biodiversity but their impacts are rarely assessed simultaneously. We modelled 1476 tree species distributions in Southeast Asia under four Shared Socioeconomic Pathways (SSPs) with varying global change intensities, and classified species into 12 spatially associated groups. We found both global changes to cause severe losses in tree distribution area. Only under SSP1-2.6, the sustainable pathway with low intensities in both global changes, were distribution losses mitigated and even gains achieved. Unexpectedly, losses were overall greatest under intermediate climate change pathways SSP2-4.5 and SSP3-7.0 than under the most extreme pathway SSP5-8.5. This was because, although climate-driven losses were greatest under SSP5-8.5, land-use-driven losses were much more extensive under SSP2-4.5 and SSP3-7.0 than SSP5-8.5. Additionally, other than SSP1-2.6, each SSP led to worst-case scenarios for several species groups. Our findings highlight that to most effectively conserve Southeast Asian tree distributions, policymakers need to prioritise a sustainable pathway that minimises both global changes.

130. Multi-temporal species distribution models to characterize ecological niche

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Understanding how biodiversity responds to environmental changes is crucial for conservation planning and decision-making. Species distribution models (SDMs) are widely used to characterize species environmental niches and forecast future biodiversity patterns and trends. However, current SDMs have some limitations, such as assuming that species distributions are in equilibrium with the contemporary climate and using long-term mean climate variables to characterize species' niches. These assumptions may not reflect the actual environmental conditions experienced by different groups of species with varying degrees of mobility and longevity, and may ignore the effects of historical climate on species' niches. In this study, we develop a novel multi-temporal SDM approach that incorporates time into SDMs to account for historical climate effects and species' longevity. We test our approach on various tree species using biodiversity data from GBIF, climate data from CHELSA, and remote sensing data from MODIS, Landsat, and Sentinel-2 platforms. We compare our approach with conventional SDMs using different performance metrics and evaluate how different time lags (years prior to observations) and time windows (length of time span) affect the predictions of SDMs for different groups of species. Our results show how multi-temporal SDMs perform compared to conventional SDMs in terms of accuracy and discrimination. We also demonstrate whether historical climate conditions are more important than contemporary climate conditions in explaining current biodiversity patterns, and whether the optimal time lag and window vary depending on longevity of species. Our study demonstrates the potential of multi-temporal SDMs to better characterize species' niches under variable environmental conditions and to improve biodiversity forecasting under future scenarios.

131. What defines the range limits of alpine plants?

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Against the backdrop of accelerating climate change, the need to comprehend species range shifts, lags, and associated extinction risks within the alpine biome has become of paramount importance. This understanding ultimately relies on what it is that defines the range limits of species. In alpine environments, the conventional notion posits that abiotic factors, namely temperature, determine the position of upper elevational range limits and that biotic factors, namely competition, drive lower elevational range limits. However, these assumptions have so far not been validated systematically. In an extensive systematic literature review, we analyzed the current state of knowledge, spanning ecological, evolutionary, and physiological perspectives on determining factors of range limits of alpine plant species.Temperature indeed stands out as the main driver of upper range limits, but what 'temperature' refers to is everything but simple. Up to date, it remains unclear which aspect of temperature is decisive, but current evidence suggests that the answer might be species-specific and depends on life stages. What defines the position of lower elevational limits is even less clear. Current scientific evidence suggests that it is shaped by diverse biotic interactions, comprising competition, herbivory, disease, and additional abiotic factors such as drought. The significance of other drivers, such as soil moisture and nutrient availability, seems not crucial if considered alone but several abiotic and biotic factors are assumed to have intervening effects. Here, I will provide a comprehensive summary of our current understanding and highlight knowledge gaps and future research directions.

132. Worldwide Late Pleistocene and Early Holocene population declines in extant megafauna are due to Homo sapiens rather than climate

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The worldwide extinction of megafauna during the Late Pleistocene and Early Holocene is evident from the fossil record, with dominant theories suggesting a climate, human or combined impact cause. Consequently, two disparate scenarios are possible for the surviving megafauna during this time period - they could have declined due to similar pressures, or increased in population size due to reductions in competition or other biotic pressures. We therefore inferred population histories of 139 extant megafauna species using genomic data which revealed population declines in 91% of species throughout the Quaternary period, with larger species experiencing the strongest decreases. Declines became ubiquitous 32-76 kya across all landmasses, a pattern better explained by worldwide *Homo sapiens* expansion than by changes in climate. We estimate that, in consequence, total megafauna abundance, biomass, and energy turnover have decreased by 92-95% over the past 50,000 years, implying major human-driven ecosystem restructuring at a global scale.

133. Species richness gradients are not universal, but change systematically across the phylogeny

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Species richness gradients are often viewed as universal. However, their variation has rarely been systematically evaluated, especially across the phylogeny. It is possible that well-known gradients, such as the latitudinal diversity gradient, hold consistently only for clades of certain age and size. Here, we analyze how species richness changes with latitude, environmental productivity and temperature for all clades within birds and mammals (~15,000 species). We use multiple gradient measures (raw richness, log-transformation, log-log transformation, parametric and non-parametric correlations), which we correlate with clade age and size to identify phylogenetic trends. To tease apart biological and statistical causes of the trends, we construct null models and use simulations. We find that, as clade age and size increase, the gradients become steeper and more consistent. Yet, even relatively large clades (up to 500 species) regularly show reverse gradients (35% of the clades within birds and mammals). Similar, albeit less pronounced, phylogenetic trends arise even within simulations and null models, suggesting that the trends might be partly statistical. We conclude that species richness gradients follow phylogenetic trends, which arise equally for biological and statistical reasons. Based on our results, we formulate guidelines on how to measure the gradients for more meaningful cross-taxa and cross-study comparisons, depending on the tested theory and research purpose. Knowledge of the phylogenetic trends paves the way toward a synthesis of the wide variety of gradients reported across taxa and previous studies.

134. Stochastic process, environmental filtering and species association jointly shape community assemblages along elevational gradients in Qinling mountain, China

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Understanding how mechanistic processes shape species occurrence and abundance is a central goal in community ecology. However, how environmental and biotic effects shift their importance in community assembly along elevational gradients remain unclear. By using inventory data of 246 plant plots in Qinling mountain in China, we conducted different joint species distribution models (JSDMs), a hierarchical Bayesian model that allow joint analysis of environments, phylogeny, trait data and community attributes. We compared performance of different models: (1) ModelEnv, only use environment; (2) Modelfull, containing environment, biotic association and phylogeny. Variance partitioning was used to quantify the relative importance of each environmental and biotic effects on both species occurrence and abundance. Our result showed that biotic association and phylogeny can significantly improve model performance for occurrence (R2 rising from 0.328 to 0.359, WAIC decreasing from 7.456 to 7.163). For abundance, integrating biotic association and phylogeny greatly improved model R2 (from 0.281 to 0.591), but increased WAIC from 6.984 to 7.824. Variance partitioning showed that mean annual temperature is the dominant factor of both occurrence and abundance. Notably, biotic effect was more important to abundance (~0.2) than occurrence (~0.05). We also found that environmental and biotic effects shift significantly along the elevational gradient. For example, annual mean temperature increased its importance at higher latitude, while soil variables generally decreased their importance as latitude increased. Overall, our findings highlight the importance of incorporating both abiotic and biotic factors in models to better reflect assembly processes underlying distribution and diversity patterns.

135. **Connecting spatial scaling of biodiversity change to per-individual ecological processes**

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Unprecedented extinctions, extirpations, and invasions have likely been taking place all over the world, and they combine to complex patterns of biodiversity change. The rate and direction of this change depends on spatial grain (resolution, scale); plausible are completely opposite trends at different grains, i.e. biodiversity losses at one grain but gains at another grain. Ecological mechanisms behind this discrepancy between fine and coarse grains are unclear. We hypothesized that the direction and magnitude of the relationship between biodiversity change (ΔS) and spatial grain (the average area of observation) depends on the magnitude of classical ecological processes such as the Allee effect, Janzen-Connell effect, and possibly the “target effect” (from the equilibrium theory of island biogeography).

Specifically, we focused on the smallest level of a single individual of an organism. We attempted to link this individual’s probability of death to population density in a larger geographic area. Similarly, we linked the individual’s dispersal potential to the area of the target location. We then examined how these processes translate to spatial patterns of biodiversity change at coarser grains.

We found that spatial scaling of extinction rates depends on how individual-level probability of death scales with overall population density, and thus on rarity or commonness species. We thus theoretically demonstrate a low-level mechanism that can explain different rates of biodiversity change which several authors observed at different spatial grains in empirical data.

136. **Land-use management impacts on species habitat suitability and functional diversity**

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Land-use land-cover (LULC) change contributes to major ecological impacts particularly in areas undergoing land abandonment, inducing modifications on habitat structure and species distributions. Alternative land-use policies are potential solutions to alleviate negative impacts of contemporary LULC change tendencies on biodiversity. This work analyses these tendencies in the Montesinho Natural Park (Portugal), an area representative of European abandoned mountain rural areas. Species distribution models were built for 264 species of vertebrates (amphibians, birds, mammals and reptiles) and plants, using a consensus modelling approach available in the R package ‘biomod2’. The models were projected to contemporary (2018) and future (2050) LULC scenarios. Four scenarios were simulated for 2050: an afforestation and rewilding scenarios focused on climate-smart management strategies, and a farmland recovery and agroforestry recovery scenarios focused on re-establishing human traditional activities to secure relevant ecosystem services and biodiversity conservation. The influences of these scenarios on biodiversity were quantified through species habitat suitability changes for 2018-2050. Functional indices were quantified to analyse how these management strategies could influence functional diversity within the park. Habitat suitability changes revealed complementary patterns among scenarios. Afforestation and rewilding scenarios benefited more species adapted to habitats with low human influence, such as forests and open woodlands. The recovery of traditional activities benefited mainly bird species adapted to agricultural landscapes. The highest functional richness was predicted for rewilding scenarios, probably related to benefits provided to unique species assembling singular functions (this work was funded by Fundação para a Ciência e a Tecnologia, I.P. - MTS/BRB/0091/2020 project).

137. Mammal food web susceptibility to extinction cascades

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An emerging research agenda in macroecology is to identify governing principles of food web structure by investigating network variation across large spatial extents. Here we test for food web susceptibility to cascading extinctions (i.e., secondary extinction) following species loss (i.e. primary extinction) throughout the global tropics and subtropics. Mammals play critical roles in top-down regulation and more published studies describe their predator-prey interactions than other taxa. We used published mammal species lists for 391 communities throughout the Neotropical, Afrotropical, and Indo-Mayan realms, constructed regional meta-webs from published predator-prey interaction data, and subset local food webs from the meta-webs. We simulated extinction scenarios between the least and most connected species for each community and evaluated the magnitude of secondary extinctions among communities. Strikingly, 70% of communities were robust to secondary extinctions after the loss of five species. At low levels of primary extinctions (1-2 species lost), secondary extinctions were more common following removal of the least connected species, indicating that the loss of weakly interacting species can have cascading consequences on food webs. However, as the number of primary extinctions increased, more communities had secondary extinctions following the removal of the most connected species, indicating highly interactive mammal species are very important for biodiversity maintenance. We found no significant differences in robustness among regions, but mammal communities with higher habitat diversity had marginally higher robustness. Further work is needed to explore the role of geographic variation in anthropogenic pressure on mammal food web network robustness given the widespread threats mammals face.

138. Prioritizing areas to monitor genetic diversity during climate change: an approach based on niche marginality

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Genetic monitoring of populations currently attracts interest in the context of the Convention on Biological Diversity but needs long-term planning and investments. Genetic diversity has been largely neglected in biodiversity monitoring, and when addressed is treated separately, detached from other conservation issues, such as habitat alteration due to climate change. This is despite climatically marginal populations at the trailing niche margins of species are likely to hold genetic diversity that is important for adaptation to changing climate. Identifying climatically marginal populations should facilitate stratified genetic sampling designs that efficiently cover climatic gradients and provide an opportunity to adapt sampling efforts in areas of high priority for stakeholders. Here we present a climatic niche marginality index based on principal component analyses and kernel density functions to determine the distance of populations to the species niche margin. We first illustrate the approach with the Swiss stone pine and map its current and future distribution of climatically core and marginal areas. We then apply the approach to four taxonomic groups, including a large set of mammal, large bird, amphibian, and tree species with conservation interest in Europe. Current and future marginality, when mapped jointly in geographic space, provide an empirical hypothesis for the distribution of diversity of adaptive loci under climate change, indicating priority areas for targeted genetic sampling for each group. Identification of areas at the trailing climatic niche margins of species will support communication with stakeholders, as well as indicate important routes for gene flow from locally adapted populations.

139. BIOREALM: an ontology for biogeographic areas

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We would like to present BIOREALM, the first informatic ontology for comparative biogeography. We applied ontological techniques to address semantic ambiguities in protected area and conservation informatics. By doing so, we aimed to create a coherent, machine-actionable semantic representation of the biogeographic areas (which often overlap protected areas) to support more efficient and standardized informatics, supporting research, and decision-making. We convert a cladogram of biogeographic areas – generated by a process known as bioregionalization – into a series of ontological classes. Areas of endemism are treated as formal objects related by hierarchical relationships and constrained by a condition of monophyly. We use semantic web approaches to extend the Environment Ontology (ENVO) with classes for (often semantically confounded) biogeographic entities, including biogeographic areas, areas of endemism, and endemic areas. We applied this approach to a bioregionalization of Australia as a case study. We have created an ontology – formatted in the Web Ontology Language (OWL) and adhering to the practices of the Open Biomedical and Biological Ontology Foundry – which provides a rigorous, extensible, and machine-actionable framework that can improve biogeographic analyses and interoperability between systems. BIOREALM encodes a model-theoretic view of endemism using semantic web approaches, offering new avenues to express and analyse biogeographic units. This approach offers a means to identify monophyletic biogeographic areas for conservation, based on specific combinations of monophyletic endemic taxa. Such an ontology provides knowledge representation solutions which supports interoperability along the FAIR (Findable, Accessible, Interoperable, Reusable) principles, thus fostering more consistent ecological informatics.

140. Taxonomic, functional and phylogenetic dynamics and divergence during primary succession on lava flows

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Primary succession is among the most fundamental ecological processes because the creation of new surface and the subsequent development of de novo biological communities has occurred continuously throughout Earth's history. Succession is a process that affects all dimensions of species composition and diversity in biological communities, namely on a taxonomic, functional and phylogenetic level. We hypothesize that communities experiencing successional changes under differing resource availability (e.g., along an elevational gradient) will diverge in taxonomic, functional and phylogenetic aspects with time and test this using the plant communities of nine lava flows on La Palma, Canary Islands, spanning 6000 years of succession. In this study we introduce a new method based on changes of betadiversity through time to quantify successional speed for taxonomic functional and phylogenetic composition. Preliminary results indicate that species richness, functional richness and phylogenetic richness increase with time, whereas successional speed shows a hump-shaped relationship with time, peaking during early successional stages and gradually decreasing towards later successional stages. Taxonomic composition shows a divergence along the elevational gradient of La Palma towards increasingly dissimilar communities with time, whereas the patterns is not so clear for functional and phylogenetic composition. The early successional peak of successional speed is likely driven by changes in resource availability that are a function of successional processes like soil development and the establishment of different life forms (short lived vs. long-lived species). Successional speed based on betadiversity shows promising results to quantify successional dynamics and make them comparable across study systems and organisms.

141. Geometric causes of species rarity

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Understanding the factors that influence species range size is crucial, as it serves as a primary predictor for extinction probability. Species range size and shape are determined by various barriers, both outer (e.g., edges of continents) and inner (e.g., mountain ridges or boundaries of suitable habitats). We show that range size is related to the proximity to geographic barriers, and propose a geometric models that predict spatial patterns of species rarity and the approximately lognormal frequency distribution of range sizes. Additionally, we investigated the effects of diversity trends on range size distributions. Our findings indicate that while simple richness gradients do not impact range size distributions, more complex diversity trends do have an effect. Since the geometric model predicts fundamental patterns comprising range sizes, namely their frequency distribution and geographic patterns, it can be taken as the first-order theory of species geographic ranges.

142. Nutrient use by tropical ant communities varies among three extensive elevational gradients: a cross-continental comparison

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Many studies demonstrate that climate limits invertebrates along tropical elevational gradients, but we have only a rudimentary understanding of the role of nutrient limitation and climatic seasonality. Here we examined the relationships between ant community structure, nutrient use and season along three undisturbed elevational gradients, each from a different continent (Ecuador: South America, PNG - Oceania, Tanzania - Africa). Along each of the three gradients, we placed six distinct nutrients (amino acid, sucrose, sucrose + amino acid, lipid, NaCl, H_2O). In total, we distributed 2370 baits at 38 sites from 203 m to 3972 m. We tested the effects of elevation and season on ant species richness and activity and relative nutrient use. We also examined if changes in ant trophic guilds corresponded to changes in the use of particular nutrients. Both species richness and activity decreased similarly with elevation along each gradient. However, there were significant interaction effects among elevation, region and season, as ant activity in the dry season was higher in Ecuador but lower in PNG. The relative nutrient preferences were affected differently by season and elevation in each region. In contrast, the trends in the ant trophic guilds were consistent along the three gradients and thus did not explain the nutrient use patterns. We conclude that while the structure of ant communities change similarly with elevation, both the seasonal and elevational effects on nutrient use differ between continents. We argue that regional differences in climate and nutrient availability rather than functional community composition shape nutrient use by ants.

143. The fungi among us: Contrasting turnover between rare and common fungal endophytes across the global distribution of two widespread C4 grass genera

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Understanding the drivers of endophyte compositional turnover represents a major unresolved issue within microbial ecology. Host identity is often reported as the strongest predictor with abiotic factors and spatial distance displaying variable importance depending on the region or scale considered. Such findings have mostly been based off measures of beta diversity, which are heavily influenced by rare species. This necessitates an alternative measure of diversity capable of capturing the turnover of the full range of rare to common species. Zeta diversity can fulfil this need. Our aim was to assess the drivers of turnover of rare to common endophytes in two widespread grass genera. Endophyte community composition was quantified from *Themeda* and *Heteropogon* collected over a large portion of the grass' global range, using ITS rDNA metabarcoding. We applied zeta diversity analysis together with MS-GDMs to disentangle the relative contribution of host, abiotic and spatial variables in explaining turnover at both global and regional scales. Host identity was only a moderate predictor of rare endophyte turnover at both scales. Abiotic factors and spatial distance were consistently strong predictors of turnover of rare and common taxa at both scales, but the importance of different abiotic factors differed between geographic regions. Therefore, zeta diversity more robustly differentiated the factors affecting the full range of endophyte turnover compared to beta-diversity analyses alone. We show that across the range of rare to common species, host identity is less important than previously proposed, and abiotic factors and distance play an important role in predicting turnover in endophyte communities.

144. Predicting functional trait variation across climatic gradients with mechanistic models

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Climate imposes constraints on organismal trait diversity and evolution through its effects on physiological performance and fitness. As climatic conditions vary across space and time, these constraints also change, leading to predictable variation in functional traits such as body size and shape, skin color, physiological thermal tolerance, and behavior. Yet, understanding the mechanisms underpinning these patterns remains a challenge and the role of climate in modulating functional trait variation has been questioned. Here, we propose a mechanistic approach using biophysical models to numerically predict how different traits (body size, skin color, thermal tolerance limits, preferred body temperature and thermoregulatory capacity) should vary in relation to climate in order to maximize thermal performance in ectotherms. We show that climate drives macro-evolutionary patterns in body size, cold tolerance, and preferred body temperatures among lizards, and that trait variation is more constrained in regions where selection is predicted to be stronger. These findings provide a mechanistic explanation for observations on how climate drives trait variation in ectotherms through its effect on thermal performance. By connecting physical, physiological, and macro-evolutionary principles, the model and results provide an integrative, mechanistic framework for predicting organismal responses to present climates and climate change.

145. Temperature attributes responsible for local distributions of alpine plants

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The local distributions of alpine plants are predominantly determined by their temperature requirements. Therefore, the recent climate warming is expected to trigger strong changes in alpine plant communities. Predictions on climate-induced effects on alpine plants often rely on few, rather coarse, climatic parameters (e.g., annual and seasonal temperature means). However, temperature is a complex phenomenon with a myriad of impacts on plant performance and little is known about which temperature attributes are the most relevant for alpine plants. In this study, we relate the species composition of 900 plots located at Mt. Schrankogel (3,497 m a.s.l., Austrian Alps) to soil temperature measured for a two-year period using temperature loggers. We derived a set of 27 temperature attributes (e.g., daily means, daily maxima, GDH), each with annual, seasonal, and monthly temporal resolutions. We then (1) examined which temperature attributes are most relevant for the alpine plant distributions. In particular, we were interested if extreme values are better predictors of species distributions than long-term averages. And (2) we investigated whether the responsiveness of alpine plants to different temperature attributes can be explained by their function traits. We found that monthly and seasonal temperature attributes performed only slightly better than annual ones and that long-term averages were better than extremes. The profound variation between species was better explained by habitat affinity than their functional traits.

146. Global spatial potential for implementing land-based climate solutions

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Reducing climate change requires widespread deployment of land-based climate solutions (LBCS) - land use and land management strategies that reduce carbon emissions and increase carbon sequestration. The degree to which LBCS can address climate change depends on how much land is available for implementing climate solutions, but no studies to date have explored the global extent and distribution across which LBCS might compete for land. To address this gap, we derived high resolution spatially-explicit estimates of where 20 different LBCS could be implemented across Earth's surface. We asked how much land is available for mitigating climate change, and how much of this area encompasses an overlap between incompatible (e.g., solar and reforestation) vs. complementary climate solutions (e.g., enhanced weathering and natural forest management). We estimated 10.5 billion ha where climate solutions could be deployed, including 6 billion ha suitable for only one solution and 4.5 billion ha suitable for multiple LBCS. Complementary climate solutions were common in croplands and pastures, with global hotspots for increasing carbon sequestration in the Midwestern United States and parts of China. Conflicting climate solutions were most common in grassland habitats, in which large portions of grasslands could either be conserved, converted to forest, or used to expand renewable energy infrastructure. These overlaps indicate a large area of potential for LBCS to reduce global climate change. However, overlaps indicate choices society must make in terms of how we use land to mitigate climate. A better understanding of trade-offs across LBCS is therefore needed.

147. The opportunities and challenges of using genomic offset metrics to integrate local adaptation to climate into forecasts of future habitat suitability

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Ecological and evolutionary genomics and associated analyses of local adaption to climate increasing are being incorporated into macroecological forecasting models to assess climate change impacts on biodiversity and inform potential mitigation strategies. So called "genomic offsets", which quantify the expected disruption of genotype-environment associations under environmental change (i.e., the magnitude of expected maladaptation a population would experience under a future climate), allow for the incorporation of intraspecific climate-associated genomic differentiation into forecasts of habitat suitability and thereby provide a means to move beyond species-level assessment of climate vulnerability. Using red spruce, a cool temperature conifer endemic to forests of eastern North America, as a case study, we discuss opportunities and challenges regarding the use of genomic offset predictions to: (1) assess *in situ* climate risks, (2) map future habitat suitability while accounting for local adaptation to climate, and (3) identify populations harboring genotypes that, if transferred to new target locations, would minimize disruption of local adaptation to climate. In addition to discussing several novel offset-based metrics, we present how decisions made during the modeling process affect forecasts and induce uncertainty.

148. Increasing landscape connectivity can allow megaherbivores to maintain ecological function

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Mammalian herbivores are critical components of functioning ecosystems that are adapted to specific habitats. However, as climates change and anthropogenic footprints expand, ecological function will be threatened as trait-environment relationships become strained. Many species will need to move to track the climates that best suit them, but potentially be hindered by anthropogenic barriers. Here, we identified communities of large herbivores across continental Africa that will likely require re-composition due to shifting climates, and we assessed their potential to undergo such change. We did so by integrating ecometrics (the study of functional trait-environment relationships at the community level) and landscape connectivity (the study of the ability of landscapes to facilitate species movements). Using ecometric models, we identified the communities in which the relationship of body mass with temperature and/or hypsodonty with precipitation may be weakened in the future. We then used connectivity models to determine where the landscape may facilitate or impede the species movements necessary for certain communities to maintain strong ecometric relationships. Over 50% of communities could exhibit weak future ecometric relationships with respect to at least one trait, putting them at risk of depleted ecological function. Many communities that are at risk occur in low-connectivity regions, like the Sahel. Our results identify conservation strategies that are appropriate for different communities. In the Sahel, for example, landscape connectivity must be enhanced to maintain functioning communities. In regions where communities are at lower risk of depleted function, strategies that protect communities with their present species compositions could be implemented instead.

149. Legacy of climate change in the global relationship between mammal trait variation and ecosystem stability

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The natural processes promoting temporal stability in ecosystems are being disrupted by the global extinction crisis. Beyond the importance of species richness, the diversity of species' traits in an ecosystem confers stability and resilience to environmental disturbances. Although traits evolve to match the environmental conditions a species encounters, specific combinations of traits usually determine which species go extinct following a disturbance. However, most trait-related stability mechanisms (i) have been assessed by using different metrics of trait-abundance distributions within and across species, challenging application to rare/extinct species, and (ii) mostly focus on responses to short-term perturbation, thus disregarding longer-term trends (e.g., climate change) that make some regions more sensitive to disturbance than others. We developed and applied a new multidimensional trait-space approach to quantify spatial changes in different aspects of mammal trait diversity in response to variation in regional ecosystem stability worldwide. We first defined ecological stability in terms of resistance, resilience, and temporal variability based on the last 20 years of the satellite-derived MODIS enhanced vegetation index. We then explored the relative role of the last 20,000 years of climate change derived from general circulation model hindcasts to test a potential “long-term legacy effect” on spatial regional changes in mammal trait space and ecosystem stability. Our trait-space metrics identify which species and regions are more likely to respond to variation in ecosystem stability and we discuss the implications of our results in the context of changing ecosystem stability driven by climate change.

150. myClim: Microclimate data handling and standardised analyses in R

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Microclimates, influenced by climate, topography, and vegetation, yield distinct local dynamics crucial for ecological processes. However, the diverse array of microclimatic loggers and data handling methods has hindered data comparability and integration. To address this gap, we developed the myClim R package, offering a standardized, reproducible microclimatic workflow. Embracing open-source principles, myClim facilitates seamless data import from the fast-growing networks of microclimatic loggers. Processing and calculating ecologically relevant variables from microclimatic time-series with myClim ensure consistency across diverse studies. Unlike existing tools, myClim emphasizes simplicity and adaptability, accommodating various sensor types and field installations. Our package, outlined here, fills a critical void in microclimate research, promoting data integrity and comparability, which is beneficial for global microclimate time-series databasing and sharing. By providing a common ground for microclimate data analysis, myClim propels the field toward cohesive, global-scale ecological insights. The stable version of the myClim package, documentation, tutorials, and example data are available on CRAN (https://cran.r-project.org/web/packages/myClim). The development version and source code can be accessed on GitHub (https://github.com/ibot-geoecology/myClim).

151. Lagged plant species responses to recent climate change and their associated traits

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Understanding species' responses to climate change is an urgent inquiry, often obscured by delayed responses and extinction debts. Distinguishing these delayed responses from genuine resilience is crucial for accurate biodiversity forecasts. Moreover, discerning species traits linked to delayed responses could provide broad insights into species’ vulnerability to long-term climate change, enabling more timely and effective management. This study pioneers temporally dynamic species distribution models (TD-SDMs) and developed such models for plant species across Europe, using data from the European Vegetation Archives. TD-SDMs are calibrated using a moving chronological window of annual climatic predictors with increasing age from the time of sampling and validated against changes in relative abundance from resampled plot data. Hence, TD-SDMs are evaluated based on their ability to predict plot-specific changes in relative abundance, while accounting for potential delays in those responses to changing climatic suitability. Identified delays were then associated with species' plant functional traits and life-history data. Our resulting TD-SDMs represent unparalleled accuracy in predicting distributional responses to climate change at a continental scale covering thousands of species. These models revealed variations in past climatic windows (lags) that best predict changes in relative abundance. Associating delays with species' plant functional traits and life-history data, we found greater lags among species with tree growth forms, particularly those with greater wood density, seed mass, and leaf longevity. Our findings deepen our understanding of the factors underpinning species' vulnerability to long-term climate change, shedding new light on this complex ecological phenomenon.

152. Predicting range dynamics of butterfly species and their host plants with CATS during the 21st century: species interactions matter

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Anthropogenic climate warming causes various kinds of changes in species' ranges such as expansions, shifts, contractions or even total losses. These dynamics are influenced by the combined effects of the magnitude of climatic change, local population dynamics, the mobility of individuals, and interactions with other species. We extended CATS, a spatially and temporally explicit population and dispersal modelling framework, to predict the range dynamics of 21 oligophagous butterfly species across Europe at a 100 m spatial resolution. These species are not only affected by the spatial shift of their own climatic niche, but also by the climate change responses of their 101, less mobile, host plants. We were able to show that the climatic effect on host plant ranges will significantly affect the likelihood of whether and where future butterfly species ranges will coincide with their larval host plants under a warming climate. This result underlines the importance of considering species interactions in future biodiversity predictions.

153. Understanding the leading drivers of tree decline in semi-arid Zagros forests

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The decline of trees in semi-arid ecosystems is a multifaceted issue with substantial environmental consequences. This research explores the potential contributors to tree and forest decline within the Zagros forests of Iran. It primarily focuses on environmental drivers such as soil, climate, topography, and tree attributes. The outcomes reveal that certain environmental factors including slope and precipitation have a considerable impact on tree decline and exhibit variations across four categories healthy, slightly declining, moderately declining, and severely declining trees. This conclusion is derived from a comprehensive analysis using a generalized additive model (GAM), with the best combination of variables being slope, terrain wetness index (TWI), and BioClim-16 climate parameters. Notably, only two of these variables, slope, and precipitation were statistically significant (p-values: slope = 0.009, BioClim-16 = 0.02). In the case of forest decline within tree groups, the best GAM model highlighted the significance of soil organic carbon (SOC) among variables that included slope and silt, with a p-value of 0.03. Furthermore, a spectral analysis was conducted to compare bare soil in areas with forest decline and those without any noticeable signs of decline. This analysis revealed significantly decreased spectral values in the declining areas across all studied Sentinel-2 bands (i.e., VNIR-3, SWIR-2, red, green, and blue) using the Wilcoxon test. Our study advances our understanding of the leading drivers governing tree and forest decline in semi-arid forests, underscoring the importance of considering the spectral properties of bare soil in patchy forests to fully grasp the tree decline. **Keywords:** Tree decline, tree groups, Zagros forests, driver analysis, bare soil, Sentinel-2.

154. **Occupancy modelling based on automatically identified species data: tackling false positives**

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Occupancy models determine the probability of the presence of a species at a site. While they commonly address imperfect species detection (i.e., false negative errors), the problem of species misidentification (i.e., false positive errors) is often overlooked. This is because the inclusion of false positive parameters in occupancy models often requires confidence scores along with species detections, which are difficult to obtain from human surveys. However, with the growing popularity of automated species identification software (e.g. from image and audio data) and associated confidence scores, the issue of false positives is receiving attention in the context of occupancy models reliant on this type of data. In this study, we introduce an occupancy modelling framework specifically designed to tackle the issue of false positives arising from automated species identification tools. We have integrated a classification model into the traditional occupancy model, allowing us to categorize species identifications as either true or false positive detections based on corresponding confidence scores. This categorization then facilitates the estimation of species occupancy and detection probabilities. To evaluate our proposed model, we first examine the consequences of disregarding false positives and false negatives on variable inference and predictive performance using simulated data. Subsequently, we apply this proposed model to real-world bird survey data collected through passive acoustic monitoring, using the avian species identification software BirdNET. Finally, based on our findings, we illustrate how this modelling framework offers a robust approach for improving species predictions in biogeographical research.

155. **TABS: R package for reconstructing altitudinal shifts in biogeographical systems over time**

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Paleoclimatic variations have had a major impact on the spatial distribution of global ecosystems, shaping present-day biodiversity. To truly understand these dynamic alterations in spatial arrangement, extent, and connectivity of ecosystems, we require spatially detailed reconstructions over continuous time series. Examples of key systems include oceanic islands and alpine regions influenced by altering coastlines and treelines respectively. However, a comprehensive and reproducible methodology to capture this dynamism remains elusive. Here, we introduce the Temporal Altitudinal Biogeographical Shifts (TABS) R package: a tool designed for constructing spatial configurations over time, focusing on biogeographical systems with altitudinal gradients. We demonstrate the use of TABS to model the historical shifts in island areas and archipelago configurations influenced by past sea level changes. Unique to TABS, it also accounts for crustal deformation due to ice sheet loading, gravitational forces, and geological changes due to uplift and subsidence. Beyond historical reconstructions, TABS can project spatial responses to future climatic and sea level transitions. This versatile package is easily adaptable to various systems, such as alpine biomes, shelf seas, and other biogeographical entities influenced by long-term climate oscillations. Understanding the shifts in ecosystems through continuous spatial reconstructions, rather than isolated snapshots in time such as the Late Glacial Maximum or specific years, captures the nuances of continuous change and provides a more complete understanding of the biogeographic history of our planet.

156. **Unveiling the effects of climate databases on ecological niche models of forest species across scales**

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Many studies have explored biases and uncertainties related to data inputs such as bioclimatic variables as predictors in ecological niche models (ENMs), but the effect of choosing a specific database among the different alternatives has not been deeply assessed across spatial scales. We addressed the effect of bioclimatic data from different open access platforms on the predictive capacity of ENMs of more abundant conifer and broadleaved species at regional (Iberian Peninsula) and continental (Europe) scales. We selected four broadly used climate databases (CHELSA, WorldClim, EuMedClim and Envirem). For each species and climate dataset, we calculated ENMs using an ensemble forecasting approach. Overall, the models performed very well based on the AUC and TSS scores across spatial scales, with coniferous species outperforming broadleaved species. The predictive capacity of ENMs based on the different climate datasets was significantly different between type of species (conifers vs. broadleaved). The contribution of each bioclimatic predictor also differed between species and datasets, being more important rainfall and temperature on broadleaved and conifer, respectively. The overlap analysis also showed a significant variability in the spatial projections of the different climatic-based ENMs. In conclusion, choosing the correct bioclimatic input data is key to avoiding erroneous conclusions when performing macroecological and biogeographic studies at different spatial scales, which is essential to develop successful decision making. This study is partially funded by national funds through FCT – Fundação para a Ciência e a Tecnologia under the MTS/BRB/0091/2020 project, and the TED2021-131722B-I00

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157. Novel model opens up new opportunities to analyse geographic patterns in animal demography

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Geographic patterns in population size and population trends are one of the most important and interesting phenomena in ecology and conservation. In studies where animals are individually marked and recaptured, even deeper insights can be acquired by decomposing the population growth (interannual change in population size) into demographic parameters – survival and recruitment. A well-known Pradel (1996) model has done this job for many taxa in more than 500 studies. Unfortunately, this model cannot be used for analyzing capture-mark-recapture data from continental-scale citizen science programmes (e.g., constant-effort sites bird ringing programmes in Europe and North America), due to the presence of transient individuals. Transient individuals are those who simply pass through the territories of local (resident) populations, not contributing to their demography. We present a long-awaited extension of the Pradel model that works also for populations with transients. This novel extension significantly opens up the use of this model, since a wide range of populations across many taxa feature transient individuals. Namely, it allows one to study continental-scale geographic patterns in the demography of populations described by the abovementioned citizen science data sets. The model can serve for a wide range of follow-up analyses to reveal geographic patterns in population dynamics and demography. For example, it immediately reveals the patterns in how variation of survival and recruitment affects the total population growth rate. We will present the model and show its practical application with examples.

158. eMaxent: an extended and improved maximum entropy algorithm for species distribution modelling

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Maxent, a versatile machine learning technique, has long been the go-to tool for modelling and predicting species distributions under limited data, spanning multiple applications. This scientific discourse's primary focus has been optimising usage and parameter tuning. Yet, the prospect of enhancing or expanding the foundational algorithm remains largely unexplored owing to its initial release as a closed-source software in Java—a programming language not widely favoured amongst ecologists. Our research introduces eMaxent, a groundbreaking extended Maxent algorithm for species distribution modelling (SDM), accommodating presence-only and abundance data. Developed in R, a preferred language among ecologists, eMaxent refines Maxent by addressing background selection, feature engineering, and regularization procedures. Notably, eMaxent offers innovative background data selection to counteract sample location bias and introduces spatially explicit features. The ELSA method measures environmental variables' local

spatial autocorrelation at pixel level over varying geographical distances. eMaxent expands on Maxent's L1 regularization with L2 and elastic net methods.

We evaluated eMaxent across multiple species and geographical scales, comparing its performance to Maxent. Results demonstrate significant model accuracy improvement, measured by AUC and TSS, particularly when used with finer scale predictor variables such as land cover data, which exhibit local variation.

The source code of this advanced modelling method will be publicly accessible via a GitHub repository for further exploration, evaluation, and expansion by the ecological and scientific community. Additionally, a complimentary R package, eMaxent, has been developed to support the user-friendly creation of SDMs.

159. Global patterns of taxonomic concept uncertainty in biodiversity databases

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Databases of species occurrences such as GBIF are increasingly important in global biodiversity monitoring and the study of species at broad spatial scales. However, the heterogeneity of data sources feeding these databases constrains their usability without flexible methods to resolve data conflicts. Taxonomic concept mismatch is one key challenge in which occurrences under the same scientific name differ in name meaning (i.e., circumscription) due to taxonomic revision. Concept mismatches create ambiguity in the taxonomic identity of occurrences, leading to frequent misassignment of stored information. Thus, methods are needed to 1) detect taxonomic concept mismatches at database scales, and 2) characterize global patterns of concept-mismatch derived taxonomic uncertainty in biodiversity databases. We share a generalizable method for detecting taxonomic concept mismatches in occurrence databases at the scale of major species groups (tested on the set of all mammal species). We created 17 metrics predictive of mismatch, based on the spatial and metadata properties of species and their occurrences. We then manually verified the mismatch status for occurrences of 200 mammal species, and used these manually classified species to train a logistic regression model predicting taxonomic mismatch status using mismatch metrics, achieving upwards of 73.5% prediction accuracy. We identify the key drivers of mismatch potential, and illustrate the corresponding global patterns of taxonomic concept uncertainty for mammalian species. Methods for flagging species with taxonomic concept mismatch, when integrated into informatics workflows, will facilitate improved documentation of taxonomic uncertainty and more responsible data use from global biodiversity databases.

160. Mapping more of biodiversity - modeling advances to improve data-deficient species distribution estimates

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In recent decades, ecology has seen unprecedented growth in the amount and variety of biodiversity data collected. Species distribution models (SDMs) are a popular tool used to relate occurrence data with environmental variables to characterize a species distribution. Conservation planning fundamentally depends on maps of species’ current and future habitat suitability. However, the accuracy with which SDMs can model species' distributions is limited by the amount of data available- as much as 30% of known species continue to lack sufficient data to allow for appropriate characterization of their geographic distributions. While SDMs have become increasingly sophisticated, they are unusable for data-deficient species. Here we present a novel modeling framework that extends SDMs to allow data-deficient species to borrow predictive strength from data-rich species. Specifically, we demonstrate how shared evolutionary history among species can inform the likelihood of shared environmental distributions and be used to estimate the spatial distributions of data-deficient species. We explore how this model can improve species richness maps of South American hummingbirds by improving individual data-deficient species estimates. This work represents a concrete way forward for SDMs to allow the integration of ancillary information and has wide applicability in helping us estimate how our biodiversity is likely to be distributed across geographic space. By better understanding how species are distributed in geographic space, we can develop more effective conservation strategies. We go a step further to demonstrate how this framework can be used to estimate data-deficient species' climate vulnerability, often for the first time.

161. Predicting vulnerability to future climate change with models and paleo-archives

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Accurately predicting biodiversity loss from climate change requires a detailed understanding of the ecological characteristics and metapopulation processes that make some species more susceptible to declines and extinction. However, the ecological attributes that increase extinction risk from climate change are poorly resolved. This is because ecological responses to climate change are complex and hard to quantify correlatively. I will show how biological data from the late Quaternary can be combined with simulation models to disentangle complex interactions between ecological traits, metapopulation dynamics, climate and other threats to megafauna. I will then show how this deeper understanding of the structure and dynamics of megafaunal extinctions is enabling species responses to climate change to be contextualized and integrated into future biodiversity projections and policy. By providing a more complete understanding of the ecological mechanisms that regulate species' responses to climate change, paleo-archives can deliver lessons to safeguard Earth's remaining large animals.

162. Substantial light woodland and open vegetation characterised the temperate forest biome before Homo sapiens

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The extent of vegetation openness in past European landscapes is widely debated. In particular, the temperate forest biome has traditionally been defined as dense, closed-canopy forest; however, some argue that large herbivores maintained greater openness or even wood-pasture conditions. Here, we address this question for the Last Interglacial period (129,000–116,000 years ago), before *Homo sapiens*-linked megafauna declines and anthropogenic landscape transformation. We applied the vegetation reconstruction method REVEALS to 96 Last Interglacial pollen records. We found that light woodland and open vegetation represented on average over 50% cover during this period. The degree of openness was highly variable and only partially linked to climatic factors, indicating the importance of natural disturbance regimes. Our results show that the temperate forest biome was historically heterogeneous rather than uniformly dense, which is consistent with the dependency of much of contemporary European biodiversity on open vegetation and light woodland.

163. The Transformative Holocene: Evaluating the influence of environmental and genetic factors in the expansion of domesticates in West Eurasia

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Humans and the environment are intimately tied to each other. Humans modify the biomes they occupy, and in turn, biotic and climatic processes determine how humans organise their livelihoods. Thus, a complete view of the human-environment relationship can only be obtained by unifying data across disparate fields, including archeology, genetics, and ecology. This will ultimately help us understand how demographic, social, cultural, ecological and evolutionary processes unfolded and influenced each other in space and time. Here, we aimed to take an interdisciplinary approach to the Neolithic and Bronze Age transitions in Western Europe - periods characterised by major movements of peoples across vast regions of Eurasia, and the concurrent spread of various agricultural and husbandry techniques, with deep changes in the vegetational landscape. We used more than 1300 ancient human genomes to infer ancestry proportions and estimate human mobility in space and time. We used these estimates to explore the spatiotemporal relationships between human movements, climate, and the effects of the expansion of domestication and cultivation of animals and crops, by combining them with archaeobotanical, archaeozoological records, and paleovegetation reconstructions stored in a database of human prehistorical and historical records (BIAD), covering vast areas across West Eurasia. By co-analyzing these disparate sources of data, we are able to obtain a comprehensive picture of the drivers and consequences of changes in human mobility, faunal and floral composition on the West Eurasian landscape over the past 10,000 years.

164. Functional Diversity Patterns Across the Ediacaran

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The Ediacaran (635-538 Ma) is characterized by profound changes in global biodiversity, with the evolution of macrofaunal communities, emergence of complex ecological interactions, and an escalation in animal ecosystem engineering. Reconstructing the paleobiology of enigmatic Ediacaran organisms and how they functioned within communities is thus pivotal to understanding the changing character of the first animal ecosystems. Here, I leverage new data surrounding the functional ecology of Ediacaran organisms to test how the evolution of new bodyplans and behaviors influenced community structure. Using genus-level occurrence and functional traits, I quantify

Ediacaran functional diversity within fossil communities for the three recognized subdivisions of the late Ediacaran: the Avalon, White Sea, and Nama ‘assemblages’. I compute three functional diversity indices – Functional Richness (FRic), Functional Evenness (FEve), Functional Divergence (FDiv) – for each community, and examine how their distributions change through time. Each functional diversity index responded differently over the late Ediacaran. The volume of community trait space (FRic) increases in the White Sea and then decrease in the Nama, reflecting fluctuating taxonomic richness and putative extinction events. Ediacaran communities remain relatively constant in the distribution of occupied trait space (high FEVe, middling FDiv). However, the contribution of different traits varies over time. Body size and branching pattern contribute heavily to FEve the Avalon, but by the Nama these have little to no effect. Functional diversity patterns in the Nama may instead be driven by niche partitioning between taxonomic groups. Thus, the effect of traits on community functional diversity likely changed with broader ecological shifts.

165. The biogeography of the Great American Biotic Interchange

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The faunal exchange between North and South America (Great American Biotic Interchange – GABI) is one of the greatest biotic exchanges at a continental scale. Diversification and dispersal dynamics of the GABI have been studied at the continental level, but the regional biogeographic patterns remain unexplored. We analyze the spatio-temporal distribution of fossil and modern mammals to evaluate biome-wide differences in GABI diversity and dispersal dynamics. We find that the success of mammals with North American origin (NAO) in South America was unequal across biomes, contrary to the traditional view of its widespread continental success in terms of species richness and persistence of lineages. NAO clades dominate in temperate biomes of both continents and the Andean highlands, but not in tropical biomes of South America. When examining the latitudinal gradients of speciation rates, NAO clades show higher rates than South American origin (SAO) clades, especially at higher latitudes of South America. For lowland forests and grasslands, the NAO clades have higher rates of speciation in temperate regions than SAO clades, and this difference decreases toward the tropics. Our results suggest that biome preference and size played a major role in GABI dispersal and diversification dynamics. Moreover, the latitudinal distribution of SAO and NAO clades shows that the modern latitudinal diversity gradient is mostly driven by the SAO clades, which show the strongest gradient. Pliocene extinction of several SAO fossil clades in temperate South America seems to be the primary reason for the strong latitudinal diversity gradient seen in SAO clades today.

166. I estimate the rains down in Africa: Building ecometric models using small mammal hypsodonty to estimate paleoprecipitation across eastern Africa

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Ecometric analyses examine the relationships between functional traits and the environment at the community level to quantitatively estimate past climatic and environmental variables at fossil sites.

Hypsodonty (tooth crown height) in North American rodent and lagomorph (Glires) communities is correlated with mean annual temperature and annual precipitation. Here, we examine community hypsodonty of Africa Glires to test if this relationship exists on a continent with many extreme climates. Categorical hypsodonty values were gathered from the literature and museum collections for 94 modern African taxa (88%). Hypsodonty had a stronger linear correlation with annual precipitation ($r^2=0.61$, $p<.001$) than with mean annual temperature ($r^2=0.09$, $p<.001$). We modeled trait-based estimates of paleoprecipitation for 26 well-sampled fossil localities from eastern Africa. Precipitation trends were highly variable across Kenya, Ethiopia, and Tanzania over the last 5.7 Ma. We confirmed other regional studies by identifying increasing aridity and decreasing annual precipitation (824 mm to 480 mm) in the Late Miocene of Kenya. From the Ethiopian Shungura Formation, we estimated temporal fluctuations in precipitation that correspond with presence or absence of paleolakes and rivers. Small mammal community hypsodonty illustrates that communities have converged towards a mesodont mean and high standard deviation in response to climate change.

167. The effects of climate change on fossil diversity of Asian mammals through the Paleogene: regional aridification vs. global cooling

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Due to conflicting results of paleobiological studies, it is unclear how global vs. regional climate changes in Earth history have affected large-scale biodiversity dynamics through time. Here, we reconstruct the diversity of fossil Asian mammals through the Paleogene, ca. 66-23 million years ago (Ma). Starting with mammalian diversification in global warmhouse climates, the Paleogene contains a striking global cooling event at the Eocene-Oligocene transition (EOT) ca. 34 Ma, which has been linked to Antarctic icesheet formation and extensive regional aridification. In Asia, previous studies have shown mammalian compositional changes across the EOT (the “Mongolian Remodeling”), with assemblages shifting from perissodactyl-dominated faunas to those dominated by smaller-bodied Glires, argued to be better adapted to dry environments with limited resources. However, recent palaeoenvironmental records and novel climate models show much earlier drying in west-central China during the mid-Eocene at roughly 40 Ma. Contrasting these two climatic events, the earlier regional aridification and the later global cooling, we quantify sampling-corrected mammalian alpha and beta diversity in central East Asia. We recover substantially lower mammalian diversity in the mid-Eocene and declines after the EOT. In addition, we show increased compositional turnover at both events. This suggests that regional mid-Eocene aridification in Central Asia may have driven faunal shifts similar in magnitude to those linked to the EOT global cooling event. Furthermore, our analyses indicate declines in both perissodactyl and rodent diversity across the EOT, suggesting that the “Mongolian Remodelling” may be partially influenced by sampling biases in the fossil record.

168. Warming worlds of the past: paleobiogeographic changes in the Asian continental interior during early Eocene hyperthemals

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The early Eocene (c. 56–48 million years ago (Ma)) was a time of global greenhouse conditions, with polar regions devoid of ice and a much less pronounced latitudinal diversity gradient than at present. To reconstruct the biotic communities of this much warmer world, it is essential to study the fossil record in combination with paleoclimate proxies such as isotopic records and precise dating methods. The Xining Basin, situated on the Northeastern Tibetan Plateau (China), presents this opportunity, as it holds an extensive and well-dated Paleogene (c. 66 to 34 Ma) sedimentary sequence with abundant fossil sporomorphs (i.e. pollen and spores) that enabled us to reconstruct past vegetation composition. The Eocene sedimentary record in this basin is composed of red mudrocks, sandstones and gypsum beds, suggestive of alluvial plain and sabkha conditions, whereas the palynological record points at a vegetation composed of steppe-desert shrub taxa. However, the sedimentary record also includes evidence for at least one hyperthermal event (i.e. a period of sudden warmer and wetter conditions) in the early Eocene. Notably, the palynological record for this event shows that trees and ferns took over much of the area that was previously occupied by the aridity-minding shrubs, resulting in a phase of ‘greening-the-desert’. The presence of conifer pollen from podocarps further indicates the (temporary) northwards expansion of southern hemisphere-temperate forest taxa. Although it is challenging to translate the biotic response in the Eocene to future scenarios of global warming, our data show that the Eocene hyperthermal turned the Central Asian deserts into a landscape with lush vegetation that accommodated species that immigrated from far afield.

169. **Late-Quaternary megafauna extinctions have greatly reduced mammalian vegetation consumption**

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How much stronger would the effects of herbivorous mammals be in natural ecosystems if human-linked extinctions and extirpations had not occurred? Many mammal species have experienced range contractions, and numerous species have gone extinct in the late Quaternary due to human pressures. Therefore, herbivore consumption rates in seemingly natural ecosystems likely deviate from their pre-anthropogenic state.
We estimated and mapped the reduction in mammal plant consumption. We accomplished this by estimating the natural densities and dietary requirements for all late-Quaternary terrestrial mammals. We mapped their consumption rate in both current ranges and present-natural ranges, i.e., estimated ranges in the absence of human-linked range contractions and extinctions. We compared

these estimated consumption rates to the current net primary productivity. We summarized the results across all ecosystem types, including the remaining wilderness areas.

We estimate that wild mammals consume approximately 11% of the net primary productivity in natural areas. However, if extinctions and extirpations had not occurred, the consumption rate would have been much higher, specifically 21%. The loss of mammals results in a median 42% reduction in consumption rate. Importantly, we estimate very similar declines in herbivory in what are considered the last remaining wilderness areas.

Our findings indicate that the natural interaction between mammalian herbivores and vegetation in ecosystems across the globe has greatly declined due to prehistoric, historic, and recent species loss. This reduction in interaction is evident even in the few remaining wilderness areas and is likely to have significant impacts on the structure and functioning of ecosystems.

170. Environmental filtering, not dispersal history drives global patterns of phylogenetic turnover in seed plants at deep phylogenetic timescales

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Phylogenetic beta diversity quantifies dissimilarities in the evolutionary relatedness among assemblages and is important for understanding the underlying mechanisms structuring biodiversity. Environmental filtering and dispersal history are two main processes that limit plant distributions and determine biogeographical patterns, and their relative importance might vary across evolutionary timescales. Here, we examined the effects of environmental dissimilarity and past and current geographical distances on the turnover component of phylogenetic and species beta diversity of seed plants globally and across phylogenetic timescales. To calculate species and phylogenetic turnover, we used a global dataset of regional plant inventories across 675 geographic regions comprising ~ 320,000 species matched to a mega-phylogeny of seed plants. To account for past and present dispersal opportunities, we used historical reconstructions of tectonic plate arrangements and calculated geographical linear distances and cost distances accounting for the cost of crossing water bodies, mountains, or unsuitable climates. Geographical distances and environmental dissimilarity together explained species turnover better (up to 86.4% of deviance explained) than phylogenetic turnover (up to 65.7%). The effect of geographical distances diminished when moving back in evolutionary time, while environmental dissimilarity always showed strong effects on phylogenetic turnover. Past cost distances across barriers explained a comparatively low amount of variation across all timescales, peaking slightly at intermediate phylogenetic timescales (20 – 50 Ma BP). Our results suggest that old lineages had enough time to disperse widely, but the fingerprints of environmental limitations on spatial patterns of plant diversity persist, providing insights into the biogeographic and evolutionary processes underlying global biodiversity patterns.

171. Equilibrium Theory of Biodiversity Dynamics: Identifying patterns, parameters, and predictions using simulations

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Recent evidence has come to light supporting the existence of biodiversity limits at multiple spatiotemporal scales, yet the mechanisms behind these limits remain poorly understood. An emerging theory, (the equilibrium theory of biodiversity dynamics; ETBD), suggests that there is a carrying capacity for species richness (an equilibrium) which is driven by the relationship between

energy availability, species richness, total abundance, and population size dependent extinction or speciation rates. To explore this theory in more detail, we developed an R package to make simulation models that produce patterns in species richness and evolution *via* the assumptions of ETBD. We performed a full factorial exploration of parameter space and assessed the relative importance of the parameters on the variation of emergent patterns. We show that ETBD can produce ecologically realistic patterns. We also find that diversity dependent speciation and extinction generate distinct and predicable patterns in phylogenetic trees. Lastly, we note that explicit population-based parameters like species abundance distribution and asymmetry in speciation splitting are the key parameters responsible for these patterns. This exploration reveals that population level processes may be important drivers of larger macroecological and evolutionary processes.

172. The Potential for Re-evaluating Biodiversity Patterns in Environmental Space

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Macroecological questions addressing diversity-environment relationships have been evaluated almost entirely in geographic space, yet most hypotheses are formulated in terms of environmental conditions. The few recent examples that have evaluated patterns directly in environmental space indicate that such refocusing provides different perspectives on the mechanisms driving broad scale patterns of diversity. Yet we lack both conceptual frameworks and macroecological studies to fully evaluate the potential contribution of such a re-focusing on environmental space. Here we introduce the concept of environmental space and briefly review how the concept has been used in four main endeavors: species distribution modeling, macroecological, correlates of species diversity, macroecological rules and macroevolution. In doing so, we lay the groundwork for how the concept, methodology and common language could be extended and used in future cross-field research aimed at uncovering new knowledge about the generation and maintenance of diversity and protecting current biodiversity on our changing plant. A focus on environmental space will likely not only reinforce geographically based hypotheses but also reveal hidden effects of the environment on biological diversity that are missed when the focus is on geographic space alone. We encourage a re-evaluation of hypotheses ad frameworks that have dominated ecological theory since the foundations of ecology with a very simple shift in the lens, that is from geographical to environmental space.

173. Environmental space and species turnover explain the land-sea biodiversity paradox

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Why do some areas of the globe have more species than others? Providing an answer to this simple question has proved difficult, but answering it is crucial to understand how Earth's biodiversity has formed and to ensure its survival into the future. One often-invoked driver of species richness is total geographic area, yet while more than 70% of the Earth is covered by ocean, most species are found on land- the so-called land-sea biodiversity paradox. In an attempt to resolve this paradox, we compiled a distributional dataset of 307,467 terrestrial, freshwater and marine taxa, spanning plants, vertebrates and invertebrates, and combined it with data on major climatic axes of temperature and productivity. We find that while terrestrial and freshwater taxa occupy less geographic space, they span several times more environmental space than marine taxa. In addition, terrestrial taxa have smaller range sizes and higher assemblage turnover than oceanic taxa. Taken together, our results suggest that size of the available climatic niche space, and how this environmental space is packed, is more important for determining richness than sheer geographic area. Our results provide a general understanding of global biodiversity accumulation and point to new strategies to conserve biodiversity by protecting the environmental space that species occupy, as opposed to only the geographic space.

174. Reclassifying biomes: a new climatic R function

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The existing relationship between climate and terrestrial biomes offers a valuable opportunity to investigate how past and future climate changes impact both the environments and the fauna that inhabits them. Such relationship enables biome characterization through climatic features alone, without the need for detailed information on other essential factors, such as vegetation. The emergence of new geospatial methodologies in parallel with the development and widespread use of cutting-edge programming tools ushers in the opportunity of applying new and improved techniques for the analysis of climatic variables and the distribution of biomes. In the context of climatic-induced biome changes, and in alignment with this methodological trend, we harness Geographic Information System (GIS) tools in R language to develop a novel function designed to reclassify the data and identify global biomes based on climatic characteristics, building upon Walter's (1970) biome classification. Our reclassification function solely relies on mean monthly temperature and precipitation data, from which it calculates various other variables linked to aspects as hydric and thermal seasonality. To illustrate the potential of this new function, we present the current configuration of global biomes using pre-industrial data. Our work provides researchers with a new, easy-to-use, and reliable tool for biome projection, adaptable to diverse temporal and spatial scales.

175. Range overlap, clade density and the evolution of diversity-dependent diversification

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The assumption of an ecological limit to the number of species in a given region is frequently invoked in evolutionary studies, yet its empirical basis is remarkably meager. We explore this assumption by integrating data on geographical distributions and phylogenetic relationships of nearly six thousand terrestrial vertebrate species. In particular, we test whether sympatry with closely-related species leads to decreasing speciation rates. We introduce the concept of clade density, which is the sum of the areas of overlap between a given species and other members of its higher taxon, weighted by their phylogenetic distance. Our results showed that, regardless of the chosen taxon and uncertainty in the phylogenetic relationships between the studied species, there is no significant relationship between clade density and speciation rate. We argue that the mechanistic foundation of diversity-dependent diversification is fragile, and that a better understanding of the mechanisms driving regional species pools is sorely needed.

176. Biogeographical cradles and museums segregating within Andean hotspots of endemism

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Global vertebrate diversity concentrates within tropical mountains, with the Andes as the World's most species-rich region. The Andes' extraordinarily high diversity derives from numerous local hotspots with immense concentrations of endemic species. A classic explanation for hotspot of endemism is that they are both cradles for young species and museums for old species caused by high speciation rates combine with the long-term persistence of local populations, respectively. Broad-scale patterns in species distributions confirm that young and old lineages tend to aggregate within tropical mountains. However, such patterns are typically obtained at coarse spatial resolutions and may not scale down to valley systems of mountain regions where the hypothesised speciation–extinction dynamics is proposed to occur. Using high-resolution occurrence and phylogenetic data on Andean hummingbirds at the scale of valleys, we find contrary to the classic hypothesis that old and young endemic species are spatially segregated, not aggregated, and associated with distinct habitat types. The young endemic species tend to have non-overlapping distributions scattered along the Andean treeline, a long and narrow habitat where populations quickly become fragmented by environmental and demographic stochasticity. By contrast, the old endemic species have more aggregated distributions, mainly within the broad cloud forest belt at the mid-elevation. These findings contradict the premise that biogeographical cradles and museums should overlap in valley systems where pockets of stable climate persist through periods of climate change. Instead, Andean biodiversity hotspots may derive from large-scale fluctuating climate complexity in conjunction with local-scale variability in available area and habitat connectivity.

177. Genetic diversity and habitat stability in Sahara-Sahel vertebrates

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In North Africa, Plio-Pleistocene climatic fluctuations between green and desert states left deep imprints in biodiversity patterns. Mountain and coastal areas seem to have functioned as refugia, at least for more mesic species, and a series of trans-Saharan mesic corridors have been hypothesised. However, these biogeographic hypotheses have only been based on a handful of species. Xeric species should also present different patterns, but even less work has been done on them. Thus, this work aims to map vertebrate diversity patterns in the Sahara-Sahel and consolidate and test biogeographic scenarios for the post-Miocene. We used nearly 8500 geo-referenced DNA sequences and 28000 occurrence points from 107 species to map intra-specific genetic diversity (ISD), and model past species range shifts. By analysing the concordance between genetic and ecology-based inferences, we attempted to identify diversity hotspots, refugia and corridors, and compare spatial patterns among mesic and xeric species. For xeric taxa, northern Sahara and southwestern Sahel were identified as diversity hotspots. Genetics and ecology supported northern Sahara refugia, which extended southwards. Discrepancies between genetics and ecology were detected in the Libyan desert and most of the Sahel. For mesic taxa, ISD hotspots covered most Saharan highlands, the Nile Valley, coastal areas, and the Niger Delta. Refugia were mostly concordant, with inconsistencies in highlands in eastern Sahel, and the western Nile Valley. Xeric corridors included the Atlantic Sahara, the Nile Valley outskirts, and the eastern Sahel. Mesic corridors included the Atlantic coast, Central Sahara highlands, and western Sahel.

178. Spatial patterns in vertebrate attractiveness reveal hotspots of untapped flagship potential

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In the CBD Post-2020 Global Biodiversity Framework nations have committed to protecting 30% of land and sea by the year 2030. However, current protected areas can already suffer from suboptimal management and significant funding shortfalls, raising questions over how area-based conservation can be efficiently, rapidly and equitably expanded to meet these ambitious goals. In this context, many have advocated the use of conservation marketing techniques to influence policy and conservation funding streams. One widely used conservation marketing technique is the flagship species concept, whereby highly charismatic and attractive species are leveraged to promote conservation and drive public and private investment in nature. However, such promotions have largely focused on a small number of species, with many 'Cinderella' species - overlooked species with flagship potential – remaining underutilised. Here, we present findings from trait-based predictive models of species attractiveness to humans for 24,750 terrestrial vertebrates, mapping the distribution of vertebrate attractiveness globally. From these data we identify global hotspots of species attractiveness and 'Cinderella Zones' in Ethiopia, south-southeast Asia, and the Amazon Basin. Cinderella Zones support a high richness of attractive species but a paucity of existing flagships, and represent spatial priorities for investment in area-based conservation and developing wildlife tourism opportunies, where appropriate. Finally, we use species distribution models to assess how future climate and land use change will alter the distribution of threatened and attractive species, to identify priorities for protected area expansion where refugia for threatened biodiversity aligns with high numbers of attractive species with untapped flagship potential.

179. USING ECOLOGICAL NICHE MODELING AND BIOGEOGRAPHY AS A MODEL FOR PREVENTING BAT BORNE RABIES

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In the era of global change and anthropogenic disturbance, rabies remains one of the oldest and most lethal of all zoonotic diseases currently impacting human and animal health. A key reservoir of the rabies virus in wildlife are bats, who have been found to carry the virus across the American continents. In Colombia, the common vampire bat (*Desmodus rotundus)* functions as a main transmissor of the rabies virus to humans, other wildlife, and to domesticated livestock species such as cattle. As such, this species has massive social and economic impacts on the health and agricultural sectors of Colombia. Vaccination has proven to limit the scope and spread of rabies outbreaks, but where and when to target vaccination efforts remains uncertain, especially in resource limited areas. Ecological niche modeling has proven to be an effective tool to identify and anticipated current and future species distributions using different predictor variables. This study aimed to use curated rabies outbreak and agricultural intelligence, targeted field sampling, and country level geographic information to identify vampire bat and rabies outbreak hotspots within Colombia. We also identified key factors which facilitate rabies outbreaks, and used this information to forecast areas in which vaccination can be targeted. By utilizing biogeographic principles and methods, our modeling framework could be used to elucidate areas of concern for bat borne rabies outbreaks in other countries and regions, and could be used functionally for preventative interventions by public health and agricultural organizations.

180. Drivers of long-term occupancy trends in three insect taxa in Central Europe

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Recent changes in climate and land-use substantially impact biological organization including population declines, range shifts, and changes in community composition, while conservation policy like the European Habitats Directive aims to protect biodiversity from negative impacts. However, few studies have managed to compare these drivers among multiple taxa in insects especially, particularly because of a lack of standardized long-term time series data. In addition, existing datasets are typically of low resolution or poor coverage, thereby limiting what inferences can be made from their use. Here, we analyse occupancy changes in butterflies, grasshoppers, and dragonflies using an extensive dataset of heterogeneous observation data collected in the central European region of Bavaria over a 40-year period. Using occupancy models, we show that the occupancies of cold-adapted species across taxa declined in past decades, while those of warm-adapted species increased. In butterflies, habitat specialists decreased, while in the other taxa there was no difference between habitat generalists and specialists. Ant-dependence may have had a stabilizing effect on Lycaenid butterflies. We show that contrary to its main goal, the European Habitats Directive did not prevent a worsening of species status as the occupancy trends of species protected in ist annexes both improved and deteriorated after its implementation.

Our findings illustrate not only why butterflies, grasshoppers, and dragonflies showed differing trends in the past as well as the effectiveness of Europe's most important nature protection instrument, but also how we might mitigate the detrimental effects of human development on species' diversity in the future.

181. A global model of changes in human terrestrial impacts over five decades

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Identifying socioeconomic and ecological factors that contribute to global human environmental impacts is needed to understand how to mitigate these impacts, and their consequent effects on humans. Human appropriation of net primary production (HANPP) is a measure of human resource use and land use change that indicates the global extent of terrestrial human impacts. Models to predict HANPP have been limited spatially, temporally, and/or by data. We investigate possible predictors of national-level HANPP at a global scale from 1960 to 2010 using Bayesian methods with R-INLA. R-INLA advances beyond other spatiotemporal methods because of its computational efficiency and by using time-steps as iterative priors rather than vague random effects. I compared models with economic, social, and agricultural predictors, alone or in combinations. A model combining economic and social predictors best predicted HANPP over time and space (lowest DIC; observed values: fitted values R2 = 0.99) and showed overall spatial stability in global HANPP through the five decades. However, HANPP increased in countries with large population growth, such as India, China, the United States, and Brazil, and decreased in Russia. As expected, population and greenhouse gas emissions were major predictors of HANPP. Models here can be a basis for future projections of international HANPP.

182. Priorities in spatial nature protection: case of Czechia

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The European landscape is highly human-transformed and has many competing interests (e.g. economic, environmental, social). While sustainability and a balance of all interests is the desired goal, economics is often the strongest driver. Therefore, an effective approach is needed to protect valuable parts of the landscape. Strategic and legislative documents such as EU Biodiversity Strategy and EU Restoration Law contain legislative commitments to protect significant part of EU's land area. This is the reason why we are trying to find localities suitable for the designation of new national parks and protected landscape areas in Czechia to contribute to the EU commitments. We have used four thematic groups of data: habitat suitability models for selected species (about 200 amphibians, birds, butterflies, mammals, molluscs and reptiles), data on natural and cultural landscape quality (habitat, landscape and geo- diversity; presence of cultural historical landscapes) and level of anthropogenic transformation of the landscape. Based on these data, we methodically made prioritization by using ZONATION software, a spatial conservation planning tool for hierarchical prioritization that works with biodiversity features as inputs. The result shows a relative proportion of the most valuable (=priority) areas for the designation of protected areas. Poster will present the workflow including used the data, methods and preliminary results.

183. Differential ecological impacts of feral cats among continents

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Introduced predators can have devastating effects on native prey on islands, but their ecological impacts on continents depend on complex co-evolutionary and biogeographical histories. To assess how these histories affect relationships between introduced predators and native prey, we investigated factors that make species vulnerable to predation by the domestic cat (*Felis catus*) in Australia, Europe, and North America. For each continent, we built datasets of prey, either corresponding to species already empirically recorded as prey or with no records but assigned to a high probability of predation via machine learning, as well as of non-prey of *F. catus,* for birds and mammals. Our findings reveal continent-specific prey preferences, with a higher proportion of bird consumption in Europe and North America and a preference for mammals in Australia. Bird prey species demonstrated cross-continental similarity, while mammal prey species exhibited divergence in Australia. Moreover, within each continent, significant distinctions emerged between prey and non-prey species, encompassing variations in size, geographic distribution, and reproductive characteristics—except for Australian mammals, where prey and non-prey shared similar body mass characteristics. Notably, a substantial proportion of Australian mammals were classified as threatened on the IUCN Red List (2022), underscoring the vulnerability of this group, while European and North American prey species were less threatened. These results offer valuable insights into species vulnerability to predation by *F. catus* and other introduced predators, highlighting the influence of eco-evolutionary context on the severity of these impacts.

184. The biogeographies of Anthropocene Biogeography

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Since *Homo sapiens sapiens* L. established itself as the predominant and, subsequently, unique hominid species, its role and influence in modifying its immediate surroundings became greater, as its population and geographic distribution increased, seeking more natural resources for their existence and their establishment in a certain area, dispersing and then changing from nomadic to sedentary. Correlating environmental variables with the dispersion and geographic distribution of all living beings has been a theme of Biogeography for at least two centuries, but the current context of humanity has allowed a speed and scope of this dispersion never experienced in those same centuries. Adopting an interdisciplinary approach to better understand the context of anthropogenic environmental changes and applying an anthropogenic approach to biogeographic studies is to place biogeography in its current time and space, at the time of intense and drastic anthropogenic interference on our planet, and to understand it as having one of its areas, the Biogeography of the Anthropocene. It is proposed that the Biogeography of the Anthropocene can be divided according to the anthropic influence that is considered to determine and modify the dispersal and geographic distribution of species: 1) Biogeography of Phytozootechnological Systems, 2) Biogeography of Conservation, 3) Biogeography of Translated, 4) Biogeography of Anthropogenic Impacts, 5) Biogeography of Indigenous and Traditional Knowledge and 6) Urban Biogeography.

185. Forest legacies of the pre-contact Maya

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Humans have shaped ecosystems through time with modern environments partly attributable to human alterations over thousands of years. Understanding the ways ecosystems have been affected by human presence is essential towards understanding the ecosystems, themselves. In northern Central America, the Maya civilization has persisted for thousands of years and the pre-contact Maya had an indisputable impact on the landscape. At the same time, how these impacts are reflected in the modern vegetation composition and distribution is disputed. In order to assess the relationship between the pre-contact Maya and the modern environment we use high-resolution lidar data from the Rio Bravo Conservation Management Area in northwestern Belize to describe the distribution of Maya modifications and canopy characteristics. Using both lowland and upland areas, we statistically compare vegetation structure with evidence of Maya landscape modification. Statistical and geospatial analyses are performed to determine the significance or lack thereof of previous human influence on modern vegetation structure and distribution.

186. Sample coverage-based standardization of species diversity improves description and prediction of biogeographic patterns

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The availability of species occurrence records (i.e., when, where, and what species were observed) has been rapidly increased, which greatly helps analyze species distributions and geographic biodiversity patterns. On the other hand, because occurrence data were originally acquired by local researchers for their own purposes, naïve use of occurrence records can lead to poor biodiversity description, interpretation, and prediction performance and, in turn, to erroneous conservation decisions based on them. We created a global-scale species diversity map using 13,959,780 points of occurrence records for 82,974 woody plant species. We calculated Hill number-based species diversity and standardized them by interpolation and extrapolation based on sample completeness (sample coverage). Observed species diversity was influenced by geographic bias of sampling efforts (higher in temperate regions and lower in the tropics), which tended to underestimate species diversity in tropical and subtropical regions. Standardized species diversity based on sample coverage showed deviations from observed species diversity patterns: for example, species-rich areas in central Africa and in mid-latitudes of East Asia. Standardization has also moderately improved the performance of the prediction model with environmental factors. The relative importance of the predictors was relatively robust to the presence or absence of standardization, with actual evapotranspiration being the most powerful factor at the global scale. In addition, we overlaid the standardized species diversity and sample coverage with spatial layers of habitat protection status and human footprint trends to identify priority areas for future sampling: the priority areas were found in the Amazon, central Africa, island Southeast Asia, and continental subtropical East Asia. The macro-scale assessment of sampling priorities would contribute to effectively filling the knowledge gaps and to construct an interactive system between local- and macro-scale studies.

187. Effect of past megafauna on genetic structure and demographic histories of megafruit plants in mainland Africa and Madagascar

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The largest animals in ecosystems (megafauna) can feed on large-seeded megafruit plants (fruits diameter > 4 cm) and disperse massive seed loads across long distances, thus playing a vital role in maintaining biotic connectivity and population structures of megafruit plants. However, it remains unclear how the global extinction of most megafauna since the late Quaternary affected megafruit plant populations. Here, we hypothesize that the loss of specialized megafaunal seed dispersers led to dispersal limitation of megafruit plants, resulting in high population genetic structure and decreases in population size that coincided temporally with the decline and extinction of co-occurring megafauna. We focus on the megafaunal palm species *Hyphaene coriacea*, which naturally occurs in savannas in Madagascar (where all seed-dispersing megafauna – e.g. giant lemurs, elephant birds – have gone extinct) and mainland Africa (where more intact elephant populations are still functioning as seed dispersers of *H. coriaceae*). Using RAD-seq from 22 populations and 151 individuals, we found that *H. coriaceae* population structure is primarily shaped by distance, and we detected signatures of population size declines in Madagascar as well as mainland Africa. This suggests that alternative dispersal mechanisms such as human-mediated dispersal and dispersal by surface runoff may have at least partly substituted the dispersal functions by past megafauna in Madagascar. These results provide important insights in the role of elephants in maintaining seed dispersal and population structure of plants in mainland Africa, and how megafruit plants have been able to persist since the late Quaternary extinction of all their primary seed dispersers.

188. Environmental Change Through Time and Its Relation to Biotic Homogenization/Differentiation of North American Birds

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Humans are rapidly changing the biotic and abiotic components of the environment. Since the past century the environment, in terms of land use and coverage, has experienced dramatic changes due to human activities. Major crops such as corn and wheat, and urban infrastructure, such as cities, are becoming dominant features of the land surface. This should cause a homogenisation of the environment as agricultural and urban intensification increases over time. Yet, the current state of the environment can also suggest a differentiation trend of the environment, which can be attributed to, e.g., crop introduction into areas of natural forest. This can lead to an increase in the heterogeneity of the environment. It is well known that environmental changes are tightly linked to biodiversity change. Human activities have led to widespread declines in biodiversity and biotic homogenisation, where assemblages of species across regions become similar. However, the direction of the environmental change and its relationship to biotic homogenisation or differentiation is unknown. Here, I investigated how the changes in environmental heterogeneity over time (1992-2018) relate to the biotic homogenization of bird diversity in the United States using beta diversity estimation. We found that some changes are happening in tandem but others changes are not. Temporal environmental homogenization (via increased dominance of specific land types e.g., crops) positively relates to the homogenization of bird species. On the other hand, increasing environmental heterogeneity (via the introduction of new land types, e.g., urban areas) can lead to species differentiation. Our findings highlight the diverse relationship between the environment and bird diversity, indicating that both coupled and decoupled changes may be contingent on the specific nature of environmental alterations.

189. Naturally occurring and anthropogenic-driven gene flow in Carpathian ox-eye daisies (Leucanthemum, Asteraceae)

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In the Carpathian Mountains (Central Europe), an elevational gradient hosts three ox-eye daisy species: the lowland *Leucanthemum ircutianum* (4*x*), the montane *L. rotundifolium* (2*x*), and the alpine *L. gaudinii* (2*x*). While previous studies documented hybridization between the latter two, our recent field observations reveal a higher prevalence of crossing than previously acknowledged. We collected and genotyped over 600 individuals, employing SNP analysis to uncover the genetic basis of this hybridization network. Our findings corroborate the observed morphological characteristics, demonstrating that hybridization is possible across all three species, and likely includes additional hybridization events among the hybrids themselves. While hybridization naturally takes place in contact zones, anthropogenic factors such as tourist traffic, roadworks, and related activities are intensifying this phenomenon. Spatial distribution and niche overlap analyses among the studied species provide additional insights. The data clearly demonstrate a high degree of niche overlap, indicating that the studied species share requirements for many bioclimatic variables, with only partial niche isolation. Reduced upward migration opportunities and increased pressure from more

thermophilic species threaten mountain taxa. As a result, potential habitat for mountain taxa faces a significant reduction, forcing them into closer coexistence with other species, thereby intensifying hybridization dynamics. Among the species, *L. gaudinii*, the alpine representative, is at the highest risk of being overwhelmed by hybridization with other species, while lowland *L. ircutianum* will witness an expansion of its available habitat. The signs of these changes are already discernible, aligning with the findings presented here.

190. Integrating biogeography and behavioral ecology to rapidly address biodiversity loss

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Addressing climate change and biodiversity loss will be the defining ecological, political, and humanitarian challenge of our time. Alarmingly, policymakers face a narrowing window of opportunity to prevent the worst impacts, necessitating complex decisions about which land to set aside for biodiversity preservation. Yet, our ability to make these decisions is hindered by our limited capacity to predict how species will respond to synergistic drivers of extinction risk. We argue that a rapid integration of biogeography and behavioral ecology can meet these challenges because of the distinct, yet complementary levels of biological organization they address, scaling from individuals to populations, and from species and communities to continental biotas. This union of disciplines will advance efforts to predict biodiversity's responses to climate change and habitat loss through a deeper understanding of how biotic interactions and other behaviors modulate extinction risk, and how responses of individuals and populations impact the communities in which they are embedded. Fostering a rapid mobilization of expertise across behavioral ecology and biogeography is a critical step toward slowing biodiversity loss.

191. Threatened at home but naturalized elsewhere: conservation conflict or opportunity?

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Human-caused environmental changes threaten numerous plant species. At the same time, humans have introduced plants into novel areas, where some of them have become naturalized. Most of the naturalized species are also common in their native ranges, but some of them may actually be threatened. Naturalization of species threatened at home could be considered an accidental kind of ex-situ conservation, but if they threaten native species they pose a conservation conflict. It remains, however, unknown how many threatened species are naturalized elsewhere, and in which regions they are native and naturalized. To address this, we combined global databases on threat status and naturalization success of the world's seed plants. As many naturalized species were introduced for economic usage, we also considered economic usage in our analysis. We found only 216 threatened species that have become successfully naturalized elsewhere. Geographically, most of them are native to the Southern Hemisphere, specifically to Africa or Australasia, and they tend to be naturalized in countries of the Northern Hemisphere. These threatened but naturalized species are often used by humans for environmental purposes or industrial materials. The main threats for these species in their native range are residential or commercial development and over-farming. Our study illustrates that, although their number is low, some threatened plant species have managed to become naturalized outside their native range. Most of them are also cultivated for economic uses, but particularly for the ones that are not cultivated, naturalization may provide an accidental means of ex-situ conservation.

192. **Large-scale dietary changes over the past 30 years in African forest elephants (Loxodonta cyclotis) in Lopé National Park, Gabon.**

William Tejler, University of Gothenburg, Sweden

Anthropogenic activities are rapidly causing many environmental changes that could negatively impact wild populations. For example, in Lopé National Park in Gabon climate change-induced fruit decline has been linked to body condition loss in African forest elephants – a frugivorous keystone species in this ecosystem. However, there is as-yet no direct evidence that the diet of forest elephants has changed in response to declining fruit availability. We investigated seasonal and decadal changes to the diet of these elephants, using 30-year-old dung data, as well as newly collected dung data from 2021-22. From both sets of samples we identified different types of foods, and categorized the amount recovered within each dung pile. We then analysed these data using generalized additive ordinal mixed models, which allow robust characterisation of the annual phenologies for each food type or species. Our results showed that the diet differed substantially between decades. First, the breadth (number of unique items) of non-fruit foods such as grass and wood dramatically increased in recent samples relative to those from 1990. Furthermore, these non-fruit foods were typically recovered at much larger quantities than before. In addition, there were substantial changes in the presence and abundance of distinct fruit species across decades, but there was no consistent direction for this change among fruits that were "important" in 1990. Altogether the species composition of fruit was vastly different between the decades. The changes in diet observed here raise concerns about the robustness of one of the most pristine ecosystems in the world.

193. **Hotspots of human pressure on the threatened European gastropods**

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Human activities are rapidly changing the biosphere as the planet has entered into a novel epoch, the Anthropocene. Anthropogenic pressure drives unprecedented rates of species' loss (current extinction rates are 1000 times higher than the background rate) and life on Earth faces a sixth mass extinction. Although the main drivers of this biodiversity crisis are mostly anthropogenic, little is known about the ranges of these threats and how they impact sensitive species. Gastropods remain poorly represented in conservation studies and conservation initiatives, despite their high number of species threatened with extinction (58.6% of freshwater species) and their high levels of endemism in Europe (>87% of all species are endemic). In this study, we aim to estimate the extent of overlap between gastropod species' distributions and each pressure layer that a species is sensitive to. We intersected individual ranges of threatened gastropod species distributed in the European region with cumulative human pressure, as defined in the Human Footprint global maps (i.e., global standardized maps of cumulative human pressures such as built environments, population density, roads, etc.). Through this intersection, our analyses indicated hotspots of impacted and coolspots of unimpacted gastropod biodiversity, providing information for future conservation planning. The research project was supported by the Hellenic Foundation for Research and Innovation (H.F.R.I.) under the "3rd Call for H.F.R.I. Research Projects to support Post-Doctoral Researchers" (Project Number: 07339).

194. Evidence of Neotropical carnivores' continental geographic range contractions over the last two decades

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Anthropogenic changes can significantly impact the geographic distributions of species, causing range contractions or expansions. However, data to assess these changes are often insufficient, heterogeneous, and spatially and temporally biased. A promising solution to overcome these data issues is to use Integrated Species Distribution Models (ISDM). In this study, we aimed to assess the changes in the geographic range distribution of eight Neotropical carnivores using ISDMs. To evaluate how the species diversity and dissimilarity among assemblages changed, we combined presence-absence and presence-only data and modelled the species' distributions at two time periods (2000-2013 and 2014-2021) using a Bayesian model based on a Poisson point process in JAGS. The model integrates the different data sources, accounts for sampling effort and spatial autocorrelation, and includes the species expert maps as a covariate (i.e., distance to the range's edge).

Our results show that most species decreased their ranges relative to the initial range size, and beta diversity in the region increased. We also reveal areas where contractions and expansions are accumulating. Our study illustrates the use of ISDMs to model the dynamics of the geographic range of species despite the data deficiencies. This modelling framework can be applied to assess other species and regions that also lack high-quality data, providing a promising solution to overcome the issue of high-quality data scarcity in the study of range dynamics.

195. Microclimate buffering and plant biogeography in temperate forests

Martin Kopecký, Institute of Botany of the Czech Academy of Sciences, Pruhonice, Czech Republic

Forests canopies buffer temperature in the understory, which in turn affects species physiology, controls species distribution and modifies key environmental processes. Here I will summarize current knowledge of the forest buffering, highlight recent advances in understanding and modelling of forest temperature buffering across space and time, and finally discuss the importance of forest temperature buffering for plant species distribution and show how its incorporation can increase our understanding of forest plant biogeography.

196. Palaeoecological trajectories of non-native vegetation and plant homogenization on islands globally

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Islands biodiversity is the result of a complex interplay of natural and anthropogenic drivers. While natural environmental settings provide the framework within which ecological species communities establish, humans have become an additional factor influencing insular biodiversity during the last centuries and millennia. However, the extent of past changes to insular biodiversity is often unknown. We combine palaeoecological data from islands globally dating back 5,000 years with extant floral checklists to 1) reconstruct trajectories of non-native plants on islands and 2) detect plant homogenization patterns. Fossil pollen data reveals that non-native plants are on the rise for more than 1,000 years which is longer than censuses and written scientific records suggest (500 years). Floristic homogenization has increased in the South Pacific over the last 5,000 years even though this trend is thought to be a contemporary issue. The results contribute to discussions about the emergence of novel ecosystems and the conservation of native insular biodiversity.

197. Biological Consequences of Global Change

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Global changes, including climate change, land productivity, oceans and other water resources, atmospheric chemistry, and ecological systems, are significantly altering the habitats, reproduction and even survival of countless species on our planet. Evidence shows that industrial, agricultural, and other human activities, coupled with an expanding world population, are contributing to the process of global change that may significantly alter the earth’s ecosystems and thus shape our future.

It was under sush circumstances that the International Society of Zoological Sciences (ISZS) initiated an international research program – Biological Consequences of Global Change (BCGC) – in 2008 to promote international scientific research, communication between scientists and information exchange, to unite scientists in different countries and disciplines to set up an international working platform for international BCGC research collaboration, data integration and information exchange so as to improve our understanding and forecasting of those potential BCGC.

The focus of BCGC is to organize a diverse group of international experts with expertise in many scientific disciplines to understand the biological consequences of endangered species, biological invasion and biological disasters, such as diseases, that are a direct result of global change.

198. Travelling on the Silk Road: grassland degradation in the high mountains of Kyrgyzstan

Sherry Young[1], Steven Brownlee[1], Ron Ydenberg[1]

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Montane ecosystems are global biodiversity hotspots that are sensitive to climate change and widely used for their ecosystem services. In Kyrgyzstan, mountains cover 94% of the country, providing suitable habitats for snow leopards (*Panthera uncia*) and many other key species. These alpine rangelands are the main source of livelihood for Kyrgyz herders, who are increasingly concerned about pasture degradation occurring throughout the region. Monitoring these rugged and remote habitats requires large, time-consuming, and often expensive human and technical resources. Satellite images are commonly used to assess rangeland degradation, which is key from a bottom-up approach to evaluate ecosystem productivity and resource availability. While these datasets are free to use, they are limited to broader spatial scales and prevent the study of processes at finer spatial scales. Large conservation efforts have been ongoing for many years for snow leopards, mostly using camera traps that can be deployed and left for a full year at a time. These cameras capture wildlife but also the environment, providing a large pool of data at specific sites about vegetation (e.g. growing season), abiotic (e.g. snow cover, temperature), wildlife presence/absence, and phenology. Here, we present how motion-triggered images from camera traps deployed for wildlife since 2016 in the Naryn State Reserve and multi-spectral imagery helped us improve our understanding of the shifts in the timing of the growing season and the incidence of unseasonal snow patterns across elevational gradients at fine and coarse resolutions.

199. **Lags in the response of plant assemblages to global warming depends on temperature-change velocity**

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Current global warming is driving changes in species assemblages by increasing the number of thermophilic species while reducing the number of cold adapted species, leading to thermophilization process. However, there is increasing evidence that thermophilization might not keep pace with global warming, resulting in thermal lags. We quantified the magnitude of thermal lags of plant assemblages in Norway during the last century and assess how their spatio-temporal variation is related to variables associated with temperature change velocity, topographic heterogeneity, and habitat type. We conducted an analysis of floristic temperature using data from a vast dataset, 16,351 plant assemblages. Our research spanned from 1905 to 2007, during which we calculated the thermophilization, and the thermal lag index. We analyzed different factors influencing observed lags, including temperature change velocity (magnitude, rate of temperature change, and distance to past analogous thermal conditions), topographic heterogeneity, and habitat type (forest and non-forest). The thermophilization increases overall during the study period. However, thermophilization falls behind temperature change, causing a constantly increasing lag. The thermal lag increases most strongly after 1980, the lag is best explained by variables related to temperature change velocity, suggesting specifically that limited migration is an important contributor to the observed lags.

200. **Ecologist in a tough spot: Communicating plant shifts responses to a young audience**

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Researchers often find themselves immersed in their specialized fields, which can make it challenging to connect with audiences who lack their level of expertise. This challenge becomes even more pronounced when attempting to transmit complex concepts to young audiences. Our poster showcases our endeavor to overcome this communication barrier by publishing a paper in Frontiers for Young Minds, a peer-reviewed journal for children. Our aim was to communicate to a young audience aged 9–12 years our research about the implications of climate change on the shifting patterns of plant distribution, addressing pivotal questions like "How do we know that plants are shifting their distributions?" and "Why are plants shifting their distributions?".

To accomplish this, we used diverse communication tools, including relatable metaphors, captivating storytelling, and scientifically informative illustrations. These techniques enable us to explain complex ecological concepts such as climatic lags, sampling methods such as permanent plots, and the process of resampling historical data.

Our research received feedback not only from scientists but also from young reviewers. These reviewers are known for their direct and honest comments, which have significantly contributed to our development as science communicators. This feedback strongly contributed to improving our explanations of core concepts, such as sessile organisms, species distribution, and vegetation zones, and finding a balance between simplifying information and maintaining accuracy to effectively communicate the essence of our research.

201. A multifaceted and multi-taxa approach for Mediterranean forests conservation

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Nowadays, most conservation approaches are based on species richness, aiming to protect biodiversity on endemism hotspots, or specific species. However, recent studies have highlighted the importance for conservation of preserving the diversities in traits and evolutionary heritages, referred to as functional and phylogenetic diversity respectively. In the few cases a three-faceted approach to biodiversity assessment has been used, it relied on the study of a single taxonomic group. Yet, species interactions shape species assemblages and can affect how species respond to climatic changes. In this poster, we'll describe our proposed approach to assess what drives the change in taxonomic, functional and phylogenetic diversity of three key taxa of Mediterranean forests (birds, butterflies and trees).

Our approach focuses on assessing three questions:

- How much past changes in environmental conditions determine current diversity patterns? We'll use multiple regression, considering not only climatic factors but also soil characteristics, herbivores consumption, fire regimes, and land use.

- How related are the changes in biodiversity facets with and between groups? We'll use Structural Equation Modeling to evaluate the relative importance of biotic interactions and environmental conditions in influencing diversity patterns.

- What are the expected changes in Mediterranean biodiversity in the near future? We'll use models built in the previews questions to assess the expected changes in diversity through different socio-economic scenarios.

The end goal of this project is to quantify the ongoing biodiversity changes in the Mediterranean region, focusing on the relevance of the current protected area network to safeguard biodiversity in a changing world, and identify future hotspots of diversity for three key taxa and across all three facets of diversity. This project is part of the INTEGRADIV consortium funded via the BIODIVERSA+.

202. Microclimate, an inseparable part of ecology and biogeography

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Brief introduction: what are microclimates and why are they important? Microclimate science has developed into a global discipline. Microclimate science is increasingly used to understand and mitigate climate and biodiversity shifts. Here, we provide an overview of the current status of microclimate ecology and biogeography in terrestrial ecosystems, and where this field is heading next. **Microclimate investigations in ecology and biogeography.** We highlight the latest research on interactions between microclimates and organisms, including how microclimates influence individuals, and through them populations, communities, and entire ecosystems and their processes. We also briefly discuss recent research on how organisms shape microclimates from the tropics to the poles. **Microclimate applications in ecosystem management.** Microclimates are also important in ecosystem management under climate change. We showcase new research in microclimate management with examples from biodiversity conservation, forestry, and urban ecology. We discuss the importance of microrefugia in conservation and how to promote microclimate heterogeneity. **Methods for microclimate science.**
We showcase the recent advances in data acquisition, such as novel field sensors and remote sensing methods. We discuss microclimate modelling, mapping, and data processing, including accessibility of modelling tools, advantages of mechanistic and statistical modelling, and solutions for computational challenges that have pushed the state-of-the-art of the field. **What's next?** We identify major knowledge gaps that need to be filled for further advancing microclimate investigations, applications, and methods. These gaps include spatiotemporal scaling of microclimate data, mismatches between macroclimate and microclimate in predicting responses of organisms to climate change, and the need for more evidence on the outcomes of microclimate management.

203. A novel evaluation of alternative species distribution models using population genomics

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In rapidly changing environments it is unclear if species can migrate to keep up with movement of suitable habitats. One indicator of a species' ability to track climate change across landscapes is its

past movement. Species distribution models (SDMs) provide a powerful means to understand past movement of suitable habitat and, indirectly, species movement. Nevertheless, different SDMs can produce markedly different predictions of habitat suitability both in the past and in the near future, yet perform similarly in predicting current-day occurrences. To evaluate the ability of SDMs to hindcast and forecast movement of a North American tree, *Fraxinus pennsylvanica*, we developed 24 SDMs to describe its past habitat from 21Kybp. These SDMs then parameterized a demo-genetic model that predicts population genetic diversity in *F. pennsylvanica*. Approximate Bayesian Computation (ABC) was then used to assess which SDMs best predicted current-day population genetics observed in this species. Models had similar performance when assessed using contemporary occurrences, but genetics consistently supported SDMs based on a CCSM climate model, an intermediate calibration extent, and generalized linear modeling. Furthermore, we projected the future range of *F. pennsylvanica*. with each of the 24 SDMs and 4 alternative climate projections. SDMs selected through the ABC analysis of genetic data forecast limited future changes in habitat locations in contrast to rejected models that predicted more dramatic changes. In conclusion, we demonstrate that integrating historical information encoded in the genetics into SDM evaluation may better inform predictions about habitat suitability in a changing environment.

204. Microrefugia for Alpine Plant Life (MAPLe)

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Mountains are home to an exceptional diversity of plant species specialised to the cold alpine climate. At the same time, temperatures in mountain areas have increased even faster than the global average, reducing the available habitat for alpine plants. Some areas within heterogeneous mountain landscapes, however, have warmed more slowly than their immediate surroundings, and could help populations of cold-adapted alpine plants to survive. With the MAPLe project, we aim to identify the extent and impact of these so-called microrefugia across mountains globally. We will use mechanistic microclimate modelling based on climate reanalysis data from the last four decades as well as in-situ microclimate records and large-scale vegetation, soil and terrain data. In addition, we will use the European Alps as a case study to integrate plant species records through time with distribution models, to test how effective these potential microrefugia have actually been for supporting the diversity of alpine plant species. The outcomes of MAPLe will thus be of great interest for local and regional conservation efforts, as well as for future research on mountain biodiversity dynamics.

205. Predicting the distribution and potential range shifts of northern pikas incorporating microclimates

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While species distributions are often modeled as functions of various environmental factors, the spatial scales of these covariates are typically larger than the scale that target organisms respond to. Incorporating fine-scale thermal conditions into the analysis will likely yield more realistic delineations of species distributions and potential range shifts, which should serve as valuable information for species conservation under the threats of climate change. In this study, we focused

on the northern pika (*Ochotona hyperborea*), a small lagomorph found in rocky patches harboring cool microclimates, to understand how species distribution predictions differ by accounting for the occurrence of microclimates. To do so, we use three Maxent models based on relevant macroclimate data (1-km resolution; macroclimate model), downscaled macroclimate data (100-m; local-climate model), and estimated microclimate data based on observed ambient-microclimate relationships (100-m; microclimate model), to predict the species baseline distribution (1961-2010) and future range shifts (2016-2100) under two emission scenarios. The overall pattern of habitat suitability was similar among all models, with higher elevations predicted to be suitable for northern pikas. However, areas with moderate suitability at lower elevations were greater in the microclimate model prediction, implying that potential habitats might be ignored in macroclimate and local-climate model predictions. All future predictions indicated unidirectional habitat losses, but such losses were smallest in the microclimate model. Our findings suggest that predictions based only on macroclimate data could overlook potential habitats, and thus may overpredict extinction probability under climate change. More nuanced assessments of species distributions are required in future studies.

206. Is averaging the answer?: Uncertainty in consensus predictions of plant species' vulnerability to climate change

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Variation in the spatial predictions produced by different species distribution models (SDMs) has been recognized as a significant source of uncertainty when modeling species' responses to climate change. Ensemble forecasting, in which a variety of modeling approaches are used to generate and explore a range of future biodiversity scenarios, has become increasingly popular in assessing species' vulnerability to environmental change. Consensus techniques are often used to summarize the variability in an ensemble of habitat suitability predictions and provide information on areas of agreement between different models; however, uncertainty in predictions of species vulnerability to climate change made by different consensus approaches has not been extensively studied. We evaluated how habitat suitability change varied among different SDM consensus methods, relative to the variation introduced by different global climate models (GCMs), representative concentration pathways (RCPs), and dispersal assumptions for 82 plant species found in the California Floristic Province, a biodiversity hotspot. We also explored the relationship between uncertainty in projected habitat change and species ecological and geographic characteristics. We found that variability between estimates of habitat suitability made by different consensus methods often outweighed the uncertainty introduced by GCMs and RCPs, especially under "full dispersal" assumptions. Uncertainty between vulnerability estimates were especially high for species with low prevalence and small range sizes, including the critically endangered tree species Pinus torreyana. The variability between spatial predictions produced by different consensus techniques highlights the need for continued evaluation of different uncertainty sources when assessing the vulnerability of biodiversity under climate change.

207. Using museum collections and species distribution modelling to understand the potential impacts of environmental change on Neolindus rove beetles

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This study seeks to analyze the quality and quantity of insect occurrence data in entomological collections, identify biases and limitations in the available information, and evaluate their impact on our understanding of changes in biodiversity. To overcome these limitations, we used a species distribution modelling approach to predict the potential distribution of a *Neolindus* genus, using occurrence data from museum collections and yearly selected environmental variables from 1958. *Neolindus* is a Neotropical genus of rove beetles, widely distributed in the region, with records from 1960 to 2022. Our modelling techniques accounted for changes in environmental conditions over time, incorporating different algorithms and multiple testing sets of data and matching the climate data with the occurrence data period. The findings of this study will have implications for biodiversity monitoring and conservation initiatives by showing changes in the suitability areas in short periods of time but with limitations in the presence prediction. Our study sheds light on the distribution and habitat preferences of *Neolindus* species and also provides a framework for evaluating the impact of environmental change on other insects. It demonstrates the potential for using species distribution models to enhance our understanding of insect biodiversity in the Neotropics. Our results highlight the importance of entomological collections in tracking changes in insect populations over time and provide a workflow for using occurrence data to improve our understanding of the ecology and distribution of rove beetles and other neglected insect groups**.**

208. Has butterfly wing colour lightness changed over recent decades in Canada?

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Climate change has widespread impacts on species' morphologies. Colour is an important trait for ecotherms due to its role in predation protection, maintaining homeostasis, etc. The thermal melanism hypothesis postulates that the colour lightness of an individual determines its solar absorption and predicts that lighter individuals have higher fitness in warmer environments. Therefore, ectotherms should have become lighter over recent decades in response to climatic warming. Previous work to test this has relied on space-for-time substitutions, which assume colour-temperature relationships observed over space are causal and therefore, the relationship will be the same over time, but the validity of this approach is unknown. We use a spatially and temporally extensive data set from natural history collections across Canada to test this hypothesis in a taxa known for its colour, the butterflies (Lepidoptera). Using 10 widespread species, we did not find support for the thermal melanism hypothesis using spatial-temporal variation in temperature. Despite the lack of causal link with temperature, wing colour became lighter over time. This suggests that colour lightness is responding to other factors, like complex measures of temperature, precipitation changes, habitat changes, or a combination. We found lighter butterflies experienced less change in colour over time. Lighter species have less initial pigmentation to respond to environmental changes, and thus may be responding to environmental change through other mechanisms like behavior. Regardless, an increase in wing colour lightness means that butterflies are tracking climate change in another way, but more work into the mechanisms behind this pattern are necessary.

209. Predicting the Spatial Distributions of Korean Endemic Plants under the Recent and Future Climate Change

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Increasing temperature can stress plant growth conditions, leading to phenological changes and shifts in spatial distributions of plants. Korean Fir (*Abies koreana*) and Korean Stewartia (*Stewartia koreana*) have moved northward while the average temperature in the Korean Peninsula has increased 0.35°C over the recent thirty years (1991-2020) compared to the previous normal (1981-2010). This study aims to (1) utilize high-resolution (1 km²) bioclimatic data to build species distribution models (SDMs) for the Korean endemic plants, (2) project the potential changes in their habitats under the recent and future climate change, and (3) identify the climatic factors affecting the changes in their distributions. To build the SDMs, bioclimatic data under present and future (Shared Socioeconomic Pathways, SSP) from CMIP6 UKESM1-0-LL, which exhibits good reproducibility in East Asia, were utilized. Bioclimatic variables were selected based on Principal component analysis (PCA) and growth conditions. The potential distributions of two species were projected to be changed in the late-century (2081-2100), compared to those in recent period (1991-2020). Korean Fir showed a retraction and northward shift of habitats during the late-century while Korean Stewartia expanded and moved north. These spatial patterns are attributed to decreasing the number of days with precipitation and increasing precipitation intensity. Predicting potential habitats of Korean endemic plants can serve as valuable information for conservation of endangered species and biodiversity preservation.

210. Is there stability across time between bioclimatic variables and topographic complexity in the Atlantic Forest?

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About a third of the world's biodiversity is harbored in mountain chains. The elevational gradients provided by these formations influence biotas through shifts in climate and vegetation types and are known to favor biological diversification. The environmental heterogeneity provided by mountain chains is thought to contribute to species diversity and endemism significantly. It has been proposed that topographic complexity enables the accumulation of diversity over time by promoting regional-level climatic stability: montane species in areas of steep topography are expected to move over relatively short geographical distances to encounter environments that are optimal for them. In this study, we evaluate if climatic stability is higher in topographic complex regions, using the Atlantic Forest as a study system. We hypothesize that topographic complexity is positively related to climatic stability and that areas of greater topographic complexity in the Atlantic Forest could function as climate refugia for local species. To test this hypothesis, we extracted the values of four bioclimatic variables representing changes in temperature and precipitation across the Atlantic Forest over time, sampling from paleoclimatic simulations at every one thousand years, from the Last Glacial Maximum (22.000 thousand years ago) to the current time, in a 30 arc-sec resolution. We obtained the bioclimatic variable in different altitudinal gradients over time to compare variable topographical complexity between these gradients. Through this comparison, we test whether the higher topographic complexity exhibits higher climate stability over time through a linear regression.

211. An alpine bird is reducing its distribution and moving to higher altitudes in its southernmost European distribution

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Under the current pattern of climate change, mountain bird populations are generally shifting their ranges to higher elevations, tracking their climatic optima. Nevertheless, space limitations at high altitudes constrain mountain species' resilience to climatic change, making them particularly vulnerable. In extreme cases, the climatic niche of some species can move beyond mountaintops, ultimately driving such species to extinction. This study presents the case of the Northern Wheatear (*Oenanthe oenanthe*) in Spain and compares the breeding distribution of this alpine bird from 2003 to 2022. We built environmental favourability models using information from the two most recent Spanish bird atlases and a set of variables to determine the factors affecting the occurrence of the species. The influence of climate compared to all other factors was obtained using variation partitioning analysis. The Northern Wheatear has suffered a strong reduction (67 %) in occupied areas and also in favourability throughout mainland Spain where climate change may have far-reaching consequences, including local extinctions. Climate explained more than 90 % of the variation in the model obtained for 2022. Occupied areas were, on average, 100 m higher in 2022 than in 2003. If the effects of climate change continue, the Northern Wheatear will likely disappear in its southernmost distribution limit, making the Sierra de las Nieves National Park population the most vulnerable on a continental scale. For this reason, it is necessary to implement monitoring programmes for Northern Wheatear populations, giving priority to mountain systems where they already occupy higher elevations.

212. Impact of climate change on the distribution and phenotypic diversity of a widespread Palearctic snake species using experimentally informed species distribution models

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Climate change is a critical driver of range shifts, habitat degradation, and biodiversity loss. Polymorphic species, with their varied phenotypes, present a unique opportunity to study differential responses to climatic changes. This study investigates the impact of future climate change on the distribution and phenotypic diversity of the European grass snake, *Natrix natrix*, a species distributed from Central Europe to the shores of Lake Baikal. We first create a database of *N. natrix* phenotypes across its range compiled from diverse citizen science platforms. Secondly, we conducted a split clutch design experiment, were we incubated *N. natrix* eggs at three temperatures: 25°C, 27°C, and 30°C to simulate future climate change. This experiment aimed to determine if incubation temperature affects hatchling phenotype and performance. Additionally, we constructed thermal performance curves for these hatchlings, analyzing how swimming and crawling speeds vary with temperature. Using the phenotypic database, we first constructed species distribution models (SDMs) by phenotype and for the entire species. Further, we used the experimental data to inform and refine the SDMs, to understand how climate change might influence phenotype occurrence across species range, future range expansions and local extinctions of the species. Our analysis reveals a northward shift in species distribution and substantial changes in phenotype frequencies,

especially in the midsection of species ranges. Notably, the response to climate change varies geographically, with lighter phenotypes predicted to become more prevalent in the southern part of the species range, while the future species expansions north are to be favorited by the performance of darker phenotypes in cooler environments. Our findings underscore the importance of combining citizen science data, phenotypic data, and experimental results into species distribution modeling to have a more nuanced understanding of climate-induced shifts in biodiversity.

213. Freshwater megafauna shape ecosystems and facilitate restoration

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Freshwater megafauna (i.e., animals that have a maximum reported body mass over 30 kg), including sturgeons, river dolphins, beavers, crocodylians, and large turtles, are subject to multiple and intense threats. Although there are increasing studies investigating the causes of megafaunal loss in freshwaters, little attention has been paid to the impacts of megafauna on the abiotic environment and other organisms. We demonstrate how megafauna shape ecological processes in freshwater ecosystems. Through activities such as movement, burrowing, and dam and nest building, megafauna have a profound influence on the extent of water bodies, flow dynamics, and the physical structure of shorelines and substrates, thereby increasing habitat heterogeneity. They enhance nutrient cycling within freshwaters and cross-ecosystem flows of material through foraging and reproduction activities. In addition, these large animals are highly connected to other freshwater organisms via direct consumption of species at different trophic levels, indirect trophic cascades, and through their influence on the habitats of these species. Since 1970, global monitored populations of freshwater megafauna have declined by 88%. In Europe, over 40% of all freshwater megafauna species have lost more than 40% of their historical distribution ranges. The decline in their abundance and distribution range and the loss of large individuals have reduced the extent and magnitude of megafaunal impacts in freshwater ecosystems. We propose that reinstating freshwater megafauna populations holds the potential for restoring key ecological processes such as disturbances, trophic complexity, and species dispersal, which will, in turn, promote overall biodiversity and enhance nature’s contributions to people.

214. Beneath the surface: systematic and large-scale modeling of groundwater amphipod diversity

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Groundwater ecosystems harbor a unique and highly adapted biodiversity. However, this biodiversity is still poorly studied, mainly due to difficulties in groundwater accessibility. To be able to protect groundwater ecosystems, understanding the distribution and diversity of groundwater organisms is essential. We established a very broad citizen science approach and compiled highly resolved and large-scale data on groundwater amphipods across Switzerland. Water providers were systematically integrated to collect repeated detection–nondetection data on groundwater amphipods. In total, more than 900 sites were sampled and over 2,000 groundwater amphipods were found. We identified a high species diversity of groundwater amphipods, consisting of few common and many rare species. The distribution of frequently found groundwater amphipod species could be modeled using an occupancy modeling approach and a set of environmental covariates. However, a large part of the diversity consisted of species found at a very limited number of sites. Interestingly, these rare species were distributed evenly across the study region. Our results emphasize the contribution of rare and narrowly distributed species to overall groundwater biodiversity. Integrating these species in biodiversity assessments is essential, but simultaneously, data collection and distribution modeling is challenging. We highlight the need of systematic sampling approaches to cover both, common and rare species. Such approaches are important for a better understanding and conservation of groundwater biodiversity.

215. Species Distribution Models in freshwater restoration contexts - an integrative framework

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Restoration measures are being pursued to rehabilitate degraded freshwater ecosystems and restore their essential functions. While progress has been made in restoring abiotic aspects, achieving full biological recovery remains elusive due to the complexity of biological systems, which are influenced by numerous factors operating at different spatial and temporal scales - often resulting in asymmetric recovery trajectories. Species distribution models (SDMs) are crucial in ecology, predicting species distribution under various scenarios. However, their application to predict species' distributions after restoration in freshwater ecosystems remains limited. This is attributed to the limitations of correlative SDMs in capturing the complexities of ecosystems post-restoration, where biota rarely corresponds to the reestablished abiotic conditions. To enhance the applicability of SDMs in contexts of ecological restoration we suggest an integrative strategy. First, the processes influencing the biological response of ecosystems during degradation and recovery require adequate consideration: species' tolerance, biotic interactions, and dispersal. Moreover, such processes relate to principal factors shaping species' distributions, i.e.biotic factors, abiotic factors, and movement. Here we review existing SDM approaches to address these concepts and processes separately and propose ways to integrate them. By addressing these concepts, we aim to enhance SDMs' functionality by providing a more accurate representation of the system's behaviour during degradation and recovery.

216. Cryptic biodiversity in Amazonian freshwater fishes of the genera Cyphocharax and Curimatella revealed by mitochondrial DNA (Teleostei: Curimatidae)

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Detritivores of the fish family Curimatidae are assigned to eight genera, including *Cyphocharax* with 47 species and *Curimatella* with five species with broad distribution across the Neotropics. Morphological investigations reveal, however, the existence of additional species. In this study, 246 specimens of *Cyphocharax* and *Curimatella,* primarily from the Amazon, Orinoco, Guianas, La Plata, and eastern coastal drainages, were identified morphologically and barcoded using the mitochondrial universal marker cytochrome c oxidase subunit I (*COI*). Analyses of species delimitation were undertaken using likelihood, Bayesian, and genetic distance methods. We discovered 71 well-supported clusters representing 35 recognized species of *Cyphocharax* and *Curimatella* and 36 lineages representing cryptic or undescribed species. Results show a clear delimitation of species boundaries constrained by the Araguaia, Arinos, Jari, Negro, Tapajós, Tocantins, and Xingu rivers of the Amazon basin, with three species recently described from the Araguaia, Paraguay, and Xingu rivers, and the remaining clusters requiring additional morphological study. In addition, the results demonstrate the species relationships constrained by the river systems of the Amazon basin, with lineages from Tocantins, Xingu, and Tapajós forming unique clusters along the phylogeny. This study reveals a significant gap in our understanding of the true species diversity in Neotropical freshwaters and provides a framework for future taxonomic research to rapidly characterize the exceptional Neotropical biodiversity, particularly in lesser-known Amazonian tributaries.

217. Functional reorganization of North American wintering bird communities

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Wintering birds serve as vital climate sentinels, yet they are often underrepresented in comprehensive surveys and overlooked in studies of avian diversity change. Here, we provide a continental-scale characterization of change in multiple facets of wintering avifauna and examine the effects of climate change on these dynamics. We reveal a strong functional reorganization of wintering bird communities marked by a distinct east-west gradient in functional diversity change, along with a superimposed north-south gradient in trait composition change. Assemblages in the eastern US saw an expansion of the functional space and increases in functional originality, evenness, and divergence, while the western US saw contractions of the functional space. Shifts in functional diversity were underlined by significant reshuffling in trait composition, particularly pronounced in the northern US. Finally, we find strong contributions of climate change to this functional reorganization, underscoring the importance of wintering birds in tracking climate change impacts on biodiversity.

218. Plant functional traits couple with range size and shape in European trees

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Investigating the connection between functional traits and range attributes offers an opportunity to gain perspective on what may shape species distribution across large spatial scales. Here, I examined whether plant functional traits of 98 European tree species are associated with the size and shape of their native ranges. I employed chorological maps to quantify two primary biogeographic attributes: species' range area and elongation. I considered 28 morpho–physiological traits reflecting key plant functions measured in above– and belowground organs. I used multi–response mixed models with phylogenetic covariance matrices to calculate the conservative trait correlation (CTC) and the phylogenetically independent correlation (IND) component of each functional trait with range area and elongation. Although several traits showed non–significant correlations with biogeographic attributes, two general signals emerged: 1) range area was positively associated with more resource acquisitive strategies, whereas 2) range elongation was positively coupled with more resource conservative strategies. For example, specific leaf area, specific root area, and root mycorrhizal colonization consistently increased with range area and decreased with range elongation. These relationships were generally more significant in the IND component and sometimes exhibited contrasting trends compared to results obtained from CTC. Trait–range relationships may arise from reciprocal selection, where functional traits influence range attributes and *vice versa*, or due to indirect effects, such as the joint variation of range and traits with latitude. The results suggest that factors operating in relatively recent times may contribute significantly to shaping species' biogeographic range attributes.

219. Flap or Fail: Exploring the Role of Native Functional Richness on the Establishment Success of Non-Native Birds on Oceanic Islands

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Island ecosystems contribute only a small percentage of global land area but harbour a much larger proportion of global biodiversity. Unfortunately, island ecosystems, and particularly island avifauna, have been shown to be especially susceptible to the impacts of non-native species, with a high number of species threatened with extinction as a result of species introductions. However, there is still uncertainty surrounding the exact drivers of successful introduced species establishment, particularly the roles of native richness and functional traits. Using a global dataset of island bird communities, we were able to investigate the implications of native bird diversity (taxonomic and functional) for determining successful establishment of non-native birds. Here, functional richness was calculated for island communities of native and introduced birds separately for traits related to ecology (foraging and dietary preference) and morphology, thus allowing for the detection of potentially divergent mechanisms responsible for community composition. Null models were used to compare functional richness of the native community to that of communities assembled through random processes as well as correcting for species richness. Results show that non-native birds expand both ecological and morphological trait-space of the native island communities and that both biotic interactions as well as island characteristics play a role in establishment success of non-native species. Considering the well-established impact of invasive species on local and global biodiversity it is imperative that we investigate the mechanisms involved in the invasion process to better prioritise and create effective conservation strategies and policy.

220. Cranial morphological disparity in flying squirrels across tropical and temperate biomes

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The latitudinal gradient of species richness has long intrigued scientists, with various hypotheses proposed to explain this phenomenon. One hypothesis, rooted in the ecological theory, suggests that greater diversity of niches in tropical biomes facilitates the coexistence of a higher number of species. Considering the close relationship between species morphology and ecology, a greater diversity of niches could also lead to greater morphological disparity in tropical biomes. In this study, we used geometric morphometric techniques on the ventral view of the skull of flying squirrels (Pteromyini, Sciuridae) to investigate how diet influences cranial shape and size, and to evaluate whether cranial morphology exhibits greater disparity in tropical biomes. We found that diet has a significant impact on skull shape and size, with folivorous species displaying large, wide and robust skulls, while frugivorous species display smaller and narrower skulls. This link between morphology and diet found for flying squirrels raises the possibility that biomes with more dietary niches available (i.e., tropical biomes) might show higher cranial morphological disparity. However, we found that morphological disparity in each biome was not different from the expected based on their species richness, suggesting that the factors governing morphological disparity in these biomes closely align with those driving species diversity. The only exception is the temperate evergreen forest, which shows lower levels of disparity than expected for its richness. This can be attributed to the high proportion of folivorous species in this biome, which have similar skull morphologies due to their specialized adaptations for leaf consumption.

221. How does plant functional diversity change along environmental gradients?

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The use of plant functional traits to infer ecological processes has obtained renewed popularity. However, despite over a decade of research examining how functional diversity patterns change along ecological gradients, few generalizations have emerged. To address this gap, we searched web of science using the search terms “functional diversity”, “gradient”, and “plant” for all papers published before 2021 and found a total of 547 papers. Then, we removed papers that were focused solely on methods, did not conduct on the ground measurements of alpha diversity (i.e., remote sensing, modeling), or used anthropogenic or biotic gradients. From the resulting 125 papers, we created a database that included: 1) the traits measured, 2) the metrics of functional diversity calculated, and 3) the abiotic gradient. We then used vote counting to assess how functional diversity changed along the abiotic gradients. In general, we found that functional diversity of leaf traits in forests (one of the most studied habitats) and plant height across all habitats increased with increasing soil resource availability and precipitation, but either decreased or showed no trend with increasing elevation. With both increasing soil resource availability and precipitation, CWMs shifted toward a more resource acquisitive functional strategy (i.e., higher CWM SLA). Leaf trait patterns were less consistent in other habitats. Although some general patterns emerged, there was no clear

consensus among the traits measured or functional diversity metrics calculated and represents a large barrier to synthesis. We provide recommendations for examining how functional diversity changes along ecological gradients.

222. Elevation and aspect interactively shape the functional diversity of forest plant communities

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Functional traits mediate plant community assembly along elevational gradients, reflecting adaptations to changing climatic, pedological and biotic conditions. Both environmental filtering and competitive exclusion determine viable trait strategies, which impacts local functional diversity. Mediterranean mountains are ideal ecosystems to study the functional diversity and composition of forest understory communities, as they are hotspots of forest species diversity in Europe. A factor often neglected in respective studies is slope aspect. Through insolation, aspect impacts growing season length, forest structure and ultimately functional understory composition. We conducted a transect-based field sampling on opposing slopes in the central Apennines, stretching from the valley bottom to the climatic treeline at ~2,000m. We recorded vascular plant composition, forest structure, pedological and geographical conditions to characterize changes in traits, species richness and functional richness with elevation on opposing slopes and to determine the impact of forest structure and soil conditions on the herb layer. We used multiple linear regression and publicly available trait data to compute functional richness and community-weighted means. We found that on north-facing slopes, trait strategies change with elevation from conservative to acquisitive, while species richness decreases, but functional richness remains constant. South-facing slopes have a higher herb richness and show a decrease in plant height and overall functional richness, indicating a change from competitive interactions at the valley bottom to environmental filtering at the top. Finally, our analysis shows that canopy cover and soil pH are among the strongest biotic and abiotic predictors of species and functional richness.

223. Functional Distinctiveness of the World’s Resident and Migratory Avifauna.

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Functionally distinct species have been recognized as crucial to ecological communities as their unique characteristics contribute to important ecosystem functions and increase ecosystem stability. Despite their importance, global assessments of how functional distinctiveness is distributed spatially, and how it changes throughout the year are lacking. Here, we investigate how functional distinctiveness for the world’s >10,000 species of birds varies spatially across the globe. We first examine whether the spatial variation in assemblage-level functional distinctiveness differs between breeding and wintering time periods. Second, we ask whether resident and migratory birds show different global (i.e., relative to all other species globally) and local (i.e., relative to all species in a local assemblage) functional distinctiveness from one another, and whether their local functional distinctiveness vary depending on the season. To quantify functional distinctiveness, we

compiled functional traits from publicly available data bases and expert range maps reflecting breeding and wintering distributions for all species of birds. We quantified the dissimilarity among species in functional space and then generated maps at a 100 x 100 km resolution to estimate average-level functional distinctiveness during both the breeding and wintering time periods. We predict that local functional distinctiveness will increase during breeding periods and that migratory birds are more distinct compared to all other species globally. Our study provides the first comprehensive investigation of spatiotemporal variation in avian functional distinctiveness.

224. Revealing biogeographic patterns of northern European flora through functional traits

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In community ecology and biogeography, reliance on taxonomic information has been the norm. However, a more nuanced approach is required to thoroughly comprehend the relationships within and across plant communities. Plant functional traits provide a tool to reveal patterns that taxonomic data alone might overlook, particularly useful are local trait measures that enable the quantification of intraspecific trait variation. Here, we examine the relationships between the intraspecific trait variation of 150 boreal and arctic-alpine plant species and their rarity, abundance, dominance, and reproductive efforts. We utilized over 20,000 plot-level trait measurements, covering four common plant traits (specific leaf area, leaf dry matter content, leaf area, and plant height) collected from six study areas across northern Finland, Norway, and Sweden. We complemented this dataset with in-situ measurements of microclimate and soil moisture obtained from more than 500 TOMST TMS4 loggers. Using structural equation models, we explored the hierarchical effects of the environment, biotic interactions, and plant traits on plant biogeographic patterns and fitness. Preliminary findings indicate that both environmental filtering and biotic interactions play pivotal roles in shaping species occurrence and abundance patterns by influencing the traits of individual plants within communities. However, we also observed substantial variation in the strength of these environmental and biotic effects among species, a variability that cannot be solely attributed to species' evolutionary histories or growth forms. In summary, our results emphasize the effectiveness of plot-level traits in unravelling the rules governing community assembly and biogeographic patterns, spanning from local to subcontinental scales.

225. Functional traits of habitat-specialized (succulent) plants on edaphic quartz islands

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Edaphic islands commonly host high numbers of habitat-specialized or endemic plant species. In the case of quartz islands in South Africa, many of these species are additionally characterized as dwarf succulent shrubs with unusual growth forms. Quartz islands are home to a remarkable and biodiverse flora that is found nowhere else. However, the functional traits of these plants are poorly represented in trait databases and the distinctive succulent growth forms necessitate innovative approaches to trait measurement in addition to conventional protocols. In this study, we investigate whether and how the plant functional and biogeographic traits correspond to the specific soil abiotic and spatial characteristics of the edaphic islands, in comparison to the surrounding matrix. We collected quantitative data on various traits of the most abundant perennial plant species (n = 195) found on a quartz island archipelago in the Knersvlakte nature reserve. Additionally, we supplemented these measurements with biogeographic traits obtained from existing literature. Our findings indicate that habitats on the quartz islands exhibit higher salinity levels and lower soil pH values compared to the surrounding areas. Furthermore, they are characterized by a greater proportion of leaf-succulent species with smaller growth forms, along with discernible differences in leaf traits. We discuss how the soil's environmental conditions and selected island parameters might contribute to the observed trait patterns. Additionally, we explore how a functional approach can enhance the comparison of different types of edaphic islands, enabling us to gain further insights into their unique or shared characteristics.

226. Heterogeneous trait responses of Paramo plant species and communities to experimental warming

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Climate change is leading to changes in the composition of plant communities. This is happening across mountain ecosystems, but its impact on functional composition in tropical alpine regions remains less understood. Using a warming experiment with Open Top Chambers (OTC) in the Ecuadorian Páramos (4,200 m), we measured vegetation cover between 2012 and 2019 and collected plant material for estimating morphological, chemical and genomic traits to test the effect of warming on species and communities. We found that species have a wide range of responses to warming with significant changes in the values across different functional trait combinations. The most common response to warming was an increase in height and/or leaf area, followed by changes in leaf dry matter content (LDMC, either higher or lower), among 6 other strategies. Larger leaf areas were found in all Asteraceae and Apiaceae species. We did not find significant differences in either trait responses or trait values between species that gain in vegetation cover in OTC over time and those that lost cover. Community-weighted mean values of LDMC, leaf area, genome size, leaf carbon, and leaf phosphorous were significantly higher in the OTC plots than those in the control plots over time. This study demonstrates that after 7 years of experimental warming, Páramo communities are developing heterogeneous response strategies. Both intraspecific changes (e.g. larger leaf areas) and traits of dominant species (e.g. larger LDMC and genome sizes) are contributing to community responses which gives us insight into tropical plant mechanisms to face climate change.

227. Broadening Participation in Ecometrics Research: An Initiative to Expand the Collection of Functional Trait Data

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Ecometrics research assesses the relationship between functional traits and the environments in which they occur. It is a promising approach for assessing biotic responses to environmental change and for predicting changing functional dynamics of ecosystems. Functional traits directly influence an organism's performance in an environment. Large database efforts have been focused on compiling comprehensive datasets, yet there is still limited functional trait data available for many mammal and reptile species. Here, we introduce a novel initiative aimed at expanding contributions to the gathering and reporting of functional trait data to promote broader participation in ecometrics research. Our project focuses on building a comprehensive, multi-trait, multi-taxonomic database for mammals and reptiles. We create a structure that is tractable and easy to input different functional trait measures. In our first round of implementation, we will include traits related to feeding ecology, locomotion, and body size. All collected and contributed trait data will be deposited in the Functional Trait Resource for Environmental Studies (FuTRES), ensuring open access to all researchers. Gathering functional trait data in this way could also be useful for the IUCN Green Status of Species, because the Green Status relies on understanding the functional role of species within their ecosystems. The Green Status aids in prioritizing conservation efforts and promoting sustainable management of ecosystems. We aim to improve efficiency and the comprehensive nature of ecometrics analysis. We also aim to broaden participation in ecometrics research and provide valuable data for conservation efforts such as the Green Status assessments, in addition to advancing our understanding of ecological systems by fostering inclusivity and collaboration.

228. Thepparatia, the evolution of dioecy and the lianescent habit in Hibisceae clade Trionum (Malvaceae, Malvoideae)

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Hibisceae subtribe Trionum is the largest clade within *Hibiscus s.l.* and contains genera with a wide range of growth forms: herbaceous (*Abelmoschus*), shrubs (*Malvaviscus*), trees (*Wercklea*) and exceptionally lianas. The rare and localised *Thepparatia* species are unique in that they combine a lianescent habit and trioecy. A number of problems have delayed the study of Hibisceae classification including low genetic variability, lack of synapomorphic morphological characters, transoceanic dispersal events and allopolyploidy. Here, we present a comprehensive phylogenomic hypothesis of *Thepparatia* based on analyses of the maternally inherited chloroplast and biparentally inherited nuclear ribosomal cistron sequences, and compare these results with its speciation, karyology, and breeding system. Chloroplast genomes in subtribe Trionum were highly conserved except in *Abelmoschus* where four additional genes were duplicated. Ancestral allopolyploid hybridisation is hypothesised in two clades: *Hibiscus* section *Venusti* (Pliocene c. 3.63 Mya between *Abelmoschus* and *Cenocentrum* in Asia) and *Wercklea* (Pliocene c. 3.82 Mya between *Kosteletzkya* and *Trionum* in America). Recent diploid interspecific hybridisation is suggested in *Thepparatia sipsongpannaensis* between *T. fragrans* and *T. scandens* during the Pleistocene, c. 640 000 years ago. Our observations also indicate *Thepparatia* have a trioecious breeding system that combined with a unique habit, and a highly localised distribution pattern, have created cross-pollination barriers and ecological specialisation. This suggests hybridisation events are rare but evolutionary significant in subtribe Trionum.

229. The cold range limit of prominent alpine graminoid species

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Where and why a species occurs and why it is absent at other places is a fundamental question in ecology. Nevertheless, range limits of alpine plant species are largely unexplored. We identified the cold range limits of two common alpine graminoids that intermingle in high-elevation habitats across the European Alps: *Carex curvula* and *Nardus stricta*. Ground-truth measurements at 115 microsites revealed that the distribution of these species was strongly affected by soil minimum temperatures during winter, rather than by season length, growing degree hours, or soil chemistry. *Carex* occured at sites with and without protecting snow cover and resisted low soil temperatures (-13°C). *Nardus* was absent at microsites with snow cover duration less than 5 months and soil minimum temperatures below -5°C. We explained these differences mechanistically by the higher freezing resistance of *Carex* compared to *Nardus*, employing methods such as electrolyte leakage, tetrazolium staining and survival assessments. *Carex* leaves and shoots resisted lower temperatures (LT50: -16.1°C) compared to *Nardus* (-13.3°C). In both species, shoot apices tolerated lowest temperatures: *Carex* -30°C, *Nardus* -24°C. However, regrowth after winter was only possible if the roots and vessels were intact. Our findings suggest that the cold range limits are set by thermal extremes in winter and not by thermal constrainst to growth and development. Microtopography, thus snow distribution pattern, in concert with the species' freezing resistance explains the cold edge of their fundamental niche.

230. Spatial scaling of beta diversity is broadly consistent and repeatable among ants, birds, diatoms, and trees

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Three fundamental concepts have separately accrued debates and varied measures: beta diversity (β), spatial scale, and ecological communities. In principle, the spatial scale at which maximal β is observed corresponds to the optimal size of an ecological community (without invoking external features of habitat, etc.). Here we test five alternative hypotheses about spatial scaling of β for ants, birds, diatoms, and trees across the contiguous USA, using spatial grains from 1 to 10^6 km^2. We evaluate summer and winter bird β in six consecutive years, and trees in four years, spaced 5 years apart. We also compare the deviation of β from spatially-clustered (β_{NBD}; Xing & He 2021) and spatially-homogeneous (β_{DEV}; Kraft et al. 2011) null models to observed β (β_{OBS};effective species turnover, Tuomisto 2010). β_{NBD} is less sensitive to sample size effects and more closely matches β_{OBS} patterns than β_{DEV}. Peak β_{NBD} ranged from ~200 km^2 (trees) to ~11,000 km^2 (diatoms), depending on taxon and seasonal timing (winter bird β_{NBD} < summer β_{NBD}). Bird and tree β_{NBD} patterns were repeatable across years. Consistent regional scaling of β here broadly supports the regional community concept (Ricklefs 2008) and suggests that: (a) similar patterns should occur across the tree of life; (b) ecology needs to better understand how local ecological and evolutionary forces scale up to form regional (biogeographical) community patterns; and (c) local biodiversity conservation efforts need to be coordinated at biogeographical scales to best achieve goals.

231. Bioclimatic niche similarity and species relatedness shift their influence on forest bryophyte co-occurrence across scales

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The processes driving species co-occurrence differ across taxa and scales are not well understood. Bryophytes are particularly interesting because while they disperse through long distances and have broad distributions, they are particularly affected by local conditions due to their small size. We investigated the relationship between pairwise species associations within epiphytic bryophytes and their bioclimatic niche similarities and taxonomic relatedness at four scales (global, regional, habitat and microhabitat). We used community data from 103 forests from northwest Iberian Peninsula and global occurrences for the 33 species with broad distributions to calculate pairwise co-occurrence at each scale and bioclimatic niche similarity, and obtained taxonomic distance matrices from bibliography. Co-occurrence relates to niche similarity at all scales, but this relationship decreases towards the microhabitat scale. Taxonomic similarity was also a good indicator of the pairwise co-occurrence not explained by niche similarity at the smallest scales. Interestingly, most pairwise relationships are positive or neutral rather than negative at all scales, although the direction of around 7% of these relationships shifts from positive at habitat scale to negative at regional scale. Bioclimatic requirements are progressively less important for species coexistence as scale diminishes due to the effect of local interactions and community-level processes.

232. Understanding elevational gradients in species richness, range size and niche asymmetry with ecological null models

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Empirically observed gradients in species diversity, range-size distribution, and the shapes of species response curves are influenced by various confounding factors, including geographical constraints, sampling biases, and their statistical representation. These factors can obscure or even contradict our understanding of the ecological drivers behind observed patterns. Formulating proper null expectation and applying adequate null models, specifically the 'Midpoint Attractor Models' for species range data, we successfully disentangled non-biological gradients from ecologically relevant ones. In a case study on Himalayan plant distribution data, we questioned the elevational Rapoport's rule, explained the mid-elevation species richness peak, and identified an asymmetry in species response curves, with a steeper decline towards higher and colder elevations.

233. Does the thermal niche explain the distinctness of alpine assemblages? Insights from water beetles

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High-mountain habitats are characterized by harsh living conditions that shape specific high-elevation assemblages, often composed by specialist species adapted to endure a pronounced abiotic stress, and prevent lowland species from colonizing or establishing. One of the key niche dimensions determining whether species can survive and establish at these extreme conditions relates to their thermal tolerances, which is especially important for ectothermic animals such as insects. Thus, differences in species thermal niches might explain how species assemblage along the elevational gradient. However, our understanding of how temperature sets altitudinal species distributional boundaries is still limited, especially for aquatic macroinvertebrates. In this study, we compare the thermal biology of high-mountain diving beetles (family Dytiscidae) from Sierra Nevada mountain range (southern Iberia) and closely related species from lowlands, with the aim to determine the role of thermal physiology in shaping the current distribution of species between both altitudinal zones and understanding how aquatic communities of high-mountain freshwaters will respond to climate change. Alpine species presented wider fundamental thermal niches than lowland ones, which might be associated with the broader range of climatic conditions they experience in high-mountain areas. Cold tolerance seems not to prevent lowland species from colonizing higher elevations, as most of the studied species can be considered as moderate freeze-tolerant, and survived ice enclosure. Therefore, fundamental thermal niches seem not to fully explain the species segregation along the elevational gradient, suggesting that other thermal niche traits and environmental factors, as well as biotic interactions, might play an important role.

234. Biogeography and diversity patterns of insects along an elevational gradient in a tropical-temperate transitional zone

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The Mexican Transition Zone, situated at the convergence of the Nearctic and Neotropical bioregions, is one of the most species-rich areas of North America. We surveyed insect communities along a 2000m elevational gradient in this region to evaluate species distribution, community structure and biographic affinity of different taxa. Our combined sampling protocol focused on ants, leaf litter weevils, and mobile insects captured by flight interception traps produced the region's most

comprehensive data currently available. While ants had the most species in lower and mid elevations (ground foraging ants 600m, leaf litter ants 400m), the species richness of leaf litter weevils increased with elevation and peaked at 1200m. The important factors associated with the alpha diversity of ants were tree size, annual precipitation and tree richness, while the diversity of weevils was positively associated with reduced tree height and low climate seasonality variation. On the other hand, the beta diversity of both groups was linked to tree richness and proportion of tropical and temperate vegetation. The biogeographic affinities of both groups were also contrasting. The lower elevations up to 1200m were mainly inhabited by ants with neotropical and mesoamerican affinities, while the high elevations were dominated by Nearctic species, with some notable exceptions. Surprisingly, the leaf litter weevils were mainly of Mesoamerican origin along the whole gradient. We compare these results with the distributional patterns of whole insect orders based on malaise trap sampling. Using the metabarcoding we detected 3100 insect OTUs at 10 elevations after 13 months of exposure.

235. Climate extremes and climate means importance in delimiting species ranges

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Environmental factors have been used to explain species’ distributions for centuries. The relative importance of those environmental factors in determining species’ occurrences may vary across space, being a non-stationary process. Furthermore, alternative measurements of the same variables, such as maximum, minimum, or mean values, may also have different strengths in explaining species’ distributions. Thus, although species tend to thrive under their optimal conditions, the relative importance of extreme values of environmental variables is expected to be higher towards species’ range edges. In order to quantify the contribution of individual variables across species’ ranges, we employ SHapley Additive exPlanations (SHAP) to analyse the importance of climatic variables to individual occurrence points in Species Distribution models of 50 mammal species, verifying whether extremes versus means contribute differently to species suitability across the species range. Our preliminary findings point that extreme temperatures and precipitation conditions are the variables with the highest explanatory power towards the specie range edges, while the centres of the ranges show no clear patterns.

236. The tangled biogeographic history of tarantulas: An African centre of origin rules out the centrifugal model of speciation

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Many animal groups diversify at the same place where they have originated, whereas others diversify at a place completely different from the centre of origin. Identification of the centre of origin, subsequent colonisation and diversification is crucial for understanding lineages' macroevolutionary dynamics and biogeographical patterns. The historical biogeography of the Mygalomorph spider family Theraphosidae has been confounded by two conflicting hypotheses –a South American origin for the

group, which is also the centre of its greatest extant diversity, as against an African origin. We aim to ascertain the centre of origin and directionality of inter-continental dispersal events in tarantulas by reconstructing their biogeographic history. We calibrated a previously published genome-scale phylogeny of Mygalomorph spiders using an improved interpretation of the fossil record. We reconstructed ancestral geographic ranges using the R package BIOGEOBEARS to explicitly test four different hypotheses that are likely to explain the extant diversity and distribution of tarantulas incorporating a time-stratified approach. We incorporated plate-tectonic reconstruction data and the dispersal ability of the organism in a model testing framework. Our results indicate that the ancestral stock of extant tarantulas occurred in Africa and South-America during the mid-Cretaceous, but subsequently went extinct in South-America. This points to an African origin for all modern tarantula lineages. The best-supported biogeographic model suggests multiple ‘out of Africa’ dispersal events into South America and later into India during the late Cretaceous. Localised ecological processes such as extinction, dispersal, key innovations, hybridisation and species–area relationships might cause a discordance between centre of origin and diversity.

237. Ecological legacies of past fire and human activity in a Panamanian forest

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Human activities over the past decades and centuries, including fire, cultivation, and forest opening, may have left ecological legacies that persist in modern tropical forests, particularly among palms. We investigated whether past human activities affected modern palm abundances in a well-studied plot located in a tropical semievergreen forest of Panama. We analyzed soil cores for charcoal to reconstruct past fire events and phytoliths to reconstruct past vegetation changes. We dated as many charcoal fragments as possible to place a temporal framework on past fire events. Our analysis documented widespread fires that occurred 600–900 years ago across the plot, which are similar ages radiocarbon dates obtained from the nearby Barro Colorado Island forest plot. *Oenocarpus mapora* increased in abundance as a result of these fires, though other palms did not. A subsequent increase in *O. mapora* occurred later in the relative absence of fire and was likely due to game hunting during the construction of the Panama Canal. Our results showed that the enrichment of *O. mapora* was determined by disturbance characteristics (e.g., timing, type, and intensity), but the persistence of increased abundances was likely determined by traits (life history characteristics). These data highlight the complexity of human–environment interactions and how they can persist for centuries in settings with long-lived trees such as tropical forests. These data highlight the importance of adding a historical context to further understand modern ecological patterns and processes.

238. Biogeography of the Early/Middle Pleistocene Transition in Central Europe.

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The Quaternary biotic history is marked by alternation of glacial and interglacial communities via extensive range dynamics of their members. This pattern, distinctly pronounced only in the middle and late Pleistocene, arose during the Early/Middle Pleistocene Transition (EMPT). We investigated course of underlying rearrangements based on extensive fossil record of EMPT small mammal communities obtained from complex sedimentary sequences in the Czech Republic (64 community samples with total abundance MNI=13995) which enabled to reveal faunal patterns at each of the MIS 23-14 climatostratigraphic stages. Despite invariant axial structure of EMPT communities, the EMPT turnover in a list of 88 small mammals species of the Mid-European late Early and Middle Pleistocene assemblages covered 41 % of species. Besides 6% of true extinctions and 16% of arrivals of apochoric clades not previously recorded (particularly during MIS 21-17 stages), most of the changes refer to phenotype rearrangements of resident taxa and split of them into elements of either glacial or interglacial communities. The apochoric elements were composed either by clades recently resident in Himalayan region or those adapted to deeply pronounced seasonality of the the boreal or steppe zones. A reduction of diversity during the glacial stages and the alternation mode of community response toward climatic oscillations were particularly pronounced since MIS 16. A tectonic uplift during MIS 22-17 demonstrated by onset of deep river erosion is considered the ultimate cause of the EMPT, related environmental rearrangements and unexpected transcontinental range expansions.

239. Molecular dating reveals multiple Pleistocene to Holocene faunal connectivity episodes between the Black and Caspian Sea basins

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The Black (BS) and Caspian (CS) seas have been isolated since the mid Pliocene (ca. 3 Ma) and are both remnants of the brackish Parathethys Sea, which spanned from the foothills of the Alps to the Himalayas during its Middle-Late Miocene (10-15 Ma) peak. Since their isolation, the BS and CS have undergone short-lived recursive connection episodes that influenced their biotic composition. However, the timing of these episodes remains contentious for the extant non-molluscan endemic fauna due to a sparse fossil record. Amphipod crustaceans are among the most diverse endemic faunal groups in the region, with a fossil record dating back 11 Ma, and dozens of species being distributed across BS and CS. Using a fossil-based, time-calibrated molecular phylogeny, we investigate the split times among 17 amphipod BS-CS sister lineage pairs. Although we find that divergence times range broadly and continuously from the Early (2.1 Ma) to Late Pleistocene/Holocene (20 kya), we identified two instances where multiple pairs experienced nearly simultaneous divergence. The first episode was observed in 3 pairs and dates to 1.5-1.56 Ma, while the second was observed in 4 pairs and dates to 0.26-0.3 Ma, both coinciding with major water intrusions from the CS into the BS. Interestingly, the first episode exclusively characterizes sand-dwellers, while the second exclusively hard substrate-dwellers. Overall, our findings reflect the numerous and sustained Pleistocene BS-CS connection episodes and suggest that some left a stronger biogeographic footprint than others.

240. Once upon a fly: the biogeographical odyssey of Labrundinia (Chironomidae, Tanypodinae), an aquatic non-biting midge towards diversification.

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Labrundinia is a highly recognizable lineage in the subfamily Tanypodinae (Diptera, Chironomidae). The predatory free-swimming larvae of this genus are typically present in unpolluted aquatic environments, such as small streams, ponds, lakes and bays. The group has been extensively studied in ecological research and comprises 39 species, all but one of which has been described from regions outside the Palearctic. Earlier phylogenetic studies have suggested that the initial diversification of the genus likely occurred in the Neotropical region, with its current presence in the Nearctic region and southern South America being the result of subsequent dispersal events. Through the integration of molecular and morphological data in a calibrated phylogeny, we reveal a complex and nuanced evolutionary history for *Labrundinia*, providing insights into its biogeographical and diversification patterns. In this comprehensive study, we analyze a dataset containing 46 *Labrundinia* species, totaling 10,662 characters, consisting of 10,616 nucleotide sites and 46 morphological characters. The molecular data was generated mainly by anchored enrichment hybrid methods. Our findings reveal multiple dispersal events out of the Neotropics, where the group originated in the late Cretaceous approximately 72 million years ago (69-78 Ma). We further reveal that the genus experienced an early burst of diversification rates during the Paleocene, which gradually decelerated towards the present day. We also find that the Neotropics have played a pivotal role in the evolution of *Labrundinia* by serving as both a cradle and a museum. This evidence highlights the crucial role that the region has played in shaping the evolutionary trajectory of *Labrundinia*.

241. Geodiversity in the Amazon Drainage Basin as a Corner Stone for Biodiversity?

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The variety of abiotic features in the landscape, i.e. geodiversity, is a research topic that has gained in popularity over the last decades, especially in relation to biodiversity. It is based on the notion that places with high geodiversity drive speciation and support high biodiversity. Despite being one of the most biodiverse regions in the world, geodiversity in the Amazon drainage basin (ADB) has not yet been objectively evaluated, which hampers research on the perceived geodiversity-biodiversity link. We address this knowledge gap by combining a meta-analysis of an existing global geodiversity map and its components (consisting of lithology, geomorphology, hydrology and soils) with a systematic literature review to identify the key characteristics of geodiversity in the ADB. We also evaluate how these geodiversity maps can be refined to better reflect geodiversity in the ADB. Our review shows that geology, through lithological diversity and geological structures, and hydrology, through hydrological processes that influence geomorphology and soil diversity, are the main determinants of geodiversity. These components are also mentioned as major explanatory factors in biogeographic research in the ADB. Based on these components, the ADB can be subdivided into three principal regions: 1) the Andean orogenic belt and western Amazon, 2) the eastern Amazon and craton, and 3) the Solimões-Amazon river system. Additional methods to map geodiversity have also been identified. This initial research into geodiversity in the ADB can support future research addressing biodiversity distribution patterns in the ADB and aid in conservation.

242. Assessing temporal variations in macroevolutionary rates: the reliability of the time-bin approach with an example of intercontinental dispersal during the Cenozoic

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There is a great interest among evolutionary biologists to reconstruct temporal variations in processes such as dispersal, extirpation, and speciation, and to correlate these variations with past environments. With the development of phylogenetic comparative methods, one increasingly used approach, is to reconstruct ancestral states and events, such as ancestral biogeography and dispersal events, and count the number of events occurring in successive time bins. This approach is intuitive, and it is also sometimes the only computationally tractable approach depending on the size of the data and the complexity of the biogeographical setting. Here, we test the validity of the approach with an example in the context of intercontinental dispersal during the Cenozoic. First, we construct a set of biogeographic stochastic maps and corresponding intercontinental dispersal events for a group of vertebrates, using the model of Dispersal Extinction Cladogenesis, which assumes a constant dispersal rate through time. We summarise the dispersal events across consecutive short time bins and compute dispersal rates through time. We correlate these time-binned events and rates with environmental variables that change through time such as the emerged area of landmasses and the distance between them. Next, on the same phylogeny we simulate biogeographies following the same assumption of no temporal variation in dispersal rate, carry out the same analyses of ancestral biogeography estimation on them, and compare their time-binned results with those obtained from empirical data. In light of our results, we discuss the pitfalls to avoid when assessing temporal variations in macroevolutionary processes in the past.

243. Do biome shifts promote sexual system transitions? Evolution of reproductive traits in Veronica with shifts into the New Zealand alpine zone

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Transitions between combined and separate sexes have occurred numerous times during angiosperm diversification. Such transitions are likely often driven by changes in habitat, which may be extreme during a biome shift. Here, we ask to what extent transitions in sexual system in section *Hebe* of the genus *Veronica* are associated with shifts between lowland and montane biomes in New Zealand; this clade represents the largest plant radiation in New Zealand. We use an existing phylogeny and biome occupancy data coupled with sexual system and trait data from the literature to model biome shifts, sexual system transitions, trait evolution, and associations between them. Our analysis indicates that the clade's common ancestor was likely hermaphroditic, had colourful flowers and occurred in lowland habitats, and that gender dimorphism and the production of white flowers likely evolved with transitions into the alpine biome. Transitions back to the lowland are associated with shifts back to non-white flowers. These results suggest that biome shifts might indeed facilitate sexual system transitions. We discuss the selective reasons for such shifts in terms of potential changes in the shape of so-called 'fitness gain curves' that may be associated with a reliance on

different pollinators in a new biome or with changes in the relative importance of abiotic versus biotic stress.

244. Rethinking spatial history: Envisioning a mechanistic historical biogeography

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Historical biogeography is the study of geographic distributions of organisms in space and time. Over the last 50 years, several methods have been proposed to reconstruct these histories. However, despite their particularities, conceptually they are all derived from the reconstruction of area relationships. Here we advocate that area cladograms lack explanatory power and that biogeography needs to move toward a more mechanistic approach. We discuss the ontological problems related to areas of endemism and their validity as biogeographic units. Specifically, we propose that areas of endemism are not discrete historical entities and should be abandoned by analytical biogeography. Instead, we suggest that biogeographic analyses should focus on those elements that cause diversification, namely barriers. We discuss how barriers have more discrete boundaries in space and time than do areas of endemism, which allows the identification of homologous units and the recovery of vicariant events. Reconstructing the history of vicariant events results in a better understanding of spatial evolution within a biota because barrier formation is the relevant causal mechanism of diversification. We end by acknowledging the largely ignored views of Peter Hovenkamp and his conceptual contributions to developing a mechanistic biogeography.

245. Alien ants break down biogeographic boundaries and homogenize community assemblages in the Anthropocene

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Since the appearance of life on Earth, millions of species have evolved, diverged, and diversified. Meanwhile, the geological structure of the planet has changed. As geographic distance increases species assemblages become more distinct defining global biogeographic realms with abrupt biogeographic boundaries. Those realms have been mainly described for vertebrates, but little is known about the global biogeographic boundaries for insects, even though they represent the most diverse group of animals. Human mobility and trade have exploded in the Anthropocene, causing voluntary and accidental dispersal of thousands of species worldwide. Some of these species have been able to establish outside of their native range (hereafter referred to as alien species), changing the composition of species assemblages worldwide. Yet, it remains largely unknown to what extent these realms may change because of human-mediated dispersal.

Focusing on the distributions of 292 alien ant species, we show that historical biogeographic patterns have already broken down into tropical versus non-tropical regions. Importantly, we demonstrate that these profound changes are not limited to the distribution patterns of alien ants but fundamentally alter biogeographic boundaries of all ant biodiversity (13,758 species). In total, 52% of ant assemblages have become more similar, supporting a global trend of biotic homogenization. Strikingly, this trend was strongest on islands and in the tropics, which harbor some of the most vulnerable ecosystems. Overall, we show that the pervasive anthropogenic impacts on biodiversity override biogeographic patterns resulting from millions of years of evolution, and disproportionally affect particular regions.

246. Niche dynamics of non-native plants vary between regions.

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Biological invasions pose a major risk to global biodiversity. When developing invasion risk assessments, model predictions often rely on the assumption that a species will conserve its environmental niche when introduced to a new range. While this assumption has been widely debated, recent literature suggests a tendency towards niche conservatism. The main problem, however, is that we still do not know for certain which factors determine whether a species will conserve its niche when introduced to a new range and how this might differ if an alien species is introduced to different regions. Here, we quantified the niche dynamics of more than 450 alien plant species that have been introduced to different parts of the world. Specifically, we used ordination to calculate the niche overlap between native and introduced range (based on Schoener's D) and the niche metrics stability, expansion and unfilling. Significance was tested using null models. Finally, we conducted phylogenetic and trait analyses to evaluate the impact of phylogeny, native range characteristics, and species traits on niche dynamics. Results indicate an overall high level of niche conservatism. Niche unfilling varied considerably based on geographic context, generally being higher when introduced to island compared to mainland systems. Our study provides important insights into how the niche dynamics of introduced plants differ between different regions.

247. Plants that have recently become more common in their native range are also more likely to be successful as naturalized aliens elsewhere

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Distribution patterns are dynamic; taxa have changed their occurrence frequencies and distributions naturally over geological time. Many taxa are also being introduced to new regions, and some of them succeed to naturalize. Although it is well established that plant taxa that have high occurrence frequencies (i.e. are common) in their native range are more likely to become naturalized, an analysis of how historical occurrence frequencies in the native range and recent changes therein, most likely due to environmental change, relate to naturalization success is still missing. We retrieved native occurrence frequencies of vascular plant taxa during two (or more) periods for ten European regions. After calculating for each of the taxa in each of the regions an index of change in occurrence frequency, we combined these data with data on the global naturalization success of the taxa to test whether taxa that have successfully naturalized elsewhere are mostly those that have also increased their occurrence frequencies in their native ranges (during the last decades or centuries). We found that global naturalization success increased significantly with both the historical occurrence frequencies as well as the index of change in occurrence frequency. For three native regions (the Czech Republic, the Netherlands and Switzerland), positive effect of the change index was even stronger for the taxa that were already common during the historical time period. Our results provide robust evidence that plant taxa that have become more common in their native regions are also more likely to become naturalized elsewhere in the world.

248. Reconstructing invasion spatial dynamics and life history traits from heterogeneous occurrence data

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Biological invasions play a major role in the current erosion of biodiversity and are more and more costly for our societies. Preventing invasions at minimal cost requires a good anticipation of the spatial dynamics and timing of invasions, which is often dictated life history traits, through life-stage dependent growth and spread. We introduce a bayesian hierarchical modeling framework to reconstruct spatial invasion dynamics from heterogeneous presence-only data by correcting spatio-temporal sampling bias and the variable detection rates across datasets. Life-stage structured fecundity can be explicitely accounted for along with covariate-dependent growth and additive spread components over a spatial grid to account for various invasion pathways. The framework may integrates prior information on life-history traits when available to improve estimation. The model class is especially suited to reconstruct perennial plant invasions, and we'll illustrate how we used it to show the major role of human mediated long-distance dispersal in the past dynamics of the invasive bush Plectranthus barbatus in Soutern Africa, and how targeted management could have drastically slow it down. This framework opens broad possibilities for invasion biogeography in many context where standardized data is rare. Ongoing research on parameter estimability in different data contexts and the identification of optimal algorithmic routines could then democratize its use.

249. The importance of variable selection when modelling alien species under non-analog conditions

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The sub-Antarctic is host to some of the remotest islands, characterized by a globally unique climate. Despite this, the islands have accumulated many alien species since their relatively recent discovery. In this study, we determined the degree of overlap between the bioclimatic conditions of these species' complete geographic distribution worldwide and the range of bioclimatic conditions present on each island group, expressed as 19 bioclimatic variables commonly used in species distribution modelling. Second, we determined how the inclusion of different sets of bioclimatic variables affects the predictions of species distribution models (SDMs) under the non-analog conditions of the sub-Antarctic. We found that almost all alien plant species in the sub-Antarctic occur outside of the climatic niches they occupy in the native and alien ranges off the islands with respect to at least one bioclimatic variable. Especially, summer warmth and temperature seasonality of many of the sub-Antarctic islands is almost entirely different from the conditions under which these species occur anywhere else in the world. Including these bioclimatic variables in SDMs, leads to strong over- and underpredictions of species occurrences. The results demonstrate that climatic variables commonly thought to be relevant for plant distribution and often used in SDMs, such as those indicating summer warmth, do not represent an effective filter for plant invasions on sub-Antarctic islands. Consequently, correlative methods based on currently realized niches will be unable to predict species invasions accurately under non-analog climatic conditions, which will likely become more frequent with intensifying climatic change, also outside the sub-Antarctic.

250. Trees from Australia in the Mediterranean basin

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A very large number of Australian tree species have been introduced in the Mediterranean basin for diverse purposes and uses, such as ornamental and landscaping plants, and forestry. This contribution focus on two main genera, *Acacia* and *Eucalyptus*, which include both species that have been planted very extensively in most of the countries facing the Mediterranean basin and other that are quite rare or failed to establish or persist after one or more introduction events. A limited number of species belonging to these two genera are now considered invasive and are strictly regulated, as in the case of *Acacia saligna*, a species banned in the EU according to Regulation no. 1143/2014. The present contribution will describe the ongoing work and the preliminary results of a database where all the information about the records of introduction of *Acacia* and *Eucalyptus* in the countries facing the Mediterranean basin are stored, based on data collected in the literature and information provided by an international team of researchers. The aim of the database is to more precisely quantify all the introductions that occurred in each country, the pathways of introduction, the geographical location and other available information to help understand why only a limited number of species of *Acacia* and *Eucalyptus* managed to naturalise or become invasive in the new Mediterranean range.

251. Functional trait differences between native and alien plant species in local communities of different habitat types

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The question of how alien plant species are integrated into local communities and what makes them invasive has been one of the central topics since the beginning of invasion ecology. Here, we address this question by analyzing functional trait differences between native and alien species in 12,460 invaded vegetation plots recorded in six different habitat types in the Czech Republic. We asked whether alien species integrate into the center or periphery of the trait space of each community (vegetation plot) and whether the observed pattern is consistent across habitat types. When we considered each trait separately, differences between native and alien species (either non-invasive naturalized or invasive) were very small and mostly statistically insignificant. We also did not find consistent differences across habitat types. In contrast, when we measured the distance from the center of the trait space of native community in each vegetation plot, we found that native species were significantly clustered around this center, while alien species (both naturalized and invasive) were distributed farther away in most vegetation plots across all habitat types. However, the distribution of alien species was statistically indistinguishable from the simulated (randomly assembled) communities. The alien species were thus not different from being randomly selected from the habitat species pools and inserted into the local communities. This suggests a weak effect of assembly rules and environmental filtering on alien species which makes them distributed at the edge of the trait space in local plant communities.

252. Marsh frog invasions in Western Europe: multiple biogeographical origins, opportunism and effects on native pond communities

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Whereas some biological invasions are well documented, others, more cryptic, are often underestimated. This is the case of marsh frogs (*Pelophylax ridibundus*) which have been released into the wild as part as the frog leg and captive breeding industry. Despite being one of the most studied frog in Europe, there is still a lack of an integrative overview of its invasion patterns and risks to biodiversity. To fill this gap, we carried out an inter-disciplinary study in phylogenetics, spatial and trophic ecology. By genotyping hundreds of populations in the Palearctic, we found out that more than 10 lineages, originating from three continents, were found in invaded areas. Interestingly, these invasions pathways fit well with the history of importations of live frogs in Western Europe. The introductions gave rise to nation-wide invasions, facilitated by the wide ecological opportunism of the invaders. This resulted in large niche overlaps with native amphibians which use similar aquatic environments. Diet analyses across multiple ponds showed a high trophic opportunism of marsh frogs, which were able to forage on most native amphibians but also on many invertebrate taxa and threatening some emblematic species. Altogether, these results rank the marsh frogs as one of the most invasive amphibian species in the world and call for research to highlight the complexity of patterns and effects from the different lineages as well as for a limitation of risks due to the international trade.

253. Anticipating the Global Expansion of the Monk Parakeet Invasion

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Biological invasions pose a significant threat to the environment and the economy, having acquired global proportions due to human activities such as trade and tourism. The Monk Parakeet (*Myiopsitta monachus*), a highly social parrot native to South America, has effectively colonized numerous regions across the globe, with significant prevalence in North America and the Mediterranean basin over the last decade. Recognizing the invasive potential of this species, identifying unoccupied regions with optimal environmental conditions for their establishment becomes an essential tool to predict the spread of this invasive process. By using known presences and a set of environmental variables (including topography, climate, and human activity), we applied the Favourability Function to generate a potential global distribution model for the Monk Parakeet. The model's accuracy was assessed, revealing good discrimination and classification capacity. It predicted highly favorable areas for potential invasion in regions where the species has not yet been detected, such as Australia, New Zealand, Myanmar, Ireland, or South Africa. Additionally, potential expansion areas were identified in places where the species has recently been detected, such as Morocco. The generated cartographic data could provide guidance for decision-making in managing this biological invasion, identifying territories already invaded where mitigation and control measures should be implemented, as well as unoccupied but favorable territories where preventive measures can be applied to prevent the spread of the Monk Parakeet.

254. Spatial resolution impacts projected plant responses to climate change on topographically complex islands

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Understanding how grain size affects our ability to characterize species responses to ongoing climate change is of crucial importance in the context of an increasing awareness for the substantial difference that exists between coarse spatial resolution macroclimatic data sets and the microclimate actually experienced by organisms. Climate change impacts on biodiversity are expected to peak in mountain areas, wherein the differences between macro and microclimates are precisely the largest. Based on a newly generated fine-scale environmental data for the Canary Islands, we assessed whether data at 100 m resolution is able to provide more accurate predictions than available data at 1 km resolution. We also analysed how future climate suitability predictions of 14 island endemic bryophytes differ depending on the grain size of grids. We used two climate data sets: CHELSA v1.2 (~1 km) and CanaryClim v1.0 (100 m), a downscaled version of the latter utilizing data from local weather stations. Species distribution models generated from CHELSA and CanaryClim exhibited a similar accuracy, but CanaryClim consistently returned higher proportions of newly suitable pixels (8%–28%) than CHELSA models (0%–3%). Consequently, the proportion of species predicted to occupy pixels of uncertain suitability was higher with CHELSA (3–8 species) than with CanaryClim (0–2 species). The resolution of climate data impacted the predictions rather than the performance of species distribution models. Our results highlight the crucial role that fine-resolution climate data sets can play in predicting the potential distribution of both microrefugia and new suitable range under warming climate.

255. PleistoDist: A toolbox for visualising and quantifying the effects of Pleistocene sea-level change on island archipelagos

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Pleistocene sea-level change has played a significant role in the evolution and assembly of island biotas. The formation of land bridges between islands during Quaternary glacial maxima, when sea levels were more than 120 metres below present-day sea levels, often facilitated historical dispersal and gene flow between islands that are today geographically disconnected. Despite the importance of Pleistocene sea-level change, few software packages exist that model the effects of this phenomenon in a standardised and generalised manner. Here, we present PleistoDist, an R package that allows users to visualise and quantify the effects of Pleistocene sea-level change on islands over time, and test multiple temporally explicit hypotheses of inter-island dispersal and community assembly. Re-analysing published datasets, we demonstrate how using PleistoDist to account for historical sea-level change can provide greater explanatory power when analysing extant island communities, and show how population genetic simulations can be used to generate spatiotemporally explicit neutral expectations of population genetic structure across island archipelagos.

256. Trait-dependent diversification and biogeography of Canary Island angiosperms: a community-wide approach

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Why do some island lineages radiate spectacularly, while others remain species-poor or do not radiate at all? Identifying the drivers that promote diversification is one of the key objectives of biodiversity research. Using a sample of over 800 species of Canary Islands flowering plants, comprising the majority of species and lineages that make up the native angiosperm flora of the archipelago, we are investigating whether specific traits may have influenced species diversification and colonisation in this floristically diverse oceanic archipelago. We are generating an angiosperm-wide time-calibrated molecular phylogeny using hybrid capture-based target enrichment combined with next-generation sequencing, which will include the island taxa and their closest relatives on the mainland, allowing us to gain an estimate of the times of colonisation and branching times for most angiosperm lineages of the Canary Islands. In addition, we are building trait databases on traits believed to have influenced diversification, including woodiness, fruit, and flower traits. We present here preliminary results from the project, including phylogenies for specific lineages of the Canary Islands angiosperm flora and an estimated number of independent colonisation events inferred for the archipelago. These phylogenies and trait data will be used to test a novel trait-dependent diversification model specifically tailored for islands, that is being developed in close collaboration

with this project. By combining the new model and the empirical data, we will identify plant traits that may have driven or hampered diversification, and triggered radiations in the Canary Islands.

257. MEDIS - A Comprehensive Spatial Dataset on Mediterranean Islands for Biogeographical and Evolutionary Research

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The intrinsic characteristics of islands make them unique for studying ecological and evolutionary dynamics. The Mediterranean Basin, a biodiversity hotspot, is rich in islands, hosting a significant global biodiversity proportion. Despite extensive research, a comprehensive spatial dataset for these islands is lacking. We presents the first comprehensive spatial dataset of all Mediterranean islands larger than 0.01 km2, aiding ecological investigations and interdisciplinary research on economic, environmental, and social issues. Building upon existing global coastlines and islands shapefiles, we extracted all Mediterranean island polygons, manually verified and corrected errors, and digitized missing islands. The spatial dataset offers detailed information on 38 geographic, climatic, ecological, and land-use variables, including island area, perimeter, isolation metrics, climatic space, terrain data, land cover, paleogeography, road networks, and geological information, providing a multifaceted view of each island's characteristics. The study encompasses 2212 islands in the Mediterranean Basin larger than 0.01 km2. The level of measurement is extensive, encompassing a wide range of variables and providing polygonal features rather than centroids' coordinates. This dataset aims to facilitate research in island biogeography by providing a basis for understanding the factors affecting species distribution and community dynamics on Mediterranean islands. Ultimately, we aim to provide a resource that will contribute to a better knowledge of the outstanding ecosystems of the Mediterranean Basin, streamlining conservation initiatives and defining effective management plans for their vulnerable species.

258. Diversification dynamics in a highly successful insular plant taxon are consistent with the general dynamic theory of oceanic island biogeography

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The general dynamic theory of oceanic island biogeography (GDT) views oceanic islands predominantly as sinks rather than sources of dispersing lineages. To test this, we conducted a biogeographic analysis of a highly successful insular plant taxon, *Cyrtandra*, and inferred directionality of dispersal and founder events throughout the four biogeographical units of the Indo-Australian Archipelago. Sunda was recovered as the major source area followed by Wallacea. The relatively high contribution of Wallacea is attributed to its central location in the IAA and its complex geological history selecting for increased dispersibility in *Cyrtandra*. We also tested if diversification dynamics in *Cyrtandra* follow predictions of adaptive radiation, which is the dominant process on oceanic islands as predicted by the GDT. Diversification dynamics of dispersing lineages of *Cyrtandra* in the Southeast Asian grade showed early bursts in diversification rates, followed by a plateau which is consistent with adaptive radiation. We did not detect signals of diversity-dependent diversification and this is attributed to Southeast Asian cyrtandras occupying various niche spaces as evident by its wide morphological range, particularly in habit and floral characters. The clade containing mostly Pacific members, which arrived at the early stages of the ontogeny of the Pacific islands, showed diversification dynamics predicted by the Island Immaturity Speciation Pulse (IISP) model, and their morphological range is controlled by the least action effect favoring woodiness and fleshy fruits. Our study provides a first step towards a framework for investigating diversification dynamics as predicted by the GDT in highly successful insular taxa.

259. Great speciators of the plant world: Island biogeography of Hawaiian Asteraceae

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Macroevolutionary models of island biogeography now allow inferring the processes governing biota assembly for entire communities over evolutionary time scales, such as testing diversification and equilibrium dynamics. However, to date, much of the attention has been focused on well-known vertebrate taxa, especially birds and mammals, and it is unclear whether similar diversification dynamics hold for island plants. Asteraceae - the most diverse plant family in the world - provides an excellent model system for looking at diversity dynamics on islands, due to this group's high diversity, endemism, and number of radiations across islands globally. In particular, the Asteraceae flora of the Hawaiian Islands is remarkably diverse, with 99 native of which 98 species are endemic. One of the most iconic examples of adaptive radiation on islands is the Asteraceae silversword alliance of Hawaiʻi, but, remarkably, this is just one of many Asteraceae radiations across the archipelago. Here, we compile and build new dated phylogenies for all the native Asteraceae lineages that have colonized Hawaiʻi. We then use a macroevolutionary island biogeography model (DAISIE) to analyze and reconstruct the build-up of the diversity for the entire native Asteraceae assemblage on this remote archipelago. Our approach allows us to infer the number of colonization and radiation events, estimate macroevolutionary rates of colonization, speciation and extinction,

and to test whether this system is at equilibrium.

260. Combining in-situ monitoring and remote sensing to detect impacts of volcanic sulfur in the Canary Pine forests of La Palma, Spain.

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The eruption of the volcano Tajogaite on the island of La Palma, Spain in 2021 had a significant impact on the surrounding ecosystems. Especially affected was the Canary Pine forest. Individuals of *Pinus canariensis*, the monodominant tree species forming these stands, were buried partially by a thick layer of tephra, mechanically damaged by volcanic ejecta and poisoned by volcanic gases. We make use of a combination of remote sensing methods combined with in-situ data to investigate several volcanic impacts on these forests. Sentinel-2 satellite images were used to map the initial spread of chlorotic canopy discoloration, revealing damage up to 7 km away from the crater. Needle samples were analyzed for their sulfur (S), carbon (C) and nitrogen (N) levels to investigate the impact of sulfur and subsequent resprouting on needle levels of essential building blocks. S and C levels were strongly linked to the distance to the volcano, with high levels of S leading to low levels of C, which is likely translocated as a building block during resprouting. Surprisingly, we found no clear relation between N and the distance or S levels and generally more complex patterns, with N likely affected by other environmental drivers and the fire history of these forests. Due to the volcanic origin of the Canay Islands, *Pinus canariensis* is well adapted to the prevailing disturbance regime shaped by volcanism and fire and showed remarkable resilience after the 2021 eruption, with even severely damaged trees resprouting and on their way to recovery.

261. Tropical Wetlands: Landscapes of Change

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Over the last decade our group has worked on mapping, modelling, and reconstructing the Holocene history of forested, peat-forming wetland ecosystems in lowland Amazonia and central Africa. These vast water-logged landscapes offer, through their rich palaeoecological records, a unique opportunity to understand long-term vegetation dynamics in a tropical setting and, importantly, the interactions between vegetation and the physical environment, the global carbon cycle, and the people who rely on their resources. Here we present the latest synthesis of emerging results from our interdisciplinary research which reveal the spatial and temporal patterns of vegetation change, and the processes that drive those patterns, for example, flooding regime, nutrient status, ecological succession (terrestrialization and paludification), and human activity. We show some of the ways in which palaeoecological and biogeographical data in particular are informing our conceptualisation of the processes of change in these landscapes, which in turn are demonstrably finding applications in policy development and sustainable management at global, national and local scales.

262. Missing Lynx: Dietary variability of *Lynx rufus* across space and time as inferred from dental microwear texture analysis

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Predators' prey selection is largely influenced by their geographic ranges and evolutionary history. Extant bobcat (*Lynx rufus*) distributions extend from southern Canada to central Mexico, nearly covering all twelve Level I ecoregions (e.g., temperate forests, deserts, great plains, etc.). Most previous research reports bobcats as generalized foragers in the north but more specialized in the south. This study aims to assess the feeding behavior of *Lynx rufus* throughout their range and over time, also assessing the degree to which dietary variability is correlated with biomes. Bobcats spanning from the 1890s to the Present were examined, including cats from eastern temperate forests, northern forests, northern mountain forests, great plains, Mediterranean California, deserts, etc. We find that dental patterns in these ecoregions do not significantly differ from each other, with indistinguishable mean values for *Asfc* and *epLsar* metrics ($p>0.05$). Microwear attributes also do not show significant differences between males and females or across time, though DMTA complexity values are significantly higher in the Present as compared to during the Pleistocene (when compared to *Lynx rufus* from Rancho La Brea, $n=11$). In summary, these results indicate that bobcat diets are today more generalized than at Rancho La Brea and that this dietary variability is prevalent in most ecoregions today. Understanding the dietary behavior of bobcats is crucial to bobcats' conservation, especially as their realized niche has changed dramatically over time potentially in responses to megafaunal extinctions and/or anthropogenic impacts.

263. Effects of urbanization on social spiders: the costs of urban living

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Urbanization involves dramatic changes in abiotic and biotic conditions, including higher temperatures, environmental pollution, and changes in the quality and abundance of resources for organisms. Organisms are adapting to these urban environments, often through changes in their phenotypes and ecology. For species that live in groups and cooperate, there is a lack of knowledge about how they are responding to urban pressures, particularly in the Neotropics. Social spiders (genus *Anelosimus*) form permanent colonies with hundreds or even thousands of spiders, who cooperate in various activities, including prey capture and offspring care. Social spiders live in the lowland rainforest, but they can also exploit urban areas. To evaluate group-level and individual level responses to urbanization, we studied colonies of *A. eximius* in urban and natural areas in the Amazon basin in eastern Ecuador. We found that, for nests of comparable sizes, the number of spiders was slightly lower in the cities, but spiders were smaller and captured smaller and less diverse prey. Urban social spiders also exhibited higher levels of parasitism and reduced fecundity. These findings are in line with predictions of declines in body size in cities due to lower availability of optimal prey and higher temperatures due to the urban heat island effect, and further suggest that the costs of living in cities go beyond inherent requirements of social spiders to obtain large and abundant prey. Understanding how urbanization alters the phenotypes and ecology of organisms is key to predicting the costs of adaptive responses to anthropogenic change.

264. “Flower power”: how flowering affects spectral diversity metrics and their relationship with plant diversity

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Biodiversity monitoring is constrained by cost- and labour-intensive field sampling methods. Increasing evidence suggests that remotely sensed spectral diversity (SD) is linked to plant diversity. However, studies testing such a relationship reported conflicting findings, especially in challenging ecosystems such as grasslands. With the advances in aerial sensors, it is theoretically possible to capture the direct link between the spectral information at the canopy level and plant species characteristics. Yet, to use SD for biodiversity monitoring, a thorough investigation of the key factors (e.g., metrics applied, spatial resolution) and conditions under which such a relationship exists is necessary. Thus, this study aims at assessing the applicability of SD for plant diversity monitoring at the local scale by testing seven different SD metrics while considering spatial resolution effects and the presence of flowering as confounding effect. Taxonomic diversity was calculated based on data collected in 159 1.5 × 1.5 m experimental mesic grassland communities. Spectral information was collected using a UAV-borne sensor measuring reflectance across six bands in the visible and near-infrared range at ~2 cm spatial resolution. Our results show that, in the presence of flowering, the relationship is significant and positive only when SD is calculated using categorical metrics. Despite the observed significance, the variance explained by the models had very low values, with no evident differences when resampling spectral data to coarser pixel sizes. Such findings suggest that new insights into the possible confounding effects on the SD~plant diversity in grassland communities are needed to use SD for monitoring purposes.

265. Macroecological analysis of sustainability of cashmere production at the continental- and regional level: impact of climate change and land use on biodiversity of grassland ecosystem

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Biodiversity is the foundation of natural capital that underpins society and economy. Therefore, in the sustainability of business, there is an increasing demand for a so-called biodiversity compliance that assesses nature-related risk through better understanding of the contact points between a company's activities and nature, as well as its impact on biodiversity features and dependence on ecosystem services. In this context, the relationship between cashmere production which generally considered to be the cause of desertification and biodiversity was analyzed, in collaboration with a globally operating apparel company. Specifically, we explored biogeographical patterns of cashmere production areas at the Eurasian continental level, and tested the overlap between suitable areas of cashmere goat grazing and priority areas of biodiversity conservation at the regional level. Then we evaluated the impact of cashmere goat grazing on biodiversity patterns by identifying spatial conservation priority areas of grassland ecosystems. Based on these macroecological analyses, the sustainability of cashmere production is discussed in relation to climate change and land-use.

266. Dispersion of dragonflies in cities: experimental study

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As many other species, also dragonflies can inhabit urban habitats even in the centre of big cities. This study has been focused on population dynamics of dragonflies in urban environment. Main goal has been to study their dispersion and migration in the Prague city centre using mark-release-recapture (MRR) method to observe whether urban environment does somehow act as a barrier for population dynamics. Lentic bodies located in broader centre of the city were chosen as sufficient study sites, situated mostly in city parks or other "green" areas. The whole study area is also divided by river. Field study took place in 2023 from the end of May to beginning of July. Individuals were given unique codes and the information about location of every encounter was included to track their movement. In total, 1867 individuals of different species were marked. Only two species (*Pyrrhosoma nymphula* and *Coenagrion puella*) were included in the dispersion analysis as they were the most abundant ones with occurrence on all the study sites. Preliminary results suggest that individuals from zygopteran populations are mostly bound to their parent site as migration between distant sites through urbanized space was recorded only within clusters of nearby lentic bodies. Movement across the river was minimal, only two marked *C. puella* individuals managed to cross the water, which, however, may suggest metapopulation character of respective species. Further experiments on more species through greater part of urban gradient along with habitat assessment could reveal more information about dragonflies' population dynamics in cities.

267. How detrital food webs differ from grazing food webs and how can food web models be linked to biogeochemical models

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Detrital food webs start with processing of dead organic matter while grazing food webs start with living autotrophs. In terrestrial ecosystems, most of the energy incorporated by photosynthesis ends in soil and the detrital food webs. Food web models describe the energy transfer between living biomass of individual trophic levels and focus only on trophic, prey-predator interactions. On the contrary, biogeochemical models use pools defined based on their dynamics, e.g. the rate of decomposition. More recently, biogeochemical models have started to consider soil biota, namely microbial biomass and in particular production of microbial necromass that can be stored in soil. Here we emphasize the role of soil detritivores, i.e., invertebrates feeding partly on dead plant material and partly on microbial biomass. By doing that, they affect microbes either by predation or even more importantly, by modification of the soil environment by production of feces and other soil structures.

There are three major energy flows essential for functioning of soil detrital food webs which are often neglected in food web models; i) production of dead biomass (mainly microbial necromass), ii) production of feces which affect nutrient availability and habitat for other organisms, and iii) building and disrupting various structures by detritivores such as soil aggregates and burrows which again affect conditions for other organisms. We propose that including these energy flows into food web models would allow to make these models more useful in description of major biogeochemical process and to explore the links between community structure and function.

268. From plant-soil feedback to soil biota engineering and soil formation and back: a continuum of soil and biota interactions at various spatiotemporal scales

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Plants and soil biota are important ecosystem engineers interacting via plant-soil feedback on both short and long time-scales. Here we emphasize three major pathways of plant-soil feedback: i) the biota pathway, when plants affect soil biota, such as plant symbionts or antagonists, which affect plants, ii) the soil pathway, when plants affect soil environment, which then feedback to plants and finally iii) biota-soil pathway, when plants affect soil biota, which then affect soil environment, which then affect plants. Plants drive these interactions via roots or litter. Roots are more important for the biota pathway, while litter dominates the biota-soil pathway, with soil pathway being intermediate. The pathways also differ in timing of their effect which can be either immediate, or long-term (legacy effect), affecting the next generations of plants. Immediate effects are more common for the root-driven biota pathway, while legacy effects are more common in the biota-soil pathway driven by litter interactions, with the soil pathway again intermediate. The legacy effects that include soil changes happen as slow gradual changes (over centuries or millennia), or relatively fast (in one or few decades), abruptly shifting between two steady states. In both cases, soil can reach tipping points, altering functioning of whole plant soil system. Apart from plants, also soil conditions or soil biota can be manipulated either intentionally (e.g. tillage), or non-intentionally (e.g. biological invasion). Studying all three pathways of the plant soil feedback on various spatiotemporal scales is necessary to understand how it is altered in the Anthropocene.

269. When cheating turns into a stabilizing mechanism of mutualistic networks

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Mutualistic interactions, such as plant-mycorrhizal or plant-pollinator interactions, are widespread in ecological communities and frequently exploited by cheaters, species that profit from interactions without providing benefits in return. Cheating usually negatively affects the fitness of the individuals that are cheated on, but the effects of cheating at the community level remains poorly understood. Here we describe two different kinds of cheating in mutualistic networks and use a generalized Lotka-Volterra model to show that they have very different consequences for the persistence of the community. Conservative cheating, where a species cheats on its mutualistic partners to escape the cost of mutualistic interactions, negatively affects community persistence. In contrast, innovative cheating occurs with species with whom legitimate interactions are not possible, because of a physiological or morphological barrier. Innovative cheating can enhance community persistence under some conditions: when cheaters have few mutualistic partners, cheat at low or intermediate frequency and the cost associated with mutualism is not too high. In this case, the negative effects of cheating on partner persistence are over-compensated at the community level by the positive feedback loops that arise in mutualistic networks. Using an empirical dataset of plant-bird interactions, we found that observed cheating patterns are highly consistent with theoretical cheating patterns found to increase community persistence. This result suggests that the cheating patterns observed in nature could contribute to promote species coexistence in mutualistic communities, instead of necessarily destabilizing them.

270. Combining natural history archives with models to quantify the resilience of bowhead whales to past, present, and future threats

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The Arctic is warming four times faster than the global average, causing the rapid decline of Arctic sea ice. These changes threaten bowhead whales (*Balaena mysticetus*) that depend on sea ice for feeding, calving, and escape from predation as they migrate to, and feed at, their primary summering grounds. Using modern data alone is insufficient for quantifying bowhead resilience to Arctic warming as almost four centuries of commercial whaling decimated stocks until its cessation in 1913. To address this, we assembled two natural history databases and leveraged them with ecological models. We constructed a fossil database that harmonizes biomolecular archives (radiocarbon, stable isotopes, and ancient DNA) from 11 Arctic marine mammal species since the Last Interglacial Period 130,000 years ago, and used this to understand the effects of long-term climate change on bowheads. Using an ecological niche modelling approach that incorporates high-resolution past and future climate data, we showed that bowhead habitat suitability has been largely stable throughout the Holocene, but the effects of future climate change will result in a ~75% decrease in suitable habitat extent by 2100. By using our second database to chronicle the history of commercial bowhead whaling throughout the Arctic, we were also able to identify the spatiotemporal drivers of whaling, showing that areas of thick sea ice delayed whalers' access to certain bowhead sub-populations, providing important historical refugia. Integrating these findings into process-explicit models will allow us to better quantify the susceptibility of bowheads to future extinction in an increasingly ice-free Arctic.

271. Bipolar, Antitropical, or Cosmopolitan? Untangling the presence and extent of true bipolarity in marine taxa

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Understanding why and how latitudinally disjunct distributions occur in the marine realm is necessary to fill the gaps in knowledge of evolutionary processes, biodiversity, and range limits. One of the most striking distributions is bipolarity, the presence of species at both polar regions without connecting populations in the tropics. The bipolarity concept and its extent has been debated since the 1800s, resulting in various definitions and confusion for study comparability. To our knowledge, this is the first systematic review which synthesizes available information from all previous studies to help identify future research questions on disjunct distributions in the marine realm. This included but

was not limited to investigating the temporal trends of such research and determining how many taxa are truly bipolar or antitropical with molecular confirmation. A total of 621 records were extracted from 233 articles, with 418 records defined as antitropical and 203 as bipolar. Most of the records referred to chordates, but cnidarians and retarians were also highly represented within the records of invertebrates and protists, respectively. There was more research on a species-level, which contradicts the perception that disjunct distributions are more common on a higher taxonomic level. However, while 203 records were defined as bipolar here, the Arctic and Antarctic Register of Marine Species have 530 species present in both databases, suggesting a hidden diversity of potential bipolar species. Overall, this systematic review provided a well-rounded view of marine disjunct distributions and identified the issues that need to be addressed to drive the field forward.

272. Unveiling Bergmann's Rule in Ectotherms: Processes associated with geographic gradient in body size in North Atlantic Reef Fish

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Bergmann's Rule associates the increase in an organism's size with the temperature at which it occurs. As temperature has a linear inverse relation with latitude, latitude has been used as a proxy to explain it. Its generality in ectotherms remains unclear. We aim to unveil abiotic mechanisms driving patterns of body size variance in Elasmobranchii and Actinopterygii, inhabiting reef environments at North Atlantic Ocean. Our database was assembled from: Gbif, FishBase, MarineRegions.org and Bio-oracle. Each ocean was divided into 2.5-degree latitude bands. We extracted 256 environmental variables as mean values per band. The Generalized Linear Model (GLM) were selected by the Akaike Information Criterion. The results for the Bergmann Rule showed a non-significant relationship ($p = 0.266$). The best GLM model (Gamma inverse) identified three oceanographic variables accounted for 88% of body size variation: minimum dissolved oxygen, maximum iron concentration and minimum salinity. Higher iron concentrations associated with higher dissolved oxygen seem to cause increase in body length. Iron containing proteins are involved in chlorophyll synthesis, which affects primary productivity. Marine teleost may have a disadvantage in assimilating iron due to their alkaline intestinal environment, thus lower availability of iron constrains body size. Osmoregulation mechanism in salt water fishes rely on gill ATPase, possibly indicating a constrain in body size in high salinity water masses. The positive relationship between body size and minimum dissolved oxygen is associated with the increased metabolic rates observed in large animals. These results support how Gill-Oxygen Limitation Hypothesis is related to smaller body size.

273. Expanding the known distribution range of existing species and the new North Pacific deep-sea coral species (Paracis, Paramuriceidae, Octocorallia, Anthozoa).

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Deep-sea coral habitats are often considered biodiversity hotspots in the deep ocean. They support a diverse community of associated species, including brittle stars, shrimp, crabs, and other

invertebrates, which may be specially adapted to the unique conditions of the deep-sea environment. Paramuriceidae is a family of gorgonian corals, which are a type of octocoral. Gorgonians are characterized by their branching, tree-like appearance and are often found in marine environments from the shallow to the deep. Paramuriceidae includes various species of gorgonian corals, and they can be found in different parts of the world, including the Indo-Pacific region and the Atlantic Ocean. The genus Paracis (Paramuriceidae, Octocorallia) has been relatively easily identified in situ ROV dive images with large pavement-like sclerites on the coenenchyme surface. i.e. during the Campaign to Address Pacific monument Science, Technology, and Ocean NEeds (CAPSTONE) by NOAA Ship Okeanos Explorer, U.S., between 2015 and 2017, the image identification counts ca. 190 Paracis in the database of Ocean Networks Canada SeaTube V3 (https://data.oceannetworks.ca/ExpeditionManagement). Though they have been observed such abundance in situ at the Pacific ROV expedition, the Paracis have not been re-examined since their initial description in the 19th century to the early 20th century. We have re-examined the type of the genus Paracis and re-described all known Paracis type species from the North Pacific in Matsumoto & Ofwegen, 2023. The discovery of new species and the expansion of the known distribution range of existing species are shown here.

274. Latitudinal variation in the geographical range of North Atlantic reef fishes is not driven by temperature

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The macroecological pattern that correlates the latitudinal range with the latitude in which a given species occur is called Rapoport's rule. The main hypothesis to explain it is the differential climate tolerance of tropical and temperate species, as organisms inhabiting low latitudes are subject to less seasonal variation, and thus, they would be limited to a narrower latitudinal distribution range. Although this relationship is supported across various taxonomic groups, its processes, significance, and generality remain unclear. We aim to unveil abiotic mechanisms driving patterns of range size variance in Elasmobranchii and Actinopterygii, inhabiting reef environments at North Atlantic Ocean. Our database was assembled from: Gbif, FishBase, MarineRegions.org and Bio-oracle. Each ocean was divided into 2.5° latitude bands. We extracted 256 oceanographic variables as mean values per band. The Generalized Linear Model (GLM) were selected by the Akaike Information Criterion. The results for the Rapoport's rule showed a non-significant relationship ($p = 0.973$). The best GLM model identified that three oceanographic variables accounted for 88,5% of latitudinal range variation: minimum dissolved oxygen, maximum iron concentration and minimum chlorophyll concentration at minimum bottom depth.The selected factors indicate ecological constraints on geographical ranges, since larger body sizes ($r_{pearson} = 0,87$) have higher metabolic rates and energy demands. Furthermore, the restricted species range between 10°N and 32.5°N is a historical effect related to the high endemism within these bands (34.7% of the species are endemic to this area), with 13.74% endemic to the Gulf of Mexico and the Caribbean Sea.

275. Exploring 5 Million Years of Climate-Induced Fragmentation

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Climate plays a pivotal role in shaping species distribution and evolutionary trajectories. It dictates the suitability of environments based on physiological requirements, influences resource availability, and molds selective pressures. Importantly, climate changes over time, altering species distributions and driving community turnovers. Dr. Elisabeth Vrba's Resource-Use hypothesis postulates that extreme climatic regions, such as rainforests, deserts, steppes, and tundras, serve as refuge and cradle for endemic species due to historical fragmentation during the Plio-Pleistocene. Our goal is to quantitatively assess the fragmentation patterns within the primary climatic zones, including tropical, arid, temperate, cold, and polar regions, over a span of five million years. We achieve this by leveraging the PALEO-PGEM model, aiming to elucidate whether extreme climatic regions experienced greater, lesser, or equivalent levels of fragmentation compared to other global regions during the Plio-Pleistocene

276. Comparative analysis of palaeoclimate models' estimations of treelines and alpine biomes in mountains worldwide

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Palaeoclimate models play an essential role in understanding past environmental changes, yet their accuracy in high-gradient terrains, such as mountains, remains unclear. Alpine biomes, located just above the climatic treeline along the highest elevations of mountains, are known to be high biodiversity reservoirs. Quaternary climate fluctuations caused significant shifts in their elevational distributions and likely contributed to their unique species composition. To understand how climatic variation shaped present-day biodiversity, reconstructing the past biome distributions is of paramount importance. Considering the uncertainties of palaeoclimate models in mountainous terrains, how reliable are our reconstructions of alpine biomes? We evaluated and compared the efficacy of various palaeoclimate models in simulating late Quaternary climate dynamics within mountains. We reconstruct treelines for three moments in time: the present, the Last Glacial Maximum (LGM) and an intermediate stage. We use a fixed temperature delimitation for the treeline and repeat this process for mountain ranges across varying longitudes and latitudes. We compare reconstructed treelines from PALEO-PGEM, CHELSA and WorldClim on a global scale both within and between mountain ranges. Our findings highlight variations among these models, influencing the estimated distribution of past alpine biomes. Due to these variations, the implications of model choice for biogeographical analysis are profound. A deeper understanding of palaeoclimate model outputs and dynamics in mountains is therefore essential for refining biogeographical models and predictions.

277. Climate and human land use as drivers of disequilibrium in post-glacial European tree distribution dynamics

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Global environmental change has and continues to alter biodiversity and ecosystem functioning at unprecedented rates. Paleoecological evidence as well as recently observed trends reveal strong climatic forcing of species spatial and temporal distribution. Furthermore, increasing human land use has drastically changed spatio-temporal tree species distribution since the last glacial maximum. However, responses to such environmental changes will be most likely temporally lagged (disequilibrial) which challenges the analyses and prediction of driver-response dynamics in space and time. Such temporally lagged response dynamics are hypothesized to become especially relevant when environmental conditions become more variable and unpredictable. Understanding disequilibrium conditions in response dynamics of key ecosystem actors such as trees to past changes in climatic conditions and human land use can therefore help to better understand current and future changes in European forest composition in the face of accelerating climate and land use change. In this study we developed a new method to quantify temporal disequilibrium dynamics in the continental-scale spatial distribution of ecologically and economically important European and North American tree species as response to macroclimatic fluctuations and land use change during the last 20,000 years. Preliminary results show that the degree of climatic disequilibrium considerably varied through prehistory. Results furthermore show that climate vs. direct human forcing of distributional disequilibrium significantly changed through prehistory with increasing effects of human land use change in the more recent past. However, different tree genera showed differences in their temporal responsiveness to climatic vs. human land use changes linked to the species dispersal abilities.

278. Holocene climate and the first farmers of Europe

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Over the span of 3 millennia (~9000–6000 years before present), Neolithic agriculture spread from south-west Asia to northern Europe and the British Isles. This new way of subsistence was founded on a set of select crops and livestock species, each having its own ecological character. Neolithic farmers certainly had to adapt their economic strategy to the climates and environments they encountered, and it is well known that proportions of crops and animal remains in archaeological assemblages differ between times and regions. However, quantitative analyses face challenges. Until now, continental-scale biogeographical studies targeting the role of environment for Neolithic subsistence practices have been hampered by the lack of both harmonized archaeological and paleoclimatological datasets. Recently, output of different transient paleoclimate simulations has become available. We present our results from evaluating them against proxy-based reconstructions in mid-Holocene Europe. The evaluation helps assess how feasible such data products are for driving spatio-temporal models in paleo- and archaeoecology. In addition, we present first insights from ecological niche modeling based on a new, Europe-wide database of archaeological occurrence records for Neolithic crops and livestock. Our statistical approach places particular emphasis on quantifying known uncertainties and elucidating the ways early farmers were or were not able to develop sustainable subsistence practices in a bio-social context.

279. Virtual Taphonomy: Simulating taphonomy and its influence on ecological niche reconstruction

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Forecasting distributions of organisms under novel environments is critical for the conservation and management of species in the face of historically unprecedented environmental changes. However, contemporary distributions have been heavily impacted throughout the Anthropocene and may no longer reflect their full range of abiotic limits or biotic associations. Fossil records offer an invaluable resource for understanding an organism's ecological niche prior to widespread human impacts, which can shed light on their responses to environmental changes in the past. However, the fossil record is subject to considerable preservation biases resulting from taphonomy and non-random search effort, which are often uncorrected in models of ecological niches or species distributions. Here we present reconstructions of simulated, but ecologically realistic, small mammal distributions over the late Quaternary (ca. last 22,000 years). We quantify the impact that preservation biases can have on ecological niche reconstructions, and therefore distribution models. Our results show that not all aspects of ecological niche inference are affected equally but that some of these biases can be accounted for using bias layers derived from the fossil record itself.

280. Do mammals track climate better than plants?

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Climate tracking is a central concept which lies at the heart of many models and disciplines. It supports the use of species distribution and niches models (SDM/ENM), especially in the context of assessing conservations priorities and policies in the light of ongoing climate change. Nevertheless, estimating the robustness of this concept is a complex task given that modern data offer limited temporal hindsight. In this context, paleontological data can be used to circumvent this issue. Using paleoclimate simulations and occurrences of mammals and plants in North America since the last deglaciation, we estimate species' ability to follow their climatic niches (or climatic fidelity) over the last 12,000 years. Based on this dataset, we (i) compare the climatic fidelity of plants and mammals, (ii) estimate the impact of European arrival and industrialization on plants and mammals climatic niches, (iii) evaluate which species and functional groups are prone to track climate and which are the more affected by human impact and finally we (iv) perform spatial analysis to identify which and how different habitats have impacted climate fidelity. Using a wide range of metrics to compute niche overlaps through time, we show that plants depict slightly better ability (10 to 20 % more overlap from T0 to T1) to track climate than mammals. In addition, we found how the arrival of Europeans in North America and industrialization profoundly altered mammalian climatic niches, to a greater extent than the climatic changes induced by the last deglaciation.

281. Unveiling Cryptic Species of Aquatic Macroinvertebrates through DNA Barcoding in Narupa Reserve, Napo, Ecuador

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Within the Ecuadorian jungle of Narupa Reserve lies an intriguing biological puzzle: aquatic macroinvertebrates. Striving to fathom their elusive diversity, we bridge tradition and technology. DNA sequencing with MinION Nanopore unveils the concealed identities of cryptic species. Each

DNA sequence serves as a clue in the enigma of life, every discovery drawing us closer to the jungle's profound secrets. In this verdant realm, the richness of Ecuador's biodiversity unfolds in delicate patterns. As our instruments decode the genetic signatures hidden within these aquatic creatures, we uncover stories that time has woven into their very genes. With each cryptic species unmasked, a page of the jungle's narrative is unveiled—a narrative that speaks of adaptation, coexistence, and the intricate dance of life. This study is a voyage of reverence, an exploration that pays homage to Ecuador's remarkable biodiversity. The forest canopy echoes with whispers of generations past, as we piece together the puzzle of ancient lineages and uncover connections that transcend epochs. Our journey is one of both scientific inquiry and heartfelt appreciation for the splendor that thrives within Narupa's lush heart.

As the MinION Nanopore reads the intricate code of life, we stand on the threshold of a deeper understanding. This understanding is not only a scientific triumph but a testament to the wonders concealed by crypticism. With every genome decoded, we inch closer to deciphering the jungle's tapestry of existence—a tapestry that, once deciphered, illuminates the intricate threads that sustain life in this hidden haven.

282. All about being old and shooting hairs: Clade age and Urticating hair explain the patterns of diversification in tarantulas

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Many groups of animals are exceptionally diverse in a specific geographic area, irrespective of their centre of origin. Localised ecological processes, dispersals, key innovations and climatic or environmental factors can generate this pattern. Mygalomorph spider family Theraphosidae, commonly known as tarantulas, are found in every continent (except Antarctica). However, this group is disproportionately diverse in South America. Around 70% of the extant species richness is from this continent. Whereas Africa, Indian subcontinent, Southeast Asia and Australia have much less diversity. We assembled a global time-calibrated phylogeny of tarantulas and tested several macroevolutionary hypotheses to explain the species richness distribution of tarantulas. First, we tested the clade age hypothesis to check if Neotropical clades are older than others and whether this pattern can be explained simply by the time-for-speciation effect. Then, we employed both trait-dependent and independent diversification tools to check if Neotropical clades have higher diversification rates and what are the factors influencing these rates. We tested the effect of microhabitat choice (ground-dwelling or arboreal), antipredator defence strategy (presence or absence of urticating hair) and geography (South America versus non-American) in influencing diversification rates. The results suggest that clade age significantly explains the distribution of species richness across lineages. However, the evolution of urticating hair has probably broken this pattern in Neotropical clades, inflating the diversification rates. This finding supports the "escape-and-radiate" hypothesis. Overall, a combined effect of clade age and novel antipredator strategy have shaped South America's exceptionally higher diversity of tarantulas.

283. Scaling laws reveal a unified energy theory for mountain biodiversity patterns

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Numerous studies have suggested that elevational richness patterns might reflect the availability of energy, but support for the role of energetic constraints is far from universal. Here, we developed a scaling law model that demonstrates how scale selection influences the predictive power of energy availability; it holds across taxonomic groups, trophic guilds, and ecosystems across mountains globally. Based on the energy requirement of each taxon, we first derived a mathematical equation that describes the actual scale on which energy availability determines their elevational richness patterns. Then yield a quantitative prediction that the strength of the elevational richness pattern-energy relationship varies with the match in actual and observational scales. A global-scale compilation strongly supported these predictions (R2 ranging from 0.63 to 0.98); furthermore, we compared the performance of energy availability measured at several scales for predicting the elevational richness patterns of trees, herbs, and litter fauna on Dongling Mountain China. The results showed that energy availability exhibited the best performance on the actual scale for all three taxa. Our model unravels the importance of scale selection in exploring the mechanism that produces elevational richness patterns, thus providing a unified understanding of montane biodiversity distributions across the domain of life.

284. Historical land use determines arbuscular mycorrhizal diversity in agricultural landscapes

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Soil microbes are essential to maintain terrestrial ecosystem functionality. However, their diversity and functionality are threatened by land use change due to agricultural expansion and intensification. One important microbial group mediating the exchange of nutrients between plants and soil in agricultural systems are arbuscular mycorrhizal (AM) fungi. While the effects of land use change have been well-studied in macro-organisms, the spatial and temporal scale effect is known to differ in ecologically distinct species groups. Here, we evaluate the potential role of land use change in the form of habitat loss in explaining arbuscular mycorrhizal fungi species richness at multiple spatial and temporal scales. We conducted a spatially intensive sampling of three agricultural fields in Estonia. The fields and their surrounding landscape have been recorded on maps since the turn of the 19th to 20th century, depicting the management succession from forested and seminatural areas to arable fields. We sampled these fields in a 100-meter grid comprising 100 soil samples. Soil AM fungal diversity was determined by DNA metabarcoding, supplemented by soil physical and chemical properties measurements. We analysed the relationship between species richness and natural habitat areas availability at different spatial scales (500 m, 100 m, 200 m buffer areas) and time periods (past 1894-1922, 1969-1989, and current 2022). Our results indicate that current AM fungi species richness is better explained by landscape data at a 100 m buffer scale and by historical landscape data from the late 19th century, indicating a legacy effect of past natural habitats. While management and modern anthropogenic pressures can be useful in assessing regional and macroecological species distributions, historical legacies could be persistent and affect these assessments locally.

285. Revisiting the spatial phylogenetics of North American seed plants

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A previous study (Mishler et al. 2020) conducted a preliminary assessment of phylogenetic diversity (PD) and endemism (PE) patterns of seed plants using point occurrence data of both native and nonnative taxa in North America. This current study extends that published preliminary study by: (a) using only native plant taxa in North America, (b) comparing phylodiversity patterns produced by point occurrence data with newly modeled ranges, and (c) investigating patterns of phylogenetic turnover. Additionally, we evaluated the effect of environmental conditions on the phylodiversity patterns and turnover. We used over eight million occurrence points representing over 17,000 native plant taxa only in North America. This comprises the native flora subset of the Mishler et al. 2020 spatial data (>8 million points), and additional records obtained for the United States and Eastern Canada. The spatial data was integrated with a corresponding phylogenetic tree (n = 17,526 tips) subset from the published phylogeny in Mishler et al 2020 to identify areas with significant concentrations of high and low PD, PE, phylogenetic turnover, relative PD RPD, as well as neo-, paleo-, and mixed endemism, employing PE and RPE in categorical analysis of neo and paleo-endemism (CANAPE). These spatial phylogenetic analyses were conducted at 50 km grid cells. The relationships of the areas with significant phylodiversity, as well as patterns of turnover were investigated with respect to predictor variables such as elevation, temperature, and precipitation.

286. Novel ecological and environmental data enhance our comprehension of tree species composition changes across Amazonia

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Trees are perhaps the most characteristic organisms forming the tropical rainforest biome (TRF). To date, more than 10.000 tree species were acknowledged for the Amazon. Notwithstanding, much of our knowledge on biogeographical patterns for the region is based on the distribution of vertebrate species. Furthermore, historical factors have been favored for the interpretation of biogeographic patterns within Amazonia over the equally likely role of ecological factors on those patterns. Here we present an evaluation for biogeographic pattern recovered from up-to-date knowledge on the distribution of trees and environmental gradients across the region. We compiled occurrence records for 8,765 tree species in Amazonia from GBIF and SpeciesLink. The occurrence records were aggregated in 0.1 degree grid-cells, and those grid-cells with more than 100 species were used to estimate compositional dissimilarities. We applied a generalized dissimilarity model to predict the compositional dissimilarities from their relationship with six environmental gradients across the Amazon. Soil fertility and Maximum Climatological Water Deficit were the two environmental gradients affecting most the estimated ecological distances between locations. Tree composition differs from the forests on relatively fertile soils close to the Andes to the dryer forests eastern the Negro river and in southern Amazonia. Recent advances on ecological and environmental understanding of Amazonia are already aiding to produce a refined view of biogeographic patterns depicted by plants in the most diverse TRF worldwide. Such detailed knowledge is pressing for planning upcoming biodiversity inventories, inform conservation actions, and design sustainable forest management.

287. Bat communities of savanna biome: a case study in Kruger NP.

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Savanna biome represents an essential component of global biodiversity, it occupies a fifth of the earth's land surface and hosts among other rich bat communities. Yet, whether these communities represent mere ad hoc assemblages of incidentally co-occurring forms or distinct entities strongly adapted to specificities of savanna biome is still not clear. The results of two-year acoustic monitoring of bat communities under a highly standardised design of multidisciplinary project MOSAIK (Monitoring Savanna Biodiversity in Kruger NP by repeated controls at 60 fixed points) enabled us to analyze bat communities (in total 130,888 individual bat records, 31 acoustic parataxa) in regards to seasonal and geographic variation of community structure at point, local and regional scales and effects of a large set of contextual predictors Besides variation in community characteristics among individual points and efects of some proximal factors (rivers, distances to campsites, microgeographic cohesivity etc.) explaining them the results revealed: (i) unexpected homogeneity in community structure at local and regional scales, with (ii) common between-season differences (inverse contributions of molossid and vespertilionid bats), (iii) common habitat preferences in all taxa approaching the centroid of regional habitat variation, and (iv) greatly pronounced patterns of phenetic packing and community nestedness. In these regards, the savanna bat communities of Kruger NP represent a highly consistent entity integrated with network of co-existence relations supposedly arisen during course of long savanna history. Indirectly, it strongly support an enormous conservation value of savanna biome.

288. Dark diversity reveals human impacts on biodiversity in natural vegetation worldwide

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Accelerating anthropogenic biodiversity loss threatens ecosystem functioning and its benefits to humans. Besides species disappearances from directly affected sites, biodiversity in natural areas is also threatened by increased human influence in the surrounding regions. Still, global empirical evidence has been so far lacking, probably due to a high natural variation of biodiversity. Here we show that the level of anthropogenic activities in the surrounding region is consistently negatively related to local plant diversity in natural vegetation worldwide. However, this negative effect was only evident when we estimated dark diversity – species present in the region but currently absent in a site despite being ecologically suitable. We present the results of a collaborative network DarkDivNet for global-scale standardized quantification of alpha and dark diversity of vascular plants by sampling 5211 local natural vegetation sites distributed among 117 regions. To account for natural biodiversity variation, we combined each site's alpha and dark diversity to estimate the site-specific species pool size (alpha + dark diversity) and the completeness of local communities (proportion of alpha diversity from the species pool). We found a strong negative relationship between community completeness and human influence, with anthropogenic impacts being particularly evident when averaged from regions extending several hundred kilometres around the local sites. Our results underscore the hidden risk of biodiversity loss in ecosystems that may appear directly unaffected but are influenced by human activities in the surrounding regions. Our work also highlights the potential of dark diversity to reveal the status and trend of ecosystems.

289. Correlates of zoogeographical boundaries among terrestrial vertebrates in Atlantic Forest hotspot

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Scientists have long pondered how biological change over time has interacted with climate and geology to generate variations in biota at multiple spatial scales. Here, I quantified the relative importance of climatic heterogeneity, orographic barriers, past climate change, and river barriers in explaining the zoogeographical regions defined for terrestrial vertebrates in the Atlantic Forest hotspot. To achieve this, I overlaid distribution maps onto a grid of 50 x 50 km cells covering the Atlantic Forest area, creating a presence and absence matrix of 917 bird species, 455 anuran species, 220 snake species, 202 mammal species, and 103 lizard species. Subsequently, I utilized a network approach, employing the Infomap Bioregions web application to delineate biogeographic regions. I used spatially explicit regression models to select and quantify the factors explaining the position of biogeographical boundaries among terrestrial vertebrates. The analysis revealed four ecoregions for birds and snakes, and five for anurans, lizards, and mammals. Our analyses confirmed that climatic heterogeneity, orographic barriers, and river barriers have collectively shaped the biogeographical boundaries of vertebrates in the Atlantic Forest. Climatic heterogeneity was the primary variable correlated with zoogeographical boundaries, indicating the role of eco-physiological constraints in delimiting species' range distribution. Dispersal limitations underscored the significance of mountain chains and river barriers. Thus, the congruence and limits in the spatial distribution of zoogeographical regions suggest that the Atlantic Forest biota retains a biogeographic structure, and distinct features of vertebrate classes influence the small variability in the number of regions and the positions of boundaries.

290. Global patterns and drivers of taxonomic, phylogenetic and functional diversity in specialist river birds

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Riverine ecosystems are complex, providing a variety of linear habitats aross terrestrial aquatic continuums. This complexity is reflected in specialist riverine bird communities, with many species using both terrestrial and aquatic resources to fulfil their life-history requirements. The aims of this work were to understand the taxonomic, phylogenetic and functional diversity of birds specialised to a riverine lifestyle globally and to study how well terrain complexity, river geomorphology, land-cover and climatic data can explain distribution patterns of specialist river bird species. We compiled information from distribution maps, global trait datasets and avian phylogenies for over 60 species specialised to live along streams and rivers. Mountains and uplands being the source of many rivers showed prominent roles in shaping avian specialization to riparian habitats. Taxonomic diversity peaked between latitudes of 20-40 North, in mountains with an exceptional peak in the Indo-Malayan mountains. Species-rich assemblages showed signs of species packing leading to adaptive radiation. Niche partitioning in specialist riverine birds is significantly driven by foraging strategies facilitated by morphological segregation across gradients of elevation, river width and openness of the riverine habitat. Mismatches in taxonomic, phylogenetic and functional diversity highlight the role of different processes in filtering species from different lineages towards an adaptation to a riverine lifestyle.

291. Heterogeneous dispersal networks to improve biodiversity analyses: relevance and methods

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Determining the relative influence of multiple ecological processes underlying biodiversity patterns is essential for a deeper mechanistic understanding of biodiversity dynamics. Biodiversity patterns result from the interplay between large-scale processes that regulate dispersal dynamics across local communities and small-scale processes, such as environmental selection and biotic interactions, within these communities. This interplay influences dispersal networks underpinning complex biodiversity patterns. Often overlooked, spatial heterogeneity is a pervasive characteristic of dispersal networks. This heterogeneity emerges from the interactions between variation in dispersal capacities among species and irregularities in patch configurations within landscapes. Through spatial simulation models, we demonstrate that neglecting this heterogeneity can lead to mismatches between biodiversity analyses conclusions and the true underlying ecological processes at play. We also identify the ecological contexts in which this discrepancy is most likely to happen. To address this limitation, we provide ecologists and biogeographers with practical solutions. We introduce novel analytics to evaluate the role of dispersal network heterogeneity in shaping empirical biodiversity patterns using network-informed species accumulation curves. We demonstrate that our method: (i) is robust in identifying dispersal network heterogeneity, (ii) indicates whether dispersal is limited or, conversely, acts to homogenize communities, and (iii) improves our understanding of biodiversity spatial patterns. Our goal is to raise awareness of spatial heterogeneity in dispersal networks, thereby inspiring new empirical analyses and advanced analytics. We thus also contend that accounting for dispersal network heterogeneity in biodiversity analyses is essential for advancing ecological theories and conservation biology.

292. Global and regional interaction between threats to bird species: Wind farms and other human activities

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Renewable energy developments are critical in fighting climate change but also have the potential to negatively affect biodiversity through land use changes, habitat disruptions, and species´ direct mortality. Moreover, the potential negative impacts on biodiversity from expanding renewable energy infrastructures will interact with other human pressures that are threatening wildlife species, such as land-use change due to agriculture and afforestation, unsustainable hunting, invasive species, and pollution. Thus, recognizing and explicitly accounting for the co-occurrence of threats and how they could interact is essential and can help us better understand their dynamics and impacts on ecosystems. This study aims to assess the interactions between wind farms and other human-induced threats that are affecting bird species at global and regional scales. Through a co-occurrence analysis between the locations of wind farms (ongoing and future developments separately) and threat maps of the likelihood of impact of agriculture, hunting and trapping, logging, pollution, and invasive species, developed using the data IUCN Red List, we will identify hotspots areas of threats and evaluate how these interactions might change over time. Understating the

interaction between threats could foster a more accurate view of the extinction risks species are facing.

293. How species, functional and phylogenetic diversity accumulate in vertebrates across regions, clades and scales

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How diversity accumulates over time within a clade or region remains a fundamental question in biology. Conflicting hypotheses exist, suggesting that diversity accumulates at constant, slowing, or accelerating rates, or even that diversity stays largely equilibrial over time. Additionally, while species diversity dynamics have received considerable attention, the dynamics of functional and phylogenetic diversity have been less explored. The interplay of ecological, evolutionary, and historical mechanisms underlying the dynamics of diversity have yet to be elucidated, too. To address these gaps, we combine phylogenies, geographic data, and species traits of tetrapod vertebrates (~30,000 species). Employing diversification analyses, null models and GIS, we analyse diversity dynamics across clades of different ages and sizes, as well as across ecoregions, biomes, and continents. We determine how species, functional, and phylogenetic diversity accumulate over time, elucidate the mechanisms behind these dynamics, and compare the results across clades, regions, and scales. Consequently, our findings contribute to reconciling conflicting hypotheses regarding biodiversity dynamics across multiple dimensions (species, functional, phylogenetic). Knowledge of these dynamics seems key to safeguard biodiversity and anticipate its responses to the ongoing environmental changes.

294. A Global database of habitat specific abundances for birds

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The distribution of the birds of the world are generally well-known. We have, however, less knowledge on how individuals of the global populations are dispersed across different habitats within their range. By a better understanding of the internal dispersion of individuals across different habitats within a species range we can identify the relative importance of various habitats for a species. This is a crucial piece of information for identifying the drivers of abundance of birds as well as the impact of land use changes on birds. Here we create a tool to estimate the relative importance of various habitats for terrestrial, non-migratory birds across the world. Based on openly available, scientific grade data on abundance, estimates of global population sizes, climate, human footprint, and land cover we produce a transparent environmental niche model and associate abundance with habitats to identify the relative importance of the various habitats found within any given bird’s distribution range. Our primary goal for the product, a database containing density estimates for the species in each habitat, is to provide a readily applicable tool to use for a more precise assessment of future impacts of land transformations which is essential for managing biodiversity. The resulting database will also be useful for scientific analyses of patterns and drivers of bird abundances.

295. Diversification patterns and their underlying mechanisms across phylogenetic scales

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Evolution of species diversity has fascinated biologists ever since Darwin and Wallace. Yet, how species accumulate within phylogenies over time remains largely unresolved and four conflicting macroevolutionary patterns have been reported: constant-rate accelerating slowing and equilibrial diversification. While each of these four diversification patterns has been widely observed across various phylogenies, their synthesis remains elusive. To attempt such synthesis, we study diversification patterns systematically across clades of different ages and sizes, using tetrapod vertebrates (~30,000 species) as the model system. Specifically, we combine diversification methods (Bayesian, likelihood) and tree geometry (Laplacean spectrum, phylometrics) to determine the diversification patterns and their changes with clade age and size. We then use simulations of the birth-death process to identify whether the most common diversification patterns resemble the patterns that emerge under diversification heterogeneity, mass extinctions, statistical artifacts or survival biases. Consequently, our results elucidate how the diversification patterns vary across the phylogeny, so as to reconcile the currently conflicting findings, and how different patterns might result for biological but also non-biological reasons.

296. **Missing links: predicting unknown associations of host plants with fungal endophytes and pathogens**

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Fungi growing on living plant tissue (both pathogens and endophytes) may induce physiological responses mediating growth, development, and reproduction of the host plant. Fungal pathogen outbreaks in plants can result in extirpated natural populations and crop loss. Some fungal endophytes can improve plant host tolerance to environmental stress, enhance defense against biotic antagonists, and may be employed in agriculture to increase crop yield. By characterizing the taxonomic range of plant hosts that are susceptible to infection by different endophytic and pathogenic fungi, we can better understand which plants could benefit from fungal symbiosis and predict associations that might lead to pathogen emergence. We isolated host plant species associations from hundreds of thousands of fungal observation records reported in various biological occurrence databases. We then used phylogenetic information on host plants to predict missing associations and identify the geographical regions and plant host clades with high numbers of missing links. Such predictions provide information on the distribution of potential, but as yet unobserved, plant pathogens and mutualists—and may help to quantify risk of novel fungal infection in host plants in newly introduced or expanded geographic ranges through changes in climate, global transport, and agricultural practices.

297. **Distribution and effects of trash-basket epiphytes and tank-bromeliads on canopy biodiversity and ecosystem functions**

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Epiphytes able to impound litter and water provide additional structure to habitats and communities inhabiting the forest canopy. Tank-bromeliads (TB) and trash-basket epiphytes (TBE) are well-known examples of epiphytes able to create new habitats in the canopy providing shelter to animals and rooting sites for plants. Here, we compare the occurrence of TB and TBE in literature and across biomes, and their effects on biodiversity and ecosystem functions. We performed a systematic review of the taxonomic and geographic distribution of TB and TBE, their effects on ecosystem functions, and reports of microorganisms, plants, and animals inhabiting them. We analysed the taxonomic and geographic biases in studies, and the influence of environmental factors on the distribution of TB, TBE, and their inhabitants. We identified 385 publications between 1905 and 2021, describing 121 TB and 213 TBE despite the firsts being several hundred. Both occur in tropical and southern temperate forests, with TB restricted to the Neotropics and TBE occurring also in Paleotropical regions. TBs are inhabited by 140 animal species, 12 plants, and 42 microorganisms. TBE support 110 animals, 25 plants, and 50 other organisms. TB and TBE are compelling model organisms that can be used to study ecological processes such as facilitation cascades, niche construction, extended phenotypes, or the effects of secondary FS on biodiversity and ecosystem functioning.

298. The use of mineral sources by the African forest elephant.

Claire M. Herlihy, Czech University of Life Sciences

African forest elephants (*Loxodonta cyclotis*) are an umbrella species for both the African rain forest and conservation in central Africa. They frequent "bais", natural clearings, rich in minerals in the forest of the Congo basin where they actively search for mineral deposits and reveal necessary nutrients required for their, and other species' diets. The presence of elephants in bais is therefore essential for biodiversity and the resilience of other critically endangered species.   From Feb. 24, 2022 to Feb. 18, 2023 using 24 camera traps in strategic positions across the Dibo bai (2.148852N, 14.629689E) within in Odzala-Kokoua National Park we collected over 60,000 images. We observed the behaviour and examined micro-habitat preferences of forest elephants and were able to identify individual elephants and compile a catalogue, currently containing 41 repeatably identifiable elephants. Camelot camera-trapping software was used to analyse the images, assessing: sex; age; and number of elephants present. This poster will present the catalogue alongside the abundance data. Using camera traps allows remote monitoring and we hope to expand the program to neighbouring bais within the TRIDOM forest region to establish long term monitoring of elephants and their movements between bais. Bais represent an important habitat for this critically endangered species and therefore require prioritisation in conservation and anti-poaching efforts. Using data produced by this project, more effective protection measures can be enacted.

299. A signature from the sky: using remote sensing to assess the effects of rewilding on the ecology of vegetation

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Over the last few decades, rewilding initiatives have been established around the world as an attempt to reverse the global trend of declining biodiversity and to promote ecological resilience. Rewilding is an increasingly popular approach for restoration and conservation, focusing on the restoration of natural interactions and ecosystem functions. One of the most widely reported goals of rewilding is to increase the diversity of habitats and vegetation, with the reintroduction of large herbivores as one of the main tools. In this view, herbivores act as promoters of habitat patchiness (both in terms of biodiversity and of nutrient distribution) through their interaction with the landscape. Despite the rising popularity of rewilding, however, a clear understanding of its effects, and how to measure them quantitatively, is still lacking, including the effect of large herbivores on vegetation phenology and diversity. To address this gap, our research uses satellite imagery and artificial intelligence to analyze thousands of aerial pictures from rewilding areas in the Palearctic region. We use Normalized Difference Vegetation Index (NDVI) to investigate changes in vegetation phenology and investigate leaf spectral diversity as a proxy for plant diversity. We compare and contrast these metrics across time (before vs. after the start of the rewilding) and space (inside vs. outside the rewilding area over the years), considering herbivore functional diversity and the time since herbivore's reintroduction as variables. With this approach, we will be able to assess and quantify the effects of rewilding on two fundamental aspects of ecosystem functioning,.

300. GetDiv - Global experiment on trail diversity: a call for participation

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The popularity of nature tourism is increasing the visitation to the nature trails. The visitor numbers are affected by various factors that the trail´s infrastructure or natural environment offers to the visitors. Although the tendency of people’s interest in nature is rather positive, it can also have harmful effects on biodiversity and vegetation as the extent and frequency of disturbances grow. By bringing visitors to fragile and protected areas, as well as constructing and maintaining trails, there is an impact on the surrounding environment according to changes in biodiversity, endangered species and species composition due to alien species and other disturbances. Therefore, it's relevant to know which factors are influencing visitor numbers in order to manage the trails more effectively and sustainably. There have been plenty of studies about tourism impacts on natural areas, however, most of the methodologies are incomparable. Here we present the rationale for the methodological approach, and call for a coordinated global effort - GetDiv - for collecting comparable and comprehensive data of diverse aspects of nature trails on local, regional and global scale. We carried out a pilot study in Estonia on 32 nature trails and present these preliminary results.

301. Analyzing changes in structural diversity of the agricultural landscape of Saxony using historic and modern remote sensing data

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The agricultural landscape of Central Europe underwent big changes over the last decades, especially between the 1960s and 1980s. Through measures like land consolidation, the structure of rural areas has changed significantly which affected not only farming activity but also lead to the destruction of species habitats and wildlife corridors. In order to quantify this impact on biodiversity, we analyzed historic CORONA spy imagery from the years 1965 and 1975 and modern digital orthophotos from 2021 in the German state of Saxony. Specifically, we focused on changes in field edge lengths and landscape heterogeneity. By comparing several texture and diversity metrics, we found a sharp decline of field edge lengths in all of Saxony between 1965 and 1975 which has only slightly recovered until the present day. The findings of the analysis are considerably affected by the differences in data quality.

302. **Environmental drivers of local bats species richness in Czech Republic: the role of hibernacula caves**

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Explaining the phenomenon of high biodiversity is one of the most significant challenges in the natural sciences, especially when it concerns long-living, highly mobile and cryptic taxa. Few studies investigate the influence of climatic variables on bat richness. Recent studies show that the size and complexity of a hibernaculum mainly explain the richness of bat. Our aims were analyze which variables better explain (i) bat species richness; (ii) total bat abundance and (iii) the abundance of each bat species**.** We use unpublished data from a long-term monitoring program of counting bats on hibernation sites in the Czech Republic. To test for the possible effects of four aspects (environmental, climatic, entrance position and inner roost parameters) on bats richness and abundances, we run Generalized Linear Models. In the richness model, temperature seasonality presented the highest contribution for the model, followed by the height of entrance and length of hibernaculum. For total abundance model, hibernaculum usage showed the highest contribution and the minimum temperature of the coldest month was selected as a climate predictor. Our models to predict bat richness and total abundance reveal that the hibernation site characteristics have similar or even higher importance than climate variables. Hibernation sites with the highest species richness are located at a region with a low temperature seasonality, they have a long length and their entrance has high profile. Our results showed that internal structure of hibernacula has fundamental importance in structuring bat assemblages in winter hibernation sites and in the distribution of some species.

303. **Species abundance distributions and complex relationship between diversity and extinction rates in North American birds**

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A crucial issue in ecology is to understand biodiversity variation across space and time. The large-scale diversity patterns are tightly related to variation in temperature and water availability, or in general energy availability. However, a mechanistic understanding of these diversity-environment relationships remains elusive. Species richness on a site is given by interplay between colonization and (local) extinction. Several prominent ecological theories like the Neutral Theory of Biodiversity or the recently proposed Equilibrium Theory of Biodiversity Dynamics predict that extinction rates are diversity-dependent, as (assuming constant total number of individuals) with more species present, population sizes should be lower. Here, we explore the patterns of local extinction rates using probably the most extensive community time-series data, the North American Breeding Bird Survey. We test the prediction, that extinction rates are higher in regions that are more species-rich relative to their total abundance and to their resource availability. We also try to disentangle causality in the relationships between extinction rates and species richness. We show that the sites with the lowest mean population sizes are not necessarily the ones with the highest extinction rates, because the sites differ in their species abundance distributions. We thus explore the complex relationships

between extinction rate, species richness and total abundance in relation to the species abundance distribution.

304. **Effects of conservation measures on plant diversity in grasslands in Southern Germany**

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Grasslands play an important role for biodiversity and are amongst the species richest habitats in Europe. However, biodiversity in European grasslands is declining in the last decades, as management intensifies and grassland area shrinks. Monitoring and maintaining biodiversity is crucial. A prominent tool of conservation in managed grasslands are contract-based-conservation programs, where farmers receive financial compensation to follow certain rules regarding management intensity.

We investigate the effect of conservation programs in grasslands in southern Germany on plant diversity and composition. We analyse the species diversity and composition of the study region and investigate the effects of conservation measures on plant diversity and composition. Additionally we evaluate remote sensing tools to estimate biodiversity within our study area.

We find, that species richness and composition drastically change between protected and non-protected grasslands, however, differences between conservation categories were marginal. The main differences are found in species compostion rather than in species richness. The employed remote sensing tools were able to differentiate between the different management regimes, however the application for biodiversity mapping was not straightforward and only partially successful.

305. **Modelling the future distribution and biodiversity of European fen habitats under global change**

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Along with the historical decline of fens due to anthropogenic impact, climate change is expected to jeopardise fen biodiversity by reducing their geographic extent and altering species composition. Yet, climate change impacts on fen distribution and biodiversity in the future remain unclear. We used 27,555 vegetation plots representing eight fen habitat types widely distributed in Europe to compute Ecosystem Distributional Models. For each fen habitat type, we projected their future potential occupancy area and range shift and evaluated the influence of different climate scenarios and groundwater pH on distribution and biodiversity. Our findings could be helpful for the nature protection authorities across Europe to assess conservational and restoration measures to mitigate potential future biodiversity loss in European fen habitats.

306. **Underlying linkage rules of pollination networks reveal their fragility**

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Understanding how species extinctions affect communities of interacting species is an important challenge of ecology. The presence of unfeasible interactions, termed forbidden links, due to physiological or morphological barriers, is likely to decrease the plasticity of interaction networks, affecting their robustness to extinctions. However, the existence of these forbidden links has been debating for a long time, stressing the need to shed the light on their prevalence and putative consequences for community robustness to extinctions. To tackle this gap, we used a dataset of plant-hummingbird interactions collected in Brazil, Costa Rica and Ecuador, along elevation gradients. First, we used a hierarchical Bayesian model to assess the importance of trait complementarity and exploitation barrier, evidencing exploitation barrier between flowers and hummingbirds with shorter bill than the corolla. Second, we show that average corolla length decreases with elevation while average bill length remains constant, leading to a decrease in the proportion of forbidden links over elevation. Third, using simulations and path analyses, we show that the proportion of forbidden links strongly decrease network robustness to plant extinctions, independently to network structure. This suggests that exploitation barriers are not rare and that they strongly limit interaction rewiring and thus the rescue of species experimenting partner extinction. Altogether our results provide insight on how linkage rules and species characteristics shape community robustness to extinctions.

307. Integrating the Equilibrium Theory of Biodiversity with the Metabolic Theory of Ecology to predict the effects of temperature and body mass on biodiversity

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The Equilibrium Theory of Biodiversity (ETBD) predicts how species richness and community abundance should change along gradients of speciation, extinction, and resource availability, and the role of the biodiversity-ecosystem function relationship in mediating these changes. The metabolic theory of ecology predicts how temperature and body mass should affect rates of speciation, growth, metabolism, and productivity. Here we integrate ETBD with the metabolic theory of ecology to make baseline quantitative predictions on the effects of temperature and body mass on large-scale species richness and community abundance. This theory shows how the biodiversity-ecosystem function relationship mediates the relationship between richness and temperature, with increased niche complementarity and facilitation leading to steeper temperature-diversity relationships. It also predicts that the temperature diversity relationship should be steeper in communities with large body sizes. Preliminary tests of the theory using biome-scale biodiversity data support the predictions, pointing to the role of metabolic ecology, niches, and diversity equilibria in shaping large-scale patterns of biodiversity and abundance.

308. Restoring degraded ecosystems to improve and enhance biodiversity and ecological connectivity in the Central European Green Belt

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The Central European Green Belt (CEGB) represents a European wide, unique network of ecologically important habitats and protected areas that often host high biodiversity. However, like other valuable landscapes, it is under increasing land use pressure, fragmentation and climate change, which lead to a decline in biodiversity and habitat degradation. To tackle these issues, a transnational cooperation is essential. This is reflected in the presented international project “ReCo”, which aims to restore ecosystems to enhance their connectivity and support biodiversity of CEGB. To do so, innovative measures in the form of geoinformation and data processing systems as well as community-based development approaches will be used. In particular, restoration hotspots along the CEGB will be identified by applying ecosystem services approach, using satellite and other available data. A historical analysis of the pilot region will also be carried out and will help to identify areas with a high potential of success for sustainable restoration. Community-based approach will be based on including information from multiple stakeholders’ workshops into developing restoration plans. These measures will be tested in six pilot regions in Poland, Germany, Czech Republic, Austria, Slovenia and Italy, which cover different types of habitats (from dry grasslands to alpine meadows, from inland wetlands to coastal wetlands) and species and their respective habitats (from wild cat to European bison). The outputs will include transnational restoration strategy on disturbed or degraded ecosystems, regional restoration and connectivity plans and practical guidelines with examples from the pilot regions.

309. Global Insights on Mountain Regions as Hotspots of Fungal Diversity

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Mountain ranges have long been recognized as biodiversity hotspots for many macroorganisms, yet the factors driving this phenomenon and the roles of mountains in either originating or preserving biodiversity (‘cradles’ or ‘museums’) remain unclear. For fungi, the role of high- and lowlands is even more enigmatic: While previous studies have assessed the role of highland indirectly via climate effects, they have not focused on montane diversity of fungi per se. Here, we use the GlobalFungi database (globalfungi.com) to assess fungal species richness in mountain ranges globally and compare them to lowlands. We assess local diversity describing the species abundance within samples taken in mountains and lowlands, and use different methods to predict this diversity globally, such as best-subset Generalized Linear Models (GLM) and Random Forest modelling. We extend our analysis to regional diversity, describing the Operational Taxonomic Unit (OTU) richness within mountain ranges or lowlands in each biogeographical realm, because montane diversity seems to greatly differ between realms. To illuminate the role of mountain ranges in the conservation of fungal diversity, we compare how the area of lowlands and highlands influence how much diversity is concentrated in the mountains as opposed to in the lowlands. To investigate whether the observed richness stems from climate or mountain effects, we compare regression models that incorporate both climate and topography. We present the first comprehensive study of fungal diversity in mountain ranges and its potential implications.

310. Conserving evolutionary processes of endemic amphibians in the megadiverse Atlantic Forest

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Recognizing biogeographical units is the initial step for different approaches in biogeography, revealing evolutionary processes as vicariance. Novel approaches seeking priority areas have allowed new perspectives for biological conservation, especially when it comes to imperilled areas and groups of organisms. We aimed herein to analyse the conservation of evolutionary processes of an endangered biodiversity hotspot by: (i) detecting clusters of endemic frog species; (ii) testing predictions of the vicariant model as a driver of biogeographical patterns; (iii) evaluating the conservation of patterns and processes based on protected areas and habitat loss; and (iv) highlighting priority areas for conservation of evolutionary processes. Biogeographical units were identified via Biotic Elements analysis, using range polygons for 381 endemic frogs from the South American Atlantic Forest. We tested two predictions of the vicariant model: (i) the occurrence of non-random co-occurrence patterns, forming clusters of co-occurring species (Biotic Elements, BEs); and (ii) the occurrence of closely related species (same genus) in distinct BEs. We calculated the percentage of forest remnants in each BE and their overlap with protected areas. We highlighted as priority areas for conservation those with high degrees of irreplaceability and/or vulnerability. We recovered 21 Biotic Elements. Vicariance must have played an important role in the distribution patterns of our model organisms. On average, BEs presented 28% of forest remnants, but only 12% of their total areas were protected. Mountain ranges of central Atlantic Forest harbour most of evolutionary processes, and therefore must be considered as priority areas for conservation of anuran amphibians.

311. Parasitic plants in Europe. Are they associated with high community diversity?

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Parasitic plants are recognized as a specialized plant functional group. Due to their special physiology and interactions with other plants, they may impact community structure and ecosystem functioning. Several local-scale studies have suggested that some parasitic plants may even increase community diversity. Here, we aim to contribute a large-scale perspective to this topic by addressing the question of whether hemiparasitic plants are associated with high plant community diversity across the European continent and different habitats. To do so, we explored an extensive vegetation-plot database available in the European Vegetation Archive.

We conducted a geographically explicit analysis to identify diversity associations of all plant species in the vegetation-plot database. To reduce the effect of community species pools, we compared the species richness of plots where individual species occur to those in close vicinity from which they are absent. Consequently, we compared these diversity-association values between parasitic plants and other species. Overall, we identified a significant, yet relatively weak trend of the whole functional group to occur in more species-rich vegetation than other species. Around 75% of parasitic plants showed a more positive association with diversity than the median of all species. More than 25% of parasitic plants were among the top 10% of species associated with diversity. Notably, the majority of parasitic plant species were mostly absent from species-poor vegetation.

312. Number of species of Coccinellidae in individual European countries and Iranian provinces – correlates and needs for more surveys

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We analysed the number of species of the beetle family Coccinellidae recorded so far in 40 individual European countries, including three Mediterranean islands. We plotted the numbers against predictors and found that latitude was the main factor (number of species decreasing to the north), followed by country area, whereas mean temperature, human population number and density, longitude and GDP per capita were not significantly correlated to the number of species. Within Iran, the area of provinces was a weak predictor of the number of species, while the human population was much more correlated. In both cases, we found that the sampling effort, represented e.g. by the presence of several specialists in the family, although not quantified, represents an important factor in increasing the number of species in the province/country checklist.

313. Global diversity patterns of vascular plants – occurrence point data versus checklists

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Understanding patterns of biodiversity and their drivers requires high-quality distributional data. One commonly used type of data is geo-referenced point occurrence records. However, such data are known to suffer from uneven sampling at spatial and species levels. Using georeferenced occurrences for all vascular plants from the Global Biodiversity Information Facility (GBIF) and two checklist databases, the Global Inventory of Floras and Traits (GIFT) and the World Checklist of Vascular Plants (WCVP), we compare patterns of vascular plant richness at the global scale. We show that occurrence data greatly underestimate richness in some parts of the world, particularly in arid parts of Africa, the Middle East and South Africa. At the same time, richness derived from GBIF shows a significant number of non-native species, inflating the richness of many regions. We argue that a combination of data types should be the standard for documenting macro-ecological patterns of biodiversity, as well as controlling for the biogeographic status of species.

314. Understanding Carbon Storage Dynamics in Ayeyarwady Delta's Mangrove Ecosystem in Myanmar: Insights for Restoration Efforts

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Mangroves are highly valued for their ecosystem services, providing a wide range of ecological, social, and economic benefits, including their role as carbon-rich ecosystems. Recent research suggests that preserving mangrove forests can offer a cost-effective strategy for mitigating CO_2 emissions. However, extensive deforestation has placed mangrove ecosystems under severe global threats. Currently, the assessment of mangrove restoration outcomes, particularly regarding soil carbon stocks, is inadequate. Therefore, this study aims to investigate the impact of restoration on soil organic carbon (SOC) in the Shwe Thaung Yan coastal region of Myanmar. The study aimed to

quantify and compare carbon stocks in different soil layers, examine the carbon sequestration potential of various mangrove species, and evaluate the effectiveness of mangrove restoration efforts. Method: Soil samples were collected in 2015 (pre-restoration) and 2021 (post-restoration) at various soil depths, and analyzed for SOC concentration, organic matter content, and bulk density. Soil properties were assessed using the Loss on Ignition (LOI) procedure. Significant differences in soil properties were observed between the pre-restoration period in 2015 and post-restoration in 2021, with higher SOC and carbon concentrations observed in 2021. The average soil carbon stocks in 2021 (1954.43 ± 33.24 Mg C ha^{-1}) were approximately 2.7 times higher than the estimated carbon stocks in 2015 (732.26 ± 6.99 Mg C ha^{-1}). Furthermore, the study revealed variations in SOC accumulation among different soil depths, with higher carbon stocks found in the upper soil layers. This study highlights the positive impact of mangrove restoration on SOC accumulation.

315. Decomposing abundance change to recruitment and loss: analysis of the North-American avifauna

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Species richness is the most commonly used metric to assess biodiversity crisis, but fluctuations in species number start with fluctuations in the number of individuals (*i.e.* abundance). Population abundances are known to be globally plummeting with, e.g., three billion fewer birds in the US compared to the 70's. However, assessing population decline doesn't give insight on the dynamic of the ecological processes driving abundance change, namely losses and recruitments of individuals. Here, we address this gap by decomposing the abundance change into processes of loss and recruitment using the North American Breeding Birds Survey dataset together with the hierarchical Dail-Madsen model accounting for imperfect detection. Using data on 564 bird species over 35 years (1987-2021) in 1033 local time series across North America, we also assess the change in growth rate and decompose it into processes of recruitment rate and loss rate. Doing so, we show which mechanisms are responsible for the decline of the avifauna all across North-America. We also show that the decline of growth rate is mainly due to an increase of individual loss rate at the North-American scale, and we show the spatial heterogeneity of those processes by mapping them. Disentangling the processes responsible for population change (*i.e.* loss and recruitment of individuals, and their respective rates) is critical to provide insights into the ecological mechanisms driving those changes. By providing maps of those processes all across North-America, we hope that efficient conservation measures can be taken by targeting either the recruitment or loss and thus, try to bend the curve of population decline.

316. Deep biogeographic barriers explain divergent global vertebrate communities

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Regional and historical processes can lead to differences in biodiversity across biogeographic regions. However, the influence of biogeography on global biodiversity patterns remains unclear. Although attempts to understand biogeographic effects on biodiversity generally treat regions as discrete units, differences in biogeographic distances among species assemblages are actually continuous. Here, we partition variance in the species richness, functional richness, phylogenetic diversity, and mean functional beta diversity turnover of mammal and bird assemblages across the

world into biogeographic and environmental components using phylobetadiversity, a metric that allows us to calculate continuous biogeographic distances among assemblages. We found that, on average, environment (climate, elevation, topography, and landmass area) explained global diversity patterns much better than phylobetadiversity, especially for birds. However, mammals in deeply isolated regions such as Australia were strongly influenced by biogeographic history, with lower taxonomic and functional richness than predicted by environment alone. Mammal assemblages in biogeographically isolated regions contained unique combinations of functional traits as well. Differences in Neotropical vs. Paleotropical bat functional richness also reflect the influence of biogeographic isolation. These examples show how deep, long-lasting biogeographic barriers can lead to divergent diversity patterns, against the backdrop of environmental determinism in diversity across most of the world.

317. Testing the latitudinal gradient in plant range size and environmental breadth

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The latitudinal gradient in plant diversity is one of the most famous patterns in ecology. It is hypothesised that narrow niche breadths and restricted geographic ranges in the tropics allow more species to coexist relative to high-latitude regions. Using global occurrence data and an environmental niche modelling approach, we test these hypotheses by quantifying the relationships among latitudinal range, environmental breath, and latitudinal median for over 100,000 plant species. We find limited evidence for a global latitudinal gradient in species' ranges and environmental breadths, with results varying across hemispheres and between tropical and non-tropical zones. We show support for these hypotheses only for trees in the northern hemisphere, but an inverse relationship in the southern hemisphere. Collectively, our results demonstrate that the latitudinal gradient in plant diversity is not explained by variation in species' ranges or environmental breadths, suggesting additional biotic, evolutionary, and geographic processes underpin this global pattern.

318. Conservation planning in Switzerland is central to preserve natural resources in Europe

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To meet the COP15 biodiversity framework in the European Union (EU), one target is to protect 30% of its land by 2030 through a resilient transnational conservation network. Switzerland is a key hub of this network due to its central location in the Alps, hosting high elevation ecosystems with enigmatic fauna and flora. Despite this importance, previous European research have highlighted either a severe lack of strict protected areas in the country, or the absence of comprehensive information on how biodiversity, nature contributions to people (NCPs) and adapted conservation planning are

distributed. Our research is part of the SPEED2ZERO project, a consortium and Swiss federal project aiming to halve greenhouse gas emissions by 2030 in Switzerland. We here present an overview of how the conservation network of the country may be improved according to expected changes in biodiversity and NCPs in the face of global changes. Although results reasonably vary across taxa group (e.g., vegetation, birds, and insects, >7’000 species), our conservation simulations predicted a larger protection focus on higher elevations and latitudes by 2050, yet with different notions and priorities for aquatic versus terrestrial systems. We explain this trend through biodiversity shifts induced by climate change, and more specifically spatial shifts in NCPs threatening the future availability and access to natural resources in the country. Overall, we highlight that Switzerland, although occupying a modest geographical extent, is expected to keep a central role within Europe to assist species migration and preserve mutual ecosystem services.

319. Factors and mechanisms driving functional variations in urban bird assemblages between developed and developing countries

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Urbanization is transforming biological communities worldwide, yet the specific processes driving community assembly across urban landscapes with varying socioeconomic development remain poorly understood. To address this gap, we (1) investigated the relative influence of two primary community assembly processes, niche differentiation and environmental filtering, on trait composition in urban bird assemblages, (2) tested whether the dominant assembly process varies between cities in developing and developed countries, and (3) identified which city characteristics drive this variation. Using species occurrence data from citizen scientists, expert species range maps, and information on foraging and breeding traits for 4,549 bird species, we measured the deviation of observed functional diversity from the expected value for each of bird assemblages across 106 cities worldwide. We then built regression models to examine the associations between the deviation and the biophysical and socioeconomic characteristics of the cities. Our findings revealed that bird assemblages in developed cities generally have higher-than-expected functional richness, suggesting that the assemblages were shaped by strong niche differentiation and/or weak environmental filtering. In contrast, strong environmental filtering and/or weak niche differentiation shaped bird assemblages in developing cities, resulting in lower-than-expected functional richness. This discrepancy was mainly due to high land cover diversity and high greenness (NDVI) in the developed cities. This study elucidates the predominant mechanisms shaping urban bird assemblages, highlighting their dependence on city characteristics tied to socioeconomic development. These findings offer valuable insights for sustainable urban planning efforts.

320. Rhizome or rootstock: variation in definitions of plant clonal growth organs, with implications for macroecology

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Understanding patterns of coexistence amongst plant ecological strategies or plant functional types

and how they vary between species assemblages experiencing different environmental conditions is a key aspect of macroecology. Published Floras, as compendia containing determination keys and species descriptions for a particular region, are increasingly used as sources of plant trait values to answer such macroecological questions. The strength of using published Floras in this way comes from the comprehensiveness with which they document the morphology all of the known plant species from a geographic region. However, the coverage and quality of trait data varies between sources but also between traits in question. While traits used for taxonomic determination have consistent standards of description across published Floras, other traits are described with less consistency. Such a group of traits include the morphology of belowground organs responsible for plant perennation, resprouting after injury and clonal growth. We use our own field surveys of perennial herbs from 12 regions in the northern hemisphere to consider how species assemblages differ in the proportions of species with different perennation organs and also how published Floras differ in the way they describe organs that support plant perennation. We found inconsistencies in terminology and missing information. We call for caution when using description of plant traits concerning perennating and clonal growth organs from Floras and advocate for standardisation of terms to allow large scale comparison.

321. Rodents show darker and redder coloration in warm and rainy environments

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Biogeographers have long been fascinated by how animals' colors vary across climate gradients. Gloger's rule, a well-known concept in this field, suggests that animals in warmer and wetter regions tend to have darker colors. However, this rule historically overlooked the distinction between two primary melanin pigments: eumelanin (responsible for darkness) and pheomelanin (associated with redness). In this study, we explored how these melanin types vary geographically, shedding light on the intricate interplay of ecological factors influencing pigmentation in South American Sigmodontine rodents. We collected pelage color data from 231 rodent species and quantified geographic variations in both eumelanin (lightness) and pheomelanin (redness). Using linear multiple regression and variance partitioning, we evaluated the influence of temperature, precipitation, predator diversity, and UVA/UVB radiance on these melanin types. Our findings support the traditional version of Gloger's rule, confirming that rodents in warmer and rainier regions typically exhibit darker-colored pelage. Additionally, we observed redder pelage in warmer environments. Surprisingly, rainier regions exhibited more intensely red rodents, challenging our expectations. This study pioneers novel research into Gloger's rule within a continental mammalian group, providing compelling evidence that pelage color closely corresponds to temperature and rainfall gradients. While our results supported predictions regarding eumelanin, the relationship between pheomelanin pigmentation and ecological factors proved more complex. These findings underscore the intricate nature of coloration patterns in response to climate, suggesting that selective pressures act distinctly on dark and reddish pigmentation in rodents.

322. Locally evolutionarily distinct species in frugivore networks have fewer links and more specialized partners

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Ecological networks describe the complex set of interconnections among species and their environment, and network structure can inform the stability, resilience, and functioning of ecosystems. Increasing attention is being paid to the mechanisms that determine species interactions. Phylogeny has informed our understanding of connections within networks, mostly by describing the strength of phylogenetic conservation of interactions. Here, we examine how the phylogenetic placement of a species relates to its functional position within a network. Using a large dataset of bipartite frugivore networks and a measure of local evolutionary distinctiveness (ED), a phylogenetic metric that describes how much unique evolutionary history a species represents within a community, we show that species with high local ED tend to have fewer interactions and that their interacting partners tend to be more specialized. Our analysis illustrates how evolutionary relationships affect present day ecologies and underscores the unique ecological contribution of evolutionary outliers.

323. Secondary sympatry and syntopy in birds: methods, patterns, and processes

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The evolution of range overlap (sympatry) that follows allopatric speciation allows for the build-up of regional diversity. However, species co-existing at regional scales might not co-occur in local syntopy. At the same time, syntopy is needed for the build-up of local, alpha diversity. We studied predictors of syntopy in songbirds worldwide using citizen-science occurrence data. First, we developed a new method to quantify syntopy that controls for range sympatry. Without this control, estimates of syntopy were heavily negatively biased. Second, we studied geographic predictors of syntopy in songbirds of the world using complete checklists from the eBird citizen-science program. Syntopy was higher in species pairs with high range sympatry and symmetry (ranges of similar size), and it was also slightly higher in northern temperate latitudes than elsewhere. Third, we studied ecological predictors of secondary syntopy in songbirds. We did this using the ABC citizen-science program of Australia, where we used 116 species pairs of honeyeaters, thornbills, fairywrens and allies (Meliphagoidea). Here, syntopy was related to ecological divergence in species pairs: it increased with divergence in foraging stratum, but it decreased with divergence in food consumed. Overall, we show that the evolution of secondary syntopy in birds is related to spatial configuration of ranges (range sympatry and symmetry), latitude (faster in the northern temperate regions), and species ecology (facilitated by the divergence in foraging stratum). Our next step will be to study a broader set of predictors of secondary syntopy (morphological, climatic, ecological) in songbirds worldwide.

324. Revealing macroecological dynamics to understand biodiversity shifts in the Anthropocene

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The ongoing biodiversity crisis presents a complex challenge for ecological sciences. Beyond the consensus about decline in biodiversity, apparent discrepancies in reported diversity trends are reported. In this presentation, I will present how integrating macroecology theory with temporal and trait-based perspectives can provide fundamental insights on ongoing biodiversity changes. First, considering temporal changes in macroecological patterns such as species area relationships and distance decay of similarity can reconcile and synthesize conflicting outcomes in biodiversity observations. Second, macroecology theory allows to link change in macroecological patterns to more fundamental biodiversity components (total number of individuals, species abundance distribution, spatial aggregation). Third, coupling these patterns with species traits can enhance our understanding of how human activities impact biological diversity over time. I will finally present how this comprehensive approach can be used to attribute human-driven changes to biodiversity shifts via changes in fundamental biodiversity components.

This framework can facilitate a deeper comprehension of the fundamental levers driving diversity changes across scales, leading to more informed conservation and mitigation strategies.

325. The Seed Dispersal Database for the European flora

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The dispersal ability of plants is a pivotal factor influencing the spatial dynamics of species, yet it remains a trait for which comprehensive data is largely lacking across most species. Measuring dispersal ability is indeed extremely tedious and challenging. Therefore, we compiled an extensive database of seed dispersal-distance classes and primary dispersal modes for the majority of European vascular plant species. In our database, we classified species into seven dispersal-distance classes based on a classification scheme, which included criteria considering diaspore or propagule morphology, life form, predominant dispersal mode, seed release height, seed mass, and habitat preferences. Each class thus contains species with comparable dispersal ability, serving as a semi-quantitative trait. We validated our assignments to dispersal-distance classes by relating them to estimated dispersal distances derived from an alternative approach. This seed dispersal database contains information about dispersal-distance classes and the most effective dispersal modes for nearly 10,000 of the most prevalent and locally dominant European vascular plant species. It is openly accessible through the FloraVeg.EU online database and can be used in functional biogeography, dynamic vegetation modeling, and ecological studies that consider plant dispersal from local to continental scales.

326. Fuzzy competitive exclusion explains parapatric distributions and highlights areas of concern for native species due to biological invasions

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The application of the fuzzy concepts of favorability (the degree to which environmental conditions are propitious for the occurrence of individual species) and favorableness (the degree to which environmental conditions are simultaneously favorable for competing species) operationalize a fuzzy version of the competitive exclusion principle that may be applied at biogeographic scales. Favorability was obtained by performing species distribution models applying favorability functions, while favorableness was derived from the application of the fuzzy intersection between the favorability for competing species. Potentially competing species would coexist in high-favorableness locations, as the demands of all species would be well fulfilled. In locations of low favorableness, the result would be either autecological exclusion of species or autecological segregation, as abiotic conditions are unfavorable for at least one of the species. Competitive exclusion would occur at the intermediate stretch of the favorableness gradient, as the conditions would be good enough for persistence of each species separately but not enough for permanent coexistence. After plotting individual favorability values along the gradient of favorableness for potentially competing species of turtles, deer, hares and vipers, the pairs of species and the specific geographical areas affected by competitive exclusion were identified. Among native species (hares and vipers) this resulted in parapatric distributions. In the case of native and introduced species (turtles and deer) this may be used to identify the particular areas where the native species are threatened of exclusion by the introduced species. This is important both theoretically and for biodiversity conservation planning.

327. Climatic stability predicts the congruence between species abundance and genetic diversity

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Unified models of biological diversity across organizational levels (genes, species, communities) can provide key insight into fundamental ecological processes. Theory predicts that the strength of the correlation between species abundance and genetic diversity in island communities should be related to community age. Historical climatic events are expected to impact assembly processes, hence affecting both the Species Abundance Distribution (SAD) and the Species Genetic Distribution (SGD) in a community. However, the signature of such historical processes in continental communities may be weak given that communities are unlikely to be fully isolated. We here test whether higher correlation between species abundance and genetic diversity (i.e. higher congruence between SAD and SGD ranks) would be observed in localities where climate has been more stable over time in a continental setting.

We assessed this hypothesis using abundance and genetic diversity data for 20 communities of Iberian leaf beetles. Our results show that the congruence between SAD and SGD ranks is only explained by climatic stability, but not by current climatic conditions.

Our results thus bring three important implications. First, the degree of congruence between SADs and SGDs could be used as a proxy of community stability, related not only to historical climatic variation but also to any other disrupting factors, including human pressure. Second, in climatically stable localities, species abundance could be used as a proxy of genetic diversity. Third, when genetic diversity data were available, deviations from SAD/SGD congruence in any particular species could be used to infer recent colonizations of these species.

328. Priority areas based on the spatial structure of evolutionary uniqueness at a global scale

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Evolutionary distinctness of biological communities is a less known but still key attribute of biodiversity at a global scale. From a conservation standpoint, a beta diversity framework of evolutionary uniqueness ensures the identification of priority areas based on its degree of differentiation from other communities while also incorporating long-term evolutionary processes. Community evolutionary uniqueness is scale dependent, so we here introduce a method for its spatial scaling and apply it to identify priority areas for terrestrial vertebrates (amphibians, reptiles, birds, and mammals). Our results allow estimating the proportion of global phylogenetic diversity that will be protected by preserving the biological communities in any given proportion of the land (cells of 10000 km^2). Our results show that the patterns of spatial scaling of community evolutionary uniqueness change among biological groups and geographical regions. Taking altogether, uniqueness and complementarity to select the priority areas for conservation resulted in a low degree of cross-taxon congruence and revealed that the high uniqueness of these priority cells can be derived either by long-term spatial gradients of continuous community differentiation, or long-term isolation at small spatial distances (i.e. two contrasting scenarios both leading to higher values of community evolutionary uniqueness). Worryingly, priority cells broadly overlap with ecoregions with insufficient protection and thus imperilled.

329. Spatial and temporal patterns of shrew diversification

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Unraveling patterns of diversification across different mammalian taxa is vital for understanding the recent composition of biodiversity. Shrews (Soricidae), a clade of small insectivorous mammals with approximately 460 species, have played a crucial role in shaping ecosystem dynamics. Shrews comprise two well-supported, morphologically and genetically distinct subfamilies – the cold-adapted Soricinae and the warm-adapted Crocidurinae. The unique adaptations in two shrew subfamilies offer a rare opportunity to test various hypotheses about the speciation and origin of species. Our research presents a comprehensive phylogenetic tree of shrew species, including the most up-to-date taxonomic information, calibrated using fossil data, and employs advanced biogeographical and phylogenetic analyses to examine shifts in diversification rates across different epochs and geographic regions. This analysis reveals compelling patterns of shrew diversification, providing a valuable perspective on their historical evolution and its implications for recent mammalian communities. Notable shifts in diversification rates underscore the influence of geological events,

climatic fluctuations, and ecological interactions on shrew evolution.

330. The role of niche conservatism and niche divergence in driving in situ speciation in the Alps

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Diversification patterns in species can be strongly influenced by niche conservatism (when species maintain their ancestral ecology over time) or niche divergence (when species change their ecology). In the Alps, the extent to which these processes play a role across multiple taxa, encompassing both terrestrial and freshwater realms, remains uncertain. To address this issue, we reconstructed the environmental niche of 123 species of butterflies, 24 amphipods, 119 fishes, 26 amphibians, and 76 flowering plants. Then, we assessed the degree of niche overlap among species within each group and examined whether closely related species exhibit more similar environmental niches than unrelated ones. Our analysis revealed that in situ speciated fishes exhibited the highest degree of niche divergence. We attribute this result to adaptive radiation playing a more significant role in generating biodiversity in lacustrine fish compared to other taxa. In the case of amphipods and terrestrial groups, a stronger influence of niche conservatism can be explained by the persistence of these species during glaciations. Therefore, much of the in situ speciation in amphipods and terrestrial organisms might have resulted from population fragmentation in refugia, leading to allopatric speciation but under similar environmental conditions. This phenomenon was unlikely to have occurred in fishes, as open water was completely erased during the last glaciation.These findings reveal that the influence of niche conservatism and divergence on speciation in the Alps varies among taxa, likely due to the differential impact of the last glaciation on each taxon's environment.

331. Cocos: effects of climatic extremes on ecosystem stability

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The frequency of extreme climatic events (ECE) is rapidly rising, as is their negative impact on natural systems and on our societies. ECE disrupt the stability of ecosystem functions, with unpredictable consequences for the provision of ecosystem services important for human welfare. Determining the capacity of ecosystems to resist (i.e., maintain their properties) and to recover (i.e., return to their functioning) after ECE is a pressing task. Equally important is to identify biodiversity-mediated mechanisms underpinning ecosystem response to ECE. Here, we present COCOS, a new project funded by the European Union, which will investigate both research aspects. Within COCOS, we will use extensive datasets on vegetation functions (e.g., plant biomass and cover) and on climatic parameters to assess the relationship between ecosystem stability, biodiversity and ECE at the global scale. From LOTVS, a worldwide collection of long-term vegetation time-series collected in permanent plots, we will obtain measures of resistance and recovery for different ecosystem types, and of plant community taxonomic and functional diversity. Using ERA5-Land climatic variables, we will compute indices of precipitation and temperature-related ECE, which we will then use to identify years in LOTVS time-series featuring anomalous climatic conditions. Focusing on those years, we will analyse the association between stability, biodiversity and ECE of varying intensity, which will allow generating predictions of ecosystem-specific resistance and recovery. Research questions and the state of the art of COCOS will be presented, along with preliminary results on the analysis of the stability-ECE relationship.

332. **Spatial patterns in farmland bird population trends across Europe**

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European farmland hosts rich biodiversity, but it is threatened by deep land use changes occurring since the second half of the 20th century. Birds represent an important farmland biodiversity component and their populations declined considerably. To combat these declines, we need to uncover the most important drivers that may differ across regions. In this respect, food availability and nest predation are the most promising candidates as they directly influence bird breeding productivity, and thus population abundance. Here we tested relationships between long-term population trends and two traits reflecting these drivers, insectivory and nest site. We found that population trends of insectivores show a clear gradient from precipitous declines in north-western Europe to stable populations in the East, whereas the trends of ground-nesters did not show any spatial patterns and their declines were uniform across space. These patterns indicate lowering insect food availability along the gradient, likely due to increasing agricultural intensity, while the impact of predation probably remained constant in different regions. Next, we specifically focused on central and eastern European countries considered as farmland bird population strongholds, and tested whether their accession to the EU's Common Agricultural Policy (CAP) resulted in changes in population trends. Taking part in CAP means marked increase in funding for agriculture which may accelerate intensification (by direct payments), but may also improve conservation management (by agri-environmental schemes). Farmland bird population trends indicate that the former option applies as they switched to decline after EU accession. The decline was steeper in countries with stronger intensification.

333. **The influence of niche partitioning and evolutionary dynamics on reef fish diversity**

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Species richness is unevenly distributed across spatial scales, yet the factors responsible for this variation are still hotly debated, especially in marine systems where comparatively less work has been done. Reef fishes are widely distributed, coupled with remarkable taxonomic, functional, and phylogenetic diversity. Currently, explanations for reef fish richness emphasize environmental drivers while often neglecting ecological factors, such as niche partitioning. We explore whether niche partitioning and environmental drivers combined can better explain reef fish species richness and diversification dynamics in three different marine realms using distributional, functional, and phylogenetic data for reef fish species. To assess niche partitioning, we calculated the hypervolume of each reef fish species based on a defined set of functional traits. Using the latest phylogenetic information for the group, we quantified the diversification dynamics in relation to reef fish diversity, considering distinct modes: acceleration, slowdowns, and saturation. We found considerable niche partitioning among reef fish species in highly diverse reef regions, such as the Indo-Australian Archipelago and the Caribbean, but less in low diversity reefs, such as those in Brazil and isolated oceanic islands in the Atlantic Ocean. Diversification dynamics varied across marine realms reflecting different biogeographic histories of the realms. Taken together, our results suggest that both niche partitioning and realm specific diversification dynamics shaped global patterns of reef fish richness.

334. Using the Global Inventory of Floras and Traits (GIFT) for plant biogeography and macroecology

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Answering the most pressing questions in the biogeography and macroecology of plants requires knowledge of species distributions and plant functional characteristics. Much of this information has accumulated over centuries of botanical exploration and is contained in regional Floras and checklists, which offer curated information on the species composition, species' biogeographic status and functional traits. Here, we outline how the Global Inventory of Floras and Traits (GIFT; https://gift.uni-goettingen.de), a repository of information from regional Floras and checklists, can be used for macroecological and biogeographic research. GIFT integrates plant distributions, functional traits, phylogenetic information, and region-level geographic, environmental, and socio-economic data. Version 3.0 of GIFT holds species lists for 3,400 regions with full global coverage, including ~367,854 taxonomically standardized plant species names and ~4 million species-by-region occurrences. GIFT also includes species-level information for 109 functional traits and ~2.97 million trait-by-species combinations. Data from GIFT is openly available via the GIFT R-package (https://CRAN.R-project.org/package=GIFT). As exemplified by several studies, GIFT allows for assessing the taxonomic, functional, and phylogenetic composition of regional floras from regional to global scale. Recently, GIFT has been used to produce global predictions of taxonomic and phylogenetic diversity of vascular plants, to describe diversity patterns across life and growth forms, and to assess drivers of phylogenetic endemism in seed plants worldwide. As such, GIFT opens up new avenues for investigating regional patterns of global plant diversity and testing hypotheses related to past and present geographic and environmental drivers and anthropogenic influence.

335. The global distribution of ferns with chlorophyllous spores

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About 14% of all fern species have short-lived chlorophyllous spores. These spores have long been considered to have limited long-distance dispersal capacity and to be highly susceptible to harsh climatic conditions, raising questions about the evolutionary and ecological advantages of this trait. Here, we examine the global distribution of chlorophyllous-spored species and their underlying environmental drivers. We studied the global distribution of 10,995 fern taxa across 556 geographical regions and assessed the association of the richness proportion of chlorophyllous-spored ferns with environmental variables using generalized linear mixed models. To assess the

influence of phylogenetic relationships of the species sharing this trait on their distribution, we used the phylogenetic mean pairwise distance and the mean nearest taxon distance. Species richness of chlorophyllous-spored ferns peaked in the tropics while their proportion was highest in temperate zones. The richness proportion was positively influenced by variables representing water availability, but negatively by variables representing temperature. Although spore type was strongly conserved phylogenetically, we found weak negative correlations between phylogenetic relatedness and species richness proportions. We found that, generally, assemblages were phylogenetically clustered in higher latitudes and overdispersed in tropical zones. Contrary to previous assumptions, our study provides strong evidence that chlorophyllous spores do not limit the distribution of ferns. Indeed, chlorophyllous-spored ferns prevail in higher latitudes where overall fern species richness is lower. Moreover, they are overrepresented on islands, and their global distribution might be explained by the tropical niche conservatism hypothesis.

336. Floral traits predict hummingbird visitation rates better than conspecific and heterospecific flower abundance

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Multiple factors interact to determine if, how often, and by whom a flower is visited. Here we use a macroecological perspective to search for emerging patterns in how flower abundance, floral traits, and functional dissimilarity influence hummingbird visitation frequency across three highly biodiverse regions. We sampled 32 sites monthly for 2 years along elevation gradients in Ecuador, Costa Rica, and Brazil and collected interaction data using time-lapse cameras, counted floral abundance and measured flower traits of all species along a 1.5 km transect. We used generalized linear mixed models to relate visitation frequency corrected for sampling effort to conspecific and heterospecific abundances, a series of floral traits, flower functional dissimilarity and flowering length (n = 6,280 flowers). Our results reveal that floral traits have a stronger influence on hummingbird foraging preferences than flower abundance. Consistent with expectations from pollination syndromes, hummingbirds preferred visiting flowers with elongated, straight, tubular corollas, and the relative importance of each trait varied among countries. We found only week evidence of both, positive and negative effects of abundance, suggesting that the importance of competition and facilitation is context-dependent. Abundance interacted with functional dissimilarity, being more important when the focal flower is more dissimilar to the others coflowering species in the community. In conclusion, while flower abundance may provide a general indication of resource availability, floral traits play a more crucial role in determining hummingbird foraging preferences.

337. Diversity Unveiled: Exploring Evolutionary Diversification Patterns in Clonal and Non-Clonal Plants

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About a half of plant species are clonal. Clonality in plants is likely to have a substantial impact on diversification, as clonality affects effective population size, meiosis frequency, and genet lifetime, all of which can affect diversification. Yet, the possible role of clonal lineages in shaping the diversity of species within ecosystems has often been overlooked. In this study, our objective is to determine the evolutionary dynamics of clonal lineages across a comprehensive phylogenetic scope. We took data on clonality traits from several existing databases, specifically TRY and CLO-PLA and linked it with existing phylogenetic information on these species, such as the Smith & Brown (2018) Angiosperm phylogeny. This dataset enables us to investigate whether diversification patterns differs in clades with prevailing clonality from the clades composed mainly of non-clonal species. We will employ distinct approaches that operate on varying phylogenetic scales, involve different assumptions, and have distinct data quality criteria. To assess diversification rates, we employ hypothesis-free tip rate estimations through various methods like BAMM, ClaDS, or DR metrics. These tip diversification rates are statistically analyzed by regression against the clonal status of plants, employing phylogenetic linear models. This study holds the potential to show whether clonality contribute significantly to the variability observed in diversification metrics. Such analysis, reveals how much phylogenetic patterns are related to clonality, thus providing insights into the distribution of clonality throughout plant lineages.

338. Beyond climate control: soil pH and phylogenetic composition mediate drought-deciduousness in the species-rich Latin American tree flora

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Deciduousness is a common drought-avoidance strategy amongst tropical trees, especially in Latin American flora. However, how climatic and soil conditions influence the leaf phenology (deciduous versus evergreen) remains unquantified. Here, by integrating leaf phenology, climatic (Vapor Pressure Deficit – VPD), and soil (soil pH) data for 5,227 plots of tree assemblages, we use generalized linear models to investigate the extent to which these variables affect the prevalence of deciduousness across Latin America and whether their effects differ among the main Latin American ecosystems. After classifying plots into rainforests, savannas, and seasonally dry forests, we used a multigroup structural equation model (SEM) approach for each of the three ecosystems to determine the direct and indirect effects (i.e., mediated by the phylogenetic composition of tree assemblage plots) of VPD and soil pH on deciduousness. We found that the deciduousness was greater in alkaline soils and under high VPD across Latin America. The direct effects of soil pH and VPD on deciduousness were most significant in seasonally dry forests. Savannas exhibited the lowest direct effect of soil pH on deciduousness. Also, only in savannaa, the direct effect of VPD on deciduousness was stronger than the direct effect of soil pH. Indirect effect (i.e. mediated by phylogenetic composition) of soil pH on deciduousness was most pronounced in rainforests. Our findings highlight that the effects of VPD, soil pH, and phylogenetic composition can synergistically influence the proportion of deciduousness throughout Latin America and in the different ecosystems.

339. Patterns of spatial and temporal autocorrelation of species richness and distributions across scales

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Understanding the dynamics of spatial and temporal biodiversity change has become crucial in the Anthropocene. These dynamics depend on the spatial and temporal grain of study, explaining why we sometimes observe local increases in richness despite an overall global loss through extinction. Species' diversity and distributions are also spatially and temporally correlated, with points located closer in space and time tending to exhibit similar values, emphasising the grain-dependent nature of this autocorrelation. Analysing this autocorrelation can help us fill knowledge gaps in species diversity and distributions and help us identify how species are changing over time. Previous studies analysing autocorrelation have mostly focused on its spatial component, overlooking the influence of time and its interaction with space. Here, we examine the spatial and temporal autocorrelation patterns of birds in the Northern Hemisphere across multiple spatial scales and time periods, using distribution data from Breeding Bird Atlases with more than one replication. We computed both global and local spatial autocorrelation of richness at different grain sizes, comparing these patterns across time periods. We found a decrease in spatial autocorrelation as grain size increases, a trend that was consistent across time periods. We then calculated the spatial autocorrelation for each species' distribution and compared them across time periods. This allowed us to determine whether distributions are becoming more aggregated or disjoint over time, helping identify species that might become susceptible to extinction due to increased isolation and separation of their populations.

340. The dynamics of the diversity-energy relationship during the last 21,000 years differs for woody and herbaceous species

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Spatial diversity patterns are linked to energy availability, but how the diversity-energy relationship changes in space and time is unclear. There are three possible scenarios: (1) equilibrium dynamics, where diversity is always positively related to energy availability in both time and space; (2) out-of-equilibrium dynamics, where diversity is determined by energy availability in equilibrium but diversity variation lags behind changes in energy availability, leading to a mismatch between temporal and spatial diversity-energy relationship, and (3) disequilibrium dynamics where the equilibrium does not exist or is irrelevant. We attempt to distinguish these scenarios using spatiotemporal pollen data for woody and herbaceous species. Applying spatiotemporal paleoecological data, we evaluated the correlation between pollen type diversity for each growth form and energy availability worldwide, as indicated by temperature and precipitation, in 1000-year intervals. Our findings reveal that for woody species, a positive temporal diversity-energy relationship emerges only amidst rapid energy level shifts, while a positive spatial relationship is significant when these levels stabilize, aligning with the out-of-equilibrium scenario. This suggests the existence of diversity equilibria acting as attractors, yet diversity often remains out of equilibrium. Conversely, the diversity-energy relationship for herbaceous species is typically weaker and inverse to that of woody species, indicating their distinct strategies and unique environmental constraints.

341. A macroevolutionary perspective on how dispersal can affect biodiversity and vice versa

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Patterns of species diversity emerge from the interactions between multiple interacting processes, such as dispersal and speciation. While the link from dispersal-to-diversity is relatively well understood, the reverse, diversity-to-dispersal, is relatively understudied. This is especially true within a macroevolutionary perspective over large eco-evolutionary time scales. Here we investigate how dispersal and diversity interact through space and time in shaping emergent biodiversity patterns. We model eco-evolutionary processes (allopatric speciation, ecological niche, dispersal and interspecific competition abilities that evolve, as well as trade-offs) to unveil dispersal-diversity feed-backs considering the abiotic structure of dynamic landscapes and biotic interactions (i.e. interspecific competition). Highest diversity (i.e. alpha, gamma and phylogenetic) occurred at intermediate levels of connectivity among patches (dispersal regime). Interspecific competition increased diversity closest to highest dispersal for every dispersal regime within the landscape. This stresses the interaction effects of interspecific competition and dispersal on populations connectivity, with lasting imprints on biodiversity patterns that are highly dependent on landscape structure and historical context. Assumptions regarding the evolution and ecology of dispersal and competitive abilities hold for these patterns, while possible historical signatures of macro-eco-evolutionary processes on emergent biodiversity patterns could be identified.

342. **Macrobehaviour - do you want to join the challenge?**

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Have you ever wondered how animal (plant, fungi, anything else...!) behaviour could impact or explain the biogeographical patterns you are finding or are interested in? Interested in the distributions of behaviours over large scales but don't know where to start with tying it to behavioural ecology theory? The new field of macrobehaviour encompasses the ‘investigation of variation in behaviour over large geographic, taxonomic, and temporal scales, and the ecological and evolutionary consequences of this variation’ and is particularly pertinent in an era of rapid environmental change where behaviour is often a first response. There are so many questions and we need YOU to begin to do tackle them. If you are up for the challenge (or you are on of those rare people who is already doing this), come and chat, get some ideas to point you towards promising avenues, and share your thoughts on my interactive poster. Hopefully we can build a new community of "biogeographers for macrobehaviour".

343. **Mismatched environmental variable scale in SDM cause misspecified inference**

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Categorical variables such as landscape and forest type are taking major part of habitat components while how species respond to these predictors is still undiscovered. Many researches have included categorical variables in their species distribution models(SDMs), but these variables have often been incorporated to the model as they are measured without concerning spatial scale and ecological process that actually affect the species’ distribution. We analyzed the effect of discrepancy between how species respond to categorical variables and how they were spatially transformed on SDM under virtual species simulation. Three different processes of species-variable response(circular range, distance, category) were purposely cross-matched to mimic discrepancies. Errors from SDM prediction in habitat map and SDM interpretation in response curve were measured and analyzed its relationship under different types of discrepancies, SDM algorithms, interpretation methods, and evaluation metrics. As a result, error patterns occurred differently depending on the context, with low errors in habitat prediction but high errors in model interpretation, which could hinder proper estimation of response curves. Error metrics and SDM algorithms were sensitive to the discrepancies, suggesting more consideration is needed in variable transformation method which could reflect the true response process of the target species. From analyzing error distribution patterns, we explain the causes of model degradation and robust algorithms for prediction and interpretation. We expect to discourage the arbitrary transformation of categorical variables by presenting errors in prediction and interpretation which could deliver misleading insights far from true species niches and responses.

344. bamm: An R package for estimating the dynamics of species distributions using the concepts of the BAM diagram

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According to the heuristic BAM diagram, species distribution is determined by a set of locations that have been accessible through dispersal (M) and have favorable biotic (B) and abiotic conditions (A). Most modeling platforms estimate factor A in a static manner using correlative niche models. Exceptionally, the other factors are dynamically modeled. We present the bamm package, which has tools to dynamically model the area of distribution based on the theoretical principles of the BAM diagram and demonstrate its use through realistic examples.

The mathematical model behind the package is a cellular represented as the product of three matrices: B, A, and M. The package provides functions for determining distribution patterns based on simulations and spectral analysis of the BAM matrix equation. These calculations are performed using sparse matrices, which allows simulations to be carried out over wide extensions and fine resolutions. The package can be used in conjunction with the correlative niche models to estimate: 1) the dynamics of the distribution area and 2) the connectivity-suitability-dispersal diagram, which is a method that identifies suitable sites connected through dispersal. Applications of the package include estimating invasive areas given a spread hypothesis, determining invasion routes of alien species, and analyzing range dynamics in response to changing environmental conditions.

345. voluModel: Modelling species distributions in three-dimensional space

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Many common ecological niche modeling (ENM) workflows organize and analyze occurrence and environmental data based on two-dimensional latitude and longitude coordinates. However, pelagic marine environments can vary strikingly with depth, and extracting environmental data based only on 2D data may result in poorly trained models and subsequent inaccurate prediction of species' geographical distributions. We developed the voluModel R package, presented here, to efficiently extract environmental data at three-dimensional coordinates (i.e. latitude, longitude, and depth) to train more precise ENMs. We present the main features of the voluModel R package and demonstrate a simple modelling workflow for Luminous Hake, *Steindachneria argentea*, as an example. voluModel includes tools for processing 3D environmental data, generating training regions, sampling data for model calibration, estimating extrapolation risk, and visualizing 3D geographic distributions based on conditions inferred as suitable based on ENMs. In addition to providing more precise models and distribution estimates, 3D niche modeling will more accurately estimate how climate dynamics may have shaped past and future changes in both the horizontal and vertical dimensions of species' geographic ranges.

346. #modelevaluation – generating spatial splits for ecological models using a hashtag sampling method

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Georeferenced locations of species occurrences are essential for understanding the relationship between species and their environments. These data can be used in a variety of ecological applications, including predictive modeling which can inform conservation and management decisions. To build trust and confidence in predictive models for use in decision-making, it is critical to assess model performance. In species distribution modeling, this assessment is commonly performed using *k*-fold cross-validation (CV) but there is an increasing recognition of the potential for models to overestimate performance when training and CV data are not independent. Multiple studies have emphasized how spatial data partitions provide more realistic assessments of model performance. Here, we extend current data partitioning methods to allow for a rigorous multi-phased workflow in which model selection and a final performance assessment each operate on separate, spatially independent data. We look toward machine learning workflows in other fields and their calls for three distinct data partitions (training, CV, testing), such that CV data are used for tuning and model selection and a separate, withheld testing dataset is used to assess performance of the selected model. We introduce a novel spatial partitioning method that combines recent advances in spatial-block sampling design with the unique geometry of the hashtag shape (#) to simultaneously generate species-specific training, CV and testing partitions. We illustrate the use of this hashtag method in the context of a species distribution modeling workflow and highlight its flexibility to a breadth of spatial patterns using examples from 280 invasive terrestrial plant species.

347. Spatial patterns of marine litter accumulation on the remote island of Santa Luzia (Cabo Verde)

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Santa Luzia, an uninhabited island in the archipelago of Cabo Verde, serves as a natural laboratory and important nesting site for loggerhead turtles (Caretta caretta). The island constitutes an Integral Natural Reserve and a Marine Protected Area. We assessed marine litter accumulation on sandy beaches of the island and analysed their spatial patterns using two sampling methods: at a fine scale, sand samples from 1×1 m squares were collected, identifying debris larger than 1 mm; at a coarse scale, drone surveys were conducted to identify visible marine debris (> 25 mm) in aerial

images. We sampled six points on three beaches of the island: Achados (three points), Francisca (two points) and Palmo Tostão (one point). Additionally, we modelled the abundance of marine debris using topographical variables as explanatory factors. Our findings reveal that the island is a significant repository for marine litter (> 84% composed of plastics), with up to 917 plastic items per m2 in the sand samples and a maximum of 38 macro-debris items per m2 in the drone surveys. Plastic fragments dominate, followed by plastic pellets (at the fine-scale approach) and fishing materials (at the coarse-scale approach). We observed that north-facing, higher-elevation beaches accumulate more large marine litter, while slope and elevation affect their spatial distribution within the beach. Achados Beach faces severe marine debris pollution challenges, and the upcoming climate changes could exacerbate this problem.

348. The Botanical Information and Ecology Network Database: a tool for plant biogeography

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The Botanical Information and Ecology Network (BIEN) is a global network of botanical institutions and individuals working to improve the understanding of plant diversity and ecology. BIEN provides a platform for collaboration and information sharing, and supports research and education in botany. This presentation will provide an overview of BIEN, its activities, and its potential to contribute to the study of plant biogeography. The presentation will also discuss the importance of plant diversity and ecology for understanding urgent questions in global change and conservation, the role of Open informatics workflows in the study of biogeography, and the role that BIEN can play in this effort.

349. Identifying Marine Food Web Homogenization Patterns

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Ongoing climate change is causing a novel heterogeneity, resulting in asymmetry in physical and abiotic properties, which is causing structural variations in ecosystems. At the local scale, homogenized ecosystems are believed to be an inevitable result of global change. Food web homogenization is a phenomenon that reflects several state characteristics of an ecosystem. One of these characteristics is topological simplification, which leads to an increased similarity in link structure and reduced network modularity. It is probably presented as a series of network topology problems. Secondly, functional non-redundancy is one of the manifestations of FwH, where multiple species have similar ecological roles and functions in the food web, leading to increased competition in the ecosystem. Additionally, FwH can also lead to resource centralization, where middle and low-level species occupy core importance, resulting in the formation of hub resource nodes and making the system more vulnerable to directional disturbances. Phenotypic differences in state characteristics can lead to various ecosystem risks, including biodiversity decline, nutrient cycling imbalances, and eutrophication. Therefore, it is important to identify the types of food web homogeneity in order to explore systematic risks. In this research, we aimed to identify various homogenization patterns in marine food webs and established an indicators system to classify

them. The work will provide a comprehensive concept of food web homogenization and improve our understanding of the risks associated with homogenizing systems, which will contribute to the development of nature-based ecosystem management countermeasures against future climate change.

350. To clamp or not to clamp? That is the extrapolation question.

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Ecological niche models (ENMs) are commonly used to predict species' potential distributions in different locations and time periods. However, transferring ENMs often requires predicting into novel environmental conditions that fall outside the range of the training dataset. When transferring ENMs, a choice must be made (at least for some algorithms): should the model extrapolate without any constraint, or should the prediction be “clamped” to the extreme values of the training data? Regression-based techniques (like GAM and even Maxent) allow for either choice, while many other techniques, like boosted regression trees and random forests, typically allow for clamping only. Although decisions about extrapolation affect the accuracy and realism of ENM transfers, there have been few assessments to determine best practices. To address this, we first transferred Maxent ENMs to novel environments (Last Glacial Maximum: ~21 kya) for a montane Mexican rodent (*Peromyscus melanotis*) by flexibly making decisions for individual variables (based on the direction of the response when truncated) and assessing the number of pixels in novel environments using kernel density plots. Results illustrate the value of making decisions about extrapolation for every variable, considering whether the response is increasing or decreasing at the truncation point and evaluating the quantity of non-analog conditions for each tail. In the cases where different extrapolation methods were suggested, applying clamping to some specific tails of variables (‘custom clamping’) was helpful to obtain a less risky prediction. We are finalizing general code to facilitate these analyses and inform decisions regarding the manner of extrapolation.

351. Stability in ecological niche models measured with the standard deviation

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Validating ecological niche models is a complex task. The most used validating metrics are discrimination (e.g. AUC, TSS) and calibration metrics (e.g. Boyce index, Miller’s statistic). A complement to these metrics is the stability of a set of replicated models through dispersion metrics such as the standard deviation (SD). We compared the variability of replicated empirical and null models hypothesizing that empirical models should have a smaller mean variability than null models. Concretely, we tested four assumptions: (1) empirical models should have a higher correlation than null models; (2) the differences between the habitat suitability or occurrence probability values of empirical and null models should be significant; (3) the subtraction between the mean empirical and null models should be different from 0; and (4) the similarity (Schoener’s D) between the empirical models should tend to 1 while the similarity between the null models should tend to 0. The models were conducted for real and virtual species, using seven modelling algorithms (GLM, GAM, GBM, MARS, RF, SVM, and Maxent). We compared the empirical and null models of virtual and real species based on the AUC, TSS, and SD values. Empirical models had a higher mean SD than null models only in some algorithms. The dispersion metrics increased with AUC/TSS. The mean and SchD of SD decreased with AUC and TSS: the lower the variability, the higher the performance. This work is funded by national funds through FCT – Fundação para a Ciência e a Tecnologia, I.P., under the MTS/BRB/0091/2020 project.

352. SPARSE 1.0: a template for databases of species inventories, with an open example of Czech birds

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Here we introduce SPARSE (acronym for "SPecies AcRoss ScalEs"), a simple and portable template for databases that can store data on species composition derived from ecological inventories, surveys, and checklists, with emphasis on metadata describing sampling effort and methods. Sparse can accommodate resurveys and time series, and data from different spatial scales, as well as complex sampling designs. SPARSE focuses on inventories that report multiple species for a given site, together with sampling methods and effort, which can be used in statistical models of true probability of occurrence of species. SPARSE is spatially explicit, and can accommodate nested spatial structures from multiple spatial scales, including sampling designs where multiple sites within a larger area have been surveyed, and the larger area can again be nested in an even larger region. Each site in SPARSE is represented either by a point, line (for transects), or polygon, stored in an ESRI shapefile. SPARSE implements a new combination our own field definitions with Darwin Core biodiversity data standard and its Humboldt core extension. The use of Humboldt core also makes SPARSE suitable for biodiversity data with temporal replication. We provide an example use of the SPARSE framework by digitizing data on birds from the Czech Republic, from 348 sites and 524 sampling events, with 15,969 unique species-per-event observations of presence, abundance, or population density. To facilitate use without the need for a high-level database expertise, the Czech bird example is implemented as MS Access .accdb file, but can be ported to other database engines. The example of Czech birds complements other bird datasets from the Czech Republic, specifically the four gridded national atlases and the breeding bird survey which cover a similar temporal extent, but different locations and spatial scales.

353. Using Google Earth Engine as a framework for Ecological Niche Modelling in northeastern Portugal

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Ecological Niche Models (ENMs) require robust data and powerful computational resources to convey meaningful insights on species distribution. Google Earth Engine constitutes a recent and versatile cloud-based modelling solution, allowing the development of fast-processing ENMs and expediting the analyses of species distributions at different spatial and temporal scales. We implemented a parametrized, customizable and user-friendly modelling framework within Google Earth Engine (GEE). The modelling framework consists in conducting ENMs in GEE using time series of remote sensing variables to estimate species vulnerability based on the trends of habitat suitability over time. We used publically available biodiversity data from vascular flora, amphibians, reptiles, and mammals and MODIS products from 2001-2022 as environmental variables. We implemented our GEE app in Montesinho Natural Park (northeastern Portugal), a natural area of European importance for biodiversity conservation. We used Maxent as modelling algorithm and the Mann-Kendall test to analyse habitat suitability trends. Written in JavaScript programming language, the GEE app provides a map for each species representing increasing or decreasing habitat suitability trends over space and time. Our results demonstrate the potential of programming frameworks based on ENMs, remote sensing data and their consequent application in areas with ecological and conservation interest. This work is funded by national funds through FCT – Fundação para a Ciência e a Tecnologia, I.P., under the MTS/BRB/0091/2020 project.

354. **Testing Assumptions of Historical Occurrence Use in Species Distribution Models**

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Occurrence data used to build species distribution models often include historical records from locations in which the species is declining or no longer exists. When these records are paired with contemporary environmental values that no longer represent the conditions the species experienced in the past, the model can create false associations that hurt predictive performance. The extent of mismatching increases with the number of historical occurrences and with inclusion of environmental variables that are more prone to change over time. The mismatch between occurrence data and contemporaneous environmental variables is a common dilemma when modeling rare or cryptic species with limited number and distribution of observation records that would otherwise improve model performance. Herein, we assess (1) the impact of historical occurrences on model performance across three sets of environmental variables of increasing persistency and (2) the performance of models built using selected-historical occurrences from locations that showed evidence of limited environmental change over time.

355. **Inferring land use legacies for Denmark using historical aerial photography**

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Obtaining detailed information about land cover is essential when allocating resources to nature protection, and in prioritising restoration efforts. With the increasing proliferation of satellite imagery, land cover datasets have been created at a variety of spatial, taxonomic and temporal resolutions.

Satellite data are only reliably available for the last 40 years, however. This leaves key gaps in our understanding of previous land cover transitions, transitions that may have enduring impacts on contemporary biodiversity and ecosystem functioning. Historical aerial photography campaigns, such as those flown after the Second World War in Europe, have the potential to be valuable sources of high resolution land cover information. These can be difficult to work with, however, due to issues with alignment, glare, and warping. Here, using a digital archive of scanned aerial photographs which spans the entirety of Denmark, we showcase an automated workflow to account for these problems, transforming historical images into usable sources of land cover information. We use structure-from-motion to produce both sub-metre resolution image composites and elevation models from the 1940s onwards. By quantifying how land cover has changed across parts of Denmark throughout the last 80 years, we then demonstrate how historical data can complement satellite-derived land cover maps. In addition, we also explore how this information could be used to support ecological restoration and prioritisation. We hope that our findings will improve our understanding of land cover change, and the legacy of human impact on the environment, both in Denmark and beyond.

356. Apparent effect of range size and fruit colour on palm diversification may be spurious

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Fruit selection by animal dispersers with different mobility directly impacts plant geographical range size, which, in turn, may impact plant diversification. We examine the interaction between fruit colour, range size and diversification rate in palms by testing two hypotheses: (1) species with fruit colours attractive to birds have larger range sizes due to high dispersal ability and (2) disperser mobility affects whether small or large range size has higher diversification, and intermediate range size is expected to lead to the highest diversification rate regardless of disperser. Species with fruit colours associated with mammal dispersal had larger ranges than those with colours associated with bird dispersal. The best fitting SecSSE models indicated that the examined traits were not the primary driver of the heterogeneity in diversification rates in the model. Extinction rate complexity had a marked impact on model performance and on diversification rates. Two traits related to dispersal mobility, range size and fruit colour, were not identified as the main drivers of diversification in palms. Increased model extinction rate complexity led to better performing models, which indicates that net diversification should be estimated rather than speciation alone. However, increased complexity may lead to incorrect SecSSE model conclusions without careful consideration. Finally, we find palms with more mobile dispersers do not have larger range sizes, meaning other factors are more important determinants of range size.

357. hsbm: A novel R-package for ecological network analysis and reconstruction

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Graph analysis tools can aid in the comprehension of complex species interaction systems (e.g., of predators and preys, hosts and parasites, or plants and pollinators) by identifying missing or inaccurate species links in poorly described networks. Amongst the hundreds of network completion algorithms that have been devised for this kind of task, one with a broadly proven effectivity is based on the Hierarchical Stochastic Block Model (HSBM). This HSBM implementation can create a nonparametric network reconstruction based on Bayesian inference that assigns error probabilities to observed and unobserved links. The method minimizes subjective decisions and enables statistical inference and model selection through a formally correct statistical validation. However, despite being a module of the popular Python-based graph-tool package, the largely R-biased community of ecologists is not utilizing this method. To bridge this gap, we introduce the hsbm R package (beta version) which includes functions designed to reconstruct bipartite species interaction networks from incomplete or unreliable data, estimate the probability of missing species links, provide error estimates for potentially misrecorded links, identify species groups, and visualize their hierarchical partition. The hsbm R package offers ecologists an accessible tool to reconstruct complex species interaction networks, address data quality issues, and gain a more precise understanding of the underlying structures of these complex systems. The package's accessibility to R users has the potential to increase the number of researchers who can benefit from this tool.

358. Can we accurately predict the distribution of soil microorganisms occurences and relative abundances? A case study in the Western Swiss Alps

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Soil microbes play a key role in shaping terrestrial ecosystems. It is therefore essential to understand what drives their distributions. While multivariate analyses have been used to characterise microbial communities and drivers of their spatial patterns, few studies focused on modelling the distribution of Operational Taxonomic Units (OTUs). Here, we evaluate the potential of species distribution models (SDMs), to predict the presence-absence and relative abundance distribution of bacteria, archaea, fungi and protist OTUs from the Swiss Alps. Advanced automatic selection of abiotic covariates was used to circumvent the lack of knowledge on the ecology of each OTU. 'Presence-absence' SDMs were successfully applied to most OTUs, yielding better predictions than null models. 'Relative-abundance' SDMs were less successful to predict absolute values, yet, they were able to correctly rank sites according to their relative abundance values. Archaea and bacteria SDMs displayed better predictive power than fungi and protist ones, indicating a closer link with the abiotic covariates used. Microorganism distributions were mostly related to edaphic covariates. In particular, pH was the most selected covariate across models. The study shows the potential of using SDM frameworks to predict the distribution of OTUs obtained from eDNA data. It underscores the importance of edaphic covariates and the need for further development of precise edaphic mapping and scenario modelling to enhance prediction of microorganism distributions in the future.

359. How sensitive are species distribution models to the selection of background points?

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Species distribution models (SDMs) are central tools in biogeography. Most commonly, they are fit with simple occurrences combined with background points (BP). But how to sample these

background points, and how does this choice affect SDMs? BPs are typically sampled randomly in geographic space, yet theory suggests, if a species is at equilibrium with the environment, it is better to sample them in a stratified way in environmental space. But this has never been tested. Furthermore, SDMs assume that the modelled species are at equilibrium. But how do these models perform when species are in disequilibrium? To answer these questions, we selected 40 different species (20 invasive and 20 equilibrium) and for each we calibrated SDMs with different types of background selections: random in environmental space, random-stratified in environmental space, random in geographic space, and random-stratified in geographic space. For each SDM we assessed both predictive performance using standard metrics and their stability using a new approach that compares the model's habitat suitability projection with those of a SDM calibrated with virtual occurrence data generated from the most suitable areas. We found that, both for species at equilibrium and for species at disequilibrium, sampling BP stratified random in environmental space yields the highest performance metrics and that sampling fully randomly in environmental space yields the most stable models. This has implications for the use of SDMs in conservation, as the classical fully random in geographic space BG is found to produce both less accurate and less stable models.

360. Is the distribution of non-native species predicted from the same environmental descriptors as native species?

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Human-driven environmental change is a major determinant of species distributions. Yet, spread by natural processes still occurs. The spreading of non-native species can be used as a large-scale "natural experiment" to investigate what drives changes in species distributions. However, exhaustive mapping of species distributions is hardly feasible and field surveys are costly and work intensive. Therefore, species distribution models (SDMs) can be used to understand, describe, and predict the potential current and future distributions of species. In this study, we investigated the differences in the covariate selection results of SDMs obtained for 147 native and non-native Swiss species. Covariate selection was done by using the covsel R package, an automated tool for species distribution modelling developed based on penalization and regularization functions, that also allows to measure the relative importance of each covariate. First, we compared the environmental categories of covariates retained for predicting the species distributions between native and non-native species. In addition, we analyzed the naturality of the variables. We found that anthropogenic covariates were more often selected by non-native species models (i.e., covariates from the transport, vegetation, and land use categories). In addition, the naturality score of the land use variables selected by native species models were higher on average. These results have implications for conservation, as they provide insight into the mechanisms behind native and non-native species distributions at a large spatial scale.

361. Improving Local-scale Species Distribution Models through Interpretable Machine Learning: A case of Cormorants in South Korean Rivers

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The machine learning method can better estimate non-linear relationships between organisms and environments at smaller scales than other methods, but has the disadvantage of being difficult to interpret the results. However, with the development of interpretable machine learning methods, it is expected that its use in species distribution models will allow for a more detailed analysis of environmental variables that contribute to habitat suitability as well as distribution prediction. In this study, we used the SHAP(SHapley Additive exPlanations), one of the interpretable machine learning methods, to interpret the spatial distribution of cormorants predicted through a maximum entropy-based species distribution model(MaxEnt) and to quantitatively understand habitat characteristics using the presence data of two species of cormorants living in South Korean rivers collected from 2019 to 2022, as well as geomorphic and vegetation data. After fitting the model that accounts for the landscape perception range of cormorants and analyzing the contribution of each variable, and interaction among them, the model was highly reliable, and a certain area of water near which wetland woody vegetation is scattered, and an appropriate proportion of river island were found to be suitable habitats. This study complements the interpretation limitations of existing prediction-oriented species distribution models and presents a method for converting geomorphic and vegetation landscape variables considering landscape perception range, suggesting the possibility of ecological interpretation through species distribution models at local scales.

362. Estimating ungulate distributions and relative abundance at a continental scale

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Growing evidence recognizes that large herbivores (mainly ungulates) have strong controls on terrestrial ecosystems. However, previous studies have mainly focused on some specific ecosystems at local scale, lacking the generality covering multiple ecosystems at large spatial extents (regional to global). Filling these knowledge gaps requires quantitative data on ungulate spatial distributions, which are scarce at large spatial scales. Rapidly growing citizen science programs provide an excellent opportunity to quantify the spatial occurrence of ungulates, which are usually attractive to citizens. However, as citizen science data at large spatial scales (e.g., records in iNaturalist) are mostly opportunistic presence-only data, inferring species distributions based on these data can suffer from the problems of sampling bias and low sampling intensity. In this project, I plan to develop a robust quantitative tool incorporating the sampling process (thus reducing the influences of sampling biases) to estimate ungulate spatial distributions. I also combine the results with snapshot data from camera traps to estimate ungulate relative abundance at continental scale, which will be the key to assessing ungulate effects on ecosystem dynamics.

363. Do SDM performance scores tell us anything about reality? A test with virtual species

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Species distribution models (SDMs) can be powerful tools for conservation biogeography, and this power is commonly assessed by model performance scores (e.g., TSS, ROC, and Kappa). However, it is not clear that internal validity (i.e., model performance) indicates external validity (i.e., reality), because model predictions are based on available data and cannot be compared to a perfectly-known reality. Virtual species enable such comparisons with user-defined habitat requirements and derived *a priori* distributions. We created four different types of virtual species (eurytopic and stenotopic organisms at each of global and regional distributions) to evaluate SDM performance given a virtual reality. For each virtual species, we predicted SDMs (11 algorithms) and compared these to the virtually-known SDMs (where R^2 between predicted and known habitat

suitabilities quantified model “virtual reality”). We then compared R^2 to performance scores for each model. Importantly, high performance scores (i.e., internal validities) did not consistently correlate with high R^2 values (i.e., external validities). Algorithms varied widely, but GLM, GAM, MARS, and MAXNET produced relatively high internal and external validities. ROC scores were consistently inflated, whereas Kappa scores more reliably matched external validities, especially at larger scales. Ideally, SDMs should perform well internally and match external reality, and work here helps to steer toward that potential. Recommendations on how to best assess SDM reality will derive from this work, with applications to applied conservation work that relies on these predictive models.

364. Diversity of fishes of the Napo and Arajuno rivers, with potential of handling, in the Parish Ahuano, Canton Tena, Napo Province

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Iván Bladymir Morillo-Villarreal, Paula Adriana Andrade-Galán et al The study is carried out to establish the diversity of fish in the Napo and Arajuno rivers in the segments that cross the Ahuano parish of the Tena Canton, Napo Province in the Ecuadorian Amazon. Several studies indicate that the Napo River basin would have up to 680 species of fish (Barriga, 2012). A monitoring effort was carried out for 12 months. Trammel and trawl nets were used to collect the specimens. Sampling was carried out at five stations in each river, every 1,000 meters, once a month during the 11 months of study. As a general result, the record of 27 species of bony fish was obtained. Of the order Characiformes, 16 species were obtained, being the most diverse, while at the taxonomic family level, Characidae was more frequent with 9 corresponding species. Additionally, a survey was carried out among 5 indigenous and peasant communities on the banks of the two rivers to establish the preference for fish consumption and the potential species for management, which were: Prochilodus nigricans for 28%, followed by Pimelodus blochii 18%, Mylosoma duriventre, Leporinus pearsoni, Hypostomus oculeus, Aguarunichthys torosus, Leporinus friederici and Triportheus angulatus with 9% each.

365. Unveiling niche-based responses and patterns of local occupancy of dryland species

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Alterations in climate and land use (e.g., increased grazing pressure), are key drivers of global environmental change in drylands. Understanding the responses of dryland biodiversity to these novel stressors is imperative due to their extensive coverage and their importance in providing key ecosystems services and supporting many human populations. Such importance is further exacerbated due to the high number of endemic plant and animal species that are unique to these environments. In this study, we explore the Grinnellian niches of the more than 1,500 plant species that inhabit the most important dryland ecosystems worldwide, extracted from BIODESERT dataset. We downloaded and filtered species’ occurrence locations from GBIF and BIEN data portals. Then, we used ensembles of Environmental Niche Models (ENMs) to represent the Grinnellian niches of each species, built on an individual species-specific selection of uncorrelated predictors from a set of 74 variables accounting for climate, soil, and topography, at a 10km resolution for the entire world. For each species, we projected the models onto each of the seven biogeographical realms where it can be found nowadays. This allowed us to validate model projections against the empirical data on dryland communities from the BIODESERT dataset and assess the coverage of potentially suitable places that are actually inhabited by the species adapted to dry environments. This may enhance our understanding of the relationship between species' potential distributions and the establishment and maintenance of local populations in drylands, which can ultimately help informing ecosystem-level adaptation strategies to global change in extreme environments.

366. Predicting spatial distribution of nature's contributions to people from individual species

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We are engaged to run against the time. The Intergovernmental Panel on Climate Change has joined Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services to integrate human and Nature relationship to change the way of future. Based on the establishment of relationship between more of 2,000 species and 17 nature's contributions to people (NCP) we proposed the first predictions of NCP based on species distribution modelling for the current and for the future scenarios (RCP 4.5 and RCP 8.5) on 3 periods (2020-2049; 2045-2074; 2070-2099). Localised in Swiss alps area, the study site allows to observe change in complex environment across multiple time-scenarios. Although these results are only based on vertebrates and tracheophytes species, they showed the highest NCP richness for the current followed by scenario RCP 8.5 and RCP 4.5. A shiny web app completes this study to support mapping visualization. These preliminary results showed us all the potential considering direct relationship between species and NCPs. This vision could be helping decision makers to support biodiversity conservation in view of the 30x30 target fixed with the "Accord de Paris".

367. Contrasting elevational zonation patterns of forest birds on Mt. Cameroon, west-central Africa, and Mt. Wilhelm, Papua New Guinea

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We compared the elevational distribution of forest birds on Mt. Cameroon (CMR) and Mt. Wilhelm (WHL), in west-central Africa and Papua New Guinea, respectively. The two mountains represent some of the few elevational systems characterized by similar altitude and complete forest gradient, yet differing in treeline location (2300 m for CMR; 3700 m for WHL). We estimated species' elevational ranges in 200-m and 500-m bands and assessed the impact of mid-domain effect (MDE) on avian species richness, species turnover, and nestedness. We found distinct patterns between the two mountains. CMR exhibited a low-altitude peak in richness followed by a decline with elevation, while WHL showed a continuous decrease. Beta diversity and the frequency of range limits also indicated differences in elevational zonation between the two mountains. Species turnover peaked on WHL between 1200 and 2200 m, whereas turnover peaked at 750-1150 m on CMR. High levels of nestedness were observed due to the decreasing number of lowland species moving upslope at intermediate elevations on both gradients. Range limits indicated that replacement of lowland by montane fauna occurred at lower elevations on CMR compared to WHL. Higher frequency of species' upper range limits at the treeline was recorded on CMR than on WHL. We hypothesize that a considerable number of highland species are restricted upwards by the lower-located treeline on CMR. The MDE was not supported as the driver of the observed patterns. These findings highlight the importance of gradient length in shaping elevational diversity patterns.

368. **Global biodiversity map: its completeness assessment based on temporal pattern of species occurrence records**

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The lack of information on the spatial distribution of species (Wallacean shortfall) is an inherent part of biodiversity research. Attempts have been made to reduce uncertainty arising from incomplete distribution data, such as species distribution modeling and statistical methods to estimate species richness (e.g. Chao's estimator). However, assessment of completeness of the visualized biodiversity patterns themselves have rarely been studied. Here, the current study proposes a novel method to quantify the completeness of taxonomic richness patterns by assessing the asymptotics of changes in taxonomic richness patterns obtained from datasets of occurrence records which are accumulated over time. Specifically, we tested whether a taxonomic richness map does not change by appending the data utilized for its compilation. If the variance of taxonomic richness in the present-day known patterns is well-accounted for by that in the past known patterns (as measured by a high R-squared value yielded by the linear regression), then the known taxonomic richness patterns are assumed to be invariant to further data accumulations, hence highly complete. This method was applied to taxonomic richness patterns generated by global occurrence datasets of

GBIF and OBIS. We found that the assessed completeness varies significantly by taxonomic groups and levels (i.e., family, genus and species), and spatial resolution (i.e., grain size). This approach might provide certainty measure of knowledge obtained from taxonomic richness patterns, for example, in context of biodiversity driver analyses or conservation planning.

369. Spatial patterns and quantifications of habitat loss differ between remotely sensed resolutions and those required for IUCN Redlisting

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Species distribution modeling (SDM) uses occurrence records and environmental variables to predict climatic suitability across geography. After additional postprocessing to consider currently available habitat for a species, these range estimates can be useful for conservation assessments, particularly for calculating area of occupancy (AOO), a metric used for threat level categorization by the International Union for Conservation of Nature (IUCN). However, spatial resolutions impact geographic patterns and areal estimates. To standardize assessments for comparison, the IUCN requires AOO estimates to be based on World Cylindrical Equal Area map projections, with a 2 km resolution. Here, we predicted the range for a threatened mammal (*Handleyomys chapmani*) using an SDM post-processed with remotely sensed forest cover data. We calculated the area at two spatial resolutions; the native 250 m resolution (from the forest cover data) and resampled to a 2 km grid. We calculated an AOO estimate for an updated assessment for the species, leading to a larger areal estimate than at the finer resolution (as expected). Findings suggest removing the species from the current Vulnerable level to outside the threatened categories. However, we found that spatial patterns of inferred local habitat loss differed substantially between resolutions. Much of the loss was no longer appreciable at the coarser 2 km grid, whereas the finer scale detected insufficient habitat along many rivers and valleys. This may be problematic at a regional level, such as for managing individual protected areas. This study emphasizes the importance of resolution for conservation.

370. A sky island perspective: New England alpine plant distributions across the region

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Northeastern alpine plant communities of the United States and Canada exist as mountaintop islands separated by a matrix of northern hardwood forest. These high elevation ecosystems are thought to be climatic refugia for tundra relic species. Understanding the drivers of their present-day assembly could provide insight into their vulnerability to modern climate change and other human-mediated disturbances. Because these rare mountaintop communities are often managed by separate agencies, plant distribution surveys have taken place sporadically over the last century, and standardization is lacking. Therefore, it is not entirely clear how interconnected these communities are or how they may have changed through time. To address this, in summer 2021 and 2022, we conducted vegetation transect surveys on 8 peaks in Vermont, New Hampshire, and Maine (USA) to assess whether the area, connectivity, topographic complexity, and hiker visitation of each “sky island” affects alpine specialist species presence and richness. Mountaintop locations were chosen to incorporate various sizes and levels of isolation from other peaks. We found that

while area and hiker visitation did not explain alpine specialist species richness across peaks, connectivity between peaks and topographic features like slope did. Because of these results, we conclude that there is likely some recolonization occurring and that topography plays a role in community heterogeneity on these mountaintops.

371. Modeling the relationship between climate, habitat, fire, and small mammal richness across the Sierra Nevada

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California is considered a biodiversity hotspot based on its high species richness and endemism, and the considerable threats to the ecosystems that support these species. Small mammals represent key components of healthy ecosystems as seed and fungal dispersers, important prey, and habitat engineers. Recently, the Sierra Nevada has experienced an increasing amount of change, including climate change such as prolonged drought and more severe and more frequent fires, as well as associated vegetation change. Small mammals are known to be sensitive to changes in climate and habitat. However, the long-term influence of fire on small mammal communities is poorly understood. We aim to explore the drivers of small mammal richness, focusing on changes in fire, habitat, and climate. Historical survey and resurvey projects, coupled with other collecting efforts, provide high-quality species occurrence data from the last century in the Sierra Nevada and other mountainous regions of California. Here, we examine patterns of small mammal community change seen in the Sierra Nevada, investigate the potential impacts of fire, both isolated from and in tandem with other potential factors affecting small mammals and determine whether this multivariate perspective improves understanding of how small mammal richness changes over time. Preliminary results indicate that inclusion of variables related to past fire does not improve fit based on models with just climate and habitat, though we are still exploring and refining key points of uncertainty. Overall, we hope to gain understanding of the multivariate factors influencing small mammal communities in an era of global change.

372. Plant functional groups as an input for dynamic vegetation modelling

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Ongoing climate change serves as a compelling driver for plant ecologists to develop robust plant biodiversity scenarios. However, traditional dynamic vegetation models rely on plant functional types that are often aggregated to the point of losing their ecological and functional relevance. Instead, we advocate for using a more nuanced and pragmatic concept known as plant functional groups (PFGs). PFGs aggregate plant species with shared characteristics related to demography, responses to plant-plant interactions, disturbance, and environmental niches. Here, we utilize an established framework and draw upon a vast dataset of over 2 million vegetation plots from the European Vegetation Archive to establish a comprehensive set of meaningful PFGs tailored to

Europe, encompassing a significant portion of vascular plant species. The process of creating these PFGs begins by incorporating trait information, specifically species' demography, life form, plant height, dispersal and responsiveness to ecological gradients estimated by indicator values for light, nutrient and moisture availability, tolerance to salinity and disturbance. Leveraging these trait attributes, we calculate pairwise similarities among more than 6,000 plant species found in Europe. To delineate species niches, we assess the climatic niche overlap between all species pairs based on bioclimatic data from CHELSA. Subsequently, these two pairwise distance matrices are combined, and a cluster analysis is executed to identify the optimal number of plant functional groups for Europe. The resultant PFGs undergo meticulous scrutiny and validation through expert evaluation. These PFGs will serve as a foundational framework guiding our future research agenda.

373. The Botanical Frontier: Anticipating the Revelation of over 1000 New Plant Species in Nigeria

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Biodiversity assessment is vital in the face of anthropogenic-driven extinction, yet the 'taxonomic impediment' poses a significant challenge. In tropical African countries like Nigeria, taxonomic studies occur sporadically, endangering the Convention on Biological Diversity's Global Biodiversity Framework vision 2050. Our study delves into the historical trends of vascular plant exploration in Nigeria and forecasts the description of currently unknown species over the next 50 years to assess the necessary taxonomic effort for comprehensive biodiversity assessment. Using a comprehensive dataset from the World Checklist of Vascular Plants, encompassing all vascular plant species in Nigeria, we employ Bayesian time series regressions to estimate the long-term description rate of these species. An ensemble forecast predicts the number of species descriptions by 2070, considering various scenarios of active taxonomists. Our findings reveal a stark contrast between resident and non-resident botanists in species description contributions, with the former contributing fewer descriptions. The number of authors involved in descriptions has increased but plateaued since the 1950s. Predictions for species descriptions by 2070 vary, with an ensemble forecast estimating 1140 species descriptions, but individual models range from 1004 to 2239. Our study estimates that current taxonomic activity will lead to a 20% increase in known vascular plant species in Nigeria over the next 50 years—possibly still an underestimate of the true, unknown species richness. Urgent action is imperative to combat the taxonomic impediment, enabling tropical African countries to align with the CBD's Global Biodiversity Framework vision 2050. We outline key pathways to achieve this goal.

374. Oh, the places they'll grow: Do trees' climate tolerances differ across life-history?

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Describing the role of climate as a biogeographic control on species distributions has a long history in the ecological literature. Such efforts are particularly relevant for understanding and accurately defining species' ecological niches. To date, most efforts to map, measure, and/or model species' climatic niches rely on information gleaned from adult or age-unspecified distribution data. Such approaches ignore the possibility that a species might maintain different climate tolerances as it matures from a juvenile into an adult. If adult and juvenile climatic niches differ, then the implementation and/or interpretation of age-agnostic analyses could be limited. Acknowledging this potential life-history difference, Grubb (1977) suggests an addendum to Hutchinson's (1957) niche concept by proposing that a species has a *regeneration niche,* which is expected to differ from its *adult survival niche*. Despite Grubb's postulation and its potential implications, a large-scale, multi-species test of the regeneration niche concept remains lacking in the literature. Here, we build from Grubb's hypothesis to assess whether juvenile and adult climatic niches differ, using trees as a model taxon. We estimate, measure, and compare the realized climatic niches of 198 tree species partitioned into their distinct life-history stages (seedling, sapling, adult) using tree occurrence data from the U.S. Forest Inventory and Analysis Database and climate data from the PRISM climate database. We find little difference in species' life-stage-partitioned climatic niches, suggesting potential stasis in species' environmental tolerances across life-history.

375. Ecology and Evolution of Clonal Growth Forms in the Lamiaceae Family Across Iranian Plateu

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Clonal growth, a widespread adaptation in plants, plays a crucial role in their survival and persistence, but has been studied primarily in temperate regions, with very limited data on its distribution in arid and subtropical regions. We aim to address a broader question how clonal growth strategies respond to varying environmental conditions across long climatic gradients with special focus on dry conditions. We therefore extend our focus beyond the hitherto studied regions of Central Europe and China taking Iran and the Middle East as a study region. Iran's unique climate gradients, spanning from high mountains to lowland deserts, provide a region ideally suited for understanding of the adaptive role of clonality to different biomes. We study Lamiaceae family, which diverse clonal growth forms and high diversity makes it an excellent candidate for investigating the relationship between clonality and environmental factors. We analyzed the diversity of clonal growth traits across Lamiaceae species, and linked them to species distribution patterns. We explore whether gradients in environmental conditions, namely drought, correlate with shifts in the frequency and types of clonality. Further, we use phylogenetic data to determine rates of evolution of clonality and individual clonal growth organs in the family. This will help to identify how ecological conditions have influenced the evolution of clonality as an unexplored component of the plant form response to the environment.

376. Unravelling the impact of soil data quality and resolution on species distribution models of temperate forest woody plants

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Soil properties influence plant physiology and performance, therefore playing a pivotal role in shaping species niches. However, comprehensive investigations that establish a link between soil properties and plant species distribution across extended geographical areas often lack detailed, high-resolution soil data. Here, we investigated the impact of soil data quality on the performance of species distribution models (SDMs) by comparing models based on measured soil properties with those based on digitally mapped soil properties at different spatial resolutions (25m and 250m). We draw upon an extensive dataset comprising vegetation plots and measured soil properties, enabling a comprehensive assessment of the significance of soil data quality for 41 woody plant species within Swiss forests. Additionally, we calibrated SDMs of the same species based on the nearest neighbouring sites of the Swiss National Forestry Inventory (NFI4) using digitally mapped soil properties. On average, all models based on measured and digitally mapped soil properties showed a significant improvement in model performance over those without soil information. Models based on higher-resolution soil information (25 m) outperformed coarse-resolution models (250m). Especially for species with an ‘extreme’ niche position, SDMs based on measured soil properties outperformed those based on modelled soil maps. The relevance of soil properties also decreased in models with coarser spatial resolution. The predictive power of SDMs for forest woody plants was most improved by pH, clay content and soil density of the topsoil layers. Our study highlights the advantages of using spatially-explicit, high-resolution soil information based on robust field measurements in SDMs as ecologically meaningful predictors of forest plant biodiversity.

377. A critically endangered African vulture starts breeding in Europe: escaping from extinction or entering a genetic amalgamation trap?

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Rüppell’s Vulture *Gyps rueppelli* is a tropical African species that until very recently was only found in sub-Saharan Africa. This vulture was first reported in Europe in Spain in 1992 and since then it has been increasingly observed, mostly in Spain. Since then there have been several unsuccessful breeding attempts, always by mixed pairings with Eurasian Griffon Vultures *Gyps fulvus*. Throughout 2021 and 2022, hybrid breeding attempts have consistently occurred at a breeding colony in Málaga (Southern Spain), but close monitoring of the individuals confirmed that mating did not result in egg-laying. It was in 2023 when a male Rüppell’s Vulture was repeatedly observed paired and mating with a female Griffon Vulture, culminating in successful hatching, and the first confirmed case of successful hybridisation by the two species in the wild. Paradoxically, as the Rüppell’s Vulture begins to colonise a new biogeographic realm, the Western Palearctic, its rapid decline in the Afrotropical region caused it to be reappraised in the IUCN Red List of Threatened Species as Critically Endangered. Hybridisation events will probably continue and even increase in Europe. Consequently, a large proportion of Rüppell’s Vulture progeny will be hybrids, accelerating their extinction in Europe through genetic amalgamation. This is a paradigmatic case of dynamic conservation biogeography, which may require conservation strategies that include areas outside the native range of the endangered species. We encourage international and transcontinental efforts involving the Iberian Peninsula, the Maghreb and southern Africa in action planning for the conservation of the Rüppell’s Vulture.

378. Biogeographic Implications of Saharan Refugia for Herpetofauna Diversity of Northern Africa

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Geographic refugia are integral in understanding species distributions and population connectivity through space and time. Refugia are especially influential in regions which have historically experienced great climatic change. One such region is the Sahara Desert of North Africa which has undergone many bouts of desertification and oasification beginning 11 million years ago. The most recent oasification event for the Sahara, known as the African Humid Period, occurred during the late Pleistocene as well as the early to mid-Holocene (approximately 14,600 to 5,500 years before present). As ectothermic organisms with relatively limited dispersal capabilities, herpetofaunal distributions and population dynamics are especially influenced by the presence of these refugia in these landscapes. In our study, we used previously published phylogeographic studies of herpetofaunal species (1 amphibian, and 110 reptiles) to highlight common regional refugia and make inferences about the population demographics of the herpetofaunal community in the Sahara Desert at three time periods bordering the African Humid Period (LGM, mid-Holocene, and current). We achieved this through an integrative approach which combined surveys of previously identified refugia, stacked species distribution modeling of stable climate areas using species occurrence data, and population demographic modeling from mitochondrial DNA sequences with MTML-Bayes and the R package. *PipeMaster*.

379. Modelling the potential biodiversity distribution - a tool for prioritisation in nature conservation

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Territorial nature protection is mostly targeted at the occurrence of endangered species or their habitats. However, knowledge of their distribution is often driven by the intensity of monitoring and mapping efforts. At a time when the ambition of the EU nature conservation is to increase its territorial extent up to 30% (10% of strict protection respectively), the need for precise knowledge of potential biodiversity is even higher than ever. Therefore, we prepared a set of models of potential distribution on selected taxonomic and functional groups of organisms (molluscs, butterflies, amphibians, reptiles, birds, and mammals) with significant conservation and/or indicator status. By synthesizing these particular models, hotspots of potential biodiversity were identified and evaluated. By comparing these hotpots with the existing system of protected areas, a database of territorial conservation priorities was then created. In addition, the connectivity of the most valuable habitats was analysed.
We believe that the data-based evidence can be an important tool for the proper designation of other protected areas in the Czech Republic.

380. 3D canopy structure as an indicator of grassland diversity

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Many studies find that the grassland biodiversity and the 3D canopy structure are correlated. The reasons for this relationship varies but are often linked to habitat heterogeneity, light availability and competitive exclusion. So far this relationship has not been tested beyond small-scale study sites due to the lack of broad geographic region information on both grassland diversity and 3D canopy structure across multiple sites. We evaluated the relationship across the Carpathian mountain range by using ~200 vegetation plots of semi-natural grassland plant diversity (vascular plants and bryophytes) and canopy height structure of the plots and their neighbourhoods derived from a global canopy height model. The relationship was tested using focal statistics at varying scales and transects using neighbourhood buffers at various sizes up to 3 km distance. Our results demonstrate a positive correlation between plant richness and the diversity of 3D canopy structure. We have identified conditions under which the 3D canopy structure can serve as an indicator of vascular plant and bryophyte richness.

381. Standardized data collection across continents in ecology, behaviour and conservation: Lessons learned from ÉLVONAL Shorebird Science project

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Shorebirds (sandpipers, plovers and allies) are some of the most charismatic birds, and they are often used as model systems in studies of evolutionary ecology, behaviour and conservation. Shorebirds have global distribution and they breed on all continents including Antarctica. However, a major stumbling block in comparing behaviour and ecology of different shorebird populations is the field methodology that usually differ between species, locations and research teams. With the support of Hungarian government's ÉLVONAL program, we started a 5-years project on breeding ecology of shorebirds in 2018. As part of the project, we collected data from over 50 shorebird populations globally. In order to make the data collection standardized and comparable across different species, populations and research teams, we developed: standardized protocols for behavioural records and breeding ecology, field notebook templates, weekly updates, final fieldwork reports and electronic templates for data delivery. For our collaborators, we run numerous fieldwork training camps, regular meetings and conferences as well as online tutorials, making sure that fieldwork protocols are applied the same across scales. We are currently working on multi-population publications, using effectively the data collected by different teams across our network according to the ÉLVONAL protocols. We hope that the developed framework of standardization approaches and procedures might be inspirational for any researcher working with any taxa across large scales – leading to higher standardization of data collected, making them comparable across different populations, species, research teams and continents.

382. Survival under the ice - Pleistocene glaciation imprints contemporary population genetic structure of five peri-alpine groundwater amphipods species

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Climate oscillation during the Pleistocene shaped the distribution and genetic diversity of many species, both terrestrial and aquatic. The impact of this period on subterranean organisms, however, is rarely studied. Some evidence suggested that glaciation affected distribution and recolonization patterns as well as speciation rates, yet some species might have persisted under the ice. Within the Alps, Switzerland is a particularly interesting region to study this phenomenon, as its territory comprises regions that were free of ice during the whole Pleistocene, regions that were covered periodically, and regions that were always under ice. Here, we focused on five species of groundwater amphipods from the genus *Niphargus*, and representatively collected thousands of individuals across Switzerland. We amplified a portion of the COI gene and associated the species' genetic structure to demographic changes and glaciation histories. Although all species seem to have used karstic cavities to survive, we observed very different genetic patterns. One species likely persisted under the ice during the whole Pleistocene, exhibiting a much higher and more structured genetic diversity as compared to the four other species. Contrarily, the latter have likely persisted in ice-free refugia, or in karstic cavities under the ice, and have rapidly recolonised after the glaciers retreated. These different histories are associated with different demographics, genetic structures, and distributions, also suggesting different adaptation abilities to future environmental changes. For example, species that went through a Pleistocene bottleneck might exhibit a restricted pool of genetic variation making them more vulnerable to ongoing climate change.

383. C4 photosynthesis provided an immediate demographic advantage to populations of the grass Alloteropsis semialata

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C_4 photosynthesis is a key innovation in the evolution of land plants but its short-term effects remain elusive. We explore the early impact of the C_4 trait on the trajectories of C_4 and non-C_4 populations from the grass *Alloteropsis semialata*, combining niche models projected into paleoclimate layers for the last 5 million years with demographic models based on genomic data. C_4 clade IV populations occupy the widest environmental space, rendering a large potential geographic range over time despite recurrent climatic changes, contrary to other clades. The initial split between C_4 and non-C_4 populations was followed by a more intense expansion of the ancestral C_4 population and the divergence between current clades led to the unparalleled success of C_4 clade IV, which spread over three continents and achieved the highest population growth among all clades. The posterior transfer of some C_4-like characters to non-C_4 populations probably facilitated the expansion of non-C_4 clade II in the region of origin. The varying demographic trajectories observed across populations, however, emphasize the significant contribution of other traits and/or local factors to the populations' fate. Our findings support that C_4 photosynthesis provided an immediate demographic advantage to *A. semialata* populations, but its effect was context dependent.

384. Host-Virus Cophylogeny Trajectories: Investigating Molecular Relationships between Coronaviruses and Bat Hosts

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Bats, with their virus tolerance and mobility, are key reservoirs for emerging viruses like coronaviruses (CoVs). The study of their interaction offers insights into disease transmission, host adaptation, and the origin of infections. This research explores the connections between 69 host-virus pairs and their coevolution. Among these pairs, 47 showed significant coevolution, highlighting strong associations. Focusing on two viral proteins, ORF1ab and spike, specific sequence regions were found to be pivotal for their coevolution.

Recombination events were identified within these proteins, indicating their role in viral adaptation to different host environments. Additionally, partial gene transfer was observed, not only within host species but also across species boundaries, revealing a complex pattern of genetic exchange.

In this study, the role of phylogeography, or the study of how species evolve and distribute across geographic regions, is evident, as it helps reveal the connections between viral lineages and their hosts in different locations.

385. Molecular diversity of spring fen macrozoobenthos from two geomorphological regions

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Recent studies on diversity of stream amphipods indicated that the Western Carpathians may have served as an important glacial refugium of freshwater fauna. If this scenario is true, a considerably high molecular diversity can be expected in this biogeographic region also for other aquatic taxa. In our project, we aim to uncover and characterize molecular diversity of benthic macroinvertebrate fauna of calcareous spring fens (a well-studied and hence convenient model community) of the Western Carpathians. For a comparison we also sampled macroinvertebrates in comparable habitats of the Bohemian Massif, the adjacent region, but with different geomorphological history. Using a DNA metabarcoding approach, we sequenced a fragment of the COI gene of pooled spring fen invertebrate communities from 21 Carpathian and 8 Bohemian Massif localities. Here the up-to-date insights about the comparison of molecular diversity of the same habitats in these two geomorphological regions will be presented. We observed a considerable lack of reference sequences in public databases (Barcoding of Life Database, GenBank) for a large portion of the detected molecular operational taxonomic units (MOTUs), indicating that the studied regions are not yet sufficiently covered by barcoding efforts, and/or suggesting that there indeed may be a considerable unrecognized diversity of macrozoobenthos. We also found large amount of NUMTs in some taxa. Furthermore we aim to compare the MOTU diversity with the morphological diversity, already well studied in most of the localities, and to detect the spatial variation associated with distinct molecular/morphological communities/phenotypes.