Package ‘HIPPO’

January 5, 2024

Type Package
Title Heterogeneity-Induced Pre-Processing Tool
Version 1.14.0
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
git_url https://git.bioconductor.org/packages/HIPPO
git_branch RELEASE_3_18
git_last_commit 7d5a5b2
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-01-05
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## ensg_hgnc

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### 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**

```r
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
**hippo_diagnostic_plot**

**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)
```

**Description**

Conduct feature selection by computing test statistics for each gene

**Usage**

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

**Arguments**

- `sce` SingleCellExperiment object with count matrix
- `show_outliers` boolean to indicate whether to circle the outliers with given `zvalue_thres`
- `zvalue_thres` 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_thres = 2)
```
Description

HIPPO's differential expression

Usage

```r
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

```r
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

```r
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

```r
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_feature_heatmap  
**HIPPO's feature heatmap**

**Description**

HIPPO's feature heatmap

**Usage**

```r
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**

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

**Description**
visualize each round of hippo through t-SNE

**Usage**

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

**Arguments**

- `sce`: SingleCellExperiment 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**

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

---

hippo_tsne_plot

**Description**
visualize each round of hippo through t-SNE

**Usage**

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

**Description**
visualize each round of hippo through t-SNE

**Usage**

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

sce  SingleCellExperiment 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)


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

```r
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

```r
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

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

---

### pois_prob_zero

*Expected zero proportion under Poisson*

#### Description

Expected zero proportion under Poisson

#### Usage

```r
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
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)
```
Expected zero proportion under Negative Binomial

**Usage**

```r
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**

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

---

**re-export magrittr pipe operator**

---

**Description**

re-export magrittr pipe operator
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