Package 'HIPPO'

November 12, 2026

Type Package

Title Heterogeneity-Induced Pre-Processing tOol

Version 1.24.0

Description For scRNA-seq data, it selects features and clusters the cells simultaneously for single-cell UMI data. It has a novel feature selection method using the zero inflation instead of gene variance, and computationally faster than other existing methods since it only relies on PCA+Kmeans rather than graph-clustering or consensus clustering.

License GPL (>=2)

Depends R (>= 3.6.0)

Encoding UTF-8

LazyData true

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL https://github.com/tk382/HIPPO

BugReports https://github.com/tk382/HIPPO/issues

Imports ggplot2, graphics, stats, reshape2, gridExtra, Rtsne, umap, dplyr, rlang, magrittr, irlba, Matrix, SingleCellExperiment, ggrepel

RoxygenNote 7.1.0

biocViews Sequencing, SingleCell, GeneExpression, DifferentialExpression, Clustering

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Contents

ensg_hgnc . . . 2
get_data_from_sce . . . 3
get_hippo . . . 3
get_hippo_diffexp . . . 4
hippo . . . 4
hippo_diagnostic_plot . . . 5
hippo_diffexp . . . 6
hippo_dimension_reduction . . . 7
hippo_feature_heatmap . . . 8
hippo_pca_plot . . . 9
hippo_tsne_plot . . . 9
hippo_umap_plot . . . 10
nb_prob_zero . . . 11
pois_prob_zero . . . 11
preprocess_heterogeneous . . . 12
preprocess_homogeneous . . . 12
toydata . . . 13
zero_proportion_plot . . . 13
zinb_prob_zero . . . 15
%>% . . . 15

Index **16**

`ensg_hgnc` *A reference data frame that matches ENSG IDs to HGNC symbols*

Description

A reference data frame that matches ENSG IDs to HGNC symbols

Usage

```
ensg_hgnc
```

Format

A data frame with 46606 rows and 2 columns

ensg Ensembl ENSG IDs

hgnc HGNC symbols

Source

http://www.biomart.org/

get_data_from_sce *Access data from SCE object*

Description

Access data from SCE object

Usage

```
get_data_from_sce(sce)
```

Arguments

sce	SingleCellExperiment object

Value

count matrix

Examples

```
data(toydata)
X = get_data_from_sce(toydata)
```

get_hippo *Access hippo object from SingleCellExperiment object.*

Description

Access hippo object from SingleCellExperiment object.

Usage

```
get_hippo(sce)
```

Arguments

sce	SingleCellExperiment object

Value

hippo object embedded in SingleCellExperiment object

Examples

```
data(toydata)
set.seed(20200321)
toydata = hippo(toydata,K = 10,z_threshold = 1,outlier_proportion = 0.01)
hippo_object = get_hippo(toydata)
```

get_hippo_diffexp *Return hippo_diffexp object*

Description

Return hippo_diffexp object

Usage

```
get_hippo_diffexp(sce, k = 1)
```

Arguments

sce	SingleCellExperiment object with hippo
k	integer round of result of interest

Value

data frame of differential expression test

Examples

```
data(toydata)
set.seed(20200321)
toydata = hippo(toydata,K = 10,z_threshold = 1,outlier_proportion = 0.01)
toydata = hippo_diffexp(toydata)
result1 = get_hippo_diffexp(toydata)
```

hippo *HIPPO's hierarchical clustering*

Description

HIPPO's hierarchical clustering

Usage

```
hippo(sce, K = 20, z_threshold = 2, outlier_proportion = 0.001, verbose = TRUE)
```

Arguments

sce	SingleCellExperiment object
K	number of clusters to ultimately get
z_threshold	numeric > 0 as a z-value threshold for selecting the features
outlier_proportion	numeric between 0 and 1, a cut-off so that when the proportion of important features reach this number, the clustering terminates
verbose	if set to TRUE, it shows progress of the algorithm

Value

a list of clustering result for each level of k=1, 2, ... K.

Examples

```
data(toydata)
toydata = hippo(toydata,K = 10,z_threshold = 1,outlier_proportion = 0.01)
```

`hippo_diagnostic_plot` *Conduct feature selection by computing test statistics for each gene*

Description

Conduct feature selection by computing test statistics for each gene

Usage

```
hippo_diagnostic_plot(sce, show_outliers = FALSE, zvalue_thresh = 10)
```

Arguments

`sce`	SingleCellExperiment object with count matrix
`show_outliers`	boolean to indicate whether to circle the outliers with given zvalue_thresh
`zvalue_thresh`	a numeric v for defining outliers

Value

a diagnostic plot that shows genes with zero inflation

Examples

```
data(toydata)
hippo_diagnostic_plot(toydata, show_outliers=TRUE, zvalue_thresh = 2)
```

hippo_diffexp *HIPPO's differential expression*

Description

HIPPO's differential expression

Usage

```
hippo_diffexp(
  sce,
  top.n = 5,
  switch_to_hgnc = FALSE,
  ref = NA,
  k = NA,
  plottitle = ""
)
```

Arguments

sce	SingleCellExperiment object with hippo
top.n	number of markers to return
switch_to_hgnc	if the current gene names are ensemble ids, and would like to switch to hgnc
ref	a data frame with columns 'hgnc' and 'ensg' to match each other, only required when switch_to_hgnc is set to TRUE
k	number of rounds of clustering that you'd like to see result. Default is 1 to K
plottitle	title of the resulting plot

Value

list of differential expression result

Examples

```
data(toydata)
set.seed(20200321)
toydata = hippo(toydata,K = 10,z_threshold = 1,outlier_proportion = 0.01)
result = hippo_diffexp(toydata)
```

hippo_dimension_reduction *compute t-SNE or umap of each round of HIPPO*

Description

compute t-SNE or umap of each round of HIPPO

Usage

```
hippo_dimension_reduction(
  sce,
  method = c("umap", "tsne"),
  perplexity = 30,
  featurelevel = 1
)
```

Arguments

sce	SingleCellExperiment object with hippo object in it.
method	a string that determines the method for dimension reduction: either 'umap' or 'tsne
perplexity	numeric perplexity parameter for Rtsne function
featurelevel	the round of clustering that you will extract features to reduce the dimension

Value

a data frame of dimension reduction result for each k in 1, ..., K

Examples

```
data(toydata)
set.seed(20200321)
set.seed(20200321)
toydata = hippo(toydata,K = 10,z_threshold = 1,outlier_proportion = 0.01)
toydata = hippo_dimension_reduction(toydata, method="tsne")
hippo_tsne_plot(toydata)
```

`hippo_feature_heatmap` *HIPPO's feature heatmap*

Description

HIPPO's feature heatmap

Usage

```
hippo_feature_heatmap(
  sce,
  switch_to_hgnc = FALSE,
  ref = NA,
  top.n = 50,
  kk = 2,
  plottitle = ""
)
```

Arguments

`sce`	SingleCellExperiment object with hippo
`switch_to_hgnc`	if the current gene names are ensemble ids, and would like to switch to hgnc
`ref`	a data frame with columns 'hgnc' and 'ensg' to match each other, only required when switch_to_hgnc is set to TRUE
`top.n`	number of markers to return
`kk`	integer for the round of clustering that you'd like to see result. Default is 2
`plottitle`	title for the plot

Value

list of differential expression result

Examples

```
data(toydata)
set.seed(20200321)
toydata = hippo(toydata,K = 10,z_threshold = 1,outlier_proportion = 0.01)
hippo_feature_heatmap(toydata)
```

`hippo_pca_plot` *visualize each round of hippo through t-SNE*

Description

visualize each round of hippo through t-SNE

Usage

```
hippo_pca_plot(sce, k = NA, pointsize = 0.5, pointalpha = 0.5, plottitle = "")
```

Arguments

`sce`	SincleCellExperiment object with hippo and t-SNE result in it
`k`	number of rounds of clustering that you'd like to see result. Default is 1 to K
`pointsize`	size of the point for the plot (default 0.5)
`pointalpha`	transparency level of points for the plot (default 0.5)
`plottitle`	title for the ggplot

Value

ggplot for pca in each round

Examples

```
data(toydata)
set.seed(20200321)
toydata = hippo(toydata, K = 10,z_threshold = 1)
hippo_pca_plot(toydata, k = 2:3)
```

`hippo_tsne_plot` *visualize each round of hippo through t-SNE*

Description

visualize each round of hippo through t-SNE

Usage

```
hippo_tsne_plot(sce, k = NA, pointsize = 0.5, pointalpha = 0.5, plottitle = "")
```

Arguments

sce	SincleCellExperiment object with hippo and t-SNE result in it
k	number of rounds of clustering that you'd like to see result. Default is 1 to K
pointsize	size of the point for the plot (default 0.5)
pointalpha	transparency level of points for the plot (default 0.5)
plottitle	title for the ggplot output

Value

ggplot object for t-SNE in each round

Examples

```
data(toydata)
set.seed(20200321)
toydata = hippo(toydata,K = 10,z_threshold = 1,outlier_proportion = 0.01)
toydata = hippo_dimension_reduction(toydata, method="tsne")
hippo_tsne_plot(toydata)
```

---

hippo_umap_plot *visualize each round of hippo through UMAP*

Description

visualize each round of hippo through UMAP

Usage

```
hippo_umap_plot(sce, k = NA, pointsize = 0.5, pointalpha = 0.5, plottitle = "")
```

Arguments

sce	SingleCellExperiment object with hippo and UMAP result in it
k	number of rounds of clustering that you'd like to see result. Default is 1 to K
pointsize	size of the point for the plot (default 0.5)
pointalpha	transparency level of points for the plot (default 0.5)
plottitle	title of the resulting plot

Value

ggplot object for umap in each round

Examples

```
data(toydata)
set.seed(20200321)
toydata = hippo(toydata,K = 10,z_threshold = 1,outlier_proportion = 0.01)
toydata = hippo_dimension_reduction(toydata, method="umap")
hippo_umap_plot(toydata)
```

---

nb_prob_zero *Expected zero proportion under Negative Binomial*

Description

Expected zero proportion under Negative Binomial

Usage

```
nb_prob_zero(lambda, theta)
```

Arguments

lambda	numeric vector of means of negative binomial
theta	numeric vector of the dispersion parameter for negative binomial, 0 if poisson

Value

numeric vector of expected zero proportion under Negative Binomial

Examples

```
nb_prob_zero(3, 1.1)
```

---

pois_prob_zero *Expected zero proportion under Poisson*

Description

Expected zero proportion under Poisson

Usage

```
pois_prob_zero(lambda)
```

Arguments

lambda	numeric vector of means of Poisson

Value

numeric vector of expected proportion of zeros for each lambda

Examples

```
pois_prob_zero(3)
```

`preprocess_heterogeneous` *Preprocess UMI data without cell label so that each row contains information about each gene*

Description

Preprocess UMI data without cell label so that each row contains information about each gene

Usage

```
preprocess_heterogeneous(X)
```

Arguments

`X`	a matrix object with counts data

Value

data frame with one row for each gene.

Examples

```
data(toydata)
df = preprocess_heterogeneous(get_data_from_sce(toydata))
```

`preprocess_homogeneous` *Preprocess UMI data with inferred or known labels*

Description

Preprocess UMI data with inferred or known labels

Usage

```
preprocess_homogeneous(sce, label)
```

Arguments

sce	SingleCellExperiment object with counts data
label	a numeric or character vector of inferred or known label

Value

data frame with one row for each gene.

Examples

```
data(toydata)
labels = SingleCellExperiment::colData(toydata)$phenoid
df = preprocess_homogeneous(toydata, label = labels)
```

---

toydata *A sample single cell sequencing data subsetted from Zheng2017*

Description

A sample single cell sequencing data subsetted from Zheng2017

Usage

```
toydata
```

Format

Single Cell experiment object with 10,000 genes and 100 cells

Source

https://www.nature.com/articles/ncomms14049

---

zero_proportion_plot *visualize each round of hippo through zero proportion plot*

Description

visualize each round of hippo through zero proportion plot

Usage

```
zero_proportion_plot(
  sce,
  switch_to_hgnc = FALSE,
  ref = NA,
  k = NA,
  plottitle = "",
  top.n = 5,
  pointsize = 0.5,
  pointalpha = 0.5,
  textsize = 3
)
```

Arguments

sce	SingleCellExperiment object with hippo element in it
switch_to_hgnc	boolean argument to indicate whether to change the gene names from ENSG IDs to HGNC symbols
ref	a data frame with hgnc column and ensg column
k	select rounds of clustering that you would like to see result. Default is 1 to K
plottitle	Title of your plot output
top.n	number of top genes to show the name
pointsize	size of the ggplot point
pointalpha	transparency level of the ggplot point
textsize	text size of the resulting plot

Value

a ggplot object that shows the zero proportions for each round

Examples

```
data(toydata)
set.seed(20200321)
toydata = hippo(toydata,K = 10,z_threshold = 1,outlier_proportion = 0.01)
data(ensg_hgnc)
zero_proportion_plot(toydata, switch_to_hgnc = TRUE, ref = ensg_hgnc)
```

zinb_prob_zero *Expected zero proportion under Negative Binomial*

Description

Expected zero proportion under Negative Binomial

Usage

```
zinb_prob_zero(lambda, theta, pi)
```

Arguments

lambda	gene mean
theta	dispersion parameter, 0 if zero-inflated poisson
pi	zero inflation, 0 if negative binomial

Value

Expected zero proportion under Zero-Inflated Negative Binomial

Examples

```
zinb_prob_zero(3, 1.1, 0.1)
```

%>% *re-export magrittr pipe operator*

Description

re-export magrittr pipe operator

Index

∗ **datasets**
ensg_hgnc, 2
toydata, 13
%>%, 15

ensg_hgnc, 2

get_data_from_sce, 3
get_hippo, 3
get_hippo_diffexp, 4

hippo, 4
hippo_diagnostic_plot, 5
hippo_diffexp, 6
hippo_dimension_reduction, 7
hippo_feature_heatmap, 8
hippo_pca_plot, 9
hippo_tsne_plot, 9
hippo_umap_plot, 10

nb_prob_zero, 11

pois_prob_zero, 11
preprocess_heterogeneous, 12
preprocess_homogeneous, 12

toydata, 13

zero_proportion_plot, 13
zinb_prob_zero, 15