

Package ‘Trendy’

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Type Package

Title Breakpoint analysis of time-course expression data

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Description Trendy implements segmented (or breakpoint) regression models to estimate breakpoints which represent changes in expression for each feature/gene in high throughput data with ordered conditions.

Depends R (>= 3.4)

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biocViews TimeCourse, RNASeq, Regression, ImmunoOncology

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| | |
|----------------|------------------------------------|
| breakpointDist | <i>Distribution of breakpoints</i> |
|----------------|------------------------------------|

Description

calculates number of breakpoints at each time.

Usage

```
breakpointDist(topTrendyData, NDigits = 0)
```

Arguments

topTrendyData results from topTrendy() function
 NDigits how many digits to be used when rounding (default is 0 (return integers))

Value

The function takes significant genes called from the topTrendyData() function. For any time point, this function calculates how many genes have a breakpoint at this time point. The output is the numbers of genes sorted by time point.

Author(s)

Ning Leng

Examples

```
m1 <- matrix(c(c(rnorm(50,5,1),sort(rnorm(50, 15, 5))), rnorm(100, 50,10)), 2, 100, TRUE)
rownames(m1) <- c("g1","g2")
colnames(m1) <- paste0("time", seq_len(100))
myTrends <- results(trendy(m1))
topGenes <- topTrendy(myTrends)
bpDist <- breakpointDist(topGenes)
```

| | |
|---------------|-------------------------|
| breakpointFit | <i>break point fits</i> |
|---------------|-------------------------|

Description

break point fits

Usage

```
breakpointFit(J, tVectIn, lmLinear, numTry)
```

Arguments

| | |
|----------|---|
| J | number of breakpoints in the model |
| tVectIn | a numerical vector indicating the time-points or the order of samples. If it is NULL (default), then the time/order will be assumed to be equally spaced from 1:N (N is number of samples). |
| lmLinear | the linear model fit; no breakpoints |
| numTry | the number of different seeds to try. If all numTry runs fail, then the linear regression (no breakpoints, one segment) model will be returned. |

| | |
|----------------|--|
| extractPattern | <i>Extract pattern from segmented regression</i> |
|----------------|--|

Description

find dynamic genes that follow a given pattern

Usage

```
extractPattern(trendyOutData, Pattern = NULL, adjR2Cut = 0.5,
  Delay = 0)
```

Arguments

| | |
|---------------|---|
| trendyOutData | output from trendy() function |
| Pattern | vector containing pattern to search genes/features (e.g, c("up", "down")), no-change is designated by "same". If length is one (e.g c("up")) then it will only consider features with constant pattern across the entire time-course. |
| adjR2Cut | only consider features with adjusted R ² > adjR2Cut. Default = .5. |
| Delay | search for pattern starting after certain time-point (e.g. only genes with a break-point > 10). |

Value

Genes: names of genes/features containing pattern and the breakpoints corresponding to the pattern.

Author(s)

Rhonda Bacher

Examples

```
myTrends <- trendy(trendyExampleData[seq_len(5),], tVect=seq_len(40))
myTrends <- results(myTrends)
#extractPattern(myTrends, Pattern = c("up")) #increasing only features
#extractPattern(myTrends, Pattern = c("same", "down"))
#extractPattern(myTrends, Pattern = c("up", "down"), Delay = 20)
```

fitSegBIC

*Fit segmented regression models on a feature/gene***Description**

fits segmented regression models

Usage

```
fitSegBIC(Data, maxK = 2, tVectIn = NULL, minNumInSeg = 5,
  pvalCut = 0.1, numTry = 5, keepFit = FALSE)
```

Arguments

| | |
|-------------|--|
| Data | a matrix of normalized expression measurements. Rows are genes/features and columns are samples. |
| maxK | maximum number of breakpoints to consider. For each gene, trendy will fit maxK + 1 models containing 0 -> maxK breakpoints (1 -> (maxK + 1) segments). The model with the lowest BIC value will be selected (unless forceRsq = TRUE, see below). |
| tVectIn | a numerical vector indicating the time-points or the order of samples. If it is NULL (default), then the time/order will be assumed to be equally spaced from 1:N (N is number of samples). |
| minNumInSeg | minimum number of samples required to be within a segment. If a breakpoint model has a segment with fewer than minNumInSeg point in any segment, then the model is not considered valid. |
| pvalCut | p-value cutoff. If the p-value of a segment is greater than PvalCut, then the segment will be called as 'no change'. |
| numTry | the number of different seeds to try. If all numTry runs fail, then the linear regression (no breakpoints, one segment) model will be returned. |
| keepFit | whether to report the fitted object (default is FALSE). |

Value

Trend: direction of each sample; -1: down, 0: no change, 1: up Slope: fitted slopes, Slope.Trend: sign of fitted slopes, Slope.Pvalue: p value of each segment, Breakpoint: estimated breakpoints, Fitted.Values: fitted values AdjustedR2: adjusted r value of the model Fit: fit object

Author(s)

Rhonda Bacher and Ning Leng

| | |
|------------|---|
| formatFunc | <i>internal helper function to format results</i> |
|------------|---|

Description

helper function to format result

Usage

```
formatFunc(IN)
```

Arguments

IN the object to be formatted

Value

a formatted matrix of results

Author(s)

Rhonda Bacher

| | |
|---------------|---|
| formatResults | <i>Function to format results for saving.</i> |
|---------------|---|

Description

format data from Trendy which can be saved for later use.

Usage

```
formatResults(topTrendyData, featureNames = NULL)
```

Arguments

topTrendyData results from topTrendy() function
featureNames an optional vector of features (if only interested in outputting a subset of features/genes).

Value

The function will reformat the output from Trendy so that it can be easily save as a .txt or .csv file. If featureNames is supplied then only the information for those features/genes is returned.

Author(s)

Rhonda Bacher

Examples

```

data(trendyExampleData)
myTrends <- trendy(Data=trendyExampleData[seq_len(2),])
myTrends <- results(myTrends)
topTrendyRes <- topTrendy(myTrends)
resToSave <- formatResults(topTrendyRes)

```

| | |
|-----------|------------------|
| getCounts | <i>getCounts</i> |
|-----------|------------------|

Description

Convenient helper function to extract the normalized expression matrix from the SummarizedExperiment

Usage

```
getCounts(DATA)
```

Arguments

| | |
|------|--|
| DATA | An object of class SummarizedExperiment that contains expression data and metadata |
|------|--|

Value

A matrix which contains the expression data where genes/features are in rows and samples are in columns

Examples

```

m1 <- matrix(c(c(rnorm(50,5,1),sort(rnorm(50, 15, 5))), rnorm(100, 50,10)), 2, 100, TRUE)
ExampleData <-
SummarizedExperiment::SummarizedExperiment(assays=list("Counts"=m1))
myData <- getCounts(ExampleData)

```

| | |
|-------------|----------------------------------|
| plotFeature | <i>Plot features of interest</i> |
|-------------|----------------------------------|

Description

plot each feature with (or without) the fitted trend.

Usage

```

plotFeature(Data, tVectIn = NULL, featureNames, showFit = TRUE,
  simple = FALSE, showLegend = TRUE, trendyOutData = NULL,
  cexLegend = 1, legendLocation = "side", xlab = "Time",
  ylab = "Normalized Expression", segColors = c("chartreuse3",
  "coral1", "black", "cornflowerblue"), customTitle = NULL,
  customLabels.x = NULL, spacing.x = NULL)

```

Arguments

| | |
|----------------|--|
| Data | a matrix of normalized expression measurements. Rows are genes/features and columns are samples. |
| tVectIn | a numerical vector indicating the time-points or the order of samples. If it is NULL (default), then the time/order will be assumed to be equally spaced from 1:N (N is number of samples). |
| featureNames | a list of genes or features to plot |
| showFit | whether to plot the segmented regression fitting (default is TRUE) |
| simple | if TRUE the plot will not highlight the breakpoints and segments and will only display a black fitted line. (default is FALSE) |
| showLegend | if TRUE and simple=FALSE then a legend will be output (default = TRUE) |
| trendyOutData | segmented regression fitting result from running trendy(); if showFit is TRUE and trendyOutData is NULL, then the segmented regression will be fit for each of the genes and it may take longer to run |
| cexLegend | cex option for sizing of legend text, default is 1. |
| legendLocation | whether to place the legend to the right 'side' of each plot or at the 'bottom' of a multo-panelled plot (default is 'side'). |
| xlab | x-axis name |
| ylab | y-axis name |
| segColors | define colors for the 'breakpoint', and 'up', 'same', 'down' segments (default: segColors = c("chartreuse3", "coral1", "black", "cornflowerblue")) |
| customTitle | default is set the plot title as the name of the feature. Otherwise this should be a named vector, with the featureName as the name and the element as the desired plot title. (i.e. customTitle <- c("MyTitle" = gene1)). |
| customLabels.x | specify x-axis tick labels instead of using the default values from tVectIn. |
| spacing.x | specify x-axis tick spacing, smaller values give more tick marks. |

Value

plot of gene expression and fitted line

Author(s)

Ning Leng and Rhonda Bacher

Examples

```
d1 <- matrix(c(c(rnorm(50,5,1),sort(rnorm(50, 15, 5))), rnorm(100, 50,10)), 2, 100, TRUE)
rownames(d1) <- c("g1", "g2")
colnames(d1) <- paste0("time", seq_len(100))
plotFeature(d1, featureNames=c("g1", "g2"))
```

| | |
|---------|----------------|
| results | <i>results</i> |
|---------|----------------|

Description

Convenient helper function to extract the results of running Trendy. Results data.frames/matrices are stored in the metadata slot and can also be accessed without the help of this convenience function by calling `metadata()`.

Usage

```
results(DATA, type = c("TrendyFits"))
```

Arguments

| | |
|------|--|
| DATA | An object of class SummarizedExperiment that contains normalized expression and other metadata, and the output of the Trendy function. |
| type | A character variable specifying which output is desired, with possible values "TrendyFits". By default <code>results()</code> will return <code>type="TrendyFits"</code> , which is the matrix of normalized counts from SCnorm. |

Value

A data.frame containing output as detailed in the description of the type input parameter

Examples

```
data(trendyExampleData)
Conditions = rep(c(1), each= 90)
trendyOut <- trendy(Data=trendyExampleData[seq_len(2),])
trendyResults <- results(trendyOut)
```

| | |
|-----------|---|
| topTrendy | <i>obtain top genes from trendy results</i> |
|-----------|---|

Description

reformats the list output for genes with a given adjusted R² cutoff

Usage

```
topTrendy(trendyOutData, adjR2Cut = 0.5)
```

Arguments

| | |
|---------------|--|
| trendyOutData | output from the trendy function |
| adjR2Cut | cutoff for the adjusted R ² . Genes whose adjusted R ² is greater than adjR2Cut are called as significant. |

Value

only significant genes will be included in the output. The output is reformatted as: Trend direction of each sample; -1: down, 0: no change, 1: up Slope: fitted slopes, Slope.Trend: sign of fitted slopes, Slope.Pvalue: p value of each segment, Breakpoint: estimated breakpoints, Fitted.Values: fitted values AdjustedR2: adjusted r value of the model Fit: fit object

Examples

```
d1 <- matrix(c(c(rnorm(50,5,1),sort(rnorm(50, 15, 5))), rnorm(100, 50,10)), 2, 100, TRUE)
rownames(d1) <- c("g1","g2")
colnames(d1) <- paste0("time", seq_len(100))
seg.all <- trendy(d1)
seg.all <- results(seg.all)
top.genes <- topTrendy(seg.all)
```

trendHeatmap

Draw heatmap of gene expression trends

Description

heatmap of the fitted trends

Usage

```
trendHeatmap(topTrendyData, featureNames = NULL, cexRow = 0.5,
  cexCol = 0.5)
```

Arguments

topTrendyData results from topTrendy() function.

featureNames names of features/genes to plot if the heatmap should be restricted. Deafult is to plot all genes from topTrendy() function.

cexRow relative text size of row labels, default=.5.

cexCol relative text size of column labels, default=.5.

Value

The function takes significant genes/features called from the topTrendyData() function. These genes are further grouped into three groups: up, down, or no change in the first segment. Within each group, the genes are sorted by their first break point. The heatmap shows expression trends of these three groups of genes. In the heatmap, red/blue/black represents up/down/nochange. A list of genes in the heatmap order is returned.

Author(s)

Ning Leng and Rhonda Bacher

Examples

```

m1 <- matrix(c(c(rnorm(50,5,1),sort(rnorm(50, 15, 5))), rnorm(100, 50,10)), 2, 100, TRUE)
rownames(m1) <- c("g1","g2")
colnames(m1) <- paste0("time", seq_len(100))
myTrends <- results(trendy(m1))
topGenes <- topTrendy(myTrends)
#makeHeat <- trendHeatmap(topGenes)

```

trendy

*Trendy***Description**

Segmented regression models are fit for each gene. The number of model fits is 1 -> maxK.

Usage

```

trendy(Data = NULL, tVectIn = NULL, saveObject = FALSE,
       fileName = NULL, meanCut = 10, maxK = 3, minNumInSeg = 5,
       pvalCut = 0.1, numTry = 5, keepFit = FALSE, NCores = NULL,
       featureNames = NULL)

```

Arguments

| | |
|--------------|--|
| Data | a matrix of normalized expression measurements. Rows are genes/features and columns are samples. |
| tVectIn | a numerical vector indicating the time-points or the order of samples. If it is NULL (default), then the time/order will be assumed to be equally spaced from 1:N (N is number of samples). |
| saveObject | if TRUE then the trendy object produced will be saved to use in the Shiny app (default is FALSE). |
| fileName | the file name (and file path) to save the Trendy object, only used if saveObject=TRUE (default name is trendyOutputForShiny.RData). |
| meanCut | genes whose mean is less than MeanCut will not be considered, default is 10. |
| maxK | maximum number of breakpoints to consider. For each gene, trendy will fit maxK + 1 models containing 0 -> maxK breakpoints (1 -> (maxK + 1) segments). The model with the lowest BIC value will be selected (unless forceRSq = TRUE, see below). |
| minNumInSeg | minimum number of samples required to be within a segment. If a breakpoint model has a segment with fewer than minNumInSeg point in any segment, then the model is not considered valid. |
| pvalCut | p-value cutoff. If the p-value of a segment is greater than PvalCut, then the segment will be called as 'no change'. |
| numTry | the number of different seeds to try. If all numTry runs fail, then the linear regression (no breakpoints, one segment) model will be returned. |
| keepFit | whether to report the fitted object (default is FALSE). |
| NCores | number of cores to use, default is detectCores() - 1. |
| featureNames | optional parameter to specify an explicit subset of features/genes to fit the segmented regression model to. |

Value

Trend: direction of each sample; -1: down, 0: no change, 1: up Slope: fitted slopes, Slope.Trend: sign of fitted slopes, Slope.Pvalue: p value of each segment, Breakpoint: estimated breakpoints, Fitted.Values: fitted values AdjustedR2: adjusted R squared value of the model Fit: fit object

Author(s)

Ning Leng and Rhonda Bacher

Examples

```
m1 <- matrix(c(c(rnorm(50,5,1),sort(rnorm(50, 15, 5))), rnorm(100, 50,10)), 2, 100, TRUE)
rownames(m1) <- c("g1","g2")
colnames(m1) <- paste0("time", seq_len(100))
myTrends <- trendy(m1)
```

| | |
|-------------------|-----------------------------------|
| trendyExampleData | <i>Example dataset for Trendy</i> |
|-------------------|-----------------------------------|

Description

Example time-course dataset.

Usage

```
data(trendyExampleData)
```

Format

data matrix

Examples

```
data(trendyExampleData)
```

| | |
|-------------|--|
| trendyShiny | <i>Trendy shiny app to interactively visualize results after running trendy().</i> |
|-------------|--|

Description

Trendy shiny app to interactively visualize results after running trendy().

Value

Opens a browser window with an interactive shiny app and visualize all precomputed Trendy fits.

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