### Package ‘hoodscanR’

March 8, 2024

**Title**  Spatial cellular neighbourhood scanning in R

**Version**  1.0.0

**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 functions to perform neighborhood colocalization analysis and neighborhood-based cell clustering.

**biocViews**  Spatial, Transcriptomics, SingleCell, Clustering

**License**  GPL-3 + file LICENSE

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

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

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**LinkingTo**  Rcpp

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**VignetteBuilder**  knitr

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Method to identify cellular spatial neighbourhood from single cell spatial transcriptomics data.

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.

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

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

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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 required 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:

- **Entropy H(x)**: \(-P(x)\log_2(P(x))\)
- **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))
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_names = "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_names Character. Column names 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.
findNearCells

Examples

```r
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

```r
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 information 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.
mergeByGroup

*Merge probability matrix based on annotations*

**Description**

Merge probability matrix based on annotations

**Usage**

```r
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**

```r
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

```r
# Example code

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

Plot heatmap for neighbourhood analysis

Description

Plot heatmap for neighbourhood analysis
plotColocal

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 required for SpatialExperiment input. Assuming that the probability is stored in the colData.
- **self_cor**: Logical. By default is TRUE, indicating 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")

\section*{plotHoodMat}

\textit{Plot probability matrix as a heatmap}

\section*{Description}

Plot probability matrix as a heatmap.

\section*{Usage}

\begin{verbatim}
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"
)
\end{verbatim}
plotProbDist

Plot probability distribution

Description

Plot probability distribution

Arguments

object A probability matrix or SpatialExperiment.
... Ignore parameter.
targetCells Character. Optional. Can specify 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))
**Usage**

```r
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,
  ...
)
```

**Arguments**

- **object**: A probability matrix or SpatialExperiment.
- **...**: aesthetic mappings to pass to `ggplot2::aes_string()`.
- **targetCells**: Character. Optional. Can specify one or more cells to be plotted.
- **pm_cols**: The colnames of probability matrix. This is required 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 plotted, 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 cells from each cluster to be plotted.

**Value**

A ggplot object.

**Examples**

```r
data("spe_test")

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

fnc <- findNearCells(spe, k = 100)

pm <- scanHoods(fnc$distance)

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

```r
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.
- **targetssize**: 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**

```r
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**

```r
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**

```r
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
```R
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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