

Supporting Information

Nowakowski et al. 10.1073/pnas.1714891115

SI Materials and Methods

Data Collection. We searched the literature using the Institute for Scientific Information Web of Science and Google Scholar to compile amphibian species abundances in natural habitats and in nearby modified habitats, as reported from published field surveys. Our search terms included amphibian*, in combination with land use, logging, silviculture, agriculture, crops, grazing, pasture, plantation, habitat disturbance, habitat alteration, habitat destruction, habitat modification, habitat loss, habitat fragmentation, or matrix. We supplemented these searches by including papers from reference sections of metaanalyses (1, 2) and from the “latest papers” on amphibian conservation listed at <https://amphibiaweb.org>. We extracted abundances from data tables and figures for all studies that sampled amphibian assemblages in natural and modified habitats in the same landscape, that used standardized sampling methods (e.g., transects or pitfall traps), and that reported sampling effort and replication. Most studies had balanced sampling designs; however, in some cases, we corrected for unequal replication by randomly selecting an equal number of natural- and altered-habitat sites from data tables (five studies), and we standardized counts by sampling effort when studies had unequal sampling effort among habitats (six studies). Additional details of the dataset are reported in ref. 3, and all studies included in the dataset are listed in [Dataset S1](#). The extracted species abundances are included in [Dataset S2](#).

Species Imputation. We compared two imputation methods to add missing species to the large-scale amphibian phylogeny (4). In both methods, placement of missing taxa was constrained by the genus of those taxa. First, we inserted missing species into the full Pyron (4) tree by randomly attaching branches along the subtree representing the genus of each species. The probability of attaching a missing branch to any existing branch was proportional to the length of branches already present in the genus, and the tip addition was equally probable along any point of the focal branch. This random insertion method is a modification of the approach implemented in the “add.species.to.genus” function to the phytools package in R (5).

We also used the PASTIS species imputation method (6), which defines a large number of topological constraints based on a constraint tree, here using the Pyron (4) tree pruned to species in the study and an outgroup, and taxonomic constraints for missing taxa, here using each species’ genus. These constraints were then passed to MrBayes to generate a posterior distribution of trees. The PASTIS method specifies a homogenous birth-death prior so that edge lengths are sampled under a common framework for both included and missing species. We specified the GTR substitution model with gamma-distribute rate variation along with other default parameters defined in the PASTIS package (6). We conducted the analysis with two replicate runs of 26 million generations. We discarded the first 6 million generations and sampled 100 random trees from this posterior distribution for downstream analyses. Parameters had reached stationarity, and potential scale reduction factor values for each parameter were ~ 1 . The depth of the root of the posterior trees were scaled to the depth of the corresponding node of the original Pyron (4) tree.

Phylogenetic Signal. We examined phylogenetic signal in habitat affiliation by way of a GLMM with a phylogenetic response to habitat conversion (slope) term implemented using Markov chain Monte Carlo (MCMC). Specifically, the number of individuals observed of a given species at a given site (Y), was assumed to come from:

$$Y[i] \sim \text{Pois}(\Lambda[i]),$$

where the expected number of individuals ($\Lambda[i]$) was predicted from a log-linear model:

$$\log(\Lambda[i]) = \beta_0 + \beta_1 \text{Hab}[i] + \gamma_0[\text{spp}[i]] + \gamma_1[\text{spp}[i]] * \text{Hab}[i] + \gamma_2[\text{spp}[i]] * \text{Hab}[i] + \varepsilon[i],$$

where $\text{Hab}[i]$ represents the habitat associated with the i th observation (converted habitats coded as 1 and natural habitat coded as -1). The β terms represent fixed effects (the mean intercept and mean response to habitat conversion across species), and gamma terms are random effects according to:

$$\begin{aligned} \gamma_0[\text{spp}] &\sim \text{Norm}(0, \sigma_0) \\ \gamma_1[\text{spp}] &\sim \text{Norm}(0, \sigma_1) \\ \gamma_2[\text{spp}] &\sim \text{MVN}(\mathbf{0}, \sigma_2 * \mathbf{C}[\text{spp} \times \text{spp}]). \end{aligned}$$

Here, γ_1 and γ_2 are dual components of the species slopes in response to habitat conversion. As a result, γ_1 corresponds to the component of the response that is not phylogenetically conserved, whereas γ_2 represents the component that can be described by Brownian motion evolution in the phylogeny. Here, \mathbf{C} is the correlation matrix derived from the phylogeny. In practice, \mathbf{C} was chosen at each iteration of the MCMC from 1 of 100 samples of the posterior from PASTIS, with equal prior probability. This effectively integrated over the phylogenetic uncertainty so that the remaining parameters reflected the full possibility of phylogenetic topologies (7).

Finally, the residual error, $\varepsilon[i] \sim \text{Norm}(0, \sigma_3)$, accounted for additional variation not conserved between species or species by habitat interactions.

We expressed phylogenetic signal as the proportion of total variance in species responses to habitat conversion that can be ascribed to Brownian motion evolution. Specifically, Pagel’s $\lambda = (\sigma_2^2 / (\sigma_1^2 + \sigma_2^2))$.

Models were fit by using JAGS through the R environment. For MCMC analysis, diffuse priors were used throughout. β terms had priors drawn from normal distributions with means of 0 and variances of 1,000, and σ terms were drawn from uniform distributions with minima at 0 and maxima at 10. In no cases were posterior distributions on the σ terms near the upper bound of the priors. Three chains were run for 10,000 iterations each, with the first 2,000 discarded as burn-in, and a thin rate of 16. Convergence was confirmed by verifying that the Gelman–Rubin statistic was < 1.1 and by visually inspecting trace plots for proper mixing. JAGS model code is available in [Dataset S3](#).

1. Gardner TA, Barlow J, Peres CA (2007) Paradox, presumption and pitfalls in conservation biology: The importance of habitat change for amphibians and reptiles. *Biol Conserv* 138:166–179.
2. Newbold T, et al. (2015) Global effects of land use on local terrestrial biodiversity. *Nature* 520:45–50.
3. Nowakowski AJ, Thompson ME, Donnelly MA, Todd BD (2017) Amphibian sensitivity to habitat modification is associated with population trends and species traits. *Glob Ecol Biogeogr* 26:700–712.

4. Pyron RA (2014) Biogeographic analysis reveals ancient continental vicariance and recent oceanic dispersal in amphibians. *Syst Biol* 63:779–797.
5. Revell L (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol Evol* 3:217–223.
6. Thomas GH, et al. (2013) PASTIS: An R package to facilitate phylogenetic assembly with soft taxonomic inferences. *Methods Ecol Evol* 4:1011–1017.
7. de Villemereuil P, Wells JA, Edwards RD, Blomberg SP (2012) Bayesian models for comparative analysis integrating phylogenetic uncertainty. *BMC Evol Biol* 12:102.

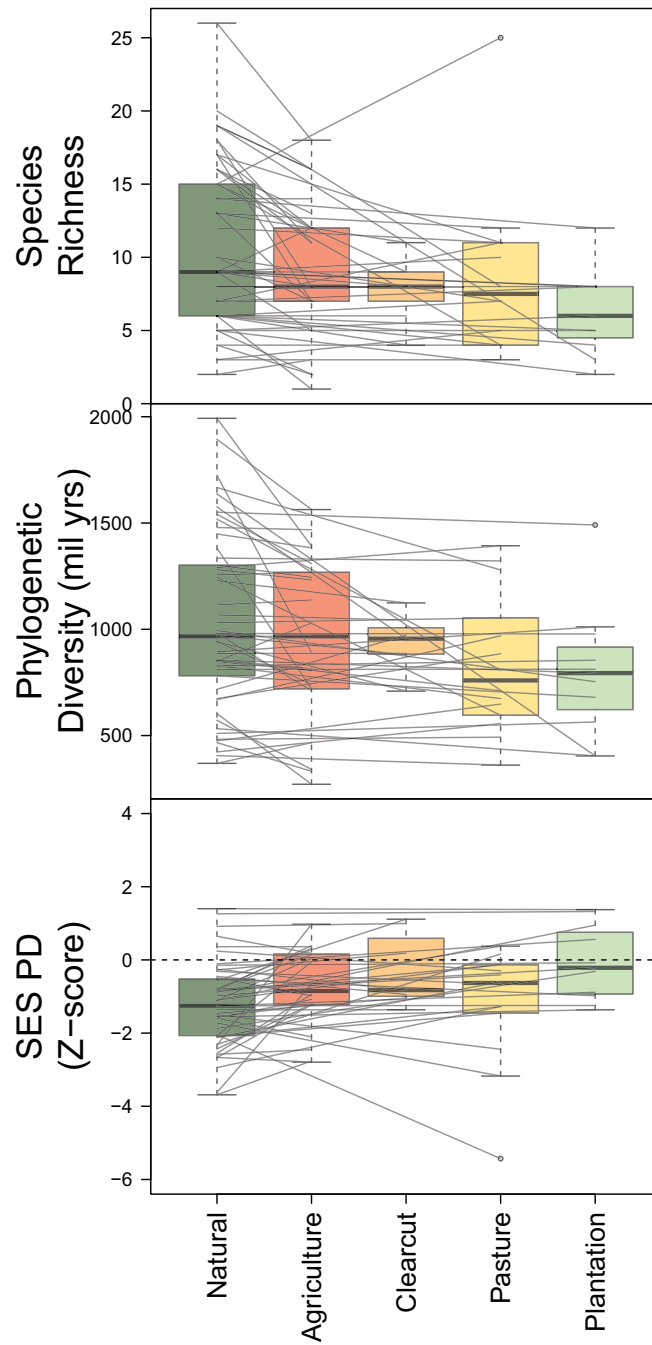


Fig. S2. Observed α -diversity by habitat type.

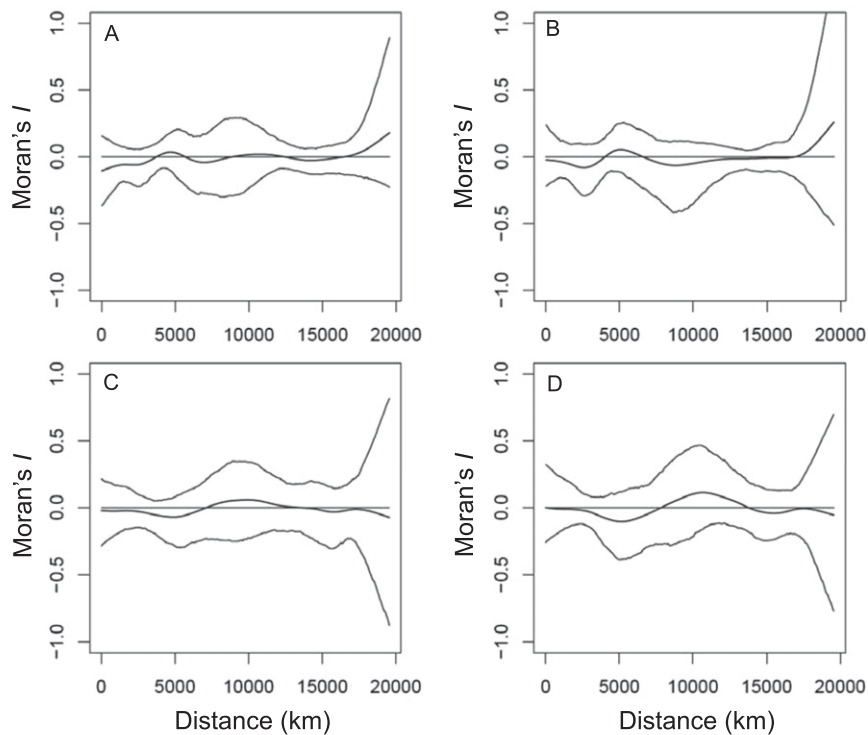


Fig. 53. Spline correlograms show lack of significant spatial autocorrelation (Moran's I) in model residuals among studies in the dataset. Residuals are from best-supported models of variation among studies in changes in taxonomic α -diversity (A) and phylogenetic α -diversity (B) and patterns of taxonomic β -diversity (C) and phylogenetic β -diversity (D). The 95% pointwise confidence envelopes were generated from a distribution of 1,000 bootstrapped samples of the estimator.

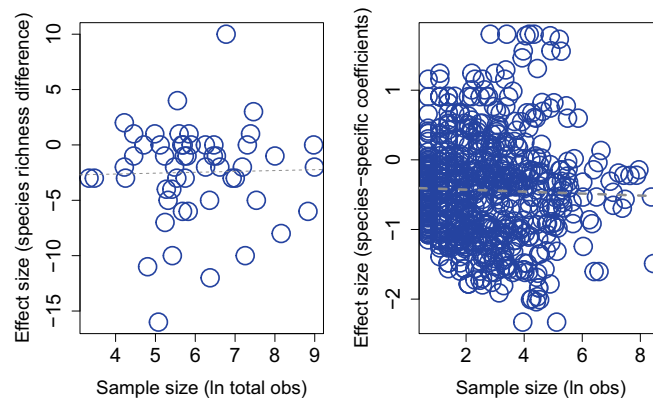


Fig. 54. Plots show lack of relationships between effect sizes and sampling effort, represented here as the total number of observations. (Left) Species richness differences between natural and converted habitats for each study in relation to the total number of observations for that study as an index of sampling effort ($P = 0.866$, $R^2 < 0.001$). (Right) Species-specific responses to habitat conversion in relation to total number of observations for each species across habitats ($P = 0.391$, marginal $R^2 = 0.001$).

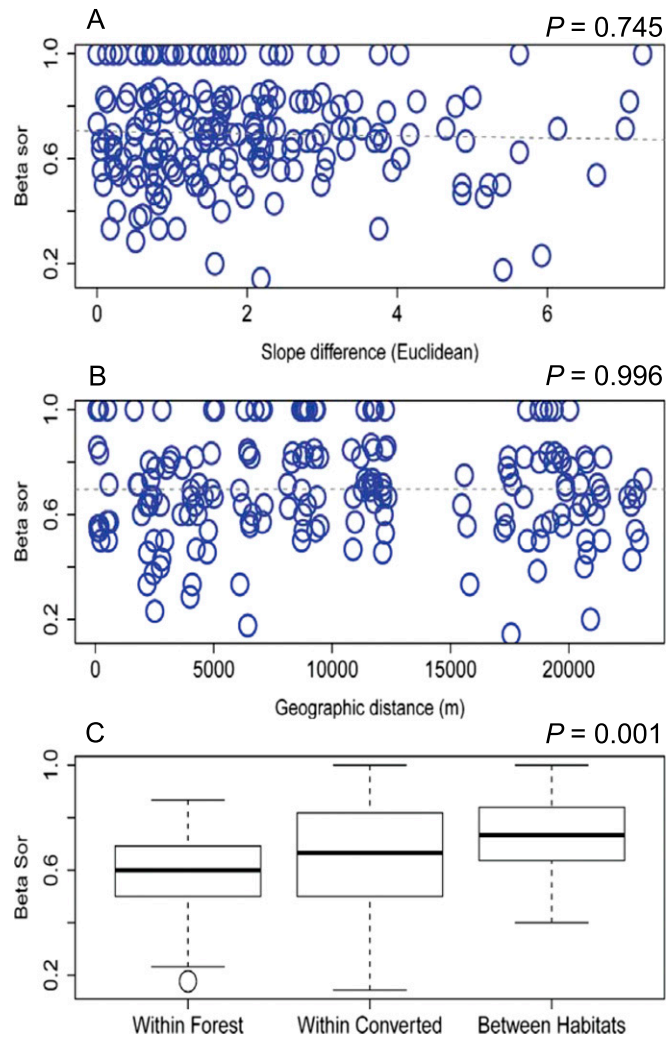


Fig. S7. Examination of within-study β -diversity; data shown are from Kurz et al. (1). (A and B) Variables that reflect indices of environmental gradients that existed before habitat conversion, such as topographic differences (A) and geographic distances (B) among pairs of sites, did not explain variation in beta diversity (here, taxonomic Sorensen index). (C) β -diversity was significantly different, however, among pairwise comparisons of habitat types. To statistically examine predictors of β -diversity, we used regression with distance matrices (A and B) and analysis of similarity (C), where P values were calculated by using permutation tests.

1. Kurz DJ, Nowakowski AJ, Tingley MW, Donnelly MA, Wilcove DS (2014) Forest-land use complementarity modifies community structure of a tropical herpetofauna. *Biol Conserv* 170: 246–255.

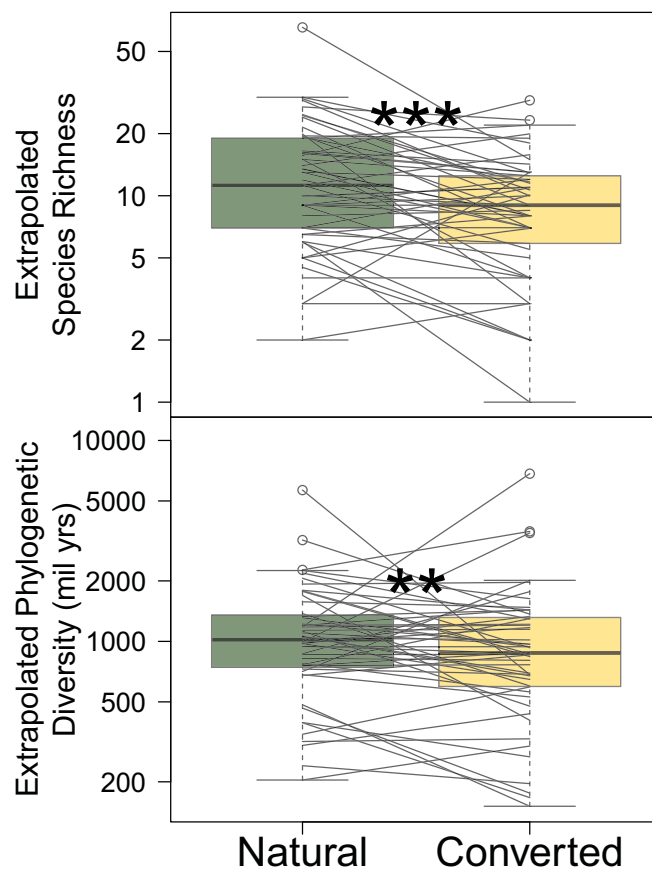


Fig. S8. Changes in taxonomic and phylogenetic α -diversity using extrapolated measures of species richness and PD from accumulation curves. $**P < 0.01$; $***P < 0.001$.

Table S1. Univariate predictors from binomial GLMs of interhabitat taxonomic and phylogenetic β -diversity across regions

Model term	Intercept	Coef	Pseudo- R^2	P	Sig
Taxonomic β-diversity					
MnAnnualTemp, °C	-2.313	0.094	0.280	<0.001	***
MaxMeanTmp, °C	-2.040	0.068	0.075	0.046	*
TotalPrecip, m	-1.374	0.498	0.194	0.001	**
Hfootprint_25 km	-0.320	0.002	0.001	0.852	
SD_MN_Temp	0.164	-0.216	0.301	<0.001	***
Elevation (1,000 m)	-0.281	-0.193	0.017	0.335	
abs(Lat), °	0.241	-0.034	0.184	0.002	**
Phylogenetic β-diversity					
MnAnnualTemp, °C	-2.902	0.087	0.317	<0.001	***
MaxMeanTmp, °C	-2.587	0.062	0.083	0.041	*
TotalPrecip, m	-1.866	0.384	0.176	0.002	**
Hfootprint_25 km	-0.805	-0.009	0.016	0.363	
SD_MN_Temp	-0.584	-0.021	0.360	<0.001	***
Elevation (1,000 m)	-0.949	-0.260	0.042	0.149	
abs(Lat), °	-0.567	-0.029	0.186	0.002	**

P values are based on likelihood ratio tests against the null model. Significant differences are shown by asterisks. $*P < 0.05$; $**P < 0.01$; $***P < 0.001$. Coef, coefficient; sig, significance.

Table S2. Best-fit binomial GLM based on forward model selection describing interhabitat taxonomic and phylogenetic β -diversity across regions

Coef name	Coef	<i>P</i>	Sig
Taxonomic β -diversity			
Intercept	0.463		
SD_MN_Temp, °C	-0.243	<0.001	***
Elevation, km	-0.407	0.021	*
R ²	0.377		
Phylogenetic β -diversity			
Intercept	-0.277		
SD_MN_Temp, °C	-0.240	<0.001	***
Elevation, km	-0.442	0.003	**
R ²	0.482		

Coef, coefficient; sig, significance. **P* < 0.05; ***P* < 0.01; ****P* < 0.001.

Other Supporting Information Files

[Dataset S1 \(PDF\)](#)

[Dataset S2 \(CSV\)](#)

[Dataset S3 \(PDF\)](#)