

# Package ‘spatialDE’

May 21, 2024

**Title** R wrapper for SpatialDE

**Date** 2024-02-08

**Version** 1.11.0

**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.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** FALSE

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

**URL** <https://github.com/sales-lab/spatialDE>,  
<https://bioconductor.org/packages/spatialDE/>

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

**Depends** R (>= 4.3)

**Imports** reticulate, basilisk (>= 1.9.10), checkmate, stats,  
SpatialExperiment, methods, SummarizedExperiment, Matrix,  
ggplot2, ggrepel, scales, gridExtra

**Suggests** knitr, BiocStyle, rmarkdown, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**biocViews** Software, Transcriptomics

**StagedInstall** no

**Config/testthat/edition** 3

**git\_url** <https://git.bioconductor.org/packages/spatialDE>

**git\_branch** devel

**git\_last\_commit** 8c1ba06

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-05-20

**Author** Davide Corso [aut] (<<https://orcid.org/0000-0001-8845-3693>>),  
 Milan Malfait [aut] (<<https://orcid.org/0000-0001-9144-3701>>),  
 Lambda Moses [aut] (<<https://orcid.org/0000-0002-7092-9427>>),  
 Gabriele Sales [cre]

**Maintainer** Gabriele Sales <gabriele.sales@unipd.it>

## Contents

<code>.importPyModule</code>	2
<code>FSV_sig</code>	3
<code>MOB_sample_info</code>	4
<code>mockSVG</code>	5
<code>modelSearch</code>	5
<code>model_search</code>	7
<code>multiGenePlots</code>	8
<code>regress_out</code>	10
<code>Rep11_MOB_0</code>	11
<code>run</code>	11
<code>spatialDE</code>	12
<code>spatialPatterns</code>	14
<code>spatial_patterns</code>	16
<code>stabilize</code>	17

**Index** 19

---

<code>.importPyModule</code>	<i>Import SpatialDE</i>
------------------------------	-------------------------

---

## Description

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

## Usage

```
.importPyModule(proc, patch_tqdm)
```

## Arguments

<code>proc</code>	A process object generated by <code>basilisk::basiliskStart()</code>
<code>patch_tqdm</code>	If TRUE patch calls to tqdm.

## Value

An R wrapper for the SpatialDE Python module.

**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](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 <a href="#">SpatialExperiment</a> . 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 [SpatialIDE](#) 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**

x	A numeric matrix of counts where genes are rows and cells are columns. Alternatively, a <code>SpatialExperiment</code> object.
de_results	data.frame resulting from <code>run()</code> or <code>spatialDE()</code> .
...	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 de_results. Only rows in de_results with <code>qval &lt; qval_thresh</code> will be kept. To disable, set <code>qval_thresh = NULL</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**

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 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
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 <a href="#">regress_out()</a> .
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 <a href="#">run()</a> .
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,
  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

x	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.
...	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 <code>SpatialExperiment</code> method, coordinates are taken from <code>spatialCoords(x)</code> .
genes_plot	character vector specifying which genes are to be plotted.
viridis_option	This function uses the <code>viridis</code> 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").
ncol	Number of columns to arrange the plots.
point_size	Point size of each plot.
dark_theme	Whether dark background should be used; this is helpful to highlight cells with high expression when using the <code>viridis</code> palette.
assay_type	A character string specifying the assay from x 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](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 <a href="#">regress_out()</a> .
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 <a href="#">SpatialExperiment</a> 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)
```

---

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 <a href="#">SpatialExperiment</a> object.
de_results	data.frame resulting from <a href="#">run()</a> or <a href="#">spatialDE()</a> .
...	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 <a href="#">spatialCoords(x)</a> .
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 &lt; 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 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,
  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 &lt; 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 with 400 cells and 3 genes
set.seed(42)
mock <- mockSVG(20, 3, 1)

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

# Index

- \* **datasets**
  - MOB\_sample\_info, 4
  - Rep11\_MOB\_0, 11
- \* **internal**
  - .importPyModule, 2
  - .importPyModule, 2
- basilisk::basiliskStart(), 2
- FSV\_sig, 3
- MOB\_sample\_info, 4
- mockSVG, 5
- model\_search, 7
- model\_search(), 7, 9, 13
- modelSearch, 5
- modelSearch, matrix-method
  - (modelSearch), 5
- modelSearch, SpatialExperiment-method
  - (modelSearch), 5
- multiGenePlots, 8
- multiGenePlots, matrix-method
  - (multiGenePlots), 8
- multiGenePlots, SpatialExperiment-method
  - (multiGenePlots), 8
- regress\_out, 10
- regress\_out(), 7, 11, 13, 15, 16
- Rep11\_MOB\_0, 11
- run, 11
- run(), 6, 7, 13, 14, 16
- spatial\_patterns, 16
- spatial\_patterns(), 9, 13, 15
- spatialDE, 12
- spatialDE(), 6, 9, 14
- spatialDE, matrix-method (spatialDE), 12
- spatialDE, SpatialExperiment-method
  - (spatialDE), 12
- SpatialExperiment, 5, 6, 9, 13, 14
- spatialPatterns, 14
- spatialPatterns, matrix-method
  - (spatialPatterns), 14
- spatialPatterns, SpatialExperiment-method
  - (spatialPatterns), 14
- stabilize, 17
- stabilize(), 7, 9, 10, 13, 15