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MetaCommunityMetrics.jl: A Julia Package for  
Spatiotemporal Metacommunity Analysis

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Software

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Summary

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Community ecologists are often interested in inferring ecological processes from observational data. This involves calculating different metrics such as beta diversity. Calculating these metrics is easy and fast due to the availability of R packages. However, community ecology today is growing beyond analysing single datasets. Large biodiversity databases have expanded the sets of spatio-temporal community data, and there is a growing interest in using simulations to study ecological processes. For these applications, R packages become slow to use.

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MetaCommunityMetrics.jl is a Julia package that helps ecologists to analyze large datasets of species observations to understand how community composition varies across space and time. By implementing computationally optimized versions of established software and new complementary functions that are designed for handling large spatiotemporal datasets, this package enables ecologists to efficiently analyze large-scale spatiotemporal community datasets that would be computationally prohibitive with existing tools. We designed intuitive interfaces that would feel familiar to ecologists transitioning from R. Our function naming conventions closely match their R equivalents, and we maintained parameter naming and ordering consistency where possible. Some of the metrics we have implemented include beta diversity decompositions in space and time, dispersal-niche continuum index, and variability metric, but a full list of metrics is listed in [Table 1](#). Full documentation and examples, including installation instructions and help files, are available at <https://cralibe.github.io/MetaCommunityMetrics.jl/>.

**Table 1:** A summary of the metrics and functions available in MetaCommunityMetrics.jl.

Metrics	Functions	Details
Beta diversity decompositions in space and time	<code>beta_diversity()</code>	Re-implementation of R package <code>adespatial</code> ( <a href="#">Dray et al., 2023</a> )
	<code>spatial_beta_div()</code>	Re-implementation of R script from Guzman et al. ( <a href="#">2022</a> )
	<code>temporal_beta_div()</code>	Re-implementation of R script from Guzman et al. ( <a href="#">2022</a> )
Dispersal-niche continuum index (DNCI)	<code>create_groups()</code>	A novel grouping function for DNCI analysis
	<code>plot_groups()</code>	A novel visualization function for DNCI analysis
	<code>DNCI_multigroup()</code>	Re-implementation of R script from R package <code>DNCImper</code> ( <a href="#">Gibert, 2024</a> )
Niche overlap index	<code>niche_overlap()</code>	Novel implementation
Occupied patches proportion	<code>prop_patch()</code>	Re-implementation of R script from Guzman et al. ( <a href="#">2022</a> )

Metrics	Functions	Details
Variability Metric	CV_meta( )	Re-implementation of R script from Wang et al. (2019)
Niche hypervolume measurements	MVNH_det( )	Re-implementation from R package MVNH(Lu et al., 2021)
	MVNH_dissimilarity( )	Re-implementation from R package MVNH(Lu et al., 2021)
	average_MVNH_det( )	Novel extension of MVNH_det( )
	average_MVNH_dissimilarity( )	Novel extension of MVNH_dissimilarity( )

24 **Statement of need**

25 Many valuable R (R Core Team, 2024) packages have been developed to aid in community  
26 analyses by providing ecological metrics that can summarize processes from biodiversity patterns  
27 and have been widely adopted in the field, such as adespatial (Dray et al., 2023), codyn  
28 (Hallett et al., 2020), and vegan (Oksanen et al., 2024). However, conducting community  
29 analyses in R is often computationally expensive, especially when working with large datasets,  
30 a limitation that becomes critical in workflows requiring repeated metric calculations. These  
31 include simulation studies for method validation, bootstrap resampling for uncertainty estimation  
32 (Efron, 1992), null model approaches for statistical testing (Gotelli & Graves, 1996), and the  
33 analysis of large biodiversity databases, such as BioTime, all of which can create significant  
34 computational bottlenecks when processing multiple large datasets iteratively. To improve  
35 the efficiency of these computationally intensive analyses, Julia becomes a logical choice  
36 for re-implementations. Julia is known for its just-in-time compilation that optimizes code  
37 execution to levels comparable with lower-level languages like C or Fortran (Bezanson et al.,  
38 2017), yet Julia remains relatively uncommon in ecological workflows.

39 **State of the field**

40 To position MetaCommunityMetrics.jl within the Julia ecosystem, we conducted a  
41 comprehensive review of existing Julia packages under the EcoJulia organization, a  
42 community-driven effort providing tools for ecological and environmental analysis, and the  
43 PoisotLab, which develops many Julia packages focusing on quantitative and computational  
44 ecology. We ensured that our package builds beyond the tools currently existing in Julia even  
45 when sharing similar ecological concepts. For example, our beta diversity metrics share the  
46 concept of beta diversity with Diversity.jl (Robert Reeve & Harris, 2024). However, our  
47 implementation decomposes beta diversity into species replacement and richness differences  
48 (or abundance difference when abundance data is used instead of occurrence data) (Baselga,  
49 2010, 2012, 2013; Legendre, 2014), which differentiates our approach from Diversity.jl,  
50 which emphasizes alpha, beta, and gamma diversity measures at the metacommunity and  
51 community levels (Richard Reeve et al., 2014). To our knowledge, no existing Julia packages  
52 implement the specific metrics listed in Table 1. MetaCommunityMetrics.jl addresses this  
53 gap by providing the first Julia implementations of these metrics, which are essential for  
54 research in community ecology but were previously only available through computationally  
55 expensive R implementations.

56 **Software Design**

57 We built MetaCommunityMetrics.jl on three design principles: computational efficiency,  
58 usability for spatiotemporal data, and methodological validation.

59 First, we extended single-snapshot metrics (single site and/or time point) to operate on  
60 multidimensional datasets (multiple sites and/or time points) via aggregation functions  
61 (`spatial_beta_div()`, `temporal_beta_div()`, `average_MVNH_det()`, `average_MVNH_dissimilarity()`),  
62 trading complexity for usability and eliminating manual looping.

63 Second, we prioritized performance over comprehensive coverage (compared to the R  
64 implementations). Our beta diversity focuses on the Podani family approach rather than all  
65 five coefficient families, `MVNH_dissimilarity` implements only Bhattacharyya distance, and  
66 `DNCI` lacks built-in visualizations. We plan to expand these in future releases.

67 Third, we use vectorized operations where possible. We also employ Cholesky decomposition  
68 for covariance calculations (a computational optimization over LU decomposition in the original  
69 R implementation), providing substantial performance gains for positive-definite matrices  
70 (Haddad, 2024).

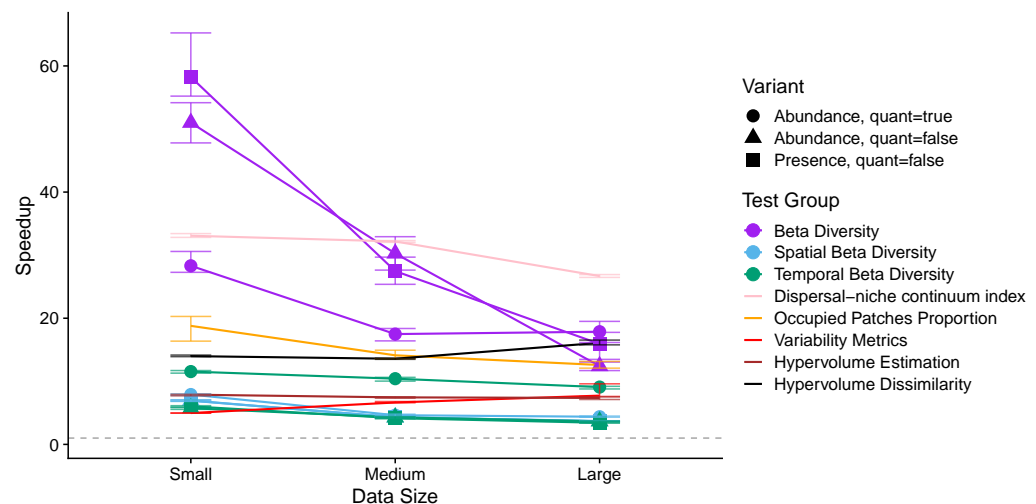
71 Fourth, our `DNCI` implementation accepts empty sites and singletons using Zero-adjusted  
72 Bray-Curtis dissimilarity, filters uninformative species (completely absent or ubiquitous),  
73 and implements status flags for five edge cases rather than throwing errors or returning  
74 NAs, supporting simulation workflows where sparse matrices are meaningful. We developed  
75 `create_groups()` and `plot_groups()` to automate site grouping (required by Vilmi et al.  
76 (2021) but manual in R) and visualize results. See [documentation](#) for details.

77 Finally, all implementations were validated against R equivalents to ensure methodological  
78 consistency (see [documentation](#)).

## 79 Research Impact Statement

80 `MetaCommunityMetrics.jl` delivers substantial computational advantages over existing tools.  
81 For example, we re-implemented the `beta.div.comp` function from the R package `adespatial`  
82 (Dray et al., 2023), achieving up to  $\sim 58\times$  faster execution times while maintaining  
83 methodological consistency (see [Figure 1](#)). As shown in [Figure 1](#), performance gains range  
84 from  $\sim 3\times$  to  $58\times$  across all re-implemented functions using [three testing datasets](#) (large:  
85 53,352 observations; medium: 26,676 observations; small: 5,325 observations), positioning  
86 `MetaCommunityMetrics.jl` as an efficient solution for diverse ecological research needs, from  
87 standard biodiversity analyses to computationally intensive simulation studies and large-scale  
88 data processing.

89 Further, the first empirical application of Approximate Bayesian Computation methods to  
90 connect metacommunity theory with observed data (a long-term phytoplankton community  
91 monitoring data) is using this package to calculate summary statistics. The manuscript of this  
92 application is under preparation.



**Figure 1:** A plot showing the speedup of all benchmarked functions across three datasets: small (5,335 observations), medium (26,676 observations), and large (53,352 observations). Speedup is calculated as the R median execution time divided by the Julia median execution time. Median speedup and its confidence interval of each comparison is shown. The grey dashed line shows where speedup equals to 1, that is both R and Julia's implementations require the same amount of time. The calculation of beta diversity has two variants: quant = true (abundance data is used) and quant = false (occurrence data is used). Details about this benchmarking can be found in the documentation under the [benchmark results section](#).

## AI usage disclosure

We used Claude, a generative AI tool, for proofreading and identifying grammatical errors in the manuscript and software documentation, and for providing optimization suggestions during software development. All writing suggestions were manually reviewed by the authors and selectively accepted. For optimization suggestions during software development, all suggestions were manually reviewed by the authors and selectively accepted, verified to produce the same results as before optimization, and benchmarked to confirm improvements in execution time and/or memory usage.

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