Contribution to the development of a multifaceted diversity framework in the context of the Biology–Ecology–Environmental Sciences–Environmental Engineering–and–(Human) Society (BEES) System.

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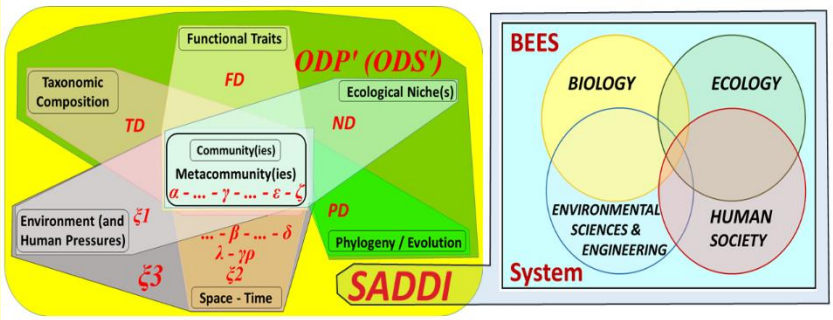
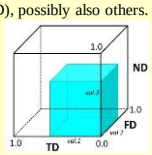
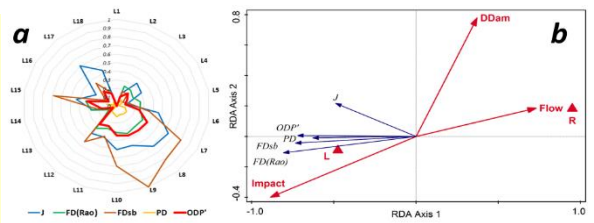


(**Left**). Overview of our contribution to the development of a multifaceted diversity framework in the context of the **Biology - Ecology - Environmental Sciences - Environmental Engineering - and - (Human) Society (BEES) System.** The figure summarizes multiple dimensions of diversity, including (1) **traditional metrics:** TD—taxonomic diversity, FD—functional diversity, ND—niche-based diversity, PD—phylogenetic (or genetic-based) diversity, α—alpha diversity, γ—gamma diversity, ε—epsilon diversity (overall diversity within large biogeographic areas), ζ—zeta diversity, β—beta diversity, δ—delta diversity (change between large biogeographic areas), and (2) **newly introduced metrics:** λ—lambda diversity, γρ— relative sequential cumulative gamma diversity, ξ— xi ecological diversities (ξ1—environment-life diversity, ξ2—life-space diversity, ξ3—integrative ecological diversity), OD'—overall diversities (ODP'—product-based, ODS'—sum-based expressions), SADDI—Standardized Average Diversity Distinctness Index. For clarity, only the primary relationship—through SADDI—is illustrated; other interrelations between diversity measures and the BEES System components are not shown.

Workflow 1. Overall Diversity Index (ODP and ODS)
Purpose: combining, integrating, and synthesizing multiple facets of diversity
Inputs: community-level values for taxonomic diversity (TD), functional diversity (FD), p-distances- or genetic-based diversity (or phylogenetic diversity, if available, PD), niche-based diversity (ND), possibly also others.
Steps: 1. If needed or desired standardize the diversity indices (on a scale [0,1]).
2. Choose combination methods:
Product: ODP, or Sum: ODS
3. Use an averaged version (arithmetic or geometric mean)
ODP' = Geometric mean of ODP components
ODS' = Arithmetic mean of ODS components
4. Compute estimation errors and confidence limits (inferential statistics)
5. If desired use regression analysis, canonical ordination analysis, variation partitioning etc. for liking diversity measures to different types of predictors (e.g., environmental, spatial).
Outputs: ODP or ODS (ODP' or ODS') with confidence intervals and errors. Interpretation as nD hypervolumes and drawing if necessary. Illustrative methods: radar plots, cubes or surfaces, direct ordination diagrams, etc.





(**Up**) a. ODP' including four diversity measures and its constituents depicted as a radar graphic along the river's sector (sites from L1 to L18). b. ODP' and the other diversity measures in relation to the environmental variables (data from the empirical study). J—Pielou's evenness index, FD(Rao)—Rao's quadratic entropy index, FDsb—niche-based diversity measured by the standardized index, PD—genetic-based diversity calculated on p-distances, ODP'—the geometric mean of these diversity measures, Flow—flow, DDam—distance to the nearest downstream dam, Impact—intensity of human pressure, R—lotic, and L—lentic river's sectors

Workflow 2. The Lambda Diversity
Purpose: measures sequential compositional change along a gradient (e.g., spatial, environmental)
Inputs: site-by-species matrix (data table) with binary or quantitative data (workflow and example are on binary data) ordered along a gradient.
Steps: 1. Compute the sequential beta diversity measure:

$$\beta_{w,w+1} = \frac{c^2_{w,w+1}}{(a_w + c_{w,w+1}) \cdot (b_{w+1} + c_{w,w+1})}$$

where a_w denotes the species found only in station or sequence w, b_{w+1} the species found only in the next w+1 station, $c_{w,w+1}$ the common species found in stations w and w+1, where w takes consecutive values from 1 to $(n-1)$.
2. Calculate the *lambda diversity cumulative sequential similarity matrix*, with the lower triangular matrix calculated as:

$$\Lambda = \lambda_{w,z} = \frac{c^2_{w,z}}{(a_{w,z} + c_{w,z}) \cdot (b_{w,z} + c_{w,z})}$$

where w and z are the indexes of summation, which take values between 1 and n (being a triangular matrix $w \geq z$), c are the common species, i.e., present both in the upstream (or former) sector defined by the first z-1 sampling sites and in the next site z, a are the species unique for the sector defined by site 1 to (z-1) and b are the species newly identified in the site z.
3. Establish three triangular matrices, namely A—with species unique for the upstream sector (group of sampling sites), B—with species appearing in each downstream site, and C—the common species, are summarized in the matrix Λ. A and B contain on the main diagonal zero, C contains the total number of species s_w in each station, and Λ the value of 1.
4. Calculate αrs_w the ratio of species from each site along the gradient (line transect or time series) as a relative measure of the alpha diversity:

$$\alpha rs_w = \frac{s_w}{S}$$

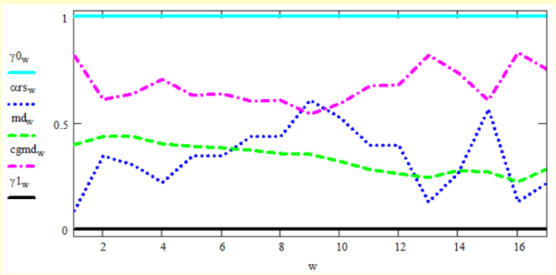
where s_w is the number of species in the sampling site, and S is the total number of species identified along the gradient.
5. Calculate the mean cumulative sequential lambda diversity (md_w). Denote with *ma*, *mb*, and *mc* the mean values for each column in the A, B, and C matrices, namely the mean value for each step (lag) for the species disappearing, appearing, or shared between sectors. Then:

$$md_w = \frac{mc^2_w}{(ma_w + mc_w) \cdot (mb_w + mc_w)}$$

6. Calculate the cumulative sequential gamma diversity (gmd) defined as:

$$gmd_w = \sqrt{\alpha rs_w \cdot md_w}$$

7. Compare with null or benchmark simulated extreme cases of communities
8. If needed use the formulas given in the article and the R code to compute the following measures:
- relative geometrical gamma change (Acgm).
- relative length ratio between the graphical display of the gamma complement and the total possible length of change (Rlgm).
- difference in relative changes in successive gamma diversity measure compared to the maximum possible value (Drgm).
- the relative sequential cumulative gamma diversity change along a gradient (γρ) as the geometric mean of the formerly defined measures of changes—Acgm, Rlgm, and Drgm.
9. Interpretation and visualization:
- line plots, maps, ordination diagrams, etc. Continuum/discontinuum, extent of changes, fragmentation, disturbance.
Outputs: lambda diversity, sequential cumulative gama diversity, plots, regression analysis, etc.



(**Up**) The relative alpha (αrs), mean lambda (md), and corresponding complement of gamma ($cgmd$) diversities plotted against the sample w along the gradient. Extreme values of γ1 = 0 ("nothing changes") and γ0 = 1 ("everything changes") are plotted for comparison and for defining the relative changes.

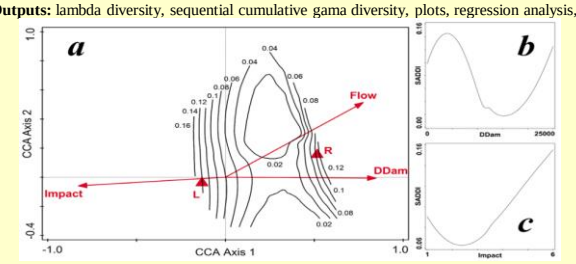
Workflow 3. The Xi (ξ) diversity
Purpose: Integrate biological, spatial and environmental heterogeneity as a dissimilarity measure (metrics based on distance matrix)
Inputs: community dissimilarity matrix (e.g., based on a 1-Jaccard index), spatial distance matrix (e.g., Euclidean distances between sites, distances from a Moran Eigenvector Maps method), and an environmental dissimilarity matrix between sites (based on Gower distance or any suitable dissimilarity metrics).
Steps:
1. Establish the biological dissimilarity matrix (general term d)
2. Build the environmental distance matrix (general term p)
3. Build the spatial distance matrix (general term p)
4. Calculate *ξ1—the xi environment-life diversity* measure, for each site q (q, w, and z take values from 1 to n):

$$\xi 1_q = \frac{1}{2} \sum_{w=1}^{n} \sum_{z=1}^{n} p_{q,w} \cdot p_{q,z} \cdot d_{w,z}$$

5. The same for *ξ2—life-space ecological diversity* (p are spatial dissimilarities)
6. Calculate the *ξ3—integrative ecological diversity*:

$$\xi 3_q = \sqrt{\xi 1_q \cdot \xi 2_q} = \sqrt{\xi\_environment \cdot \xi\_space}$$

7. Use ξ as reponse variable in regression analysis (or ordination) with different types of predictors (such as human impact or pressure, landscape features)
Outputs: xi diversities, combining ecological communities with spatial and environmental heterogeneities, etc. Visualization by regression plots, plots by isolines in ordination space.



(**Up**) a. Loess function-based isolines of SADDI (Standardized Average Diversity Distinctness Index) defined by the 7th root of the distance matrix determinant of diversity measures for each of the 18 sampling stations, plotted on the canonical correspondence analysis (CCA) ordination space of species weights (not shown in the diagram) predicted by the environmental variables (r^2 = 55.0%), b. loess function of SADDI related to DDam (distance to nearest downstream dam, r^2 = 31.4%) and c. to human impact (r^2 = 39.4%)

Workflow 4. The Standardized Average Diversity Distinctness Index (SADDI)
Purpose: Combines different facets of diversity, calculates a matrix of distances or absolute value differences and expresses in a deterministic manner the multidimensional parallelotope (hypervolume) as the determinant of that matrix.
Inputs: matrices of diversity measures (sites-by-diversity measures).
Steps: 1. If necessary normalize or standardize the scale of biodiversity measures to [0,1].
2. Calculate distance matrix between diversity measures (as |x-y|) or its squared form for each site and denote it as D.
3. Calculate the determinant for each matrix describing each site (the determinant is interpreted as the volume of the parallelotope in n-dimensions)
4. Compute the geometric average of the determinant as the n-th root of the value (where n means the number of diversities or the dimension of the parallelotope) as a unit cube.

$$SADDI_w = \sqrt[n]{|\det(D)_w|}$$

5. Use the SADDI measured in the former step as dependent variable in different types of regression and ordination analyses.
Outputs: SADDI values per site–or system, regression models, 2D or 3D plots, isolines plotted by different types of regression methods on canonical ordination spaces and diagrams, etc.

References
1. Sîrbu, I., Benedek, A.M., Sîrbu, M. (2021). Variation partitioning in double-constrained multivariate analyses: linking communities, environment, space, functional traits, and ecological niches. Oecologia 197: 43-59. https://link.springer.com/article/10.1007/s00442-021-05006-6.
2. Sîrbu, I., Benedek, A.M., Sîrbu, M. (2025). Rethinking composite quantification by capturing biological and ecological diversity across multiple dimensions. *Scientific Reports* 15, 27822. https://doi.org/10.1038/s41598-025-13161-6.