

# Package ‘spatialDE’

February 2, 2026

**Title** R wrapper for SpatialDE

**Version** 1.17.0

**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

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

**Maintainer** Gabriele Sales <[gabriele.sales@unipd.it](mailto:gabriele.sales@unipd.it)>

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|                 |                         |
|-----------------|-------------------------|
| .importPyModule | <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

- 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](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

|                         |                                                                                                                                               |
|-------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|
| <code>size</code>       | An integer scalar. Cells will be spatially arranged on a <code>size</code> x <code>size</code> grid. Default: 10, corresponding to 100 cells. |
| <code>tot_genes</code>  | An integer scalar. Total number of genes. Default: 1000.                                                                                      |
| <code>de_genes</code>   | An integer scalar. The number of spatially variable genes. Default: 100.                                                                      |
| <code>return_SPE</code> | 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 [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 <a href="#">SpatialExperiment</a> object.                                                                                                              |
| <code>de_results</code>  | <code>data.frame</code> resulting from <a href="#">run()</a> or <a href="#">spatialDE()</a> .                                                                                                                                                  |
| <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'.<br>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 &lt; 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 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 <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> . |
| 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.<br>Alternatively, a <code>SpatialExperiment</code> object.                                              |
| ...            | For the generic, arguments to pass to specific methods.                                                                                                                                                                                   |
| coordinates    | A <code>data.frame</code> with sample coordinates. Each row is a sample, the columns with coordinates should be named 'x' and 'y'.<br>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 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](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 <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**

|                          |                                                                                                                                                                                                                                           |
|--------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>           | A numeric matrix of counts where genes are rows and cells are columns. Alternatively, a <a href="#">SpatialExperiment</a> 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'.<br>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 <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'.<br>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 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 &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 wit 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> |
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**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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