Package 'traviz'

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Type Package

Title Trajectory functions for visualization and interpretation.

Version 1.10.0

Description traviz provides a suite of functions to plot trajectory related objects from Bioconductor packages. It allows plotting trajectories in reduced dimension, as well as averge gene expression smoothers as a function of pseudotime. Asides from general utility functions, traviz also allows plotting trajectories estimated by Slingshot, as well as smoothers estimated by tradeSeq. Furthermore, it allows for visualization of Slingshot trajectories using ggplot2.

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LazyData false

Imports ggplot2, viridis, mgcv, SingleCellExperiment, slingshot, princurve, Biobase, methods, RColorBrewer, SummarizedExperiment, grDevices, graphics, rgl

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`counts` *A count matrix, used for testing.*

Description

This object contains the gene expression counts from the data described in Paul et al. (2015).

Usage

```
data("counts", package = "traviz")
```

Format

An object of class `standardGeneric` of length 1.

Details

#' @references Franziska Paul, Yaara Arkin, Amir Giladi, DiegoAdhemar Jaitin, Ephraim Kenigsberg, Hadas KerenShaul, Deborah Winter, David Lara-Astiaso, Meital Gury, Assaf Weiner, Eyal David, Nadav Cohen, FeliciaKathrineBratt Lauridsen, Simon Haas, Andreas Schlitzer, Alexander Mildner, Florent Ginhoux, Steen Jung, Andreas Trumpp, BoTorben Porse, Amos Tanay, and Ido Amit. Transcriptional Heterogeneity and Lineage Commitment in Myeloid Progenitors. Cell, 163(7):1663–1677, 12 2015. ISSN 0092- 8674. doi: 10.1016/J.CELL.2015.11.013. URL https://www.sciencedirect.com/scie
ii/S0092867415014932?via

crv *A SlingshotDataset object, used for testing.*

Description

This dataset contains the Slingshot trajectory from the data described in Paul et al. (2015).

Usage

```
data("crv", package = "traviz")
```

Format

An object of class `SlingshotDataSet` of length 1.

References

Franziska Paul, Yaara Arkin, Amir Giladi, DiegoAdhemar Jaitin, Ephraim Kenigsberg, Hadas KerenShaul, Deborah Winter, David Lara-Astiaso, Meital Gury, Assaf Weiner, Eyal David, Nadav Cohen, FeliciaKathrineBratt Lauridsen, Simon Haas, Andreas Schlitzer, Alexander Mildner, Florent Ginhoux, Steen Jung, Andreas Trumpp, BoTorben Porse, Amos Tanay, and Ido Amit. Transcriptional Heterogeneity and Lineage Commitment in Myeloid Progenitors. Cell, 163(7):1663–1677, 12 2015. ISSN 0092- 8674. doi: 10.1016/J.CELL.2015.11.013. URL https://www.sciencedirect.com/science/article/ii/S0092867415014932?via

plot-SlingshotDataSet *Plot Slingshot output*

Description

Tools for visualizing lineages inferred by `slingshot`.

Usage

```
## S4 method for signature 'SlingshotDataSet,ANY'
plot(
  x,
  type = NULL,
  linInd = NULL,
  show.constraints = FALSE,
  add = FALSE,
  dims = seq_len(2),
  asp = 1,
  cex = 2,
  lwd = 2,
  col = 1,
```

```
  ...
)

## S4 method for signature 'SlingshotDataSet'
lines(x, type = NULL, dims = seq_len(2), ...)
```

Arguments

x	a SlingshotDataSet with results to be plotted.
type	character, the type of output to be plotted, can be one of "lineages", "curves", or "both" (by partial matching), see Details for more.
linInd	integer, an index indicating which lineages should be plotted (default is to plot all lineages). If col is a vector, it will be subsetted by linInd.
show.constraints	logical, whether or not the user-specified initial and terminal clusters should be specially denoted by green and red dots, respectively.
add	logical, indicates whether the output should be added to an existing plot.
dims	numeric, which dimensions to plot (default is 1:2).
asp	numeric, the y/x aspect ratio, see plot.window.
cex	numeric, amount by which points should be magnified, see par.
lwd	numeric, the line width, see par.
col	character or numeric, color(s) for lines, see par.
...	additional parameters to be passed to lines.

Details

If type == 'lineages', straight line connectors between cluster centers will be plotted. If type == 'curves', simultaneous principal curves will be plotted.

When type is not specified, the function will first check the curves slot and plot the curves, if present. Otherwise, lineages will be plotted, if present.

Value

returns NULL.

Examples

```
library(slingshot)
data("slingshotExample", package="slingshot")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
pto <- slingshot(rd, cl, start.clus = "1")
plot(SlingshotDataSet(pto), type = 'b')

# add to existing plot
sds <- as.SlingshotDataSet(pto)
plot(rd, col = 'grey50', asp = 1)
lines(sds, lwd = 3)
```

plot3d-SlingshotDataSet

Plot Slingshot output in 3D

Description

Tools for visualizing lineages inferred by `slingshot`.

Usage

```
## S3 method for class 'SlingshotDataSet'
plot3d(
  x,
  type = NULL,
  linInd = NULL,
  add = FALSE,
  dims = seq_len(3),
  aspect = "iso",
  size = 10,
  col = 1,
  ...
)
```

Arguments

`x`	a `SlingshotDataSet` with results to be plotted.
`type`	character, the type of output to be plotted, can be one of `"lineages"`, `curves`, or `both` (by partial matching), see Details for more.
`linInd`	integer, an index indicating which lineages should be plotted (default is to plot all lineages). If `col` is a vector, it will be subsetted by `linInd`.
`add`	logical, indicates whether the output should be added to an existing plot.
`dims`	numeric, which dimensions to plot (default is `1:3`).
`aspect`	either a logical indicating whether to adjust the aspect ratio or a new ratio, see `plot3d`.
`size`	numeric, size of points for MST (default is `10`), see `plot3d`.
`col`	character or numeric, color(s) for lines, see `par`.
`...`	additional parameters to be passed to `lines3d`.

Details

If `type == 'lineages'`, straight line connectors between cluster centers will be plotted. If `type == 'curves'`, simultaneous principal curves will be plotted.

When `type` is not specified, the function will first check the `curves` slot and plot the curves, if present. Otherwise, `lineages` will be plotted, if present.

Value

returns NULL.

Examples

```
library(rgl)
library(slingshot)
data("crv", package="traviz")
rd <- slingReducedDim(crv)
rd <- cbind(rd, rnorm(nrow(rd), sd=.1))
cl <- apply(slingClusterLabels(crv), 1, which.max)
sds <- slingshot::slingshot(rd, clusterLabels=cl, start.clus=1)
slingshot::plot3d.SlingshotDataSet(as.SlingshotDataSet(sds), type = 'b')

# add to existing plot
plot3d(rd, col = cl, aspect = 'iso')
slingshot::plot3d.SlingshotDataSet(as.SlingshotDataSet(sds), lwd = 3, add = TRUE)
```

---

plotExpression *Plot gene expression along pseudotime.*

Description

Plot gene expression along pseudotime.

Plots a fast loess smoother of gene expression for each lineage.

Usage

```
plotExpression(counts, sds, gene, ...)

## S4 method for signature 'matrix,SlingshotDataSet,character'
plotExpression(
  counts,
  sds,
  gene,
  type = "loess",
  span = 0.75,
  alpha = 1,
  lwd = 1,
  size = 2/3
)

## S4 method for signature 'matrix,PseudotimeOrdering,character'
plotExpression(
  counts,
  sds,
```

```
  gene,
  type = "loess",
  span = 0.75,
  alpha = 1,
  lwd = 1,
  size = 2/3
)
```

Arguments

counts	The matrix of gene expression counts.
sds	A SlingshotDataSet or PseudotimeOrdering object, typically obtained after trajectory inference using Slingshot.
gene	Gene name of gene to plot.
...	parameters including:
type	The type of smoother. Defaults to "loess".
span	If type is "loess", the span of the smoother. See loess documentation.
alpha	Numeric between 0 and 1, determines the transparency of data points, see scale_color_viridis_d.
lwd	Line width of the smoother. Passed to geom_line.
size	Character expansion of the data points. Passed to geom_point.

Value

A ggplot object.

Examples

```
library(ggplot2)
data(crv, package="traviz")
data(counts, package="traviz")
plotExpression(counts = counts, sds=crv, gene=rownames(counts)[1])
```

---

plotGeneCount *Plot gene expression in reduced dimension.*

Description

Plot the gene in reduced dimensional space.

Usage

```
plotGeneCount(curve, ...)

## S4 method for signature 'SlingshotDataSet'
plotGeneCount(
  curve,
  counts = NULL,
  gene = NULL,
  clusters = NULL,
  models = NULL,
  title = NULL
)

## S4 method for signature 'SingleCellExperiment'
plotGeneCount(
  curve,
  counts = NULL,
  gene = NULL,
  clusters = NULL,
  models = NULL,
  title = NULL
)
```

Arguments

curve	One of two • A SlingshotDataSet object. The output from trajectory inference using Slingshot. • A SingleCellExperiment object. The output from trajectory inference using Slingshot.
...	parameters including:
counts	The count matrix, genes in rows and cells in columns. Only needed if the input is of the type SlingshotDataSet and the gene argument is not NULL.
gene	The name of gene for which you want to plot the count or the row number of that gene in the count matrix. Alternatively, one can specify the clusters argument.
clusters	The assignation of each cell to a cluster. Used to color the plot. Either clusters or gene and counts must be supplied.
models	The fitted GAMs, typically the output from fitGAM. Used to display the knots.
title	Title for the plot.

Details

If both gene and clusters arguments are supplied, the plot will be colored according to gene count level. If none are provided, the function will fail.

Value

A ggplot object

Examples

```
set.seed(97)
library(slingshot)
data(crv, package="traviz")
data(counts, package="traviz")
plotGeneCount(crv, counts, gene = "Mpo")
```

---

plotSmoothers *Plot the log-transformed counts and the fitted values for a particular gene along all lineages*

Description

Plot the smoothers estimated by tradeSeq.

Usage

```
plotSmoothers(models, ...)

## S4 method for signature 'gam'
plotSmoothers(
  models,
  nPoints = 100,
  lwd = 2,
  size = 2/3,
  xlab = "Pseudotime",
  ylab = "Log(expression + 1)",
  border = TRUE,
  alpha = 1,
  sample = 1
)

## S4 method for signature 'SingleCellExperiment'
plotSmoothers(
  models,
  counts,
  gene,
  nPoints = 100,
  lwd = 2,
  size = 2/3,
  xlab = "Pseudotime",
  ylab = "Log(expression + 1)",
  border = TRUE,
```

```
  alpha = 1,
  sample = 1,
  pointCol = NULL,
  curvesCols = NULL,
  plotLineages = TRUE
)
```

Arguments

models	Either the SingleCellExperiment object obtained after running fitGAM, or the specific GAM model for the corresponding gene, if working with the list output of tradeSeq.
...	parameters including:
nPoints	The number of points used to extrapolate the fit. Defaults to 100.
lwd	Line width of the smoother. Passed to geom_line.
size	Character expansion of the data points. Passed to geom_point.
xlab	x-axis label. Passed to labs.
ylab	y-axis label. Passed to labs.
border	Logical: should a white border be drawn around the mean smoother.
alpha	Numeric between 0 and 1, determines the transparency of data points, see scale_color_viridis_d.
sample	Numeric between 0 and 1, use to subsample the cells when there are too many so that it can plot faster.
counts	The matrix of gene expression counts.
gene	Gene name or row in count matrix of gene to plot.
pointCol	Plotting colors for each cell. Can be either character vector of length 1, denoting a variable in the colData(models) to color cells by, or a vector of length equal to the number of cells.
curvesCols	Plotting colors for each curve Should be a list of colors of the exact same length as the number of curves, i.e. the number of lineages (if there is no conditions) or the number of lineages by the number of conditions. In the second case, the colors are grouped by condition (lineage 1 - condition 1, lineage 1 - condition 2,...).
plotLineages	Logical, should the mean smoothers for each lineage be plotted?

Value

A ggplot object

Examples

```
set.seed(82)
library(ggplot2)
data(crv, package="traviz")
data(counts, package="traviz")
data(sce, package="traviz")
```

```
plotSmoothers(sce, counts, rownames(counts)[1])
# show only one curve
curvesCols <- c("#440154FF", "transparent")
plotSmoothers(sce, counts, rownames(counts)[1], curvesCols = curvesCols,
border = FALSE)
# Show only first curve and cells assigned to first lineage
plotSmoothers(sce, counts, rownames(counts)[1], curvesCols = curvesCols,
  border = FALSE) +
  ggplot2::scale_color_manual(values = curvesCols)
```

---

sce *A SingleCellExperiment object, used for testing.*

Description

This object contains fitted smoothers using `tradeSeq`.

Usage

```
data("sce", package = "traviz")
```

Format

An object of class `SingleCellExperiment` with 240 rows and 2660 columns.

Details

#' @references Franziska Paul, Yaara Arkin, Amir Giladi, DiegoAdhemar Jaitin, Ephraim Kenigsberg, Hadas KerenShaul, Deborah Winter, David Lara-Astiaso, Meital Gury, Assaf Weiner, Eyal David, Nadav Cohen, FeliciaKathrineBratt Lauridsen, Simon Haas, Andreas Schlitzer, Alexander Mildner, Florent Ginhoux, Steen Jung, Andreas Trumpp, BoTorben Porse, Amos Tanay, and Ido Amit. Transcriptional Heterogeneity and Lineage Commitment in Myeloid Progenitors. Cell, 163(7):1663–1677, 12 2015. ISSN 0092- 8674. doi: 10.1016/J.CELL.2015.11.013. URL https://www.sciencedirect.com/scie
ii/S0092867415014932?via

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