Package ‘hoodscanR’

July 23, 2025

Title Spatial cellular neighbourhood scanning in R

Version 1.6.0

Description hoodscanR is an user-friendly R package providing functions to assist cellular neighborhood analysis of any spatial transcriptomics data with single-cell resolution. All functions in the package are built based on the SpatialExperiment object, allowing integration into various spatial transcriptomics-related packages from Bioconductor. The package can result in cell-level neighborhood annotation output, along with funtions to perform neighborhood colocalization analysis and neighborhood-based cell clustering.

biocViews Spatial, Transcriptomics, SingleCell, Clustering

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URL `https://github.com/DavisLaboratory/hoodscanR`,
`https://davislaboratory.github.io/hoodscanR/`

BugReports `https://github.com/DavisLaboratory/hoodscanR/issues`

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Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Imports knitr, rmarkdown, SpatialExperiment, SummarizedExperiment, circlize, ComplexHeatmap, scico, rlang, utils, ggplot2, grid, methods, stats, RANN, Rcpp (>= 1.0.9)

LinkingTo Rcpp

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Contents

`hoodscanR-package` *Method to identify cellular spatial neighbourhood from single cell spatial transcriptomics data.*

Description

`hoodscanR` implements a novel method to scan for cell neighbourhood from spatial transcriptomics data at single cell level, such as CosMx and MERFISH etc. `hoodscanR` takes the cellular position and cell type annotations as inputs, allowing cellular spatial neighbourhood analysis.

Details

Key neighborhood analysis functions include `findNearCells`,`scanHoods`, `mergeByGroup`, `calcMetrics`,`clustByHood`.

Key visualisation functions include `plotTissue`, `plotHoodMat`, `plotColocal`,`plotProbDist`.

Author(s)

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See Also

Useful links:

- `https://github.com/DavisLaboratory/hoodscanR`
- `https://davislaboratory.github.io/hoodscanR/`
- Report bugs at `https://github.com/DavisLaboratory/hoodscanR/issues`

`calcMetrics` *Calculate metrics for probability matrix*

Description

Calculate metrics for probability matrix

Usage

```
calcMetrics(spe, pm = NA, pm_cols = NA, val_names = c("entropy", "perplexity"))
```

Arguments

`spe`	A SpatialExperiment object.
`pm`	Optional. The probability matrix.
`pm_cols`	The colnames of probability matrix. This is requires for SpatialExperiment input. Assuming that the probability is stored in the colData.
`val_names`	Character vector with length of 2. Column names used to store calculated entropy and perplexity.

Value

A SpatialExperiment object. Calculated entropy and perplexity are saved as columns in the colData of the SpatialExperiment object. Entropy and perplexity are calculated based on information theory:

P(x) is the probability calculated from the scanHoods function.

Entropy H(x) = -P(x)log2(P(x))

Perplexity P(x) = 2^H(x)

By default, the calculated entropy and perplexity will be stored in the colData of the input spe, with column name as entropy and perplexity.

Examples

```
data("spe_test")

spe <- readHoodData(spe, anno_col = "celltypes")

fnc <- findNearCells(spe, k = 100)

pm <- scanHoods(fnc$distance)

pm2 <- mergeByGroup(pm, fnc$cells)

spe <- mergeHoodSpe(spe, pm2)

spe <- calcMetrics(spe, pm_cols = colnames(pm2))
```

`clustByHood` *Cluster the probability matrix with K-means*

Description

Cluster the probability matrix with K-means

Usage

```
clustByHood(object, ...)

## S4 method for signature 'matrix'
clustByHood(object, k = 2^ncol(object) - 1, iter_max = 1000, nstart = 5)

## S4 method for signature 'SpatialExperiment'
clustByHood(
  object,
  pm_cols,
  k = 0,
  iter_max = 1000,
  nstart = 5,
  algo = "Hartigan-Wong",
  val_name = "clusters"
)
```

Arguments

`object`	A probability matrix or a SpatialExperiment.
`...`	Ignore parameter.
`k`	The number of clusters. By default is 2^ncol(object)-1.
`iter_max`	the maximum number of iterations allowed.

`nstart`	how many random sets should be chosen.
`pm_cols`	The colnames of probability matrix. This is requires for SpatialExperiment input. Assuming that the probability is stored in the colData.
`algo`	Algorithm to be used. Options include Hartigan-Wong, Lloyd, and MacQueen.
`val_name`	Character. Column name used to store the clusters.

Value

A probability matrix or a SpatialExperiment object. For latter, the clustering results are saved in the colData of the SpatialExperiment object.

Examples

```
m <- matrix(abs(rnorm(1000 * 100)), 1000, 100)

clust <- clustByHood(m, k = 3)
```

`findNearCells` *Find the k-th nearest cells for each cell*

Description

Find the k-th nearest cells for each cell

Usage

```
findNearCells(
  dat,
  k = 100,
  targetCell = FALSE,
  reportCellID = FALSE,
  reportDist = TRUE,
  anno_col = 0
)
```

Arguments

`dat`	A SpatialExperiment object, can be generated using function `readHoodData`.
`k`	The maximum number of nearest cells to compute.
`targetCell`	Specify the cells to be the target cell for finding nearest cells.
`reportCellID`	Logical. Set to TRUE to report cell id instead of cell types.
`reportDist`	Logical. Set to TRUE to report the distance matrix.
`anno_col`	Character vector. The name of annotation column to use.

Details

The `findNearCells` function uses the `nn2` function from the `RANN` package, which uses the Approximate Near Neighbor (ANN) C++ library. For more infromation on the ANN library please see http://www.cs.umd.edu/~mount/ANN/.

Value

A list includes a data.frame and a matrix, describing the cell types and distances of the k-th nearest cells of each cell.

Examples

```
data("spe_test")

spe <- readHoodData(spe, anno_col = "celltypes")

fnc <- findNearCells(spe, k = 100)
```

`mergeByGroup` *Merge probability matrix based on annotations*

Description

Merge probability matrix based on annotations

Usage

```
mergeByGroup(pm, group_df)
```

Arguments

`pm`	A numeric matrix. Probability matrix generated by the soft_max function.
`group_df`	A character matrix. Annotation of the neighboring cells to be used.

Value

A probability matrix, describing the probability of each cell being in each cellular neighborhood.

Examples

```
data("spe_test")

spe <- readHoodData(spe, anno_col = "celltypes")

fnc <- findNearCells(spe, k = 100)

pm <- scanHoods(fnc$distance)
```

```
pm2 <- mergeByGroup(pm, fnc$cells)
```

`mergeHoodSpe` *Merge probability matrix into SpatialExperiment object.*

Description

Merge probability matrix into SpatialExperiment object.

Usage

```
mergeHoodSpe(spe, pm, val_names = NULL)
```

Arguments

`spe`	A SpatialExperiment object.
`pm`	Probability matrix. Can be obtained by the function mergeByGroup.
`val_names`	Character vector with length of the ncol of pm.

Value

A SpatialExperiment object. Cell-level neighborhood information are saved in the colData of the SpatialExperiment object.

Examples

```
data("spe_test")

spe <- readHoodData(spe, anno_col = "celltypes")

fnc <- findNearCells(spe, k = 100)

pm <- scanHoods(fnc$distance)

pm2 <- mergeByGroup(pm, fnc$cells)

spe <- mergeHoodSpe(spe, pm2)
```

`perplexityPermute` *Compute p-value for perplexity via permutation*

Description

Compute p-value for perplexity via permutation

Usage

```
perplexityPermute(spe, pm = NA, pm_cols = NA, n_perm = 1000)
```

Arguments

`spe`	A SpatialExperiment object.
`pm`	Optional. The probability matrix.
`pm_cols`	The colnames of probability matrix. This is requires for SpatialExperiment input. Assuming that the probability is stored in the colData.
`n_perm`	Integer number. The number of permutation. 1000 by default.

Value

A SpatialExperiment object. Calculated P-value and adjusted P-value are saved as columns in the colData of the SpatialExperiment object. P-value and adjusted P-value are calculated based on permutation test and Benjamini Hochberg correction.

Examples

```
data("spe_test")

spe <- readHoodData(spe, anno_col = "celltypes")

fnc <- findNearCells(spe, k = 100)

pm <- scanHoods(fnc$distance)

pm2 <- mergeByGroup(pm, fnc$cells)

spe <- mergeHoodSpe(spe, pm2)

spe <- perplexityPermute(spe, pm_cols = colnames(pm2))
```

---

plotColocal *Plot heatmap for neighbourhood analysis*

Description

Plot heatmap for neighbourhood analysis

Usage

```
plotColocal(object, ...)

## S4 method for signature 'matrix'
plotColocal(object, hm_width = 5, hm_height = 5)

## S4 method for signature 'SpatialExperiment'
plotColocal(
  object,
  pm_cols,
  self_cor = TRUE,
  by_group = NULL,
  hm_width = 5,
  hm_height = 5,
  cluster_row = TRUE,
  cluster_col = TRUE,
  return_matrix = FALSE
)
```

Arguments

`object`	A probability matrix or SpatialExperiment.
`...`	Ignore parameter.
`hm_width`	Integer. The width of heatmap.
`hm_height`	Integer. The height of heatmap.
`pm_cols`	The colnames of probability matrix. This is requires for SpatialExperiment input. Assuming that the probability is stored in the colData.
`self_cor`	Logical. By default is TRUE, inidicating running a correlation between neighbourhoods to perform a simple co-localization analysis. When this set to FALSE, it will plot the average probability of each neighbourhood by group using the by_group parameter.
`by_group`	Character. This is required when self_cor is set to FALSE.
`cluster_row`	Logical. Cluster rows.
`cluster_col`	Logical. Cluster columns.
`return_matrix`	Logical. Export a numeric matrix .

Value

A ComplexHeatmap plot. When return_matrix is set to TRUE, return a matrix Object.

Examples

```
data("spe_test")

spe <- readHoodData(spe, anno_col = "celltypes")

fnc <- findNearCells(spe, k = 100)

pm <- scanHoods(fnc$distance)

pm2 <- mergeByGroup(pm, fnc$cells)

spe <- mergeHoodSpe(spe, pm2)

plotColocal(spe, pm_cols = colnames(pm2))

plotColocal(spe, pm_cols = colnames(pm2), self_cor = FALSE, by_group = "cell_annotation")
```

`plotHoodMat` *Plot probability matrix as a heatmap*

Description

Plot probability matrix as a heatmap

Usage

```
plotHoodMat(object, ...)

## S4 method for signature 'matrix'
plotHoodMat(
  object,
  targetCells = NA,
  n = 30,
  hm_width = 4,
  hm_height = 15,
  clusterRows = TRUE,
  clusterCols = TRUE,
  title = "Probability of neighborhoods"
)

## S4 method for signature 'SpatialExperiment'
plotHoodMat(
  object,
```

```
    pm_cols,
    targetCells = NA,
    n = 30,
    hm_width = 4,
    hm_height = 15,
    clusterRows = TRUE,
    clusterCols = TRUE,
    title = "Probability of neighborhoods"
  )
```

Arguments

`object`	A probability matrix or SpatialExperiment.
`...`	Ignore parameter.
`targetCells`	Character. Optional. Can speicify one or more cells to be plotted.
`n`	Integer. The number of randomly selected cells to be plotted. This parameter will be used when targetCells is not specify.
`hm_width`	Integer. The width of heatmap.
`hm_height`	Integer. The height of heatmap.
`clusterRows`	Logical. Cluster rows or not.
`clusterCols`	Logical. Cluster columns or not.
`title`	Title of the heatmap.
`pm_cols`	The colnames of probability matrix. This is requires for SpatialExperiment input. Assuming that the probability is stored in the colData.

Value

A ComplexHeatmap plot.

Examples

```
data("spe_test")

spe <- readHoodData(spe, anno_col = "celltypes")

fnc <- findNearCells(spe, k = 100)

pm <- scanHoods(fnc$distance)

pm2 <- mergeByGroup(pm, fnc$cells)

spe <- mergeHoodSpe(spe, pm2)

plotHoodMat(spe, pm_cols = colnames(pm2))
```

`plotProbDist` *Plot probability distribution*

Description

Plot probability distribution

Usage

```
plotProbDist(object, ...)

## S4 method for signature 'matrix'
plotProbDist(object, targetCells = NA, ...)

## S4 method for signature 'SpatialExperiment'
plotProbDist(
  object,
  pm_cols,
  targetCells = NA,
  by_cluster = FALSE,
  show_clusters = as.character(seq(6)),
  plot_all = FALSE,
  sample_size = 2,
  val_name = "clusters",
  ...
)
```

Arguments

`object`	A probability matrix or SpatialExperiment.
`...`	aesthetic mappings to pass to `ggplot2::aes_string()`.
`targetCells`	Character. Optional. Can speicify one or more cells to be plotted.
`pm_cols`	The colnames of probability matrix. This is requires for SpatialExperiment input. Assuming that the probability is stored in the colData.
`by_cluster`	Logical. By default is TRUE, to plot distribution by each cluster.
`show_clusters`	Character. The cluster to be ploted, by default is 1 to 6.
`plot_all`	Logical. By default is FALSE, set this to true to plot box plot instead of bar plot to show all cells in each cluster.
`sample_size`	Integer. By default is 2, sampling two cell from each cluster to be plotted.
`val_name`	Character. Column name used to store the clusters.

Value

A ggplot object.

Examples

```
data("spe_test")

spe <- readHoodData(spe, anno_col = "celltypes")

fnc <- findNearCells(spe, k = 100)

pm <- scanHoods(fnc$distance)

pm2 <- mergeByGroup(pm, fnc$cells)

spe <- mergeHoodSpe(spe, pm2)

plotProbDist(spe, pm_cols = colnames(pm2))
```

`plotTissue` *Plot cells based on cell position on tissue.*

Description

Plot cells based on cell position on tissue.

Usage

```
plotTissue(
  spe,
  targetcell = FALSE,
  k_near = 100,
  targetsize = 3,
  targetshape = 1,
  targetcolor = "red",
  scaleFactor = 1,
  reverseY = TRUE,
  ...
)
```

Arguments

`spe`	SpatialExperiment object.
`targetcell`	Optional. Can input ONE specific cell id to zoom-in on the region of a specific cell.
`k_near`	Optional. If targetcell is specified, the k_near cells around the targetcell will be plotted.
`targetsize`	Dot size of the targetcell.
`targetshape`	Shape of the targetcell.

`targetcolor`	Colour of the targetcell.
`scaleFactor`	Scale factor to align with the image.
`reverseY`	Reverse y coordinates.
`...`	aesthetic mappings to pass to `ggplot2::aes_string()`.

Value

A ggplot object.

Examples

```
data("spe_test")

plotTissue(spe, color = celltypes)
```

`readHoodData` *Read cellular position and annotation data into a list object.*

Description

Read cellular position and annotation data into a list object.

Usage

```
readHoodData(
  spe = NA,
  anno_col = NA,
  cell_pos_dat = NA,
  cell_anno_dat = NA,
  pos_col = NA
)
```

Arguments

`spe`	SpatialExperiment object.
`anno_col`	Character. The column name of the annotation to be used in the following neighbourhood analysis.
`cell_pos_dat`	data.frame object contains the cellular positions.
`cell_anno_dat`	data.frame object contains the cell annotations.
`pos_col`	Character. If the x and y are in the colData instead of in the SpatialCoords of spe, can specify this parameter.

Value

A SpatialExperiment object.

Examples

```
data("spe_test")

spe <- readHoodData(spe, anno_col = "celltypes")
```

`scanHoods` *Scan cellular neighbourhoods.*

Description

Scan cellular neighbourhoods.

Usage

```
scanHoods(
  m,
  mode = c("proximityFocused", "smoothFadeout"),
  tau = NA,
  t_init = NA
)
```

Arguments

`m`	Distance matrix. Can be obtained from function findNearCells.
`mode`	Character. Either proximityFocused or smoothFadeout. By default is proximityFocused.
`tau`	The hyperparameter tau, by default is median(m**2)/5
`t_init`	An initial tau. In the smoothFadeout mode, user can provide an initial tau for optimization.

Value

A probability matrix.

Examples

```
m <- matrix(abs(rnorm(1000 * 100)), 1000, 100)

pm <- scanHoods(m)
```

`spe_test` *Example test spatial transcriptomics data*

Description

hoodscanR-package has 1 datasets:

- spe_test Example test spatial transcriptomics data in SpatialExperiment format. This test data is randomly subsetting from the publicly available CosMx non-small cell lung cancer data. Source data: https://nanostring.com/products/cosmx-spatial-molecular-imager/nsclc-ffpe-dataset/.

Usage

```
data("spe_test")
```

Format

A SpatialExperiment object

Value

A SpatialExperiment object

Examples

```
data(spe_test)
```

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