Package ‘ccrepe’

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Title ccrepe_and_nc.score
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Description The CCREPE (Compositionality Corrected by REnormalizaion and PErmutation) package is designed to assess the significance of general similarity measures in compositional datasets. In microbial abundance data, for example, the total abundances of all microbes sum to one; CCREPE is designed to take this constraint into account when assigning p-values to similarity measures between the microbes. The package has two functions:
ccrepe: Calculates similarity measures, p-values and q-values for relative abundances of bugs in one or two body sites using bootstrap and permutation matrices of the data.
nc.score: Calculates species-level co-variation and co-exclusion patterns based on an extension of the checkerboard score to ordinal data.
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VignetteBuilder knitr
Suggests knitr, BiocStyle, BiocGenerics, testthat
biocViews ImmunoOncology, Statistics, Metagenomics, Bioinformatics, Software

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ccrepe-package ......................................................... 2
ccrepe ................................................................. 2
ccrepeSampleTestFunction ......................................... 5
nc.score .............................................................. 6
Index

ccrepe-package

A package for analysis of sparse compositional data. Allows calculation of the similarity measure nc-score and calculation of compositionality-corrected p-values for arbitrary similarity scores (including user-defined) applied to compositional data.

Description

ccrepe was developed for use with microbial relative abundance data, which is both sparse and compositional in nature.

Details

<table>
<thead>
<tr>
<th>Package</th>
<th>ccrepe</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>Package</td>
</tr>
<tr>
<td>Version</td>
<td>1.0</td>
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</tbody>
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Author(s)

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ccrepe

Calculates compositionality-corrected p-values and q-values for compositional data using an arbitrary distance metric.

Description

ccrepe calculates compositionality-corrected p-values and q-values for compositional data by generating first a null distribution of the distance metric generated by permutation and renormalization of the data, and then by generating an alternative distribution of the distance metric by bootstrap resampling of the data. For greater detail, see References.

The two distributions are compared using a pooled-variance Z-test to give a compositionality-corrected p-value. The p-values can be calculated for all appropriate (passing certain quality-control measures) pairwise comparisons, or for a subset of user-specified ones.

Q-values are additionally calculated using the Benjamin-Hochberg-Yekutieli procedure (see References).
Usage

ccrepe(
x = NA,
y = NA,
sim.score = cor,
sim.score.args = list(),
min.subj = 20,
iterations = 1000,
subset.cols.x = NULL,
subset.cols.y = NULL,
errthresh = 1e-04,
verbose = FALSE,
iterations.gap = 100,
distributions = NA,
compare.within.x = TRUE,
concurrent.output = NA,
make.output.table = FALSE)

Arguments

x First dataframe or matrix containing the relative abundances in cavity1: columns are bugs, rows are samples. (Rows should therefore sum to a constant.) The subjectIDs, if present, are assumed to be the row names and NOT the first column of data.

y Second dataframe or matrix (optional) containing the relative abundances in cavity2: columns are bugs, rows are samples. The subjectIDs, if present, are assumed to be the row names. If both x and y are specified, they will be merged by row names. If no row names are specified for either or both datasets, the default is to use the row numbers as subject IDs.

sim.score A function defining a similarity measure, such as cor or nc.score. This similarity measure can be a pre-defined R function or user-defined. If the latter, certain properties should be satisfied as detailed below (also see examples). The default similarity measure is Spearman correlation. A user-defined similarity measure should:
1. Be able to take either two inputs which are vectors or one input which is either a matrix or a dataframe
2. In the case of two inputs, return a single number
3. In the case of one input, return a matrix in which the (i,j)th entry is the similarity score for column i and column j in the original matrix
4. Resulting matrix (in the case of one input) must be symmetric
5. The inputs must be named x and y

sim.score.args A list of arguments for the measurement function. For example: In the case of cor, the following would be acceptable: sim.score.args = list(method='spearman',use='complete.obs').

min.subj Minimum number of samples that must be non-missing in a bug/feature/column in order to apply the similarity measure to that bug/feature/column. This is to ensure that there are sufficient subjects to perform a bootstrap (default: 20).
iterations  The number of iterations of bootstrap and permutation (default: 1000).
subset.cols.x  A vector of column indices from x to indicate which features to compare
subset.cols.y  A vector of column indices from y to indicate which features to compare
errthresh  If feature has number of zeros greater than errthresh^\(\frac{1}{n}\), that feature is excluded
verbose  Logical: an indicator whether the user requested verbose output, which prints periodic progress of the algorithm through the dataset(s), as well as including more detailed output. (default:FALSE)
iterations.gap  If output is verbose - number of iterations after issue a status message (Default=100 - displayed only if verbose=TRUE).
distributions  Output Distribution file (default:NA).
compare.within.x  A boolean value indicating whether to do comparisons given by taking all subsets of size 2 from subset.cols.x or to do comparisons given by taking all possible combinations of subset.cols.x or subset.cols.y. If TRUE but subset.cols.y=NA, returns all comparisons involving any features in subset.cols.x. This argument is only used when y=NA.
concurrent.output  Optional output file to which each comparison will be written as it is calculated.
make.output.table  A boolean value indicating whether to include table-formatted output.

Value

Returns a list containing the calculation results and the parameters used.
Default parameters shown:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>min.subj</td>
<td>Description above</td>
</tr>
<tr>
<td>errThresh</td>
<td>Description same as errthresh above</td>
</tr>
<tr>
<td>sim.score</td>
<td>A matrix of the similarity scores for all the requested comparisons. The (i,j)th element of sim.score corresponds to the similarity score of column i (or the ith column of subset.cols.1) and column j (or the jth column of subset.cols.1) in one dataset, or to the similarity score of column i (or the ith column of subset.cols.1) in dataset x and column j (or the jth column of subset.cols.2) in dataset y in the case of two datasets.</td>
</tr>
<tr>
<td>p.values</td>
<td>A matrix of the p-values for all the requested comparisons. The (i,j)th element of p.values corresponds to the p-value of the (i,j)th element of sim.score.</td>
</tr>
<tr>
<td>q.values</td>
<td>A matrix of the Benjamini-Hochberg-Yekutieli FDR corrected p-values. The (i,j)th element of q.values corresponds to the q-value of the (i,j)th element of sim.score.</td>
</tr>
<tr>
<td>z.stat</td>
<td>A matrix of the z-statistics for all the requested comparisons. The (i,j)th element corresponds to the z-statistic which gave rise to the (i,j)th p-value.</td>
</tr>
<tr>
<td>output.table</td>
<td>(Only if make.output.table=TRUE) A table where each row is one comparison. Each row contains the features being compared with their similarity scores, z-statistics, p-values and q-values</td>
</tr>
</tbody>
</table>

Additional parameters if verbose=TRUE:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>iterations</td>
<td>Description Above</td>
</tr>
</tbody>
</table>
Description

This simple example of a test measurement function to be used with ccrepe used in the same fashion that cor would be used.

Some properties of the function:
1. Be able to take either two inputs which are vectors or one input which is either a matrix or a data frame.
2. In the case of one input, return a matrix in which the (i,j)th entry is the similarity score for column i and column j in the original matrix.
3. Resulting matrix must be symmetric.
4. The inputs must be named x and y.
Usage
ccrepeSampleTestFunction(x, y = NA)

Arguments
x  x is a vector or a matrix
y  y is a vector.
   if y selected then x must be a vector too

Value
If x and y are vectors it returns a number: 0.5 If x is a matrix it returns a matrix of all 0.5

Author(s)
Emma Schwager <emma.schwager@gmail.com>

description
nc.score calculates species-level co-variation and co-exclusion patterns based on an extension of
the checkerboard score to ordinal data.
It is an extension to Diamond’s checkerboard score (See references below) to ordinal data and
implements a framework for robust detection of species-level association patterns in metagenomic
data.

Usage
nc.score(x,
y = NULL,
use = "everything",
nbins = NULL,
bin.cutoffs = NULL
)

Arguments
x  A numeric vector, data frame, or matrix. The first entity to be processed. Columns
    are bugs, rows are samples.
y  NULL(default) or a numeric vector, data frame, or matrix with compatible di-
    mensions to x. Columns are features, rows are samples.
use  An optional character string giving a method for computing covariances in the
    presence of missing values. This must be (an abbreviation of) one of the strings
    "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs".
nbins  A non-negative integer of the number of bins to generate (cutoffs will be gen-
    erated by the discretize function from the infotheo package).
bin.cutoffs  A list of values demarcating the bin cutoffs. The binning is performed using the
    findInterval function.
**Value**

Matrix or vector of normalized scores.

**Author(s)**

Craig Bielski <craig.bielski@gmail.com>

**References**

Emma Schwager and Colleagues. Detecting statistically significant associations between sparse and high dimensional compositional data. In Progress.

**Examples**

```r
data <- matrix(rlnorm(40, meanlog=0, sdlog=1), nrow=10)
data.rowsum <- apply(data, 1, sum)
data.norm <- data / data.rowsum
testdata <- data.norm
dimnames(testdata) <- list(paste("Sample", seq(1,10)), paste("Feature", seq(1,4)))

nc.score.results <- nc.score( x=testdata )
cnc.score.results.bins <- nc.score( x=testdata )
cnc.score.results.bin.cutoffs <- nc.score( x=testdata )
cnc.score.results
cnc.score.results.bins
cnc.score.results.bin.cutoffs
```
Index

ccrepe, 2
cccrepe-package, 2
cccrepeSampleTestFunction, 5
nc.score, 6