

Package ‘spatialDE’

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Title R wrapper for SpatialDE

Version 1.15.1

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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<code>.importPyModule</code>	<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 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
```

```

results <- spatialDE(spe)

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

plot <- FSV_sig(results, msearch)

```

MOB_sample_info	<i>Mouse Olfactory Bulb sample metadata</i>
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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

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.

mockSVG	<i>Generate count matrix for spatially variable genes.</i>
---------	--

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 <code>run()</code> or <code>spatialDE()</code> .
<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 regress_out() .
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 run() .
qval_thresh	numeric scalar, specifying the q-value significance threshold to filter de_results. Only rows in de_results with qval < qval_thresh will be kept. To disable, set qval_thresh = NULL.
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,
  qval_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 stabilize() .
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

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.

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

x	A numeric matrix of counts where genes are rows and cells are columns. Alternatively, a SpatialExperiment object.
...	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> .
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 `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)
```

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

<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>n_patterns</code>	integer The number of spatial patterns
<code>length</code>	numeric The characteristic length scale of the clusters
<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 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 with 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,
  qval_thresh = NULL, n_patterns = 4L, length = 1.5,
  verbose = FALSE
)

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

spatial_patterns

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

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

<code>x</code>	matrix-like object of normalized counts. E.g. resulting from <code>regress_out()</code> .
<code>coordinates</code>	<code>data.frame</code> with sample coordinates. Each row is a sample, the columns with coordinates must be named 'x' and 'y'.
<code>de_results</code>	<code>data.frame</code> resulting from <code>run()</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>n_patterns</code>	integer The number of spatial patterns
<code>length</code>	numeric The characteristic length scale of the clusters
<code>verbose</code>	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 for 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,
  qval_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 with 400 cells and 3 genes
set.seed(42)
mock <- mockSVG(20, 3, 1)

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

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