

Material & Methods

Danet, A, Giam, X, Olden, J, Comte, L

15 août, 2022

1 Fish community time series

We used the RivFishTime database(Comte et al. 2021), a compilation of more than 12,000 time series containing species abundances of riverine fish communities. The database mainly covers western and northern Europe, northern America, and southeastern Australia. We completed the database with time series from Canada and United States (Table S1), following the same criteria than RivFishTime for integration(Comte et al. 2021).

We selected time series having at least 5 years of data over a 10 year period as well as a consistent sampling protocol. As several sites had been sampled using different sampling methods (e.g. electrofishing, seining) and/or over different periods of the year, we selected for each site only the sampling events that were performed using the most frequent protocol (i.e. the mode) and within 1.5 month of the most frequently sampled month (i.e. 45 days before or after). When there were several sampling events the same year, we selected the sampling that took place at the closest date from the most sampled date of the site. We further checked that the reported unit of abundance was consistent for each time series.

The data selection resulted in 4476 fish community time series, totalling 46932 sampling events, 326717 species abundance records, and 806 freshwater fish species. The median time span was of 17 [13,23] years ([25th quantile, 75th quantile]), the median baseline of the time series was 1997 [1992,2003], and the median completeness of the time series was of 55% [38%,78%] (see Fig. S2 for the complete distribution). The sites were mostly located in Palearctic (75%), Nearctic (20%) and Australasia (5%). Four countries gathered 85% of the sites, namely Great Britain (29%), France (21%), Sweden (18%), and the United States (18%, Table S4).

2 Community metrics

We assessed community changes in riverine fish communities using several biodiversity facets related to community composition, non-native species, species richness and total abundance (Table S7).

2.1 Dissimilarity metrics

We characterized temporal dissimilarity in community composition in each site, taking the first year of sampling of a community as the reference community. We first used the complement of the Jaccard similarity index (J). This index is based on presence/absence and is simply the sum of species gains and losses over the total number of species across two samples (eq. (2.1)). It thus measures the proportion of species not shared between two samples.

$$J = \frac{S_{gain} + S_{loss}}{S_{tot}}$$

with S_{gain} , S_{loss} , S_{tot} being the numbers of immigrant, extirpated and total species respectively.

We further partitioned the Jaccard dissimilarity index into two sets of complementary indices. The first set was Appearance and Disappearance, respectively the proportion of colonizing species (S_{gain}/S_{tot}) and the proportion of extirpated species (S_{loss}/S_{tot}). The second set was Turnover (J_t) and Nestedness (J_n), respectively $J_t = (2 * \min(S_{loss}, S_{gain})) / (S_{common} + (2 * \min(S_{loss}, S_{gain})))$ and $J_n = 1 - J_t$ (Baselga and Orme 2012), S_{common} being the number of species present in both communities. High Turnover values indicate that the changes in community composition resulting from species replacement, whereas high values of Nestedness indicate species gains or losses from a nested community, i.e. that a community is a subset of the other (Baselga, Bonthoux, and Balent 2015).

We further characterized temporal dissimilarity with the Simpson-based dissimilarity index (Hillebrand et al. 2018) (H_d , (2.1)). This index is based on species relative abundances and their variation across two samples. Simpson-based dissimilarity index is based on the Simpson diversity index and thus gives higher weight to changes in the abundant species, whereas Jaccard dissimilarity index gives equal weight to each species. Simpson-based dissimilarity index thus quantifies the extent of changes in the identity of dominant species (Hillebrand et al. 2018). Both high Jaccard and Simpson dissimilarity values thus indicate changes in composition implying changes in the abundant species, whereas conjointly high Jaccard and low Simpson dissimilarity values indicate composition changes in species of low relative abundances.

$$H_d = 1 - H$$

$$H_d = 1 - \frac{\sum_i (p_i - p'_i)^2}{\sum_i p_i^2 + \sum_i p'^2_i - \sum_i p_i p'_i}$$

with i : species i , p : relative abundance and $'$: the focal community

2.2 Total abundance

Total abundance was reported in number of individuals (47.00% of the sampling events), density of individuals per 100 m^2 (51.81%), Catch Per Unit Effort (1.05%), and Leslie index (0.14%, Table S3). Although we selected for strict protocol consistency, 70% or more of the sampling events by unit of abundance did not reported sampling effort, preventing us to harmonize count, abundance density and Catch Per Unit Effort (Comte et al. 2021).

2.3 Species richness

As sampled species richness is a negatively biased estimator of the “true” species richness, we corrected sampled species richness with the coverage-based rarefaction and extrapolation methodology (Chao and Jost 2012). The estimated coverage of a sample is positively related to the number of individuals and negatively related to number of singletons. We fixed the coverage of all samples at 98.5% via rarefaction and extrapolation using the R package `iNEXT` [hsieh_inext_2016], to make species richness to be comparable across samples.

We did not always have direct access to the number of individuals and number of singletons to compute the sampling coverage, as 51.81% of the abundances were measured as density by 100 m^2 and 1.05% as Catch per Unit Effort. In this case, we first divided each species abundance (x_i) by the minimum values of abundance in the community (i.e. $x'_i = 1/\min(x_i)$), which we further rounded so that each community had at least one singleton species, i.e. a species with one individual. The correlation was very high between raw species richness and Chao richness (Spearman’s $\rho = 0.97$ for both raw variables and log transformed ones, Fig. S3).

3 Stream gradient and anthropogenic pressures

In dendritic networks, the environmental heterogeneity and connectivity along the longitudinal (upstream-downstream) gradient strongly shape species occurrences, immigration rates and community composition (Altermatt, Seymour, and Martinez 2013). To capture this stream gradient, we described stream

characteristics at each site by the altitude (m), slope (deg.), average annual discharge ($m^3.s^{-1}$), distance from source (km), and strahler order that we extracted from the HydroAtlas database (Linke et al. 2019; Robinson, Regetz, and Guralnick 2014, Table S8). We did so by snapping the sites to the closest stream segment using a one kilometer buffer (99% of the sites). We performed a Principal Component Analysis over the site stream characteristics after log transforming (added absolute minimum values plus one to avoid negative values, $x'_i = x_i + \min(x_i) + 1$) and standardizing all the variables, i.e. centering and scaling. We orthogonally rotated the two first principal components, using the varimax criterion (Kaiser 1958; Revelle 2019), to increase the quality of the variable representation (i.e. their loadings) on the two first principal components. The first rotated component was positively related to average annual discharge, distance from source and Strahler order and capturing 56% of the variance (Fig. S4), and then was used as a composite variable describing the stream gradient from upstream to downstream.

We quantified the degree of anthropogenic pressures using the human footprint index (Venter et al. 2016a, 2016b). The human footprint index aggregates an array of human pressures, including population density, the extent of forested, cropland and pasture land areas, but also the extent of built environments such as roads, railways, electric infrastructures, and navigable pathways (Fig. S5). It does so by combining remote sensing data, systematic surveys and modelling from ground data, making it less prone to errors (Venter et al. 2016a). The human footprint index ranges from 0 to 50, with values superior to four being considered in a degraded state (Williams et al. 2020). To capture both the effects of the legacy of past anthropogenic pressures and its recent changes, we considered the human footprint index computed in 1993 and 2009 (i.e. 16 years span). Specifically, the human footprint index of 1993 was used as a measure of the legacy of past anthropogenic pressures and the ratio between the human footprint of 2009 and 1993 as a measure of the recent changes in anthropogenic pressures. In order to obtain interpretable coefficients of recent changes in human footprint, we log-transformed the ratio of human footprint with a base 2. Then, a value of minus one and one represent a division by two and a multiplication by two of the human footprint between 1993 and 2009, respectively. Only 7% of the samplings took place before 1993, while 58% took place between 1993 and 2009 and 34% after 2009 (Fig. S1). The human footprint index values were extracted from the HydroAtlas database at the reach scale (original resolution of 450meters, Linke et al. 2019). The human footprint indexes of 1993 and 2009 were not correlated with the stream gradient (Spearman's ρ of 0.08 and 0.1 respectively).

3.1 Non-native species data

The biogeographic origin of the fish species describing whether species were native or introduced to a given drainage basin was retrieved using the global database of Tedesco et al. (2017) (94.4% of the species occurrences). For the sites falling outside of the river basins provided in Tedesco et al. (2017), such as for the sites located close to the shore, we used the closest basin in the country. For species not included in a given drainage basin, we determined the origin of the species at the country scale using Fishbase (Froese, Pauly, and others 2021) (5.5% of species occurrences). Given the spatial extent of the United States, we completed the global database with the Nonindigenous Aquatic Species (NAS) database developed by the U.S. Geological Survey (<https://nas.er.usgs.gov/>), at the US state scale (0.05% of the species occurrences). We completed the remaining species origins at the country scale, using national atlases and Fishbase data in neighboring countries, such as for *Piaractus brachipomus* and *Rutilus rutilus* in the United States (0.1% of the species occurrences, Table S6). We then estimated the percentage of non-native species for each sampling events, both for species richness and abundances (Table S7).

4 Statistical analysis

4.1 General statistical model

We modelled the temporal trends of the different biodiversity facets (Y) as dependant of time ($\beta_0 Time_t$, eq. (4.1)) measured as the number of years since the beginning of the sampling at each site with $t_0 = 0$, the stream gradient measured by the rotated PCA axis over stream characteristics, the legacy of past anthropogenic pressures measured by the human footprint index of 1993, and the recent changes in anthropogenic

pressures measured by the ratio between the human footprint index of 2009 and 1993. We included all the predictors as main effects ($\sum_{k=1} \beta_k X_k$) to capture the differences in biodiversity facets attributed to spatial effects of the ecological drivers. We further included interactions between time and the ecological drivers ($\sum_{k=0, l \neq k} \beta_{kl} X_k X_l$) to test how stream gradient and anthropogenic pressures affect the temporal trends in biodiversity facets. Finally, we included the triple interactions between time and the pairs of other ecological drivers ($\sum_{k=0, m \neq n \neq k} \beta_{kmn} X_k X_m X_n$) to test for the presence synergistic or antagonistic effects of the stream gradient and anthropogenic pressures on the temporal trends in biodiversity facets.

Furthermore, the statistical model (eq. (4.1)) was adapted according of the nature of the variables, namely total abundance and dissimilarity metrics. For total abundance, we added the measurement unit of abundance as a categorical variable both as a main effect and in interaction with time (Klink et al. 2020). We set raw count as the reference factor level such as the temporal trends in total abundance in the main text and supplementary materials are expressed in raw count. We modelled dissimilarity metrics with the intercept fixed at zero as dissimilarity metrics at each site was 0 at the beginning of the time series. Furthermore, we did not include the main effects of ecological drivers ($\sum_{k=1} \beta_k X_k$ term from eq. (4.1)) in the modelling of dissimilarity metrics, i.e. we only included the effects of ecological drivers on the temporal trends. We did so because dissimilarity metrics were relative to the site and bounded between 0 and 1, so we did not expect average differences in dissimilarity which are not due to differences in the temporal trends.

We accounted for the spatial structure of the data by adding random effects to the intercept (α) and the slope of the temporal trends (β_0) on the basin identity (n) and on the site identity (i), nested in basin ($i|n$). The random effects and the error terms were modelled as a Normal distribution of mean 0 and variance (σ^2).

$$Y_{i|n,t} = \alpha + \beta_0 Time_t + \sum_{k=1} \beta_k X_k + \sum_{k=0, l \neq k} \beta_{kl} X_k X_l + \sum_{k=0, m \neq l \neq k} \beta_{klm} X_k X_l X_m + \epsilon_{i|n,t}$$

- $\alpha = \alpha_0 + a_n + a_{i|n}$
- $\beta_0 = \mu + b_n + b_{i|n}$
- $k, l, m \in [1, 2, 3]$: ecological drivers including stream gradient, legacy of past and recent changes in anthropogenic pressures
- $a_n, a_{i|n}, b_n, b_{i|n}, \epsilon_{i|n,t} \sim \mathcal{N}(0, \sigma^2)$
- n : hydrographic basin, i : site i , t : time t

All the response variables were modelled with a Gaussian distribution following previous studies modelling temporal trends of community composition, species richness and total abundance at the global scale (Dornelas et al. 2014; Blowes et al. 2019; Klink et al. 2020). Other error structures might be more appropriate to model response variables bounded between 0 and 1 and representing ratio of discrete numbers such as the dissimilarity metrics and the proportion of non-native species, doing so allows to obtain easily interpretable coefficients across all biodiversity facets (e.g. temporal trends are not interpretable as rates of change when modelled using a logit scale such as when using a beta distribution). In addition, Blowes et al. (2019) previously found that slope coefficients estimated with a gaussian error and a beta error had a Spearman correlation superior to 0.90 and give qualitatively similar results. We therefore believe that this choice is not likely to alter our conclusions.

4.2 Variable transformations

We log-transformed the number of years as $\log(year + 1)$ as it improved the quality of the model fitting to the data, decreasing the WAIC (Watanabe-Akaike information criterion, Gelman, Hwang, and Vehtari 2014; Vehtari, Gelman, and Gabry 2017) by -575 in average (-11%) (Table S11). It suggests the presence of non-linearity in the temporal trends, which is particularly expected in the case of bounded variables such as the dissimilarity metrics. The rate of community change per decade is then found for a time value of $\log(10 + 1)$, i.e. 2.4. We further log-transformed with a base 2 the recent changes in anthropogenic pressures quantified by the ratio of human footprint index between 2009 and 1993, i.e. $\log_2(HFT_{2009}/HFT_{1993})$. Then, a value of minus one and one represent respectively a division by two and a multiplication by two of the human footprint between 1993 and 2009. We log-transformed total abundance and Chao species richness, then their temporal trends are multiplicative and can be expressed in percentage change by unit of time. We

derived percentage change by decade in species richness and total abundance by back transforming β_0 such as: $(e^{\beta_0 \times \log(10+1)} - 1) \times 100$.

4.2.1 Variable standardization

In order to compare the magnitude of the effects of time, stream gradient, and anthropogenic pressures among biodiversity facets and to compare the magnitude of the effects of the predictors, we scaled both biodiversity facets and the predictors by their standard deviation prior to the model evaluation.

As our models contain interactions, the individuals slope coefficients can be difficult to interpret without centering the predictors around ecological relevant values (Gelman 2008). As an example, the average temporal trends estimated by β_0 in eq.(4.1) can only be interpreted when all the $X_k = 0$. Without centering, it means that β_0 is interpretable when the past anthropogenic pressures and the stream gradient are equal to 0. Hence, we centered past antropogenic pressures and stream gradient around their average values. The variables quantifying recent changes in anthropogenic pressures was not centered, as 0 values indicate no recent changes in anthropogenic pressures. Time variable was not centered either because then the main effects of the ecological drivers ($\sum_{k=1} \beta_k$) can be interpreted as a baseline effect, i.e. when time is equal to 0.

4.2.2 Model evaluation and confidence intervals

The models were evaluated in a Bayesian framework using Integrated Nested Laplacian Approximation (INLA), which approximates the posterior distribution of the parameters and then do not rely on Markov chains and Monte Carlo simulations, and then is a computationally efficient method to evaluate Bayesian models (Rue, Martino, and Chopin 2009; Rue et al. 2017). When estimating conjointly the temporal trends at multiple locations, an advantage of the Bayesian approach is the estimation of credible intervals around the temporal trends estimated at each location. A second advantage is that it allows the computation of credible intervals, which translates in the probability that an unobserved parameter falls in a given interval, to the difference with frequentist approach (Greenland et al. 2016). We computed the credible intervals at 80%, 90% and 95% using Highest Posterior Density method (Hyndman 1996). When 0 is outside the credible intervals of the coefficients at 80%, 90% and 95%, they can respectively be interpreted as weak, moderate and strong evidence of an effect (Klink et al. 2020; Mastrandrea et al. 2010). The model evaluation was performed with the INLA R package (Rue, Martino, and Chopin 2009).

4.2.3 Bayesian priors

INLA models were evaluated with defaults uninformative priors. The prior distribution of fixed coefficients followed a flat zero centered normal distribution ($\mathcal{N}(\mu, \sigma^2) = \mathcal{N}(0, 1000)$). The prior distribution of the random effects and the gaussian error (ϵ_{it} , eq. (4.1)) followed a log gamma distribution with shape and inverse scale parameters ($\mathcal{G}(s, \tau) = \mathcal{G}(1, 5.10^{-5})$). We then back-transformed the estimated coefficients to to the standard deviations attributed to the random effects and the gaussian error ($\sigma = 1/\sqrt{\tau}$). We checked that the slope coefficients, random effects and the temporal trends by basin and site were similar than with an implementation in frequentist. Then, we concluded that the quality of parameter inference did not suffer from the uninformative priors.

4.2.4 Model validity

We checked the model validity visually by plotting the fitted versus the observed values (Fig. S6). We visually inspected the PIT and CPO (respectively Posterior Integral Transform and Conditional Predictive Ordinate) distribution to assess both the overall quality of fitting, and the frequency of outliers. There was very multicollinearity in the model, as all Variance Inflation Factors were around 1 (Table S10).

We computed R^2 to assess the quality of the fit of the bayesian models. We then computed marginal (R_m^2) and conditional (R_c^2) R-squared, respectively associated to the variance explained by fixed effects and the one explained by both fixed and random effects (Nakagawa and Schielzeth 2013). We only included the random effects on the intercept in the R^2 computation, i.e. the basin effect (a_n) and the site effect ($a_{i|n}$), as the inclusion of the variance attributed to random slopes is much complex and was shown to not change the

results (Nakagawa and Schielzeth 2013; LaHuis et al. 2014). We computed the variance associated of each predicted values from their posterior distribution (`inla.rmarginal` in INLA R package), following Gelman et al. (2019) recommendations to take in account the variability associated with the priors (θ). As we computed the variance of predicted values for each observation, we computed R-squared values associated to each observation to obtained the R-squared distribution (Gelman et al. 2019). We then reported the mean marginal and conditional R-squared associated the 95% credible interval computed using the Highest Posterior Density method.

$$R_m^2 = \frac{Var_{fit}}{Var_{fit} + Var_{res}} = \frac{\sigma^2(\hat{y}_i)}{\sigma^2(\hat{y}_i) + \sigma^2(y_i - \hat{y}_i)}$$

$$R_c^2 = \frac{Var_{fit} + (a_n)^2 + (a_{i|n})^2}{Var_{fit} + (a_n)^2 + (a_{i|n})^2 + Var_{res}}$$

y_i and \hat{y}_i being respectively the observations and the predicted values, Var_{fit} and Var_{res} being respectively the variance of predictive means and the variance of the residuals, Gelman et al. (2019). a_n and $a_{i|n}$ are respectively the standard deviation on the random intercept associated to the hydrographic basin and the site.

4.3 Assessing the dimensionality of temporal community changes

We performed a PCA over the temporal trends of community metrics at the site level to find the linear combination of variables that explained the most variance and separates linearly uncorrelated variables. In complement, we performed a clustering analysis to identity types of community trajectories. The temporal trends for each biodiversity facet and site were extracted by the Best Linear Unbiased Prediction method. We did not include the temporal trends of the variables describing composition of non-native species as the they are part of biodiversity (Schlaepfer 2018) and the changes in the proportion of non-native species displayed little variation, then it was of little interest to include them in the dimensionality analysis.

We performed clustering using the trimmed k-means method (Fritz, García-Escudero, and Mayo-Iscar 2012), a robust clustering method because it avoids the identification of spurious clusters. The method consists of trimming the α most outlying data while taking in account the multidimensional structure, the number of dimension being the number of community metric. To choose a relevant number of clusters, we plotted the trimmed log-likelihood of the function as a function of the proportion of the most outlying data trimmed (α) (Fig. S7). We thus selected a partition of temporal community changes in six clusters with $\alpha = 5\%$. We did not constraint the algorithm for the relative size of shape of the clusters, as we had no apriori expectation about them. The clustering algorithm was run for a minimum number of one hundred iterations and up to 125. To further control for the quality of each fish community changes assignment to a given cluster, we discarded any fish community for which the second best cluster assignment was 50% better than the first one, we did so by comparing the degree of affiliation to the clusters (Fritz, García-Escudero, and Mayo-Iscar 2012). The clustering was performed using `tclust` R package.

5 Reproducibility and open science statement

The main text, the present document and the supplementary materials are written in Rmarkdown, i.e. combining code and text, and are available on github. We further implement a code pipeline using the `targets` R package to ensure that all the code, the data, the figures, the manuscript and the results are up to date.

References

- Altermatt, Florian, Mathew Seymour, and Nicolas Martinez. 2013. “River Network Properties Shape - Diversity and Community Similarity Patterns of Aquatic Insect Communities Across Major Drainage Basins.” *Journal of Biogeography* 40 (12): 2249–60. <https://doi.org/10.1111/jbi.12178>.

- Baselga, Andrés, Sébastien Bonthoux, and Gérard Balent. 2015. “Temporal Beta Diversity of Bird Assemblages in Agricultural Landscapes: Land Cover Change Vs. Stochastic Processes.” *PLOS ONE* 10 (5): e0127913. <https://doi.org/10.1371/journal.pone.0127913>.
- Baselga, Andrés, and C. David L. Orme. 2012. “Betapart : An R Package for the Study of Beta Diversity: *Betapart Package*.” *Methods in Ecology and Evolution* 3 (5): 808–12. <https://doi.org/10.1111/j.2041-210X.2012.00224.x>.
- Blowes, Shane A., Sarah R. Supp, Laura H. Antão, Amanda Bates, Helge Bruehlheide, Jonathan M. Chase, Faye Moyes, et al. 2019. “The Geography of Biodiversity Change in Marine and Terrestrial Assemblages.” *Science* 366 (6463): 339–45. <https://doi.org/10.1126/science.aaw1620>.
- Chao, Anne, and Lou Jost. 2012. “Coverage-Based Rarefaction and Extrapolation: Standardizing Samples by Completeness Rather Than Size.” *Ecology* 93 (12): 2533–47. <https://doi.org/10.1890/11-1952.1>.
- Comte, Lise, Juan Carvajal-Quintero, Pablo A. Tedesco, Xingli Giam, Ulrich Brose, Tibor Erős, Ana F. Filipe, et al. 2021. “RivFishTIME: A Global Database of Fish Time-Series to Study Global Change Ecology in Riverine Systems.” *Global Ecology and Biogeography* 30 (1): 38–50. <https://doi.org/10.1111/geb.13210>.
- Dornelas, Maria, Nicholas J. Gotelli, Brian McGill, Hideyasu Shimadzu, Faye Moyes, Caya Sievers, and Anne E. Magurran. 2014. “Assemblage Time Series Reveal Biodiversity Change but Not Systematic Loss.” *Science* 344 (6181): 296–99. <https://doi.org/10.1126/science.1248484>.
- Fritz, Heinrich, Luis A. García-Escudero, and Agustín Mayo-Iscar. 2012. “Tclust: An R Package for a Trimming Approach to Cluster Analysis.” *Journal of Statistical Software* 47 (May): 1–26. <https://doi.org/10.18637/jss.v047.i12>.
- Froese, Rainer, Daniel Pauly, and others. 2021. *FishBase*. Fisheries Centre, University of British Columbia.
- Gelman, Andrew. 2008. “Scaling Regression Inputs by Dividing by Two Standard Deviations.” *Statistics in Medicine* 27 (15): 2865–73. <https://doi.org/10.1002/sim.3107>.
- Gelman, Andrew, Ben Goodrich, Jonah Gabry, and Aki Vehtari. 2019. “R-Squared for Bayesian Regression Models.” *The American Statistician* 73 (3): 307–9. <https://doi.org/10.1080/00031305.2018.1549100>.
- Gelman, Andrew, Jessica Hwang, and Aki Vehtari. 2014. “Understanding Predictive Information Criteria for Bayesian Models.” *Statistics and Computing* 24 (6): 997–1016. <https://doi.org/10.1007/s11222-013-9416-2>.
- Greenland, Sander, Stephen J. Senn, Kenneth J. Rothman, John B. Carlin, Charles Poole, Steven N. Goodman, and Douglas G. Altman. 2016. “Statistical Tests, P Values, Confidence Intervals, and Power: A Guide to Misinterpretations.” *European Journal of Epidemiology* 31: 337–50. <https://doi.org/10.1007/s10654-016-0149-3>.
- Hillebrand, Helmut, Bernd Blasius, Elizabeth T. Borer, Jonathan M. Chase, John A. Downing, Britas Klemens Eriksson, Christopher T. Filstrup, et al. 2018. “Biodiversity Change Is Uncoupled from Species Richness Trends: Consequences for Conservation and Monitoring.” *Journal of Applied Ecology* 55 (1): 169–84. <https://doi.org/10.1111/1365-2664.12959>.
- Hyndman, Rob J. 1996. “Computing and Graphing Highest Density Regions.” *The American Statistician* 50 (2): 120–26. <https://doi.org/10.1080/00031305.1996.10474359>.
- Kaiser, Henry F. 1958. “The Varimax Criterion for Analytic Rotation in Factor Analysis.” *Psychometrika* 23 (3): 187–200. <https://doi.org/10.1007/BF02289233>.
- Klink, Roel van, Diana E. Bowler, Konstantin B. Gongalsky, Ann B. Swengel, Alessandro Gentile, and Jonathan M. Chase. 2020. “Meta-Analysis Reveals Declines in Terrestrial but Increases in Freshwater Insect Abundances.” *Science* 368 (6489): 417–20. <https://doi.org/10.1126/science.aax9931>.
- LaHuis, David M., Michael J. Hartman, Shotaro Hakoyama, and Patrick C. Clark. 2014. “Explained Variance Measures for Multilevel Models.” *Organizational Research Methods* 17 (4): 433–51. <https://doi.org/10.1177/1094428114541701>.

- Linke, Simon, Bernhard Lehner, Camille Ouellet Dallaire, Joseph Ariwi, Günther Grill, Mira Anand, Penny Beames, et al. 2019. “Global Hydro-Environmental Sub-Basin and River Reach Characteristics at High Spatial Resolution.” *Scientific Data* 6 (1): 283. <https://doi.org/10.1038/s41597-019-0300-6>.
- Mastrandrea, Michael D., Christopher B. Field, Thomas Stocker F., Ottmar Edenhofer, Kristie Ebi L., David Frame J., Hermann Held, et al. 2010. “Guidance Note for Lead Authors of the IPCC Fifth Assessment Report on Consistent Treatment of Uncertainties.” Jasper Ridge, CA, USA: ntergovernmental Panel on Climate Change (IPCC). https://www.ipcc.ch/site/assets/uploads/2017/08/AR5_Uncertainty_Guidance_Note.pdf.
- Nakagawa, Shinichi, and Holger Schielzeth. 2013. “A General and Simple Method for Obtaining R² from Generalized Linear Mixed-Effects Models.” *Methods in Ecology and Evolution* 4 (2): 133–42. <https://doi.org/10.1111/j.2041-210x.2012.00261.x>.
- Revelle, William. 2019. “Psych: Procedures for Psychological, Psychometric, and Personality Research.” Evanston, Illinois: Northwestern University. <https://CRAN.R-project.org/package=psych>.
- Robinson, Natalie, James Regetz, and Robert P. Guralnick. 2014. “EarthEnv-DEM90: A Nearly-Global, Void-Free, Multi-Scale Smoothed, 90m Digital Elevation Model from Fused ASTER and SRTM Data.” *ISPRS Journal of Photogrammetry and Remote Sensing* 87 (January): 57–67. <https://doi.org/10.1016/j.isprsjprs.2013.11.002>.
- Rue, Håvard, Sara Martino, and Nicholas Chopin. 2009. “Approximate Bayesian Inference for Latent Gaussian Models Using Integrated Nested Laplace Approximations (with Discussion).” *Journal of the Royal Statistical Society B* 71: 319–92.
- Rue, Håvard, Andrea I. Riebler, Sigrunn H. Sørbye, Janine B. Illian, Daniel P. Simpson, and Finn K. Lindgren. 2017. “Bayesian Computing with INLA: A Review.” *Annual Reviews of Statistics and Its Applications* 4 (March): 395–421. <http://arxiv.org/abs/1604.00860>.
- Schlaepfer, Martin A. 2018. “Do Non-Native Species Contribute to Biodiversity?” *PLOS Biology* 16 (4): e2005568. <https://doi.org/10.1371/journal.pbio.2005568>.
- Tedesco, Pablo A., Olivier Beauchard, Rémy Bigorne, Simon Blanchet, Laëtitia Buisson, Lorenza Conti, Jean-François Cornu, et al. 2017. “A Global Database on Freshwater Fish Species Occurrence in Drainage Basins.” *Scientific Data* 4 (October): 170141. <https://doi.org/10.1038/sdata.2017.141>.
- Vehtari, Aki, Andrew Gelman, and Jonah Gabry. 2017. “Practical Bayesian Model Evaluation Using Leave-One-Out Cross-Validation and WAIC.” *Statistics and Computing* 27 (5): 1413–32. <https://doi.org/10.1007/s11222-016-9696-4>.
- Venter, Oscar, Eric W. Sanderson, Ainhua Magrath, James R. Allan, Jutta Beher, Kendall R. Jones, Hugh P. Possingham, et al. 2016a. “Global Terrestrial Human Footprint Maps for 1993 and 2009.” *Scientific Data* 3 (1): 160067. <https://doi.org/10.1038/sdata.2016.67>.
- . 2016b. “Sixteen Years of Change in the Global Terrestrial Human Footprint and Implications for Biodiversity Conservation.” *Nature Communications* 7 (1): 12558. <https://doi.org/10.1038/ncomms12558>.
- Williams, Brooke A., Oscar Venter, James R. Allan, Scott C. Atkinson, Jose A. Rehbein, Michelle Ward, Moreno Di Marco, et al. 2020. “Change in Terrestrial Human Footprint Drives Continued Loss of Intact Ecosystems.” *One Earth* 3 (3): 371–82. <https://doi.org/10.1016/j.oneear.2020.08.009>.