

Package: spatialDESeq (via r-universe)

September 23, 2026

Title Spatial Differential Expression via Spatial Autoregressive GLMs

Version 0.99.2

Description A robust, parallelized statistical framework optimized for identifying spatially differential expression in high-throughput spatial transcriptomics datasets. The package extends standard negative binomial generalized linear models (GLMs) by incorporating continuous physical tissue spot coordinates as distance-weighted local smoothing covariates. This configuration models spatial context seamlessly without relying on pre-annotated categorical tissue clusters. The underlying distance matrix evaluations and coordinate smoothing routines are accelerated natively via an optimized C++ Armadillo matrix engine to guarantee computational efficiency. Built to integrate natively into the Bioconductor ecosystem, the package operates directly on SpatialExperiment containers, incorporates robust library-size normalization scaling factor offsets, calculates adjusted p-values for multi-gene profiles, and supplies an interactive Shiny-based point-and-click visualization dashboard tool for downstream exploratory data analysis.

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Encoding UTF-8

biocViews GeneExpression, RNASeq, Sequencing, Spatial, Transcriptomics, DifferentialExpression, Software

URL <https://github.com>

BugReports <https://github.com/issues>

Depends R (>= 4.4.0), BiocGenerics

Imports methods, SpatialExperiment (>= 1.12.0), SummarizedExperiment (>= 1.32.0), BiocParallel (>= 1.36.0), Rcpp (>= 1.0.11), ggplot2 (>= 3.4.0), stats

LinkingTo Rcpp, RcppArmadillo (>= 0.12.0)

Suggests testthat (>= 3.0.0), shiny (>= 1.8.0), BiocStyle (>= 2.30.0), knitr (>= 1.45), rmarkdown (>= 2.25)

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make_mock_spatial	<i>Generate Mock Spatial Transcriptomics Data</i>
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Description

Generate Mock Spatial Transcriptomics Data

Usage

make_mock_spatial()

Value

A SpatialExperiment object with synthetic counts and coordinates.

Examples

se <- make_mock_spatial()

plotSpatialDESeq	<i>Plot Spatial Differential Expression Results</i>
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Description

Plot Spatial Differential Expression Results

Usage

```
plotSpatialDESeq(se, gene_id, metric = c("expression", "spatial_effect"))
```

Arguments

se	An analyzed SpatialExperiment object.
gene_id	Character. Gene target to visualize.
metric	Character. Choose "expression" or "spatial_effect".

Value

A ggplot2 object.

Examples

```
se <- make_mock_spatial()
analyzed <- spatialDESeq(se, design = ~ condition, radius = 2.5)
plotSpatialDESeq(analyzed, gene_id = "Gene1", metric = "expression")
```

plotVolcano	<i>Generate Volcano Plot for Spatial Differential Expression</i>
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Description

Generate Volcano Plot for Spatial Differential Expression

Usage

```
plotVolcano(se, alpha = 0.05, effect_cutoff = 0.5)
```

Arguments

se	An analyzed SpatialExperiment object.
alpha	Numeric. Significance value cutoff.
effect_cutoff	Numeric. Threshold for effect markings.

Value

A ggplot2 object.

Examples

```
se <- make_mock_spatial()
analyzed <- spatialDESeq(se, design = ~ condition, radius = 2.5)
plotVolcano(analyzed)
```

rcpp_spatial_weights *Compute Row-Normalized Spatial Weights*

Description

Compute Row-Normalized Spatial Weights

Usage

```
rcpp_spatial_weights(coords, radius)
```

Arguments

coords	Numeric matrix of physical spots coordinates.
radius	Distance radius.

Value

Matrix of physical distance weights.

Examples

```
coords <- matrix(runif(20), ncol = 2)
rcpp_spatial_weights(coords, radius = 0.5)
```

runExplorer *Launch Interactive Spatial Data Explorer*

Description

Launch Interactive Spatial Data Explorer

Usage

```
runExplorer(se)
```

Arguments

se An analyzed SpatialExperiment object.

Value

Opens an interactive Shiny dashboard page in the web browser. None returned.

Examples

```
## Not run:
se <- make_mock_spatial()
analyzed <- spatialDESeq(se, design = ~ condition, radius = 2.5)
runExplorer(analyzed)

## End(Not run)
```

spatialDESeq	<i>Multithreaded Spatial Differential Expression Analysis</i>
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Description

Multithreaded Spatial Differential Expression Analysis

Usage

```
spatialDESeq(se, design, radius = 2.5, BPPARAM = BiocParallel::bpparam())
```

Arguments

se A SpatialExperiment object.

design A formula specifying experimental variables (e.g., ~ condition).

radius Numeric. Distance radius for local spatial neighbors.

BPPARAM A BiocParallelParam object defining core backend allocation.

Value

A SpatialExperiment object with analysis results appended to rowData.

Examples

```
se <- make_mock_spatial()
analyzed <- spatialDESeq(se, design = ~ condition, radius = 2.5)
```

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