

# Package ‘HIPPO’

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**Type** Package

**Title** Heterogeneity-Induced Pre-Processing tOol

**Version** 1.19.0

**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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---

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

<code>sce</code>	SingleCellExperiment object with hippo
<code>k</code>	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

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

**Value**

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

**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	<i>visualize each round of hippo through t-SNE</i>
----------------	--

---

**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	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**

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

---

hippo_tsne_plot	<i>visualize each round of hippo through t-SNE</i>
-----------------	--

---

**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	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)
```

---

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	<i>A sample single cell sequencing data subsetted from Zheng2017</i>
---------	--

---

**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	<i>visualize each round of hippo through zero proportion plot</i>
----------------------	---

---

**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	<i>Expected zero proportion under Negative Binomial</i>
----------------	---

---

**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)
```

---

%>%	<i>re-export magrittr pipe operator</i>
-----	---

---

**Description**

re-export magrittr pipe operator

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