The Journal of Open Source Software

mapme.biodiversity: Efficient Monitoring of Global Biodiversity Portfolios

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DOI: 10.xxxxxx/draft

Software

- Review
- Repository
- Archive

Editor: Jack Atkinson

Submitted: 06 November 2025
Published: unpublished

Summary

The `mapme.biodiversity` R package provides an open and reproducible framework for computing biodiversity-related indicators from multiple global geospatial datasets. It streamlines access, preprocessing, and analysis of spatial data to produce standardized, area-based metrics that can be used for conservation monitoring, policy evaluation, and research. By enabling reproducible, scalable, and extendable analyses across thematic datasets, `mapme.biodiversity` helps to bridge the gap between raw geospatial information and decision-relevant biodiversity indicators.

Statement of need

To prevent biodiversity loss at scale, conservation researchers and practitioners require area-based indicators derived from diverse spatial datasets. However, relevant data sources are dispersed across multiple repositories and platforms, each with distinct access protocols, formats, and documentation standards.

Most existing tools focus on a specific data source or domain, offering limited interoperability and requiring users to learn multiple interfaces. This fragmentation imposes a high cognitive and technical burden, especially on users who are not remote sensing specialists but need spatial data for research, monitoring, or policy evaluation.

The `mapme.biodiversity` R package provides a unified interface to access and process a wide range of spatial datasets relevant to conservation and environmental management. It enables users to derive standardized, area-based indicators at scale, supports reproducible workflows in R, and facilitates integration with other tools via export to standard spatial formats.

State of the field

The Digital Observatory for Protected Areas provides a centralized, server-based system developed by the European Commission to compute global protected-area indicators through standardized, automated workflows (Juffe-Bignoli et al., 2024). In contrast, `mapme.biodiversity` offers an R-native, decentralized framework that enables users to reproduce similar area-based analyses locally, adapt them to specific contexts, and extend them with additional datasets.

The Global Forest Watch (`GFW`) API, developed by the World Resource Institute, provides access to selected global forest monitoring datasets such as tree cover, loss, gain, biomass, and fire activity derived from satellite products like Hansen et al. (2013). It allows users to delegate computations to a remote cloud infrastructure and retrieve aggregated statistics for defined areas. `mapme.biodiversity` instead performs all processing locally or on user-managed servers and is designed to handle a wider set of environmental and socio-economic data sources.

`BON in a Box`, developed by the Group on Earth Observations Biodiversity Observation Network (GEO BON), is an open platform for biodiversity monitoring and indicator computation(Griffith et al., 2024). It enables users to assemble and share modular workflows that generate Essential Biodiversity Variables and policy-relevant indicators aligned with the Kunming–Montreal Global Biodiversity Framework. While `mapme.biodiversity` focuses on reproducible computation of area-based indicators within R, BON in a Box emphasizes cross-language interoperability and integration with national biodiversity monitoring systems.

Research Impact Statement

The package is actively used by several institutions for both operational and research purposes. At the Kreditanstalt für Wiederaufbau (KfW) and the Agence Française de Développement – the German and French public development banks for international development – it is used for internal impact evaluations and reporting on funded conservation and development programs. At the French National Research Institute for Sustainable Development (IRD), the package is used in policy evaluation projects and in initiatives aimed at strengthening research capacity in the Global South, notably in Madagascar and Senegal. For instance, `mapme.biodiversity` is a central to the pre-analysis plans and ongoing empirical studies evaluating the impacts of protected areas on deforestation, including a registered study accepted at PLOS ONE (Ramiandrisoa, 2026). The software has been incorporated into training materials used for capacity-building activities with government analysts and researchers, including workshops delivered to evaluation teams at the Ministry of Economy and Finance in Madagascar and to graduate students and early-career researchers at the University of Antananarivo (see online materials at BETSAKA).

Software design

Key features include:

- **Data acquisition and preparation**: automated download and preprocessing of global geospatial datasets with spatial–temporal filtering for user-defined areas of interest, optional local or cloud-based caching (e.g., through GDAL's virtual file system drivers, such as `/vsis3`).
- **Indicator computation and aggregation**: harmonized routines for summarizing and aggregating results across spatial units.
- **Scalability**: Utilizes existing R packages for spatial data handling (`terra`, `sf`), data manipulation (`dplyr`), and parallel processing (`future`) and progress monitoring (`progressr`) to handle large datasets. Supports multiple area of interest as input, enabling the processing of many regions of interest in a single run.
- **Reproducibility**: supports standardized, modular, scriptable workflows to enable replication of analysis, auditing and sharing.
- **Extensibility**: the framework allows users to add datasets add datasets and create their own indicators to meet specific research, monitoring or evaluation needs.
- **Interoperability**: outputs in standard geospatial formats, compatible with external GIS and statistical software.

The following minimal example illustrates a typical workflow:

```r
library(mapme.biodiversity)
# Define one or several areas of interest
```

```r
aoi_path <- system.file("extdata", "gfw_sample.gpkg",
                        package = "mapme.biodiversity")
aoi <- sf::read_sf(aoi_path)
# Get the resource data
res <- get_resources(aoi,
                     get_gfw_treecover(version = "GFC-2024-v1.12"),
                     get_gfw_lossyear(version = "GFC-2024-v1.12"))
# Compute the indicator
ind <- calc_indicators(res,
                       calc_treecover_area(years = 2000:2024,
                                           min_size = 1, min_cover = 30))
# Save portfolio data to GeoPackage
write_portfolio(ind, "example.gpkg")
# Transform into long format for plotting
out <- portfolio_long(ind)
# plot the results
plot(out$datetime, out$value, col =  "blue", pch = 16, xlab = "year",
     ylab = sprintf("%s (%s)", out$variable[1], out$unit[1]),
     main =  "Treecover loss")
```

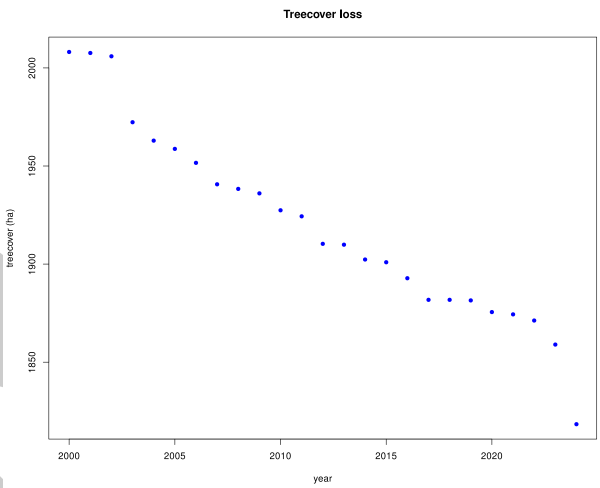

Figure 1: Treecover Loss Time-Series Plot

Availability

The mapme.biodiversity R package is implemented as an extension package to the R statistical computing environment (R Core Team, 2022). It is available on the CRAN (Görgen & Bhandari, 2025). Development versions are available on an online code repository. In addition to extensive online documentation that provides detailed information about the package, mapme.biodiversity provides an applied workshop using a real-world use-case scenario.

AI usage disclosure

No generative AI tools were used in the development of this software, the writing of this manuscript, or the preparation of supporting materials.

Acknowledgments

The development and maintenance of the `mapme.biodiversity` package have been funded by the KfW German Development Bank. The authors thank all users and contributors who provided feedback and suggestions that helped improve the package.

Conflicts of interest

This software was developed through collaboration between KfW staff, contracted developers, and independent researchers. DG, OB, ZK, and AP contributed to the development under KfW funding; JS is employed by KfW; and FB uses the package for research activities, some of which are funded by the KfW. The authors declare that KfW support did not hinder in any way the accuracy, reliability or performance of this software, nor the objectivity with which it is presented in the present article. All views expressed in this paper are those of the authors and do not necessarily reflect those of KfW.

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