

# 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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<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(patch_tqdm)
```

### Arguments

`patch_tqdm` 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**

```

set.seed(42)
spe <- mockSVG(size = 10, tot_genes = 200, de_genes = 20, 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	<i>Mouse Olfactory Bulb sample metadata</i>
-----------------	---

---

**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**

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

---

**Description**

Generate count matrix for spatially variable genes.

**Usage**

```
mockSVG(size = 10, tot_genes = 1000, de_genes = 100, return_SPE = FALSE)
```

**Arguments**

size	An integer scalar. Cells will be spatially arranged on a size $\times$ 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(10, tot_genes = 200, de_genes = 20, 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, qual_thresh = 0.05, verbose = FALSE)

## S4 method for signature 'SpatialExperiment'
modelSearch(
  x,
  de_results,
  assay_type = "counts",
  qual_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 <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> .
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 wit 100 cells, 200 genes
set.seed(42)
spe <- mockSVG(size = 10, tot_genes = 200, de_genes = 20, 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	<i>Compare model fits with different models</i>
--------------	---

---

**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 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	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**

```
set.seed(42)
mock <- mockSVG(size = 10, tot_genes = 300, de_genes = 10)
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

x	A numeric matrix of stabilized counts (e.g. resulting from <a href="#">stabilize()</a> ) 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> .



genes_plot	character vector specifying which genes are to be plotted.
viridis_option	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").
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 viridis 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 with 100 cells, 200 genes
set.seed(42)
spe <- mockSVG(size = 10, tot_genes = 200, de_genes = 10, 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[1:4, ]$g,
  point_size = 4,
  viridis_option = "D"
)
```

---

regress_out	<i>Regress out library size effect</i>
-------------	--

---

**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 <a href="#">stabilize()</a> .
sample_info	data.frame with samples as rows and at least a column with <code>total_counts</code> .

**Value**

matrix of normalized counts.

**Examples**

```
set.seed(42)
mock <- mockSVG(10, 1000, 10)
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	<i>Mouse Olfactory Bulb spatial gene expression data</i>
-------------	--

---

**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**

```
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	<i>Perform SpatialDE test</i>
-----	-------------------------------

---

## 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 <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'.
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

```
set.seed(42)
mock <- mockSVG(size = 10, tot_genes = 500, de_genes = 10)
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 with 100 cells, 200 genes
set.seed(42)
spe <- mockSVG(size = 10, tot_genes = 200, de_genes = 20, 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,
  qual_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 <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 &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, 200 genes
set.seed(42)
spe <- mockSVG(size = 10, tot_genes = 200, de_genes = 20, 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,
  qual_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> .
qual_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; qual_thresh</code> will be kept. To disable, set <code>qual_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

```
set.seed(42)
mock <- mockSVG(size = 10, tot_genes = 500, de_genes = 10)
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

*Stabilize variance of counts*

---

### 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**

```
set.seed(42)
mock <- mockSVG(10, 1000, 10)
stabilized <- stabilize(mock$counts)
```

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