R documentation

of 'barPlotCellTypes.Rd'

September 3, 2020

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barPlotCellTypes *Plot a bar plot with deconvoluted cell type proportions.*

Description

This function allows to plot a bar plot with the deconvoluted cell type proportions of a given bulk RNA-seq sample using ggplot2.

Usage

```
barPlotCellTypes(
  data,
  colors,
  simplify = NULL,
  color.line = NA,
  x.label = "Bulk samples",
  rm.x.text = FALSE,
  title = "Results of deconvolution",
  legend.title = "Cell types",
  angle = 90,
  ...
)

## S4 method for signature 'DigitalDLSorter'
barPlotCellTypes(
  data,
  colors = NULL,
  name.data = NULL,
  simplify = NULL,
  color.line = NA,
  x.label = "Bulk samples",
  rm.x.text = FALSE,
  title = "Results of deconvolution",
  legend.title = "Cell types",
  angle = 90
)
```

```
## S4 method for signature 'ANY'
barPlotCellTypes(
  data,
  colors,
  color.line = NA,
  x.label = "Bulk samples",
  rm.x.text = FALSE,
  title = "Results of deconvolution",
  legend.title = "Cell types",
  angle = 90
)
```

Arguments

`data`	`DigitalDLSorter` object with `deconv.results` slot or `data.frame`/`matrix` with cell types as columns and samples as rows.
`colors`	Vector with colors that will be used.
`color.line`	Color of border bars.
`x.label`	Label of x axis.
`rm.x.text`	Logical value indicating if remove x axis ticks (names of samples).
`title`	Title of plot.
`legend.title`	Title of legend plot.
`angle`	Angle of text ticks.
`name.data`	If a DigitalDLSorter is given, name of the element that stores the results in `deconv.results` slot. If not, forget it.
`simplified`	Vector with cell types that will be compressed into the cell type with more probability in each sample by majority voting. This option is intended for cases with exclusive cell types that they have not sense that appear in the same sample.

See Also

`deconvDigitalDLSorter` `deconvDigitalDLSorterObj`

Examples

```
## Using a matrix
barPlotCellTypes(deconvResults)

## Using a DigitalDLSorter object
barPlotCellTypes(DDLS.Chung)
```

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