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# 1 Introduction

A tool in the management and research of ecosystems is to divide them into different types: river types, ecoregions, habitat types. These examples serve to highlight the breadth of systems, spatial scales, and methods employed in this exercise. These classifications can be usefull for several discinct reasons. They are a easy to use representation of the environmental context and might be considered as a latent, discrete gradient capturing the relevant environmental variables like their continuous counterpart, the ordination axis. This environmental context can then be used to calibrate indicator metrics in biomonitoring (Szoszkiewicz et al. 2019). This is necessary as responses of biota to natural gradients (Alahuhta et al. 2017; Bogotá-Gregory et al. 2023) and anthropogenic stressors (Denison et al. 2021; Pharaoh et al. 2024; Bevan et al. 2024) can differ between ecosystem types. Such context or region-dependence has also been observed for trait-environment relationsships (Yang et al. 2018; Burner et al. 2021; Kopp et al. 2023). They are also used as a controlling variable when planning experiments. When we try to minimize the impact certain environmental features, we can focus our sampling to a small selection of types (ref). We often hold different protection goals for different regions of habitats - a typology can then facilitating the selection, combination, or priorisation of management actions. Lastly, they can also serve as a proxy for species ranges, where detailed information is lacking (Pinkert et al. 2023).

Typologies are models. Rather than describing nature, they superimpose their simplified view. A view that can be usefull if they meet the assumption that ecological communities within types are more similar to oneanother than to communities from other types. Generally this property is known as external cluster validity (insert short description), and in this context more specifically as biological validity (ref). With the advent of typology systems in different management schemes (Clean Water act, Water Framework Directive, more examples - also check CWA again.) interest in biovalidation grew and noumerous systems have to date been evaluated against noumerous (new word) taxonomic groups.

Provide some examples.

The available studies on the biovalidity of typology systems suffer from two flaws. First, there is contention which method should be used to determine biovalidity. Different studies use different methods, which reduces comparability among them. It remians difficult to compare the biovalidity of typology systems across taxa and places, because we lack an empirically grounded notion of how biovalid a biovalid typology systems is. In lieu, two practices have taken hold. Biovalidity is judged against unrealistic heurisitcs without ecological foundations or against statistical significane. Effect size heuristics exist for some commonly used metrics but not all. They are not specifically tailored to evaluate biovalidity. They are based on practically irrelevant considerations. The fact that these heuristics are disconnected from ecological realities is evident as they are context-, scale-, and taxon-independent. All three factors should influence the result.

Dichotomous decisions based on *p*-values suffer from a slew of issues. Here, we wish to highlight X issues relevent whithin this context. P-value depend on effect size and sample size. Large scale ecological studies typically have a large number of sampling sites, thus rendering even miniscule effect sizes statistcally significant. A move toward *a priori* determined relevant effect sizes seems frutiful (Popovic et al. 2024). Other ways to adress these issues have been proposed but will be considered here (Maier and Lakens 2022; Wulff and Taylor 2023; Crouch 2025)

We aim to provide a comprehensive set of benchmarks for different biovalidity metrics. These benchmarks will cover different taxonomic groups and different spatial scales. We will train a large number regression models on independent empirical data sets and use these models to simulate new biological data. These simulations will be based on artificial typology systems along a gradient of low to high expected biovalidity, thus enabling us to map plausible ranges for different metrics, spatial scales, and taxa.

## 1.1 Methods

### 1.1.1 The data sets

Within each data set, we will stratify the subsampling by year. Within each year, we will restrict it to the three consective months with the most samples. If these number of samples in these months () < 100 samples, this year will not be evaluated for this data set. If samples, our subsampling methodology will incorporate a descending-frequency approach based on one hundred-sample increments. The process will begin by dividing by 100 (rounded down) to determine the number of increments . For each increment from 1 to , we will generate independent subsamples, each containing samples. When the remainder from dividing by 100 exceeds 0.5, we will include one additional sample at the maximum size. This approach ensures thorough sampling coverage while maintaining computational feasibility. For each subsample we determined the minimum, mean, median, and maximum spatial distance between samples with the R package sf (ref). We then remove taxa that occur in less than 5% of sampling sites.

### 1.1.2 Environmental data

We will compile and extensive data base of environmental variables relevant for freshwater organisms (Table 1). Each variable will be summarized at the catchment scale, where catchments are derived from the EU hydro DEM catchment data base (REF).

| Variable | Spatial Scale | Data product | Reference |
| --- | --- | --- | --- |
| Rainfall erosivity | Ecosystem | GloREDa | Panagos et al. (2023) |
| Soil Organic Carbon | Ecosystem | European Soil Database v2.0 | Panagos et al. (2022) |
| Soil pH in Water | Ecosystem | EcoDataCube | Witjes et al. (2023) |
| Slope | Ecosystem | Hydrography90m | Amatulli et al. (2022) |
| Roughness | Ecosystem | Geomorpho90m | Amatulli et al. (2020) |
| Floodplain Area | Ecosystem | Potential Flood prone Area | EEA (2020) |
| Mean annual discharge | Ecosystem | Copernicus C3S | Berg et al. (2021) |
| Minimum annual discharge | Ecosystem | Copernicus C3S | Berg et al. (2021) |
| Saturated Soil Water Content | Ecosystem | Soil Hydraulic Properties | Tóth et al. (2015) |
| Upstream catchment area | Ecosystem | HydroATLAS | Linke et al (2019) |
| Maximum annual discharge | Ecosystem | Copernicus C3S | Berg et al. (2021) |
| Snow Cover | Ecosystem | HydroATLAS | Linke et al (2019) |
| Segment Sinuosity | Ecosystem | EU Hydro | EEA (2019) |
| Valley Bottom Flatness Index | Ecosystem | EcoDataCube | Witjes et al. (2023) |
| Stream Power Index | Ecosystem | Hydrography90m | Amatulli et al. (2022) |
| Lake Index | Ecosystem | HydroLAKES | Messager et al. (2016); Snelder et al. (2005) |
| Elevation | Region, Ecosystem | Hydrography90m | Amatulli et al. (2022) |
| Groundwater Table Depth | Region | HydroATLAS | Linke et al. (2019) |
| Glaciated Area in Catchment | Region | Randolph Glacier Inventory | RGI Consortium (2017) |
| Precipitation of Wettest Month | Region | CHELSA-BIOCLIM+ | Brun et al. (2022) |
| Precipitation of Driest Month | Region | CHELSA-BIOCLIM+ | Brun et al. (2022) |
| Minimum Temperature Coldest Month | Region | CHELSA-BIOCLIM+ | Brun et al. (2022) |
| Maximum Temperature Warmest Month | Region | CHELSA-BIOCLIM+ | Brun et al. (2022) |
| Bedrock Geology | Region | IHME | Cornu et al. (2013) |
| Catchment soil type | Region | European Soil Database v2.0 | Panagos et al. (2022) |

We will capture the impact of space using one of two different approaches: Moran’s Eigenvector Maps (MEM, ref) or Asymmetric Eigenvector Maps (AEM, ref). (ref) MEM will be used of the largest spatial distance within a subsample exceeds T, otherwise we will use AEM. For both we will evaluate the statistical significance of Moran’s I of the eigenvectos with permutation tests (Cliff and Ord 1973), and only keept those eigenvectors which had a statistically significant Moran’s I value. Both will be implemented with the adespatial R package version … (ref).

### 1.1.3 Modellings species communities

To establish the relationship between the presence/ absence of organisms and environmental variables, we will use hierarchical modelling of species communities (HMSC, ref) from the corresponding R package Hmsc (ref). This bayesian hierarchical latent variable model allows the incorporation of phylogeny and traits and has been favoribly compared to similar methdods (ref).  
We will include a non-spatiotemporal random factor for each sample. The model will be fit with a probit residual distribution. Model fit will be evaluated with the potential scale reduction factor and choose a second statistic. By default, we will run models with two chains, 2000 samples, a thinning of 2, and a transient period of 2000 samples. If either of potential scale reduction factor or Welch’s statistic suggest that the chains have not converged or that the posterior is not stationary for > 10% of regression parameters, we will iteratively increase the number of samples up to 10000. Thinning will be increased in parallel, so that it is awlways the number of chains devided by 1000, and the length of the transient equals the number of samples.

Where available, we include both functional traits and phylogenetic data in the HMSC model. For fish, funcitonal data is available through Traits of Freshwater Fish (TOFF, Lecocq et al. 2019) and the phylogenetic data from Rabosky et al. (2018). For diatoms, … . For macroinvertebrates, functional data is available through Kunz et al. (2022), but highly resolved phylogenetic data is only available for certain orders (see García-Girón et al. 2024). For macrophytes,

Rather than evaluating the explained variation based on point estimates derived from the parameter’s posterior distribution, we will compute the full posterior of the VP (see ref) and use point estiamtes from the latter. Due to Jensen’s inequality these two values are not equal.

We will interpret all the variance explained by environmental variables as abiotic filering, the variance explained by spatial eigenvectors as spatial filtering, and the variance of the latent variables as biotic interactions. The last point is highly contentions (Dormann et al. 2018; e.g., Blanchet et al. 2020; Vallé et al. 2023), as the latent variables can also captured unmeasured enviornmental driveres. In our case this will likely include local scale variables such as sediment composition. We expect therefore to slightly overestimate the relevance of biotic interactions and will keep this in mind in any interpretations of the results. Tjur’s (Tjur 2009) will be used to evaluate the overall explained variation in the biotic data.  
The unexplained variance , will be interpreted as stoachistcity in communitiy composition. Each of these values will be averaged across species. For each fitted model, we thus obtain a vector of four numbers, which sum to 1, which estimate the assembly mechanisms of this metacommunity. Over all the models we will run, we will be able to derive a multivariate proability distribution of assembly mechanisms. As each mechanism itself can range between 0 and 1, their distribution can likely be captured by a beta distribution. The dirichlet distribution is a multivariate distribution with beta marginals, and thus able to represent this.

### 1.1.4 Simulating typologies

The fitted models will be used to simulate new bitoic data.

### 1.1.5 Evaluating typologies

We will evaluate each typology with a selection of recommended or practically used methods (see box 1).

| Method | Equation | Metrics | Reference |
| --- | --- | --- | --- |
| Classification Strength | - | cs statistic, **p**-value | Van Sickle (1997) |
| Analysis of Similarity |  | R statistic, **p**-value | Clarke (1993) |

including classification strength, analysis of similarities, area under the zetadiversity decline curve, permutation analysis of variance, silhouette width, indicator value analysis, Indicator Species Analysis Minimizing Intermediate Constancies. A short explanation of each metric is provided in box X.

### 1.1.6 Deriving benchmarks

### 1.1.7 Software

To ensure replicability, we will use the groundhog R package () to use the packageversions that were available on the (add date). Posterior checks were conducted with coda … (), Data wrangling was done with data.table, and tidyverse packages.

# 2 Acknowledgements

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