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ecodive: Parallel and Memory-Efficient R Package for Ecological Diversity Analysis

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Summary

Understanding the complexity of biological communities - whether bacteria in the human gut, trees in a forest, or plankton in the ocean - is a central goal of ecology. Researchers quantify this complexity using "diversity metrics," which describe the variety of species within a single site (alpha diversity) or the differences in composition between two sites (beta diversity). `ecodive` is an R package designed to calculate these metrics efficiently. It bridges the gap between complex ecological theory and practical data analysis, providing researchers with a unified toolset to process large-scale datasets that were previously computationally prohibitive. By leveraging parallel processing and optimized memory management, `ecodive` enables rapid, high-throughput analysis of microbial and macro-ecological communities.

Statement of Need

A primary challenge in modern ecological analysis is the management of high-dimensional data. As sequencing technologies improve, datasets are growing to include thousands of samples and tens of thousands of unique taxa. Beta diversity calculations, which involve comparing every sample to every other sample, exhibit $O(n^2)$ complexity. This quadratic scaling creates a significant bottleneck; a dataset that doubles in size requires four times the processing power, often overwhelming standard desktop computers.

Furthermore, the software landscape for ecological metrics is fragmented. A researcher needing to calculate a specific set of indices—for example, Faith's Phylogenetic Diversity, Bray-Curtis dissimilarity, and UniFrac distances—often must install and manage multiple R packages (`picante`, vegan, `GUniFrac`), each with different dependencies, input formats, and performance limitations.

`ecodive` solves these problems by providing a centralized, high-performance library. It targets ecologists, microbiologists, and bioinformaticians who require a robust, dependency-free solution for diversity analysis. By consolidating 50 standard metrics into a single, optimized framework, it eliminates the need for "package hopping" and enables the analysis of massive datasets on standard hardware.

State of the Field

Several R packages exist for diversity analysis, but `ecodive` offers a unique contribution through its scope and performance. The standard package for community ecology, vegan (Oksanen et al., 2001), provides excellent implementations of non-phylogenetic metrics (e.g., Bray-Curtis)

but lacks phylogenetic awareness (e.g., UniFrac). Conversely, packages like `picante` (Kembel et al., 2010) and `GUniFrac` (Chen et al., 2023) specialize in phylogenetic metrics but do not offer a comprehensive suite of general-purpose indices. The `phyloseq` (McMurdie & Holmes, 2013) package wraps many of these tools but relies on their underlying, often serial, implementations.

More generalized packages like `philentropy` (Drost, 2018) offer an impressive breadth of 46 distinct distance measures. However, `philentropy` focuses on information theory and general probability distributions rather than ecology. Critically, it includes many asymmetric divergences (where distance $A \to B \neq B \to A$) which, while mathematically valuable, are unsuitable for standard ecological ordination methods like PCoA that require symmetric distance matrices. Furthermore, `philentropy` lacks critical domain-specific metrics such as the UniFrac family and alpha diversity richness estimators like Chao1.

`ecodive` builds upon this landscape by unifying these distinct domains. It implements 50 symmetric metrics chosen specifically for their relevance to ecological ordination and analysis. Crucially, unlike the serial R or C implementations found in most peer packages (see **Research Impact**), `ecodive` is built entirely on a parallelized C engine, providing orders-of-magnitude faster performance while ensuring numerical identity with established tools.

Software Design

The architecture of `ecodive` balances the user-friendly conventions of R with the raw performance of C. A critical design trade-off centered on data representation.

Most R users work with dense matrices where samples are rows and features are columns. Standard R functions like `dist()` expect this format. However, ecological matrices are typically 90-99% zeros (sparse). Storing them as dense matrices wastes gigabytes of RAM, and processing them row-by-row is cache-inefficient for many distance algorithms.

To address this, `ecodive` maintains the standard R interface (samples-as-rows) but fundamentally alters the backend data structure:

1. **Transparent Transformation:** When a standard matrix is passed to `ecodive`, it is internally converted into a column-compressed sparse matrix (`dgCMatrix`) with samples transposed to columns. This incurs a one-time overhead but allows the C engine to skip zeros entirely and access memory in a cache-friendly, column-major pattern.
2. **Power User Bypass:** For extremely large datasets where the overhead of this transformation is non-trivial, users can manually provide data in the native `dgCMatrix` format (samples as columns). `ecodive` detects this optimized state and bypasses the transformation step, operating directly on the existing C pointers. This allows for "zero-copy" analysis of massive datasets.
3. **Parallelization Strategy:** `ecodive` employs a direct implementation using the standard POSIX threads (`pthreads`) library, avoiding the memory duplication overhead of forking processes found in R's `parallel` package. This design enables fine-grained, dynamic load balancing, ensuring efficient execution even when calculating partial distance matrices.

Research Impact Statement

`ecodive` has demonstrated immediate utility in high-dimensional microbiome studies. The core C algorithms in `ecodive` were originally developed for and deployed in the `rbiom` package (Smith, 2020). As part of `rbiom`, these optimized metrics have already been utilized in diverse microbial ecology studies, including research on preterm infant microbiomes (Ahearn-Ford et al., 2025), dietary interventions (DiMattia et al., 2025), and relationship satisfaction (Cheng et al., 2023). `ecodive` extracts these proven, high-performance components into a standalone, lightweight library to make them accessible to the broader R ecosystem without `rbiom`'s specific visualization and data structure dependencies.

In benchmarks comparing 15 ecological R packages, `ecodive` consistently ranked as the fastest and most memory-efficient solution:

- **Speed:** For the widely-used Unweighted UniFrac metric ($N = 50$), `ecodive` completed calculations in 6.4ms, compared to 2.5s for `picante` (396x faster) and 297ms for `phyloseq` (46x faster).
- **Scalability:** For standard Bray-Curtis dissimilarity ($N = 1006$), `ecodive` processed the matrix in ~20ms, whereas vegan required 1.68s.
- **Memory:** `ecodive`'s sparse architecture reduced memory allocation for large operations from gigabytes (in `abdiv` or `tabula`) to megabytes, enabling analyses on laptops that previously required clusters.

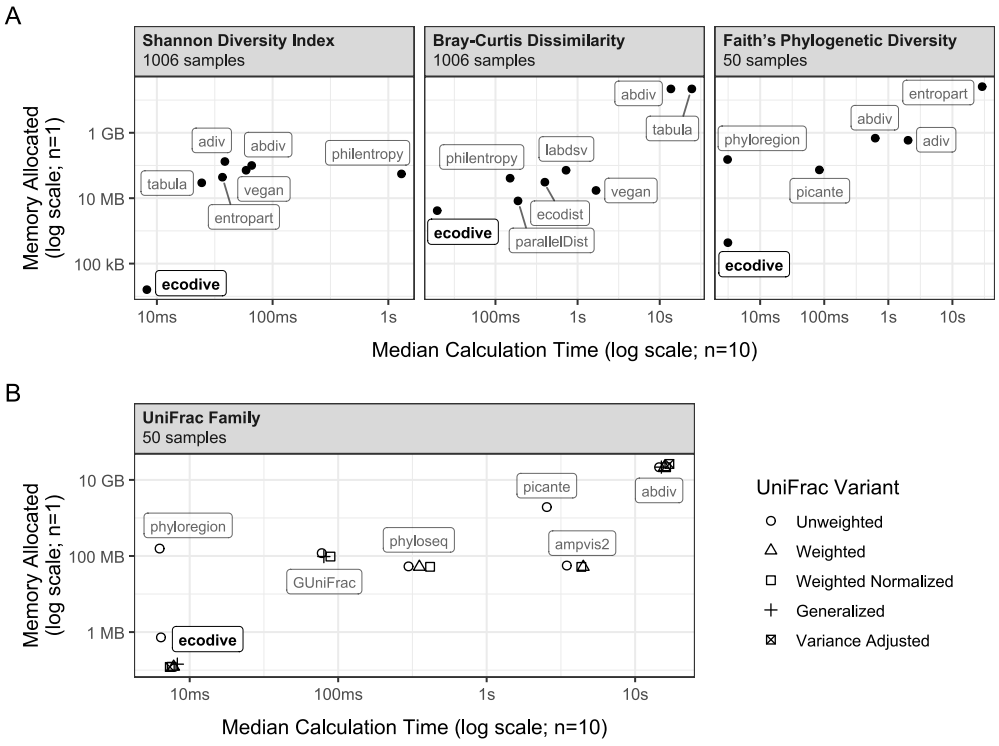

Figure 1: Benchmarking results. Execution time (x-axis) vs. peak memory usage (y-axis) for various diversity metrics across 15 R packages. `ecodive` (highlighted) consistently occupies the bottom-left quadrant, indicating high speed and low memory footprint. Note the log scale on both axes.

The package is fully documented with vignettes covering performance tuning and metric selection, and is available for installation with zero external R dependencies, ensuring high community readiness and long-term stability.

Example Usage

`ecodive` is designed for ease of use and integrates seamlessly with existing bioinformatics workflows, such as those using `phyloseq` objects. For example, calculating weighted UniFrac distances is straightforward:

```
data(esophagus, package = 'phyloseq')
ecodive::weighted_unifrac(esophagus)
#>           B         C
```

```
#> C 0.1050480
#> D 0.1401124 0.1422409
```

AI Usage Disclosure

Generative AI tools (Google Gemini) were used to assist in the drafting and revision of this manuscript and the generation of documentation. No AI tools were used to write the functional source code (R or C) of the software. All AI-generated text was critically reviewed, verified for accuracy, and edited by the authors.

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