

Package: RTCC (via r-universe)

September 24, 2026

Type Package

Title Detecting Trait Clustering in Environmental Gradients

Version 0.1.1

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Description The Randomized Trait Community Clustering method (Triado-Margarit et al., 2019, <[doi:10.1038/s41396-019-0454-4](https://doi.org/10.1038/s41396-019-0454-4)>) is a statistical approach which allows to determine whether if an observed trait clustering pattern is related to an increasing environmental constrain. The method 1) determines whether exists or not a trait clustering on the sampled communities and 2) assess if the observed clustering signal is related or not to an increasing environmental constrain along an environmental gradient. Also, when the effect of the environmental gradient is not linear, allows to determine consistent thresholds on the community assembly based on trait-values.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

Imports matrixStats, vegan, Rcpp

Suggests testthat, knitr, rmarkdown

LinkingTo testthat, Rcpp

NeedsCompilation yes

Depends R (>= 3.5.0)

Config/pak/sysreqs cmake make libuv1-dev

Repository <https://mateumenendez.r-universe.dev>

Date/Publication 2020-06-12 16:50:03 UTC

RemoteUrl <https://github.com/cran/RTCC>
RemoteRef HEAD
RemoteSha 028d47d02e698ac9e074f0fd70aa60252e8ae298

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group_information	<i>Genomic data linked to saline lagoons.</i>
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Description

A dataset containing genomic data of 544 genomes that matched 16s rRNA data from saline lagoons of the Monegros desert area.

Usage

group_information

Format

A data frame with 544 rows and 14 variables:

- genome** Genome IMG code
- Genome_Size** Genome size
- GC_perc** GC percentage
- Coding_base_perc** Condong base percentage
- CDS_perc** CDS percentage
- RNA_perc** RNA percentage
- rRNA_count** rRNA count
- Transporter_perc** Transporter proteins percentage
- Signal_peptide_perc** Signal peptide percentage
- Transmembrane_perc** Transmembrane proteins percentage
- Gene_Count** Gene count
- min_env** Minimum environmental value where the organism has been observed

max_env Minimum environmental value where the organism has been observed

rel_abundance Relative abundance of the organism on the metacommunity

...

Source

Triadó-Margarit, X., Capitán, J.A., Menéndez-Serra, M. et al. A Randomized Trait Community Clustering approach to unveil consistent environmental thresholds in community assembly. ISME J 13, 2681–2689 (2019).

metadata

Salinity values of saline lagoons.

Description

A dataset containing salinity values of 136 lagoons on the Monegros desert area.

Usage

metadata

Format

A data frame with 136 rows and 2 variables:

sample_ID Sample internal code

salinity Sample salinity value

Source

Triadó-Margarit, X., Capitán, J.A., Menéndez-Serra, M. et al. A Randomized Trait Community Clustering approach to unveil consistent environmental thresholds in community assembly. ISME J 13, 2681–2689.2019.

RTCC

RTCC: Detecting trait clustering in environmental gradients with the Randomized Trait Community Clustering method

Description

A set of functions which allows to determine if the observed traits present clustering/overdispersion patterns on the observed samples, and if so, to establish if the observed pattern is linked to the effect of an environmental gradient.

Details

The study of phenotypic similarities and differences within species along environmental gradients might be used as a powerful tool complementing taxon-based approaches when assessing the contribution of stochastic and deterministic processes in community assembly. For this, this package allows an easy implementation of a method for detecting clustering/overdispersion patterns along an environmental gradient (Triado-Margarit et al., 2019). A first function assesses if the observed traits exhibit a clustering/overdispersion pattern on the tested samples. If positive, two subsequent functions determine whether the observed pattern is linked to the effect of an environmental variable and its statistical significance.

Data entry

The data consists on presence-absence observations along a measured environmental gradient and trait quantitative information of the observed organisms.

References

Triado-Margarit, X., Capitan, J.A., Menendez-Serra, M. et al. (2019) A Randomized Trait Community Clustering approach to unveil consistent environmental thresholds in community assembly. *ISME J* **13**, 2681–2689 . <https://doi.org/10.1038/s41396-019-0454-4>

rtcc1

Trait selection

Description

This function determines whether the selected traits exhibit or not a clustering/overdispersion signal on the tested samples. For each trait, compares the observed Mean Pairwise Distance (MPD) of each sample against a distribution of synthetic communities MPDs obtained by a randomization test. Each synthetic community is build maintaining the original sample richness and randomly selecting organisms form the global pool.

Usage

```
rtcc1(table1, table2, table3, traits_columns, repetitions)
```

Arguments

table1	A data frame containing organisms names on the first column and its trait values on the consecutive ones. It also has to contain two columns with the maximum and the minimum values of the tested environmental variable where the organisms have been observed.
table2	A presence-absence observations table with the organisms names on the first column and the sample names as consecutive colnames.
table3	A dataframe containing sample names on the first column and environmental parameters on the consecutive ones.
traits_columns	Table 1 column numbers where different trait values appear.
repetitions	Number of simulated synthetic communities distributions.

Value

The function returns a dataframe with trait names as colnames and the p-value distribution of the different traits.

Examples

```
data(group_information)
data(table_presence_absence)
data(metadata)
rtcc1(group_information, table_presence_absence, metadata, 2:11, 100)
```

rtcc2

Clustering signal along an environmental gradient

Description

For a given trait, this function determines whether the observed trait clustering/overdispersion on the metacommunity is linked to an environmental gradient. For this, it sequentially remove samples in decreasing order of the environmental variable and computes at each step the remaining metacommunity h-index. This index is based on the percentage of samples on a metacommunity presenting significant trait clustering/overdispersion.

Usage

```
rtcc2(
  table1,
  table2,
  table3,
  species_abundances,
  trait_col_number,
  min_env_col,
  max_env_col,
  env_var_col,
  h_iteration,
  repetitions,
  model
)
```

Arguments

table1	A data frame containing organisms names on the first column and its trait values on the consecutive ones. It also has to contain two columns with the maximum and the minimum values of the tested environmental variable where the organisms have been observed.
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table2	A presence-absence observations table with the organisms names on the first column and the sample names as consecutive colnames.
table3	A dataframe containing sample names on the first column and environmental parameters on the consecutive ones.
species_abundances	A vector containing the relative abundance of the organisms on the whole data set on the same order as appear on Table 1.
trait_col_number	Table 1 column number of the tested trait.
min_env_col	Table 1 column number indicating the minimum value of the environmental variable were each organism has been observed.
max_env_col	Table 1 column number indicating the maximum value of the environmental variable were each organism has been observed.
env_var_col	Table 2 column number indicating the tested environmental variable.
h_iteration	Number of h-index calculations for computing a confidence interval.
repetitions	Number of simulated synthetic communities distributions.
model	Model selection. All models build synthetic communities based on the organisms richness of the observed communities. - Model 1: organism are selected randomly from the global pool. - Model 2: organism are selected randomly with a probability based on its relative abundance on the global pool. - Model 3: organism are selected randomly, but only those whose environmental range includes the value of the simulated community are eligible. - Model 4: organism are selected randomly, but only those whose environmental range includes the value of the simulated community are eligible and the selection probability is based on its relative abundance on the global pool.

Value

The function returns a dataframe with the maximum of the environmental variable on the remaining metacommunity after the sequential removal, h-index calculation for each environmental value, and its confidence standard deviation.

Examples

```
data(group_information)
data(table_presence_absence)
data(metadata)
rtcc2(group_information, table_presence_absence, metadata, group_information$sums,
9, 12, 13, 2, 100, 100, model = 1)
```

rtcc3

*Clustering signal significance.***Description**

For a given trait and environmental variable, this function creates a null model of the clustering/overdispersion pattern in order to test if the observed pattern statistically differs from the expected by random. For this, it sequentially remove random samples from the metacommunity and computes at each step the remaining metacommunity h-index. This index is based on the percentage of samples on a metacommunity presenting significant trait clustering/overdispersion. After h iterations, computes a 95 obtained h-index for each point of the environmental gradient.

Usage

```
rtcc3(
  table1,
  table2,
  table3,
  species_abundances,
  trait_col_number,
  min_env_col,
  max_env_col,
  env_var_col,
  h_iteration,
  repetitions,
  model
)
```

Arguments

table1	A data frame containing organisms names on the first column and its trait values on the consecutive ones. It also has to contain two columns with the maximum and the minimum values of the tested environmental variable where the organisms have been observed.
table2	A presence-absence observations table with the organisms names on the first column and the sample names as consecutive colnames.
table3	A dataframe containing sample names on the first column and environmental parameters on the consecutive ones.
species_abundances	A vector containing the relative abundance of the organisms on the whole data set on the same order as appear on Table 1.
trait_col_number	Table 1 column number of the tested trait.
min_env_col	Table 1 column number indicating the minimum value of the environmental variable were each organism has been observed.

max_env_col	Table 1 column number indicating the maximum value of the environmental variable were each organism has been observed.
env_var_col	Table 2 column number indicating the tested environmental variable.
h_iteration	Number of h-index calculations for computing a confidence interval.
repetitions	Number of simulated synthetic communities distributions.
model	Model selection. All models build synthetic communities based on the organisms richness of the observed communities. - Model 1: organism are selected randomly from the global pool. - Model 2: organism are selected randomly with a probability based on its relative abundance on the global pool. - Model 3: organism are selected randomly, but only those whose environmental range includes the value of the simulated community are eligible. - Model 4: organism are selected randomly, but only those whose environmental range includes the value of the simulated community are eligible and the selection probability is based on its relative abundance on the global pool.

Value

The function returns a dataframe with the maximum value of environmental variable corresponding to the same number of samples on the ordered removal, h-index calculation for each environmental value, and the percentiles 0.025, 0.5 and 0.975 of the obtained distribution for each point (mean value and 95

Examples

```
data(group_information)
data(table_presence_absence)
data(metadata)
rtcc3(group_information, table_presence_absence, metadata, group_information$sums,
9, 12, 13, 2, 50, 20, model = 1)
```

table_presence_absence

Genome presence-absence data of 136 saline lagoons.

Description

A dataset containing presence-absence data of 544 genomes on 136 saline lagoons of the Monegros desert area.

Usage

```
table_presence_absence
```

Format

A data frame with 544 rows and 137 variables:

genome Genome IMG code

MON_10 Sample presence-absence observations

MON_100 Sample presence-absence observations

MON_101 Sample presence-absence observations

MON_103 Sample presence-absence observations

MON_104 Sample presence-absence observations

MON_106 Sample presence-absence observations

MON_107 Sample presence-absence observations

MON_108 Sample presence-absence observations

MON_109 Sample presence-absence observations

MON_11 Sample presence-absence observations

MON_110 Sample presence-absence observations

MON_111 Sample presence-absence observations

MON_112 Sample presence-absence observations

MON_113 Sample presence-absence observations

MON_114 Sample presence-absence observations

MON_116 Sample presence-absence observations

MON_117 Sample presence-absence observations

MON_118 Sample presence-absence observations

MON_119 Sample presence-absence observations

MON_12 Sample presence-absence observations

MON_120 Sample presence-absence observations

MON_122 Sample presence-absence observations

MON_123 Sample presence-absence observations

MON_124 Sample presence-absence observations

MON_125 Sample presence-absence observations

MON_126 Sample presence-absence observations

MON_127 Sample presence-absence observations

MON_128 Sample presence-absence observations

MON_129 Sample presence-absence observations

MON_13 Sample presence-absence observations

MON_130 Sample presence-absence observations

MON_131 Sample presence-absence observations

MON_133 Sample presence-absence observations

MON_134 Sample presence-absence observations

MON_135 Sample presence-absence observations
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MON_95 Sample presence-absence observations
MON_96 Sample presence-absence observations
MON_97 Sample presence-absence observations
MON_98 Sample presence-absence observations
MON_99 Sample presence-absence observations ...

Source

Triadó-Margarit, X., Capitán, J.A., Menéndez-Serra, M. et al. A Randomized Trait Community Clustering approach to unveil consistent environmental thresholds in community assembly. *ISME J* 13, 2681–2689 (2019).

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