GRICAD

LECA Laboratoire d'Ecologie Alpine

UGA Université Grenoble Alpes

JUG - 2021

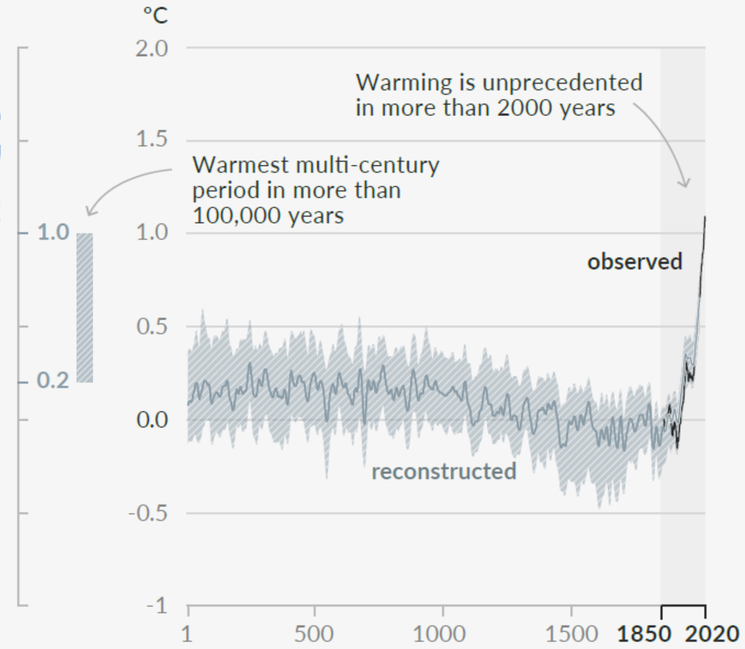
Phylogenomic Study of the Whole Alpine Flora

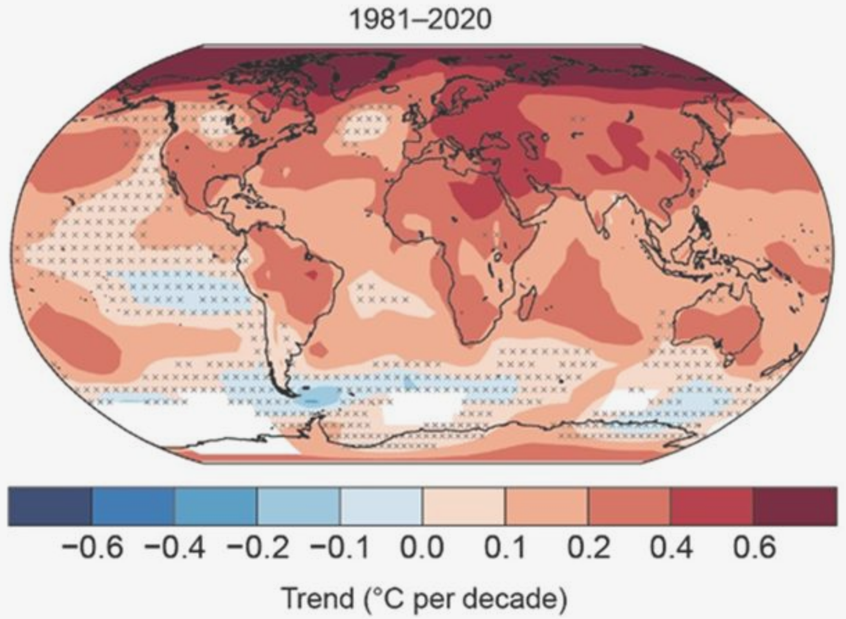
Charles Pouchon (LECA, UNIGE-MuseumLab)

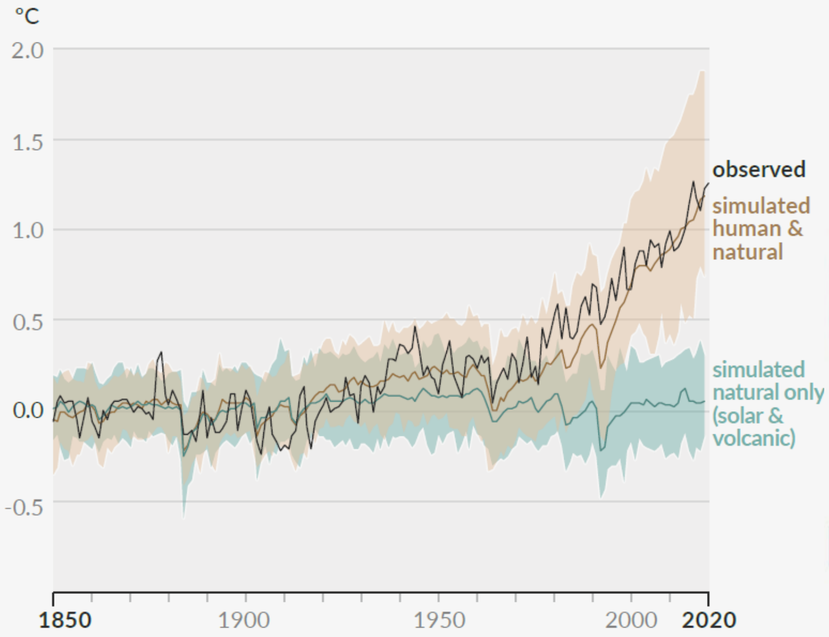
Ranunculus glacialis (Galibier) - © C. Pouchon

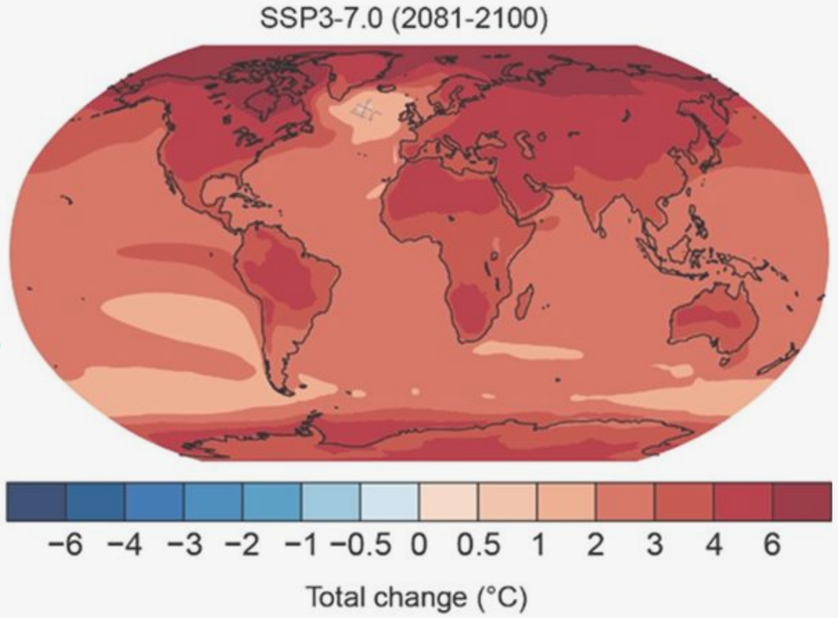
How is the Climate Changing…

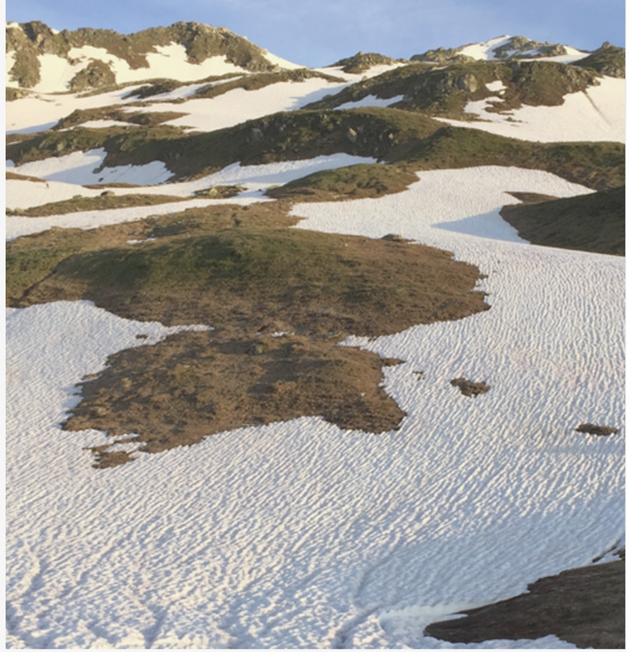
an evidence: a very significant increase of the climate change induced by human activities

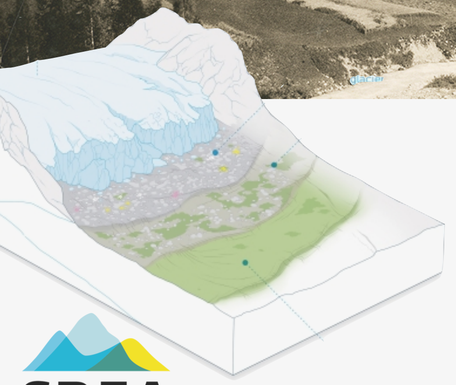




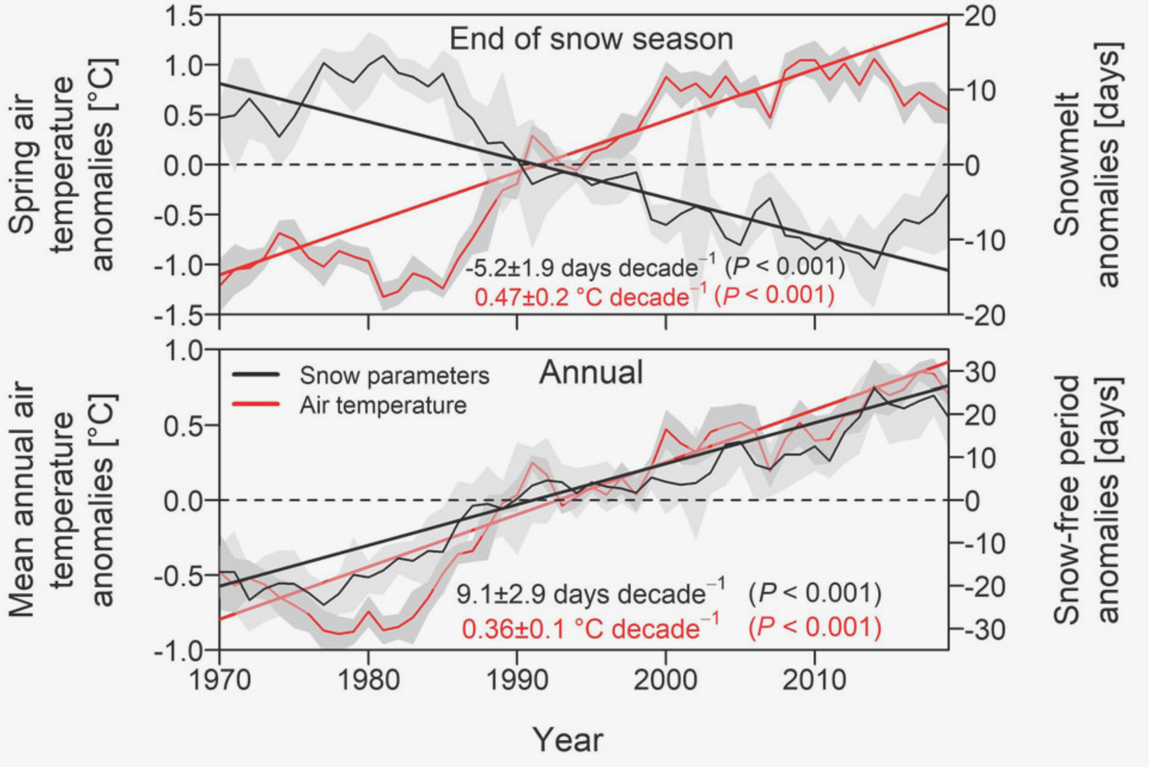








CREA
-MONT-BLANC-



Snow cover changes in Swiss Alps (Vitasse et al. 2021; data from Klein et al. 2016)

Consequences of climate change on mountain landscapes

Glacier retreat and changes on snow cover periods

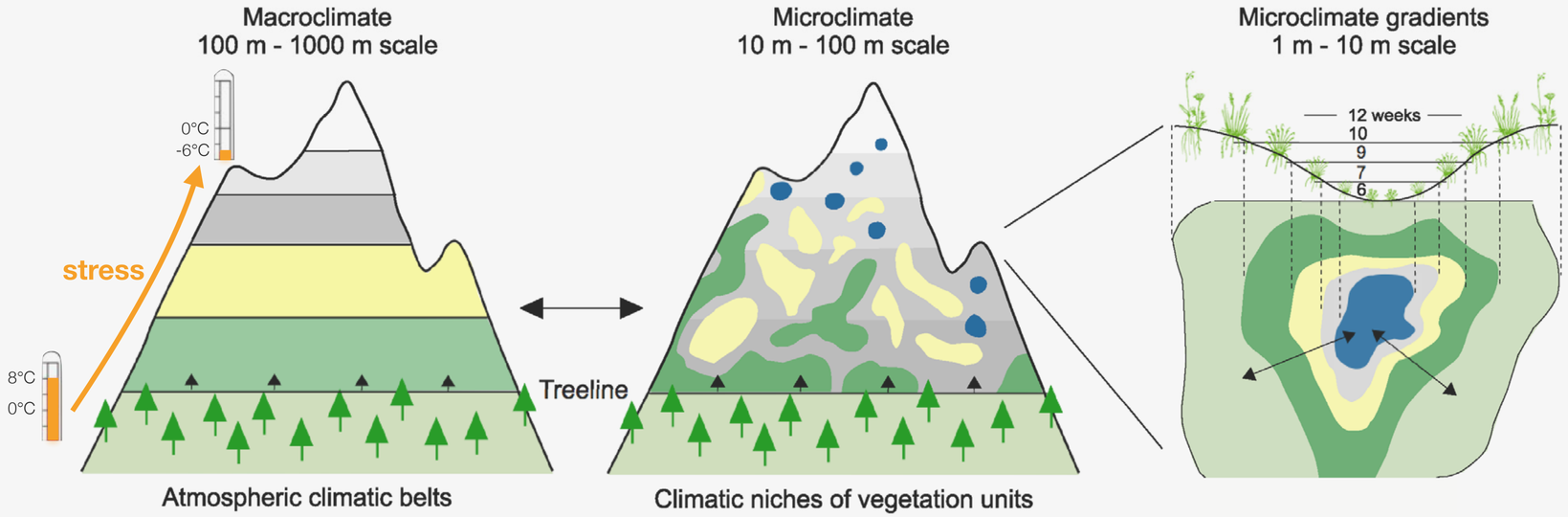
diversity

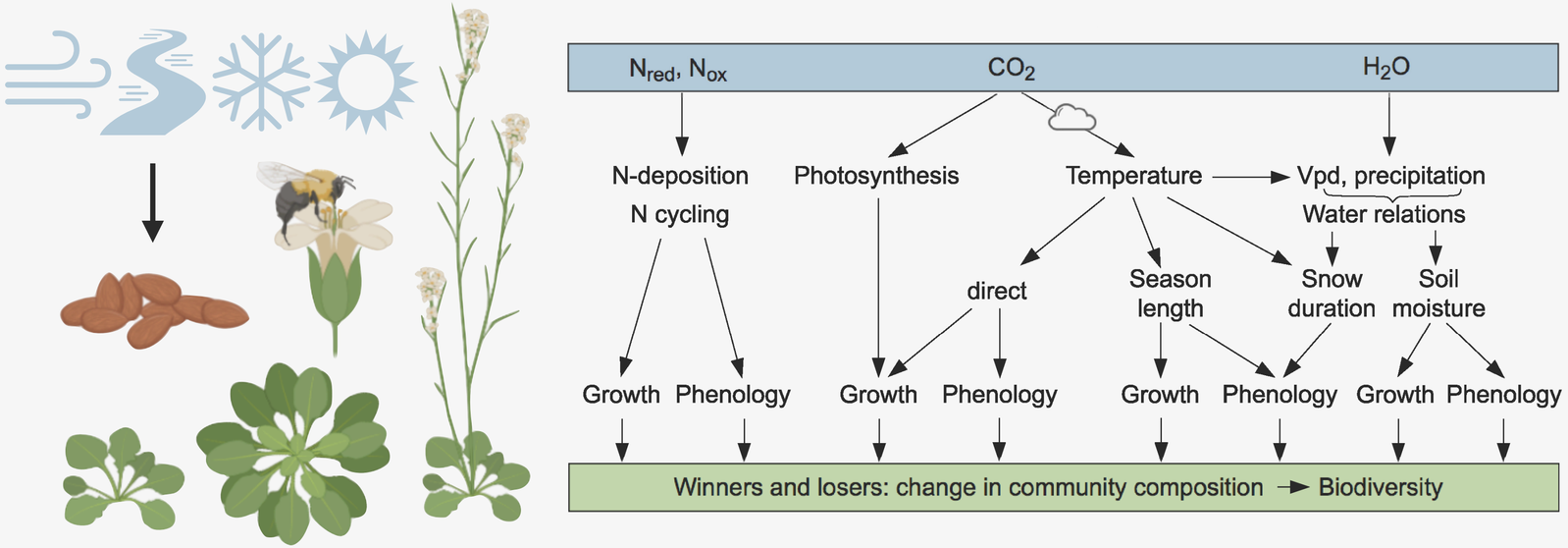
MDPI

Review

Why Is the Alpine Flora Comparatively Robust against Climatic Warming?

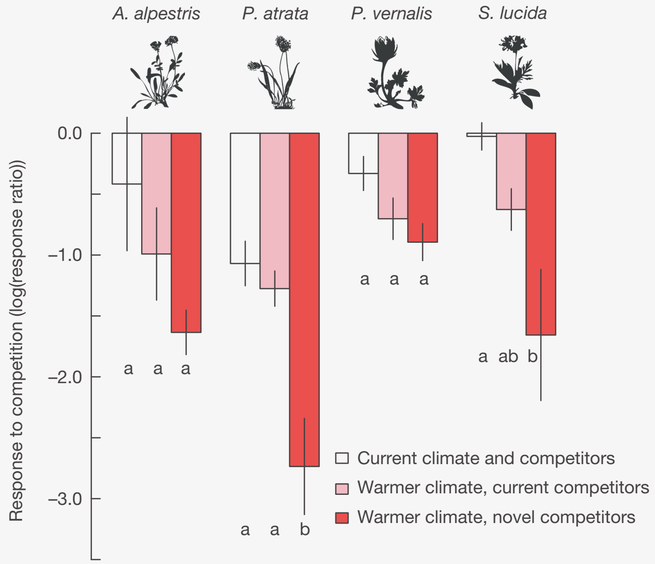
Christian Körner * and Erika Hiltbrunner

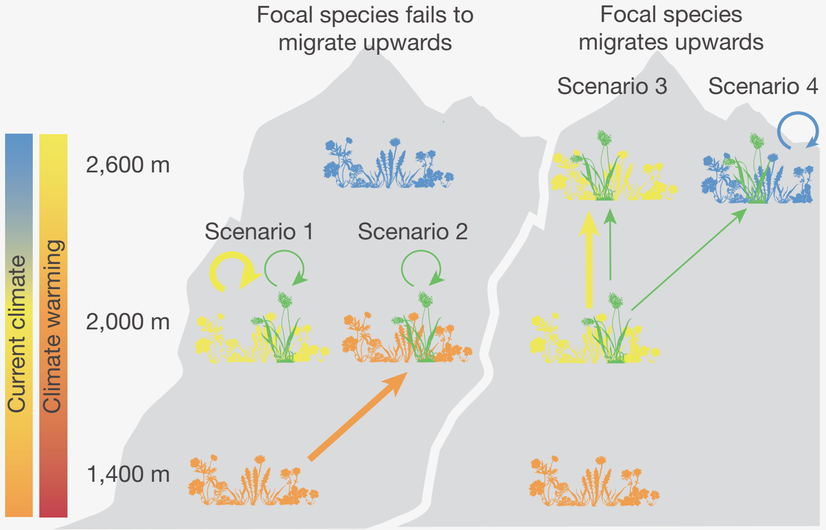




Effects on Alpine Plant Communities

life conditions for alpine plant communities create by climate and topography





LETTER

doi:10.1038/nature14952

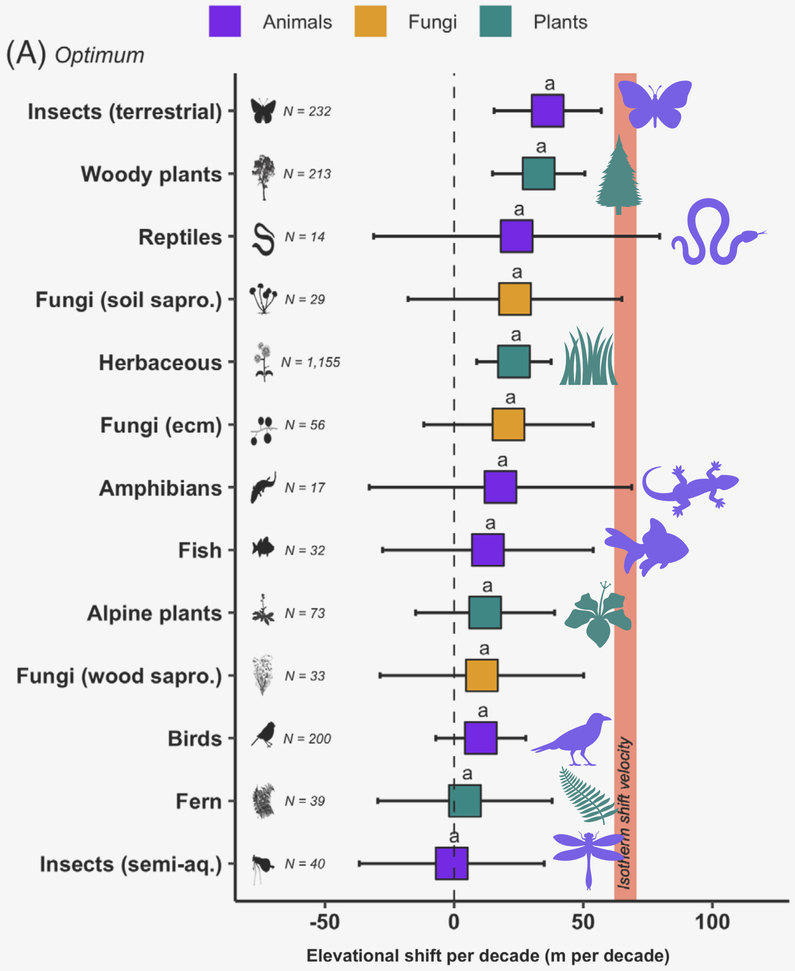
Novel competitors shape species' responses to climate change

Jake M. Alexander[1], Jeffrey M. Diez[2] & Jonathan M. Levine[1]

BIOLOGICAL REVIEWS
Cambridge Philosophical Society
Biol. Rev. (2021), pp. 000–000.
doi: 10.1111/brv.12727

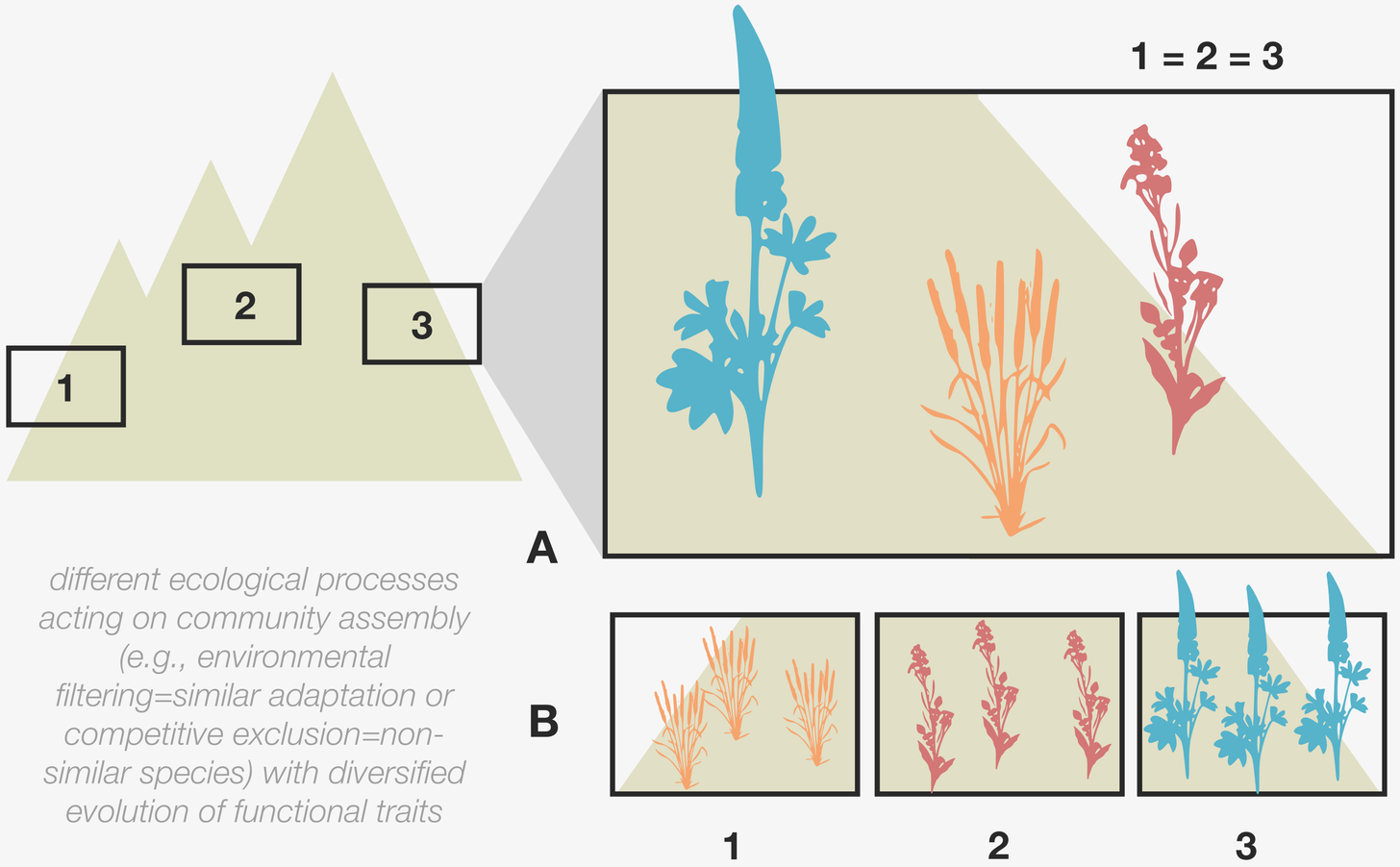
Phenological and elevational shifts of plants, animals and fungi under climate change in the European Alps

Yann Vitasse[1*], Sylvain Ursenbacher[2,3], Geoffrey Klein[1,4], Thierry Bohnenstengel[2], Yannick Chittaro[2], Anne Delestrade[5,6], Christian Monnerat[2], Martine Rebetez[1,4], Christian Rixen[7], Nicolas Strebel[8], Benedikt R. Schmidt[2,9], Sonja Wipf[7,10], Thomas Wohlgemuth[1], Nigel Gilles Yoccoz[11] and Jonathan Lenoir[12]

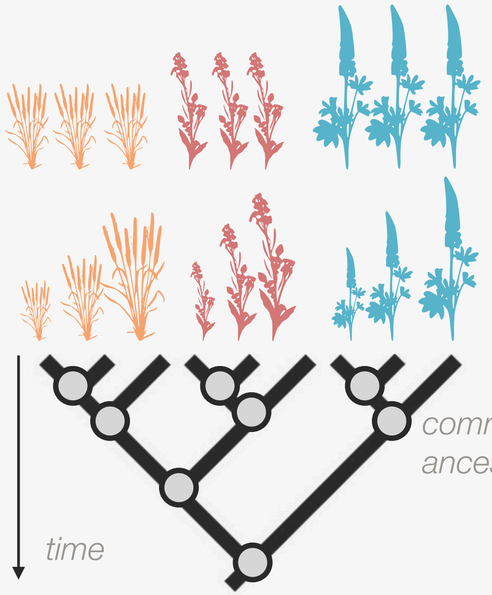


Effects on Alpine Plant Communities

Phenological and elevational shifts under climate change, depending on dispersal capacity and leading to new species composition (competition)



different ecological processes acting on community assembly (e.g., environmental filtering=similar adaptation or competitive exclusion=non-similar species) with diversified evolution of functional traits



C conserved trait

D convergent trait

phylogeny

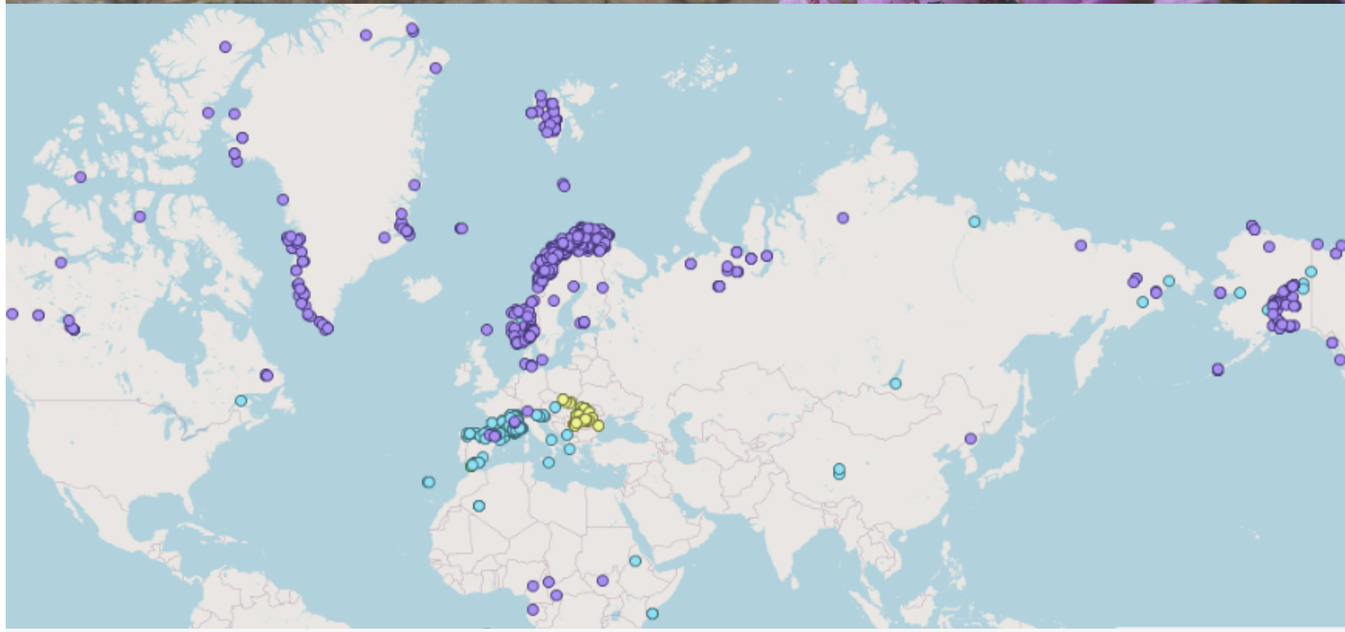
AC: competitive exclusion and conserved traits
AD: environmental fitering and convergent traits
BC: environmental filtering and conserved traits
BD: competitive exclusion and convergent traits

How to preserve it ?

understanding how plant communities are assembled (functional or phylogenetic diversity) is a paramount..

OriginAlps/Phylo[Alps/Norway] projects

understanding the evolutionary and ecologic assembly of the whole artico-alpine flora



PhyloAlps

PhyloCarpates

PhyloNorway

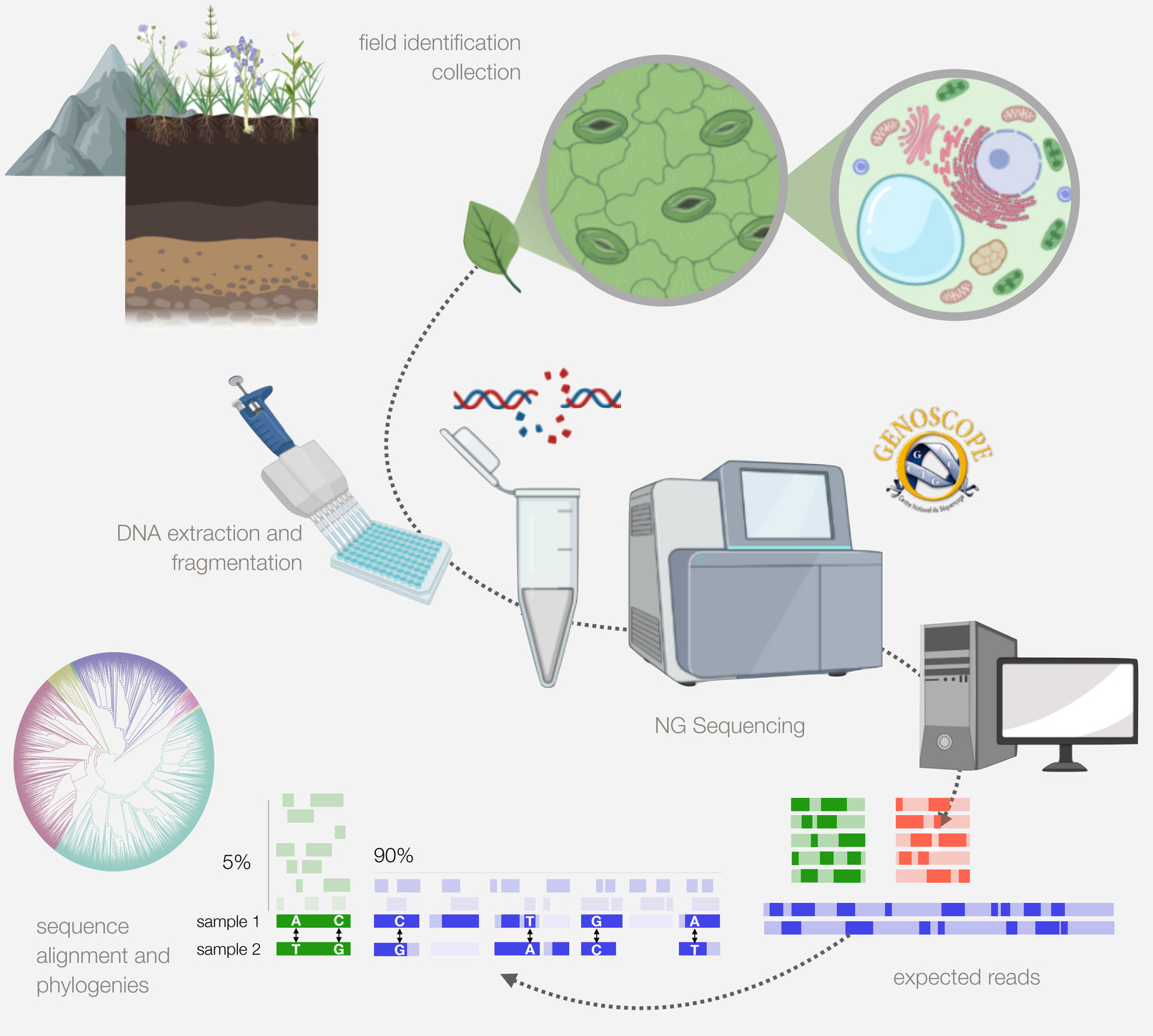
4726 samples (fresh)
4437 taxa

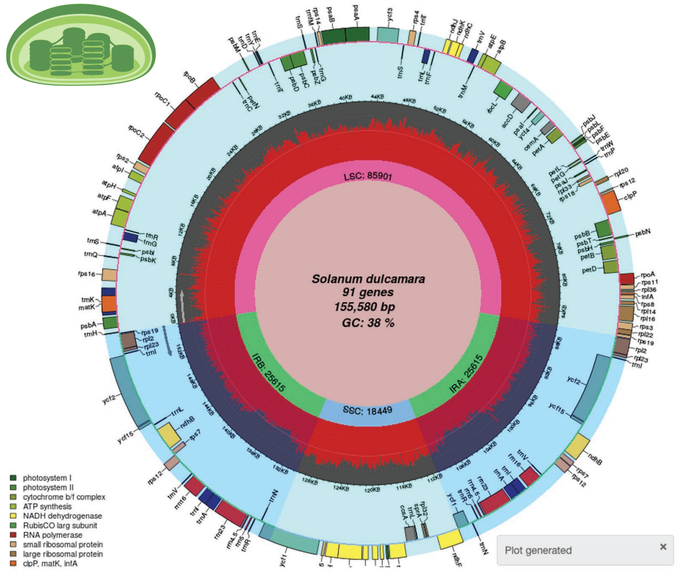
2091 samples (herbarium)
1899 taxa

6817 samples
5575 taxa
1037 genera
161 families

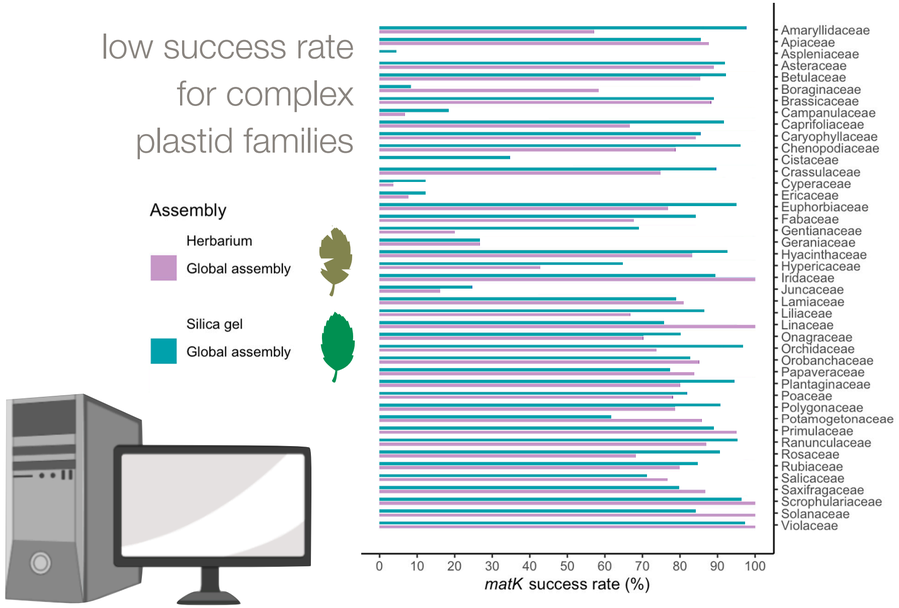
A Genome Skimming Approach

Whole genome sequencing at very low coverage sufficient to capture organelle genomes





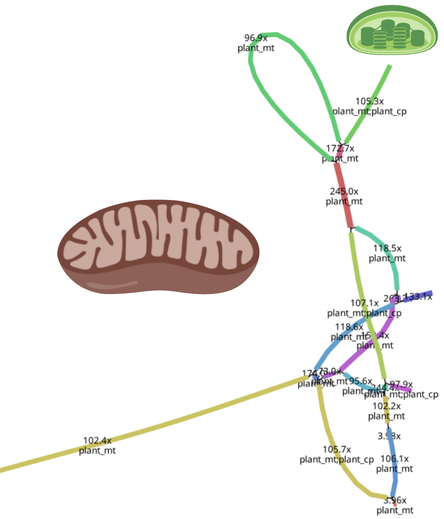
low success rate for complex plastid families



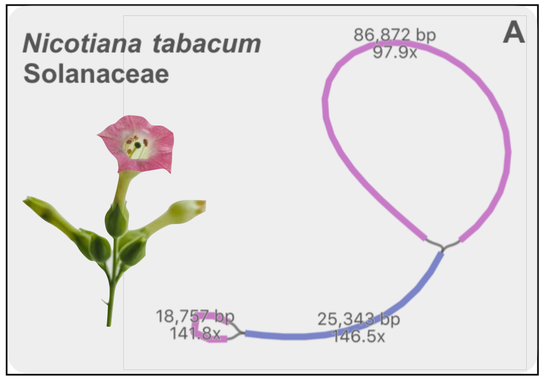
plants
MDPI
Article

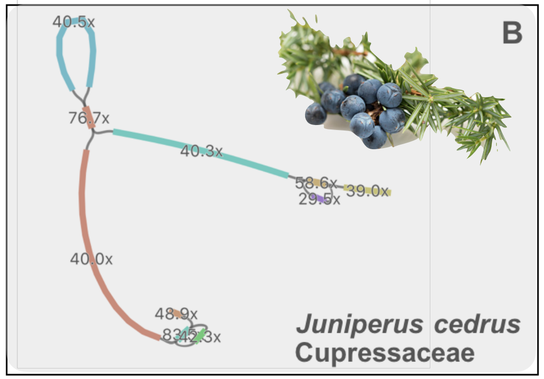
The Treasure Vault Can be Opened: Large-Scale Genome Skimming Works Well Using Herbarium and Silica Gel Dried Material

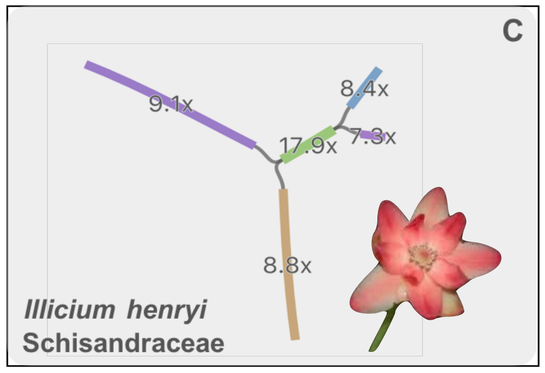
Inger Greve Alsos [1,*], Sebastien Lavergne [2], Marie Kristine Foreid Merkel [1], Marti Boleda [2], Youri Lammers [1], Adriana Alberti [3], Charles Pouchon [2], France Denoeud [3], Iva Pitelkova [1], Mihai Puşcaş [4], Cristina Roquet [2,5], Bogdan-Iuliu Hurdu [6], Wilfried Thuiller [2], Niklaus E. Zimmermann [7], Peter M. Hollingsworth [8] and Eric Coissac [2,*]

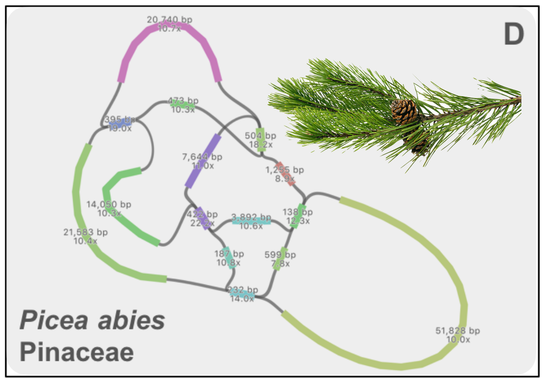


examples of assembly graphs for cpDNA and mtDNA genomes



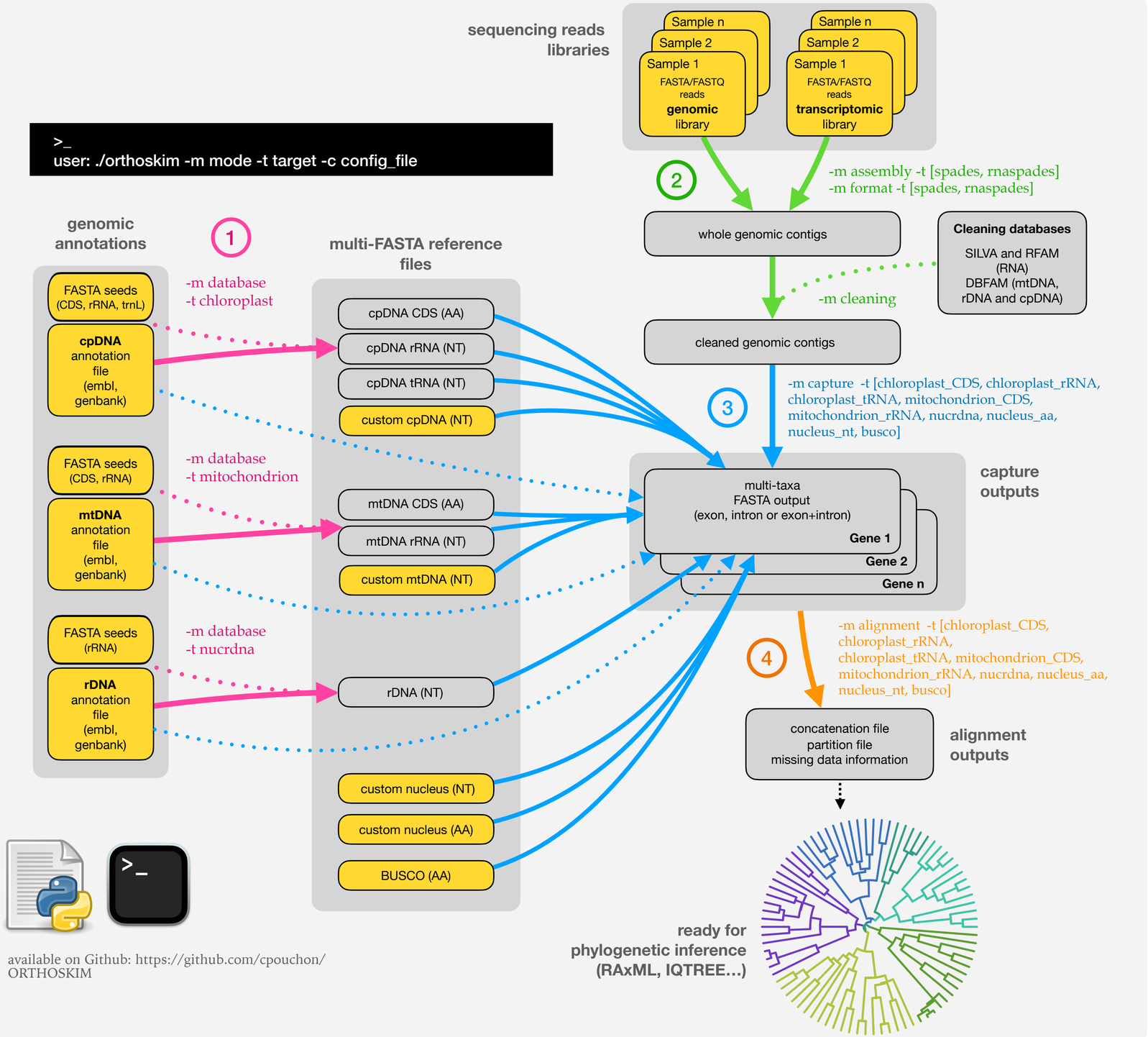






Bioinformatic Challenges I

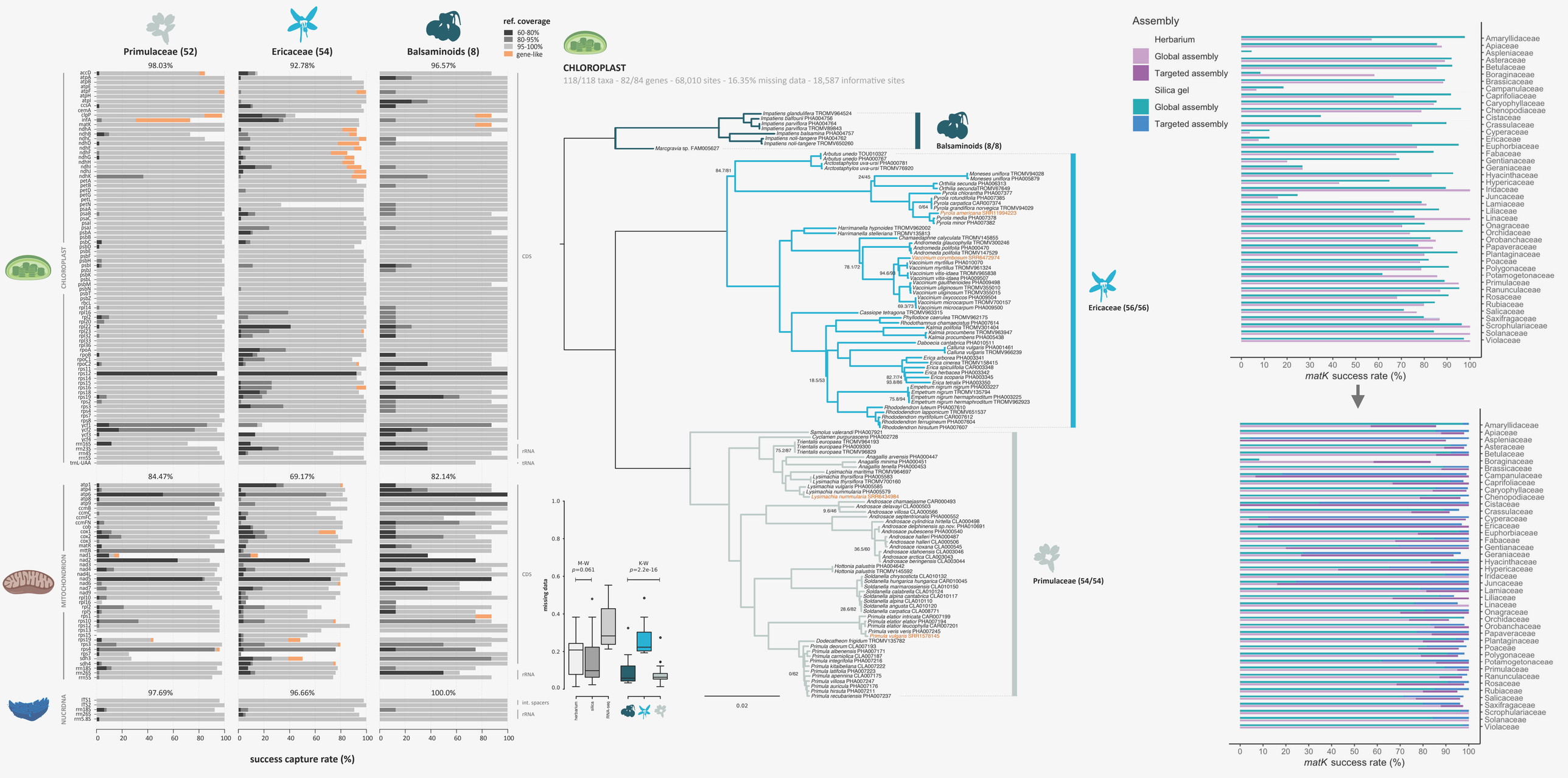
new computational tool need to overcome complex plastid structure, mtDNA assembly and organelle transfers issues using traditional assembler



available on Github: https://github.com/cpouchon/ORTHOSKIM

Bioinformatic Challenges I

development of ORTHOSKIM pipeline to perform *in silico* sequence capture (Pouchon et al. accepted.)



example of ORTHOSKIM capture and phylogenetic application

gene recovery using ORTHOSKIM

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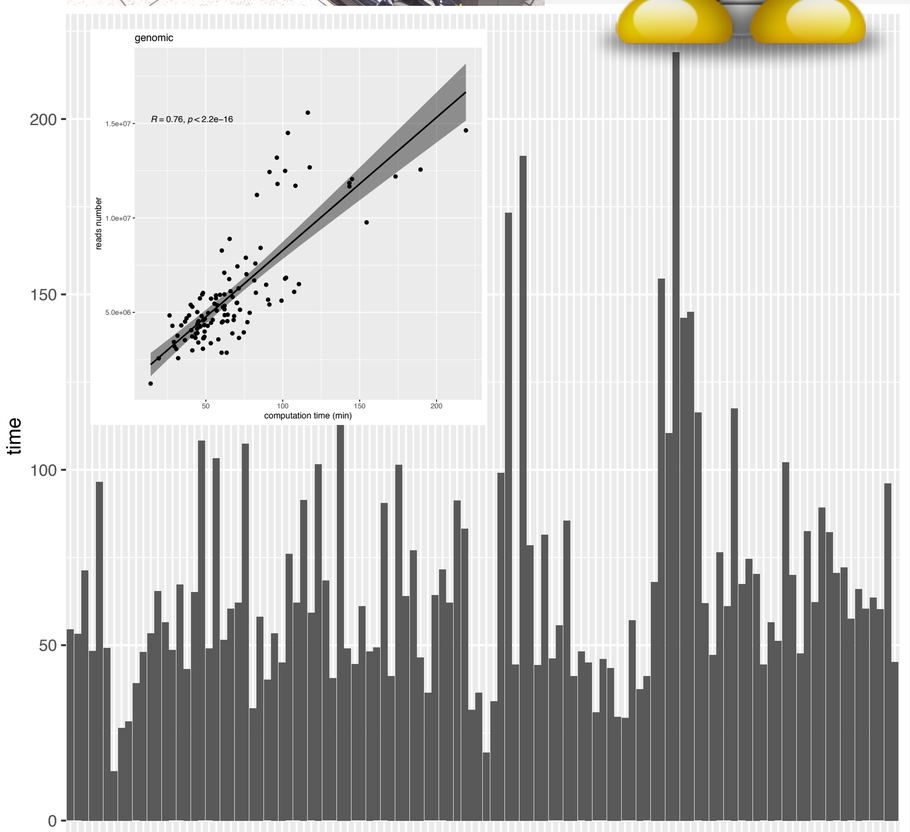
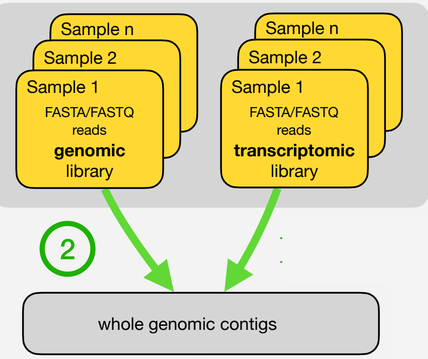
GRENOBLE ALPES RECHERCHE | INFRASTRUCTURE DE CALCUL INTENSIF ET DE DONNÉES

Bioinformatic Challenges II

high resource and computational time requirements

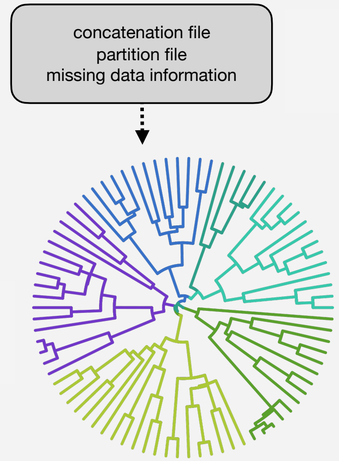
luke23: 20 CPUs, 128 Gb
luke49: 24 CPUs, 128 Gb





median assembly time : 1h:5m:0s (24 CPUs)/library

expected time for all libraries: 6943h:38m:30s ~ 290 days



phylogenetic inference time: **154h:3m:1s (24 CPUs) ~ 1 week**

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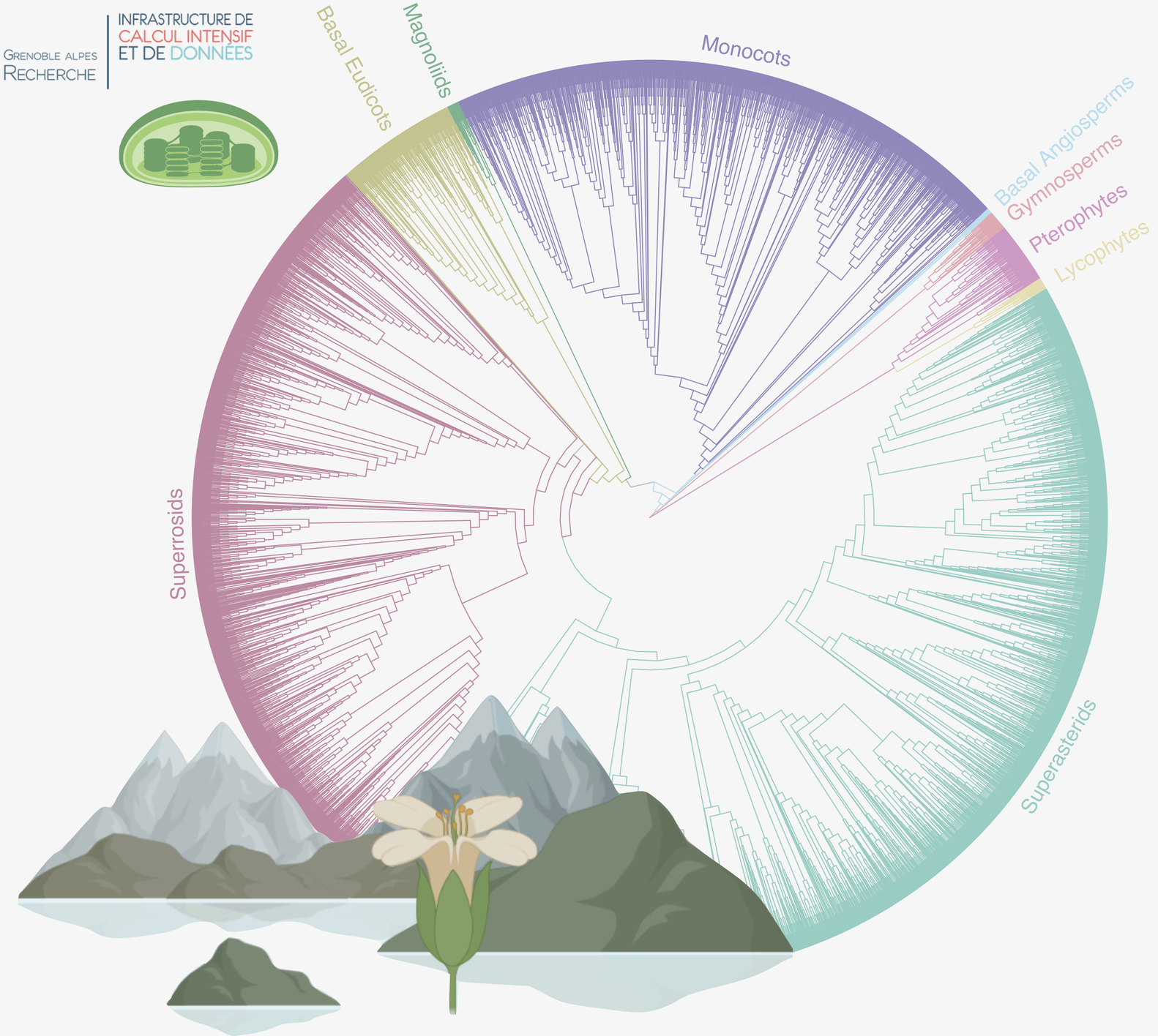
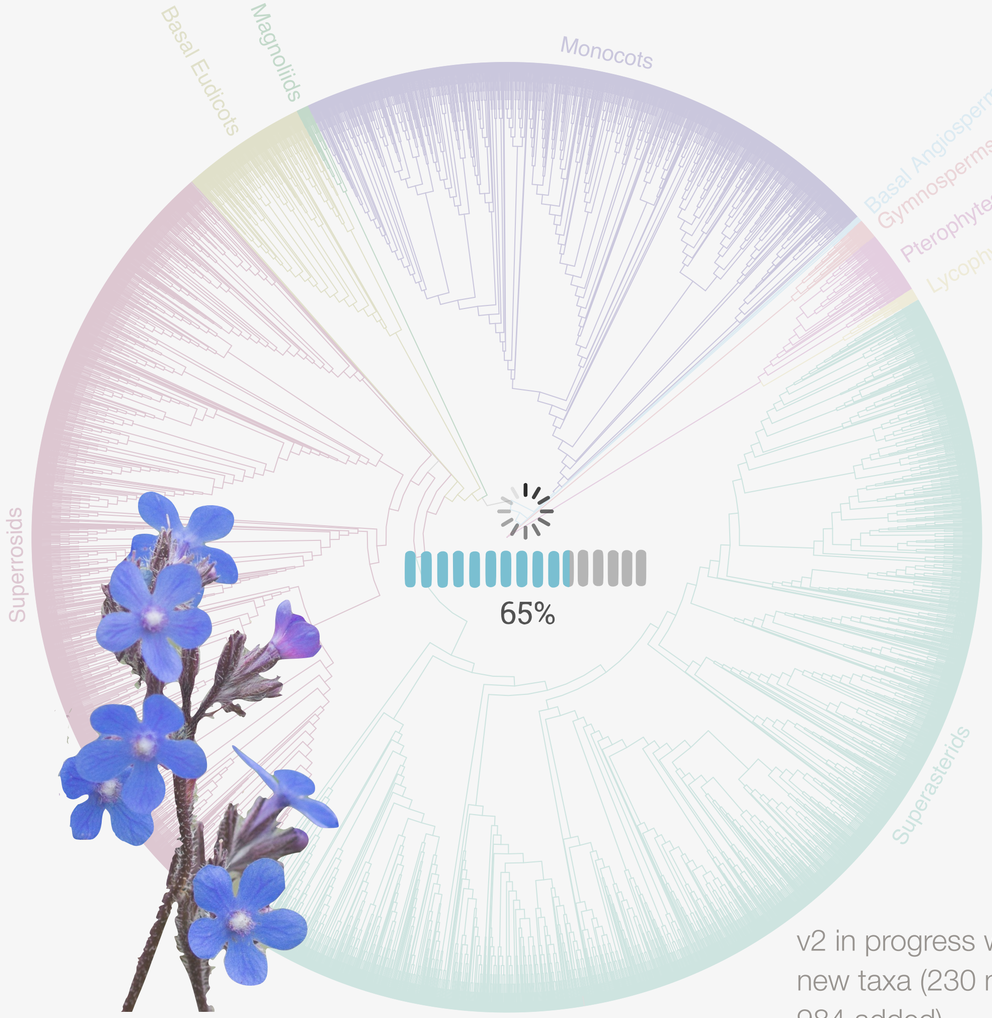
A First Phylogeny of a Whole Biogeographic Area

6986 taxa - 4,775 full cpDNA + 2,211 ORTHOSKIM) - 84 genes (79 CDS, 4 rRNA, trnL-UAA) - 62,049 Nt (49,660 informative; 9.05% missing)



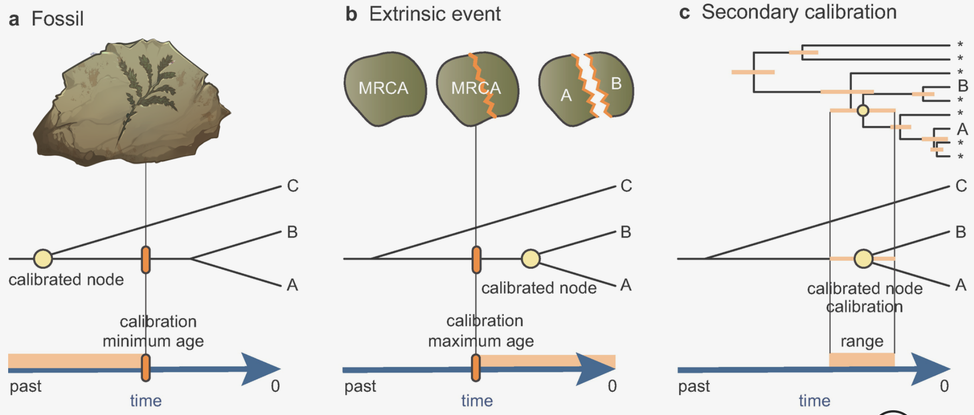


Anchusa italica Retz.

v2 in progress with new taxa (230 new + 984 added)

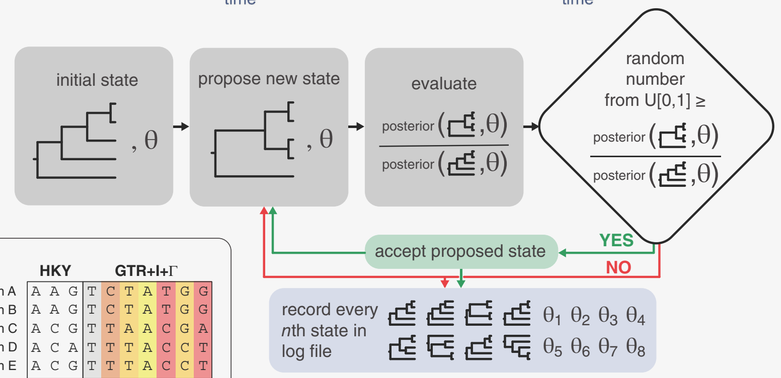
RefSeq

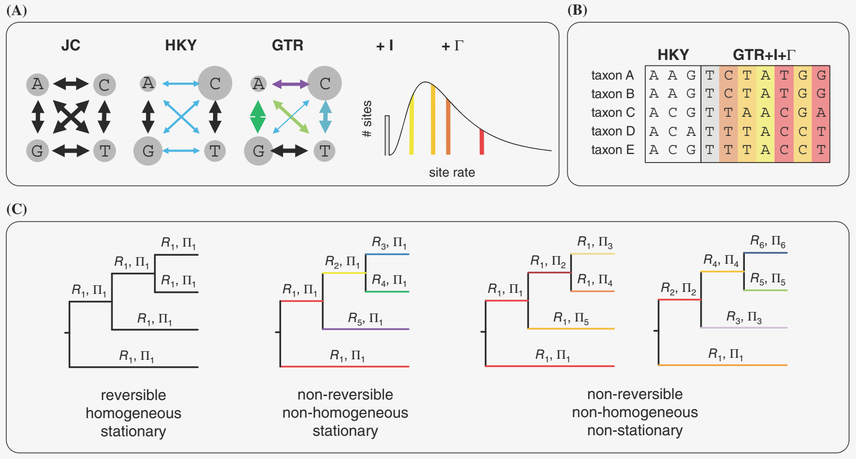
Calibration for molecular dating (fig from Magallón 2021) needs additional taxa (NCBI)



Beast2

Bayesian evolutionary analysis by sampling trees





Model of nucleotide substitution process (bottom left) and process of MCMC for bayesian molecular dating (top right) - Bromham et al. 2017

Where is it Going?

more data, more taxa and more complex models (phylogeny and dating): utopia vs reality (Dahu)?

Thank you

in behalf of the PhyloAlps consortium

Saxifraga oppositifolia (Galibier) - © C. Pouchon