

# Package ‘spicyR’

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**Type** Package

**Title** Spatial analysis of in situ cytometry data

**Version** 1.18.0

**Description** The spicyR package provides a framework for performing inference on changes in spatial relationships between pairs of cell types for cell-resolution spatial omics technologies. spicyR consists of three primary steps: (i) summarizing the degree of spatial localization between pairs of cell types for each image; (ii) modelling the variability in localization summary statistics as a function of cell counts and (iii) testing for changes in spatial localizations associated with a response variable.

**License** GPL (>=2)

**LazyData** true

**biocViews** SingleCell, CellBasedAssays, Spatial

**Encoding** UTF-8

**Depends** R (>= 4.1)

**VignetteBuilder** knitr

**BugReports** <https://github.com/SydneyBioX/spicyR/issues>

**URL** <https://ellispatrick.github.io/spicyR/>

<https://github.com/SydneyBioX/spicyR>,

<https://sydneybiox.github.io/spicyR/>

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bind	<i>Produces a dataframe showing L-function metric for each imageID entry.</i>
------	---

---

## Description

Produces a dataframe showing L-function metric for each imageID entry.

## Usage

```
bind(results, pairName = NULL)
```

## Arguments

results	Spicy test result obtained from spicy.
pairName	A string specifying the pairwise interaction of interest. If NULL, all pairwise interactions are shown.

## Value

A data.frame containing the colData related to the results.

**Examples**

```
data(spicyTest)
df <- bind(spicyTest)
```

---

colTest	<i>Perform a simple wilcoxon-rank-sum test or t-test on the columns of a data frame</i>
---------	---

---

**Description**

Perform a simple wilcoxon-rank-sum test or t-test on the columns of a data frame

**Usage**

```
colTest(df, condition, type = NULL, feature = NULL, imageID = "imageID")
```

**Arguments**

df	A data.frame or SingleCellExperiment, SpatialExperiment
condition	The condition of interest
type	The type of test, "wilcox", "ttest" or "survival".
feature	Can be used to calculate the proportions of this feature for each image
imageID	The imageID's if presenting a SingleCellExperiment

**Value**

Proportions

**Examples**

```
# Test for an association with long-duration diabetes
# This is clearly ignoring the repeated measures...
data("diabetesData")
diabetesData <- spicyR::format_data(
  diabetesData, "imageID", "cellType", c("x", "y"), FALSE
)
props <- getProp(diabetesData)
condition <- spicyR::getImagePheno(diabetesData)$stage
names(condition) <- spicyR::getImagePheno(diabetesData)$imageID
condition <- condition[condition %in% c("Long-duration", "Onset")]
test <- colTest(props[names(condition), ], condition)
```

---

convPairs	<i>Converts colPairs object into an abundance matrix based on number of nearby interactions for every cell type.</i>
-----------	--

---

### Description

Converts colPairs object into an abundance matrix based on number of nearby interactions for every cell type.

### Usage

```
convPairs(cells, colPair, cellType = "cellType", imageID = "imageID")
```

### Arguments

cells	A SingleCellExperiment that contains objects in the colPairs slot.
colPair	The name of the object in the colPairs slot for which the dataframe is constructed from.
cellType	The cell type if using SingleCellExperiment.
imageID	The image ID if using SingleCellExperiment.

### Value

Matrix of abundances

### Examples

```
data("diabetesData")
images <- c("A09", "A11", "A16", "A17")
diabetesData <- diabetesData[
  , SummarizedExperiment::colData(diabetesData)$imageID %in% images
]

diabetesData_SPE <- SpatialExperiment::SpatialExperiment(diabetesData,
  colData = SummarizedExperiment::colData(diabetesData)
)
SpatialExperiment::spatialCoords(diabetesData_SPE) <- data.frame(
  SummarizedExperiment::colData(diabetesData_SPE)$x,
  SummarizedExperiment::colData(diabetesData_SPE)$y
) |>
  as.matrix()

SpatialExperiment::spatialCoordsNames(diabetesData_SPE) <- c("x", "y")

diabetesData_SPE <- imcRtools::buildSpatialGraph(diabetesData_SPE,
  img_id = "imageID",
  type = "knn",
  k = 20,
  coords = c("x", "y")
)

pairAbundances <- convPairs(diabetesData_SPE,
```

```
colPair = "knn_interaction_graph"
)
```

---

diabetesData	<i>Diabetes IMC data in SCE format.</i>
--------------	---

---

### Description

This is a subset of the Damond et al 2019 imaging mass cytometry dataset. The data contains cells in the pancreatic islets of individuals with early onset diabetes and healthy controls. The object contains single-cell data of 160 images from 8 subjects, with 20 images per subject.

### Usage

```
data("diabetesData")
```

### Format

diabetesData\_SCE a SingleCellExperiment object

### Details

Converted into a SingleCellExperiment format.

---

getPairwise	<i>Get statistic from pairwise L curve of a single image.</i>
-------------	---

---

### Description

Get statistic from pairwise L curve of a single image.

### Usage

```
getPairwise(
  cells,
  from = NULL,
  to = NULL,
  window = "convex",
  window.length = NULL,
  Rs = c(20, 50, 100),
  sigma = NULL,
  minLambda = 0.05,
  edgeCorrect = TRUE,
  includeZeroCells = TRUE,
  BPPARAM = BiocParallel::SerialParam(),
  imageIDCol = "imageID",
  cellTypeCol = "cellType",
  spatialCoordCols = c("x", "y")
)
```

**Arguments**

cells	A SummarizedExperiment that contains at least the variables x and y, giving the location coordinates of each cell, and cellType.
from	The 'from' cellType for generating the L curve.
to	The 'to' cellType for generating the L curve.
window	Should the window around the regions be 'square', 'convex' or 'concave'.
window.length	A tuning parameter for controlling the level of concavity when estimating concave windows.
Rs	A vector of the radii that the measures of association should be calculated.
sigma	A numeric variable used for scaling when fitting inhomogeneous L-curves.
minLambda	Minimum value for density for scaling when fitting inhomogeneous L-curves.
edgeCorrect	A logical indicating whether to perform edge correction.
includeZeroCells	A logical indicating whether to include cells with zero counts in the pairwise association calculation.
BPPARAM	A BiocParallelParam object.
imageIDCol	The name of the imageID column if using a SingleCellExperiment or SpatialExperiment.
cellTypeCol	The name of the cellType column if using a SingleCellExperiment or SpatialExperiment.
spatialCoordCols	The names of the spatialCoords column if using a SingleCellExperiment.

**Value**

Statistic from pairwise L curve of a single image.

**Examples**

```
data("diabetesData")
# Subset by imageID for fast example
selected_cells <- diabetesData[
  , SummarizedExperiment::colData(diabetesData)$imageID == "A09"
]
pairAssoc <- getPairwise(selected_cells)
```

---

getProp

*Get proportions from a SummarizedExperiment.*

---

**Description**

Get proportions from a SummarizedExperiment.

**Usage**

```
getProp(cells, feature = "cellType", imageID = "imageID")
```

**Arguments**

cells	A SingleCellExperiment, SpatialExperiment or data.frame.
feature	The feature of interest
imageID	The imageID's

**Value**

Proportions

**Examples**

```
data("diabetesData")
prop <- getProp(diabetesData)
```

---

signifPlot	<i>Plots result of signifPlot.</i>
------------	------------------------------------

---

**Description**

Plots result of signifPlot.

**Usage**

```
signifPlot(
  results,
  fdr = FALSE,
  type = "bubble",
  breaks = NULL,
  comparisonGroup = NULL,
  colours = c("#4575B4", "white", "#D73027"),
  marksToPlot = NULL,
  cutoff = 0.05,
  contextColours = NULL,
  contextLabels = waiver()
)
```

**Arguments**

results	A spicy results object
fdr	TRUE if FDR correction is used.
type	Whether to make a bubble plot or heatmap. Note: For survival results a bubble plot will be used.
breaks	Vector of 3 numbers giving breaks used in legend. The first number is the minimum, the second is the maximum, the third is the number of breaks.
comparisonGroup	A string specifying the name of the outcome group to compare with the base group.
colours	Vector of colours to use to colour legend.
marksToPlot	Vector of marks to include in plot.

cutoff	significance threshold for circles in bubble plot.
contextColours	Used for <a href="#">Kontextual</a> results. A named list specifying the colours for each context. By default the Tableau colour palette is used.
contextLabels	Used for <a href="#">Kontextual</a> results. A named list to change the default labels for each context.

**Value**

a ggplot or pheatmap object

**Examples**

```
data(spicyTest)

p <- signifPlot(spicyTest, breaks = c(-3, 3, 0.5))
# plot includes unicode characters, do not use default pdf device
ggplot2::ggsave(p, filename = tempfile(), device = cairo_pdf)
```

---

spicyBoxPlot	<i>Plots boxplot for a specified cell-cell relationship</i>
--------------	---

---

**Description**

Plots boxplot for a specified cell-cell relationship

**Usage**

```
spicyBoxPlot(results, from = NULL, to = NULL, rank = NULL)
```

**Arguments**

results	Data frame obtained from spicy.
from	Cell type which you would like to compare to the to cell type.
to	Cell type which you would like to compare to the from cell type.
rank	Ranking of cell type in terms of p-value, the smaller the p-value the higher the rank.

**Value**

a ggplot2 boxplot

**Examples**

```
data(spicyTest)

spicyBoxPlot(spicyTest,
             rank = 1)
```

---

SpicyResults-class      *Performs spatial tests on spatial cytometry data.*

---

## Description

Performs spatial tests on spatial cytometry data.

## Usage

```
spicy(
  cells,
  condition,
  subject = NULL,
  covariates = NULL,
  from = NULL,
  to = NULL,
  imageIDCol = "imageID",
  cellTypeCol = "cellType",
  spatialCoordCols = c("x", "y"),
  alternateResult = NULL,
  verbose = FALSE,
  weights = TRUE,
  weightsByPair = FALSE,
  weightFactor = 1,
  window = "convex",
  window.length = NULL,
  BPPARAM = BiocParallel::SerialParam(),
  sigma = NULL,
  Rs = NULL,
  minLambda = 0.05,
  edgeCorrect = TRUE,
  includeZeroCells = FALSE,
  ...
)
```

## Arguments

cells	A SummarizedExperiment or data frame that contains at least the variables x and y, giving the location coordinates of each cell, and cellType.
condition	A character specifying which column which contains the condition or ‘Surv’ objects
subject	Vector of subject IDs corresponding to each image if cells is a data frame.
covariates	Vector of covariate names that should be included in the mixed effects model as fixed effects.
from	vector of cell types which you would like to compare to the to vector
to	vector of cell types which you would like to compare to the from vector
imageIDCol	The image ID if using SingleCellExperiment.
cellTypeCol	The cell type if using SingleCellExperiment.

<code>spatialCoordCols</code>	The spatial coordinates if using a <code>SingleCellExperiment</code> .
<code>alternateResult</code>	An pairwise association statistic between each combination of celltypes in each image.
<code>verbose</code>	logical indicating whether to output messages.
<code>weights</code>	logical indicating whether to include weights based on cell counts.
<code>weightsByPair</code>	logical indicating whether weights should be calculated for each cell type pair.
<code>weightFactor</code>	numeric that controls the convexity of the weight function.
<code>window</code>	Should the window around the regions be 'square', 'convex' or 'concave'.
<code>window.length</code>	A tuning parameter for controlling the level of concavity when estimating concave windows.
<code>BPPARAM</code>	A <code>BiocParallelParam</code> object.
<code>sigma</code>	A numeric variable used for scaling when fitting inhomogeneous L-curves.
<code>Rs</code>	A vector of radii that the measures of association should be calculated. If <code>NULL</code> , <code>Rs = c(20, 50, 100)</code> is specified by default.
<code>minLambda</code>	Minimum value for density for scaling when fitting inhomogeneous L-curves.
<code>edgeCorrect</code>	A logical indicating whether to perform edge correction.
<code>includeZeroCells</code>	A logical indicating whether to include cells with zero counts in the pairwise association calculation.
<code>...</code>	Other options.

**Value**

Data frame of p-values.

**Examples**

```
data("diabetesData")

# Test with random effect for patient on a pairwise combination of cell
# types.
spicy(diabetesData,
      condition = "stage", subject = "case",
      from = "Tc", to = "Th"
)

# Test all pairwise combinations of cell types without random effect of
# patient.
## Not run:
spicyTest <- spicy(diabetesData, condition = "stage", subject = "case")

## End(Not run)

# Test all pairwise combination of cell types with random effect of patient.
## Not run:
spicy(diabetesData, condition = "condition", subject = "subject")

## End(Not run)
```

---

spicyTest	<i>Results from spicy for diabetesData</i>
-----------	--

---

**Description**

Results from the call: `spicyTest <- spicy(diabetesData, condition = "condition", subject = "subject")`

**Usage**

```
data("spicyTest")
```

**Format**

spicyTest a spicy object

---

survBubble	<i>Plots survival results from spicy.</i>
------------	---

---

**Description**

Plots survival results from spicy.

**Usage**

```
survBubble(
  result,
  fdr = FALSE,
  cutoff = 0.05,
  colourGradient = c("#4575B4", "white", "#D73027"),
  marksToPlot = NULL,
  contextColours = NULL,
  contextLabels = waiver()
)
```

**Arguments**

result	A <code>spicyResults</code> object that contains survival results.
fdr	TRUE if FDR correction is used.
cutoff	Significance threshold for circles in bubble plot.
colourGradient	A vector of colours, used to define the low, medium, and high values for the colour scale.
marksToPlot	Vector of marks to include in bubble plot.
contextColours	Used for <a href="#">Kontextual</a> results. A named list specifying the colours for each context. By default the Tableau colour palette is used.
contextLabels	Used for <a href="#">Kontextual</a> results. A named list to change the default labels for each context.

**Value**

A `ggplot` object.

---

`topPairs`*A table of the significant results from spicy tests*

---

**Description**

A table of the significant results from spicy tests

**Usage**

```
topPairs(x, coef = NULL, n = 10, adj = "fdr", cutoff = NULL, figures = NULL)
```

**Arguments**

<code>x</code>	The output from spicy.
<code>coef</code>	Which coefficient to list.
<code>n</code>	Extract the top n most significant pairs.
<code>adj</code>	Which p-value adjustment method to use, argument for <code>p.adjust()</code> .
<code>cutoff</code>	A p-value threshold to extract significant pairs.
<code>figures</code>	Round to 'figures' significant figures.

**Value**

A data.frame

**Examples**

```
data(spicyTest)
topPairs(spicyTest)
```

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