# Package 'spatialDE'

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**Title** R wrapper for SpatialDE

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**Version** 1.4.3

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

**Depends** R (>= 4.1)

**Imports** reticulate, basilisk (>= 1.9.10), checkmate, stats, SpatialExperiment, methods, SummarizedExperiment, Matrix, S4Vectors, ggplot2, ggrepel, scales, gridExtra

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# R topics documented:



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`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 *Mouse Olfactory Bulb sample metadata*

### Description

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

### Usage

```
data(MOB_sample_info)
```

### Format

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

### References

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 *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` scaler. 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

| | |
|---|---|
| `x` | A numeric `matrix` of counts where genes are rows and cells are columns.<br>Alternatively, a SpatialExperiment object. |
| `de_results` | `data.frame` resulting from `run()` or `spatialDE()`. |
| `...` | For the generic, arguments to pass to specific methods. |
| `coordinates` | A `data.frame` with sample coordinates. Each row is a sample, the columns with coordinates should be named 'x' and 'y'.<br>For the *SpatialExperiment* method, coordinates are taken from `spatialCoords(x)`. |

| | |
|---|---|
| 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 | 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 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 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(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 `stabilize()`) where genes are rows and cells are columns.<br>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'.<br>For the *SpatialExperiment* method, coordinates are taken from `spatialCoords(x)`. |
| `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 `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

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

---

`run` *Perform SpatialDE test*

---

## Description

Wraps the `run` function from the SpatialDE Python package.

## Usage

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

## Arguments

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

## Value

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

The most important columns are:

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

## References

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

## Examples

```
## Mock up a SpatialExperiment object 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(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.<br>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'.<br>For the *SpatialExperiment* method, coordinates are taken from `spatialCoords(x)`. |
| `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.<br>Alternatively, a SpatialExperiment object. |
| de_results | `data.frame` resulting from `run()` or `spatialDE()`. |
| ... | For the generic, arguments to pass to specific methods. |
| coordinates | A `data.frame` with sample coordinates. Each row is a sample, the columns with coordinates should be named 'x' and 'y'.<br>For the *SpatialExperiment* method, coordinates are taken from `spatialCoords(x)`. |
| 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`. |
| 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,
    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

| | |
|---|---|
| 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. |
| 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` *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

```
## 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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