

Package ‘scBin’

March 25, 2019

Type Package

Title scBin: single-cell RNA-seq Data Plotter and Binarizer

Version 0.1.0

Date 2019-03-25

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Description Plots single-cell RNA-seq flow marker gene counts and binarizes data using a cutoff.

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NeedsCompilation no

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scBinarizer	<i>Binarize count matrix using a cutoff</i>
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Description

Replace counts greater than cutoff with 1, and counts less than or equal to cutoff with 0.

Usage

```
scBinarizer(x, cutoff = 0)
```

Arguments

x	count matrix. Rows: samples (cells). Columns: features (genes).
cutoff	numeric. The applied cutoff.

Value

Binarized count matrix.

Author(s)

Peter Vegh

scPlot

Plot protein vs gene expression

Description

Plots protein expression for specified marker genes and calculates a count cutoff for expression, a confusion matrix, and generates a plot.

Usage

```
scPlot(x, meta, markers, tnr = 0.95, jitter = F)
```

Arguments

x	count matrix. Rows: samples (cells). Columns: features (genes).
meta	metadata dataframe, where one of the columns is a binary vector of flow (protein) sorting bins. Count and metadata cells must be the same and in the same order.
markers	list of vectors of length 2. The first element of each vector is a marker gene column name in 'x', the second element is the matching marker protein name in 'meta'. This column of 'meta' must contain only 0 and 1.
tnr	desired true negative rate of nonzero counts.
jitter	jitters the dots on the plot if set TRUE.

Value

List of three:

cutoff	the calculated cutoff for given specificity for nonzero counts
confusion	confusion matrix of all values after applying the cutoff
plots	the saved plots of protein expression vs gene count

Author(s)

Peter Vegh