Package 'slingshot'

March 30, 2021

Title Tools for ordering single-cell sequencing

Version 1.8.0

Description Provides functions for inferring continuous, branching lineage structures in low-dimensional data. Slingshot was designed to model developmental trajectories in single-cell RNA sequencing data and serve as a component in an analysis pipeline after dimensionality reduction and clustering. It is flexible enough to handle arbitrarily many branching events and allows for the incorporation of prior knowledge through supervised graph construction.

License Artistic-2.0

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R topics documented:

`embedCurves` *Embed trajectory in new space*

Description

This function takes the output of `slingshot` (or `getCurves`) and attempts to embed the curves in a different coordinate space than the one in which they were constructed. This should be considered as a visualization tool, only.

Usage

```
embedCurves(x, newDimRed, ...)

## S4 method for signature 'SlingshotDataSet,matrix'
embedCurves(
  x,
  newDimRed,
  shrink = NULL,
  stretch = NULL,
  approx_points = NULL,
  smoother = NULL,
```

```
  shrink.method = NULL,
  ...
)

## S4 method for signature 'SingleCellExperiment,matrix'
embedCurves(
  x,
  newDimRed,
  shrink = NULL,
  stretch = NULL,
  approx_points = NULL,
  smoother = NULL,
  shrink.method = NULL,
  ...
)

## S4 method for signature 'SingleCellExperiment,character'
embedCurves(
  x,
  newDimRed,
  shrink = NULL,
  stretch = NULL,
  approx_points = NULL,
  smoother = NULL,
  shrink.method = NULL,
  ...
)
```

Arguments

x	an object containing slingshot output.
newDimRed	a matrix representing the new coordinate space in which to embed the slingshot curves.
...	Additional parameters to pass to scatter plot smoothing function, smoother.
shrink	logical or numeric between 0 and 1, determines whether and how much to shrink branching lineages toward their average prior to the split.
stretch	numeric factor by which curves can be extrapolated beyond endpoints. Default is 2, see principal_curve.
approx_points	numeric, whether curves should be approximated by a fixed number of points. If FALSE (or 0), no approximation will be performed and curves will contain as many points as the input data. If numeric, curves will be approximated by this number of points; preferably about 100 (see principal_curve).
smoother,	choice of scatter plot smoother. Same as principal_curve, but "lowess" option is replaced with "loess" for additional flexibility.
shrink.method	character denoting how to determine the appropriate amount of shrinkage for a branching lineage. Accepted values are the same as for kernel in density (default is "cosine"), as well as "tricube" and "density". See 'Details' for more.

Details

Many of the same parameters are used here as in `getCurves`. This function attempts to translate curves from one reduced dimensional space to another by predicting each dimension as a function of pseudotime (ie. the new curve is determined by a series of scatterplot smoothers predicting the coordinates in the new space as a function of pseudotime). Because the pseudotime values are not changed, this amounts to a single iteration of the iterative curve-fitting process used by `getCurves`.

Note that non-linear dimensionality reduction techniques (such as tSNE and UMAP) may produce discontinuities not observed in other spaces. Use caution when embedding curves in these spaces.

Value

a `SlingshotDataSet` containing curves in the new space.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl)
rd2 <- cbind(rd[,2] + rnorm(nrow(rd)), -rd[,1] + rnorm(nrow(rd)))
sds.new <- embedCurves(sds, rd2)
sds.new

plot(rd2, col = cl, asp = 1)
lines(sds.new, lwd = 3)
```

---

getCurves *Construct Smooth Lineage Curves*

Description

This function takes a reduced data matrix `n` by `p`, a vector of cluster identities (optionally including `-1`'s for "unclustered"), and a set of lineages consisting of paths through a forest constructed on the clusters. It constructs smooth curves for each lineage and returns the points along these curves corresponding to the orthogonal projections of each data point, along with corresponding arclength (`pseudotime` or `lambda`) values.

Usage

```
getCurves(sds, ...)

## S4 method for signature 'SlingshotDataSet'
getCurves(
  sds,
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
```

```
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)

## S4 method for signature 'SingleCellExperiment'
getCurves(
  sds,
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)
```

Arguments

sds	The SlingshotDataSet for which to construct simultaneous principal curves. This should already have lineages identified by getLineages.
...	Additional parameters to pass to scatter plot smoothing function, smoother.
shrink	logical or numeric between 0 and 1, determines whether and how much to shrink branching lineages toward their average prior to the split.
extend	character, how to handle root and leaf clusters of lineages when constructing the initial, piece-wise linear curve. Accepted values are 'y' (default), 'n', and 'pc1'. See 'Details' for more.
reweight	logical, whether to allow cells shared between lineages to be reweighted during curve-fitting. If TRUE, cells shared between lineages will be iteratively reweighted based on the quantiles of their projection distances to each curve. See 'Details' for more.
reassign	logical, whether to reassign cells to lineages at each iteration. If TRUE, cells will be added to a lineage when their projection distance to the curve is less than the median distance for all cells currently assigned to the lineage. Additionally, shared cells will be removed from a lineage if their projection distance to the curve is above the 90th percentile and their weight along the curve is less than 0.1.
thresh	numeric, determines the convergence criterion. Percent change in the total distance from cells to their projections along curves must be less than thresh. Default is 0.001, similar to principal_curve.
maxit	numeric, maximum number of iterations, see principal_curve.
stretch	numeric factor by which curves can be extrapolated beyond endpoints. Default is 2, see principal_curve.

approx_points	numeric, whether curves should be approximated by a fixed number of points. If FALSE (or 0), no approximation will be performed and curves will contain as many points as the input data. If numeric, curves will be approximated by this number of points; preferably about 100 (see principal_curve).
smoother,	choice of scatter plot smoother. Same as principal_curve, but "lowess" option is replaced with "loess" for additional flexibility.
shrink.method	character denoting how to determine the appropriate amount of shrinkage for a branching lineage. Accepted values are the same as for kernel in density (default is "cosine"), as well as "tricube" and "density". See 'Details' for more.
allow.breaks	logical, determines whether curves that branch very close to the origin should be allowed to have different starting points.

Details

When there is only a single lineage, the curve-fitting algorithm is nearly identical to that of principal_curve. When there are multiple lineages and shrink > 0, an additional step is added to the iterative procedure, forcing curves to be similar in the neighborhood of shared points (ie., before they branch).

The extend argument determines how to construct the piece-wise linear curve used to initiate the recursive algorithm. The initial curve is always based on the lines between cluster centers and if extend = 'n', this curve will terminate at the center of the endpoint clusters. Setting extend = 'y' will allow the first and last segments to extend beyond the cluster center to the orthogonal projection of the furthest point. Setting extend = 'pc1' is similar to 'y', but uses the first principal component of the cluster to determine the direction of the curve beyond the cluster center. These options typically have little to no impact on the final curve, but can occasionally help with stability issues.

When shink = TRUE, we compute a shrinkage curve, $w_l(t)$, for each lineage, a non-increasing function of pseudotime that determines how much that lineage should be shrunk toward a shared average curve. We set $w_l(0) = 1$, so that the curves will perfectly overlap the average curve at pseudotime 0. The weighting curve decreases from 1 to 0 over the non-outlying pseudotime values of shared cells (where outliers are defined by the 1.5*IQR rule). The exact shape of the curve in this region is controlled by shrink.method, and can follow the shape of any standard kernel function's cumulative density curve (or more precisely, survival curve, since we require a decreasing function). Different choices of shrink.method seem to have little impact on the final curves, in most cases.

When reweight = TRUE, weights for shared cells are based on the quantiles of their projection distances onto each curve. The distances are ranked and converted into quantiles between 0 and 1, which are then transformed by 1 -q^2. Each cell's weight along a given lineage is the ratio of this value to the maximum value for this cell across all lineages.

Value

An updated SlingshotDataSet object containing the oringinal input, arguments provided to getCurves as well as the following new elements:

- curves A list of principal_curve objects.
- slingParams Additional parameters used for fitting simultaneous principal curves.

References

Hastie, T., and Stuetzle, W. (1989). "Principal Curves." *Journal of the American Statistical Association*, 84:502–516.

See Also

slingshot

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- getLineages(rd, cl, start.clus = '1')
sds <- getCurves(sds)

plot(rd, col = cl, asp = 1)
lines(sds, type = 'c', lwd = 3)
```

---

getLineages *Infer Lineage Structure from Clustered Samples*

Description

Given a reduced-dimension data matrix n by p and a vector of cluster identities (potentially including -1's for "unclustered"), this function infers a forest structure on the clusters and returns paths through the forest that can be interpreted as lineages.

Usage

```
getLineages(data, clusterLabels, ...)

## S4 method for signature 'matrix,matrix'
getLineages(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3
)

## S4 method for signature 'matrix,character'
getLineages(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3
)
```

```
## S4 method for signature 'matrix,ANY'
getLineages(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3
)

## S4 method for signature 'SlingshotDataSet,ANY'
getLineages(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3
)

## S4 method for signature 'data.frame,ANY'
getLineages(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3
)

## S4 method for signature 'matrix,numeric'
getLineages(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3
)

## S4 method for signature 'matrix,factor'
getLineages(
  data,
```

```
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3
)

## S4 method for signature 'SingleCellExperiment,ANY'
getLineages(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3
)
```

Arguments

data	a data object containing the matrix of coordinates to be used for lineage inference. Supported types include matrix, SingleCellExperiment, and SlingshotDataSet.
clusterLabels	character, a vector of length n denoting cluster labels, optionally including -1's for "unclustered." If reducedDim is a SlingshotDataSet, cluster labels will be taken from it.
...	Additional arguments to specify how lineages are constructed from clusters.
reducedDim	(optional) identifier to be used if reducedDim(data) contains multiple elements. Otherwise, the first element will be used by default.
start.clus	(optional) character, indicates the cluster(s) *from* which lineages will be drawn.
end.clus	(optional) character, indicates the cluster(s) which will be forced leaf nodes in their trees.
dist.fun	(optional) function, method for calculating distances between clusters. Must take two matrices as input, corresponding to points in reduced-dimensional space. If the minimum cluster size is larger than the number dimensions, the default is to use the joint covariance matrix to find squared distance between cluster centers. If not, the default is to use the diagonal of the joint covariance matrix.
omega	(optional) numeric, this granularity parameter determines the distance between every real cluster and the artificial cluster, .OMEGA. In practice, this makes omega the maximum allowable distance between two connected clusters. By default, omega = Inf. If omega = TRUE, the maximum edge length will be set to the median edge length of the unsupervised MST times a scaling factor (omega_scale, default = 3). This value is provided as a potentially useful rule of thumb for datasets with outlying clusters or multiple, distinct trajectories, but it is not otherwise recommended.
omega_scale	(optional) numeric, scaling factor to use when omega = TRUE. The maximum edge length will be set to the median edge length of the unsupervised MST times omega_scale (default = 3).

Details

The connectivity matrix is learned by fitting a (possibly constrained) minimum-spanning tree on the clusters and the artificial cluster, .OMEGA, which is a fixed distance away from every real cluster. This effectively limits the maximum branch length in the MST to the chosen distance, meaning that the output may contain multiple trees.

Once the connectivity is known, lineages are identified in any tree with at least two clusters. For a given tree, if there is an annotated starting cluster, every possible path out of a starting cluster and ending in a leaf that isn't another starting cluster will be returned. If no starting cluster is annotated, every leaf will be considered as a potential starting cluster and whichever configuration produces the longest average lineage length (in terms of number of clusters included) will be returned.

Value

An object of class SlingshotDataSet containing the arguments provided to getLineages as well as the following new elements:

- lineages a list of L items, where L is the number of lineages identified. Each lineage is represented by a character vector with the names of the clusters included in that lineage, in order.
- connectivity the inferred cluster connectivity matrix.
- slingParams$start.given,slingParams$end.given logical values indicating whether the starting and ending clusters were specified a priori.
- slingParams$dist the pairwise cluster distance matrix.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- getLineages(rd, cl, start.clus = '1')

plot(rd, col = cl, asp = 1)
lines(sds, type = 'l', lwd = 3)
```

---

newSlingshotDataSet *Initialize an object of class* SlingshotDataSet

---

Description

Constructs a SlingshotDataSet object. Additional helper methods for manipulating SlingshotDataSet objects are also described below.

Usage

```
newSlingshotDataSet(reducedDim, clusterLabels, ...)

## S4 method for signature 'data.frame,ANY'
newSlingshotDataSet(reducedDim, clusterLabels, ...)

## S4 method for signature 'matrix,numeric'
```

```
newSlingshotDataSet(reducedDim, clusterLabels, ...)

## S4 method for signature 'matrix,factor'
newSlingshotDataSet(reducedDim, clusterLabels, ...)

## S4 method for signature 'matrix,ANY'
newSlingshotDataSet(reducedDim, clusterLabels, ...)

## S4 method for signature 'matrix,character'
newSlingshotDataSet(reducedDim, clusterLabels, ...)

## S4 method for signature 'matrix,matrix'
newSlingshotDataSet(
  reducedDim,
  clusterLabels,
  lineages = list(),
  adjacency = matrix(NA, 0, 0),
  curves = list(),
  slingParams = list()
)
```

Arguments

reducedDim	matrix. An n by p numeric matrix or data frame giving the coordinates of the cells in a reduced dimensionality space.
clusterLabels	character. A character vector of length n denoting each cell's cluster label.
...	additional components of a SlingshotDataSet to specify. This may include any of the following:
lineages	list. A list with each element a character vector of cluster names representing a lineage as an ordered set of clusters.
adjacency	matrix. A binary matrix describing the connectivity between clusters induced by the minimum spanning tree.
curves	list. A list of principal_curve objects produced by getCurves.
slingParams	list. Additional parameters used by Slingshot. These may specify how the minimum spanning tree on clusters was constructed: • start.clucharacter. The label of the root cluster. • end.clucharacter. Vector of cluster labels indicating the terminal clusters. • start.givenlogical. A logical value indicating whether the initial state was pre-specified. • end.givenlogical. A vector of logical values indicating whether each terminal state was pre-specified • distmatrix. A numeric matrix of pairwise cluster distances. They may also specify how simultaneous principal curves were constructed: • shrinklogical or numeric between 0 and 1. Determines whether and how much to shrink branching lineages toward their shared average curve. • extendcharacter. Specifies the method for handling root and leaf clusters of lineages when constructing the initial, piece-wise linear curve. Accepted values are 'y' (default), 'n', and 'pc1'. See getCurves for details.

- reweightlogical. Indicates whether to allow cells shared between lineages to be reweighted during curve-fitting. If TRUE, cells shared between lineages will be iteratively reweighted based on the quantiles of their projection distances to each curve.
- reassignlogical. Indicates whether to reassign cells to lineages at each iteration. If TRUE, cells will be added to a lineage when their projection distance to the curve is less than the median distance for all cells currently assigned to the lineage. Additionally, shared cells will be removed from a lineage if their projection distance to the curve is above the 90th percentile and their weight along the curve is less than 0.1.
- shrink.methodcharacter. Denotes how to determine the amount of shrinkage for a branching lineage. Accepted values are the same as for kernel in the density function (default is "cosine"), as well as "tricube" and "density". See getCurves for details.
- Other parameters specified by principal_curve.

Value

A SlingshotDataSet object with all specified values.

Functions

- newSlingshotDataSet,data.frame,ANY-method: returns a SlingshotDataSet object.
- newSlingshotDataSet,matrix,numeric-method: returns a SlingshotDataSet object.
- newSlingshotDataSet,matrix,factor-method: returns a SlingshotDataSet object.
- newSlingshotDataSet,matrix,ANY-method: returns a SlingshotDataSet object.
- newSlingshotDataSet,matrix,character-method: returns a SlingshotDataSet object.
- newSlingshotDataSet,matrix,matrix-method: returns a SlingshotDataSet object.

Examples

```
rd <- matrix(data=rnorm(100), ncol=2)
cl <- sample(letters[seq_len(5)], 50, replace = TRUE)
sds <- newSlingshotDataSet(rd, cl)
```

---

pairs-SlingshotDataSet

Pairs plot of Slingshot output

Description

A tool for quickly visualizing lineages inferred by slingshot.

Usage

```
## S3 method for class 'SlingshotDataSet'
pairs(
  x,
  type = NULL,
  show.constraints = FALSE,
  col = NULL,
  pch = 16,
  cex = 1,
  lwd = 2,
  ...,
  labels,
  horInd = seq_len(nc),
  verInd = seq_len(nc),
  lower.panel = FALSE,
  upper.panel = TRUE,
  diag.panel = NULL,
  text.panel = textPanel,
  label.pos = 0.5 + has.diag/3,
  line.main = 3,
  cex.labels = NULL,
  font.labels = 1,
  row1attop = TRUE,
  gap = 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.
show.constraints	logical, whether or not the user-specified initial and terminal clusters should be specially denoted by green and red dots, respectively.
col	character, color vector for points.
pch	integer or character specifying the plotting symbol, see par.
cex	numeric, amount by which points should be magnified, see par.
lwd	numeric, the line width, see par.
...	additional parameters for plot or axis, see pairs.
labels	character, the names of the variables, see pairs.
horInd	see pairs.
verInd	see pairs.
lower.panel	see pairs.
upper.panel	see pairs.
diag.panel	see pairs.
text.panel	see pairs.
label.pos	see pairs.

line.main	see pairs.
cex.labels	see pairs.
font.labels	see pairs.
row1attop	see pairs.
gap	see pairs.

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

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl, start.clus = "1")
pairs(sds, type = 'curves')
```

---

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

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

# add to existing plot
plot(rd, col = 'grey50')
lines(sds, lwd = 3)
```

plot3d-SlingshotDataSet

Plot Slingshot output in 3D

Description

Tools for visualizing lineages inferred by `slingshot`.

Usage

```
plot3d.SlingshotDataSet(
  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

```
## Not run:
library(rgl)
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
rd <- cbind(rd, rnorm(nrow(rd)))
sds <- slingshot(rd, cl, start.clus = "1")
plot3d(sds, type = 'b')

# add to existing plot
plot3d(rd, col = 'grey50', aspect = 'iso')
plot3d(sds, lwd = 3, add = TRUE)

## End(Not run)
```

---

plotGenePseudotime *Plot Gene Expression by Pseudotime*

Description

Show the gene expression pattern for an individual gene along lineages inferred by slingshot.

Usage

```
plotGenePseudotime(data, ...)

## S4 method for signature 'SlingshotDataSet'
plotGenePseudotime(data, gene, exprs, loess = TRUE, loessCI = TRUE, ...)

## S4 method for signature 'SingleCellExperiment'
plotGenePseudotime(data, gene, exprs, loess = TRUE, loessCI = TRUE, ...)
```

Arguments

data	an object containing slingshot output, either a SlingshotDataSet or a SingleCellExperiment object.
...	additional parameters to be passed to plot.
gene	the gene to be plotted. If exprs is provided, this may be either the gene name or its row index in exprs. Otherwise, this is assumed to be a vector of scaled expression values.
exprs	the genes-by-samples matrix of scaled expression values (log counts or normalized log counts).
loess	logical, whether to include a loess fit in each plot (default is TRUE).
loessCI	logical, whether to include a confidence band around the loess curve (default is TRUE).

Value

returns NULL.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl, start.clus = "1")
ex <- matrix(c(rchisq(100,1),rchisq(20,3),rchisq(20,6)),nrow=1)
rownames(ex) <- 'Gene-1'
plotGenePseudotime(sds, 'Gene-1', ex)
```

---

predict,SlingshotDataSet-method

Predict from a Slingshot model

Description

Map new observations onto simultaneous principal curves fitted by `slingshot`.

Usage

```
## S4 method for signature 'SlingshotDataSet'
predict(object, newdata = NULL)
```

Arguments

`object`	a `SlingshotDataSet` containing simultaneous principal curves to use for prediction.
`newdata`	a matrix or data frame of new points in the same reduced-dimensional space as the original input to `slingshot` (or `getLineages`).

Details

This function is a method for the generic function `predict` with `signature(object = "SlingshotDataSet")`. If no `newdata` argument is provided, it will return the original results, given by `object`.

Value

A `SlingshotDataSet` object based on the input `newdata`. New cells are treated as "unclustered" and the `lineages` and `adjacency` slots are intentionally left blank, to distinguish these results from the original `slingshot` output. The `curves` slot represents the projections of each new cell onto the existing curves. As with standard `slingshot` output, the lineage-specific pseudotimes and assignment weights can be accessed via the functions `slingPseudotime` and `slingCurveWeights`.

See Also

`slingshot`, `SlingshotDataSet`

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl, start.clus = '1')

x <- cbind(runif(100, min = -5, max = 10), runif(100, min = -4, max = 4))
predict(sds, x)
```

`slingAdjacency` *Extract Slingshot adjacency matrix*

Description

Extract the adjacency matrix from an object containing `slingshot` output.

Usage

```
slingAdjacency(x)

## S4 method for signature 'SlingshotDataSet'
slingAdjacency(x)

## S4 method for signature 'SingleCellExperiment'
slingAdjacency(x)
```

Arguments

x	an object containing `slingshot` output.

Value

the matrix of connections between clusters, inferred by the MST.

Methods (by class)

- `SlingshotDataSet`: returns the adjacency matrix between clusters from a `SlingshotDataSet` object.
- `SingleCellExperiment`: returns the adjacency matrix between clusters from a `SingleCellExperiment` object.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- getLineages(rd, cl)
slingAdjacency(sds)
```

slingBranchGraph *Construct graph of slingshot branch labels*

Description

Builds a graph describing the relationships between the different branch assignments

Usage

```
slingBranchGraph(x, ...)

## S4 method for signature 'ANY'
slingBranchGraph(x, thresh = NULL, max_node_size = 100)
```

Arguments

x	an object containing slingshot output, generally either a SlingshotDataSet or SingleCellExperiment.
...	additional arguments passed to object-specific methods.
thresh	weight threshold for assigning cells to lineages. A cell's weight on a certain lineage must be greater than this value (default = 1/L, for L lineages).
max_node_size	the size of the largest node in the graph, for plotting (all others will be drawn proportionally). See igraph.plotting for more details.

Value

an igraph object representing the relationships between lineages.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl)
slingBranchGraph(sds)
```

slingBranchID *Get slingshot branch labels*

Description

Extracts lineage assignments from slingshot results. This produces a categorical variable indicating which lineage (or combination of lineages) each cell is assigned to.

Usage

```
slingBranchID(x, ...)

## S4 method for signature 'ANY'
slingBranchID(x, thresh = NULL)
```

Arguments

x	an object containing slingshot output, generally either a SlingshotDataSet or SingleCellExperiment.
...	additional arguments passed to object-specific methods.
thresh	weight threshold for assigning cells to lineages. A cell's weight on a certain lineage must be at least this value (default = 1/L, for L lineages).

Value

a factor variable that assigns each cell to a particular lineage or set of lineages.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl)
slingBranchID(sds)
```

---

slingClusterLabels *Extract cluster labels used by Slingshot*

Description

Extract the cluster labels used by slingshot.

Usage

```
slingClusterLabels(x)

## S4 method for signature 'SlingshotDataSet'
slingClusterLabels(x)

## S4 method for signature 'SingleCellExperiment'
slingClusterLabels(x)
```

Arguments

x	an object containing slingshot output.

Value

a vector of cluster labels or a matrix of cluster assignment weights.

Methods (by class)

- SlingshotDataSet: returns the cluster labels stored in a SlingshotDataSet object.
- SingleCellExperiment: returns the cluster labels used by slingshot in a SingleCellExperiment object.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- getLineages(rd, cl)
slingClusterLabels(sds)
```

`slingCurves` *Extract simultaneous principal curves*

Description

Extract the simultaneous principal curves from an object containing `slingshot` output.

Usage

```
slingCurves(x)

## S4 method for signature 'SlingshotDataSet'
slingCurves(x)

## S4 method for signature 'SingleCellExperiment'
slingCurves(x)
```

Arguments

`x`	an object containing `slingshot` output.

Value

the list of smooth lineage curves, each of which is a `principal_curve` object.

Methods (by class)

- `SlingshotDataSet`: returns the list of smooth lineage curves from a `SlingshotDataSet` object.
- `SingleCellExperiment`: returns the list of smooth lineage curves from a `SingleCellExperiment` object.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl)
slingCurves(sds)
```

slingLineages *Extract the Slingshot lineages*

Description

Extract lineages (represented by ordered sets of clusters) identified by slingshot.

Usage

```
slingLineages(x)

## S4 method for signature 'SlingshotDataSet'
slingLineages(x)

## S4 method for signature 'SingleCellExperiment'
slingLineages(x)
```

Arguments

x	an object containing slingshot output.

Value

the list of lineages, represented by ordered sets of clusters.

Methods (by class)

- SlingshotDataSet: returns the list of lineages, represented by ordered sets of clusters from a SlingshotDataSet object.
- SingleCellExperiment: returns the list of lineages, represented by ordered sets of clusters from a SingleCellExperiment object.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- getLineages(rd, cl)
slingLineages(sds)
```

slingParams *Methods for parameters used by Slingshot*

Description

Extracts additional control parameters used by Slingshot in lineage inference and fitting simultaneous principal curves.

Usage

```
slingParams(x)

## S4 method for signature 'SlingshotDataSet'
slingParams(x)

## S4 method for signature 'SingleCellExperiment'
slingParams(x)
```

Arguments

x	an object containing slingshot output.

Value

the list of additional parameters used by Slingshot.

Methods (by class)

- SlingshotDataSet: returns the list of additional parameters used by Slingshot from a SlingshotDataSet object.
- SingleCellExperiment: returns the list of additional parameters used by Slingshot from a SingleCellExperiment object.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl, start.clus = '5')
slingParams(sds)
```

---

slingPseudotime *Get Slingshot pseudotime values*

Description

Extract the matrix of pseudotime values or cells' weights along each lineage.

Usage

```
slingPseudotime(x, ...)

slingCurveWeights(x, ...)

## S4 method for signature 'SlingshotDataSet'
slingPseudotime(x, na = TRUE)

## S4 method for signature 'SingleCellExperiment'
slingPseudotime(x, na = TRUE)
```

```
## S4 method for signature 'SlingshotDataSet'
slingCurveWeights(x, as.probs = FALSE)

## S4 method for signature 'SingleCellExperiment'
slingCurveWeights(x)
```

Arguments

x	an object containing slingshot output.
...	additional parameters to be passed to object-specific methods.
na	logical. If TRUE (default), cells that are not assigned to a lineage will have a pseudotime value of NA. Otherwise, their arclength along each curve will be returned.
as.probs	logical. If FALSE (default), output will be the weights used to construct the curves, appropriate for downstream analysis of individual lineages (ie. a cell shared between two lineages can have two weights of 1). If TRUE, output will be scaled to represent probabilistic assignment of cells to lineages (ie. a cell shared between two lineages will have two weights that sum to 1).

Value

an n by L matrix representing each cell's pseudotime along each lineage.

an n by L matrix of cell weights along each lineage.

Methods (by class)

- SlingshotDataSet: returns the matrix of pseudotime values from a SlingshotDataSet object.
- SingleCellExperiment: returns the matrix of pseudotime values from a SingleCellExperiment object.
- SlingshotDataSet: returns the matrix of cell weights along each lineage from a SlingshotDataSet object.
- SingleCellExperiment: returns the matrix of cell weights along each lineage from a SingleCellExperiment object.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl)
slingPseudotime(sds)
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl)
slingCurveWeights(sds)
```

slingshot *Perform lineage inference with Slingshot*

Description

Perform lineage inference with Slingshot

Given a reduced-dimensional data matrix n by p and a vector of cluster labels (or matrix of soft cluster assignments, potentially including a -1 label for "unclustered"), this function performs lineage inference using a cluster-based minimum spanning tree and constructing simultaneous principal curves for branching paths through the tree.

This wrapper function performs lineage inference in two steps: (1) identify lineage structure with a cluster-based minimum spanning tree with the getLineages function and (2) construct smooth representations of each lineage using simultaneous principal curves from the function getCurves.

Usage

```
slingshot(data, clusterLabels, ...)

## S4 method for signature 'matrix,character'
slingshot(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3,
  lineages = list(),
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)

## S4 method for signature 'matrix,matrix'
slingshot(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
```

```
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3,
  lineages = list(),
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)

## S4 method for signature 'SlingshotDataSet,ANY'
slingshot(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3,
  lineages = list(),
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)

## S4 method for signature 'data.frame,ANY'
slingshot(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
```

```
  omega_scale = 3,
  lineages = list(),
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)

## S4 method for signature 'matrix,numeric'
slingshot(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3,
  lineages = list(),
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)

## S4 method for signature 'matrix,factor'
slingshot(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3,
  lineages = list(),
```

```
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)

## S4 method for signature 'matrix,ANY'
slingshot(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3,
  lineages = list(),
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)

## S4 method for signature 'ClusterExperiment,ANY'
slingshot(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3,
  lineages = list(),
  shrink = TRUE,
  extend = "y",
```

```
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)

## S4 method for signature 'SingleCellExperiment,ANY'
slingshot(
  data,
  clusterLabels,
  reducedDim = NULL,
  start.clus = NULL,
  end.clus = NULL,
  dist.fun = NULL,
  omega = NULL,
  omega_scale = 3,
  lineages = list(),
  shrink = TRUE,
  extend = "y",
  reweight = TRUE,
  reassign = TRUE,
  thresh = 0.001,
  maxit = 15,
  stretch = 2,
  approx_points = FALSE,
  smoother = "smooth.spline",
  shrink.method = "cosine",
  allow.breaks = TRUE,
  ...
)
```

Arguments

data	a data object containing the matrix of coordinates to be used for lineage inference. Supported types include matrix, SingleCellExperiment, and SlingshotDataSet.
clusterLabels	character, a vector of length n denoting cluster labels, optionally including -1's for "unclustered." If reducedDim is a SlingshotDataSet, cluster labels will be taken from it.
...	Additional parameters to pass to scatter plot smoothing function, smoother.
reducedDim	(optional) identifier to be used if reducedDim(data) contains multiple elements. Otherwise, the first element will be used by default.
start.clus	(optional) character, indicates the cluster(s) of origin. Lineages will be represented by paths coming out of this cluster.
end.clus	(optional) character, indicates the cluster(s) which will be forced leaf nodes. This introduces a constraint on the MST algorithm.

dist.fun — (optional) function, method for calculating distances between clusters. Must take two matrices as input, corresponding to subsets of reducedDim. If the minimum cluster size is larger than the number dimensions, the default is to use the joint covariance matrix to find squared distance between cluster centers. If not, the default is to use the diagonal of the joint covariance matrix.

omega — (optional) numeric, this granularity parameter determines the distance between every real cluster and the artificial cluster, .OMEGA. In practice, this makes omega the maximum allowable distance between two connected clusters. By default, omega = Inf. If omega = TRUE, the maximum edge length will be set to the median edge length of the unsupervised MST times a scaling factor (omega_scale, default = 3). This value is provided as a potentially useful rule of thumb for datasets with outlying clusters or multiple, distinct trajectories, but it is not otherwise recommended.

omega_scale — (optional) numeric, scaling factor to use when omega = TRUE. The maximum edge length will be set to the median edge length of the unsupervised MST times omega_scale (default = 3).

lineages — list generated by getLineages, denotes lineages as ordered sets of clusters and contains the K x K connectivity matrix constructed on the clusters by getLineages.

shrink — logical or numeric between 0 and 1, determines whether and how much to shrink branching lineages toward their average prior to the split.

extend — character, how to handle root and leaf clusters of lineages when constructing the initial, piece-wise linear curve. Accepted values are 'y' (default), 'n', and 'pc1'. See 'Details' for more.

reweight — logical, whether to allow cells shared between lineages to be reweighted during curve-fitting. If TRUE, cells shared between lineages will be iteratively reweighted based on the quantiles of their projection distances to each curve. See 'Details' for more.

reassign — logical, whether to reassign cells to lineages at each iteration. If TRUE, cells will be added to a lineage when their projection distance to the curve is less than the median distance for all cells currently assigned to the lineage. Additionally, shared cells will be removed from a lineage if their projection distance to the curve is above the 90th percentile and their weight along the curve is less than 0.1.

thresh — numeric, determines the convergence criterion. Percent change in the total distance from cells to their projections along curves must be less than thresh. Default is 0.001, similar to principal_curve.

maxit — numeric, maximum number of iterations, see principal_curve.

stretch — numeric factor by which curves can be extrapolated beyond endpoints. Default is 2, see principal_curve.

approx_points — logical or numeric, whether curves should be approximated by a fixed number of points. If FALSE, no approximation will be performed and curves will contain as many points as the input data. If numeric, curves will be approximated by this number of points; preferably about 100 (see principal_curve).

smoother, — choice of scatter plot smoother. Same as principal_curve, but "lowess" option is replaced with "loess" for additional flexibility.

shrink.method — character denoting how to determine the appropriate amount of shrinkage for a branching lineage. Accepted values are the same as for kernel in density (default is "cosine"), as well as "tricube" and "density". See 'Details' for more.

allow.breaks logical, determines whether curves that branch very close to the origin should be allowed to have different starting points.

Details

The connectivity matrix is learned by fitting a (possibly constrained) minimum-spanning tree on the clusters and the artificial cluster, .OMEGA, which is a fixed distance away from every real cluster. This effectively limits the maximum branch length in the MST to the chosen distance, meaning that the output may contain multiple trees.

Once the connectivity is known, lineages are identified in any tree with at least two clusters. For a given tree, if there is an annotated starting cluster, every possible path out of a starting cluster and ending in a leaf that isn't another starting cluster will be returned. If no starting cluster is annotated, every leaf will be considered as a potential starting cluster and whichever configuration produces the longest average lineage length (in terms of number of clusters included) will be returned.

When there is only a single lineage, the curve-fitting algorithm is nearly identical to that of principal_curve. When there are multiple lineages and shrink == TRUE, an additional step is added to the iterative procedure, forcing curves to be similar in the neighborhood of shared points (ie., before they branch).

The extend argument determines how to construct the piece-wise linear curve used to initiate the recursive algorithm. The initial curve is always based on the lines between cluster centers and if extend = 'n', this curve will terminate at the center of the endpoint clusters. Setting extend = 'y' will allow the first and last segments to extend beyond the cluster center to the orthogonal projection of the furthest point. Setting extend = 'pc1' is similar to 'y', but uses the first principal component of the cluster to determine the direction of the curve beyond the cluster center. These options typically have little to no impact on the final curve, but can occasionally help with stability issues.

When shink == TRUE, we compute a shrinkage curve, $w_l(t)$, for each lineage, a non-increasing function of pseudotime that determines how much that lineage should be shrunk toward a shared average curve. We set $w_l(0) = 1$, so that the curves will perfectly overlap the average curve at pseudotime 0. The weighting curve decreases from 1 to 0 over the non-outlying pseudotime values of shared cells (where outliers are defined by the 1.5*IQR rule). The exact shape of the curve in this region is controlled by shrink.method, and can follow the shape of any standard kernel function's cumulative density curve (or more precisely, survival curve, since we require a decreasing function). Different choices of shrink.method seem to have little impact on the final curves, in most cases.

When reweight = TRUE, weights for shared cells are based on the quantiles of their projection distances onto each curve. The distances are ranked and converted into quantiles between 0 and 1, which are then transformed by 1 -q^2. Each cell's weight along a given lineage is the ratio of this value to the maximum value for this cell across all lineages.

Value

An object of class SlingshotDataSet containing the arguments provided to slingshot as well as the following output:

- lineages a list of L items, where L is the number of lineages identified. Each lineage is represented by a character vector with the names of the clusters included in that lineage, in order.
- connectivity the inferred cluster connectivity matrix.
- slingParamsAdditional parameters used for lineage inference or fitting simultaneous principal curves. This may include the elements start.given and end.given, logical values indicating whether the starting and ending clusters were specified a priori. Additionally, this will always include dist, the pairwise cluster distance matrix.

- curvesA list of principal_curve objects.

References

Hastie, T., and Stuetzle, W. (1989). "Principal Curves." *Journal of the American Statistical Association*, 84:502–516.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
sds <- slingshot(rd, cl, start.clus = '1')

plot(rd, col = cl, asp = 1)
lines(sds, lwd = 3)
```

SlingshotDataSet *Extract Slingshot output*

Description

This is a convenience function to extract a SlingshotDataSet from an object containing slingshot output.

Usage

```
SlingshotDataSet(data, ...)

## S4 method for signature 'SingleCellExperiment'
SlingshotDataSet(data)

## S4 method for signature 'SlingshotDataSet'
SlingshotDataSet(data)
```

Arguments

data	an object containing slingshot output.
...	additional arguments to pass to object-specific methods.

Value

A SlingshotDataSet object containing the output of slingshot.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
library(SingleCellExperiment)
u <- matrix(rpois(140*50, 5), nrow = 50)
sce <- SingleCellExperiment(assays = list(counts = u),
```

```
                            reducedDims = SimpleList(PCA = rd),
                            colData = data.frame(clus = cl))
sce <- slingshot(sce, clusterLabels = 'clus', reducedDim = 'PCA')
SlingshotDataSet(sce)
```

SlingshotDataSet-class

Class SlingshotDataSet

Description

The SlingshotDataSet class holds data relevant for performing lineage inference with the slingshot package, primarily a reduced dimensional representation of the data and a set of cluster labels. All slingshot methods can take an object of the class SlingshotDataSet as input and will output the same.

Usage

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

## S4 method for signature 'SlingshotDataSet,ANY'
reducedDim(x)

## S4 method for signature 'SlingshotDataSet'
reducedDims(x)

## S4 method for signature 'SlingshotDataSet,ANY,ANY,ANY'
x[i, j]
```

Arguments

object	a SlingshotDataSet object.
x	a SlingshotDataSet object.
i	indices to be applied to rows (cells) of the reduced dimensional matrix and cluster labels.
j	indices to be applied to the columns (dimensions) of the reduced dimensional matrix.

Details

Warning: this will remove any existing lineages or curves from the SlingshotDataSet object.

Value

The accessor functions reducedDim, clusterLabels, lineages, adjacency, curves, and slingParams return the corresponding elements of a SlingshotDataSet. The functions pseudotime and curveWeights extract useful output elements of a SlingshotDataSet, provided that curves have already been fit with either slingshot or getCurves.

Methods (by generic)

- show: a short summary of SlingshotDataSet object.
- reducedDim: returns the matrix representing the reduced dimensional dataset.
- reducedDims: returns the matrix representing the reduced dimensional dataset.
- [: Subset dataset and cluster labels.

Slots

reducedDim matrix. An n by p numeric matrix or data frame giving the coordinates of the cells in a reduced dimensionality space.

clusterLabels matrix or character. An n by K matrix of weights indicating each cell's cluster assignment or a character vector of cluster assignments, which will be converted into a binary matrix.

lineages list. A list with each element a character vector of cluster names representing a lineage as an ordered set of clusters.

adjacency matrix. A binary matrix describing the adjacency between clusters induced by the minimum spanning tree.

curves list. A list of principal_curve objects produced by getCurves.

slingParams list. Additional parameters used by Slingshot. These may specify how the minimum spanning tree on clusters was constructed:

- start.cluscharacter. The label of the root cluster.
- end.cluscharacter. Vector of cluster labels indicating the terminal clusters.
- start.givenlogical. A logical value indicating whether the initial state was pre-specified.
- end.givenlogical. A vector of logical values indicating whether each terminal state was pre-specified
- distmatrix. A numeric matrix of pairwise cluster distances.

They may also specify how simultaneous principal curves were constructed:

- shrinklogical or numeric between 0 and 1. Determines whether and how much to shrink branching lineages toward their shared average curve.
- extendcharacter. Specifies the method for handling root and leaf clusters of lineages when constructing the initial, piece-wise linear curve. Accepted values are 'y' (default), 'n', and 'pc1'. See getCurves for details.
- reweightlogical. Indicates whether to allow cells shared between lineages to be reweighted during curve-fitting. If TRUE, cells shared between lineages will be iteratively reweighted based on the quantiles of their projection distances to each curve.
- reassignlogical. Indicates whether to reassign cells to lineages at each iteration. If TRUE, cells will be added to a lineage when their projection distance to the curve is less than the median distance for all cells currently assigned to the lineage. Additionally, shared cells will be removed from a lineage if their projection distance to the curve is above the 90th percentile and their weight along the curve is less than 0.1.
- shrink.methodcharacter. Denotes how to determine the amount of shrinkage for a branching lineage. Accepted values are the same as for kernel in the density function (default is "cosine"), as well as "tricube" and "density". See getCurves for details.
- Other parameters specified by principal_curve.

slingshotExample *Bifurcating lineages data*

Description

This simulated dataset contains a low-dimensional representation of two bifurcating lineages (rd) and a vector of cluster labels generated by k-means with K = 5 (cl).

Usage

```
data("slingshotExample")
```

Format

rd is a matrix of coordinates in two dimensions, representing 140 cells. cl is a numeric vector of 140 corresponding cluster labels for each cell.

Source

Simulated data provided with the slingshot package.

Examples

```
data("slingshotExample")
rd <- slingshotExample$rd
cl <- slingshotExample$cl
slingshot(rd, cl)
```

Index