

# Package ‘CBEA’

January 27, 2023

**Title** Competitive Balances for Taxonomic Enrichment Analysis in R

**Version** 1.3.0

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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.

**License** MIT + file LICENSE

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

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

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**Author** Quang Nguyen [aut, cre] (<<https://orcid.org/0000-0002-2072-3279>>)

**Maintainer** Quang Nguyen <quangpmnguyen@gmail.com>

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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 <a href="#">cbea</a>
distr	See documentation <a href="#">cbea</a>
adj	See documentation <a href="#">cbea</a>
n_perm	See documentation <a href="#">cbea</a>
parametric	See documentation <a href="#">cbea</a>
thresh	See documentation <a href="#">cbea</a>
init	See documentation <a href="#">cbea</a>
control	See documentation <a href="#">cbea</a>
parallel_backend	See documentation <a href="#">cbea</a>
...	See documentation <a href="#">cbea</a>

### 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.

<code>parametric</code>	(Logical). Indicate whether a parametric distribution will be fitted to estimate z-scores, CDF values, and p-values. Defaults to TRUE
<code>thresh</code>	(Numeric). Threshold for significant p-values if <code>sig</code> is the output. Defaults to 0.05
<code>init</code>	(Named List). Initialization parameters for estimating the null distribution. Default is NULL.
<code>control</code>	(Named List). Additional arguments to be passed to <code>fitdistr</code> and <code>normmixEM</code> . Defaults to NULL.
<code>parallel_backend</code>	See documentation <a href="#">cbea</a>
<code>...</code>	Additional arguments not used at the moment.
<code>abund_values</code>	(Character). Character value for selecting the assay to be the input to <code>cbea</code>
<code>taxa_are_rows</code>	(Logical). Indicate whether the data frame or matrix has taxa as rows
<code>id_col</code>	(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`*This function checks for validity of arguments based on the parameters and the distribution of interest*

---

**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                      *Combining two distributions*

---

**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 probability 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**

<code>data</code>	(Numeric Vector). A vector of numbers that can be inputted to estimate the parameters of the distributional forms.
<code>distr</code>	(String). The distribution to be fitted. Right now only <code>norm</code> or <code>mnorm</code> is supported
<code>init</code>	(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
<code>args_list</code>	(List). Named list of additional arguments passed onto <code>fitdist</code> and <code>normalmixEM</code>
<code>...</code>	Other parameters passed to <code>fitdistrplus</code> or <code>normalmixEM</code>

**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 <a href="#">cbea</a>
distr	(Character). See documentation <a href="#">cbea</a>
output	(Character). See documentation <a href="#">cbea</a>
n_perm	(Numeric). The total number of permutations.
parametric	(Logical). See documentation <a href="#">cbea</a>
thresh	(Numeric). See documentation <a href="#">cbea</a>
init	(List). See documentation <a href="#">cbea</a>
control	(List). See documentation <a href="#">cbea</a>

**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**

<code>x</code>	An object of type CBEAout
<code>statistic</code>	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.
<code>...</code>	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

*Geometric mean of a vector*

---

**Description**

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

**Usage**

```
gmean(vec)
```

**Arguments**

<code>vec</code>	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	<i>Geometric mean of rows of a matrix</i>
----------	---

---

**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	<i>Gingival data set from the Human Microbiome Project</i>
--------------	--

---

**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 in 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.

Calgaro 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                      *Creating an output object of type CBEAout*

---

### 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)

---

pmnorm                              *The Two Component Mixture Normal Distribution*

---

### Description

The Two Component Mixture Normal Distribution

### Usage

```
pmnorm(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

*Print dispatch for CBEAout objects*


---

**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

*Objects exported from other packages*


---

**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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