

Package ‘CBEA’

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Title Competitive Balances for Taxonomic Enrichment Analysis in R

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Description This package implements CBEA, a method to perform set-based analysis for microbiome relative abundance data. This approach constructs a competitive balance between taxa within the set and remainder taxa per sample. More details can be found in the Nguyen et al. 2021+ manuscript. Additionally, this package adds support functions to help users perform taxa-set enrichment analyses using existing gene set analysis methods. In the future we hope to also provide curated knowledge driven taxa sets.

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URL <https://github.com/qpmnguyen/CBEA>,
<https://qpmnguyen.github.io/CBEA/>

BugReports <https://github.com/qpmnguyen/CBEA//issues>

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.cbea

Internal cbea function

Description

See main function cbea documentation for more details.

Usage

```
.cbea(
  ab_tab,
  set_list,
  output,
  distr,
  adj = FALSE,
  n_perm = 100,
  parametric = TRUE,
  thresh = 0.05,
  init = NULL,
  control = NULL,
  parallel_backend = NULL,
  ...
)
```

Arguments

| | |
|------------------|---|
| ab_tab | (Matrix). Named n by p matrix. This is the OTU/ASV/Strain table where taxa are columns. |
| set_list | (List). List of length m. This is a list of set membership by column names. |
| output | See documentation cbea |
| distr | See documentation cbea |
| adj | See documentation cbea |
| n_perm | See documentation cbea |
| parametric | See documentation cbea |
| thresh | See documentation cbea |
| init | See documentation cbea |
| control | See documentation cbea |
| parallel_backend | See documentation cbea |
| ... | See documentation cbea |

Value

A data frame of size n by m. n is the total number of samples and m is the total number of sets with elements represented in the data.

| | |
|------|--|
| cbea | <i>Enrichment analysis using competitive compositional balances (CBEA)</i> |
|------|--|

Description

cbea is used compute enrichment scores per sample for pre-defined sets using the CBEA (Competitive Balances for Enrichment Analysis).

Usage

```
cbea(  
  obj,  
  set,  
  output,  
  distr = NULL,  
  adj = FALSE,  
  n_perm = 100,  
  parametric = TRUE,  
  thresh = 0.05,  
  init = NULL,  
  control = NULL,  
  parallel_backend = NULL,  
  ...  
)  
  
## S4 method for signature 'TreeSummarizedExperiment'  
cbea(  
  obj,  
  set,  
  output,  
  distr = NULL,  
  abund_values,  
  adj = FALSE,  
  n_perm = 100,  
  parametric = TRUE,  
  thresh = 0.05,  
  init = NULL,  
  control = NULL,  
  parallel_backend = NULL,  
  ...  
)  
  
## S4 method for signature 'data.frame'  
cbea(  
  obj,  
  set,  
  taxa_are_rows = FALSE,  
  id_col = NULL,  
  output,  
  distr = NULL,  
  adj = FALSE,  
  n_perm = 100,  
  parametric = TRUE,  
  thresh = 0.05,  
  init = NULL,  
  control = NULL,  
  parallel_backend = NULL,  
  ...  
)  
  
## S4 method for signature 'matrix'
```

```

cbea(
  obj,
  set,
  taxa_are_rows = FALSE,
  output,
  distr = NULL,
  adj = FALSE,
  n_perm = 100,
  parametric = TRUE,
  thresh = 0.05,
  init = NULL,
  control = NULL,
  parallel_backend = NULL,
  ...
)

```

Arguments

| | |
|------------------|--|
| obj | The element of class <code>TreeSummarizedExperiment</code> , <code>data.frame</code> , or <code>matrix</code> . <code>phyloseq</code> is not supported due to conflicting dependencies and <code>TreeSummarizedExperiment</code> is much more compact. |
| set | <code>BiocSet</code> . Sets to be tested for enrichment in the <code>BiocSet</code> format. Taxa names must be in the same format as elements in the set. |
| output | (String). The form of the output of the model. Has to be either <code>zscore</code> , <code>cdf</code> , <code>raw</code> , <code>pval</code> , or <code>sig</code> |
| distr | (String). The choice of distribution for the null. Can be either <code>mnorm</code> (2 component mixture normal), <code>norm</code> (Normal distribution), or <code>NULL</code> if <code>parametric</code> is <code>TRUE</code> . |
| adj | (Logical). Whether correlation adjustment procedure is utilized. Defaults to <code>FALSE</code> . |
| n_perm | (Numeric). Add bootstrap resamples to both the permuted and unpermuted data set. This might help with stabilizing the distribution fitting procedure, especially if the sample size is low. Defaults to 1. |
| parametric | (Logical). Indicate whether a parametric distribution will be fitted to estimate z-scores, CDF values, and p-values. Defaults to <code>TRUE</code> |
| thresh | (Numeric). Threshold for significant p-values if <code>sig</code> is the output. Defaults to 0.05 |
| init | (Named List). Initialization parameters for estimating the null distribution. Default is <code>NULL</code> . |
| control | (Named List). Additional arguments to be passed to <code>fitdistr</code> and <code>normmixEM</code> . Defaults to <code>NULL</code> . |
| parallel_backend | See documentation cbea |
| ... | Additional arguments not used at the moment. |
| abund_values | (Character). Character value for selecting the assay to be the input to <code>cbea</code> |
| taxa_are_rows | (Logical). Indicate whether the data frame or matrix has taxa as rows |
| id_col | (Character Vector). Vector of character to indicate metadata columns to keep (for example, <code>sample_id</code>) |

Details

This function support different formats of the OTU table, however for best results please use [TreeSummarizedExperiment](#). phyloseq is supported, however CBEA will not explicitly import phyloseq package and will require users to install them separately. If use `data.frame` or `matrix`, users should specify whether taxa are rows using the `taxa_are_rows` option. Additionally, for `data.frame`, users can specify metadata columns to be kept via the `id_col` argument.

The output argument specifies what type of values will be returned in the final matrix. The options `pval` or `sig` returns either unadjusted p-values or dummy variables indicating whether a set is significantly enriched in that sample (based on unadjusted p-values thresholded at `thresh`). The option `raw` returns raw scores computed for each set without any distribution fitting or inference procedure. Users can use this option to examine the distribution of CBEA scores under the null.

Value

R An n by m matrix of enrichment scores at the sample level

Examples

```
data(hmp_gingival)
seq <- hmp_gingival$data
set <- hmp_gingival$set
# n_perm = 10 to reduce runtime
mod <- cbea(obj = seq, set = set, output = "zscore",
            abund_values = "16SrRNA",
            distr = "norm", parametric = TRUE,
            adj = TRUE, thresh = 0.05, n_perm = 10)
```

check_args

Checking arguments of the function

Description

This function extracts the parent environment (when called under the `cbea` function) and then check all the arguments.

Usage

```
check_args()
```

Value

None

| | |
|-----------------|--|
| check_distr_arg | <i>This function checks for validity of arguments based on the parameters and the distribution of interest</i> |
|-----------------|--|

Description

This function checks for validity of arguments based on the parameters and the distribution of interest

Usage

```
check_distr_arg(param, distr, .note = NULL)
```

Arguments

| | |
|-------|--|
| param | (List). Named list of parameter values |
| distr | (String). String name of the distribution being evaluated |
| .note | (String). Any additional annotation to be put in front of error messages |

Value

Returns 0 if there are no errors

| | |
|---------------|------------------------------------|
| combine_distr | <i>Combining two distributions</i> |
|---------------|------------------------------------|

Description

Pass along handling of combining distributions to avoid clogging up the main function

Usage

```
combine_distr(perm, unperm, distr, ...)
```

Arguments

| | |
|--------|--|
| perm | (List). A list of parameters for permuted distribution |
| unperm | (List). A list of parameters for the unpermuted distribution |
| distr | (String). Distribution of choice |

Value

A list of the combined distribution form based on the initial distribution of choice

dlst *Defintions for location-scale t distribution*

Description

Internal functions for defining the t-distribution in terms of location-scale.

Usage

```
dlst(x, df = 1, mu = 0, sigma = 1, log = FALSE)
```

```
plst(q, df = 1, mu = 0, sigma = 1, log = FALSE)
```

Arguments

| | |
|-------|--|
| x, q | The data vector |
| df | Degrees of freedom |
| mu | The location parameter |
| sigma | The scale parameter |
| log | Indicate whether probabilities are return as log |

Value

Numeric values representing the density and cumulative probabilitiy values of the location-scale t distribution

Functions

- dlst: Probability Density Function
- plst: Cumulative distribution function

Examples

```
val <- rnorm(10)
dlst(val, df = 1, mu = 0, sigma = 1)
val <- rnorm(10)
plst(q = val, df = 1, mu = 0, sigma = 1)
```

estimate_distr *Estimate distribution parameters from data*

Description

This function takes a numeric vector input and attempts to find the most optimal solution for the parameters of the distribution of choice. Right now only norm and mnorm distributions are supported.

Usage

```
estimate_distr(data, distr, init = NULL, args_list = NULL)
```


Arguments

| | |
|-----------|--|
| data | (Numeric Vector). A vector of numbers that can be inputted to estimate the parameters of the distributional forms. |
| distr | (String). The distribution to be fitted. Right now only norm or mnorm is supported |
| init | (List). Initialization parameters for each distribution. For mixtures, each named element in the list should be a vector with length equal to the number of components |
| args_list | (List). Named list of additional arguments passed onto fitdist and normalmixEM |
| ... | Other parameters passed to fitdistrplus or normalmixEM |

Details

The package `fitdistrplus` is used to estimate parameters of the normal distribution while the package `normalmixEM` is used to estimate parameters of the mixture normal distribution. So far we suggest only estimating two components for the mixture normal distribution. For default options, we use mostly defaults from the packages themselves. The only difference was the mixture normal distribution where the convergence parameters were loosened and requiring more iterations to converge.

Value

A named list with all the parameter names and values

| | |
|------------|---|
| fit_scores | <i>Function to compute CBEA scores for each set</i> |
|------------|---|

Description

Function to compute CBEA scores for each set

Usage

```
fit_scores(
  index_vec,
  ab_tab,
  adj,
  distr,
  output,
  n_perm,
  parametric,
  thresh,
  init,
  control
)
```

Arguments

| | |
|------------|---|
| index_vec | (Character Vector). A character vector indicating the elements of the set of interest |
| ab_tab | (Matrix). Named n by p matrix. This is the OTU/ASV/Strain table where taxa are columns. |
| adj | (Logical). See documentation cbea |
| distr | (Character). See documentation cbea |
| output | (Character). See documentation cbea |
| n_perm | (Numeric). The total number of permutations. |
| parametric | (Logical). See documentation cbea |
| thresh | (Numeric). See documentation cbea |
| init | (List). See documentation cbea |
| control | (List). See documentation cbea |

Value

This function returns a list containing output scores and other diagnostics (as sublists)

| | |
|---------------|---|
| get_adj_mnorm | <i>Function to perform the adjustment for the mixture normal distribution</i> |
|---------------|---|

Description

Function to perform the adjustment for the mixture normal distribution

Usage

```
get_adj_mnorm(perm, unperm, verbose = FALSE, fix_comp = "none")
```

Arguments

| | |
|----------|--|
| perm | (List). Parameter values of the distribution of scores |
| unperm | (List). Parameter values of the distribution of scores computed on unpermuted data |
| fix_comp | (Character). Which component to keep |

Value

A List of parameters for the adjusted mixture normal.

| | |
|-----------------|--|
| get_diagnostics | <i>Get diagnostic values using parent environment.</i> |
|-----------------|--|

Description

This function is used internally inside `fit_scores` to grab the relevant objects from the previous parent environment (i.e. the environment from `fit_scores`) and compute relevant information. The role of this function is break diagnostic component into a different function for maintenance.

Usage

```
get_diagnostics(env = caller_env())
```

Value

This function returns a list of two components: `diagnostic` represent goodness-of-fit statistics for the distribution fitting itself while `lmoment` contains the l-moment comparisons between the computed raw scores, permuted scores, and other fitted distributions.

| | |
|----------|---|
| get_mean | <i>Get the overall mean of a two component mixture distribution</i> |
|----------|---|

Description

Get the overall mean of a two component mixture distribution

Usage

```
get_mean(mu, lambda)
```

Arguments

`mu` (Vector). A two value vector of mean values.
`lambda` (Vector). A two value vector of component mixing coefficients

Value

A numeric value representing the overall mean

| | |
|---------------|--|
| get_raw_score | <i>Get CBEA scores for a given matrix and a vector of column indices</i> |
|---------------|--|

Description

Get CBEA scores for a given matrix and a vector of column indices

Usage

```
get_raw_score(X, idx)
```

Arguments

| | |
|-----|--|
| X | (Matrix). OTU table of matrix format where taxa are columns and samples are rows |
| idx | (Integer vector). Vector of integers indicating the column ids of taxa in a set |

Value

A matrix of size n by 1 where n is the total number of samples

Examples

```
data(hmp_gingival)
seq <- hmp_gingival$data
seq_matrix <- SummarizedExperiment::assays(seq)[[1]]
seq_matrix <- t(seq_matrix) + 1
rand_set <- sample(seq_len(ncol(seq_matrix)), size = 10)
scores <- get_raw_score(X = seq_matrix, idx = rand_set)
```

| | |
|--------|---|
| get_sd | <i>Get the overall standard deviation of a two component mixture distribution</i> |
|--------|---|

Description

Get the overall standard deviation of a two component mixture distribution

Usage

```
get_sd(sigma, mu, mean, lambda)
```

Arguments

| | |
|--------|---|
| sigma | (Vector). A two value vector of component-wise variances |
| mu | (Vector). A two value vector of mean values. |
| mean | (Numeric Value). The overall mean. |
| lambda | (Vector). A two value vector of component mixing coefficients |

Value

A numeric value representing the overall standard deviation

| | |
|----------------|---------------------------------|
| glance.CBEAout | <i>Glance at CBEAout object</i> |
|----------------|---------------------------------|

Description

This function cleans up all diagnostics of the cbea method (from the CBEAout object) into a nice `tibble::tibble()`

Usage

```
## S3 method for class 'CBEAout'
glance(x, statistic, ...)
```

Arguments

| | |
|-----------|---|
| x | An object of type CBEAout |
| statistic | What type of diagnostic to return. Users can choose to return <code>fit_diagnostic</code> which returns goodness of fit statistics for the different fitted distributions (e.g. log likelihoods) while <code>fit_comparison</code> returns comparisons across different distributions and raw values (and data) across the 4 l-moments. |
| ... | Unused, kept for consistency with generics |

Value

A `tibble::tibble()` summarizing diagnostic fits per set (as row)

Examples

```
# load the data
data(hmp_gingival)
mod <- cbea(hmp_gingival$data, hmp_gingival$set, abund_values = "16SrRNA",
  output = "sig", distr = "norm", adj = FALSE, n_perm = 5, parametric = TRUE)
glance(mod, "fit_diagnostic")
```

| | |
|-------|-----------------------------------|
| gmean | <i>Geometric mean of a vector</i> |
|-------|-----------------------------------|

Description

Compute geometric mean of a vector using `exp(mean(log(.x)))` format

Usage

```
gmean(vec)
```

Arguments

| | |
|-----|----------------------------------|
| vec | A vector of values with length n |
|-----|----------------------------------|

Value

A numeric value of the geometric mean of the vector `vec`

Examples

```
ex <- abs(rnorm(10))
gmean(ex)
```

`gmeanRow`

Geometric mean of rows of a matrix

Description

This function computes the geometric mean by row of a numeric matrix

Usage

```
gmeanRow(X)
```

Arguments

`X` A numeric matrix with `n` rows and `p` columns

Value

A numeric vector of the geometric mean of the matrix `X` with length `n`

Examples

```
ex <- matrix(rnorm(100), nrow = 10, ncol = 10)
ex <- abs(ex)
gmeanRow(ex)
```

`hmp_gingival`

Gingival data set from the Human Microbiome Project

Description

Gingival data set from the Human Microbiome Project

Usage

```
data(hmp_gingival)
```

Format

A list with two elements

data The microbiome relative abundance data with relevant metadata obtained from the Human Microbiome Project via the HMP16SData package (snapshot: 11-15-2021). The data set is hosted the container of type phyloseq. Using the mia package users can convert it to the TreeSummarizedExperiment type.

set Sets of microbes based on their metabolism annotation at the Genera level. Annotations obtained via Calagaro et al.'s repository on Zenodo (<https://doi.org/10.5281/zenodo.3942108>)

References

Data can be downloaded directly from <https://hmpdacc.org/hmp/>

R interface of the data from <https://doi.org/doi:10.18129/B9.bioc.HMP16SData>

Beghini F, Renson A, Zolnik CP, Geistlinger L, Usyk M, Moody TU, et al. Tobacco Exposure Associated with Oral Microbiota Oxygen Utilization in the New York City Health and Nutrition Examination Study. *Annals of Epidemiology*. 2019;34:18–25.e3. doi:10.1016/j.annepidem.2019.03.005

Consortium THMP, Huttenhower C, Gevers D, Knight R, Abubucker S, Badger JH, et al. Structure, Function and Diversity of the Healthy Human Microbiome. *Nature*. 2012;486(7402):207–214. doi:10.1038/nature11234.

Calgareo M, Romualdi C, Waldron L, Risso D, Vitulo N. Assessment of Statistical Methods from Single Cell, Bulk RNA-Seq, and Metagenomics Applied to Microbiome Data. *Genome Biology*. 2020;21(1):191. doi:10.1186/s13059-020-02104-1

Schiffer L, Azhar R, Shepherd L, Ramos M, Geistlinger L, Huttenhower C, et al. HMP16SData: Efficient Access to the Human Microbiome Project through Bioconductor. *American Journal of Epidemiology*. 2019;doi:10.1093/aje/kwz006.

merge_lists

This function handles the ability to merge supplied and defaults

Description

This function handles the ability to merge supplied and defaults

Usage

```
merge_lists(defaults, supplied)
```

Arguments

defaults (List). Default options
supplied (List). Supplied options

Value

A merged list

| | |
|-------------|--|
| new_CBEAout | <i>Creating an output object of type CBEAout</i> |
|-------------|--|

Description

This function takes a list of lists from each object and turns it into a CBEAout type object

Usage

```
new_CBEAout(out, call)
```

Arguments

| | |
|------|--|
| out | A list containing scores for each set |
| call | A list containing all important arguments for printing |

Value

A new CBEAout object (which is a cleaner list of lists)

| | |
|---------|--|
| pmmnorm | <i>The Two Component Mixture Normal Distribution</i> |
|---------|--|

Description

The Two Component Mixture Normal Distribution

Usage

```
pmmnorm(q, mu, sigma, lambda, log = FALSE, verbose = FALSE)
dmnorm(x, mu, sigma, lambda, log = FALSE, verbose = FALSE)
```

Arguments

| | |
|---------|---|
| q, x | (Vector). Values to calculate distributional values of. |
| mu | (Vector). A two value vector of mean values. |
| sigma | (Vector). A two value vector of component-wise variances |
| lambda | (Vector). A two value vector of component mixing coefficients |
| log | (Boolean). Whether returning probabilities are in log format |
| verbose | (Boolean). Whether to return component values. |

Value

A numeric value representing the probability density value of a two-component mixture distribution

Functions

- pmnorm: Cumulative Distribution Function
- dmnorm: Probability Density Function

Examples

```
library(mixtools)
lambda <- c(0.7,0.3)
mu <- c(1,2)
sigma <- c(1,1)
v <- rnormmix(100, lambda=lambda, mu=mu, sigma=sigma)
pmnorm(v, lambda=lambda,mu=mu,sigma=sigma)
dmnorm(v, lambda=lambda,mu=mu,sigma=sigma)
```

| | |
|---------------|---|
| print.CBEAout | <i>Print dispatch for CBEAout objects</i> |
|---------------|---|

Description

Print dispatch for CBEAout objects

Usage

```
## S3 method for class 'CBEAout'
print(x, ...)
```

Arguments

| | |
|-----|---|
| x | The CBEAout object |
| ... | Undefined arguments, keeping consistency for generics |

Value

Text for printing

| | |
|-----------|---|
| reexports | <i>Objects exported from other packages</i> |
|-----------|---|

Description

These objects are imported from other packages. Follow the links below to see their documentation.

generics [glance](#), [tidy](#)

| | |
|--------------|--|
| scale_scores | <i>Scaling scores based on estimated null distribution</i> |
|--------------|--|

Description

Scaling scores based on estimated null distribution

Usage

```
scale_scores(scores, method, param, distr, thresh = 0.05)
```

Arguments

| | |
|--------|---|
| scores | (Numeric Vector). Raw CBEA scores generated without permutations |
| method | (String). The final form that the user want to return. Options include cdf, zscore, pval and sig. |
| param | (List). The parameters of the estimated null distribution. Names must match distribution. |
| thresh | (Numeric). The threshold to decide whether a set is significantly enriched. Only available if method is sig |

Value

A vector of size n where n is the sample size

| | |
|--------------|------------------------------|
| tidy.CBEAout | <i>Tidy a CBEAout object</i> |
|--------------|------------------------------|

Description

This function takes in a CBEA type object and collects all values across all sets and samples that were evaluated.

Usage

```
## S3 method for class 'CBEAout'
tidy(x, ...)
```

Arguments

| | |
|-----|--|
| x | A CBEAout object. |
| ... | Unused, included for generic consistency only. |

Value

A tidy `tibble::tibble()` summarizing scores per sample per set.

Examples

```
# load the data
data(hmp_gingival)
mod <- cbea(hmp_gingival$data, hmp_gingival$set, abund_values = "16SrRNA",
  output = "sig", distr = "norm", adj = FALSE, n_perm = 5, parametric = TRUE)
tidy(mod)
```

| | |
|-----------|---|
| var_setup | <i>Setting up parameter arrays for vectorized call to d/pnorm functions for multi-component mixture distributions</i> |
|-----------|---|

Description

Setting up parameter arrays for vectorized call to d/pnorm functions for multi-component mixture distributions

Usage

```
var_setup(mu, sigma, lambda, vlen)
```

Arguments

| | |
|--------|--|
| mu | See pmnorm documentation |
| sigma | See pmnorm documentation |
| lambda | See pmnorm documentation |
| vlen | (Integer). Length of the x or p vector to be evaluated |

Value

A list containing lambda, mu, and sigma

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