Package 'spectre'

July 17, 2021

Type Package

Title Predict Regional Community Composition

Version 1.0.2

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Description Predict regional community composition at a fine spatial resolution using only sparse biological and environmental data. The package is based on the DynamicFOAM algorithm described in Mokany et al. (2011) <doi:10.1111/j.1461-0248.2011.01675.x>.

License GPL-3

Depends R (>= 3.5)

Imports ggplot2, Rcpp (>= 1.0.1)

Suggests dplyr, testthat (>= 3.0.2), knitr, rmarkdown, covr, RcppProgress

LinkingTo Rcpp, RcppProgress, testthat

ByteCompile true

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

SystemRequirements C++11

VignetteBuilder knitr

NeedsCompilation yes

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Repository CRAN

Date/Publication 2021-07-17 06:30:02 UTC

R topics documented:

`alpha_list` *Matrix of predicted alpha diversity in each cell.*

Description

Matrix of predicted alpha diversity in each cell.

Usage

```
alpha_list
```

Format

vector.

`calc_commonness_error` *calc_commonness_error*

Description

Calculate commonness error

Usage

```
calc_commonness_error(x, objective_matrix)
```

Arguments

`x`	Results object from run_optimization_min_conf.
`objective_matrix`	Matrix from (modeled) alpha-diversity and Bray-Curtis dissimilarity

Details

Calculate mean absolute commonness error (MAE_c) and relative commonness error in percentage (RCE).

Value

vector

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estimated_gamma *Total (estimated) species in the system.*

Description

Total (estimated) species in the system.

Usage

```
estimated_gamma
```

Format

numeric

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generate_commonness_matrix_from_gdm *generate_commonness_matrix_from_gdm*

Description

Creates a pairwise site by site commonness matrix from estimates of species richness and Bray-Curtis dissimilarity.

Usage

```
generate_commonness_matrix_from_gdm(gdm_predictions, alpha_list)
```

Arguments

gdm_predictions	a square pairwise matrix of Bray-Curtis dissimilarity estimates between site pairs. We recommend using the gdm-package (Fitzpatrick et al. 2020) to generate this matrix
alpha_list	a vector of species richness for every site in the study area. The length of this vector must be equivalent to one of the dimensions of the gdm_predictions

Details

`generate_commonness_matrix_from_gdm` uses a vector of estimated species richness per site and a pairwise matrix of site by site Bray-Curtis dissimilarity (we recommend using the gdm-package (Fitzpatrick et al. 2020) to generate this matrix) to produce a matrix of the estimated species in common between site pairs (referred to as a commonness matrix). The commonness between sites is calculated using

$$C_{ij} = (1 - \beta_{ij})(S_i + S_j)/2$$

Where β_{ij} is the dissimilarity between sites, C_{ij} is the species in common between sites, and S is the number of species in each site. For more details see Mokany et al 2011.

Value

A pairwise site by site `matrix` of the number of species in common between each site pair, with dimensions equal to that of the provided dissimilarity matrix.

References

Mokany, K., Harwood, T.D., Overton, J.M., Barker, G.M., & Ferrier, S. (2011). Combining α and β diversity models to fill gaps in our knowledge of biodiversity. Ecology Letters, 14(10), 1043-1051.

`minimal_example_data` *List with example data created using the* `gdm` *package*

Description

List with example data created using the `gdm` package

Usage

```
minimal_example_data
```

Format

list

plot_commonness *plot_commonness*

Description

Plot commonness between observed and optimized data

Usage

```
plot_commonness(x, target)
```

Arguments

x	Results object of run_optimization_min_conf()
target	Pairwise matrix of species in common.

Details

Plot a heatmap of commonness between observed data and optimized data. This visual style allows for easier spatial understanding of commonness differences to be ascertained.

Value

ggplot

plot_error *plot_error*

Description

Plot the absolute error

Usage

```
plot_error(x)
```

Arguments

x	Results object from run_optimization_min_conf

Details

Plot error over time

Value

ggplot

References

xxx

`run_optimization_min_conf` *run_optimization_min_conf*

Description

Generate an optimized estimate of community composition (species presences and absences) for every site in the study area.

Usage

```
run_optimization_min_conf(
  alpha_list,
  total_gamma,
  target,
  max_iterations,
  partial_solution = NULL,
  fixed_species = NULL,
  seed = NA,
  verbose = TRUE,
  interruptible = TRUE
)
```

Arguments

`alpha_list`	`Matrix` of predicted alpha diversity (species richness) in each cell.
`total_gamma`	Total number of species present throughout the entire landscape.
`target`	Pairwise matrix of species in common between each site by site pair. Only the upper triangle of the matrix is actually needed.
`max_iterations`	The maximum number of iterations that the optimization algorithm may run through before stopping.
`partial_solution`	An initial `matrix` of species presences and absences for each site in the landscape. The total number of presences must match the estimated species richness of each site.
`fixed_species`	Fixed partial solution with species that are considered as given. Those species are not going to be changed during optimization.
`seed`	Seed for random number generator. Seed must be a positive integer value. `seed = NA` means that a random integer is used as seed.
`verbose`	If `TRUE` (default), a progress report is printed during the optimization run.
`interruptible`	Allow a run to be interrupted before completion.

Details

run_optimization_min_conf is the core function of the spectre package. The underlying algorithm of this function is adapted from Mokany et al. (2011). A pairwise commonness matrix (having the same structure as the target matrix) is calculated from the partial_solution matrix and the value difference with the target determined. If a difference is present and depending on the set stopping criteria the algorithm continues. A random site in the presence/absence matrix is selected, and a random presence record at this site replaced with an absence. Every absence in the selected site is then individually flipped to a presence and the value difference with the objective recorded. The presence record which resulted in the lowest value difference (minimum conflict) is retained. This cycle continues, with a random site selected every iteration, until the pairwise commonness and objective matrices match or the algorithm runs beyond the max_iterations.

Value

A species presence/absence matrix of the study landscape.

References

Mokany, K., Harwood, T.D., Overton, J.M., Barker, G.M., & Ferrier, S. (2011). Combining α and β diversity models to fill gaps in our knowledge of biodiversity. Ecology Letters, 14(10), 1043-1051.

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spectre *spectre*

Description

The goal of spectre is to provide an open source tool capable of predicting regional community composition at fine spatial resolutions using only sparse biological and environmental data.

Author(s)

Maintainer: Craig Simpkins <simpkinscraig063@gmail.com>

Authors:

- Sebastian Hanss
- Maximilian Hesselbarth
- Matthias Spangenberg
- Jan Salecker

`target_matrix` *Pairwise matrix of species in common.*

Description

Pairwise matrix of species in common.

Usage

```
target_matrix
```

Format

matrix

Index