Package ‘CytoSimplex’

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Type Package

Title Simplex Visualization of Cell Fate Similarity in Single-Cell Data

Version 0.1.1

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Description Create simplex plots to visualize the similarity between single-cells and selected clusters in a 1-/2-/3-simplex space. Velocity information can be added as an additional layer. See Liu J, Wang Y et al (2023) <doi:10.1101/2023.12.07.570655> for more details.


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colNormalize Normalize each column of the input matrix by the column sum

Description

Normalize each column of the input matrix by the column sum

Usage

colNormalize(x, scaleFactor = NULL, log = FALSE, ...)

## Default S3 method:
colNormalize(x, scaleFactor = NULL, log = FALSE, ...)

## S3 method for class 'dgCMatrix'
colNormalize(x, scaleFactor = NULL, log = FALSE, ...)

## S3 method for class 'Seurat'
colNormalize(
  x,
  scaleFactor = NULL,
  log = FALSE,
  assay = NULL,
  layer = "counts",
  ...)

## S3 method for class 'SingleCellExperiment'
colNormalize(x, scaleFactor = NULL, log = FALSE, assay.type = "counts", ...)
**plotBinary**

Arguments

- **x**: Feature by observation matrix. Alternatively, Seurat object or SingleCellExperiment object with raw counts available are also supported.

- **scaleFactor**: Multiplier on normalized data. Default NULL.

- **log**: Logical. Whether to take log1p transformation after scaling. Default FALSE

- **assay**: For "Seurat" method, the specific assay to get data from. Default NULL to the default assay.

- **layer**: For "Seurat" method, which layer of the assay to be used. Default "counts".

- **assay.type**: For "SingleCellExperiment" method, the assay type to get data from. Default "counts".

Value

Normalized matrix of the same size

- A Seurat object with normalized data in the specified slot of the specified assay.

- A SingleCellExperiment object with normalized data in the specified assay. "normcounts" if log = FALSE and "logcounts" if log = TRUE.

Examples

```r
rnaNorm <- colNormalize(rnaRaw)

# Seurat example
library(Seurat)
srt <- CreateSeuratObject(rnaRaw)
srt <- colNormalize(srt)

# SingleCellExperiment example
library(SingleCellExperiment)
sce <- SingleCellExperiment(assays = list(counts = rnaRaw))
sce <- colNormalize(sce)
```

---

**plotBinary**

Create binary plots

Description

Create binary plots that show similarity between single cells and two selected terminals in a barycentric coordinate. The two vertices are placed at the left and right of a 2D plot where x-axis measures the similarity. Y-axis is jittered for a clear view. A density (histogram) curve is added for indicating the distribution.

See plotTernary manual for more details.
Usage

plotBinary(x, ...)

## Default S3 method:
plotBinary(
  x,
  clusterVar,
  vertices,
  features = NULL,
  byCluster = NULL,
  processed = FALSE,
  method = c("euclidean", "cosine", "pearson", "spearman"),
  force = FALSE,
  sigma = 0.08,
  scale = TRUE,
  dotColor = "grey60",
  returnData = FALSE,
  ...
)

## S3 method for class 'Seurat'
plotBinary(
  x,
  layer = "counts",
  assay = NULL,
  clusterVar = NULL,
  processed = FALSE,
  ...
)

## S3 method for class 'SingleCellExperiment'
plotBinary(x, assay.type = "counts", clusterVar = NULL, processed = FALSE, ...)

## S3 method for class 'simMat'
plotBinary(
  x,
  dotSize = 0.6,
  dotColor = "grey60",
  densLinewidth = 0.8,
  labelColors = c("#3B4992FF", "#EE0000FF"),
  title = NULL,
  ...
)

Arguments

x Input data. Can be a matrix or dgCMatrix object with cells as columns, a Seurat or SingleCellExperiment object. "simMat" method takes intermedi-
... Arguments passed to other methods.

clusterVar A vector/factor assigning the cluster variable to each column of the matrix object. For "Seurat" method, NULL (default) for Idents(x), or a variable name in meta.data slot. For "SingleCellExperiment" method, NULL (default) for colLabels(x), or a variable name in colData slot.

vertices Vector of three unique cluster names that will be used for plotting. Or a named list that groups clusters as three terminal vertices. There must not be any overlap between groups.

features Valid matrix row subsetting index to select features for similarity calculation. Default NULL uses all available features.

byCluster Default NULL to generate one plot with all cells. Set "all" to split cells in plot by cluster and returns a list of subplots for each cluster as well as the plot including all cells. Otherwise, a vector of cluster names to generate a list of subplots for the specified clusters.

processed Logical. Whether the input matrix is already processed. TRUE will bypass internal preprocessing and input matrix will be directly used for similarity calculation. Default FALSE and raw count input is recommended. If missing in call, using slot = "counts" in "Seurat" method or using assay.type = "counts" in "SingleCellExperiment" method will force this argument to be FALSE and others for TRUE.

method Similarity calculation method. Default "euclidean". Choose from "euclidean", "cosine", "pearson", "spearman".

force Whether to force calculate the similarity when more than 500 features are detected, which is generally not recommended. Default FALSE.

sigma Gaussian kernel parameter that controls the effect of variance. Only effective when using a distance metric (i.e. method is "euclidian" or "cosine"). Larger value tighten the dot spreading on figure. Default 0.08.

scale Whether to min-max scale the distance matrix by clusters. Default TRUE.

returnData Logical. Whether to return similarity data instead of generating plot. Default FALSE.

layer For "Seurat" method, which layer of the assay to be used. Default "counts".

assay For "Seurat" method, the specific assay to get data from. Default NULL to the default assay.

assay.type For "SingleCellExperiment" methods. Which assay to use for calculating the similarity. Default "counts".

dotSize, dotColor Dot aesthetics passed to geom_point. Default 0.6 and "grey60".

densLinewidth Density plot line aesthetic. Default 0.8.

labelColors Color of the axis lines and vertex labels. Default c("#3B4992FF", "#EE0000FF") (blue and red).

title Title text of the plot. Default NULL.
plotQuaternary

Value

For 'simMat' method, a ggplot object. For other methods, a ggplot object when splitCluster = FALSE, or a list of ggplot objects when splitCluster = TRUE.

Examples

gene <- selectTopFeatures(rnaRaw, rnaCluster, c("RE", "OS"))
plotBinary(rnaRaw, rnaCluster, c("RE", "OS"), gene)

# Seurat example
library(Seurat)
srt <- CreateSeuratObject(rnaRaw)
Idents(srt) <- rnaCluster
gene <- selectTopFeatures(srt, vertices = c("OS", "RE"))
plotBinary(srt, features = gene, vertices = c("OS", "RE"))

# SingleCellExperiment example
library(SingleCellExperiment)
sce <- SingleCellExperiment(assays = list(counts = rnaRaw))
colLabels(sce) <- rnaCluster
gene <- selectTopFeatures(sce, vertices = c("OS", "RE"))
plotBinary(sce, features = gene, vertices = c("OS", "RE"))

plotQuaternary

Create quaternary simplex plots

Description

Create quaternary plots that show similarity between single cells and selected four terminals in a baricentric coordinate.

See plotTernary for more details on methodologies.

A dynamic rotating view in a GIF image file can be created with writeQuaternaryGIF. Package magick must be installed in advance. Linux users may refer to this installation guide.

Usage

plotQuaternary(x, ...)

## Default S3 method:
plotQuaternary(
  x,
  clusterVar,
  vertices,
  features = NULL,
  veloGraph = NULL,
plotQuaternary

byCluster = NULL,
processed = FALSE,
method = c("euclidean", "cosine", "pearson", "spearman"),
force = FALSE,
sigma = 0.05,
scale = TRUE,
dotColor = "grey60",
returnData = FALSE,
...

## S3 method for class 'Seurat'
plotQuaternary(
  x,
  layer = "counts",
  assay = NULL,
  clusterVar = NULL,
  processed = FALSE,
  ...
)

## S3 method for class 'SingleCellExperiment'
plotQuaternary(
  x,
  assay.type = "counts",
  clusterVar = NULL,
  processed = FALSE,
  ...
)

## S3 method for class 'simMat'
plotQuaternary(
  x,
  veloMat = NULL,
nGrid = 10,
radius = 0.2,
dotSize = 0.6,
dotColor = "grey60",
labelColors = c("#3B4992FF", "#EE0000FF", "#008B45FF", "#631879FF"),
arrowLinewidth = 0.6,
arrowAngle = 20,
arrowLen = 0.1,
vertexLabelSize = 1,
edgeLinewidth = 1,
title = NULL,
titleSize = 1,
tintColor = "black",
theta = 20,
plotQuaternary

phi = 0,
interactive = FALSE,
...
)

Arguments

x  Input data. Can be a matrix or dgCMatrix object with cells as columns, a Seurat or SingleCellExperiment object. "simMat" method takes intermediate values.

...  Arguments passed to other methods.

classVar  A vector/factor assigning the cluster variable to each column of the matrix object. For "Seurat" method, NULL (default) for Idents(x), or a variable name in meta.data slot. For "SingleCellExperiment" method, NULL (default) for colLabels(x), or a variable name in colData slot.

vertices  Vector of three unique cluster names that will be used for plotting. Or a named list that groups clusters as three terminal vertices. There must not be any overlap between groups.

features  Valid matrix row subsetting index to select features for similarity calculation. Default NULL uses all available features.

veloGraph  Cell x cell dgCMatrix object containing velocity information. Shows velocity grid-arrow layer when specified. Default NULL does not show velocity.

byCluster  Default NULL to generate one plot with all cells. Set "all" to split cells in plot by cluster and returns a list of subplots for each cluster as well as the plot including all cells. Otherwise, a vector of cluster names to generate a list of subplots for the specified clusters.

processed  Logical. Whether the input matrix is already processed. TRUE will bypass internal preprocessing and input matrix will be directly used for similarity calculation. Default FALSE and raw count input is recommended. If missing in call, using slot = "counts" in "Seurat" method or using assay.type = "counts" in "SingleCellExperiment" method will force this argument to be FALSE and others for TRUE.

method  Similarity calculation method. Default "euclidean". Choose from "euclidean", "cosine", "pearson", "spearman".

force  Whether to force calculate the similarity when more then 500 features are detected, which is generally not recommended. Default FALSE.

sigma  Gaussian kernel parameter that controls the effect of variance. Only effective when using a distance metric (i.e. method is "euclidian" or "cosine"). Larger values tighten the dot spreading on figure. Default 0.05.

scale  Whether to min-max scale the distance matrix by clusters. Default TRUE.

returnData  Logical. Whether to return similarity and aggregated velocity data if applicable instead of generating plot. Default FALSE.

layer  For "Seurat" method, which layer of the assay to be used. Default "counts".

assay  For "Seurat" method, the specific assay to get data from. Default NULL to the default assay.
assay.type

For "SingleCellExperiment" methods. Which assay to use for calculating the similarity. Default "counts".

veloMat

Aggregated velocity matrix. Output of aggrVeloGraph.

nGrid

Number of grids along the x-axis of the tetrahedron triangle. Default 10.

radius

Arrow length of unit velocity. Lower this when arrows point outside of the tetrahedron. Default 0.2.

dotSize, dotColor

Dot aesthetics. Default 0.6 and "grey60".

labelColors

Colors of the vertex labels. Default c("#3B4992FF", "#EE0000FF", "#008B45FF", "#631879FF") (blue, red, green and purple).

arrowLinewidth

Arrow aesthetics. Default 0.6.

arrowAngle, arrowLen

Arrow aesthetics passed to grid::arrow. The length of the arrow will be internally converted to unit object in inches. Default 20 and 0.1.

vertexLabelSize

Numeric, size of vertex text label relative to default size. Default 1.

dotSize, dotColor

Dot aesthetics. Default 0.6 and "grey60".

labelColors

Colors of the vertex labels. Default c("#3B4992FF", "#EE0000FF", "#008B45FF", "#631879FF") (blue, red, green and purple).

arrowLinewidth

Arrow aesthetics. Default 0.6.

arrowAngle, arrowLen

Arrow aesthetics passed to grid::arrow. The length of the arrow will be internally converted to unit object in inches. Default 20 and 0.1.

vertexLabelSize

Numeric, size of vertex text label relative to default size. Default 1.

edgeLinewidth

Controls the linewidth of the edges of the tetrahedron. Default 1.

title

Title text of the plot. Default NULL.

titleSize, titleColor

Setting on the main title text. Default 1, and "black".

theta, phi

Numeric scalar. The angles defining the viewing direction. theta gives the azimuthal direction and phi the colatitude. Default 20 and 0.

interactive

Logical. Whether to use "rgl" library to create interactive device. Default FALSE.

Value

For "simMat" method, a "plist" (plot3D package product) object. For other methods, a "plist" object when splitCluster = FALSE, or a list of "plist" objects when splitCluster = TRUE. A "plist" object can be viewed with print(), show() or a direct run of the object variable name in interactive console.

Examples

gene <- selectTopFeatures(rnaRaw, rnaCluster, c("RE", "OS", "CH", "ORT"))
plotQuaternary(rnaRaw, rnaCluster, c("RE", "OS", "CH", "ORT"), gene)

# Seurat example
library(Seurat)
srt <- CreateSeuratObject(rnaRaw)
Idsents(srt) <- rnaCluster
gene <- selectTopFeatures(srt, vertices = c("OS", "RE", "CH", "ORT"))
plotQuaternary(srt, features = gene,
vertices = c("OS", "RE", "CH", "ORT"))

# SingleCellExperiment example
library(SingleCellExperiment)
plotTernary

Create ternary plots

Description

Create ternary plots that show similarity between single cells and selected three terminals in a ternary baricentric coordinate.

Usage

plotTernary(x, ...)

## Default S3 method:
plotTernary(
  x,
  clusterVar,
  vertices,
  features = NULL,
  veloGraph = NULL,
  byCluster = NULL,
  processed = FALSE,
  method = c("euclidean", "cosine", "pearson", "spearman"),
  force = FALSE,
  sigma = 0.08,
  scale = TRUE,
  dotColor = "grey60",
  returnData = FALSE,
  ...
)

## S3 method for class 'Seurat'
plotTernary(
  x,
  layer = "counts",
  assay = NULL,
  clusterVar = NULL,
  processed = FALSE,
  ...
)
## S3 method for class 'SingleCellExperiment'
plotTernary(
  x,
  assay.type = "counts",
  clusterVar = NULL,
  processed = FALSE,
  ...
)

## S3 method for class 'simMat'
plotTernary(
  x,
  title = NULL,
  veloMat = NULL,
  nGrid = 10,
  radius = 0.1,
  dotSize = 0.6,
  dotColor = "grey60",
  labelColors = c("#3B4992FF", "#EE0000FF", "#008B45FF"),
  vertexLabelSize = 5,
  vertexLabelDrift = 0.03,
  axisBreak = 5,
  axisTextShow = TRUE,
  axisTextSize = 4,
  axisTextDrift = 0.02,
  gridLineAlpha = 0.6,
  arrowLinewidth = 0.25,
  arrowAngle = 20,
  arrowLen = 0.2,
  titleSize = 14,
  equilateral = TRUE,
  margin = 0.1,
  ...
)

### Arguments

**x**
Input data. Can be a matrix or dgCMatrix object with cells as columns, a Seurat or SingleCellExperiment object. "simMat" method takes intermediate values.

**...**
Arguments passed to other methods.

**clusterVar**
A vector/factor assigning the cluster variable to each column of the matrix object. For "Seurat" method, NULL (default) for Idents(x), or a variable name in meta.data slot. For "SingleCellExperiment" method, NULL (default) for colLabels(x), or a variable name in colData slot.

**vertices**
Vector of three unique cluster names that will be used for plotting. Or a named list that groups clusters as three terminal vertices. There must not be any overlap between groups.
features Valid matrix row subsetting index to select features for similarity calculation. Default NULL uses all available features.

veloGraph Cell x cell dgCMatrix object containing velocity information. Shows velocity grid-arrow layer when specified. Default NULL does not show velocity.

byCluster Default NULL to generate one plot with all cells. Set "all" to split cells in plot by cluster and returns a list of subplots for each cluster as well as the plot including all cells. Otherwise, a vector of cluster names to generate a list of subplots for the specified clusters.

processed Logical. Whether the input matrix is already processed. TRUE will bypass internal preprocessing and input matrix will be directly used for similarity calculation. Default FALSE and raw count input is recommended. If missing in call, using slot = "counts" in "Seurat" method or using assay.type = "counts" in "SingleCellExperiment" method will force this argument to be FALSE and others for TRUE.

method Similarity calculation method. Default "euclidean". Choose from "euclidean", "cosine", "pearson", "spearman".

force Whether to force calculate the similarity when more then 500 features are detected, which is generally not recommended. Default FALSE.

sigma Gaussian kernel parameter that controls the effect of variance. Only effective when using a distance metric (i.e. method is "euclidean" or "cosine"). Larger values tighten the dot spreading on figure. Default 0.08.

scale Whether to min-max scale the distance matrix by clusters. Default TRUE.

returnData Logical. Whether to return similarity and aggregated velocity data if applicable instead of generating plot. Default FALSE.

layer For "Seurat" method, which layer of the assay to be used. Default "counts".

assay For "Seurat" method, the specific assay to get data from. Default NULL to the default assay.

assay.type For "SingleCellExperiment" methods. Which assay to use for calculating the similarity. Default "counts".

title Title text of the plot. Default NULL.

veloMat Aggregated velocity matrix. Output of aggrVeloGraph.

nGrid Number of grids along the bottom side of the equilateral triangle. Default 10.

radius Arrow length of unit velocity. Lower this when arrows point outside of the coordinate. Default 0.1.

dotSize, dotColor Dot aesthetics passed to geom_point. Default 0.6 and "grey60".

labelColors Colors of the axis lines and vertex labels. Default c("#3B4992FF", "#EE0000FF", "#008B45FF") (blue, red and green)

vertexLabelSize, vertexLabelDrift Adjustment on the three vertex text labels. Drift means the distance that the labels should be moved against the center of the plot. Default size 5, drifted distance 0.03.

axisBreak Number of breaks to be labeled along axis. Default 5.
axisTextShow Logical, whether to show axis text. Default TRUE.
axisTextSize, axisTextDrift
  Similar to the vertex adjustment applied to the text label along the axis breaks.
  Default size 4, drifted distance 0.02.
gridLineAlpha Transparency of background grid lines. Default 0.6.
arErrLinewidth, arrowAngle, arrowLen
  Arrow aesthetics, see Details.
titleSize Size of title text. Default 14.
equilateral Logical, whether to always display the triangle as equilateral. Default TRUE.
margin Margin allowed around of the triangle plotting region when equilateral = TRUE

Details

Argument inheritance - For matrix/dgCMatrix ("default" method), we first calculate the similarity matrix and obtain a "simMat" object. Then the "simMat" method is internally called. For data container objects (e.g. Seurat), we obtain the correct data matrix first and then call the "default" method. The arguments inherits as the flow described above.

The calculation of similarity matrix - The similarity is calculated either by converting a distance metric ("euclidean" or "cosine") with Gaussian kernel, or directly computed with correlation metrics ("pearson" or "spearman"). The centroid of each terminal is obtained first, and the specified metric from each cell to each terminal is calculated. The similarity matrix (n cells by v terminals) is lastly normalized to sum to 1 for each cell, so it becomes a baricentric coordinate.

Arrow aesthetics parameters - The shape of arrows is controlled by 3 arguments. Considering an arrow as the combination of a line segment and a triangle, arrowLinewidth controls the width of the line as well as the edge line of the triangle; arrowAngle equals to angle of the arrow-tip vertex of the triangle devided by 2 (e.g. the triangle is equilateral when arrowAngle = 20); arrowLen controls the absolute length from the arrow-tip vertex to its opposite edge.

Value

For "simMat" method, a ggplot object. For other methods, a ggplot object when splitCluster = FALSE, or a list of ggplot objects when splitCluster = TRUE.

Examples

gene <- selectTopFeatures(rnaRaw, rnaCluster, c("OS", "RE", "CH"))
plotTernary(rnaRaw, rnaCluster, c("OS", "RE", "CH"), gene)

# Seurat example
library(Seurat)
srt <- CreateSeuratObject(rnaRaw)
Idents(srt) <- rnaCluster
gene <- selectTopFeatures(srt, vertices = c("OS", "RE", "CH"))
plotTernary(srt, features = gene, vertices = c("OS", "RE", "CH"))

# SingleCellExperiment example
library(SingleCellExperiment)
sce <- SingleCellExperiment(assays = list(counts = rnaRaw))
collLabels(sce) <- rnaCluster
gene <- selectTopFeatures(sce, vertices = c("OS", "RE", "CH"))
plotTernary(sce, features = gene, vertices = c("OS", "RE", "CH"))

**rnaCluster**

*Major cell type annotation of the example mouse bone marrow data*

**Description**

Major cell type annotation of the example mouse bone marrow data

**Usage**

rnaCluster

**Format**

factor object

**Source**

https://www.nature.com/articles/s41467-023-38034-2

**References**


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**rnaRaw**

*Mouse bone marrow scRNAseq example data*

**Description**

Mouse bone marrow scRNAseq example data

**Usage**

rnaRaw

**Format**

dgCMatrix object
**Source**
https://www.nature.com/articles/s41467-023-38034-2

**References**

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**rnaVelo**

*Velocity graph of the example mouse bone marrow data*

**Description**

Velocity graph of the example mouse bone marrow data

**Usage**

rnaVelo

**Format**

dgCMatrix object

**Source**
https://www.nature.com/articles/s41467-023-38034-2

**References**

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**selectTopFeatures**

*Pick top differentially presented features for similarity calculation*

**Description**

Performs wilcoxon rank-sum test on input matrix. While `clusterVar` and `vertices` together defines the groups of cells to be set as terminals of the simplex, this function will test each of these groups against the rest of the cells. The U-Statistics (statistic), p-value (pval) and adjusted p-value (padj), together with average presence in group (avgExpr), log fold-change (logFC), AUC (auc), percentage in group (pct_in) and percentage out of group (pct_out) will be calculated. Set `returnStats = TRUE` to return the full statistics table.

Top features are selected by sorting primarily on adjusted p-value, and secondarily on log fold-change, after filtering for up-regulated features.
Usage

`selectTopFeatures(x, clusterVar, vertices, ...)`

```r
# Default S3 method:
selectTopFeatures(
  x,
  clusterVar,
  vertices,
  nTop = 30,
  processed = FALSE,
  lfcThresh = 0.1,
  returnStats = FALSE,
  ...
)
```

```r
# S3 method for class 'Seurat'
selectTopFeatures(
  x,
  clusterVar = NULL,
  vertices,
  assay = NULL,
  layer = "counts",
  processed = FALSE,
  ...
)
```

```r
# S3 method for class 'SingleCellExperiment'
selectTopFeatures(
  x,
  clusterVar = NULL,
  vertices,
  assay.type = "counts",
  processed = FALSE,
  ...
)
```

Arguments

- **x**: Dense or sparse matrix, observation per column. Preferably a raw count matrix. Alternatively, a Seurat object or a SingleCellExperiment object.
- **clusterVar**: A vector/factor assigning the cluster variable to each column of the matrix object. For "Seurat" method, NULL (default) for Idents(x), or a variable name in meta.data slot. For "SingleCellExperiment" method, NULL (default) for colLabels(x), or a variable name in colData slot.
- **vertices**: Vector of cluster names that will be used for plotting. Or a named list that groups clusters as a terminal vertex. There must not be any overlap between groups.
- **nTop**: Number of top features to return. Default: 30.
- **processed**: Logical. Whether to use processed data. Default: FALSE.
- **lfcThresh**: Log fold change threshold. Default: 0.1.
- **returnStats**: Logical. Whether to return statistics. Default: FALSE.
- **...**: Additional arguments passed to methods.
show.plist-method

Description

Show plist object produced with plot3D package

Usage

```
## S4 method for signature 'plist'
show(object)

## S3 method for class 'plist'
print(x, ...)
```
writeQuaternaryGIF

Arguments

object, x   plist object
...
Graphic parameters passed to plot. mar is pre-specified.

Value

No return value. It displays the plot described in a 'plist' object returned by plotQuaternary, internally created by package 'plot3D'.

Examples

gene <- selectTopFeatures(rnaRaw, rnaCluster, c("RE", "OS", "CH", "ORT"))
plistObj <- plotQuaternary(rnaRaw, rnaCluster, c("RE", "OS", "CH", "ORT"), gene)
print(plistObj)
# equivalent to
show(plistObj)

writeQuaternaryGIF Create GIF image for dynamic rotating view of 3D quaternary simplex plot

Description

Create GIF image for dynamic rotating view of 3D quaternary simplex plot

Usage

writeQuaternaryGIF(
  x,
  ..., cluster = NULL,
  gifPath = "quaternary.gif",
  tmpDir = tempdir(),
  fps = 10,
  degreePerFrame = 10
)

Arguments

x      Input object that plotQuaternary accepts.
...
All other arguments needed for plotQuaternary. Must be specified with exact argument names instead of a positional manner.
cluster    One cluster that exists in clusterVar, if users need to view the plot for specific group. Default NULL plot all cells.
gifPath    Output GIF image file path. Default "quaternary.gif"
writeQuaternaryGIF

- **tmpDir**: A temporary directory to store all PNG files for all perspectives created. Default tempdir().
- **fps**: Number of frame per second, must be a factor of 100. Default 10.
- **degreePerFrame**: Number of degree that the tetrahedron is rotated per frame. Default 10.

**Value**

No object is returned. The tmpDir folder will be created with $360 / \text{degreePerFrame}$ PNG image files in it. A GIF image file will be created at gifPath.

**Examples**

```r
gene <- selectTopFeatures(rnaRaw, rnaCluster, c("RE", "OS", "CH", "ORT"))
writeQuaternaryGIF(rnaRaw, clusterVar = rnaCluster, features = gene,
vertices = c("RE", "OS", "CH", "ORT"),
gifPath = paste0(tempfile(), ".gif"))
```
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