Package ‘scatterHatch’

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Title  Creates hatched patterns for scatterplots
Version  1.8.0
Description  The objective of this package is to efficiently create scatterplots
where groups can be distinguished by color and texture. Visualizations in computational biology tend to have many groups
making it difficult to distinguish between groups solely on color.
Thus, this package is useful for increasing the accessibility of scatterplot visualizations to those with visual impairments such as
color blindness.
License  MIT + file LICENSE
BugReports  https://github.com/FertigLab/scatterHatch/issues
Encoding  UTF-8
LazyData  false
Roxygen  list(markdown = TRUE)
RoxygenNote  7.1.1
VignetteBuilder  knitr
Suggests  knitr, rmarkdown, testthat
Imports  grid, ggplot2, plyr, spatstat.geom, stats, grDevices
Depends  R (>= 4.1)
biocViews  Visualization, SingleCell, CellBiology, Software, Spatial
URL  https://github.com/FertigLab/scatterHatch
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Author  Atul Deshpande [aut, cre] (<https://orcid.org/0000-0001-5144-6924>)
Maintainer  Atul Deshpande <adeshpande@jhu.edu>
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pdacData  
*Tissue-CyCIF data of Pancreatic Ductal Adenocarcinoma (PDAC)*

Description

Single-cell resolution of 4 cellular compartments in a human Pancreatic Ductal Adenocarcinoma sample that spans across three distinct tissues: the pancreas, small intestine, and tumor. Contains cartesian coordinates of each cell along with the frame it was identified from in t-CyCIF imaging.

Usage

data(pdacData)

Format

A data frame with 158159 rows and 3 variables:

frame  10x frame from t-CyCIF imaging. Used to identify tissue type of cell.
Xt  Cartesian x-coordinate of cell across entire tissue sample (across all frames).
Yt  Cartesian y-coordinate of cell across entire tissue sample (across all frames)

Source

Shortened version of t-CyCIF single-cell data of Pancreatic Ductal Adenocarcinoma (PDAC) resection specimen from *Lin et. al* with only the cartesian coordinates and frames each cell is in present.

Entire dataset can be downloaded from [http://lincs.hms.harvard.edu/wordpress/wp-content/uploads/2017/05/rawdata_Figure78_PDAC.zip](http://lincs.hms.harvard.edu/wordpress/wp-content/uploads/2017/05/rawdata_Figure78_PDAC.zip)

References

Lin et al. (2018) eLife 2018;7:e31657 (*eLife*)
scatterHatch

Creates a scatterplot with hatched patterns.

Description
This function creates a scatterplot with hatched patterns by using geom_segment(). Also creates the legend to represent each hatched group. The aesthetics defining each pattern, like the lineType and lineColor are all passed to geom_segment().

Usage
scatterHatch(
  data,
  x,
  y,
  color_by,
  legendTitle = "",
  pointSize = 1,
  pointAlpha = 0.5,
  gridSize = NULL,
  sparsePoints = NULL,
  patternList = NULL,
  colorPalette = NULL
)

Arguments
data Dataset to be used
x Column name of x-coordinates
y Column name of y-coordinates
color_by Column name of factor that defines groupings
legendTitle Title of the legend
pointSize Point size for the scatterplot
pointAlpha Transparency of points in the scatterplot
gridSize Controls the precision of the hatched pattern. Larger values correspond to greater precision. Default follows a exponential decay function based on point size.
sparsePoints Logical Vector denoting points annotated as sparse. If NULL, default sparsity detector will be used to annotate sparse points.
patternList Aesthetics to be passed for each pattern (must be a list where each element has a named pattern)
colorPalette Colors to be used for each group. Default is color-blind friendly.

Value
ggplot2 object of scatterplot with hatched patterns for each group.
Examples

```r
data(pdacData)
scatterHatch(pdacData, "Xt", "Yt", "frame")
```
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