Package ‘traviz’

March 28, 2024

Type Package
Title Trajectory functions for visualization and interpretation.
Version 1.8.0
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 average 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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'plotGeneCount.R' 'plotSmoothers.R' 'plot_SlingshotDataSet.R'
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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

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


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
```r
library(slingshot)
data("slingshotExample", package="slingshot")
rd <- slingshotExample$rd
c1 <- slingshotExample$c1
pto <- slingshot(rd, c1, 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

```r
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

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

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

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

```r
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

```r
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

```r
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

```r
plotSmoothers(models, ...)
```

```r
## 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
)
```

```r
## 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**
```
```
Index

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