Package ‘groHMM’

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Description

groHMM was developed for analysis of GRO-seq data, which provides a genome wide 'map' of the position and orientation of all transcriptionally active RNA polymerases. groHMM predicts the boundaries of transcriptional activity across the genome de novo using a two-state hidden Markov model (HMM). The model essentially divides the genome into 'transcribed' and 'non-transcribed' regions in a strand specific manner.

We also use HMMs to identify the leading edge of Pol II at genes activated by a stimulus in GRO-seq time course data. This approach allows the genome-wide interrogation of transcription rates in cells.

In addition to these advanced features, groHMM provides wrapper functions for counting raw reads, generating wiggle files for visualization, and creating metagene (averaging) plots. Although groHMM is tailored towards GRO-seq data, the same functions and analytical methodologies can, in principal, be applied to a wide variety of other short read data sets.
averagePlot

**Details**

- **Package**: groHMM
- **Type**: Package
- **Version**: 0.99.0
- **Date**: 2014-04-02
- **License**: GPL (>=3)
- **LazyLoad**: yes
- **Depends**: R (>= 2.14.0), MASS, GenomicRanges, rtracklayer, parallel

**Author(s)**

Charles G. Danko, Minho Chae, Andre Martins

Maintainer: Minho Chae<minho.chae@gmail.com>

**References**


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**averagePlot**

*Returns the average profile of tiling array probe intensity values or wiggle-like count data centered on a set of genomic positions (specified by 'Peaks').*

**Description**

Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors, use the argument 'mc.cores'.

**Usage**

```r
averagePlot(ProbeData, Peaks, size = 50, bins = seq(-1000, 1000, size))
```
**Arguments**

- **ProbeData** Data frame representing chromosome, window center, and a value.
- **Peaks** Data frame representing chromosome, and window center.
- **size** Numeric. The size of the moving window. Default: 50 bp.
- **bins** The bins of the meta gene – i.e. the number of moving windows to break it into. Default +/- 1kb from center.

**Value**

A vector representing the 'typical' signal centered on the peaks of interest.

**Author(s)**

Charles G. Danko and Minho Chae

---

**breakTranscriptsOnGenes**

*breakTranscriptsOnGenes Breaks transcripts on genes*

**Description**

Breaks transcripts when they are overlapped with multiple well annotated genes.

**Usage**

`breakTranscriptsOnGenes(tx, annox, strand = "+", geneSize = 5000, threshold = 0.8, gap = 5, plot = FALSE)`

**Arguments**

- **tx** GRanges of transcripts.
- **annox** GRanges of non-overlapping annotations for reference.
- **strand** Takes "+" or "." Default: "+"
- **geneSize** Numeric. Minimum gene size in annox to be used as reference. Default: 5000
- **threshold** Numeric. Ratio of overlapped region relative to a gene width. Transcripts only greater than this threshold are subjected to be broken. Default: 0.8
- **gap** Numeric. Gap (bp) between broken transcripts. Default: 5
- **plot** Logical. If set to TRUE, show each step in a plot. Default: FALSE

**Value**

Returns GRanges object of broken transcripts.
**Author(s)**

Minho Chae and Charles G. Danko

**Examples**

```r
tax <- GRanges("chr7", IRanges(1000, 30000), strand="+")
annox <- GRanges("chr7", IRanges(start=c(1000, 20000),
          width=c(10000,10000)), strand="+)

bPlus <- breakTranscriptsOnGenes(tx, annox, strand="+")
```

---

**Description**

Combines transcripts that are within the same gene annotation, combining smaller transcripts for genes with low regulation into a single transcript representing the gene.

**Usage**

```r
combineTranscripts(tx, annox, geneSize = 1000, threshold = 0.8,
          plot = FALSE)
```

**Arguments**

- `tx` : GRanges of transcripts.
- `annox` : GRanges of non-overlapping annotations for reference.
- `geneSize` : Numeric. Minimum gene size in annotations to be used as reference. Default: 1000
- `threshold` : Numeric. Ratio of overlapped region relative to transcript width. Transcripts only greater than this threshold are subjected to be combined. Default: 0.8
- `plot` : Logical. If set to TRUE, show each step in a plot. Default: FALSE

**Value**

Returns GRanges object of combined transcripts.

**Author(s)**

Minho Chae and Charles G. Danko

**Examples**

```r
tax <- GRanges("chr7", IRanges(start=c(1000, 20000),
          width=c(10000,10000)), strand="+)
annox <- GRanges("chr7", IRanges(1000, 30000), strand="+")
combined <- combineTranscripts(tx, annox)
```
countMappableReadsInInterval

countMappableReadsInInterval counts the number of mappable reads in a set of genomic features.

Description

Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors, use the argument 'mc.cores'.

Usage

countMappableReadsInInterval(features, UnMap, debug = FALSE, ...)

Arguments

- features: A GRanges object representing a set of genomic coordinates. The meta-plot will be centered on the start position.
- UnMap: List object representing the position of un-mappable reads. Default: not used.
- debug: If set to TRUE, provides additional print options. Default: FALSE
- ...: Extra argument passed to mclapply

Value

Returns a vector of counts, each representing the number of reads inside each genomic interval.

Author(s)

Charles G. Danko and Minho Chae

detectTranscripts
detectTranscripts detects transcripts de novo using a two-state hidden Markov model (HMM).

Description

Read counts can be specified as either a GRanges object (reads), or using a fixed-step wiggle-format passed in a list (Fp and Fm). Either reads or BOTH Fp and Fm must be specified.

Usage

detectTranscripts(reads = NULL, Fp = NULL, Fm = NULL, LtProbA = -5, LtProbB = -200, UTS = 5, size = 50, threshold = 0.1, debug = TRUE, ...
detectTranscripts

Arguments

- **reads**: A GRanges object representing a set of mapped reads.
- **Fp**: Wiggle-formatted read counts on "+" strand. Optionally, Fp and Fm represent list() filled with a vector of counts for each chromosome. Can detect transcripts starting from a fixed-step wiggle.
- **Fm**: Wiggle-formatted read counts on "-" strand.
- **LtProbA**: Log probability of t... . Default: -5. One of these is just an initialization, and the final value is set by EM. The other is a holdout parameter.
- **LtProbB**: Log probability of t... . Default: -200.
- **UTS**: Variance in read counts of the untranscribed sequence. Default: 5.
- **size**: Log probability of t... . Default: -5.
- **threshold**: Threshold change in total likelihood, below which EM exits.
- **debug**: If set to TRUE, provides additional print options. Default: FALSE
- ...: Extra argument passed to mclapply

Details

Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors set the option 'mc.cores'.


Value

Returns a list of emisParams, trnasParams, viterbiStates, and transcripts. The transcript element is a GRanges object representing the predicted genomic coordinates of transcripts on both the + and - strand.

Author(s)

Charles G. Danko and Minho Chae

Examples

```r
S0mR1 <- as(readGAlignments(system.file("extdata", "S0mR1.bam", 
package="groHMM")), "GRanges")
## Not run:
# hmmResult <- detectTranscripts(S0mR1, LtProbB=-200, UTS=5, threshold=1)
# txHMM <- hmmResult$transcripts
```
evaluateHMMInAnnotations

Function evaluates HMM calling.

Description
Evaluates HMM calling of transcripts compared to known annotations.

Usage
evaluateHMMInAnnotations(tx, annox)

Arguments
- tx: GRanges of transcripts predicted by HMM.
- annox: GRanges of non-overlapping annotations.

Value
A list of error information: merged annotations, dissociated annotations, total, and rate.

Author(s)
Minho Chae

Examples
```r
tx <- GRanges("chr7", IRanges(start=seq(100, 1000, by=200),
width=seq(100, 1000, by=100)), strand="+")
annox <- GRanges("chr7", IRanges(start=seq(110, 1100, by=150),
width=seq(100, 1000, by=150)), strand="+")
error <- evaluateHMMInAnnotations(tx, annox)
```

expressedGenes

Function identifies expressed features using the methods introduced in Core, Waterfall, Lis; Science, Dec. 2008.

Description
Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors use the argument 'mc.cores'.

Usage
expressedGenes(features, reads, Lambda = NULL, UnMap = NULL,
debug = FALSE, ...)

**getCores**

**Arguments**

- **features** A GRanges object representing a set of genomic coordinates. The meta-plot will be centered on the start position. There can be optional "ID" column for gene ids.
- **reads** A GRanges object representing a set of mapped reads.
- **UnMap** List object representing the position of un-mappable reads. Default: not used.
- **debug** If set to true, returns the number of positions. Default: FALSE.
- **...** Extra argument passed to mclapply

**Value**

Returns a data.frame representing the expression p.values for features of interest.

**Author(s)**

Charles G. Danko

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**getCores**

*Returns the number of cores.*

**Description**

Returns the number of cores.

**Usage**

getCores(cores)

**Arguments**

- **cores** the number of cores, it is 1 in windows platform.

**Examples**

```r
cores <- getCores(2L)
```
**getTxDensity**

Calculates transcript density.

**Description**

Calculates transcript density for transcripts which overlap with annotations. For 'run genes together' or 'broken up a single annotation' errors, best overlapped transcripts or annotations are used.

**Usage**

```r
getTxDensity(tx, annox, plot = TRUE, scale = 1000L, nSampling = 0L, samplingRatio = 0.1, ...)
```

**Arguments**

- `tx`: GRanges of transcripts.
- `annox`: GRanges of non-overlapping annotations.
- `plot`: Logical. If TRUE, plot transcript density. Default: TRUE
- `scale`: Numeric. Scaled size of a gene for transcript density calculation. Default: 1000L
- `nSampling`: Numeric. Number of subsampling. Default: 0L
- `samplingRatio`: Numeric. Ratio of sampling for annotations. Default: 0.1
- `...`: Extra argument passed to mclapply.

**Details**

Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors set the option 'mc.cores'.

**Value**

Returns a list of FTD, TTD, PostTTS, and AUC.

**Author(s)**

Minho Chae

**Examples**

```r
tx <- GRanges("chr7", IRanges(start=seq(1000,4000, by=1000), width=seq(1000, 1300, by=100)), strand=rep("+", 4))
annox <- GRanges("chr7", IRanges(start=seq(1100,4100, by=1000), width=seq(900, 1200, by=100)), strand=rep("+", 4))
## Not run:
# density <- getTxDensity(tx, annox)
```
**limitToXkb**

**Description**

`limitToXkb` truncates a set of genomic intervals at a constant, maximum size.

**Usage**

`limitToXkb(features, offset = 1000, size = 13000)`

**Arguments**

- **features**: A GRanges object representing a set of genomic coordinates. The meta-plot will be centered on the start position.
- **offset**: Starts the interval from this position relative to the start of each genomic feature.
- **size**: Specifies the size of the window.

**Value**

Returns GRanges object with new genomic coordinates.

**Author(s)**

Minho Chae and Charles G. Danko

**Examples**

```r
tx <- GRanges("chr7", IRanges(1000, 30000), strand="+")
newTX <- limitToXkb(tx)
```

---

**makeConsensusAnnotations**

**Description**

`makeConsensusAnnotations` Makes a consensus annotation

Makes a non-overlapping consensus annotation. Gene annotations are often overlapping due to multiple isoforms for a gene. In consensus annotation, isoforms are first reduced so that only redundant intervals are used to represent a genomic interval for a gene, i.e., a gene id. Remaining unresolved annotations are further reduced by truncating 3’ end of annotations.
Usage

makeConsensusAnnotations(ar, minGap = 1L, minWidth = 1000L, ...)

Arguments

- **ar**
  - GRanges of annotations to be collapsed.
- **minGap**
  - Minimum gap between overlapped annotations after truncated. Default: 1L
- **minWidth**
  - Minimum width of consensus annotations. Default: 1000L
- **...**
  - Extra argument passed to mclapply.

Details

Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors, use the argument 'mc.cores'.

Value

Returns GRanges object of annotations.

Author(s)

Minho Chae

Examples

```r
## Not run:
# library(TxDb.Hsapiens.UCSC.hg19.knownGene)
# txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
# tx <- transcripts(txdb, columns=c("gene_id", "tx_id", "tx_name"),
#        filter=as.character(seqnames(tx)), invert=TRUE),]
# ca <- metaGene(ar, minGap = 1L, minWidth = 1000L, ...)
```

---

**Description**

Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors, set the option 'mc.cores'.

**Usage**

```r
metaGene(features, reads = NULL, plusCVG = NULL, minusCVG = NULL,
        size = 100L, up = 100000L, down = NULL, ...)
```

**metaGene**

*Returns a histogram of the number of reads in each section of a moving window centered on a certain feature.*
**Arguments**

- **features**: A GRanges object representing a set of genomic coordinates. The meta-plot will be centered on the transcription start site (TSS).
- **reads**: A GRanges object representing a set of mapped reads. Instead of 'reads', 'plusCVG' and 'minusCVG' can be used. Default: NULL.
- **plusCVG**: An IntegerRangesList object for reads with '+' strand.
- **minusCVG**: An IntegerRangesList object for reads with '-' strand.
- **size**: The size of the moving window.
- **up**: Distance upstream of each feature to align and histogram. Default: 10 kb.
- **down**: Distance downstream of each feature to align and histogram. If NULL, same as up. Default: NULL.
- **...**: Extra argument passed to mclapply

**Value**

Returns a integer-Rle representing the 'typical' signal centered on a point of interest.

**Author(s)**

Charles G. Danko and Minho Chae

**Examples**

```r
features <- GRanges("chr7", IRanges(1000, 1000), strand="+")
reads <- GRanges("chr7", IRanges(start=c(1000:1004, 1100),
   width=rep(1, 6)), strand="+")
mg <- metaGene(features, reads, size=4, up=10)
```

---

**metaGene_nL**

*Returns a histogram of the number of reads in each section of a moving window of #' variable size across genes.*

**Description**

Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors, use the argument 'mc.cores'.

**Usage**

```r
metaGene_nL(features, reads, n_windows = 1000, debug = FALSE, ...)
```
metaGeneMatrix

Arguments

features  A GRanges object representing a set of genomic coordinates.
reads     A GRanges object representing a set of mapped reads.
n_windows The number of windows to break genes into.
debug     If set to TRUE, provides additional print options. Default: FALSE
...       Extra argument passed to mclapply

Value

Returns a vector representing the 'typical' signal across genes of different length.

Author(s)

Charles G. Danko and Minho Chae

Description

Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors, use the argument 'mc.cores'.

Usage

metaGeneMatrix(features, reads, size = 50, up = 1000, down = up,
               debug = FALSE, ...)

Arguments

features  A GRanges object representing a set of genomic coordinates.
reads     A GRanges object representing a set of mapped reads.
size      The size of the moving window.
up        Distance upstream of each f to align and histogram Default: 1 kb.
down      Distance downstream of each f to align and histogram Default: same as up.
debug     If set to TRUE, provides additional print options. Default: FALSE
...       Extra argument passed to mclapply

Value

Returns a vector representing the 'typical' signal across genes of different length.

Author(s)

Charles G. Danko and Minho Chae
pausingIndex  

**Returns the pausing index for different genes. TODO: DESCRIBE THE PAUSING INDEX.**

**Description**

Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors, use the argument 'mc.cores'.

**Usage**

```r
pausingIndex(features, reads, size = 50, up = 1000, down = 1000,
             UnMAQ = NULL, debug = FALSE, ...)
```

**Arguments**

- `features`: A GRanges object representing a set of genomic coordinates.
- `reads`: A GRanges object representing a set of mapped reads.
- `size`: The size of the moving window.
- `up`: Distance upstream of each f to align and histogram.
- `down`: Distance downstream of each f to align and histogram (NULL).
- `UnMAQ`: Data structure representing the coordinates of all un-mappable regions in the genome.
- `debug`: If set to TRUE, provides additional print options. Default: FALSE
- `...`: Extra argument passed to mclapply

**Value**

Returns a data.frame of the pausing indices for the input genes.

**Examples**

```r
features <- GRanges("chr7", IRanges(2394474,2420377), strand="+")
reads <- as(readGAlignments(system.file("extdata", "S0mR1.bam",
                                      package="groHMM")), "GRanges")

## Not run:
# pi <- pausingIndex(features, reads)
```
polymeraseWave

\textit{Given GRO-seq data, identifies the location of the polymerase 'wave' in up- or down-regulated genes.}

\section*{Description}

The model is a three state hidden Markov model (HMM). States represent: (1) the 5' end of genes upstream of the transcription start site, (2) upregulated sequence, and (3) the 3' end of the gene through the polyadenylation site.

\section*{Usage}

\begin{verbatim}
polymeraseWave(reads1, reads2, genes, approxDist, size = 50, upstreamDist = 10000, TSmooth = NA, NonMap = NULL, prefix = NULL, emissionDistAssumption = "gamma", finterWindowSize = 10000, limitPCRDups = FALSE, returnVal = "simple", debug = TRUE)
\end{verbatim}

\section*{Arguments}

- \textbf{reads1} Mapped reads in time point 1.
- \textbf{reads2} Mapped reads in time point 2.
- \textbf{genes} A set of genes in which to search for the wave.
- \textbf{approxDist} The approximate position of the wave. Suggest using 2000 [bp/ min] * time [min], for mammalian data.
- \textbf{size} The size of the moving window. Suggest using 50 for direct ligation data, and 200 for circular ligation data. Default: 50.
- \textbf{upstreamDist} The amount of upstream sequence to include Default: 10 kb.
- \textbf{TSmooth} Optimally, outlying windows are set a maximum value over the inter-quantile interval, specified by TSmooth. Reasonable value: 20; Default: NA (for no smoothing). Users are encouraged to use this parameter ONLY in combination with the normal distribution assumptions.
- \textbf{NonMap} Optionally, un-mappable positions are treated as missing data. NonMap passes in the list() structure for un-mappable regions.
- \textbf{prefix} Optionally, writes out png images of each gene examined for a wave. 'Prefix' denotes the file prefix for image names written to disk. Users are encouraged to create a new directory and write in a full path.
- \textbf{emissionDistAssumption} Takes values 'norm', 'normExp', and 'gamma'. Specifies the functional form of the 'emission' distribution for states I and II (i.e. 5' of the gene, and inside of the wave). In our experience, "gamma" works best for highly-variable 'spikey' data, and 'norm' works for smooth data. As a general rule of thumb, "gamma" is used for libraries made using the direct ligation method, and 'norm' for circular ligation data. Default: "gamma".
polymeraseWave

finterWindowSize
   Method returns 'quality' information for each gene to which a wave was fit. Included in these metrics are several that define a moving window. The moving window size is specified by filterWindowSize. Default: 10 kb.

limitPCRDups
   If true, counts only 1 read at each position with >= 1 read. NOT recommended to set this to TRUE. Default: FALSE.

returnVal
   Takes value "simple" (default) or "alldata". "simple" returns a data.frame with Pol II wave end positions. "alldata" returns all of the available data from each gene, including the full posterior distribution of the model after EM.

debug
   If TRUE, prints error messages.

Details

The model computes differences in read counts between the two conditions. Differences are assumed fit a functional form which can be specified by the user (using the emissionDistAssumption argument). Currently supported functional forms include a normal distribution (good for GRO-seq data prepared using the circular ligation protocol), a gamma distribution (good for 'spikey' ligation based GRO-seq data), and a long-tailed normal+exponential distribution was implemented, but never deployed.

Initial parameter estimates are based on initial assumptions of transcription rates taken from the literature. Subsequently all parameters are fit using Baum-Welch expectation maximization.


Arguments:

Value

Returns either a data.frame with Pol II wave end positions, or a List() structure with additional data, as specified by returnVal.

Author(s)

Charles G. Danko

Examples

genes <- GRanges("chr7", IRanges(2394474,2420377), strand="+", SYMBOL="CYP2W1", ID="54905")
reads1 <- as(readGAlignments(system.file("extdata", "S0mR1.bam", package="groHMM")), "GRanges")
reads2 <- as(readGAlignments(system.file("extdata", "S40mR1.bam", package="groHMM")), "GRanges")
approxDist <- 2000*10
# Not run:
# pw <- polymeraseWave(reads1, reads2, genes, approxDist)
readBed

**Description**

Bed file format is assumed to be either four column: seqnames, start, end, strand columns; or six column: seqnames, start, end, name, score, and strand. Three column format is also possible when there is no strand information.

**Usage**

```r
readBed(file, ...)
```

**Arguments**

- `file`: Path to the input file.
- `...`: Extra argument passed to `read.table`.

**Details**

Any additional arguments available to `read.table` can be specified.

**Value**

Returns GRanges object representing mapped reads.

**Author(s)**

Minho Chae and Charles G. Danko.

RgammaMLE

**Description**

RgammaMLE fits a gamma distribution to a specified data vector using maximum likelihood.

**Usage**

```r
RgammaMLE(X)
```

**Arguments**

- `X`: A vector of observations, assumed to be real numbers in the interval [0,+Inf).
**Value**

Returns a list of parameters for the best-fit gamma distribution (shape and scale).

**Author(s)**

Charles G. Danko

---

**Rnorm**  
*Rnorm fits a normal distribution to a specified data vector using maximum likelihood.*

**Description**

Rnorm fits a normal distribution to a specified data vector using maximum likelihood.

**Usage**

```r
Rnorm(X)
```

**Arguments**

- `X`  
  A vector of observations, assumed to be real numbers in the interval (-Inf,+Inf).

**Value**

Returns a list of parameters for the best-fit normal distribution (mean and variance).

**Author(s)**

Charles G. Danko

---

**Rnorm.exp**  
*Rnorm.exp fits a normal+exponential distribution to a specified data vector using maximum likelihood.*

**Description**

Distribution function defined by: \( \alpha \cdot \text{Normal}(\text{mean}, \text{variance}) + (1-\alpha) \cdot \text{Exponential}(\lambda) \).

**Usage**

```r
Rnorm.exp(xi, wi = rep(1, NROW(xi)), guess = c(0.5, 0, 1, 1),
           tol = sqrt(.Machine$double.eps), maxit = 10000)
```
Arguments

- **xi**: A vector of observations, assumed to be real numbers in the interval (-Inf, +Inf).
- **wi**: A vector of weights. Default: vector of repeating 1; indicating all observations are weighted equally. (Are these normalized internally?! Or do they have to be [0,1]?)
- **guess**: Initial guess for parameters. Default: c(0.5, 0, 1, 1).
- **tol**: Convergence tolerance. Default: sqrt(.Machine$double.eps).
- **maxit**: Maximum number of iterations. Default: 10,000.

Details

Fits nicely with data types that look normal overall, but have a long tail starting for positive values.

Value

Returns a list of parameters for the best-fit normal distribution (alpha, mean, variance, and lambda).

Author(s)

Charles G. Danko

---

**runMetaGene**  
*Runs metagene analysis for sense and antisense direction.*

Description

Supports parallel processing using mclapply in the `parallel` package. To change the number of processors, set the option `mc.cores`.

Usage

```r
runMetaGene(features, reads, anchorType = "TSS", size = 100L,
            normCounts = 1L, up = 10000L, down = NULL, sampling = FALSE,
            nSampling = 1000L, samplingRatio = 0.1, ...)
```

Arguments

- **features**: GRanges A GRanges object representing a set of genomic coordinates, i.e., set of genes.
- **reads**: GRanges of reads.
- **anchorType**: Either 'TSS' or 'TTS'. Metagene will be centered on the transcription start site(TSS) or transcription termination site(TTS). Default: TSS.
- **size**: Numeric. The size of the moving window. Default: 100L
- **normCounts**: Numeric. Normalization vector such as average reads. Default: 1L
tlsDeming

up Numeric. Distance upstream of each feature to align and histogram. Default: 1 kb
donw Numeric. Distance downstream of each feature to align and histogram. If NULL, down is same as up. Default: NULL
sampling Logical. If TRUE, subsampling of Metagene is used. Default: FALSE
nSampling Numeric. Number of subsampling. Default: 1000L
samplingRatio Numeric. Ratio of sampling for features. Default: 0.1
...
Extra argument passed to mclapply.

Value
A list of integer-Rle for sense and antisene.

Author(s)
Minho Chae

Examples
features <- GRanges("chr7", IRanges(start=1000:1001, width=rep(1,2)),
  strand=c("+", "-"))
reads <- GRanges("chr7", IRanges(start=c(1000:1003, 1100:1101),
  width=rep(1, 6)), strand=rep(c("+","-"), 3))
## Not run:
# mg <- runMetaGene(features, reads, size=4, up=10)

Description
A 'total least squares' implementation using demming regression.

Usage
tlsDeming(x, y, d = 1)

Arguments
  x X values.
  y Y values.
  d Ratio of variances. Default: 1, for orthogonal regression.

Value
Parameters for the linear model.
**Author(s)**

Charles G. Danko

---

**tlsLoess**  
_A 'total least squares'-like hack for LOESS. Works by rotating points 45 degrees, fitting LOESS, and rotating back._

**Description**

A 'total least squares'-like hack for LOESS. Works by rotating points 45 degrees, fitting LOESS, and rotating back.

**Usage**

```r
tlsLoess(x, y, theta = -pi/4, span = 1)
```

**Arguments**

- `x`: X values.
- `y`: Y values.
- `theta`: Amount to rotate, sets the ratio of variances that are assumed by the hack. Default: -pi/4 radians (45 degrees) for orthogonal regression.
- `span`: The LOESS span parameter. Default: 1

**Value**

List of input values and LOESS predictions.

---

**tlsSvd**  
_A 'total least squares' implementation using singular value decomposition._

**Description**

A 'total least squares' implementation using singular value decomposition.

**Usage**

```r
tlsSvd(x, y)
```
windowAnalysis

Arguments

x X values.
y Y values.

Value
Parameters for the linear model $Y = aX + e$.

Author(s)
Charles G. Danko

windowAnalysis Returns a vector of integers representing the counts of reads in a moving window.

Description
Supports parallel processing using mclapply in the 'parallel' package. To change the number of processors, set the option 'mc.cores'.

Usage

windowAnalysis(reads, strand = '*', windowSize = stepSize, stepSize = windowSize, chrom = NULL, limitPCRDups = FALSE, ...)

Arguments

reads GenomicRanges object representing the position of reads mapping in the genome.
strand Takes values of '+' , '-' , or '*'. '*' denotes collapsing reads on both strands. Default: '*'.
windowSize Size of the moving window. Either windowSize or stepSize must be specified.
stepSize The number of bp moved with each step.
chrom Chromosome for which to return data. Default: returns all available data.
limitPCRDups Counts only one read mapping to each start site. NOTE: If set to TRUE, assumes that all reads are the same length (don't use for paired-end data). Default: FALSE.
...
Extra argument passed to mclapply

Value
Returns a list object, each element of which represents a chromosome.

Author(s)
Charles G. Danko and Minho Chae
Examples

```r
S0mR1 <- as(readGAlignments(system.file("extdata", "S0mR1.bam", package="groHMM")), "GRanges")
## Not run:
# Fp <- windowAnalysis(S0mR1, strand="+", windowSize=50)
```

**writeWiggle**
writeWiggle writes a wiggle track or BigWig file suitable for uploading to the UCSC genome browser.

**Description**
writeWiggle writes a wiggle track or BigWig file suitable for uploading to the UCSC genome browser.

**Usage**

```r
writeWiggle(reads, file, strand = "*", fileType = "wig", size = 50,
            normCounts = NULL, reverse = FALSE, seqinfo = NULL,
            track.type.line = FALSE, ...)
```

**Arguments**

- **reads**: GenomicRanges object representing the position of reads mapping in the genome.
- **file**: Specifies the filename for output.
- **strand**: Takes values of "+", "-", or "*". Computes writes a wiggle on the specified strand. "*" denotes collapsing reads on both strands. Default: "*".
- **fileType**: Takes values of "wig" or "BigWig". Default: "wig".
- **size**: Size of the moving window.
- **normCounts**: A normalization factor correcting for library size or other effects. For example, total mappible read counts might be a reasonable value. Default: 1 (i.e. no normalization).
- **reverse**: If set to TRUE, multiplies values by -1. Used for reversing GRO-seq data on the negative (-) strand. Default: FALSE
- **seqinfo**: Seqinfo object for reads. Default: NULL.
- **track.type.line**: If set to TRUE, prints a header identifying the file as a wiggle. Necessary to upload a custom track to the UCSC genome browser. Default: TRUE
- **...**: Extra argument passed to mclapply.

**Author(s)**
Minho Chae and Charles G. Danko
writeWiggle

Examples

```r
S0mR1 <- as(readGAlignments(system.file("extdata", "S0mR1.bam", package="groHMM")), "GRanges")
## Not run:
# writeWiggle(reads=S0mR1, file="S0mR1_Plus.wig", fileType="wig", 
# strand="+", reverse=FALSE)
```
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