Science
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Supplementary Materials for

Amphibian fungal panzootic causes catastrophic ~~unprecedented~~ and ongoing loss of biodiversity

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Materials and Methods

Other Supplementary Materials for this manuscript include the following:

Data S1 (Excel format)

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Materials and Methods

Compilation of declined-species dataset

Chytridiomycosis and amphibian declines

Chytridiomycosis is a lethal disease of amphibians that was discovered in 1998 (*4*). In amphibians, chytridiomycosis can develop from infection with one of two fungal species, *Batrachochytrium dendrobatidis* (described in 1999, *31*) or *B. salamandrivorans* (described in 2013, *5*). We identified chytridiomycosis-associated declines caused by infection with either *B. dendrobatidis* or *B. salamandrivorans*. We found evidence for the decline of only one amphibian species (*Salamandra salamandra*) associated with infection with *B. salamandrivorans*, and subsequently for convenience in the following Supplementary Materials, we focus on chytridiomycosis-associated declines resulting from infection with *B. dendrobatidis*.

Several previous efforts have attempted to quantify the number of amphibian species that have experienced declines associated with chytridiomycosis. First, the International Union for the Conservation of Nature (IUCN) Global Amphibian Assessment (GAA), conducted from 2001 to 2004, concluded that 202 amphibian species had experienced "enigmatic" declines, but did not directly attribute these declines to chytridiomycosis (*9*). However, the GAA was conducted when knowledge of chytridiomycosis and its impacts on amphibians was rudimentary. Building on the GAA, Skerratt et al. (*2*) used multiple lines of evidence to argue that *B. dendrobatidis* was the agent driving "enigmatic" declines identified in the GAA.

Since the 2001–2004 GAA, *B. dendrobatidis* has continued to spread into new regions (*6*) and understanding of chytridiomycosis and its impacts on amphibian hosts has greatly increased. For example, a search for "*Batrachochytrium dendrobatidis*" yields 40 results on the

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Web of Science from 2004 and earlier, but 1,258 results for 2005–2017. However, despite these advances, the scale and number of global amphibian declines associated with chytridiomycosis has yet to be empirically quantified, or examined in light of major developments in our understanding of this disease.

Identifying declined species

We developed an expert-curated list of species that have experienced declines associated with chytridiomycosis (a method analogous with the IUCN approach to evaluating conservation status). We used a two-step process to identify declined species. First, at a continental scale, we searched for evidence of amphibian declines associated with chytridiomycosis. This involved searching the scientific literature and discussions with amphibian experts. Second, if chytridiomycosis-associated declines were identified for a particular continent, we then engaged regional amphibian experts, generally at the country level, to thoroughly compile information on all chytridiomycosis-associated amphibian declines, using the framework and methods described below. Regional experts were chosen based on their professional experience in amphibian ecology in the region, and knowledge of chytridiomycosis. In the case of Asia, there was no evidence for chytridiomycosis-associated declines, and as such, further assessments of amphibians from that continent were not conducted. We acknowledge that this approach could fail to identify some very recent or only locally known declines. However, such cases are unlikely to substantially affect our analyses as existing knowledge would likely be insufficient to determine the role of chytridiomycosis in the decline.

Our focus was on identifying species that had experienced declines due to chytridiomycosis (as specified below), rather than on identifying species in which infection with

either *B. dendrobatidis* or *B. salamandrivorans* has been documented. This is an important distinction, as some amphibian species can be infected with either pathogen, but not experience morbidity or mortality (asymptomatic) or population declines (*7, 8*). The global database *B. dendrobatidis*-maps [http://www.bd-maps.net] provides information on species in which infections have been documented.

For the second step of our assessment conducted in 2017, we assembled a team of 41 researchers with expertise in both amphibian ecology and chytridiomycosis to undertake country-level assessments for 24 countries where there was evidence that chytridiomycosis has contributed to amphibian declines. Following the methodology of Scheele et al. (*32*), for each species, experts collated all available peer-reviewed articles, government technical reports, theses, conference proceedings, books, information from IUCN assessments, and unpublished data on species' status and trends recorded by amphibian ecologists. The scientific literature was searched through Google Scholar and ISI Web of Knowledge. Bibliographies of relevant papers were checked to identify further literature. Relevant information and sources underpinning the inclusion of each declined species in the dataset is provided in data S1. Prior to commencing their assessments, each expert thoroughly discussed the assessment methodology with the lead author (B.C.S.) to ensure consistent interpretation and implementation of the assessment framework.

Because initial outbreaks of chytridiomycosis occurred in many regions before its discovery, and many impacted amphibian species are difficult to observe and/or occur in remote habitats, quantifying the role of chytridiomycosis in declines is, for many species, challenging and retrospective. As such, we developed an epidemiological framework (see Metadata tab in data S1) to integrate all available evidence (including laboratory, experimental and field data) to

evaluate the severity, distribution, and timing of amphibian declines caused by chytridiomycosis. This approach of incorporating multiple lines of evidence is commonly used in health disciplines (*33*), has previously been applied to a continent-wide assessment of chytridiomycosis-associated declines (*32*), and uses published criteria (*2*) for determining disease causation in population declines.

We identified species that had undergone declines in abundance caused by chytridiomycosis. We define decline severity as the total estimated reduction (%) in abundance across a species' range, associated with chytridiomycosis. Most of the assessed species have undergone declines in both abundance and range. However, we elected to focus on changes in abundance because, in the context of chytridiomycosis, declines in abundance and range are often conflated due to environmental context influencing disease impacts, with range reductions cumulating from population extinctions driven by reductions in abundance.

Our quantification of *B. dendrobatidis*-associated declines is likely conservative for three main reasons. First, *B. dendrobatidis* has caused the decline of undescribed species, a phenomenon that might be particularly relevant in the Neotropics where there are many undescribed species (REFS). Second, species may have declined due to chytridiomycosis, but there is currently no evidence linking their decline to chytridiomycosis. In such cases, these species have not been included in our assessment. Third, the true extent of a species decline associated with *B. dendrobatidis* may be unrecognized. As such, species may be categorized in a less severe decline category because, while there is evidence for the role of *B. dendrobatidis* in the species' decline in parts of its range, declines in other parts of its range have not (yet) been attributed to *B. dendrobatidis*. Finally, declines could be under-documented in species with large

> **Comentado [BS1]:** (see the Panama study by Crawford et al., 2010 PNAS which found undescribed species were lost following a *Bd* outbreak)

ranges, due to logistical challenges associated with monitoring and surveying widely distributed species.

Declined species were grouped into five broad classes of severity: (1) minor decline <20% in abundance; (2) severe decline >20% but <90%; (3) extreme decline >90%; (4) presumed extinct in the wild (no known extant populations, and no individuals detected at known historical locations, but some reasonable doubt that the last individual has died); and (5) confirmed extinct in the wild (as per IUCN listing). Note that the class "Extinct" includes both "Extinct" and "Extinct in the Wild" sensu IUCN. For each declined species, we also assessed whether there was evidence for ongoing population declines due to chytridiomycosis (i.e. populations experiencing continued declines following the initial emergence of chytridiomycosis) (yes, no, unknown, not applicable [for presumed or confirmed extinct species]), and whether partial recovery of declined species had been observed (yes, no, unknown, not applicable [for presumed or confirmed extinct species]). Species were classified as experiencing ongoing decline if chytridiomycosis was causing continuing reductions in abundance after initial declines associated with chytridiomycosis outbreaks. Species were classified as experiencing partial recovery if increases in abundance were reported after initial declines caused by chytridiomycosis outbreaks. We report the year recovery commenced for populations of species subject to regular surveys. For species where signs of recovery have been reported, but the absence of regular surveys prevent identification of when recoveries commenced, we provide the first year that recoveries were reported. No date is provided when precise information is unavailable. We note that a high degree of caution is needed in interpreting information on species recovery. In many cases, declined species have only shown signs of recovery in some populations, and in generally still have greatly reduced abundance

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compared with historical levels. Detailed examples of how declines were categorized for eight species with varying decline severities are provided in the 'Worked_examples' worksheet in data S1.

Timing of species declines

Species were assigned either a year of decline commencement (n = 104), or if this was not known, an uncertainty interval during which the decline was thought to have occurred (n = 345). If known, experts provided the year that decline commenced. If the year was unknown, experts estimated a range of years during which the decline could have occurred, or provided a year which could be indirectly related to the timing of decline (e.g. the last year the species was observed as abundant, or the first year that observations were made of populations post-decline (*24*). In such cases, we represented uncertainty by defining an interval of years. Intervals were either provided directly by experts, or where experts provided only a start- or end-year for decline, we conservatively assumed a ten-year interval, respectively, before or after the stated year. For some Mesoamerican species (particularly in Panama), rather than an interval, the contributors provided temporal information about the first detection of *B. dendrobatidis* in different areas of the region, and based on that information, we inferred the period during which decline might have occurred as a five-year interval on both sides of the first known detection of *B. dendrobatidis* within the range of the species, based on the IUCN distribution maps (*34*). In total, information about the timing of declines was available for 449 species out of 501 in our dataset. Species for which no data about the timing of declines were available (n = 52) were excluded from later statistical models (Timing of declines and Predictors of declines and recoveries below). In those models, each species was assigned a single year of decline, to avoid

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overrepresentation of species with longer uncertainty intervals. For species with a two- or three-year interval, we used the first and middle year respectively. Where the uncertainty interval of the timing of decline was longer than three years, we drew a random year within that interval to avoid systematic bias towards the beginning, mid- or endpoints of the interval.

Evidence for the role of chytridiomycosis in species declines

For each declined species, assessors evaluated the following: 1) Was *B. dendrobatidis* diagnosed using histopathology and/or PCR to confirm infection during mass die-offs or sudden declines? 2) Did declines coincide with the documented emergence and spread of *B. dendrobatidis* in the region? 3) Is the declined species highly susceptible to *B. dendrobatidis* in laboratory experiments (i.e. >75% individuals die post exposure in the laboratory) or demographic field studies? 4) Did sympatric species decline simultaneously due to *B. dendrobatidis?* For each question, species were assigned 'yes', 'no', or 'no data'. The strength of evidence linking *B. dendrobatidis* to each species decline was then scored from one to four, with four being the strongest evidence of *B. dendrobatidis*-associated declines. One = expert opinion of the assessor only. Two = single line of correlative evidence. Three = multiples lines of correlative evidence. Four = robust before-after decline sampling demonstrating declines were caused by *B. dendrobatidis*.

<u>Statistical analyses</u>

We used generalized linear models to assess the temporal trend in the overall number of declines, in the severity of those declines, and in the probability of a species' recovery. We also sought to identify attributes of species distributions (e.g. range size, climatic region, elevation)

and life-history traits that were associated with decline severity and recovery. We selected these variables based on previous work on extinction risk in vertebrates (*35*), life-history traits previously linked to chytridiomycosis-associated declines (*10, 11, 36*), as well as known bioclimatic preference of *B. dendrobatidis* (*8, 37, 38*). All models described below were fit in JAGS (*39*), using uninformative priors for all parameters, and run for 150,000 iterations on three Markov chains, with a burn-in of 75,000 and a thinning rate of 10. Convergence was assessed by visual inspection of the chain histories and using the *R*-hat statistic.

Timing of declines

First, we modelled the temporal trend in the overall number of declines. As outlined above, we associated each species with a year of decline (as explained in section 'Timing of species declines' above). For each year between 1970 (the earliest year in our dataset) and 2016, we counted the number of species that had that year as the stated or inferred year of decline and used this as a Poisson-distributed response variable, with year of decline as a predictor.

We compared three alternative functions: null (constant number, i.e. no temporal trend), linear (constant increasing or decreasing trend in the number of declines) and quadratic (to reflect an initial increase, followed by a decrease in the number of declines). Given the simple structure of the models, we compared models on the basis of the coefficient estimates and discarded terms for which the 95% credible interval of the posterior distribution of the regression coefficient encompassed zero (analogous to failure to reject the null hypothesis with $\alpha=0.05$ if working with a null hypothesis significance test). Results are summarized in Table S1.

We also modelled the severity of individual declines as a function of time. Because severity was a categorical variable, ordered from 1 to 5, we used a multinomial logit link

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regression with year of decline, defined as above, as a predictor (moderator). The output of the model can be interpreted as the probability that a species falls in a given severity class. Consequently, a positive coefficient for time (year) would indicate that species with later declines were more likely to suffer more severe impacts. To account for the varying degree of evidence supporting the decline of each species, we took an approach analogous to a meta-analysis (*13*). We defined the prior variance of the linear estimator for the multinomial probability of a species falling in a higher severity class as a function of the corresponding amount of evidence (1, 10, 100 and 1000 for the four levels of evidence from highest to lowest— see *Evidence for the role of chytridiomycosis in species declines*). We added a random effect to account for taxonomic autocorrelation (using the genus of each species as a blocking factor, nested within its family).

We also modelled species recovery (yes/no) using logistic regression and year of decline as a predictor, following the same procedure as above. Here, a negative regression coefficient would suggest species with earlier declines were more likely to have recovered (as expected if there was a time lag between decline and recovery). We excluded species from this analysis if they had gone extinct or if there was no data on population trajectory after the initial decline, leading to a final set of 254 species (including 59 known recoveries).

Finally, visual analysis of the dataset also led us to hypothesize that declines (particularly less severe ones) may have been under-reported or supported by less evidence before 1975. Therefore, we repeated all analyses described below selecting only those species for which the exact or inferred year of decline was 1975 or later. All results were confirmed with and without pre-1975 data.

Predictors of declines and recoveries

We sought to identify factors that explained the severity of declines and the probability of species recovery. With severity of decline (1 to 5) and recovery (yes/no) as the respective response variables, we used the same model formulations as above, respectively, multinomial and logistic regression. For severity of impact, we again used the level of evidence to weigh the prior variance of the linear predictor. For both analyses, we again added a random effect at the genus and family level to account for taxonomic autocorrelation.

We began the analysis for severity with a full model that included 10 covariates, selected on the basis of data availability, hypotheses about host and pathogen ecology, and preliminary visual analysis of the data (see next paragraph for detailed descriptions). The 10 covariates were: (1) Geographic range, expressed as the $\log_{10}$ of the extent of the species range in km^2; (2) Latitude, calculated as the absolute value for the centroid of the species' distribution; (3) Mean elevation across the species range (included because it is associated with a range of factors that may either affect suitability for *B. dendrobatidis*, such as temperature and precipitation, or host characteristics that may affect vulnerability to declines, such as lower connectivity in high elevation species and increased age to maturity (refs); (4) Elevational range, expressed as the $\log_{10}$ of the difference between the maximum and minimum elevations across the species' range; (5) Body size, expressed as the $\log_{10}$ of the mean snout-to-vent length for the species; (6) Clutch size, expressed as the $\log_{10}$ of the average number of eggs/offspring for the species; (7) Three variables describing association with aquatic habitat: use of aquatic habitat (1 if adults of the species use aquatic habitats for at least part of the year, 0 for species fully terrestrial as adults), association with permanent water bodies, and direct development (note that because these three variables were highly correlated with each other (Pearson's $r > 0.5$, see below), only one was

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included in the model at a time); (8) Activity pattern of the species (0 for nocturnal species, 1 for all other species not strictly nocturnal); (9) Maximum temperature of the warmest month, averaged over the species range from BIOCLIM05 variable (*40*); and (10) Precipitation of the driest quarter of the year, averaged over the species range from the BIOCLIM17 variable (*40*). Another 20 additional variables potentially associated with chytridiomycosis were discarded after preliminary modelling and visual analysis (clear absence of visual patterns when plotted, large credible intervals for regression coefficients centered close to zero), leaving the 10 listed above as the set we analysed in detail. These discarded variables included environmental specialization, expressed as the number of environments (arid, temperate, sub-tropical, tropical, sub-alpine, alpine) where the species is known to occur, habitat topography, additional reproductive modes such as use of bromeliads, lakes, wetlands or terrestrial clutches, all BIOCLIM variables other than BIO05 and BIO17, including maximum and minimum annual temperature and precipitation as well as seasonality patterns. The final set of 10 variables covered a wide range of ecological hypotheses about chytridiomycosis-related declines (see below).

Species distribution maps were obtained from the IUCN Red List of Threatened Species (*12*), from which the geographical range was calculated in ArcGIS 10.1. Minimum and maximum elevations used to acquire elevational ranges (with median elevation calculated as the midpoint) were obtained from species-specific online IUCN Red List accounts. Body size and clutch size were extracted from the AmphiBIO database (*41*) and were included to reflect life history strategies. Data about association with aquatic habitat were provided by contributors of our dataset and were included to reflect the previously demonstrated link between *B. dendrobatidis*-driven declines and aquatic habitats (*11, 42*); activity patterns of the species were

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compiled from AmphibiaWeb (*43*) and Stuart et al. (*44*), and were included due to the

thermoregulatory behavior of some species that can inhibit *B. dendrobatidis* growth (*45, 46*).

Finally, averaged temperature and precipitation data spanning each species' range were obtained

from the corresponding BIOCLIM variables of the WorldClim 2 dataset (*40*) at 30 arc second

(±1x1 km) resolution, calculated across the IUCN Red List distribution maps in ArcGIS 10.1.

We chose the BIOCLIM05 and 17 variables to reflect whether, within a species range, part of the

year was especially unsuitable for *B. dendrobatidis* persistence and growth, due to a marked dry

and/or warm season. We also evaluated interaction terms between environmental (BIOCLIM)

and elevation/range covariates. Finally, we added to the initial model a covariate for year of

decline where the previous analysis (see above) suggested a significant relationship between time

of decline and severity/recovery. For recovery, given the smaller initial dataset, we fitted the

initial model with a subset of these variables, following the rule of thumb of at least ten

observations in the less represented class (recovery yes/no) for each predictor, and assessing all

possible combinations of covariates within that constraint. Because species that have experienced

very large declines are unlikely to recover for demographic reasons, we excluded from the

analysis all species known or presumed extinct, for which recovery would be impossible by

definition, and included an additional predictor to reflect such small-population bottlenecks (0 if

the species suffered a decline > 90%, and 1 otherwise). This allowed us to account for

demographic barriers to recovery, and identify environmental and life history correlates of

recovery among species that may have remained unaffected by such barriers.

Preliminary analysis confirmed that correlation between pairs of predictors did not

exceed $r = 0.5$, except for the three variables describing association with aquatic habitat, of

which only one at a time was included in models. In particular, we noted that median elevation

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and elevational range of species had a Pearson's correlation of $r = 0.01$, allowing the inclusion of both variables in the models. We centered all continuous variables by subtracting their mean to improve convergence. Rather than using complex imputation techniques, for each combination of covariates we removed species for which values of at least one covariate were missing. We fit the model in JAGS using the settings and convergence diagnostics described above. We then progressively simplified the model by removing covariates for which the 95 % credible interval of the posterior distribution of the regression coefficient encompassed zero (analogous to failure to reject the null hypothesis with $\alpha = 0.05$ if working with a null hypothesis significance test). As a covariate was dropped from the model, we added back to the data set any species that had been removed because they missed a value for that covariate, after confirming there was no taxonomic or geographic bias in species that were added at a later stage. When two or more covariates had to be removed, we removed one at a time, beginning from the covariate with the smallest available sample size. Because the three variables describing association with aquatic habitat were highly correlated, only one was included in the model at a time, so we repeated the entire process for each of them. For decline severity and recovery, respectively, the full models contained 102 and 84 species (mostly reflecting limited information about body size and clutch size). As explained above, in the multinomial logistic regression for severity of decline, a positive coefficient for a given covariate would indicate that species with higher values of that covariate (e.g. larger body size) were more likely to be classified in a higher severity class. In the logistic regression for recovery, a positive coefficient would indicate that species with higher values of that covariate were more likely to have recovered from the decline. Results are summarized in Tables S2-S3.

We also evaluated the realized effect of each covariate on the response variable, calculating the multiplicative effect size of covariate i as the product of the estimated regression coefficient by the range of that covariate in the dataset: $E_i = e^{\beta_i(max_i - min_i)}$. Multiplicative effect sizes indicate how much the odds of the response variable (i.e. being classified in a higher severity of decline or having recovered from decline) increase or decrease across the observed range of the covariate: values greater and smaller than one indicate positive and negative effects respectively, while a value of one suggests no effect. Figure S2 illustrates the cumulative effect sizes for all predictors of decline severity (Figure S2A) and recovery (Figure S2B).
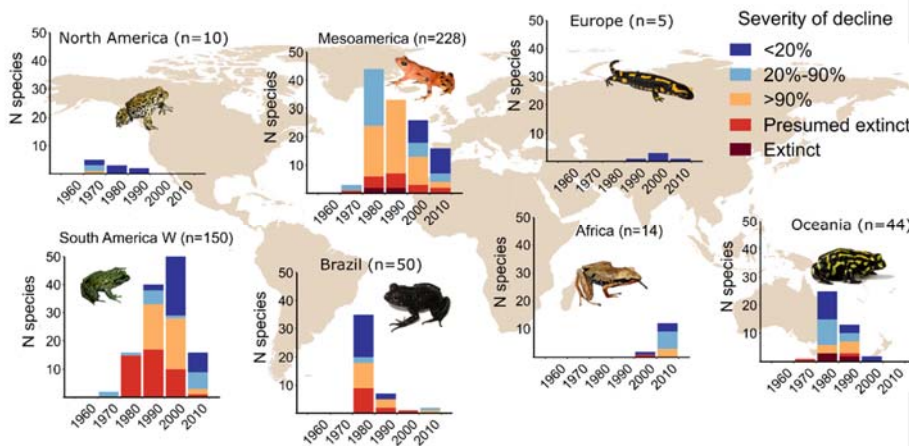
Figure S1. Timing of species declines by geographic area. Bars indicate the cumulative number of declines in a given year, stacked by decline severity and grouped by decade for readability. For species in which the exact year of decline is uncertain, the figure uses the middle year of the interval of uncertainty, as stated by experts or inferred from available data. Brazilian species are plotted separately from all other South American species (South America W); Mesoamerica includes Central America, Mexico and the Caribbean Islands; Oceania includes Australia and New Zealand. No declines have been reported in Asia. [Photo credits (left to right): *Anaxyrus boreas*, Chris Brown; *Telmatobius sanborni*, Ignacio De la Riva; *Atelopus varius*, Brian Gratwicke; *Cycloramphus boraceiensis*, L. F. Toledo; *Cardioglossa melanogaster*, Mareike Hirschfeld; *Salamandra salamandra*, Didier Descouens; *Pseudophryne corroboree*, Corey Doughty].
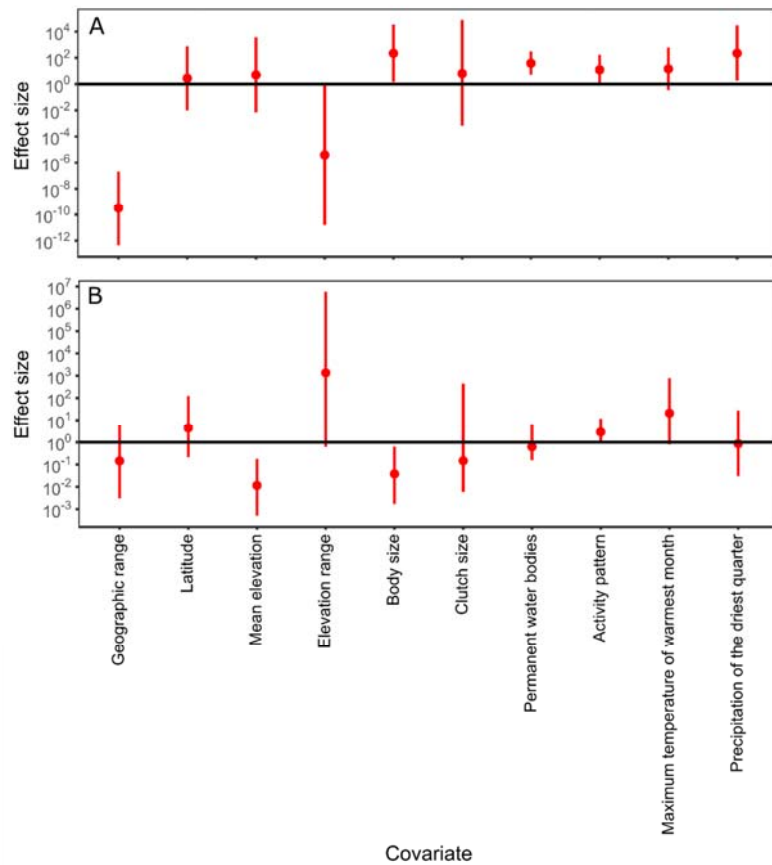
Figure S2. Multiplicative effect sizes for predictors of (A) severity and (B) recovery. Values greater and smaller than one indicate positive and negative effects respectively; a value of one (horizontal line) suggests no effect. Values are calculated from the ranges and coefficients in Tables S2 and S3. Bars indicate 95% credible intervals.

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Table S1. Summary of modelling results for the timing of species declines. Estimates refer to the mean estimate of the regression coefficients for each model, respectively, intercept α, linear term β_{time} and quadratic term β_{time2} (95% credible intervals in parentheses). "Retained" refers to whether the variable was retained as significantly influencing the severity of declines (when the 95% credible interval of the regression coefficient's posterior distribution did not encompass zero).

Model	**Mean β (95% CRI)**	Retained
Total number of declines (n=449)		
Decline ~ .	α = 2.25 (2.16,2.34)	No
Decline ~ time	α = 2.53 (2.35, 2.71) β_{time} = -1.13 (-1.84, -0.41)	No
Decline ~ time^2	α = 1.28 (0.94, 1.59) β_{time} = 14.37 (11.33, 17.51) β_{time2} = -34.88 (-41.86, 28.19)	Yes
Severity of decline (n=449)		
Severity ~ .	α = -1.46 (-7.08, 3.79)	No
Severity ~ time	α = -1.32 (-6.08, 4.02) β_{time} = -9.65 (-15.36, -3.96)	Yes
Severity ~ time^2	α = -0.17 (-6.04, 4.75) β_{time} = -9.04 (-18.37, 0.31) β_{time2} = -0.84 (-17.46, 15.68)	No
Recovery (n=254)		

Recovery ~ .	α = -1.86 (-3.05, -0.92)	No
Recovery ~ time	α = -0.86 (-2.15, 0.33) β_{time} = -5.45 (-10.14, -1.04)	Yes
Recovery ~ time^2	α = -1.13 (-2.52, 0.15) β_{time} = -1.85 (-10.12, 6.19) β_{time2} = -8.49 (-24.56, 7.55)	No

Table S2. Summary of results for predictors of the severity of species declines. "Range" refers to the range of a variable in the largest analysed dataset (all continuous variables were centred and modelled on the $\log_{10}$ scale). "β" refers to the mean estimate of the regression coefficient for each variable (95% credible intervals in parentheses). "Sample size" refers to the size of the largest fitted dataset which included the variable. "Retained" refers to whether the variable was retained as significantly influencing the severity of declines (when the 95% credible interval of the regression coefficient's posterior distribution did not encompass zero).

Variable	Range ($\log_{10}$)	Mean β (95% CRI)	Sample size	Retained
Geographic range (km^2)	-5.04, 3.36	-2.60 (-3.39, -1.83)	297	Yes
Latitude	-1.58, 0.62	0.46 (-2.12, 3.01)	217	No
Mean elevation (m asl)	-1.24, 0.61	0.87 (-2.69, 4.46)	217	No
Elevation range (m)	-4.84, 0.70	-2.25 (-4.49, -0.03)	297	Yes
Body size (SVL in mm)	-0.55, 0.77	4.09 (0.28, 7.93)	297	Yes
Clutch size (n)	-1.50, 1.97	0.53 (-2.10, 3.25)	102	No
Permanent water bodies (yes/no)	0, 1	3.66 (1.64, 5.72)	297	Yes
Activity pattern (strictly nocturnal yes/no)	0, 1	2.5 (-0.26, 5.15)	217	No

Maximum temperature of warmest month (C)	-0.27, 0.15	6.35 (-2.55, 15.26)	297	No
Precipitation of the driest quarter (mm)	-1.26, 0.88	2.53 (0.28, 4.81)	297	Yes

Table S3. Summary of results for predictors of species ~~declining from~~ recovery (yes/no). "Range" refers to the range of a variable in the largest analysed dataset (all continuous variables were centred and modelled on the $\log_{10}$ scale). "β" refers to the regression coefficient for the variable (on the $\log_{10}$ scale for continuous variables). "Sample size" refers to the size of the largest fitted dataset which included the variable (number of known recoveries in parentheses). "Retained" refers to whether the variable was retained as significantly influencing the ~~severity of declines~~probability of recovery.

Variable	Range	Mean β (95% CRI)	Sample size	Retained
Geographic range (km^2)	-11.86, 7.47	-0.10 (-0.30, 0.09)	209 (50)	No
Latitude	-1.60, 0.62	0.67 (-0.70, 2.18)	210 (48)	No
Mean elevation (m asl)	-1.06, 0.49	-2.88 (-4.90, -1.10)	164 (41)	Yes
Elevation range (m)	-2.89, 0.83	1.94 (-0.13, 4.19)	164 (41)	No
Body size (SVL in mm)	-0.46, 0.77	-2.66 (-5.19, -0.37)	164 (41)	Yes
Clutch size (n)	-1.52, 1.85	-0.57 (-1.52,1.81)	84 (28)	No
Permanent water bodies (yes/no)	0, 1	-0.47 (-0.87, 1.87)	164 (41)	No
Activity pattern (strictly nocturnal yes/no)	0, 1	1.07 (0.05, 2.46)	154 (37)	Yes

Maximum temperature of warmest month (C)	-0.66, 0.32	3.10 (-0.24, 6.81)	158 (40)	No
Precipitation of the driest quarter (mm)	-1.30, 0.87	-0.07 (-1.61, 1.52)	158 (40)	No

Table S4. Complete legend of taxonomic groups as indicated in Figure 2 (main text).

Order	Family	Genus	Species	Severity	Recovery
Anura	Alsodidae	Alsodes	*Alsodes tumultuosus*	1	no
	Alytidae	Alytes	*Alytes muletensis*	1	yes
			Alytes obstetricans	1	unknown
		Discoglossus	*Discoglossus sardus*	1	unknown
	Aromobatidae	Allobates	*Allobates alessandroi*	3	no
			Allobates capixaba*	3	yes
			Allobates olfersioides	4	n/a
			Allobates talamancae	2	unknown
		Aromobates	*Aromobates meridensis*	3	no
		Mannophryne	*Mannophryne collaris*	3	no
			Mannophryne cordilleriana	3	no
	Arthroleptidae	Arthroleptis	*Arthroleptis variabilis*	1	no
		Cardioglossa	*Cardioglossa manengouba*	3	no
			Cardioglossa pulchra	2	no
			Cardioglossa trifasciata	3	no
	Brachycephalidae	Brachycephalus	*Brachycephalus alipioi*	2	no
		Ischnocnema	*Ischnocnema epipeda*	3	no
			Ischnocnema paranaensis	4	n/a
			Ischnocnema parva	1	yes
			Ischnocnema pusilla	3	no
			Ischnocnema sp. aff. guentheri	1	yes
	Bufonidae	Anaxyrus	*Anaxyrus baxteri*	5	n/a
			Anaxyrus boreas	2	no
			Anaxyrus canorus	2	no
		Atelopus	*Atelopus andinus*	2	unknown
			Atelopus angelito	4	n/a
			Atelopus arthuri	4	n/a
			Atelopus balios	3	no
			Atelopus bomolochos	3	no
			Atelopus boulengeri	4	n/a
			Atelopus carbonerensis	4	n/a
			Atelopus certus	3	no
			Atelopus chiriquiensis	4	n/a
			Atelopus chrysocorallus	4	n/a
			Atelopus coynei	4	n/a
			Atelopus cruciger	3	unknown
			Atelopus dimorphus	4	n/a
			Atelopus elegans	3	no
			Atelopus epikeisthos	4	n/a

Order	Family	Genus	Species	Severity	Recovery
			Atelopus erythropus	3	no
			Atelopus eusebiodiazi	4	n/a
			Atelopus exiguus	3	no
			Atelopus glyphus	3	no
			Atelopus guanujo	4	n/a
			Atelopus halihelos	4	n/a
			Atelopus ignescens	3	no
			Atelopus limosus	3	no
			Atelopus longirostris	3	no
			Atelopus lynchi	4	n/a
			Atelopus mindoensis	4	n/a
			Atelopus mucubajiensis	3	no
			Atelopus nanay	3	no
			Atelopus nepiozomus	3	no
			Atelopus onorei	4	n/a
			Atelopus orcesi	4	n/a
			Atelopus oxyrhynchus	4	n/a
			Atelopus pachydermus	3	unknown
			Atelopus palmatus	3	no
			Atelopus pastuso	4	n/a
			Atelopus patazensis	3	yes
			Atelopus peruensis	4	n/a
			Atelopus petersi	4	n/a
			Atelopus pinangoi	4	n/a
			Atelopus planispina	4	n/a
			Atelopus podocarpus	4	n/a
			Atelopus pulcher	3	no
			Atelopus pyrodactylus	4	n/a
			Atelopus reticulatus	4	n/a
			Atelopus senex	4	n/a
			Atelopus sorianoi	4	n/a
			Atelopus sp.	4	n/a
			Atelopus spurrelli	3	unknown
			Atelopus tamaense	4	n/a
			Atelopus tricolor	3	no
			Atelopus varius	3	no
			Atelopus zeteki	4	n/a
		Incilius	*Incilius aucoinae*	1	unknown
			Incilius coniferus	1	unknown
			Incilius epioticus	1	unknown
			Incilius fastidiosus	3	no
			Incilius holdridgei	3	no

Order	Family	Genus	Species	Severity	Recovery
			Incilius ibarrai	3	no
			Incilius macrocristatus	2	no
			Incilius periglenes	5	n/a
			Incilius signifer	1	unknown
		Melanophryniscus	*Melanophryniscus moreirae*	3	yes
		Nectophrynoides	*Nectophrynoides asperginis*	5	n/a
		Rhaebo	*Rhaebo haematiticus*	2	no
		Rhinella	*Rhinella alata*	1	unknown
			Rhinella arunco	1	no
			Rhinella centralis	1	unknown
			Rhinella leptoscelis	3	yes
			Rhinella quechua	3	no
			Rhinella spinulosa	2	yes
			Rhinella veraguensis	3	no
		Werneria	*Werneria tandyi*	2	no
	Calyptocephalellidae	Calyptocephalella	*Calyptocephalella gayi*	2	no
	Centrolenidae	Centrolene	*Centrolene buckleyi*	1	unknown
			Centrolene daidaleum	1	no
		Cochranella	*Cochranella euknemos*	2	no
			Cochranella granulosa	1	no
		Espadarana	*Espadarana prosoblepon*	1	unknown
		Hyalinobatrachium	*Hyalinobatrachium aureoguttatum*	2	unknown
			Hyalinobatrachium bergeri	1	no
			Hyalinobatrachium chirripoi	1	unknown
			Hyalinobatrachium colymbiphyllum	2	yes
			Hyalinobatrachium fleischmanni	1	yes
			Hyalinobatrachium talamancae	2	unknown
		Hyalinobatrachium	*Hyalinobatrachium valerioi*	1	unknown
		Nymphargus	*Nymphargus griffithsi*	1	no
			Nymphargus pluvialis	3	no
			Nymphargus truebae	4	n/a
		Rulyrana	*Rulyrana spiculata*	3	no
		Sachatamia	*Sachatamia albomaculata*	2	yes
			Sachatamia ilex	3	unknown
		Teratohyla	*Teratohyla pulverata*	1	unknown
			Teratohyla spinosa	2	unknown
		Vitreorana	*Vitreorana eurygnatha*	1	yes
	Craugastoridae	Bryophryne	*Bryophryne cophites*	1	no
			Bryophryne zonalis	1	unknown
		Craugastor	*Craugastor anciano*	4	n/a
			Craugastor andi	3	no

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Order	Family	Genus	Species	Severity	Recovery
			Craugastor angelicus	3	no
			Craugastor aurilegulus	3	no
			Craugastor azueroensis	3	unknown
			Craugastor bransfordii	2	unknown
			Craugastor catalinae	3	no
			Craugastor chrysozetetes	5	n/a
			Craugastor crassidigitus	2	unknown
			Craugastor cruzi	4	n/a
			Craugastor emleni	4	n/a
			Craugastor escoces	3	unknown
			Craugastor evanesco	3	no
			Craugastor fitzingeri	2	unknown
			Craugastor fleischmanni	3	no
			Craugastor gollmeri	3	unknown
			Craugastor megacephalus	2	yes
			Craugastor melanostictus	1	unknown
			Craugastor mexicanus	2	no
			Craugastor milesi	3	no
			Craugastor monnichorum	2	unknown
			Craugastor noblei	3	unknown
			Craugastor obesus	4	n/a
			Craugastor omoaensis	4	n/a
			Craugastor opimus	2	unknown
			Craugastor podiciferus	1	unknown
			Craugastor punctariolus	4	n/a
			Craugastor ranoides	3	no
			Craugastor rhyacobatrachus	4	n/a
			Craugastor rugosus	2	unknown
			Craugastor stadelmani	4	n/a
			Craugastor stejnegerianus	1	unknown
			Craugastor tabasarae	3	no
			Craugastor talamancae	2	unknown
			Craugastor taurus	3	no
			Craugastor underwoodi	2	unknown
		Holoaden	*Holoaden bradei*	4	n/a
		Pristimantis	*Pristimantis anolirex*	2	no
			Pristimantis caryophyllaceus	2	yes
			Pristimantis cerasinus	2	unknown
			Pristimantis cosnipatae	3	unknown
			Pristimantis cruentus	2	unknown
			Pristimantis danae	1	unknown
			Pristimantis gaigei	2	yes

Order	Family	Genus	Species	Severity	Recovery
			Pristimantis gracilis	1	no
			Pristimantis gryllus	1	no
			Pristimantis melanoproctus	2	no
			Pristimantis mondolfii	1	no
			Pristimantis moro	2	unknown
			Pristimantis museosus	3	unknown
			Pristimantis nicefori	1	no
			Pristimantis palmeri	1	yes
			Pristimantis pardalis	2	yes
			Pristimantis pharangobates	1	unknown
			Pristimantis platydactylus	1	yes
			Pristimantis ridens	2	unknown
			Pristimantis salaputium	1	unknown
			Pristimantis taeniatus	1	unknown
			Pristimantis toftae	1	yes
		Strabomantis	*Strabomantis bufoniformis*	3	no
		Tachiramantis	*Tachiramantis douglasi*	2	no
	Cycloramphidae	Cycloramphus	*Cycloramphus boraceiensis*	1	no
			Cycloramphus duseni	4	n/a
			Cycloramphus fuliginosus	1	no
			Cycloramphus granulosus	3	no
			Cycloramphus semipalmatus	2	no
			Cycloramphus stejnegeri	4	n/a
			Cycloramphus valae	4	n/a
		Thoropa	*Thoropa petropolitana*	3	no
			Thoropa taophora	1	no
	Dendrobatidae	Ameerega	*Ameerega flavopicta*	1	yes
		Andinobates	*Andinobates minutus*	1	unknown
		Colostethus	*Colostethus panamansis*	3	yes
			Colostethus pratti	3	no
		Dendrobates	*Dendrobates auratus*	2	yes
		Hyloxalus	*Hyloxalus abditaurantius*	3	no
			Hyloxalus fascianigrus	3	no
			Hyloxalus lehmanni	1	no
		Oophaga	*Oophaga arborea*	2	unknown
			Oophaga granulifera	2	unknown
			Oophaga histrionica	2	no
			Oophaga pumilio	1	unknown
			Oophaga speciosa	4	n/a
			Oophaga vicentei	1	unknown
		Phyllobates	*Phyllobates lugubris*	2	unknown

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		Ranitomeya	*Ranitomeya claudiae*	2	unknown
		Silverstoneia	*Silverstoneia flotator*	2	yes
			Silverstoneia nubicola	2	unknown
	Eleutherodactylidae	Adelophryne	*Adelophryne baturitensis*	3	no
		Diasporus	*Diasporus diastema*	1	unknown
			Diasporus hylaeformis	1	unknown
			Diasporus quidditus	1	unknown
		Eleutherodactylus	*Eleutherodactylus coqui*	1	yes
			Eleutherodactylus eneidae	5	n/a
			Eleutherodactylus jasperi	5	n/a
			Eleutherodactylus karlschmidti	5	n/a
			Eleutherodactylus locustus	3	yes
			Eleutherodactylus portoricensis	1	yes
			Eleutherodactylus richmondi	3	yes
			Eleutherodactylus wightmanae	2	yes
	Hemiphractidae	Fritziana	*Fritziana ohausi*	1	no
		Gastrotheca	*Gastrotheca antoniiochoai*	1	unknown
			Gastrotheca cornuta	3	no
			Gastrotheca dendronastes	1	no
			Gastrotheca excubitor	1	no
			Gastrotheca helenae	2	no
			Gastrotheca nebulanastes	1	no
			Gastrotheca nicefori	1	no
			Gastrotheca testudinea	1	no
		Hemiphractus	*Hemiphractus fasciatus*	2	unknown
			Hemiphractus helioi	1	no
	Hylidae	Aplastodiscus	*Aplastodiscus flumineus*	4	n/a
			Aplastodiscus musicus	3	no
		Boana	*Boana boans*	1	unknown
			Boana gladiator	1	unknown
			Boana pugnax	1	unknown
			Boana rosenbergi	1	unknown
			Boana rufitela	2	unknown
			Boana xerophyla	1	no
		Bokermannohyla	*Bokermannohyla circumdata*	1	no
			Bokermannohyla izecksohni	3	no
		Bromeliohyla	*Bromeliohyla bromeliaceae*	3	no
		Charadrahyla	*Charadrahyla altipotens*	3	no
			Charadrahyla nephila	2	no
		Cruziohyla	*Cruziohyla calcarifer*	1	unknown
		Dendropsophus	*Dendropsophus ebraccatus*	1	unknown

Order	Family	Genus	Species	Severity	Recovery
			Dendropsophus meridensis	2	no
			Dendropsophus microcephalus	1	unknown
			Dendropsophus pelidna	1	no
			Dendropsophus phlebodes	1	unknown
			Dendropsophus ruschii	3	yes
		Diaglena	*Diaglena spinosa*	2	unknown
		Dryophytes	*Dryophytes euphorbiacea*	1	no
			Dryophytes walkeri	2	no
		Duellmanohyla	*Duellmanohyla ignicolor*	2	no
			Duellmanohyla schmidtorum	2	no
			Duellmanohyla soralia	2	no
			Duellmanohyla uranochroa	3	no
		Ecnomiohyla	*Ecnomiohyla echinata*	2	no
			Ecnomiohyla miliaria	2	no
			Ecnomiohyla minera	3	no
			Ecnomiohyla rabborum	4	n/a
		Exerodonta	*Exerodonta melanomma*	2	no
		Hyla	*Hyla bocourti*	4	n/a
			Hyla hazelae	2	unknown
		Hyloscirtus	*Hyloscirtus armatus*	3	no
			Hyloscirtus colymba	2	no
			Hyloscirtus palmeri	3	unknown
			Hyloscirtus phyllognathus	3	no
			Hyloscirtus platydactylus	1	no
		Isthmohyla	*Isthmohyla angustilineata*	3	no
			Isthmohyla calypsa	4	n/a
			Isthmohyla debilis	3	no
			Isthmohyla graceae	3	no
			Isthmohyla lancasteri	2	unknown
			Isthmohyla picadoi	1	unknown
			Isthmohyla pictipes	2	no
			Isthmohyla pseudopuma	2	no
			Isthmohyla rivularis	3	no
			Isthmohyla tica	3	no
			Isthmohyla zeteki	1	unknown
		Ololygon	*Ololygon cf. perpusillus*	2	yes
			Ololygon heyeri	3	yes
			Ololygon peixotoi	3	no
		Phyllodytes	*Phyllodytes luteolus*	1	no
		Plectrohyla	*Plectrohyla cyclada*	2	no
			Plectrohyla dasypus	3	no

Order	Family	Genus	Species	Severity	Recovery
			Plectrohyla exquisita	3	no
			Plectrohyla hartwegi	2	no
			Plectrohyla ixil	3	no
			Plectrohyla lacertosa	3	no
			Plectrohyla matudai	2	no
			Plectrohyla quecchi	2	no
			Plectrohyla sagorum	2	no
		Pseudis	*Pseudis paradoxa*	1	no
		Ptychohyla	*Ptychohyla erythromma*	2	no
			Ptychohyla hypomykter	1	yes
			Ptychohyla legleri	3	no
			Ptychohyla leonhardschultzei	2	no
		Sarcohyla	*Sarcohyla arborescandens*	2	no
			Sarcohyla sabrina	3	no
		Scarthyla	*Scarthyla vigilans*	1	no
		Scinax	*Scinax altae*	1	unknown
			Scinax boulengeri	1	unknown
			Scinax elaeochrous	1	unknown
			Scinax ruber	1	unknown
		Smilisca	*Smilisca phaeota*	2	yes
			Smilisca sila	1	unknown
			Smilisca sordida	1	unknown
		Tepuihyla	*Tepuihyla edelcae*	1	no
		Tlalocohyla	*Tlalocohyla loquax*	2	no
		Trachycephalus	*Trachycephalus typhonius*	1	unknown
	Hylodidae	Crossodactylus	*Crossodactylus cf. gaudichaudii*	1	no
			Crossodactylus dispar	4	n/a
			Crossodactylus timbuhy	3	yes
			Crossodactylus trachystomus	3	yes
			Crossodactylus werneri	3	no
		Hylodes	*Hylodes asper*	1	no
			Hylodes babax	1	no
			Hylodes glaber	4	n/a
			Hylodes lateristrigatus	1	no
			Hylodes phyllodes	1	yes
	Hyperoliidae	Afrixalus	*Afrixalus paradorsalis*	1	no
		Kassina	*Kassina decorata*	2	no
	Leiopelmatidae	Leiopelma	*Leiopelma archeyi*	1	unknown
	Leptodactylidae	Adenomera	*Adenomera andreae*	1	no
			Adenomera marmorata	1	yes
		Leptodactylus	*Leptodactylus bolivianus*	1	unknown

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			Leptodactylus colombiensis	1	no
			Leptodactylus fallax	3	no
			Leptodactylus fragilis	1	unknown
			Leptodactylus melanonotus	1	unknown
			Leptodactylus rhodonotus	1	no
			Leptodactylus savagei	1	unknown
			Leptodactylus sp.	3	no
		Paratelmatobius	*Paratelmatobius lutzii*	4	n/a
		Physalaemus	*Physalaemus henselii*	2	no
			Physalaemus jordanensis	2	no
		Pleurodema	*Pleurodema bibroni*	2	no
			Pleurodema brachyops	1	unknown
			Pleurodema marmoratum	1	unknown
	Limnodynastidae	Adelotus	*Adelotus brevis*	1	no
	Microhylidae	Chiasmocleis	*Chiasmocleis panamensis*	1	unknown
		Ctenophryne	*Ctenophryne aterrima*	1	unknown
		Hypopachus	*Hypopachus barberi*	2	no
	Myobatrachidae	Geocrinia	*Geocrinia victoriana*	1	no
		Mixophyes	*Mixophyes balbus*	2	yes
			Mixophyes fleayi	2	yes
			Mixophyes iteratus	2	yes
		Philoria	*Philoria frosti*	3	no
		Pseudophryne	*Pseudophryne bibronii*	1	no
			Pseudophryne corroboree	3	no
			Pseudophryne dendyi	1	no
			Pseudophryne pengilleyi	3	no
		Rheobatrachus	*Rheobatrachus silus*	5	n/a
			Rheobatrachus vitellinus	5	n/a
		Taudactylus	*Taudactylus acutirostris*	5	n/a
			Taudactylus diurnus	5	n/a
			Taudactylus eungellensis	2	yes
			Taudactylus liemi	1	yes
			Taudactylus pleione	3	no
			Taudactylus rheophilus	4	n/a
	Odontophrynidae	Proceratophrys	*Proceratophrys moratoi*	1	no
	Pelodryadidae	Litoria	*Litoria castanea*	3	no
			Litoria littlejohni	1	no
			Litoria verreauxii	1	yes
			Litoria verreauxii alpina	2	no
		Ranoidea	*Ranoidea aurea*	2	no
			Ranoidea barringtonensis	1	unknown

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			Ranoidea booroolongensis	2	no
			Ranoidea caerulea	1	no
			Ranoidea daviesae	1	unknown
			Ranoidea dayi	2	no
			Ranoidea jungguy	1	unknown
			Ranoidea kroombitensis	1	no
			Ranoidea lesueuri	1	unknown
			Ranoidea lorica	3	no
			Ranoidea nannotis	2	yes
			Ranoidea nudidigita	1	yes
			Ranoidea nyakalensis	5	n/a
			Ranoidea pearsoniana	2	yes
			Ranoidea piperata	4	n/a
			Ranoidea raniformis	2	no
			Ranoidea rheocola	2	yes
			Ranoidea serrata	1	yes
			Ranoidea spenceri	3	no
			Ranoidea subglandulosa	1	unknown
			Ranoidea wilcoxii	1	unknown
	Petropedetidae	Petropedetes	*Petropedetes perreti*	1	no
	Phrynobatrachidae	Phrynobatrachus	*Phrynobatrachus cricogaster*	1	no
			Phrynobatrachus jimzimkusi	2	no
			Phrynobatrachus manengoubensis	3	no
			Phrynobatrachus sandersoni	2	no
			Phrynobatrachus werneri	2	no
	Phyllomedusidae	Agalychnis	*Agalychnis annae*	3	no
			Agalychnis callidryas	1	unknown
			Agalychnis lemur	3	no
			Agalychnis moreleti	3	no
			Agalychnis spurrelli	1	unknown
		Phasmahyla	*Phasmahyla exilis*	1	no
			Phasmahyla guttata	1	yes
		Phrynomedusa	*Phrynomedusa bokermanni*	4	n/a
			Phrynomedusa marginata	4	n/a
		Phyllomedusa	*Phyllomedusa venusta*	1	unknown
	Pipidae	Pipa	*Pipa myersi*	2	unknown
	Ranidae	Lithobates	*Lithobates chiricahuensis*	2	no
			Lithobates maculatus	2	yes
			Lithobates megapoda	2	no
			Lithobates montezumae	2	no
			Lithobates neovolcanicus	1	no

Order	Family	Genus	Species	Severity	Recovery
			Lithobates pipiens	2	no
			Lithobates sierramadrensis	2	no
			Lithobates spectabilis	2	no
			Lithobates tarahumarae	2	no
			Lithobates vaillanti	1	unknown
			Lithobates vibicarius	3	yes
			Lithobates warszewitschii	2	yes
			Lithobates yavapaiensis	2	yes
		Rana	*Rana cascadae*	2	no
			Rana maculata	1	yes
			Rana muscosa	3	no
			Rana sierrae	3	yes
	Rhinodermatidae	Rhinoderma	*Rhinoderma darwinii*	2	no
			Rhinoderma rufum	4	n/a
	Telmatobiidae	Telmatobius	*Telmatobius arequipensis*	2	no
			Telmatobius atacamensis	4	n/a
			Telmatobius atahualpai	1	unknown
			Telmatobius bolivianus	4	n/a
			Telmatobius brevipes	2	no
			Telmatobius brevirostris	2	no
			Telmatobius carrillae	2	no
			Telmatobius ceiorum	4	n/a
			Telmatobius chusmisensis	1	no
			Telmatobius cirrhacelis	4	n/a
			Telmatobius colanensis	2	no
			Telmatobius contrerasi	4	n/a
			Telmatobius culeus	3	unknown
			Telmatobius edaphonastes	4	n/a
			Telmatobius espadai	4	n/a
			Telmatobius hockingi	2	no
			Telmatobius ignavus	2	no
			Telmatobius jelskii	1	unknown
			Telmatobius laticeps	4	n/a
			Telmatobius latirostris	2	unknown
			Telmatobius marmoratus	1	no
			Telmatobius mayoloi	2	unknown
			Telmatobius mendelsoni	4	n/a
			Telmatobius niger	4	n/a
			Telmatobius pefauri	4	n/a
			Telmatobius pisanoi	4	n/a
			Telmatobius punctatus	1	no

Order	Family	Genus	Species	Severity	Recovery
			Telmatobius sanborni	2	unknown
			Telmatobius schreiteri	4	n/a
			Telmatobius scrocchii	4	n/a
			Telmatobius sibiricus	4	n/a
			Telmatobius simonsi	3	unknown
			Telmatobius stephani	4	n/a
			Telmatobius timens	3	no
			Telmatobius truebae	3	no
			Telmatobius vellardi	2	unknown
			Telmatobius verrucosus	4	n/a
			Telmatobius yuracare	4	n/a
Caudata	Ambystomatidae	Ambystoma	*Ambystoma altamirani*	1	no
			Ambystoma granulosum	1	no
	Plethodontidae	Bolitoglossa	*Bolitoglossa biseriata*	1	unknown
			Bolitoglossa colonnea	2	unknown
			Bolitoglossa compacta	1	unknown
			Bolitoglossa leandrae	2	no
			Bolitoglossa lignicolor	1	unknown
			Bolitoglossa magnifica	1	unknown
			Bolitoglossa marmorea	1	unknown
			Bolitoglossa medemi	1	unknown
			Bolitoglossa minutula	1	unknown
			Bolitoglossa rostrata	2	no
			Bolitoglossa schizodactyla	3	unknown
			Bolitoglossa tamaense	1	no
		Chiropterotriton	*Chiropterotriton dimidiatus*	2	no
			Chiropterotriton magnipes	3	no
		Oedipina	*Oedipina grandis*	2	unknown
			Oedipina parvipes	1	unknown
		Parvimolge	*Parvimolge townsendi*	2	no
		Pseudoeurycea	*Pseudoeurycea brunnata*	4	n/a
			Pseudoeurycea cochranae	3	no
			Pseudoeurycea exspectata	4	n/a
			Pseudoeurycea goebeli	3	no
			Pseudoeurycea lineola	2	no
			Pseudoeurycea melanomolga	2	no
			Pseudoeurycea nigromaculata	2	no
			Pseudoeurycea papenfussi	3	no
			Pseudoeurycea rex	2	no
			Pseudoeurycea smithi	3	no

Order	Family	Genus	Species	Severity		Recovery
			Pseudoeurycea unguidentis		4	n/a
		Thorius	*Thorius aureus*		1	no
			Thorius boreas		1	no
			Thorius dubitis		3	no
			Thorius magnipes		3	no
			Thorius pennatulus		2	no
			Thorius pulmonaris		2	no
			Thorius troglodytes		3	no
	Salamandridae	Euproctus	*Euproctus platycephalus*		1	unknown
		Salamandra	*Salamandra salamandra*		1	no

Data S1. For the complete dataset of declined species, see the separate Excel file.

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