Package ‘groHMM’

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Author Charles G. Danko, Minho Chae, Andre Martins, W. Lee Kraus
Maintainer Anusha Nagari <anusha.nagari@utsouthwestern.edu>, Venkat Malladi <venkat.malladi@utsouthwestern.edu>, Tulip Nandu <tulip.nandu@utsouthwestern.edu>, W. Lee Kraus <lee.kraus@utsouthwestern.edu>
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Description A pipeline for the analysis of GRO-seq data.
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BugReports https://github.com/Kraus-Lab/groHMM/issues
License GPL-3
biocViews Sequencing, Software
LazyLoad yes
NeedsCompilation yes

R topics documented:

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groHMM-package

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.

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
averagePlot

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

References


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

averagePlot(ProbeData, Peaks, size = 50, bins = seq(-1000, 1000, size))

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ProbeData</td>
<td>Data.frame representing chromosome, window center, and a value.</td>
</tr>
<tr>
<td>Peaks</td>
<td>Data.frame representing chromosome, and window center.</td>
</tr>
<tr>
<td>size</td>
<td>Numeric. The size of the moving window. Default: 50 bp.</td>
</tr>
<tr>
<td>bins</td>
<td>The bins of the meta gene – i.e. the number of moving windows to break it into. Default +/- 1kb from center.</td>
</tr>
</tbody>
</table>

Value

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

Author(s)

Charles G. Danko and Minho Chae
breakTranscriptsOnGenes

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>tx</code></td>
<td>GRanges of transcripts.</td>
</tr>
<tr>
<td><code>annox</code></td>
<td>GRanges of non-overlapping annotations for reference.</td>
</tr>
<tr>
<td><code>strand</code></td>
<td>Takes &quot;+&quot; or &quot;-&quot;. Default: &quot;+&quot;</td>
</tr>
<tr>
<td><code>geneSize</code></td>
<td>Numeric. Minimum gene size in annox to be used as reference. Default: 5000</td>
</tr>
<tr>
<td><code>threshold</code></td>
<td>Numeric. Ratio of overlapped region relative to a gene width. Transcripts only greater than this threshold are subjected to be broken. Default: 0.8</td>
</tr>
<tr>
<td><code>gap</code></td>
<td>Numeric. Gap (bp) between broken transcripts. Default: 5</td>
</tr>
<tr>
<td><code>plot</code></td>
<td>Logical. If set to TRUE, show each step in a plot. Default: FALSE</td>
</tr>
</tbody>
</table>

Value

Returns GRanges object of broken transcripts.

Author(s)

Minho Chae and Charles G. Danko

Examples

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

**combineTranscripts** Combines transcripts.

**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**

```
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**

```
tx <- GRanges("chr7", IRanges(start=c(1000, 20000), width=c(10000,10000)), strand="+")
annox <- GRanges("chr7", IRanges(1000, 30000), strand="+")
combined <- combineTranscripts(tx, annox)
```
detectTranscripts
detectTranscripts detects transcripts de novo using a two-state hidden
Markov model (HMM).

detectTranscripts

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

descr

detectTranscripts

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

descr

detectTranscripts

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

descr

detectTranscripts

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

descr

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,
...)

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
evaluateHMMInAnnotations

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

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

evaluateHMM 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 annotation, total, and rate.

Author(s)

Minho Chae
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

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

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
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

cores <- getCores(2L)

getTxDensity

getTxDensity Calculates transcript density.

Description

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

Usage

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

Arguments

tax 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'.
limitToXkb

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

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 features.
- `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(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)
```

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

makeConsensusAnnotations Makes a consensus annotation

Description

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

```r
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=list(tx_chrom="chr7"))
# tx <- tx[seqnames(tx),]
# ca <- makeConsensusAnnotations(tx)
```
**metaGene**

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

**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 = 10000L, down = NULL, ...)
```

**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`: A RangesList object for reads with '+' strand.
- `minusCVG`: A RangesList object for reads with '-' strand.
- `size`: The size of the moving window.
- `up`: Distance upstream of each features to align and histogram. Default: 10 kb.
- `down`: Distance downstream of each features to align and histogram. If NULL, same as up. Default: NULL.
- `...`: Extra argument passed to mclapply.

**Value**

Returns an 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(start=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)
```
metaGeneMatrix  

**Description**

Returns a matrix, with rows representing read counts across a specified gene, or other features of interest.

**Usage**

```r
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

---

metaGene_nL  

**Description**

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

**Usage**

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

**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, ...)
```
pausingIndex

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

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.

Returns the pausing index for different genes.

Author(s)

Charles G. Danko and Minho Chae
polymeraseWave

Examples

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

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.

Usage

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)

Arguments

reads1 Mapped reads in time point 1.
reads2 Mapped reads in time point 2.
genes A set of genes in which to search for the wave.
approxDist The approximate position of the wave. Suggest using 2000 [bp/ min] * time [min], for mammalian data.
size The size of the moving window. Suggest using 50 for direct ligation data, and 200 for circular ligation data. Default: 50.
upstreamDist The amount of upstream sequence to include Default: 10 kb.
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.
NonMap Optionally, un-mappable positions are treated as missing data. NonMap passes in the list() structure for un-mappable regions.
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.
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

readBed Returns a GenomicRanges object constructed from the specified bed file.

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

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

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

Description

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

Usage

RgammaMLE(x)

Arguments

x  A vector of observations, assumed to be real numbers in the interval [0, +\infty).

Value

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

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*Normal(mean, variance)+(1-alpha) *Exponential(lambda).

Usage

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
- **up**: Numeric. Distance upstream of each feature to align and histogram. Default: 1 kb
- **down**: 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 antisense.
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)

---

tlsDeming

A 'total least squares' implementation using demming regression.

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 variences. 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

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

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.

Author(s)
Charles G. Danko

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

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

Usage
tlsSvd(x, y)

Arguments
x X values.
y Y values.

Value
Parameters for the linear model Y~a*X+e.

Author(s)
Charles G. Danko
windowAnalysis

*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**

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

**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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