Package ‘singleCellHaystack’

March 28, 2021

Type Package

Title Finding Needles (=differentially Expressed Genes) in Haystacks (=single Cell Data)

Version 0.3.4

Description Identification of differentially expressed genes (DEGs) is a key step in single-cell transcriptomics data analysis. ‘singleCellHaystack’ predicts DEGs without relying on clustering of cells into arbitrary clusters. Single-cell RNA-seq (scRNA-seq) data is often processed to fewer dimensions using Principal Component Analysis (PCA) and represented in 2-dimensional plots (e.g. t-SNE or UMAP plots). ‘singleCellHaystack’ uses Kullback-Leibler divergence to find genes that are expressed in subsets of cells that are non-randomly positioned in a these multi-dimensional spaces or 2D representations. For the theoretical background of ‘singleCellHaystack’ we refer to Vandenbon and Diez (Nature Communications, 2020) <doi:10.1038/s41467-020-17900-3>.

Imports methods, Matrix, splines, ggplot2, reshape2

Suggests knitr, rmarkdown, SummarizedExperiment, SingleCellExperiment, SeuratObject, Rtsne, cowplot, testthat, wrswoR

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LazyData true

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VignetteBuilder knitr

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Author Alexis Vandenbon [aut, cre] (<https://orcid.org/0000-0003-2180-5732>), Diego Diez [aut] (<https://orcid.org/0000-0002-2325-4893>)

Maintainer Alexis Vandenbon <alexis.vandenbon@gmail.com>

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dat.tsne

Single cell RNA-seq dataset.

Description

Single cell RNA-seq dataset.

dat.tsne

Single cell tSNE coordingates.

Description

Single cell tSNE coordingates.
**default_bandwidth.nrd**

Default function given by function `bandwidth.nrd` in MASS. No changes were made to this function.

**Usage**

default_bandwidth.nrd(x)

**Arguments**

- **x** A numeric vector

**Value**

A suitable bandwidth.

---

**extract_row_dgRMatrix**

Returns a row of a sparse matrix of class `dgRMatrix`. Function made by Ben Bolker and Ott Toomet (see https://stackoverflow.com/questions/47997184/)

**Description**

Returns a row of a sparse matrix of class `dgRMatrix`. Function made by Ben Bolker and Ott Toomet (see https://stackoverflow.com/questions/47997184/)

**Usage**

extract_row_dgRMatrix(m, i = 1)

**Arguments**

- **m** a sparse matrix of class `dgRMatrix`
- **i** the index of the row to return

**Value**

A row (numerical vector) of the sparse matrix
extract_row_lgRMatrix  Returns a row of a sparse matrix of class lgRMatrix. Function made by Ben Bolker and Ott Toomet (see https://stackoverflow.com/questions/47997184/)

Description

Returns a row of a sparse matrix of class lgRMatrix. Function made by Ben Bolker and Ott Toomet (see https://stackoverflow.com/questions/47997184/)

Usage

extract_row_lgRMatrix(m, i = 1)

Arguments

m  a sparse matrix of class lgRMatrix
i  the index of the row to return

Value

A row (logical vector) of the sparse matrix

generate

Function to get the density of points with value TRUE in the (x,y) plot

Description

Function to get the density of points with value TRUE in the (x,y) plot

Usage

generate(  x,  y,  detection,  rows.subset = 1:nrow(detection),  high.resolution = FALSE  )
get_dist_two_sets

Arguments

x  x-axis coordinates of cells in a 2D representation (e.g. resulting from PCA or t-SNE)
y  y-axis coordinates of cells in a 2D representation
detection  A logical matrix or dgRMatrix showing which gens (rows) are detected in which cells (columns)
rows.subset  Indices of the rows of 'detection' for which to get the densities. Default: all.
high.resolution  Logical: should high resolution be used? Default is FALSE.

Value

A 3-dimensional array (dim 1: genes/rows of expression, dim 2 and 3: x and y grid points) with density data

get_dist_two_sets  Calculate the pairwise Euclidean distances between the rows of 2 matrices.

Description

Calculate the pairwise Euclidean distances between the rows of 2 matrices.

Usage

get_dist_two_sets(set1, set2)

Arguments

set1  A numerical matrix.
set2  A numerical matrix.

Value

A matrix of pairwise distances between the rows of 2 matrices.
get_D_KL

Calculates the Kullback-Leibler divergence between distributions.

Description
Calculates the Kullback-Leibler divergence between distributions.

Usage
get_D_KL(classes, parameters, reference.prob, pseudo)

Arguments
- classes: A logical vector. Values are T if the gene is expressed in a cell, F if not.
- parameters: Parameters of the analysis, as set by function `get_parameters_haystack`
- reference.prob: A reference distribution to calculate the divergence against.
- pseudo: A pseudocount, used to avoid log(0) problems.

Value
A numerical value, the Kullback-Leibler divergence

get_D_KL_highD

Calculates the Kullback-Leibler divergence between distributions for the high-dimensional version of haystack().

Description
Calculates the Kullback-Leibler divergence between distributions for the high-dimensional version of haystack().

Usage
get_D_KL_highD(classes, density.contributions, reference.prob, pseudo = 0)

Arguments
- classes: A logical vector. Values are T if the gene is expressed in a cell, F if not.
- density.contributions: A matrix of density contributions of each cell (rows) to each center point (columns).
- reference.prob: A reference distribution to calculate the divergence against.
- pseudo: A pseudocount, used to avoid log(0) problems.

Value
A numerical value, the Kullback-Leibler divergence
**get_euclidean_distance**

*Calculate the Euclidean distance between x and y.*

**Description**

Calculate the Euclidean distance between x and y.

**Usage**

get_euclidean_distance(x, y)

**Arguments**

- **x**: A numerical vector.
- **y**: A numerical vector.

**Value**

A numerical value, the Euclidean distance.

---

**get_grid_points**

*A function to decide grid points in a higher-dimensional space*

**Description**

A function to decide grid points in a higher-dimensional space.

**Usage**

get_grid_points(input, method = "centroid", grid.points = 100)

**Arguments**

- **input**: A numerical matrix with higher-dimensional coordinates (columns) of points (rows).
- **method**: The method to decide grid points. Should be "centroid" (default) or "seeding".
- **grid.points**: The number of grid points to return. Default is 100.

**Value**

Coordinates of grid points in the higher-dimensional space.
**get_log_p_D_KL**

Estimates the significance of the observed Kullback-Leibler divergence by comparing to randomizations.

**Description**

Estimates the significance of the observed Kullback-Leibler divergence by comparing to randomizations.

**Usage**

```r
get_log_p_D_KL(T.counts, D_KL.observed, D_KL.randomized, output.dir = NULL)
```

**Arguments**

- `T.counts` The number of cells in which a gene is detected.
- `D_KL.observed` A vector of observed Kullback-Leibler divergences.
- `D_KL.randomized` A matrix of Kullback-Leibler divergences of randomized datasets.
- `output.dir` Optional parameter. Default is NULL. If not NULL, some files will be written to this directory.

**Value**

A vector of log10 p values, not corrected for multiple testing using the Bonferroni correction.

**get_parameters_haystack**

Function that decides most of the parameters that will be during the "Haystack" analysis.

**Description**

Function that decides most of the parameters that will be during the "Haystack" analysis.

**Usage**

```r
get_parameters_haystack(x, y, high.resolution = FALSE)
```

**Arguments**

- `x` x-axis coordinates of cells in a 2D representation (e.g. resulting from PCA or t-SNE)
- `y` y-axis coordinates of cells in a 2D representation
- `high.resolution` Logical: should high resolution be used? Default is FALSE.
Value

A list containing various parameters to use in the analysis.

get_reference

Get reference distribution

Description

Get reference distribution

Usage

get_reference(param, use.advanced.sampling = NULL)

Arguments

param Parameters of the analysis, as set by function ‘get_parameters_haystack’
use.advanced.sampling If NULL naive sampling is used. If a vector is given (of length = no. of cells) sampling is done according to the values in the vector.

Value

A list with two components, Q for the reference distribution and pseudo.

haystack

The main Haystack function

Description

The main Haystack function

Usage

haystack(x, ...)

## S3 method for class 'matrix'
haystack(
x,
dim1 = 1,
dim2 = 2,
detection,
method = "highD",
use.advanced.sampling = NULL,
dir.randomization = NULL,
scale = TRUE,
grid.points = 100,
grid.method = "centroid",
... 
)

## S3 method for class 'data.frame'
haystack(
  x,
  dim1 = 1,
  dim2 = 2,
  detection,
  method = "highD",
  use.advanced.sampling = NULL,
  dir.randomization = NULL,
  scale = TRUE,
  grid.points = 100,
  grid.method = "centroid",
  ...
)

## S3 method for class 'Seurat'
haystack(
  x,
  assay = "RNA",
  slot = "data",
  coord = "pca",
  dims = NULL,
  cutoff = 1,
  method = NULL,
  use.advanced.sampling = NULL,
  ...
)

## S3 method for class 'SingleCellExperiment'
haystack(
  x,
  assay = "counts",
  coord = "TSNE",
  dims = NULL,
  cutoff = 1,
  method = NULL,
  use.advanced.sampling = NULL,
  ...
)

Arguments

x a matrix or other object from which coordinates of cells can be extracted.
... further parameters passed down to methods.

dim1 column index or name of matrix for x-axis coordinates.

dim2 column index or name of matrix for y-axis coordinates.

detection A logical matrix showing which genes (rows) are detected in which cells (columns)

method choose between highD (default) and 2D haystack.

use.advanced.sampling
If NULL naive sampling is used. If a vector is given (of length = no. of cells) sampling is done according to the values in the vector.

dir.randomization
If NULL, no output is made about the random sampling step. If not NULL, files related to the randomizations are printed to this directory.

scale Logical (default=TRUE) indicating whether input coordinates in x should be scaled to mean 0 and standard deviation 1.

grid.points An integer specifying the number of centers (gridpoints) to be used for estimating the density distributions of cells. Default is set to 100.

grid.method The method to decide grid points for estimating the density in the high-dimensional space. Should be "centroid" (default) or "seeding".

assay name of assay data for Seurat method.

slot name of slot for assay data for Seurat method.

coord name of coordinates slot for specific methods.

dims dimensions from coord to use. By default, all.

cutoff cutoff for detection.

Value
An object of class "haystack"

haystack_2D The main Haystack function, for 2-dimensional spaces.

Description
The main Haystack function, for 2-dimensional spaces.

Usage
haystack_2D(
  x,
  y,
  detection,
  use.advanced.sampling = NULL,
  dir.randomization = NULL
)
Arguments

x  x-axis coordinates of cells in a 2D representation (e.g. resulting from PCA or t-SNE)
y  y-axis coordinates of cells in a 2D representation
detection  A logical matrix showing which genes (rows) are detected in which cells (columns)
use.advanced.sampling  If NULL naive sampling is used. If a vector is given (of length = no. of cells) sampling is done according to the values in the vector.
dir.randomization  If NULL, no output is made about the random sampling step. If not NULL, files related to the randomizations are printed to this directory.

Value

An object of class "haystack"

Examples

# using the toy example of the singleCellHaystack package
# define a logical matrix with detection of each gene (rows) in each cell (columns)
dat.detection <- dat.expression > 1

# running haystack in default mode
res <- haystack(dat.tsne, detection=dat.detection, method = "2D")
# list top 10 biased genes
show_result_haystack(res, n =10)

haystack_highD  The main Haystack function, for higher-dimensional spaces.

Description

The main Haystack function, for higher-dimensional spaces.

Usage

haystack_highD(
  x,
  detection,
  grid.points = 100,
  use.advanced.sampling = NULL,
  dir.randomization = NULL,
  scale = TRUE,
  grid.method = "centroid"
)
Arguments

- **x**: Coordinates of cells in a 2D or higher-dimensional space. Rows represent cells, columns the dimensions of the space.
- **detection**: A logical matrix showing which genes (rows) are detected in which cells (columns).
- **grid.points**: An integer specifying the number of centers (gridpoints) to be used for estimating the density distributions of cells. Default is set to 100.
- **use.advanced.sampling**: If NULL, naive sampling is used. If a vector is given (of length = no. of cells), sampling is done according to the values in the vector.
- **dir.randomization**: If NULL, no output is made about the random sampling step. If not NULL, files related to the randomizations are printed to this directory.
- **scale**: Logical (default=TRUE) indicating whether input coordinates in x should be scaled to mean 0 and standard deviation 1.
- **grid.method**: The method to decide grid points for estimating the density in the high-dimensional space. Should be "centroid" (default) or "seeding".

Value

An object of class "haystack", including the results of the analysis, and the coordinates of the grid points used to estimate densities.

Examples

```r
# I need to add some examples.
# A toy example will be added too.
```

---

**hclust_haystack**  
Function for hierarchical clustering of genes according to their expression distribution in 2D or multi-dimensional space

Description

Function for hierarchical clustering of genes according to their expression distribution in 2D or multi-dimensional space

Usage

```r
hclust_haystack(x, ...)
```

```r
## S3 method for class 'matrix'
hclust_haystack(x, dim1 = 1, dim2 = 2, ...)
```

```r
## S3 method for class 'data.frame'
hclust_haystack(x, dim1 = 1, dim2 = 2, ...)
```
hclust Haystack highD

Arguments

x a matrix or other object from which coordinates of cells can be extracted.
... further parameters passed down to methods.
dim1 column index or name of matrix for x-axis coordinates.
dim2 column index or name of matrix for y-axis coordinates.

hclust Haystack highD Function for hierarchical clustering of genes according to their distribution in a higher-dimensional space.

Description

Function for hierarchical clustering of genes according to their distribution in a higher-dimensional space.

Usage

hclust Haystack highD(  
  x,  
  detection,  
  genes,  
  method = "ward.D",  
  grid.coordinates = NULL,  
  scale = TRUE  
)

Arguments

x Coordinates of cells in a 2D or higher-dimensional space. Rows represent cells, columns the dimensions of the space.
detection A logical matrix showing which genes (rows) are detected in which cells (columns)
genes A set of genes (of the 'detection' data) which will be clustered.
method The method to use for hierarchical clustering. See '?hclust' for more information. Default: "ward.D".
grid.coordinates Coordinates of grid points in the same space as 'x', to be used to estimate densities for clustering.
scale whether to scale data.

Value

An object of class hclust, describing a hierarchical clustering tree.

Examples

# to be added
hclust_haystack_raw

Function for hierarchical clustering of genes according to their distribution on a 2D plot.

Description

Function for hierarchical clustering of genes according to their distribution on a 2D plot.

Usage

hclust_haystack_raw(x, y, detection, genes, method = "ward.D")

Arguments

x  x-axis coordinates of cells in a 2D representation (e.g. resulting from PCA or t-SNE)

y  y-axis coordinates of cells in a 2D representation

detection  A logical matrix showing which genes (rows) are detected in which cells (columns)

genes  A set of genes (of the 'detection' data) which will be clustered.

method  The method to use for hierarchical clustering. See '?hclust' for more information. Default: "ward.D".

Value

An object of class hclust, describing a hierarchical clustering tree.

Examples

# using the toy example of the singleCellHaystack package
# define a logical matrix with detection of each gene (rows) in each cell (columns)
dat.detection <- dat.expression > 1

# running haystack in default mode
res <- haystack(dat.tsne, detection=dat.detection, method = "2D")

# get biased genes, store in variable gene.subset
sorted.table <- show_result_haystack(res, p.value.threshold = 1e-5)
gene.subset <- row.names(sorted.table)

# hierarchical clustering, and cutting into 5 clusters
hc <- hclust_haystack(dat.tsne, detection=dat.detection, genes=gene.subset)
hc.clusters <- cutree(hc,k = 5)
**kde2d_faster**

*Based on the MASS kde2d() function, but heavily simplified; it's just tcrossprod() now.*

**Description**

Based on the MASS kde2d() function, but heavily simplified; it's just tcrossprod() now.

**Usage**

kde2d_faster(dens.x, dens.y)

**Arguments**

dens.x Contribution of all cells to densities of the x-axis grid points.
dens.y Contribution of all cells to densities of the y-axis grid points.

---

**kmeans_haystack**

*Function for k-means clustering of genes according to their expression distribution in 2D or multi-dimensional space*

**Description**

Function for k-means clustering of genes according to their expression distribution in 2D or multi-dimensional space

**Usage**

kmeans_haystack(x, ...)

## S3 method for class 'matrix'
kmeans_haystack(x, dim1 = 1, dim2 = 2, ...)

## S3 method for class 'data.frame'
kmeans_haystack(x, dim1 = 1, dim2 = 2, ...)

**Arguments**

x a matrix or other object from which coordinates of cells can be extracted.
...
further parameters passed down to methods.
dim1 column index or name of matrix for x-axis coordinates.
dim2 column index or name of matrix for y-axis coordinates.
Function for k-means clustering of genes according to their distribution in a higher-dimensional space.

**Usage**

```r
kmeans_haystack_highD(
  x,                     # Coordinates of cells in a 2D or higher-dimensional space. Rows represent cells, columns the dimensions of the space.
  detection,             # A logical matrix showing which genes (rows) are detected in which cells (columns)
  genes,                 # A set of genes (of the 'detection' data) which will be clustered.
  grid.coordinates = NULL, # Coordinates of grid points in the same space as 'x', to be used to estimate densities for clustering.
  k,                     # The number of clusters to return.
  scale = TRUE,          # whether to scale data.
  ...                   # Additional parameters which will be passed on to the kmeans function.
)
```

**Arguments**

- `x`: Coordinates of cells in a 2D or higher-dimensional space. Rows represent cells, columns the dimensions of the space.
- `detection`: A logical matrix showing which genes (rows) are detected in which cells (columns).
- `genes`: A set of genes (of the 'detection' data) which will be clustered.
- `grid.coordinates`: Coordinates of grid points in the same space as 'x', to be used to estimate densities for clustering.
- `k`: The number of clusters to return.
- `scale`: Whether to scale data.
- `...`: Additional parameters which will be passed on to the kmeans function.

**Value**

An object of class kmeans, describing a clustering into 'k' clusters.

**Examples**

# to be added
kmeans_haystack_raw  Function for k-means clustering of genes according to their distribution on a 2D plot.

Description
Function for k-means clustering of genes according to their distribution on a 2D plot.

Usage
kmeans_haystack_raw(x, y, detection, genes, k, ...)

Arguments
x  x-axis coordinates of cells in a 2D representation (e.g. resulting from PCA or t-SNE)
y  y-axis coordinates of cells in a 2D representation
detection  A logical matrix showing which genes (rows) are detected in which cells (columns)
genes  A set of genes (of the ‘detection’ data) which will be clustered.
k  The number of clusters to return.
...  Additional parameters which will be passed on to the kmeans function.

Value
An object of class kmeans, describing a clustering into ‘k’ clusters

Examples
# using the toy example of the singleCellHaystack package
# define a logical matrix with detection of each gene (rows) in each cell (columns)
dat.detection <- dat.expression > 1

# running haystack in default mode
res <- haystack(dat.tsne, detection=dat.detection, method = "2D")

# get biased genes, store in variable gene.subset
sorted.table <- show_result_haystack(res, p.value.threshold = 1e-5)
gene.subset <- row.names(sorted.table)

# k-means clustering into 5 clusters
km <- kmeans_haystack(dat.tsne, detection=dat.detection, genes=gene.subset, k=5)
km.clusters <- km$cluster
Description

Visualizing the detection/expression of a gene in a 2D plot

Usage

plot_gene_haystack(x, ...)

## S3 method for class 'matrix'
plot_gene_haystack(x, dim1 = 1, dim2 = 2, ...)

## S3 method for class 'data.frame'
plot_gene_haystack(x, dim1 = 1, dim2 = 2, ...)

## S3 method for class 'SingleCellExperiment'
plot_gene_haystack(
  x,
  dim1 = 1,
  dim2 = 2,
  assay = "counts",
  coord = "TSNE",
  ...
)

## S3 method for class 'Seurat'
plot_gene_haystack(
  x,
  dim1 = 1,
  dim2 = 2,
  assay = "RNA",
  slot = "data",
  coord = "tsne",
  ...
)

Arguments

x               a matrix or other object from which coordinates of cells can be extracted.
...
... further parameters passed to plot_gene_haystack_raw().
dim1            column index or name of matrix for x-axis coordinates.
dim2            column index or name of matrix for y-axis coordinates.
assay           name of assay data for Seurat method.
**plot_gene_haystack_raw**

*Visualizing the detection/expression of a gene in a 2D plot*

**Description**

Visualizing the detection/expression of a gene in a 2D plot

**Usage**

```r
plot_gene_haystack_raw(
  x,
  y,
  gene,
  expression,
  detection = NULL,
  high.resolution = FALSE,
  point.size = 1,
  order.by.signal = FALSE
)
```

**Arguments**

- `x` : x-axis coordinates of cells in a 2D representation (e.g. resulting from PCA or t-SNE)
- `y` : y-axis coordinates of cells in a 2D representation
- `gene` : name of a gene that is present in the input expression data, or a numerical index
- `expression` : a logical/numerical matrix showing detection/expression of genes (rows) in cells (columns)
- `detection` : an optional logical matrix showing detection of genes (rows) in cells (columns). If left as NULL, the density distribution of the gene is not plotted.
- `high.resolution` : logical (default: FALSE). If set to TRUE, the density plot will be of a higher resolution
- `point.size` : numerical value to set size of points in plot. Default is 1.
- `order.by.signal` : If TRUE, cells with higher signal will be put on the foreground in the plot. Default is FALSE.

**Value**

A plot
plot_gene_set_haystack

Examples

# using the toy example of the singleCellHaystack package
# define a logical matrix with detection of each gene (rows) in each cell (columns)
dat.detection <- dat.expression > 1
# various ways of plotting gene expression patterns
plot_gene_haystack(dat.tsne, expression=dat.expression, gene="gene_242",
                   detection = dat.detection, high.resolution = TRUE)
plot_gene_haystack(dat.tsne, expression=dat.expression, gene="gene_242",
                   detection = dat.detection, high.resolution = TRUE, point.size = .1)

plot_gene_set_haystack

Visualizing the detection/expression of a set of genes in a 2D plot

Description

Visualizing the detection/expression of a set of genes in a 2D plot

Usage

plot_gene_set_haystack(x, ...)

## S3 method for class 'matrix'
plot_gene_set_haystack(x, dim1 = 1, dim2 = 2, ...)

## S3 method for class 'data.frame'
plot_gene_set_haystack(x, dim1 = 1, dim2 = 2, ...)

## S3 method for class 'SingleCellExperiment'
plot_gene_set_haystack(
x,
   dim1 = 1,
   dim2 = 2,
   assay = "counts",
   coord = "TSNE",
   ...
)

## S3 method for class 'Seurat'
plot_gene_set_haystack(
x,
   dim1 = 1,
   dim2 = 2,
   assay = "RNA",
   slot = "data",
   coord = "tsne",
   ...
)
plot_gene_set_haystack_raw

Visualizing the detection/expression of a set of genes in a 2D plot

Arguments

- **x**: a matrix or other object from which coordinates of cells can be extracted.
- **...**: further parameters passed to plot_gene_haystack_raw().
- **dim1**: column index or name of matrix for x-axis coordinates.
- **dim2**: column index or name of matrix for y-axis coordinates.
- **assay**: name of assay data for Seurat method.
- **coord**: name of coordinates slot for specific methods.
- **slot**: name of slot for assay data for Seurat method.

Usage

```r
plot_gene_set_haystack_raw(
  x,
  y,
  genes = NA,
  detection,
  high.resolution = TRUE,
  point.size = 1,
  order.by.signal = FALSE
)
```

Arguments

- **x**: x-axis coordinates of cells in a 2D representation (e.g. resulting from PCA or t-SNE)
- **y**: y-axis coordinates of cells in a 2D representation
- **genes**: Gene names that are present in the input expression data, or a numerical index.
  If NA, all genes will be used.
- **detection**: a logical matrix showing detection of genes (rows) in cells (columns)
- **high.resolution**: logical (default: TRUE). If set to FALSE, the density plot will be of a lower resolution
- **point.size**: numerical value to set size of points in plot. Default is 1.
- **order.by.signal**: If TRUE, cells with higher signal will be put on the foreground in the plot. Default is FALSE.
**Value**

A plot

**Examples**

```
# using the toy example of the singleCellHaystack package
# define a logical matrix with detection of each gene (rows) in each cell (columns)
dat.detection <- dat.expression > 1

# define a set of genes that we want to visualize
# this might be a set of differentially expressed genes
# predicted by haystack and clustered together by hclust_haystack

# visualize the expression pattern of the set of genes
plot_gene_set_haystack(dat.tsne, detection=dat.detection, genes=gene_set)
```

---

**read_haystack**

*Function to read haystack results from file.*

**Description**

Function to read haystack results from file.

**Usage**

```r
read_haystack(file)
```

**Arguments**

- `file` A file containing 'haystack' results to read

**Value**

An object of class "haystack"

**Examples**

```
# using the toy example of the singleCellHaystack package
# define a logical matrix with detection of each gene (rows) in each cell (columns)
dat.detection <- dat.expression > 1

# running haystack in default mode
res <- haystack(dat.tsne, detection=dat.detection, method = "2D")

outfile <- file.path(tempdir(), "output.csv")
```
# write result to file outfile.csv
write_haystack(res, file = outfile)

# read in result from file
res.copy <- read_haystack(file = outfile)

show_result_haystack  
*Shows the results of the 'haystack' analysis in various ways, sorted by*  
*significance. Priority of params is genes > p.value.threshold > n.*

### Description
Shows the results of the 'haystack' analysis in various ways, sorted by significance. Priority of params is genes > p.value.threshold > n.

### Usage
`show_result_haystack(res.haystack, n = NA, p.value.threshold = NA, gene = NA)`

### Arguments
- `res.haystack`: A 'haystack' result variable
- `n`: If defined, the top "n" significant genes will be returned. Default: NA, which shows all results.
- `p.value.threshold`: If defined, genes passing this p-value threshold will be returned.
- `gene`: If defined, the results of this (these) gene(s) will be returned.

### Value
A table with a sorted subset of the 'haystack' result according to input parameters.

### Examples
```r
# using the toy example of the singleCellHaystack package
# define a logical matrix with detection of each gene (rows) in each cell (columns)
dat.detection <- dat.expression > 1

# running haystack in default mode
res <- haystack(dat.tsne, detection=dat.detection, method = "2D")

# below are variations for showing the results in a table
# 1. list top 10 biased genes
show_result_haystack(res.haystack = res, n =10)
# 2. list genes with p value below a certain threshold
show_result_haystack(res.haystack = res, p.value.threshold=1e-10)
# 3. list a set of specified genes
set <- c("gene_497", "gene_386", "gene_275")
show_result_haystack(res.haystack = res, gene = set)
```
Function to write haystack result data to file.

**Description**

Function to write haystack result data to file.

**Usage**

```r
write_haystack(res.haystack, file)
```

**Arguments**

- `res.haystack`: A 'haystack' result variable
- `file`: A file to write to

**Examples**

```r
# using the toy example of the singleCellHaystack package
# define a logical matrix with detection of each gene (rows) in each cell (columns)
dat.detection <- dat.expression > 1

# running haystack in default mode
res <- haystack(dat.tsne, detection=dat.detection, method = "2D")

outfile <- file.path(tempdir(), "output.csv")

# write result to file outfile.csv
write_haystack(res, file = outfile)

# read in result from file
res.copy <- read_haystack(file = outfile)
```
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