**Online Figures for:**

**The recovery of European freshwater biodiversity has come to a halt**

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**Driver correlations**

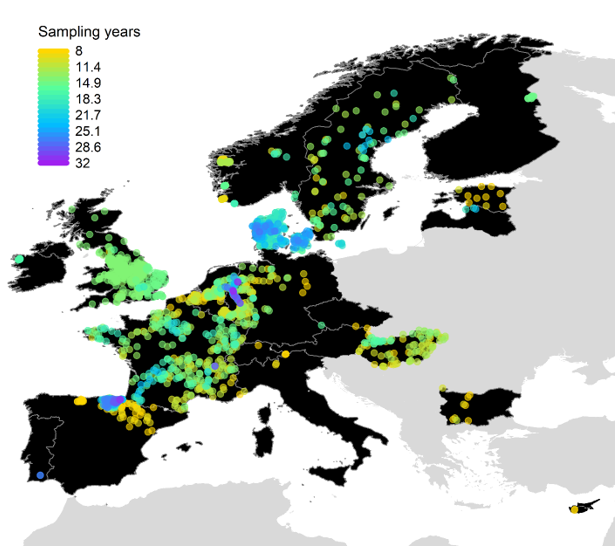
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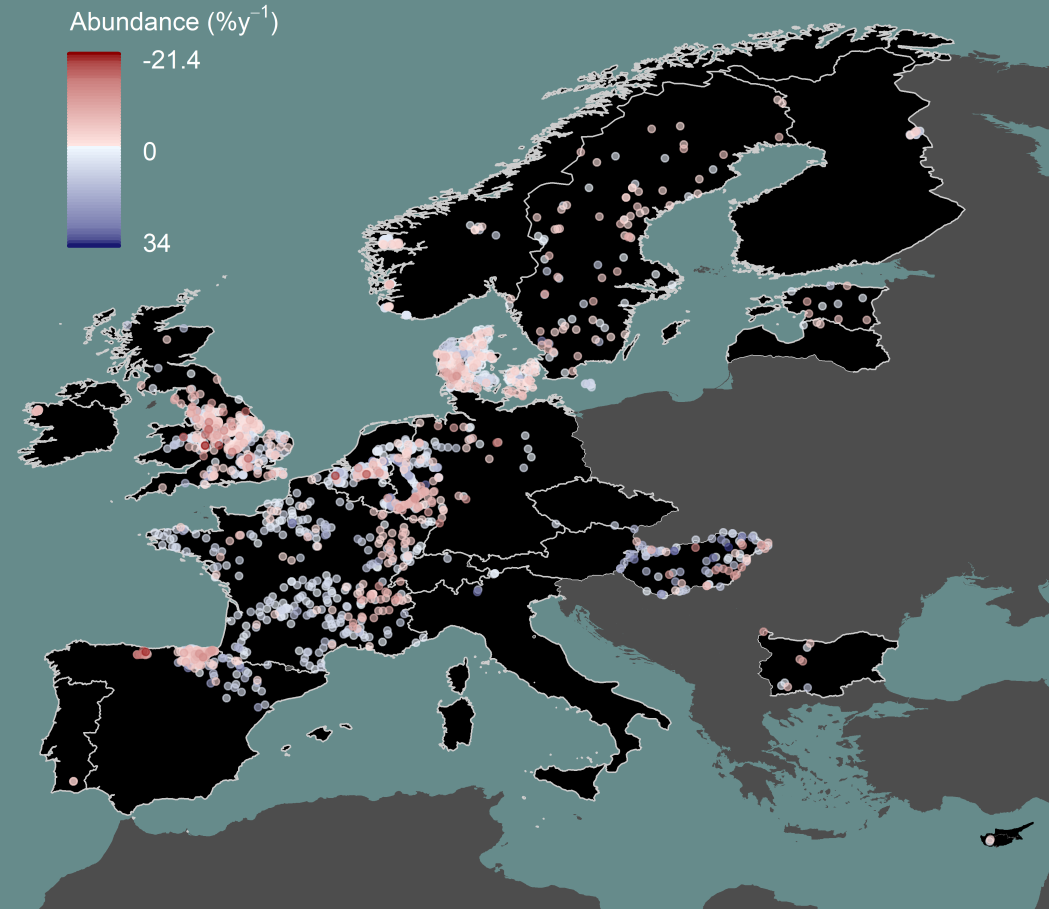
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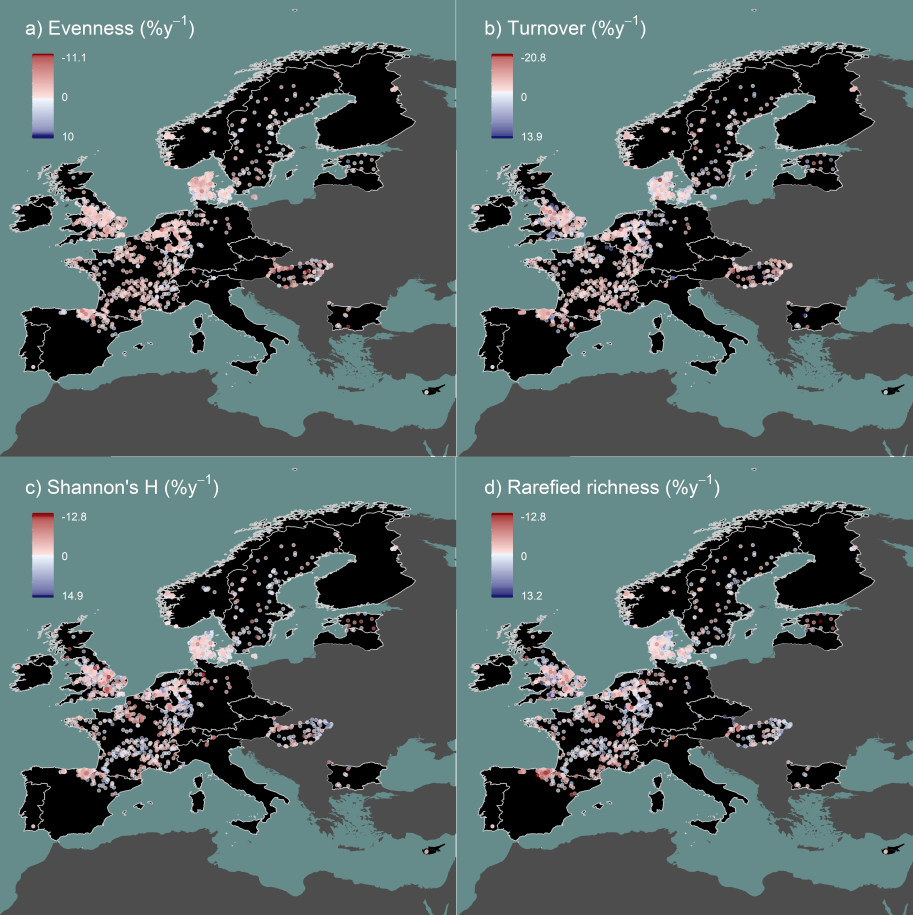
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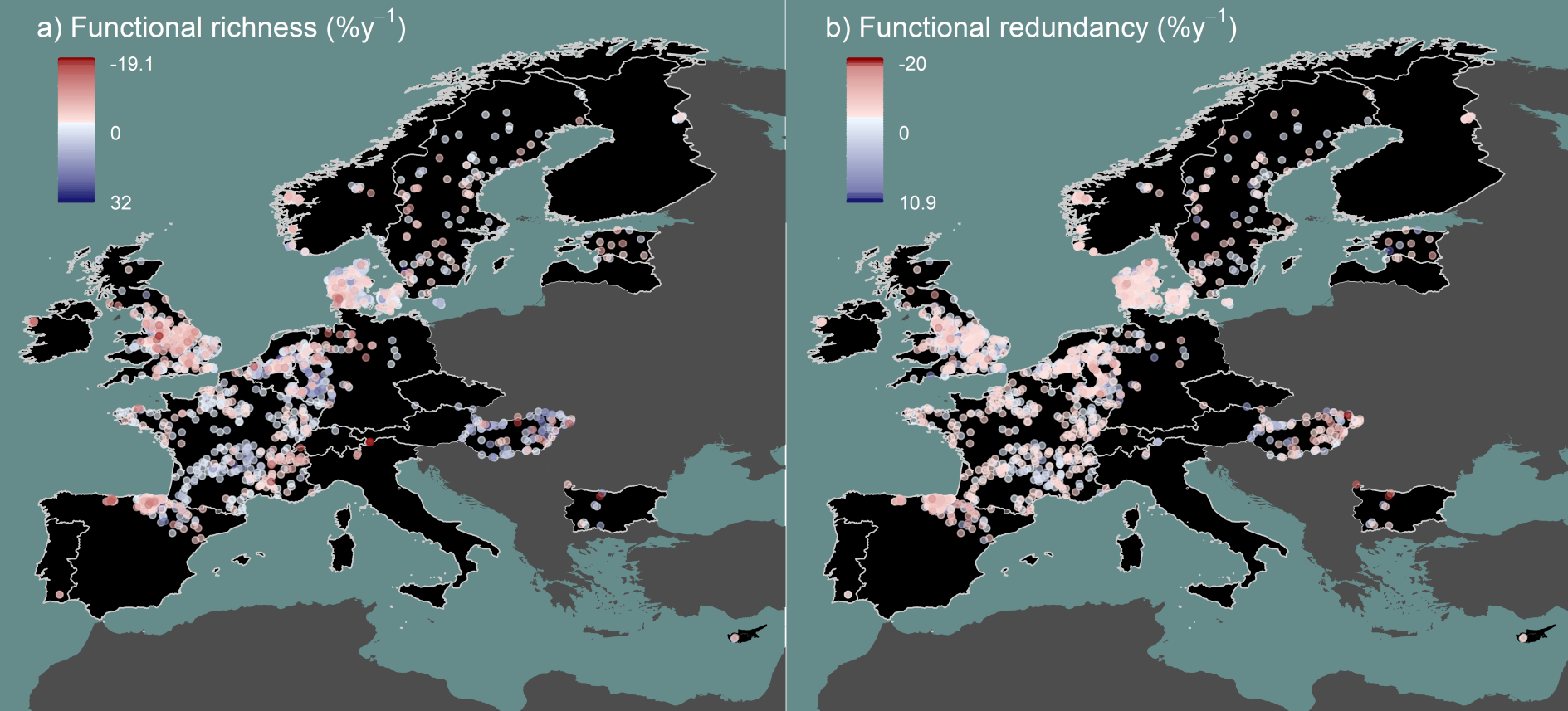
**Fig. 1 | Spatial variation in the number of sampling years across all 1,816 study sites.**

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**Fig. 2 | Spatial distribution of abundance trends.** Point colors represent site-specific abundance trends in percentage change per year.



**Fig. 3 | Spatial distribution of trends in additional taxonomic diversity metrics.** Point colors represent site trends in percentage change per year for **a)** Shannon’s evenness, **b)** taxonomic turnover, **c)** Shannon’s diversity (H), and **d)** rarefied taxon richness.



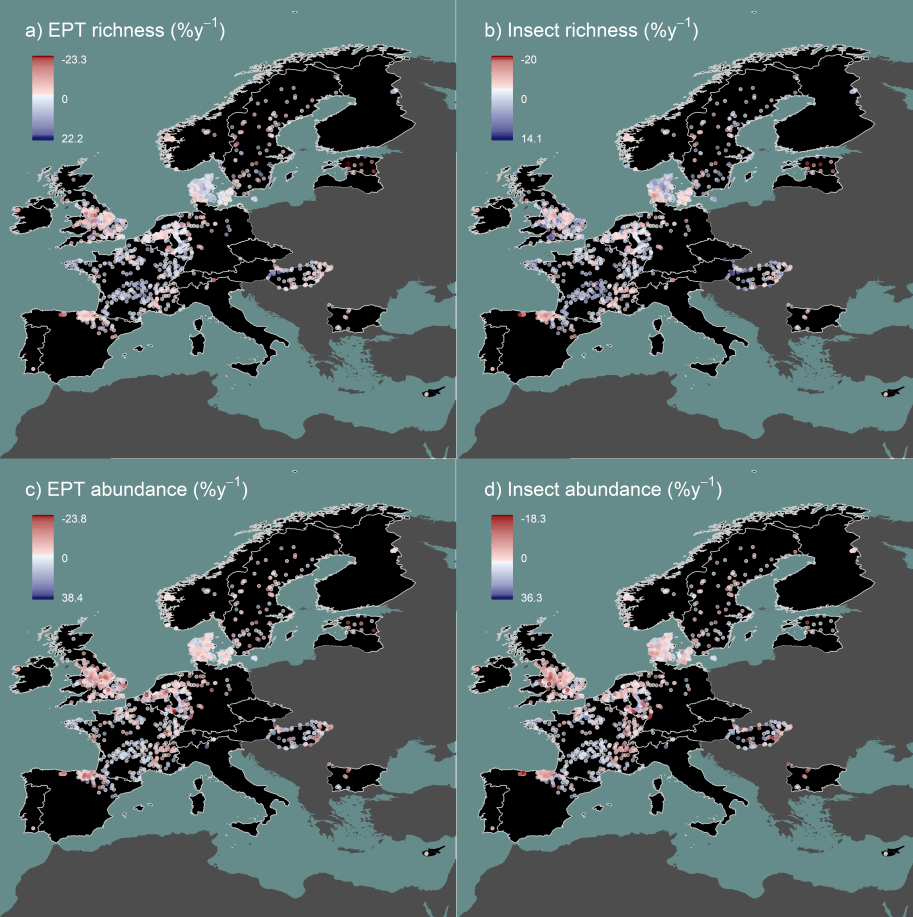
**Fig. 4 | Spatial distribution of trends in functional diversity metrics.** Point colors represent site trends in percentage change per year for **a)** functional richness and **b)** functional redundancy.



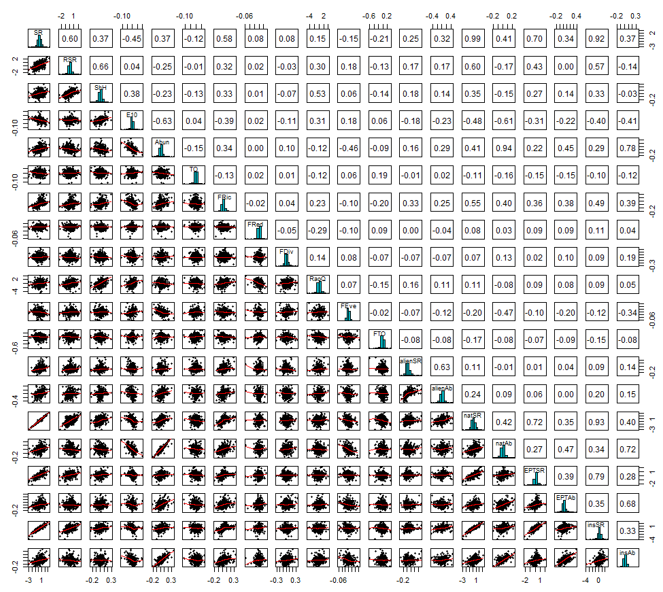
**Fig. 5 | Spatial distribution of trends in additional functional diversity metrics.** Point colors represent site trends in percentage change per year for **a)** functional evenness, **b)** functional turnover, **c)** Rao’s quadratic entropy, and **d)** functional divergence.



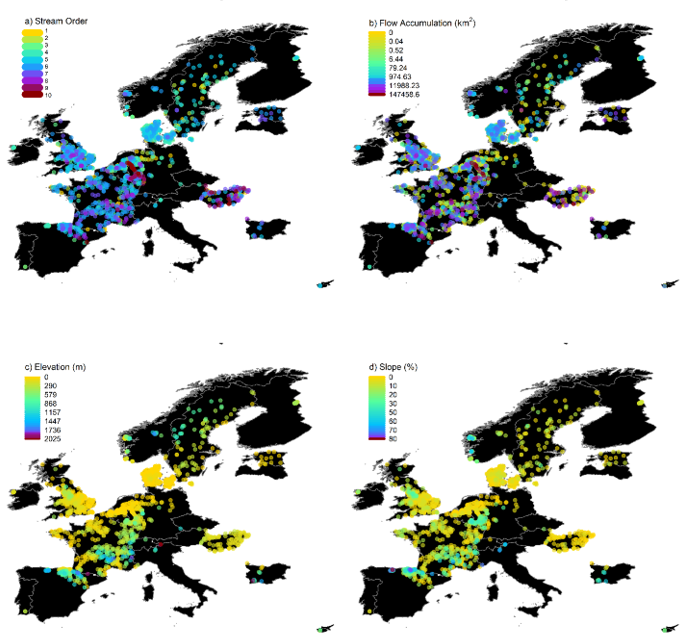
**Fig. 6 | Spatial distribution of trends in non-native and native species.** Point colors represent site trends in percentage change per year for **a)** non-native taxon richness, **b)** native taxon richness, **c)** non-native abundance, and **d)** native abundance. Only the 1,299 sites having high taxonomic resolution enabling identification of native versus non-native species are shown.



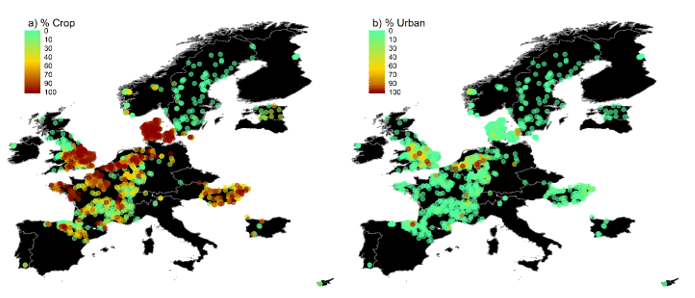
**Fig. 7 | Spatial distribution of trends in EPT and insect taxa.** Point colors represent site trends in percentage change per year for **a)** EPT taxon richness, **b)** insect taxon richness, **c)** EPT abundance, and **d)** insect abundance.



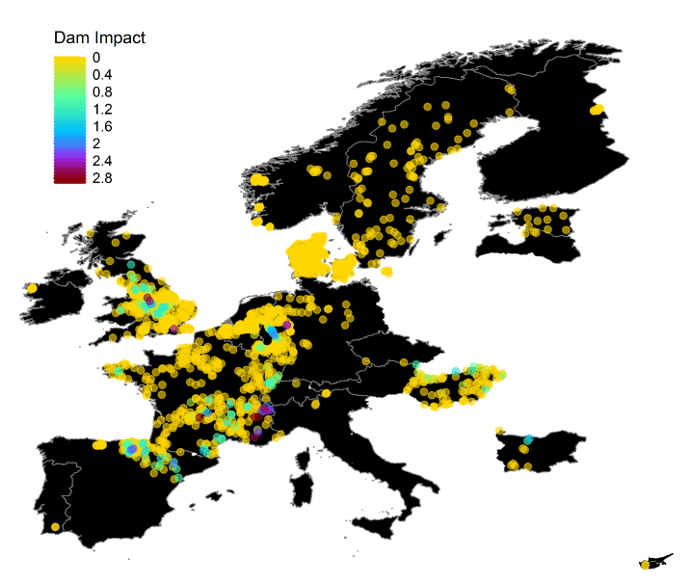
**Fig. 8 | Pearson’s correlations, histograms, and regression plots comparing all response variables.** SR = taxon richness, RSR = rarefied taxon richness, ShH = Shannon’s diversity (H), E10 = Shannon’s evenness, Abund = abundance, TO = taxonomic turnover, FRic = functional richness, FRed = functional redundancy, FDiv = functional divergence, RaoQ = Rao’s quadratic entropy, FEve = functional evenness, FTO = functional turnover, alienSR = non-native species richness, alienAb = non-native abundance, natSR = native taxon richness, natAb = native abundance, EPTSR = EPT taxon richness, EPTAb = EPT abundance, insSR = insect taxon richness, and insAb = insect abundance.



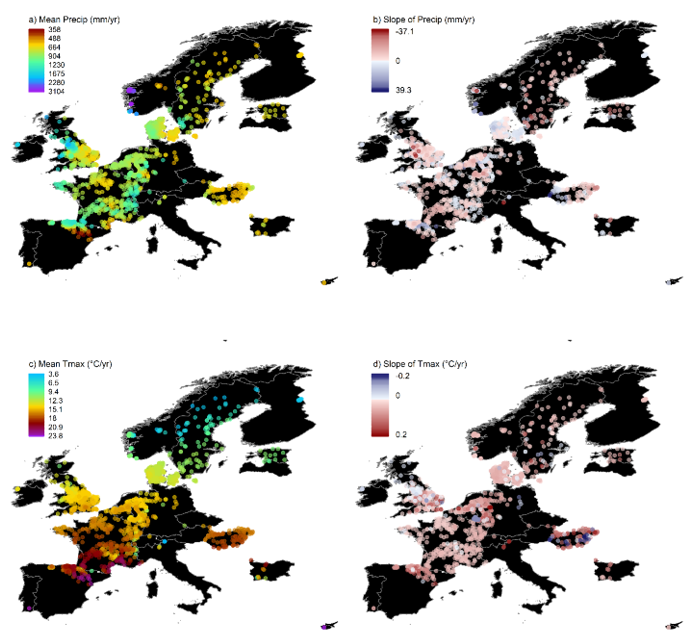
**Fig. 9 | Distribution of stream characteristics.** Spatial variation across the 1,816 study sites in **a)** Strahler stream order, **b)** flow accumulation, **c)** elevation, and **d)** slope. See Extended Data Table 4 for more details and sources of environmental data.



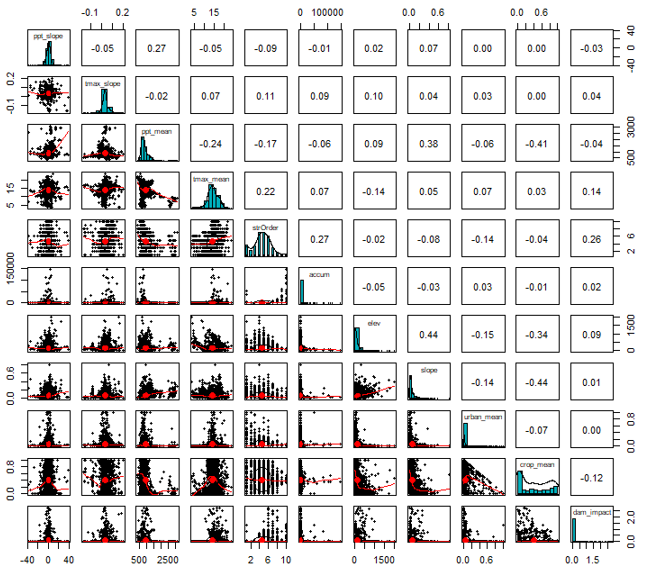
**Fig. 10 | Distribution of land cover.** Spatial variation across the 1,816 study sites in percentage upstream **a)** crop and **b)** urban land cover types. See Extended Data Table 4 for details and sources of environmental data.



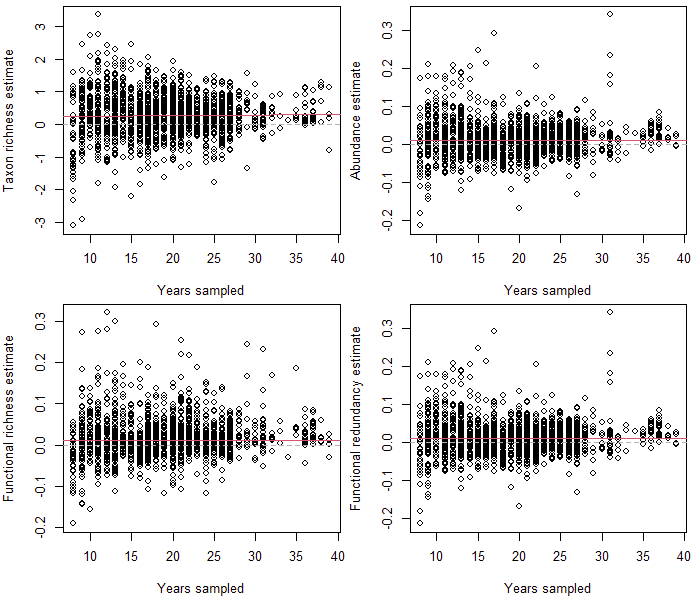
**Fig. 11 | Distribution of dam impacts.** Spatial variation across the 1,816 study sites in dam impact score based on distances between sites and upstream dams. See Extended Data Table 4 for details and the source of dam data and Methods for calculation of dam impact scores.



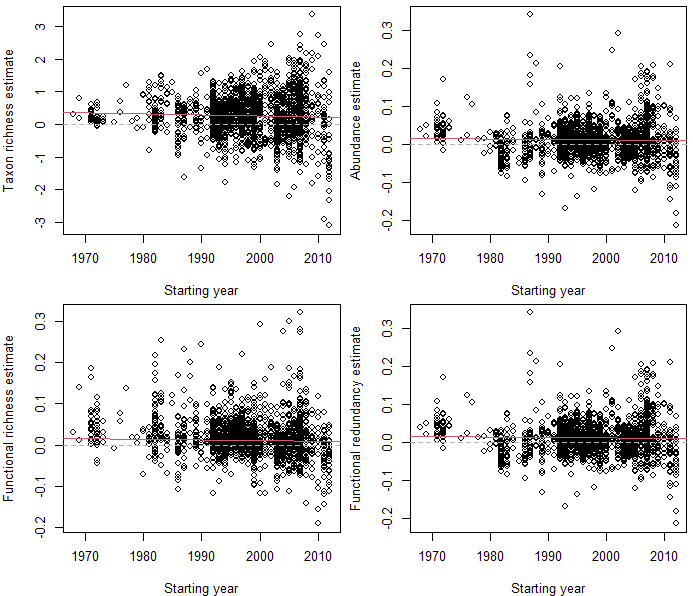
**Fig. 12 | Distribution of climate variation.** Spatial variation across the 1,816 sites and over study duration for **a)** mean cumulative annual precipitation, **b)** the change (trend) in annual precipitation per year, **c)** mean annual maximum temperature, and **d)** the change (trend) in annual mean maximum temperature per year. See Extended Data Table 4 for details and sources of climate data and the Methods for additional description of the calculations.



**Fig. 13 | Pearson’s correlations, histograms, and regression plots comparing all stream characteristics and environmental driver variables.** ppt\_slope = the change (trend) in annual precipitation per year, tmax\_slope = the change (trend) in annual mean maximum temperature per year, ppt\_mean = mean annual cumulative precipitation, tmax\_mean = mean annual maximum temperature, strOrder = Strahler stream order, accum = flow accumulation, elev = elevation, slope = slope, urban\_mean = percentage upstream urban land cover, crop\_mean = percentage upstream crop land cover, dam\_impact = dam impact score. See Extended Data Table 4 and Methods for additional information on environmental data sources and processing.



**Fig. 14 | Sensitivity check to examine effects of years sampled on biodiversity trend estimates.** Grey dashed lines mark a trend of zero and red solid lines show linear regressions relationships between years sampled and estimates.



**Fig. 15 | Sensitivity check to examine effects of the first sampling year (start year) on biodiversity trend estimates.** Grey dashed lines mark a trend of zero and red solid lines show linear regressions relationships between start year and estimates.



**Fig. 16 | Comparison of trend estimates between meta-analysis models.** Model estimates were comparable across model types including **a,** Weighted Meta-analysis: the model type used and described in the main manuscript where estimates are weighted by their uncertainty, **b,** Unweighted Meta-analysis: a two stage meta-analysis with no incorporation of uncertainty, and **c,** One Stage: a hierarchical model including site identity as a random term. Scripts including model formulas can be found at https://github.com/Ewelti/EuroAquaticMacroInverts in the “R” folder.



**Fig. 17 | Jackknife analysis of trend estimates with countries removed.** Model estimates of trends for taxonomic and functional response variables with each country sequentially removed. The removed country is labeled on the y-axis. Jackknife script including model formula can be found at https://github.com/Ewelti/EuroAquaticMacroInverts under “R/ HPC\_Meta\_analysis\_country\_jacknife.R”.



**Fig. 18 | Distribution over time for sites of a given taxonomic resolution.** Number of sites per taxonomic resolution (species, genus/mixed, family) included in each year across the study duration.



**Fig. 19 | Distribution over time for sites per country in moving window analysis.** Number of sites per country included in moving window from windows of 1990-1999 to 2011-2020 with x-axis showing mean year of each window.



**Fig. 20 | Distribution over time for sites of a given taxonomic resolution in moving window analysis.** Number of sites per taxonomic resolution (species, genus/mixed, family) included in moving window from windows of 1990-1999 to 2011-2020 with x-axis showing mean year of each window.



**Fig. 21 | Proportion of positive to negative sites in moving window trends.** Change in number of sites with positive versus negative trends in moving window analysis of **a**, taxon richness, **b**, abundance, **c**, functional richness, and **d**, functional redundancy. Values of “1” indicate equal number of sites with positive and negative trends, values >1 = more sites with positive versus negative trends, and values <1 = less sites with positive versus negative trends.



**Fig. 22 | High threshold moving window analysis 1.** Trends in **a**, taxon richness, **b**, abundance, **c**, functional richness, and **d**, functional redundancy over time from sites with ≥ 15 years of sampling between the years 2000-2018, the period most represented in our dataset. This analysis included 515 sites from 11 countries. Estimates were calculated from Bayesian mixed-effects models of trends with ≥ 6 years within 10-year moving windows (windows 2000-2009 to 2009-2018). Years on the x-axis represent the mean year of each window. Gray polygons indicate 80, 90, and 95% credible intervals.



**Fig. 23 | High threshold moving window analysis 2.** Trends in **a**, taxon richness, **b**, abundance, **c**, functional richness, and **d**, functional redundancy over time from sites with ≥ 20 years of sampling between the years 1990-2020, the period most represented in our dataset. This analysis included 308 sites from 8 countries. Estimates were calculated from Bayesian mixed-effects models of trends with ≥ 6 years within 10-year moving windows (windows 1990-1999 to 2011-2020). Years on the x-axis represent the mean year of each window. Gray polygons indicate 80, 90, and 95% credible intervals.



**Fig. 24 | Moving window analysis of sites with species level community resolution.** Trends in **a**, taxon richness, **b**, abundance, **c**, functional richness, and **d**, functional redundancy over time from sites with communities sorted to species level resolution. This analysis included 717 sites from 14 countries. Years were included when they represented a minimum of 200 sites. Estimates were calculated from Bayesian mixed-effects models of trends with ≥ 6 years within 10-year moving windows (windows 1994-2003 to 2011-2020; windows prior to 1994 had fewer than 200 sites and were not included). Years on the x-axis represent the mean year of each window. Gray polygons indicate 80, 90, and 95% credible intervals.