

Package ‘spatialDE’

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Title R wrapper for SpatialDE

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Description SpatialDE is a method to find spatially variable genes (SVG) from spatial transcriptomics data. This package provides wrappers to use the Python SpatialDE library in R, using reticulate and basilisk.

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<https://bioconductor.org/packages/spatialDE/>

BugReports <https://github.com/sales-lab/spatialDE/issues>

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.importPyModule	<i>Import SpatialDE</i>
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Description

This function loads the SpatialDE Python module and optionally monkey-patches it to remove tqdm calls.

Usage

`.importPyModule(proc, patch_tqdm)`

Arguments

proc A process object generated by `basilisk::basiliskStart()`
patch_tqdm If TRUE patch calls to tqdm.

Value

An R wrapper for the SpatialDE Python module.

FSV_sig*Plot Fraction Spatial Variance vs Q-value*

Description

Plot Fraction Spatial Variance vs Q-value

Usage

```
FSV_sig(  
  results,  
  ms_results = NULL,  
  certain_only = FALSE,  
  log_x = FALSE,  
  do_label = TRUE,  
  covariate_names = NULL  
)
```

Arguments

results	results from SpatialDE.
ms_results	model selection results, should be a data frame with columns g for gene names and model for the model selected.
certain_only	only plot results with narrow 95% confidence interval.
log_x	Whether to display x axis in log scale.
do_label	display gene names for statistically significant genes, default TRUE.
covariate_names	names of covariates as a reference, default to NULL.

Value

A ggplot2 object.

Author(s)

Davide Corso, Milan Malfait, Lambda Moses

References

Svensson, V., Teichmann, S. & Stegle, O. SpatialDE: identification of spatially variable genes. Nat Methods 15, 343–346 (2018). <https://doi.org/10.1038/nmeth.4636>

SpatialDE 1.1.3: the version of the Python package used under the hood.

Examples

```
## Mock up a SpatialExperiment object with 400 cells and 3 genes
set.seed(42)
spe <- mockSVG(size = 20, tot_genes = 3, de_genes = 1, return_SPE = TRUE)

## Run spatialDE with S4 integration
results <- spatialDE(spe)

## Run model search
msearch <- modelSearch(spe, de_results = results, qual_thresh = NULL,
  verbose = FALSE)

plot <- FSV_sig(results, msearch)
```

MOB_sample_info

Mouse Olfactory Bulb sample metadata

Description

Coordinates and total counts for the samples from the Mouse Olfactory Bulb data generated by Stahl et al. (2016). This data was originally downloaded from https://github.com/Teichlab/SpatialDE/blob/master/Analysis/MouseOB/MOB_sample_info.csv.

Usage

```
data(MOB_sample_info)
```

Format

A data.frame with 262 rows and 3 variables as columns: the x and y coordinates and total_counts corresponding to each spot.

References

Stahl, P. L. et al. (2016) 'Visualization and analysis of gene expression in tissue sections by spatial transcriptomics', *Science*, 353(6294), p. 78. doi: 10.1126/science.aaf2403.

mockSVG

*Generate count matrix for spatially variable genes.***Description**

Generate count matrix for spatially variable genes.

Usage

```
mockSVG(size, tot_genes, de_genes, return_SPE = FALSE)
```

Arguments

size	An integer scalar. Cells will be spatially arranged on a size x size grid. Default: 10, corresponding to 100 cells.
tot_genes	An integer scalar. Total number of genes. Default: 1000.
de_genes	An integer scalar. The number of spatially variable genes. Default: 100.
return_SPE	A logical, whether to return result as a SpatialExperiment . Default: FALSE.

Value

If return_SPE = TRUE, returns a [SpatialExperiment](#) object.

If not, a list containing:

- coordinates: data.frame with x and y columns;
- counts: matrix with generated gene counts.

Examples

```
spe <- mockSVG(size = 20, tot_genes = 3, de_genes = 1, return_SPE = TRUE)
spe
```

modelSearch

*Classify Spatially Variable Genes to interpretable fitting classes***Description**

Compare model fits with different models, using the [SpatialDE](#) Python package.

Usage

```

modelSearch(x, de_results, ...)

## S4 method for signature 'matrix'
modelSearch(x, de_results, coordinates, qval_thresh = 0.05, verbose = FALSE)

## S4 method for signature 'SpatialExperiment'
modelSearch(
  x,
  de_results,
  assay_type = "counts",
  qval_thresh = 0.05,
  verbose = FALSE
)

```

Arguments

<code>x</code>	A numeric matrix of counts where genes are rows and cells are columns. Alternatively, a SpatialExperiment object.
<code>de_results</code>	<code>data.frame</code> resulting from run() or spatialDE() .
<code>...</code>	For the generic, arguments to pass to specific methods.
<code>coordinates</code>	A <code>data.frame</code> with sample coordinates. Each row is a sample, the columns with coordinates should be named 'x' and 'y'. For the <i>SpatialExperiment</i> method, coordinates are taken from <code>spatialCoords(x)</code> .
<code>qval_thresh</code>	numeric scalar, specifying the q-value significance threshold to filter <code>de_results</code> . Only rows in <code>de_results</code> with <code>qval < qval_thresh</code> will be kept. To disable, set <code>qval_thresh = NULL</code> .
<code>verbose</code>	A logical controlling the display of a progress bar from the Python package.
<code>assay_type</code>	A character string specifying the assay from <code>x</code> to use as input. Defaults to "counts".

Value

`data.frame` of `model_search` results.

Author(s)

Davide Corso, Milan Malfait, Lambda Moses

References

Svensson, V., Teichmann, S. & Stegle, O. SpatialDE: identification of spatially variable genes. *Nat Methods* 15, 343–346 (2018). <https://doi.org/10.1038/nmeth.4636>

SpatialDE 1.1.3: the version of the Python package used under the hood.

See Also

The individual steps performed by this function: `stabilize()`, `regress_out()` and `model_search()`.

Examples

```
## Mock up a SpatialExperiment object wit 400 cells and 3 genes
set.seed(42)
spe <- mockSVG(size = 20, tot_genes = 3, de_genes = 1, return_SPE = TRUE)

## Run spatialDE with S4 integration
de_results <- spatialDE(spe)

## Run model search
model_search <- modelSearch(spe, de_results = de_results,
  qval_thresh = NULL, verbose = FALSE
)
```

model_search

Compare model fits with different models

Description

Classify DE genes to interpretable fitting classes.

Usage

```
model_search(x, coordinates, de_results, qval_thresh = 0.05, verbose = FALSE)
```

Arguments

x	matrix-like object of normalized counts. E.g. resulting from <code>regress_out()</code> .
coordinates	data.frame with sample coordinates. Each row is a sample, the columns with coordinates must be named 'x' and 'y'.
de_results	data.frame resulting from <code>run()</code> .
qval_thresh	numeric scalar, specifying the q-value significance threshold to filter <code>de_results</code> . Only rows in <code>de_results</code> with <code>qval < qval_thresh</code> will be kept. To disable, set <code>qval_thresh = NULL</code> .
verbose	logical controlling the display of the progress bar.

Value

data.frame of `model_search` results.

References

Svensson, V., Teichmann, S. & Stegle, O. SpatialDE: identification of spatially variable genes. Nat Methods 15, 343–346 (2018). <https://doi.org/10.1038/nmeth.4636>

Examples

```
## Mock up a SpatialExperiment object with 400 cells and 3 genes
set.seed(42)
mock <- mockSVG(size = 20, tot_genes = 3, de_genes = 1)

stabilized <- stabilize(mock$counts)
sample_info <- mock$coordinates
sample_info$total_counts <- colSums(mock$counts)
regressed <- regress_out(counts = stabilized, sample_info = sample_info)

## Run SpatialDE
de_results <- run(regressed, coordinates = mock$coordinates)

## Run model search
ms_results <- model_search(
  x = regressed,
  coordinates = mock$coordinates,
  de_results = de_results,
  qual_thresh = NULL
)
```

multiGenePlots

Plot Spatial Patterns of Multiple Genes

Description

Plot Spatial Patterns of Multiple Genes

Usage

```
multiGenePlots(x, ...)

## S4 method for signature 'matrix'
multiGenePlots(
  x,
  coordinates,
  genes_plot,
  viridis_option = "D",
  ncol = 2,
  point_size = 1,
  dark_theme = TRUE
)

## S4 method for signature 'SpatialExperiment'
multiGenePlots(
  x,
  assay_type = "counts",
```



```

    genes_plot,
    viridis_option = "D",
    ncol = 2,
    point_size = 1,
    dark_theme = TRUE
)

```

Arguments

<code>x</code>	A numeric matrix of stabilized counts (e.g. resulting from <code>stabilize()</code>) where genes are rows and cells are columns. Alternatively, a <code>SpatialExperiment</code> object.
<code>...</code>	For the generic, arguments to pass to specific methods.
<code>coordinates</code>	A <code>data.frame</code> with sample coordinates. Each row is a sample, the columns with coordinates should be named 'x' and 'y'. For the <i>SpatialExperiment</i> method, coordinates are taken from <code>spatialCoords(x)</code> .
<code>genes_plot</code>	character vector specifying which genes are to be plotted.
<code>viridis_option</code>	This function uses the viridis palette to color cells for gene expression. Four options are available: "magma" (or "A"), "inferno" (or "B"), "plasma" (or "C"), "viridis" (or "D", the default option) and "cividis" (or "E").
<code>ncol</code>	Number of columns to arrange the plots.
<code>point_size</code>	Point size of each plot.
<code>dark_theme</code>	Whether dark background should be used; this is helpful to highlight cells with high expression when using the viridis palette.
<code>assay_type</code>	A character string specifying the assay from <code>x</code> to use as input. Defaults to "counts".

Value

This function draws a plot for each specified genes

Author(s)

Davide Corso, Milan Malfait, Lambda Moses

References

Svensson, V., Teichmann, S. & Stegle, O. SpatialDE: identification of spatially variable genes. Nat Methods 15, 343–346 (2018). <https://doi.org/10.1038/nmeth.4636>

SpatialDE 1.1.3: the version of the Python package used under the hood.

See Also

The individual steps performed by this function: `stabilize()`, `spatialDE()`.

For further analysis of the DE results: `model_search()` and `spatial_patterns()`.

Examples

```
## Mock up a SpatialExperiment object wit 400 cells and 3 genes
set.seed(42)
spe <- mockSVG(size = 20, tot_genes = 3, de_genes = 1, return_SPE = TRUE)

## Run spatialDE
results <- spatialDE(spe)

ordered_spe_results <- results[order(results$qval), ]
head(ordered_spe_results)

plots <- multiGenePlots(spe,
  assay_type = "counts",
  ordered_spe_results$g,
  point_size = 4,
  viridis_option = "D"
)
```

regress_out

*Regress out library size effect***Description**

Regresses out the effect of library size. This function is a wrapper for `regress_out` from the **NaiveDE** Python package.

Usage

```
regress_out(counts, sample_info)
```

Arguments

counts	matrix of variance stabilized counts, e.g. resulting from <code>stabilize()</code> .
sample_info	data.frame with samples as rows and at least a column with total_counts.

Value

matrix of normalized counts.

Examples

```
## Mock up a SpatialExperiment object wit 400 cells and 3 genes
set.seed(42)
mock <- mockSVG(20, 3, 1)

stabilized <- stabilize(mock$counts)
sample_info <- mock$coordinates
sample_info$total_counts <- colSums(mock$counts)
```

```
regressed <- regress_out(counts = stabilized, sample_info = sample_info)
```

Rep11_MOB_0

Mouse Olfactory Bulb spatial gene expression data

Description

Replicate 11 from the spatially dependent gene expression data from the mouse olfactory bulb generated by Stahl et al. (2016). This data was originally downloaded from https://github.com/Teichlab/SpatialDE/blob/master/Analysis/MouseOB/data/Rep11_MOB_0.csv.

Usage

```
data(Rep11_MOB_0)
```

Format

A matrix with 16218 genes as rows and 262 spots as columns.

References

Ståhl, P. L. et al. (2016) 'Visualization and analysis of gene expression in tissue sections by spatial transcriptomics', *Science*, 353(6294), p. 78. doi: 10.1126/science.aaf2403.

run

Perform SpatialDE test

Description

Wraps the run function from the [SpatialDE](#) Python package.

Usage

```
run(x, coordinates, verbose = FALSE)
```

Arguments

x	matrix-like object of normalized counts. E.g. resulting from regress_out() .
coordinates	data.frame with sample coordinates. Each row is a sample, the columns with coordinates must be named 'x' and 'y'.
verbose	logical controlling the display of the progress bar.

Value

A data.frame with DE results where each row is a gene and columns contain relevant statistics.

The most important columns are:

- g: the name of the gene
- pval: the p-value for spatial differential expression
- qval: the q-value, indicating significance after correcting for multiple testing
- l: A parameter indicating the distance scale a gene changes expression over

References

Svensson, V., Teichmann, S. & Stegle, O. SpatialDE: identification of spatially variable genes. Nat Methods 15, 343–346 (2018). <https://doi.org/10.1038/nmeth.4636>

Examples

```
## Mock up a SpatialExperiment object with 400 cells and 3 genes
set.seed(42)
mock <- mockSVG(size = 20, tot_genes = 3, de_genes = 1)

stabilized <- stabilize(mock$counts)
sample_info <- mock$coordinates
sample_info$total_counts <- colSums(mock$counts)
regressed <- regress_out(counts = stabilized, sample_info = sample_info)

## Run SpatialDE
de_results <- run(regressed, coordinates = mock$coordinates)
```

spatialDE

*Find spatially variable genes with **SpatialDE***

Description

Identify genes that significantly depend on spatial coordinates with the **SpatialDE** Python package.

Usage

```
spatialDE(x, ...)

## S4 method for signature 'matrix'
spatialDE(x, coordinates, verbose = FALSE)

## S4 method for signature 'SpatialExperiment'
spatialDE(x, assay_type = "counts", verbose = FALSE)
```

Arguments

<code>x</code>	A numeric matrix of counts where genes are rows and cells are columns. Alternatively, a SpatialExperiment object.
<code>...</code>	For the generic, arguments to pass to specific methods.
<code>coordinates</code>	A <code>data.frame</code> with sample coordinates. Each row is a sample, the columns with coordinates should be named 'x' and 'y'. For the <i>SpatialExperiment</i> method, coordinates are taken from <code>spatialCoords(x)</code> .
<code>verbose</code>	A logical controlling the display of a progress bar from the Python package.
<code>assay_type</code>	A character string specifying the assay from <code>x</code> to use as input. Defaults to "counts".

Value

A `data.frame` with DE results where each row is a gene and columns contain relevant statistics.

The most important columns are:

- `g`: the name of the gene
- `pval`: the p-value for spatial differential expression
- `qval`: the q-value, indicating significance after correcting for multiple testing
- `l`: A parameter indicating the distance scale a gene changes expression over

Author(s)

Davide Corso, Milan Malfait, Lambda Moses

References

Svensson, V., Teichmann, S. & Stegle, O. SpatialDE: identification of spatially variable genes. *Nat Methods* 15, 343–346 (2018). <https://doi.org/10.1038/nmeth.4636>

SpatialDE 1.1.3: the version of the Python package used under the hood.

See Also

The individual steps performed by this function: [stabilize\(\)](#), [regress_out\(\)](#) and [run\(\)](#).

For further analysis of the DE results: [model_search\(\)](#) and [spatial_patterns\(\)](#).

Examples

```
## Mock up a SpatialExperiment object wit 400 cells and 3 genes
set.seed(42)
spe <- mockSVG(size = 20, tot_genes = 3, de_genes = 1, return_SPE = TRUE)

## Run spatialDE
de_results <- spatialDE(spe)

head(de_results)
```

spatialPatterns *Automatic expression histology in SpatialDE*

Description

Group spatially variable genes into spatial patterns using Automatic Expression Histology, using the **SpatialDE** Python package.

Usage

```
spatialPatterns(x, de_results, ...)

## S4 method for signature 'matrix'
spatialPatterns(
  x,
  de_results,
  coordinates,
  qval_thresh = 0.05,
  n_patterns,
  length,
  verbose = FALSE
)

## S4 method for signature 'SpatialExperiment'
spatialPatterns(
  x,
  de_results,
  qval_thresh = 0.05,
  n_patterns,
  length,
  assay_type = "counts",
  verbose = FALSE
)
```

Arguments

x	A numeric matrix of counts where genes are rows and cells are columns. Alternatively, a SpatialExperiment object.
de_results	data.frame resulting from run() or spatialDE() .
...	For the generic, arguments to pass to specific methods.
coordinates	A data.frame with sample coordinates. Each row is a sample, the columns with coordinates should be named 'x' and 'y'. For the <i>SpatialExperiment</i> method, coordinates are taken from <code>spatialCoords(x)</code> .
qval_thresh	numeric scalar, specifying the q-value significance threshold to filter <code>de_results</code> . Only rows in <code>de_results</code> with <code>qval < qval_thresh</code> will be kept. To disable, set <code>qval_thresh = NULL</code> .

n_patterns	integer	The number of spatial patterns
length	numeric	The characteristic length scale of the clusters
verbose	A logical	controlling the display of a progress bar from the Python package.
assay_type	A character string	specifying the assay from x to use as input. Defaults to "counts".

Value

A list of two data.frames (pattern_results, patterns):

- pattern_results: data.frame with pattern membership information for each gene.
- patterns the posterior mean underlying expression from genes in given spatial patterns.

Author(s)

Davide Corso, Milan Malfait, Lambda Moses

References

Svensson, V., Teichmann, S. & Stegle, O. SpatialDE: identification of spatially variable genes. Nat Methods 15, 343–346 (2018). <https://doi.org/10.1038/nmeth.4636>

SpatialDE 1.1.3: the version of the Python package used under the hood.

See Also

The individual steps performed by this function: [stabilize\(\)](#), [regress_out\(\)](#) and [spatial_patterns\(\)](#).

Examples

```
## Mock up a SpatialExperiment object wit 100 cells and 3 genes
set.seed(42)
spe <- mockSVG(size = 10, tot_genes = 3, de_genes = 1, return_SPE = TRUE)

## Run spatialDE
de_results <- spatialDE(spe)

spatial_patterns <- spatialPatterns(spe, de_results = de_results,
  qual_thresh = NULL, n_patterns = 4L, length = 1.5,
  verbose = FALSE
)

head(spatial_patterns$pattern_results)
head(spatial_patterns$patterns)
```

spatial_patterns	<i>Group spatially variable genes into spatial patterns using automatic expression histology (AEH)</i>
------------------	--

Description

Group spatially variable genes into spatial patterns using automatic expression histology (AEH)

Usage

```
spatial_patterns(
  x,
  coordinates,
  de_results,
  qval_thresh = 0.05,
  n_patterns,
  length,
  verbose = FALSE
)
```

Arguments

x	matrix-like object of normalized counts. E.g. resulting from <code>regress_out()</code> .
coordinates	data.frame with sample coordinates. Each row is a sample, the columns with coordinates must be named 'x' and 'y'.
de_results	data.frame resulting from <code>run()</code> .
qval_thresh	numeric scalar, specifying the q-value significance threshold to filter <code>de_results</code> . Only rows in <code>de_results</code> with <code>qval < qval_thresh</code> will be kept. To disable, set <code>qval_thresh = NULL</code> .
n_patterns	integer The number of spatial patterns
length	numeric The characteristic length scale of the clusters
verbose	logical controlling the display of the progress bar.

Value

list of two dataframe (`pattern_results`, `patterns`): `pattern_results` dataframe with pattern membership information for each gene. `patterns` the posterior mean underlying expression fro genes in given spatial patterns.

References

Svensson, V., Teichmann, S. & Stegle, O. SpatialDE: identification of spatially variable genes. Nat Methods 15, 343–346 (2018). <https://doi.org/10.1038/nmeth.4636>

Examples

```
## Mock up a SpatialExperiment object with 400 cells and 3 genes
set.seed(42)
mock <- mockSVG(size = 20, tot_genes = 3, de_genes = 1)

stabilized <- stabilize(mock$counts)
sample_info <- mock$coordinates
sample_info$total_counts <- colSums(mock$counts)
regressed <- regress_out(counts = stabilized, sample_info = sample_info)

## Run SpatialDE
de_results <- run(x = regressed, coordinates = mock$coordinates)

## Run Spatial_patterns
sp <- spatial_patterns(
  x = regressed,
  coordinates = mock$coordinates,
  de_results = de_results,
  qual_thresh = NULL,
  n_patterns = 5, length = 1.5
)

sp$pattern_results
sp$patterns
```

stabilize	<i>Stabilize variance of counts</i>
-----------	-------------------------------------

Description

Stabilize variance of negative binomial data using Anscombe's approximation. This function is a wrapper for stabilize from the **NaiveDE** Python package.

Usage

```
stabilize(counts)
```

Arguments

counts matrix with expression values for samples in columns and genes in rows.

Value

matrix of variance stabilized counts.

Examples

```
## Mock up a SpatialExperiment object wit 400 cells and 3 genes
set.seed(42)
mock <- mockSVG(20, 3, 1)

stabilized <- stabilize(mock$counts)
```

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