Package 'tomoseqr'

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Title R Package for Analyzing Tomo-seq Data

Version 1.16.0

Description `tomoseqr` is an R package for analyzing Tomo-seq data.
Tomo-seq is a genome-wide RNA tomography method that combines combining
high-throughput RNA sequencing with cryosectioning for spatially resolved transcriptomics.
`tomoseqr` reconstructs 3D expression patterns from tomo-seq data
and visualizes the reconstructed 3D expression patterns.

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`animate2d` *Animate 2D expressions along one axis and generate GIF file.*

Description

Animate 2D expressions along one axis and generate GIF file.

Usage

```
animate2d(
  tomoObj,
  geneID,
  along = "x",
  main = geneID,
  xlab = "x",
  ylab = "y",
  file = str_c(geneID, "_", along, ".gif"),
  zlim = NA,
  interval = 0.1,
  aspectX = 1,
  aspectY = 1
)
```

Arguments

tomoObj	tomoSeq object
geneID	single gene ID (string)
along	Parameter specifying along which axis the cross section should be plotted.
main	A string used for the title of the plot. Default is geneID.
xlab	Label of x axis. Default is xaxis.
ylab	Label of y axis. Default is yaxis.
file	Path of GIF file.
zlim	Limit of value of heatmap. If target="mask", it is ignored.
interval	interval of GIF animation.
aspectX	Width of figure. If you don't specify the value of this parameter, It is calculated based on the number of sections Corresponding to the horizontal axis
aspectY	Height of figure. If you don't specify the value of this parameter, It is calculated based on the number of sections Corresponding to the vertical axis

Value

It generate GIF file.

Examples

```
if(interactive()) {
    data(tomoObj)
    animate2d(tomoObj, "gene2", target = "expression", file = "example.gif")
}
```

---

doadJunker2014 *Load data of Junker2014 from cache.*

Description

Load data of Junker2014 from cache.

Usage

```
doadJunker2014(tomoseqrCache)
```

Arguments

tomoseqrCache	Cache of tomoseqr. You can get it using downloadJunker2014.

Value

List of tomo-seq data in cache.

downloadJunker2014 *Download part of the Tomo-seq data published by Junker et al.*

Description

Download part of the Tomo-seq data published by Junker et al.

Usage

```
downloadJunker2014(verbose = FALSE)
```

Arguments

verbose	If you want to force downloads with or without cache, set this to TRUE.

Value

BiocFileCache object.

estimate3dExpressions *Estimate 3d expressions*

Description

Estimate 3d expressions

Usage

```
estimate3dExpressions(x, y, z, mask, query, numIter = 100, normalize = TRUE)
```

Arguments

x	A data.frame object containing a simulated Tomo-seq data for x-axis sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.
y	A data.frame object containing a simulated Tomo-seq data for y-axis sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.
z	A data.frame object containing a simulated Tomo-seq data for z-axis sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.
mask	A 3D array that represents if each boxel is included to sample. You can make a mask using `masker`.
query	Vector of gene IDs
numIter	How many times iterate
normalize	Whether to normalize so that total expression per sample volume is equal between sections.

Value

tomoSeq object

Examples

```
data("testx", "testy", "testz", "mask")
estimate3dExpressions(
    testx,
    testy,
    testz,
    mask = mask,
    query = c("gene1"),
    normalize = TRUE
)
```

---

extractGeneList *Extract geneIDs to which hoge can be applied.*

Description

Extract geneIDs to which hoge can be applied.

Usage

```
extractGeneList(x, y, z)
```

Arguments

x	A data.frame object containing a Tomo-seq data for x-axis sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.
y	A data.frame object containing a Tomo-seq data for y-axis sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.
z	A data.frame object containing a Tomo-seq data for z-axis sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.

Value

A vector that contains genes which can be used for `estimate3dExpressions`.

Examples

```
data("testx", "testy", "testz")
extractGeneList(testx, testy, testz)
```

findAxialGenes *Find peak genes on axial*

Description

Find peak genes on axial

Usage

```
findAxialGenes(tomoSeqData, genes = "all")
```

Arguments

tomoSeqData	tomo-seq data of any axis
genes	If run for all genes

Value

A data frame consisting of gene ID, max of expression levels of the gene, mean of expression levels calculated by excluding the maximum value and section number showing the maximum expression level (0 means that there is no such section).

Examples

```
data(testx)
findAxialGenes(testx)
```

getReconstructedResult *Get reconstructed matrix*

Description

Get reconstructed matrix

Usage

```
getReconstructedResult(tomoObj, geneID)
```

Arguments

tomoObj	tomoSeq object
geneID	single gene ID

Value

Reconstruction result as matrix

Examples

```
data(tomoObj)
getReconstructedResult(tomoObj, "gene2")
```

`imageViewer` *Output the reconstructed expression pattern as an image.*

Description

Output the reconstructed expression pattern as an image.

Usage

```
imageViewer(tomoObj)
```

Arguments

`tomoObj`	tomoSeq object

Value

NA

Examples

```
if (interactive()) {
    data(tomoObj)
    imageViewer(tomoObj, "gene2")
}
```

`mask` *A matrix containing mask data.*

Description

It is a matrix representing the mask. Each element of the matrix corresponds to a voxel, and has the value 1 if the voxel is included in the mask, 0 if it is not.

masker *Make mask*

Description

Make mask

Usage

```
masker()
```

Value

NA

Examples

```
if (interactive()) {
    masker()
}
```

plot1dAllExpression *Plot expressions of all genes along an axis*

Description

Plot expressions of all genes along an axis

Usage

```
plot1dAllExpression(tomoSeqData, ...)
```

Arguments

tomoSeqData	A data.frame object containing a Tomo-seq data for any sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.
...	Arguments which are related to plot parameters. Prease refer to plot.

Value

NA

Examples

```
data("testx")
plot1dAllExpression(testx)
```

plot1dExpression *Plot expression of single gene along an axis*

Description

Plot expression of single gene along an axis

Usage

```
plot1dExpression(tomoObj, geneID, axes)
```

Arguments

tomoObj	tomoSeq object
geneID	single gene ID (string)
axes	axis ("x", "y" or "z")

Value

NA

Examples

```
data(tomoObj)
plot1dExpression(tomoObj, "gene2", "x")
```

plotLossFunction *Plot the trend of the value of the loss function.*

Description

Plot the trend of the value of the loss function.

Usage

```
plotLossFunction(tomoObj, geneID)
```

Arguments

tomoObj	tomoSeq object
geneID	single gene ID (string)

Value

NA

Examples

```
data(tomoObj)
plotLossFunction(tomoObj, "gene2")
```

`testx` *A data.frame object containing a simulated Tomo-seq data for x-axis sections.*

Description

A data.frame object containing a simulated Tomo-seq data for x-axis sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.

`testy` *A data.frame object containing a simulated Tomo-seq data for y-axis sections.*

Description

A data.frame object containing a simulated Tomo-seq data for y-axis sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.

`testz` *A data.frame object containing a simulated Tomo-seq data for z-axis sections.*

Description

A data.frame object containing a simulated Tomo-seq data for z-axis sections. The rows represent genes. The first column contains gene IDs and the second and subsequent columns contain gene expression levels in sections.

toDataFrame *Convert reconstructed matrix to data.frame.*

Description

Convert reconstructed matrix to data.frame.

Usage

```
toDataFrame(tomoObj, geneID)
```

Arguments

tomoObj	tomoSeq object
geneID	single gene ID

Value

Reconstruction result converted to dataframe.

Examples

```
data(tomoObj)
toDataFrame(tomoObj, "gene2")
```

tomoObj *A tomoSeq object.*

Description

It is a tomoSeq object generated from testx, testy, testz and mask.

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