mapme.biodiversity: Efficient Monitoring of Global Biodiversity Portfolios

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Summary

The `mapme.biodiversity` R package provides access to data and analyisis routines to several datasets relevant to conservation research. It can be used by scientists and practitioners to analyse conservation portfolios in a consistent way. The software integrates well into existing workflows and spatial analyses using the R programming environment. It has been used in impact evaluations to assess the effectivness of international donor interventions to reduce forest cover loss.

Statement of need

To prevent biodiversity losses at scale, conservation researchers require area-based indicators that monitor the state of portfolios of intervention areas over time. However, relevant spatial data resources are scattered across data repositories and servers for which access patterns can differ significantly. Most other software usually focuses on the analysis of a single (group of) data resource, increasing the cognitive burden on researchers who have to learn multiple interfaces and put substantial efforts into harmonizing output structures.

The `mapme.biodiversity` R package provides a single access pattern to a diverse set of conservation related data resources from diverse sources. It provides a common interface to derive area-based indicators for conservation portfolios in a standardized output format. Further workflows and analysis of the indicators can be conducted in the R computing environment or with other tools of one's liking through the serialization of data to standard spatial formats. It thus helps individuals and groups active in conservation research to streamline their spatial data acqusition process.

Main Features

- **Data Acquisition & Preparation**: Provides seamless access to a broad range of biodiversity-related global datasets, with automated downloading and preprocessing based on temporal and spatial filtering for user-defined AOIs, along with efficient data caching (local storage of preprocessed datasets to prevent redundant downloads).

- **Spatial Analysis, Aggregation, and Summarization**: Offers a harmonized set of tools for calculating numerous biodiversity indicators, with results that can be aggregated at user-defined spatial scales.

- **Scalability**: Utilizes existing R packages for spatial data handling (`terra`, `sf`), data manipulation (`dplyr`), and parallel processing (`future`) to efficiently handle large datasets. Supports multiple AOIs as input (vector-centric design), enabling the processing of many regions of interest in a single run.

- **Reproducibility**: Features a modular, scriptable workflow that makes analyses easy to reproduce and share.

- **Customizability**: Provides an extensible framework that allows users to add datasets and create their own indicators to meet specific research or conservation needs.

- **Output formats** (standard geospatial file formats) are compatible with a variety of tools for analysis and reporting, including other R packages and external GIS software.

Applications

- KfW: Impact evaluations (Melvin)

- KfW: Reporting to Ministry (Johannes/Sven)

- IRD: Research projects & capacity development (Florent)

- WWF and others?

Comparison with other software packages

- JRC's DOPA: https://www.preprints.org/manuscript/202408.1146/v1 & https://github.com/giacomo-gcad/dopa_workflow/
- wdpar: https://github.com/prioritizr/wdpar
- Red List Indices: https://github.com/red-list-ecosystem/rle_indices
- GFW API: https://data-api.globalforestwatch.org/
- Others?

Minimal code example

This is what a minimalistic workflow might look like:

```
library(mapme.biodiversity)
# define AOI
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))
# transform into a more suitable format
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")
```
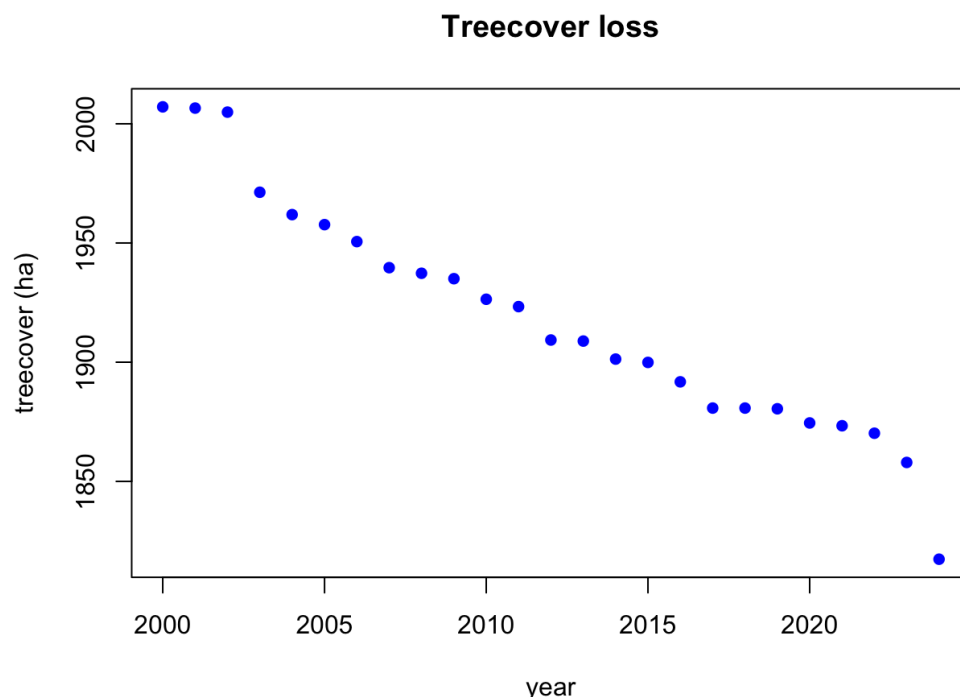
Treecover loss

Figure 1: Treecover loss plot

It demonstrates that one can perform the entire analysis – including retrieving data, computing the indicator summary for the region of interest, and plotting the results - with just a few lines of code.

The detailed documentation for the package can be found online (https://mapme-initiative.github.io/mapme.biodiversity/).

More examples can be found in the online tutorial (https://mapme-initiative.github.io/demo-madeira/).

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 Comprehensive R Archive Network (CRAN) (Görgen & Bhandari, 2025). Development versions are available on an online code repository (https://github.com/mapme-initiative/mapme.biodiversity). Documentation for the package can be found online (https://mapme-initiative.github.io/mapme.biodiversity/).

Acknowledgments

Conflict of interest

The authors declares no conflict of interest.

References

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