Package ‘COMPASS’

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Type Package

Title Combinatorial Polyfunctionality Analysis of Single Cells

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Description COMPASS is a statistical framework that enables unbiased analysis of antigen-specific T-cell subsets. COMPASS uses a Bayesian hierarchical framework to model all observed cell-subsets and select the most likely to be antigen-specific while regularizing the small cell counts that often arise in multi-parameter space. The model provides a posterior probability of specificity for each cell subset and each sample, which can be used to profile a subject’s immune response to external stimuli such as infection or vaccination.

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BugReports https://github.com/RGLab/COMPASS/issues

VignetteBuilder knitr

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LazyData yes

biocViews FlowCytometry

RoxygenNote 5.0.1

NeedsCompilation yes

R topics documented:

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COMPASS-package

COMPASS (Combinatorial Polyfunctionality Analysis of Single-Cells)

Description

This package implements a model for the analysis of polyfunctionality in single-cell cytometry experiments. The model effectively identifies combinations of markers that are differentially expressed between samples of cells subjected to different stimulations.

See Also

- COMPASSContainer, for information on getting your cytometry data into a suitable format for use with COMPASS,
- COMPASS, for the main model fitting routine.
categories

Description
Returns the categories matrix in a COMPASSResult object.

Usage
categories(x, counts)

Arguments
x A COMPASSResult object.
counts Boolean; if TRUE we return the counts (degree of functionality) as well.

CellCounts

Description
Compute the number of cells expressing a particular combination of markers for each sample.

Usage
CellCounts(data, combinations)

Arguments
data Either a COMPASSContainer, or a list of matrices. Each matrix i is of dimension N_i cells (rows) by K common markers (columns).
combinations A list of 'combinations', used to denote the subsets of interest. See the examples for usage.

See Also
Combinations

Examples
set.seed(123)
## generate 10 simulated matrices of flow data
K <- 6 ## number of markers
data <- replicate(10, simplify=FALSE, {
  m <- matrix( rnorm(1E4 * K, 2000, 1000 ), ncol=K )
  m[m < 2500] <- 0
  colnames(m) <- c("IL2", "IL4", "IL6", "Mip1B", "IFNg", "TNFa")
  return(m)
})
names(data) <- sample(letters, 10)
Combinations

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## generate counts over all available combinations of markers in data
str(CellCounts(data)) ## 64 columns, as all 2^6 combinations expressed

## generate marginal counts
combos <- list(1, 2, 3, 4, 5, 6) ## marginal cell counts
cc <- CellCounts(data, combos)

## a base R way of doing the same thing
f <- function(data) {
  do.call(rbind, lapply(data, function(x) apply(x, 2, function(x) sum(x > 0)))))
}  
cc2 <- f(data)

## check that they're identical
stopifnot(identical( unname(cc), unname(cc2) ))

## We can also generate cell counts by expressing various combinations
## of markers (names) in the data.

## count cells expressing IL2 or IL4
CellCounts(data, "IL2|IL4")

## count cells expressing IL2, IL4 or IL6
CellCounts(data, "IL2|IL4|IL6")

## counts for each of IL2, IL4, IL6 (marginally)
CellCounts(data, c("IL2", "IL4", "IL6"))

## counts for cells that are IL2 positive and IL4 negative
CellCounts(data, "IL2 & !IL4")

## expressing the same intent with indices
CellCounts(data, list(c(1, -2)))

## all possible combinations
str(CellCounts(data, Combinations(6)))

## can also call on COMPASSContainers
data(COMPASS)
CellCounts(CC, "M1&M2")

---

<table>
<thead>
<tr>
<th>Combinations</th>
<th>Generate Combinations</th>
</tr>
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</table>

**Description**

Given an integer n, generate all binary combinations of n elements, transformed to indices. This is primarily for use with the `CellCounts` function, but may be useful for users in some scenarios.

**Usage**

`Combinations(n)`
Arguments

n
An integer.

Examples

Combinations(3)

Description

This function fits the COMPASS model.

Usage

COMPASS(data, treatment, control, subset = NULL,
  category_filter = function(x) colSums(x > 5) > 2,
  filter_lowest_frequency = 0, filter_specific_markers = NULL,
  model = "discrete", iterations = 40000, replications = 8,
  keep_original_data = FALSE, verbose = TRUE, dropDegreeOne = FALSE, ...)

Arguments

data
An object of class COMPASSContainer.
treatment
An R expression, evaluated within the metadata, that returns TRUE for those samples that should belong to the treatment group. For example, if the samples that received a positive stimulation were named "92TH023 Env" within a variable in meta called Stim, you could write Stim == "92TH023 Env". The expression should have the name of the stimulation vector on the left hand side.
control
An R expression, evaluated within the metadata, that returns TRUE for those samples that should belong to the control group. See above for details.
subset
An expression used to subset the data. We keep only the samples for which the expression evaluates to TRUE in the metadata.
category_filter
A filter for the categories that are generated. This is a function that will be applied to the treatment counts matrix generated from the intensities. Only categories meeting the category_filter criteria will be kept.
filter_lowest_frequency
A number specifying how many of the least expressed markers should be removed.
filter_specific_markers
Similar to filter_lowest_frequency, but lets you explicitly exclude markers.
model
A string denoting which model to fit; currently, only the discrete model ("discrete") is available.
iterations
The number of iterations (per 'replication') to perform.
replications
The number of 'replications' to perform. In order to conserve memory, we only keep the model estimates from the last replication.
keep_original_data
  Keep the original COMPASSContainer as part of the COMPASS output? If memory
  or disk space is an issue, you may set this to FALSE.
verbose
  Boolean; if TRUE we output progress information.
dropDegreeOne
  Boolean; if TRUE we drop degree one categories and merge them with the nega-
  tive subset.
...
  Other arguments; currently unused.

Value

A COMPASSResult is a list with the following components:

fit
  A list of various fitted parameters resulting from the COMPASS model fitting pro-
  cedure.
data
  The data used as input to the COMPASS fitting procedure – in particular, the counts
  matrices generated for the selected categories, n_s and n_u, can be extracted
  from here.
orig
  If keep_original_data was set to TRUE in the COMPASS fit, then this will be the
  COMPASSContainer passed in. This is primarily kept for easier running of the
  Shiny app.

The fit component is a list with the following components:

alpha_s
  The hyperparameter shared across all subjects under the stimulated condition. It
  is updated through the COMPASS model fitting process.
A_alphas
  The acceptance rate of alpha_s, as computed through the MCMC sampling
  process in COMPASS.
alpha_u
  The hyperparameter shared across all subjects under the unstimulated condition.
  It is updated through the COMPASS model fitting process.
A_alphau
  The acceptance rate of alpha_u, as computed through the MCMC sampling
  process in COMPASS.
gamma
  An array of dimensions I x K x T, where I denotes the number of individuals,
  K denotes the number of categories / subsets, and T denotes the number of itera-
  tions. Each cell in a matrix for a given iteration is either zero or one, reflecting
  whether individual i is responding to the stimulation for subset k.
mean_gamma
  A matrix of mean response rates. Each cell denotes the mean response of indi-
  vidual i and subset k.
A_gamma
  The acceptance rate for the gamma. Each element corresponds to the number of
  times an individual’s gamma vector was updated.
categories
  The category matrix, showing which categories entered the model.
model
  The type of model called.
posterior
  Posterior measures from the sample fit.
call
  The matched call used to generate the model fit.

The data component is a list with the following components:

n_s
  The counts matrix for stimulated samples.
n_u
  The counts matrix for unstimulated samples.
counts_s
  Total cell counts for stimulated samples.
COMPASSContainer

This function generates the data container suitable for use with COMPASS.

### Usage

```r
COMPASSContainer(data, counts, meta, individual_id, sample_id,
                 countFilterThreshold = 0)
```

### Description

This function generates the data container suitable for use with COMPASS.

**counts_u**
Total cell counts for unstimulated samples.

**categories**
The categories matrix used to define which categories will enter the model.

**meta**
The metadata. Note that only individual-level metadata will be kept; sample-specific metadata is dropped.

**sample_id**
The name of the vector in the metadata used to identify the samples.

**individual_id**
The name of the vector in the metadata used to identify the individuals.

The orig component (included if keep_original_data is TRUE) is the COMPASSContainer object used in the model fit.

### Category Filter

The category filter is used to exclude categories (combinations of markers expressed for a particular cell) that are expressed very rarely. It is applied to the treatment counts matrix, which is a N samples by K categories matrix. Those categories which are mostly unexpressed can be excluded here. For example, the default criteria,

```r
category_filter=function(x) colSums(x > 5) > 2
```

indicates that we should only retain categories for which at least three samples had at least six cells expressing that particular combination of markers.

### See Also

- COMPASSContainer, for constructing the data object required by COMPASS

### Examples

```r
data(COMPASS) ## loads the COMPASSContainer 'CC'
fit <- COMPASS(CC,
               category_filter=NULL,
               treatment=trt == "Treatment",
               control=trt == "Control",
               verbose=FALSE,
               iterations=100 ## set higher for a real analysis
)
```
COMPASSContainer

Arguments

data  A list of matrices. Each matrix $M_i$ is made up of $N_i$ cells by $K$ markers; for example, it could be the intensity information from an intracellular cytokine experiment. Each element of the list should be named; this name denotes which sample the cell intensities were measured from.

counts  A named integer vector of the cell counts(of the parent population) for each sample in data.

meta  A data.frame of metadata, describing the individuals in the experiment. Each row in meta should correspond to a row in data. There should be one row for each sample; i.e., one row for each element of data.

individual_id  The name of the vector in meta that denotes the individuals from which samples were drawn.

sample_id  The name of the vector in meta that denotes the samples. This vector should contain all of the names in the data input.

countFilterThreshold  Numeric; if the number of cells expressing at least one marker of interest is less than this threshold, we remove that file. Default is 0, which means filter is disabled.

Details

The names attributes for the data and counts objects passed should match.

Value

A COMPASSContainer returns a list made up of the same components as input the model, but checks and sanitizes the supplied data to ensure that it conforms to the expectations outlined above.

Examples

```r
set.seed(123)

n <- 10  ## number of samples
k <- 3  ## number of markers

## generate some sample data
sid_vec <- paste0("sid_", 1:n)  ## sample ids; unique names used to denote samples
iid_vec <- rep_len( paste0("iid_", 1:(n/2) ), n )  ## individual ids

## generate n matrices of 'cell intensities'
data <- replicate(n, {
  nrow <- round(runif(1) * 1E2 + 1000)
  ncol <- k
  vals <- rexp( nrow * ncol, runif(1, 1E-5, 1E-3) )
  vals[ vals < 2000 ] <- 0
  output <- matrix(vals, nrow, ncol)
  output <- output[ apply(output, 1, sum) > 0, ]
  colnames(output) <- paste0("M", 1:k)
  return(output)
})
names(data) <- sid_vec

## make a sample metadata data.frame
meta <- data.frame(

table

```
sid=sid_vec,
iid=iid_vec,
trt=rep( c("Control", "Treatment"), each=5 )
)

## generate an example total counts
## recall that cells not expressing any marker are not included
## in the 'data' matrices
counts <- sapply(data, nrow) + round( rnorm(n, 1E3, 1E2) )
counts <- setNames( as.integer(counts), names(counts) )

## insert everything into a COMPASSContainer
CC <- COMPASSContainer(data, counts, meta, "iid", "sid")

### Description

This dataset contains simulated data for an intracellular cytokine staining experiment. In this data set, we have paired samples from five individuals, with each pair of samples being subjected to either a 'Control' condition or a 'Treatment' condition.

### Details

Please see COMPASSContainer for more information on the components of this object.

The dataset is exported as CC, which is a short alias for COMPASSContainer.

### COMPASSContainerFromGatingSet

Create a COMPASS Container from a GatingSet

### Description

This code expects a GatingSet or GatingSetList. It expects a regular expression for the node name (i.e. '/4+\$' would match '/4+' in a node name with the plus sign at the end of the string. Alternatively, you can supply a partial path. The user must supply the 'individual_id', which has the default value suitable for the data we commonly see. 'sample_id' is the 'rownames' of 'pData' of 'GatingSet'. Sometimes the child node names don't match the marker names exactly. This function will try to make some guesses about how to match these up. The filter.fun parameter is a function that does some regular expression string substitution to try and clean up the node names by removing various symbols that are often added to gates, {+/-}. The user can provide their own function to do string cleanup. Counts are extracted as well as metadata and single cell data, and these are fed into the COMPASSContainer constructor.

### Usage

COMPASSContainerFromGatingSet(gs = NULL, node = NULL, filter.fun = NULL,
individual_id = "PTID", mp = NULL, matchmethod = c("Levenshtein", "regex"), markers = NA, swap = FALSE, countFilterThreshold = 5000)
COMPASSDescription

Arguments

- **gs**: a GatingSet or GatingSetList
- **node**: a regular expression to match a single node in the gating tree. If more than one node is matched, an error is thrown.
- **filter.fun**: a function that does string substitution to clean up node names, i.e. turns a 'CD4+' into a 'CD4' to try and match against the parameters slot of the flowFrames in gs
- **individual_id**: a character identifying the subject id column in the gs metadata
- **mp**: a list mapping node names to markers. This function tries to guess, but may fail. The user can override the guesswork.
- **matchmethod**: a character either 'regex' or 'Levenshtein' for matching nodes to markers.
- **markers**: a character vector of marker names to include.
- **swap**: a logical default FALSE. Set to TRUE if the marker and channel names are swapped.
- **countFilterThreshold**: numeric threshold. If the number of cells expressing at least one marker of interest is less than this threshold, we remove that file. Default is 5000.

Details

There is likely not sufficient error checking.

See Also

COMPASSContainer

Examples

```r
## Not run:
## gs is a GatingSet from flowWorkspace
COMPASSContainerFromGatingSet(gs, "4+")
## End(Not run)
```

COMPASSDescription  Get and Set the Description for the Shiny Application

Description

This is used for setting an informative description used in the Shiny application.

Usage

COMPASSDescription(x)

COMPASSDescription(x) <- value
COMPASSResult-accessors

Arguments

x
value

A COMPASS fit.
A set of paragraphs describing the experiment, as a character vector.

Details

Information about the COMPASS results will be auto-generated.

COMPASSResult-accessors

COMPASSResult Accessors

Description

These functions can be used for accessing data within a COMPASSResult.
The gamma array associated with a COMPASS model fit.

Usage

Gamma(x)
MeanGamma(x)

Arguments

x

A COMPASSResult object.

COMPASSResult-data

Simulated COMPASS fit

Description

This dataset represents the result of fitting the COMPASS model on the accompanying dataset CC, as exported by data(COMPASS). Please see the vignette (vignette("COMPASS")) for more details on how to interact with a COMPASS fit.

Details

The model is fit as follows, using the COMPASSContainer CC.

CR <- COMPASS(CC,
treatment=trt == "Treatment",
control=trt == "Control",
iterations=1000
)

The dataset is exported as CR, which is a short alias for COMPASSResult.
Please see COMPASS for more information on the output from a COMPASS model fit.
FunctionalityScore

**Description**

Computes the functionality score for each observation from the gamma matrix of a COMPASS model fit. The scores are normalized according to the total number of possible subsets that could be observed \((2^M - 1)\).

**Usage**

```r
FunctionalityScore(x, n, markers = NULL)
```

### Default S3 method:

```r
FunctionalityScore(x, n, markers = NULL)
```

**Arguments**

- `x` An object of class `COMPASSResult`, as returned by `COMPASS`. Alternatively, a matrix of functionality scores, used under the assumption that the ‘null’ category has been dropped.
- `n` The number of markers included in an experiment. It is inferred from the data when `x` is a `COMPASSResult`.
- `markers` The set of markers for which to compute a Functionality score. By default uses all markers. Must match names returned by `markers()`.

**Value**

A numeric vector of functionality scores.

**Note**

The null category is implicitly dropped when computing the functionality score for a COMPASS result; this is not true for the regular matrix method.

**Examples**

```r
FunctionalityScore(CR)
```
**GetThresholdedIntensities**

*Extract Thresholded Intensities from a GatingSet*

**Description**

This function extracts thresholded intensities for children of a node `node`, as specified through the `map` argument.

**Usage**

```r
GetThresholdedIntensities(gs, node, map)
```

**Arguments**

- `gs` A GatingSet or GatingSetList.
- `node` The name, or path, of a single node in a GatingSet / GatingSetList.
- `map` A list, mapping node names to markers.

**Details**

`map` should be an R list, mapping node names (as specified in the gating hierarchy of the gating set) to channel names (as specified in either the `desc` or `name` columns of the parameters of the associated flowFrames in the GatingSet).

**Value**

A list with two components:

- `data` A list of thresholded intensity measures.
- `counts` A named vector of total cell counts at the node `node`.

**Examples**

```r
if (require("flowWorkspace")) {

## Generate an example GatingSet that could be used with COMPASS
## We then pull out the 'data' and 'counts' components that could
## be used within a COMPASSContainer

n <- 10 ## number of samples
k <- 4 ## number of markers

sid_vec <- paste0("sid_", 1:n) ## sample ids; unique names used to denote samples
iid_vec <- rep_len( paste0("iid_", 1:(n/10) ), n ) ## individual ids
marker_names <- c("TNFa", "IL2", "IL4", "IL6")

## Generate n sets of 'flow' data -- a list of matrices, each row
## is a cell, each column is fluorescence intensities on a particular
## channel / marker
data <- replicate(n, {
  nrow <- round(runif(1) * 1E4 + 1000)
```

markers

markers

ncol <- k
vals <- rexp( nrow * ncol, runif(1, 1E-5, 1E-3) )
output <- matrix(vals, nrow, ncol)
colnames(output) <- marker_names
return(output)
})

names(data) <- sid_vec

## Put it into a GatingSet
fs <- flowSet( lapply(data, flowFrame) )
gs <- GatingSet(fs)

## Add some dummy metadata
meta <- pData(gs)
meta$PTID <- 1:10
pData(gs) <- meta
gate <- rectangleGate( list(TNFa=c(-Inf,Inf)))
add(gs, gate, parent="root", name="dummy")

## Add dummy gate

invisible(lapply(marker_names, function(marker) {
    .gate <- setNames( list( c( rexp(1, runif(1, 1E-5, 1E-3)), Inf) ), marker )
gate <- rectangleGate(.gate=.gate)
    add(gs, gate, parent="dummy", name=paste0(marker, "+"))
}))
recompute(gs)

## Map node names to channel names
map=list(
    "TNFa+"="TNFa",
    "IL2+"="IL2",
    "IL4+"="IL4",
    "IL6+"="IL6"
)

## Pull out the data as a COMPASS-friendly dataset
node <- "dummy"
map <- map
system.time(
    output <- GetThresholdedIntensities(gs, "dummy", map)
)

system.time(
    output <- COMPASSContainerFromGatingSet(gs, "dummy", individual_id="PTID")
)

str(output)

Markers
melt_  

Description  
Returns the markers associated with an experiment.

Usage  
markers(object)

Arguments  
object  An R object.

melt_  

Make a 'Wide' data set 'Long'

Description  
Inspired by reshape2::melt, we melt data.frames and matrixs. This function is built for speed.

Usage  
melt_(data, ...)

## S3 method for class 'data.frame'
melt_(data, id.vars, measure.vars,  
variable.name = "variable", ..., value.name = "value")

## S3 method for class 'matrix'
melt_(data, ...)

Arguments  
data  The data.frame to melt.
...  Arguments passed to other methods.
id.vars  Vector of id variables. Can be integer (variable position) or string (variable name). If blank, we use all variables not in measure.vars.
measure.vars  Vector of measured variables. Can be integer (variable position) or string (variable name). If blank, we use all variables not in id.vars.
variable.name  Name of variable used to store measured variable names.
value.name  Name of variable used to store values.

Details  
If items to be stacked are not of the same internal type, they will be promoted in the order logical > integer > numeric > character.
merge.COMPASSContainer

*Merge Two COMPASSContainers*

**Description**

This function merges two COMPASSContainers.

**Usage**

```r
## S3 method for class 'COMPASSContainer'
merge(x, y, ...)
```

**Arguments**

- `x`: A COMPASSContainer.
- `y`: A COMPASSContainer.
- `...`: other arguments passed to 'COMPASSContainer' call.

**Examples**

```r
## Chop the example COMPASSContainer into two, then merge it back together
CC1 <- subset(CC, trt == "Control")
CC2 <- subset(CC, trt == "Treatment")
merged <- merge(CC1, CC2)
res <- identical(CC, merge(CC1, CC2)) ## should return TRUE in this case
stopifnot( isTRUE(res) )
```

---

**metadata**

*Metadata*

**Description**

Functions for getting and setting the metadata associated with an object.

**Usage**

```r
metadata(x)
```

**Examples**

```r
## S3 method for class 'COMPASSContainer'
metadata(x)
```

```r
## S3 method for class 'COMPASSResult'
metadata(x)
```

```r
metadata(x) <- value
```

```r
## S3 replacement method for class 'COMPASSContainer'
metadata(x) <- value
```
pheatmap

Arguments

x
An R object.

value
An R object appropriate for storing metadata in object x; typically a data.frame.

Usage

pheatmap(mat, color = colorRampPalette(rev(brewer.pal(n = 7, name = "RdYlBu")))(100), kmeans_k = NA, breaks = NA, border_color = "grey60", cellwidth = NA, cellheight = NA, scale = "none", cluster_rows = TRUE, cluster_cols = TRUE, clustering_distance_rows = "euclidean", clustering_distance_cols = "euclidean", clustering_method = "complete", treeheight_row = ifelse(cluster_rows, 50, 0), treeheight_col = ifelse(cluster_cols, 50, 0), legend = TRUE, legend_breaks = NA, legend_labels = NA, annotation = NA, annotation_colors = NA, annotation_legend = TRUE, drop_levels = TRUE, show_rownames = TRUE, show_colnames = TRUE, main = NA, fontsize = 10, fontsize_row = fontsize, fontsize_col = fontsize, display_numbers = FALSE, number_format = "%.2f", fontsize_number = 0.8 * fontsize, filename = NA, width = NA, height = NA, row_annotation = NA, row_annotation_legend = TRUE, row_annotation_colors = NA, cytokine_annotation = NA, headerplot = NA, polar = FALSE, order_by_max_functionality = TRUE, ...)
cluster_rows  boolean values determining if rows should be clustered.
cluster_cols  boolean values determining if columns should be clustered.
clustering_distance_rows  
distance measure used in clustering rows. Possible values are "correlation" for Pearson correlation and all the distances supported by `dist`, such as "euclidean", etc. If the value is none of the above it is assumed that a distance matrix is provided.

clustering_distance_cols  
distance measure used in clustering columns. Possible values the same as for `clustering_distance_rows`.
clustering_method  
clustering method used. Accepts the same values as `hclust`.
treeheight_row  the height of a tree for rows, if these are clustered. Default value 50 points.
treeheight_col  the height of a tree for columns, if these are clustered. Default value 50 points.
legend  
logical to determine if legend should be drawn or not.
legend_breaks  vector of breakpoints for the legend.
legend_labels  vector of labels for the `legend_breaks`.
annotation  
data frame that specifies the annotations shown on top of the columns. Each row defines the features for a specific column. The columns in the data and rows in the annotation are matched using corresponding row and column names. Note that color schemes takes into account if variable is continuous or discrete.
annotation_colors  
list for specifying annotation track colors manually. It is possible to define the colors for only some of the features. Check examples for details.
annotation_legend  
boolean value showing if the legend for annotation tracks should be drawn.
drop_levels  
logical to determine if unused levels are also shown in the legend
show_rownames  boolean specifying if column names are be shown.
show_colnames  boolean specifying if column names are be shown.
main  
the title of the plot
fontsize  
base fontsize for the plot
fontsize_row  fontsize for rownames (Default: fontsize)
fontsize_col  fontsize for colnames (Default: fontsize)
display_numbers  
logical determining if the numeric values are also printed to the cells.
number_format  
format strings (C printf style) of the numbers shown in cells. For example "%.2f" shows 2 decimal places and "%.1e" shows exponential notation (see more in `gettextf`).
fontsize_number  
fontsize of the numbers displayed in cells
filename  
file path where to save the picture. Filetype is decided by the extension in the path. Currently following formats are supported: png, pdf, tiff, bmp, jpeg. Even if the plot does not fit into the plotting window, the file size is calculated so that the plot would fit there, unless specified otherwise.
width  
manual option for determining the output file width in inches.
height  
manual option for determining the output file height in inches.
pheatmap

row_annotation  data frame that specifies the annotations shown on the rows. Each row defines the features for a specific row. The rows in the data and rows in the annotation are matched using corresponding row names. The category labels are given by the data frame column names.

row_annotation_legend  same interpretation as the column parameters.

row_annotation_colors  same interpretation as the column parameters

cytokine_annotation  A data.frame of factors, with either levels 0 = unexpressed, 1 = expressed, or optionally with a third level -1 = 'left out'. of the categories for each column. They will be colored by their degree of functionality and ordered by degree of functionality and by amount of expression if column clustering is not done.

headerplot  is a list with two components, order and data. Order tells how to reorder the columns of the matrix.

polar  Boolean; if TRUE we draw a polar legend. Primarily for internal use. Data is some summary statistic over the columns which will be plotted in the header where the column cluster tree usually appears. Cytokine ordering is ignored when the headerplot argument is passed.

order_by_max_functionality  Boolean; re-order the cytokine labels by maximum functionality?

... graphical parameters for the text used in plot. Parameters passed to grid.text, see gpar.

Details

The function also allows to aggregate the rows using kmeans clustering. This is advisable if number of rows is so big that R cannot handle their hierarchical clustering anymore, roughly more than 1000. Instead of showing all the rows separately one can cluster the rows in advance and show only the cluster centers. The number of clusters can be tuned with parameter kmeans_k.

Value

Invisibly a list of components

- tree_row the clustering of rows as hclust object
- tree_col the clustering of columns as hclust object
- kmeans the kmeans clustering of rows if parameter kmeans_k was specified

Author(s)

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Examples

# Generate some data
test = matrix(rnorm(200), 20, 10)
test[1:10, seq(1, 10, 2)] = test[1:10, seq(1, 10, 2)] + 3
test[11:20, seq(2, 10, 2)] = test[11:20, seq(2, 10, 2)] + 2
test[15:20, seq(2, 10, 2)] = test[15:20, seq(2, 10, 2)] + 4
colnames(test) = paste("Test", 1:10, sep = "")
rownames(test) = paste("Gene", 1:20, sep = "")

# Draw heatmaps
pheatmap(test)
pheatmap(test, kmeans_k = 2)
pheatmap(test, scale = "row", clustering_distance_rows = "correlation")
pheatmap(test, color = colorRampPalette(c("navy", "white", "firebrick3"))(50))
pheatmap(test, cluster_row = FALSE)
pheatmap(test, legend = FALSE)
pheatmap(test, display_numbers = TRUE)
pheatmap(test, display_numbers = TRUE, number_format = "%e")
pheatmap(test, cluster_row = FALSE, legend_breaks = -1:4, legend_labels = c("0", "1e-4", "1e-3", "1e-2", "1e-1", "1"))
pheatmap(test, cellwidth = 15, cellheight = 12, main = "Example heatmap")
# pheatmap(test, cellwidth = 15, cellheight = 12, fontsize = 8, filename = "test.pdf")

# Generate column annotations
annotation = data.frame(Var1 = factor(1:10 %% 2 == 0, labels = c("Class1", "Class2")), Var2 = 1:10)
annotation$Var1 = factor(annotation$Var1, levels = c("Class1", "Class2", "Class3"))
rownames(annotation) = paste("Test", 1:10, sep = "")
pheatmap(test, annotation = annotation)
pheatmap(test, annotation = annotation, annotation_legend = FALSE)
pheatmap(test, annotation = annotation, annotation Legend = FALSE, drop_levels = FALSE)

# Specify colors
Var1 = c("navy", "darkgreen")
names(Var1) = c("Class1", "Class2")
Var2 = c("lightgreen", "navy")
ann_colors = list(Var1 = Var1, Var2 = Var2)

# Specify row annotations
row_ann <- data.frame(A=gl(4,nrow(test)/4), B=gl(4,nrow(test)/4))
rownames(row_ann) <- rownames(test)
pheatmap(test, annotation = annotation, annotation_legend = FALSE, drop_levels = FALSE, row_annotation = row_ann)

# Using cytokine annotations
M<-matrix(rnorm(8*20),ncol=8)
row_annotation<-data.frame(A=gl(4,nrow(M)/4), B=gl(4,nrow(M)/4))
eg<-expand.grid(factor(c(0,1)), factor(c(0,1)), factor(c(0,1)))
colnames(eg)<-c("IFNg", "TNFa", "IL2")
rownames(eg)<-apply(eg,1,function(x)paste0(x,collapse=""))
colnames(M)<-1:nrow(M)
cytokine_annotation=eg
pheatmap(M, annotation=annotation, row_annotation=row_annotation, annotation_legend=TRUE, row_annotation_legend=TRUE, cluster_rows=FALSE, cytokine_annotation=eg, cluster_cols=FALSE)

# Specifying clustering from distance matrix
drows = dist(test, method = "minkowski")
dcols = dist(t(test), method = "minkowski")
pheatmap(test, clustering_distance_rows = drows, clustering_distance_cols = dcols)
Description

This function can be used to visualize the mean probability of response; that is, the probability that there is a difference in response between samples subjected to the ‘treatment’ condition, and samples subjected to the ‘control’ condition.

Usage

## S3 method for class 'COMPASSResult'
plot(x, y, subset = NULL, threshold = 0.01, minimum_dof = 1, maximum_dof = Inf, must_express = NULL, row_annotation, palette = colorRampPalette(brewer.pal(10, "Purples"))(20), show_rownames = FALSE, show_colnames = FALSE, measure = NULL, order_by = FunctionalityScore, order_by_max_functionality = TRUE, markers = NULL, ...)

Arguments

x  
An object of class COMPASSResult.

y  
This argument gets passed to row_annotation, if row_annotation is missing. It can be used to group rows (individuals) by different conditions as defined in the metadata.

subset  
An R expression, evaluated within the metadata, used to determine which individuals should be kept.

threshold  
A numeric threshold for filtering under-expressed categories. Any categories with mean score < threshold are removed.

minimum_dof  
The minimum degree of functionality for the categories to be plotted.

maximum_dof  
The maximum degree of functionality for the categories to be plotted.

must_express  
A character vector of markers that should be included in each subset plotted. For example, must_express=c("TNFa & IFNg") says we include only subsets that are positive for both TNFa or IFNg, while must_express=c("TNFa", "IFNg") says we should keep subsets which are positive for either TNFa or IFNg.

row_annotation  
A vector of names, pulled from the metadata, to be used for row annotation.

palette  
The colour palette to be used.

show_rownames  
Boolean; if TRUE we display row names (ie, the individual ids).

show_colnames  
Boolean; if TRUE we display column names (ie, the column name associated with a cytokine; typically not needed)

measure  
Optional. By default, we produce a heatmap of the mean gammas produced in a model fit. We can override this by supplying a matrix of suitable dimension as well; these can be generated with the Posterior* functions – see Posterior for examples.

order_by  
Order rows within a group. This should be a function; e.g. FunctionalityScore, mean, median, and so on. Set this to NULL to preserve the original ordering of the data.
**plot2**

Plot a pair of COMPASSResults

Description

This function can be used to visualize the mean probability of response – that is, the probability that there is a difference in response between samples subjected to the 'treatment' condition, and samples subjected to the 'control' condition.

Usage

```r
plot2(x, y, subset, threshold = 0.01, minimum_dof = 1, maximum_dof = Inf,
      must_express = NULL, row_annotation = NULL, palette = NA,
      show_rownames = FALSE, show_colnames = FALSE, ...)
```

Arguments

- `x`: An object of class COMPASSResult.
- `y`: An object of class COMPASSResult.
- `subset`: An R expression, evaluated within the metadata, used to determine which individuals should be kept.
- `threshold`: A numeric threshold for filtering under-expressed categories. Any categories with mean score < `threshold` are removed.
- `minimum_dof`: The minimum degree of functionality for the categories to be plotted.
- `maximum_dof`: The maximum degree of functionality for the categories to be plotted.
- `must_express`: A character vector of markers that should be included in each subset plotted. For example, `must_express=c("TNFa & IFNg")` says we include only subsets that are positive for both TNFa or IFNg, while `must_express=c("TNFa", "IFNg")` says we should keep subsets which are positive for either TNFa or IFNg.
- `row_annotation`: A vector of names, pulled from the metadata, to be used for row annotation.
- `palette`: A vector of names, pulled from the metadata, to be used for row annotation.
- `show_rownames`: Boolean; if TRUE we display row names (ie, the individual ids).

Value

The plot as a grid object (grob). It can be redrawn with e.g. `grid::grid.draw()`.

Examples

```r
## visualize the mean probability of response
plot(CR)

## visualize the proportion of cells belonging to a category
plot(CR, measure=PosteriorPs(CR))
```
show_colnames Boolean: if TRUE we display column names (ie, the column name associated with a cytokine; typically not needed)

Optional arguments passed to pheatmap.

Value

The plot as a grid object (grob). It can be redrawn with e.g. grid::grid.draw().

Description

Computes the Polyfunctionality score for each observation from the gamma matrix of a COMPASS model fit. The scores are normalized to one.

Usage

PolyfunctionalityScore(x, degree, n, markers = NULL)

## S3 method for class 'COMPASSResult'
PolyfunctionalityScore(x, degree, n, markers = NULL)

## Default S3 method:
PolyfunctionalityScore(x, degree, n, markers = NULL)

Arguments

x An object of class COMPASSResult, as returned by COMPASS. Alternatively, a matrix of functionality scores.
degree A vector of weights. If missing, this is the 'degree of functionality', that is, the number of markers expressed in a particular category.
n The total number of markers. This is inferred when x is a COMPASSResult, and is unused in that case.
markers A character specifying the markers for which to compute the score. Must match names in markers().

Value

A numeric vector of polyfunctionality scores.

Examples

PolyfunctionalityScore(CR)
Description

These functions can be used to retrieve different posterior measures from a COMPASS fit object.

Usage

Posterior(x)
PosteriorDiff(x)
PosteriorLogDiff(x)
PosteriorPs(x)
PosteriorPu(x)

Arguments

x An object of class COMPASSResult.

Details

The posterior items retrieved are described as follows:

PosteriorPs: The posterior probability that the samples subjected to the ‘treatment’, or ‘stimulated’, condition responded.

PosteriorPu: The posterior probability that the samples subjected to the ‘control’, or ‘unstimulated’, condition responded.

PosteriorDiff: The difference in posterior response rates, as described above.

PosteriorLogDiff: The difference in the log response rates, as described above.

Examples

Posterior(CR)
PosteriorPs(CR)
PosteriorPu(CR)
PosteriorDiff(CR)
PosteriorLogDiff(CR)
**print.COMPASSContainer**

*Print a COMPASSContainer Object*

**Description**

This function prints a COMPASSContainer object, giving basic information about the object and the data it encapsulates.

**Usage**

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

**Arguments**

- `x`  
  An object of class COMPASSContainer.

- `...`  
  Optional arguments passed to `cat`.

**Examples**

```r
print(CC)
```

---

**print.COMPASSResult**

*Print a COMPASSResult Object*

**Description**

This function prints basic information about the model fit by a COMPASS call.

**Usage**

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

**Arguments**

- `x`  
  An object of class COMPASSResult.

- `...`  
  Optional arguments; currently unused.

**Examples**

```r
print(CR)
```
scores

Fetch the table of scores and metadata from a COMPASSResult Object

Description
This function extracts the functionality and polyfunctionality scores from a COMPASS result merged with the sample metadata table, accounting for any dropped samples due to filtering.

Usage
scores(x, markers = NULL)

Arguments
x
A COMPASSResult object.
markers
A character vector of markers for which to compute the scores. Defaults to all markers. Must match the names returned by markers().

Examples
scores(CR)

shinyCOMPASS
Start a Shiny Application for Visualizing COMPASS Results

Description
This function takes a COMPASSResult object, and generates a local Shiny application for visualizing the results.

Usage
shinyCOMPASS(x, dir = NULL, meta.vars, facet1 = "None", facet2 = "None", facet3 = "None", main = "Heatmap of Ag-Specificity Posterior Probabilities", stimulation = NULL, launch = TRUE, ...)

Arguments
x
An object of class COMPASSResult.
dir
A location to write out the .rds files that will be loaded and used by the Shiny application.
meta.vars
A character vector of column names that should be used for potential facetting in the Shiny app. By default, we take all metadata variables; you may want to limit this if you know certain variables are not of interest.
facet1, facet2, facet3
Default values for facets in the Shiny app. Each should be the name of a single vector in the metadata.
**shinyCOMPASSDeps**

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SimpleCOMPASS  

Fit the discrete COMPASS Model

Description
This function fits the COMPASS model from a user-provided set of stimulated / unstimulated matrices. See the NOTE for important details.

Usage
```
SimpleCOMPASS(n_s, n_u, meta, individual_id, sample_id, iterations = 10000, replications = 8, verbose = TRUE)
```

Arguments
- **n_s**  The cell counts for stimulated cells.
- **n_u**  The cell counts for unstimulated cells.
- **meta** A data.frame of metadata, describing the individuals in the experiment. Each row in meta should correspond to a row in data. There should be one row for each sample; i.e., one row for each element of n_s and n_u.
- **individual_id** The name of the vector in meta that denotes the individuals from which samples were drawn.
- **sample_id** The name of the vector in meta that denotes the samples. This vector should contain all of the names in the data input.
- **iterations** The number of iterations (per 'replication') to perform.
- **replications** The number of 'replications' to perform. In order to conserve memory, we only keep the model estimates from the last replication.
- **verbose** Boolean; if TRUE we output progress information.

Value
A list with class COMPASSResult with two components, the fit containing parameter estimates and parameter acceptance rates, and data containing the generated data used as input for the model.

Note
n_s and n_u counts matrices should contain ALL \(2^M\) possible combinations of markers, even if they are 0 for some combinations. The code expects the marker combinations to be named in the following way: "M1&M2&!M3" means the combination represents cells expressing marker "M1" and "M2" and not "M3". For 3 markers, there should be 8 such combinations, such that n_s and n_u have 8 columns.

Examples
```r
## Not run:
set.seed(123)
n <- 10 ## number of samples
k <- 3 ## number of markers

## generate some sample data
subset.COMPASSContainer

Subset a COMPASSContainer

Description

Use this function to subset a COMPASSContainer.

Usage

## S3 method for class 'COMPASSContainer'
subset(x, subset, ...)

Arguments

x A COMPASSContainer.

subset A logical expression, evaluated within the metadata, indicating which entries to keep.

... other arguments passed to 'COMPASSContainer' call.

Examples

subset(CC, iid == "iid_1")
summary.COMPASSContainer  

**Summarize a COMPASSContainer Object**

**Description**
This function prints summary information about a COMPASSContainer object – the number of samples, basic information about the metadata, and so on.

**Usage**
```r
## S3 method for class 'COMPASSContainer'
summary(object, ...)
```

**Arguments**
- **object**: An object of class COMPASSContainer.
- **...**: Optional arguments; currently ignored.

**Examples**
```r
summary(CC)
```

summary.COMPASSResult  

**Summarize a COMPASSResult Object**

**Description**
This function prints basic information about the model fit by a COMPASS call.

**Usage**
```r
## S3 method for class 'COMPASSResult'
summary(object, ...)
```

**Arguments**
- **object**: An object of class COMPASSResult.
- **...**: Optional arguments; currently unused.

**Examples**
```r
print(CR)
```
TotalCellCounts

Compute Total Cell Counts

Description

This function is used to compute total cell counts, per individual, from a COMPASSContainer.

Usage

TotalCellCounts(data, subset, aggregate = TRUE)

Arguments

data A COMPASSContainer.
subset An expression, evaluated within the metadata, defining the subset of data over which the counts are computed. If left unspecified, the counts are computed over all samples.
aggregate Boolean; if TRUE we sum over the individual, to get total counts across samples for each individual.

Examples

TotalCellCounts(CC, trt == "Treatment")
TotalCellCounts(CC, trt == "Control")
TotalCellCounts(CC)

transpose_list Transpose a List

Description

Transpose a matrix-like list.

Usage

transpose_list(x)

Arguments

x An R list.

Examples

l <- list(1:3, 4:6, 7:9)
stopifnot(identical(transpose_list(transpose_list(l)), l))
UniqueCombinations

**Generate Unique Combinations**

**Description**
Generate all possible unique combinations of \( x \). Primarily used as a helper function for CellCounts, but may be occasionally useful to the end user.

**Usage**

```r
UniqueCombinations(x, as.matrix)
```

### S3 method for class 'COMPASSContainer'

```r
UniqueCombinations(x, as.matrix = FALSE)
```

### Default S3 method:

```r
UniqueCombinations(x, as.matrix = FALSE)
```

**Arguments**

- **x**: Either a COMPASSContainer, or a list of matrices.
- **as.matrix**: Boolean; if TRUE we return results as a matrix; otherwise, we return the results as a list.

**Examples**

```r
UniqueCombinations(CC)
```
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