Package ‘Statial’

June 7, 2023

Type Package

Title A package to identify changes in cell state relative to spatial associations

Version 1.2.0

Date 2022-09-19

VignetteBuilder knitr

Encoding UTF-8

biocViews SingleCell, Spatial

Depends R (>= 4.1.0)

Imports BiocParallel, spatstat.geom, concaveman, tidyverse, data.table, spatstat.explore, dplyr, tidyr, SingleCellExperiment, tibble, stringr, tidyselect, ggplot2, methods, stats

Suggests BiocStyle, knitr, testthat (>= 3.0.0)

Description Statial is a suite of functions for identifying changes in cell state. The functionality provided by Statial provides robust quantification of cell type localisation which are invariant to changes in tissue structure. In addition to this Statial uncovers changes in marker expression associated with varying levels of localisation. These features can be used to explore how the structure and function of different cell types may be altered by the agents they are surrounded with.

License GPL-3

RoxygenNote 7.2.1

Config/testthat/edition 3

git_url https://git.bioconductor.org/packages/Statial

git_branch RELEASE_3_17

git_last_commit 0e0efa0

git_last_commit_date 2023-04-25

Date/Publication 2023-06-06

Author Farhan Ameen [aut, cre],
Sourish Iyengar [aut],
Shila Ghazanfar [aut],
Ellis Patrick [aut]

Maintainer Farhan Ameen <fame2827@uni.sydney.edu.au>

R topics documented:

ggplotRs — *Plotting the original and konditional L values over a range of radii.*

Description

This function takes outputs from rsCurve and plots them in ggplot. If standard deviation is estimated in rsCurve, then confidence intervals will be constructed based on the standard deviation. If the confidence interval overlaps with 0, then the relationship is insignificant for that radius.

Usage

```
ggplotRs(rsDf)
```

Arguments

rsDf	A data frame from rsCurve.

Value

A ggplotly object showing the original and konditional L function values over a range of radii

Examples

```
data("kerenImage")

rsDf <- rsCurve(
  cells = kerenImage,
  from = "p53",
  to = "Immune",
  parent = c("p53", "Keratin+Tumour"),
  rs = seq(10, 510, 100),
  cores = 40
)

ggplotRs(rsDf)
```

---

headSCE — *Head and neck cutaneous squamous cell carcinoma IMC data*

Description

This is a subset of imaging mass cytometry dataset of head and neck cutaneous squamous cell carcinoma from Ferguson et al 2022. The object contains 5 images.

Usage

```
data(headSCE)
```

Format

headData a SingleCellExperiment object

References

Ferguson, A. L., Sharman, A. R., Allen, R. O., Ye, T., Lee, J. H., Low, T.-H. H., Ch'ng, S., Palme, C. E., Ashford, B., Ranson, M., Clark, J. R., Patrick, E., Gupta, R., & Palendira, U. (2022). High-Dimensional and Spatial Analysis Reveals Immune Landscape–Dependent Progression in Cutaneous Squamous Cell Carcinoma. Clinical Cancer Research, OF1-OF12. ([DOI](https://doi.org/10.1158/1078-0432.Ccr-22-1332))

---

kerenImage — *MIBI-TOF Breast cancer image*

Description

This is a single MIBI-TOF image of breast cancer from patient 6 of the Keren et al 2018 dataset.

Usage

```
data(kerenImage)
```

Format

headData a SingleCellExperiment object

References

Keren, L., Bosse, M., Marquez, D., Angoshtari, R., Jain, S., Varma, S., Yang, S. R., Kurian, A., Van Valen, D., West, R., Bendall, S. C., & Angelo, M. (2018). A Structured Tumor-Immune Microenvironment in Triple Negative Breast Cancer Revealed by Multiplexed Ion Beam Imaging. Cell, 174(6), 1373-1387.e1319. ([DOI](https://doi.org/10.1016/j.cell.2018.08.039))

`Konditional` *Evaluation of pairwise cell relationships, conditional on a 3rd population.*

Description

Konditional identifies the relationship between two cell types which are conditional on the spatial behaviour of a 3rd cell population, for a particular radius (r).

Usage

```
Konditional(
  cells,
  parentDf = NULL,
  r,
  from = NULL,
  to = NULL,
  parent = NULL,
  inhom = TRUE,
  edgeCorrect = FALSE,
  window = "convex",
  window.length = NA,
  weightQuantile = 0.8,
  includeZeroCells = TRUE,
  includeOriginal = TRUE,
  spatialCoords = c("x", "y"),
  cellType = "cellType",
  imageID = "imageID",
  cores = 1
)
```

Arguments

`cells` A SingleCellExperiment, SpatialExperiment or a list of data.frames containing columns specifying the imageID, cellType, and x and y spatial coordinates.

`parentDf` A data frame from `parentCombinations`

`r` Radius to evaluated pairwise relationships between from and to cells.

`from` The first cell type to be evaluated in the pairwise relationship.

`to` The second cell type to be evaluated in the pairwise relationship.

`parent` The parent population of the from cell type (must include from cell type).

`inhom` A logical value indicating whether to account for inhomogeneity.

`edgeCorrect` A logical value indicating whether to perform edge correction.

`window` Type of window for data, either ‘square‘, ‘convex‘ or ‘concave‘, passed into `makeWindow`

`window.length` A tuning parameter for controlling the level of concavity when estimating concave windows. Passed into `makeWindow`

`weightQuantile` A decimal value indicating what quantile of parent density used to weight the ‘from‘ cells.

`includeZeroCells` A logical value indicating whether to include cells with zero counts in the pairwise association calculation.

`includeOriginal` A logical value to return the original L function values along with the konditional values.

`spatialCoords` The columns which contain the x and y spatial coordinates.

`cellType` The column which contains the cell types.

`imageID` The column which contains image identifiers.

`cores` Number of cores for parallel processing.

Value

A Koditional result object

Examples

```
# Load data
data("headSCE")

CD4_Konditional <- Konditional(
  cells = headSCE,
  r = 50,
  from = "TC_CD4",
  to = "SC5",
  parent = c("TC_CD4", "TC_CD8"),
  cores = 40
)


head(CD4_Konditional)
```

makeWindow *Creates a window for a PPP object*

Description

This function creates a window for a ‘spatstat::ppp‘ object, the type of window can be specified using the ‘window‘ argument.

Usage

```
makeWindow(data, window = "square", window.length = NULL)
```

Arguments

`data`	A single image data frame from a SingleCellExperiment object or PPP object.
`window`	The shape of window around the regions, can be ‘square‘, ‘convex‘ or ‘concave‘
`window.length`	A tuning parameter for controlling the level of concavity when estimating concave windows.

Value

Creates an ‘owin‘ class, representing the observation window for the image.

Examples

```
data <- data.frame(x = rnorm(10), y = rnorm(10))
ow <- makeWindow(data, window = "square")

spatstat.geom::ppp(x = data$x, y = data$y, window = ow)
```

parentCombinations *Create all combinations of cell type relationships from a list of parents*

Description

This function takes in named vectors of all the parent populations in the dataset, and creates a data frame containing all pairwise cell relationships, this data frame can be inputed into the ‘parentDf‘ argument in ‘Konditional‘.

Usage

```
parentCombinations(all, ...)
```

Arguments

`all` A list of all the ‘to‘ cell types Konditional is evaluated over

`...` Vectors of each parent population

Value

A data frame containing all pairwise cell relationships and their corresponding parent

Examples

```
tcells <- c("CD4", "CD8")
tissue <- c("epithelial", "stromal")
allCells <- c("tumour", tissue, tcells)

parentCombinations(all = allCells, tcells, tissue)
```

`relabelKonditional` *Cell permutation for Konditional*

Description

Function which randomises specified cells in an image and calculates the ‘Konditional‘ value. This can be used to estimate the null distribution, of the parent cell population for significance testing.

This function relabels all specified cells within a single image, to estimate the null distribution of cell population specified.

Usage

```
relabelKonditional(
  cells,
  nSim = 1,
  r,
  from,
  to,
  parent,
  returnImages = FALSE,
  inhom = TRUE,
  edge = FALSE,
  cores = 1,
  ...
)

relabel(image, labels = NULL)
```

Arguments

`cells` A single image data frame from a SingleCellExperiment object

`nSim` Number of randomisations which will be calculated.

`r` Radius to evaluated pairwise relationships between from and to cells.

`from` The first cell type to be evaluated in the pairwise relationship.

`to` The second cell type to be evaluated in the pairwise relationship.

`parent` The parent population of the from cell type (must include from cell type).

`returnImages` A logical value to indicate whether the function should return the randomised images along with the Konditional values.

`inhom` A logical value indicating whether to account for inhomogeneity.

`edge` A logical value indicating whether to perform edge correction.

`cores` Number of cores for parallel processing.

`...` Any arguments passed into `Konditional`

`image` A single image from a Single Cell Experiment object.

`labels` A vector of CellTypes labels to be permuted If NULL all cells labels will be radomised.

Value

A data frame containing Konditional value for each randomised image. If ‘returnImages = TRUE‘ function will return a list with Konditional values and the randomised images.

A data frame containing all pairwise cell relationships and their corresponding parent

Examples

```
data("kerenImage")

relabelResult <- relabelKonditional(
  cells = kerenImage,
  nSim = 5,
  r = 250,
  from = "p53",
  to = "Immune",
  parent = c("p53", "Keratin+Tumour"),
  cores = 40
)

data("kerenImage")

# Permute CD8 T cells and T cell labels in the image
relabeledImage <- relabel(kerenImage, labels = c("p53", "Keratin+Tumour"))
plot(relabeledImage)
```

`rsCurve` *Evaluation of Konditional over a range of radii.*

Description

This function obtains ‘Kondtional‘ values over a range of radii, standard deviations for each value can be obtained using permutation for significance testing. To obtain estimates for standard deviations specify ‘se = TRUE‘.

Usage

```
rsCurve(
  cells,
  from,
  to,
  parent,
  rs = seq(10, 100, 10),
  inhom = TRUE,
  edge = FALSE,
  se = FALSE,
  nSim = 20,
  cores = 1,
  ...
)
```

Arguments

`cells`	A single image data frame from a SingleCellExperiment object
`from`	The first cell type to be evaluated in the pairwise relationship.
`to`	The second cell type to be evaluated in the pairwise relationship.
`parent`	The parent population of the from cell type (must include from cell type).
`rs`	A vector of radii to evaluate konditional over.
`inhom`	A logical value indicating whether to perform an inhomogeneous L function.
`edge`	A logical value indicating whether to perform edge correction.
`se`	A logical value to indicate if the standard deviation of konditional should be calculated to construct error bars.
`nSim`	Number of randomisations to perform using `relabelKonditional`, which will be used to calculated the SE.
`cores`	Number of cores for parallel processing.
`...`	Any arguments passed into `Konditional`.

Value

A data frame of original L values and Konditional values evaluated over a range of radii.

Examples

```
data("kerenImage")

rsDf <- rsCurve(
  cells = kerenImage,
  from = "p53",
  to = "Immune",
  parent = c("p53", "Keratin+Tumour"),
  rs = seq(10, 510, 100),
  cores = 40
)
```

Index