Package ‘ccrepe’

Type Package

Title ccrepe_and_nc.score

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Imports infotheo (>= 1.1)

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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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R topics documented:

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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

Package: ccrepe
Type: Package
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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
subset.cols.x
subset.cols.y
errthresh
verbose
iterations.gap
distributions
compare.within.x
concurrent.output
make.output.table
Value

Returns a list containing the calculation results and the parameters used.

Default parameters shown:

min.subj
errThresh
sim.score
p.values
q.values
z.stat
output.table
(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

Additional parameters if verbose=TRUE:

iterations
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ccrepeSampleTestFunction

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subset.cols.y Description Above
iterations.gap Description Above
sim.score.parameters Description Above
compare.within.x Description Above
make.output.table Description Above

Author(s)

Emma Schwager <emma.schwager@gmail.com>

References

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


Examples

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)))
ccrepe.results <- ccrepe (x=testdata, iterations=20, min.subj=10)
ccrepe.results.nc.score <- ccrepe(x=testdata,iterations=20,min.subj=10,sim.score=nc.score)
ccrepe.results
ccrepe.results.nc.score

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
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 must be symmetric
5. The inputs must be named x and y
nc.score

Usage

crepeSampleTestFunction(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)

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nc.score

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 givinga method for computing covariances in the
presence of missing values. This must be (an abbreviation of) on 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 gener-
ated 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

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