Package ‘bumphunter’

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Author Rafael A. Irizarry [cre, aut],
Martin Aryee [aut],
Kasper Daniel Hansen [aut],
Hector Corrada Bravo [aut],
Shan Andrews [ctb],
Andrew E. Jaffe [ctb],
Harris Jaffee [ctb],
Leonardo Collado-Torres [ctb]
Maintainer Rafael A. Irizarry <rafa@jimmy.harvard.edu>
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annotateNearest | Annotate the results of nearest

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**Description**

Annotate the results of nearest with more information about the type of match.

**Usage**

annotateNearest(x, subject, annotate = TRUE, ...)

**Arguments**

- **x**: The query. An IRanges or GenomicRanges object, or a data.frame with columns for start, end, and, optionally, chr or seqnames.
- **subject**: The subject. An IRanges or GenomicRanges object, or a data.frame with columns for start, end, and, optionally, chr or seqnames.
- **annotate**: Whether to annotate the result.
- **...**: Arguments passed along to nearest.

**Details**

This function runs nearest and then annotates the nearest hit. Note that the nearest subject range to a given query may not be unique and we arbitrarily chose one as done by default by nearest.

**Value**

A data frame with columns c("distance", "subjectHits", "type", "amountOverlap", "insideDistance", "size") unless annotate is FALSE, in which case only the first two columns are returned as an integer matrix.

- **dist**: Signed distance to the nearest target. Queries downstream from (i.e. past) their nearest target are given a negative distance.
- **subjectHits**: The index of the nearest target.
annotateTranscripts

Description

Annotate transcripts

Usage

annotateTranscripts(txdb, annotationPackage = NULL, by = c("tx","gene"), codingOnly=FALSE, verbose = TRUE)

Arguments

txdb A TxB database object such as TxDb.Hsapiens.UCSC.hg19.knownGene

annotationPackage An annotation data package from which to obtain gene/transcript annotation. For example org.Hs.eg.db. If none is provided the function tries to infer it from organism(txdb) and if it can’t it proceeds without annotation unless requireAnnotation = TRUE.
annotateTranscripts

by Should we create a GRanges of transcripts (tx) or genes (gene).
codingOnly Should we exclude all the non-coding transcripts.
verbose logical value. If 'TRUE', it writes out some messages indicating progress. If 'FALSE' nothing should be printed.
requireAnnotation logical value. If 'TRUE' function will stop if no annotation package is successfully loaded.
mappingInfo a named list with elements 'column', 'keytype' and 'multiVals'. If specified this information will be used with mapIds when mapping the gene ids using annotationPackage. This is useful when working with a txdb object from ENSEMBL or GENCODE among other databases.
simplifyGeneID logical value. If 'TRUE', gene ids will be shortened to before a dot is present in the id. This is useful for changing GENCODE gene ids to ENSEMBL ids.

Details

This function prepares a GRanges for the matchGenes function. It adds information and in particular adds exons information to each gene/transcript.

Value

A GRanges object with an attribute description set to annotatedTranscripts. The following columns are added. seqinfo is the information returned by seqinfo, CSS is the coding region start, CSE is the coding region end, Tx is the transcript ID used in TxDb, Entrez is the Entrez ID, Gene is the gene symbol, Refseq is the RefSeq annotation, Nexons is the number of exons, Exons is an IRanges with the exon information.

Author(s)

Harris Jaffee and Rafael A. Irizarry. 'mappingInfo' and 'simplifyGeneID' contributed by Leonardo Collado-Torres.

See Also

matchGenes

Examples

## Not run:
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
genes <- annotateTranscripts(TxDB.Hsapiens.UCSC.hg19.knownGene)

##and to avoid guessing the annotation package:
genes <- annotateTranscripts(TxDB.Hsapiens.UCSC.hg19.knownGene,annotation="org.Hs.eg.db")

## End(Not run)
**bumphunter**

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**bumphunter**  

**Bumphunter**

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**Description**

Estimate regions for which a genomic profile deviates from its baseline value. Originally implemented to detect differentially methylated genomic regions between two populations.

**Usage**

```r
## S4 method for signature 'matrix'
bumphunter(object, design, chr=NULL, pos, cluster=NULL, coef=2, cutoff=NULL, pickCutoff = FALSE, pickCutoffQ = 0.99, ... useWeights=FALSE, B=ncol(permutations), permutations=NULL, verbose=TRUE, ...)

bumphunterEngine(mat, design, chr = NULL, pos, cluster = NULL, coef = 2, cutoff = NULL, pickCutoff = FALSE, pickCutoffQ = ... smoothFunction = locfitByCluster, useWeights = FALSE, B=ncol(permutations), permutations=NULL, verbose = TRUE, ...)

## S3 method for class 'bumps'
print(x, ...)
```

**Arguments**

- **object**: An object of class matrix.
- **x**: An object of class bumps.
- **mat**: A matrix with rows representing genomic locations and columns representing samples.
- **design**: Design matrix with rows representing samples and columns representing covariates. Regression is applied to each row of mat.
- **chr**: A character vector with the chromosomes of each location.
- **pos**: A numeric vector representing the chromosomal position.
- **cluster**: The clusters of locations that are to be analyzed together. In the case of microarrays, the clusters are many times supplied by the manufacturer. If not available the function `clusterMaker` can be used to cluster nearby locations.
- **coef**: An integer denoting the column of the design matrix containing the covariate of interest. The hunt for bumps will be only be done for the estimate of this coefficient.
- **cutoff**: A numeric value. Values of the estimate of the genomic profile above the cutoff or below the negative of the cutoff will be used as candidate regions. It is possible to give two separate values (upper and lower bounds). If one value is given, the lower bound is minus the value.
- **pickCutoff**: Should bumphunter attempt to pick a cutoff using the permutation distribution?
- **pickCutoffQ**: The quantile used for picking the cutoff using the permutation distribution.
- **maxGap**: If cluster is not provided this maximum location gap will be used to define cluster via the `clusterMaker` function.
- **nullMethod**: Method used to generate null candidate regions, must be one of ‘bootstrap’ or ‘permutation’ (defaults to ‘permutation’). However, if covariates in addition to the outcome of interest are included in the design matrix (ncol(design)>2), the ‘permutation’ approach is not recommended. See vignette and original paper for more information.
smooth  A logical value. If TRUE the estimated profile will be smoothed with the smoother defined by `smoothFunction`.

smoothFunction  A function to be used for smoothing the estimate of the genomic profile. Two functions are provided by the package: `loessByCluster` and `runmedByCluster`.

useWeights  A logical value. If TRUE then the standard errors of the point-wise estimates of the profile function will be used as weights in the loess smoother `loessByCluster`. If the `runmedByCluster` smoother is used this argument is ignored.

B  An integer denoting the number of resamples to use when computing null distributions. This defaults to 0. If `permutations` is supplied that defines the number of permutations/bootstraps and B is ignored.

permutations  is a matrix with columns providing indexes to be used to scramble the data and create a null distribution when `nullMethod` is set to permutations. If the bootstrap approach is used this argument is ignored. If this matrix is not supplied and B>0 then these indexes are created using the function `sample`.

verbose  logical value. If TRUE, it writes out some messages indicating progress. If FALSE nothing should be printed.

...  further arguments to be passed to the smoother functions.

Details

This function performs the bumphunting approach described by Jaffe et al. International Journal of Epidemiology (2012). The main output is a table of candidate regions with permutation or bootstrap-based family-wide error rates (FWER) and p-values assigned.

The general idea is that for each genomic location we have a value for several individuals. We also have covariates for each individual and perform regression. This gives us one estimate of the coefficient of interest (a common example is case versus control). These estimates are then (optionally) smoothed. The smoothing occurs in clusters of locations that are ‘close enough’. This gives us an estimate of a genomic profile that is 0 when uninteresting. We then take values above (in absolute value) cutoff as candidate regions. Permutations can then performed to create null distributions for the candidate regions.

The simplest way to use permutations or bootstraps to create a null distribution is to set B. If the number of samples is large this can be set to a large number, such as 1000. Note that this will be slow and we have therefore provided parallelization capabilities. In cases where the user wants to define the permutations or bootstraps, for example cases in which all possible permutations/boostraps can be enumerated, these can be supplied via the `permutations` argument.

Uncertainty is assessed via permutations or bootstraps. Each of the B permutations/boostraps will produce an estimated ‘null profile’ from which we can define ‘null candidate regions’. For each observed candidate region we determine how many null regions are ‘more extreme’ (longer and higher average value). The ‘p.value’ is the percent of candidate regions obtained from the permutations/boostraps that are as extreme as the observed region. These p-values should be interpreted with care as the theoretical properties are not well understood. The ‘fwer’ is the proportion of permutations/boostraps that had at least one region as extreme as the observed region. We compute p.values and FWER for the area of the regions (as opposed to length and value as a pair) as well. Note that for cases with more than one covariate the permutation approach is not generally recommended; the `nullMethod` argument will coerce to ‘bootstrap’ in this scenario. See vignette and original paper for more information.

Parallelization is implemented through the `foreach` package.
An object of class bumps with the following components:

- **tab**: The table with candidate regions and annotation for these.
- **coef**: The single loci coefficients.
- **fitted**: The estimated genomic profile used to determine the regions.
- **pvaluesMarginal**: Marginal p-value for each genomic location.
- **null**: The null distribution.
- **algorithm**: Details on the algorithm.

**Author(s)**

Rafael A. Irizarry, Martin J. Aryee, Kasper D. Hansen, and Shan Andrews.

**References**


**Examples**

dat <- dummyData()
# Enable parallelization
require(doParallel)
registerDoParallel(cores = 2)
# Find bumps
bumps <- bumpHunter(dat$mat, design=dat$design, chr=dat$chr, pos=dat$pos, 
cluster=dat$cluster, coef=2, cutoff= 0.28, nullMethod="bootstrap", 
smooth=TRUE, B=250, verbose=TRUE, 
smoothFunction=loessByCluster)

bumps
# cleanup, for Windows
bumphunter:::foreachCleanup()
Arguments

- **chr**: A vector representing chromosomes. This is usually a character vector, but may be a factor or an integer.
- **pos**: A numeric vector with genomic locations.
- **assumeSorted**: This is a statement that the function may assume that the vector `pos` is sorted (within each `chr`). Allowing the function to make this assumption may increase the speed of the function slightly.
- **maxGap**: An integer. Genomic locations within `maxGap` from each other are placed into the same cluster.
- **maxClusterWidth**: An integer. A cluster large than this width is broken into subclusters.

Details

The main purpose of the function is to genomic location into clusters that are close enough to perform operations such as smoothing. A genomic location is a combination of a chromosome (`chr`) and an integer position (`pos`). Specifically, genomic intervals are not handled by this function.

Each chromosome is clustered independently from each other. Within each chromosome, clusters are formed in such a way that two positions belong to the same cluster if they are within `maxGap` of each other.

Value

A vector of integers to be interpreted as IDs for the clusters, such that two genomic positions with the same cluster ID is in the same cluster. Each genomic position receives one integer ID.

Author(s)

Rafael A. Irizarry, Hector Corrada Bravo

Examples

```r
N <- 1000
chr <- sample(1:5, N, replace=TRUE)
pos <- round(runif(N, 1, 10^5))
o <- order(chr, pos)
chr <- chr[o]
pos <- pos[o]
regionID <- clusterMaker(chr, pos)
regionID2 <- boundedClusterMaker(chr, pos)
```

dummyData

Generates dummy data for use with bumphunter functions

Description

This function generates a small dummy dataset representing samples from two different groups (cases and controls) that is used in bumphunter examples.
**dummyData**

**Usage**

```r
dummyData(n1 = 5, n2 = 5, sd = 0.2, l = 100, spacing = 100,
clusterSpacing=1e5, numClusters=5)
```

**Arguments**

- **n1** Number of samples in group 1 (controls)
- **n2** Number of samples in group 2 (cases)
- **sd** Within group standard deviation to be used when simulating data
- **l** The number of genomic locations for which to simulate data
- **spacing** The average spacing between locations. The actual locations have a random component so the actual spacing will be non-uniform
- **clusterSpacing** The spacing between clusters. (Specifically, the spacing between the first location in each cluster.)
- **numClusters** Divide the genomic locations into this number of clusters, each of which will contain locations spaced spacing bp apart.

**Value**

A list containing data that can be used with various bumphunter functions.

- **mat** A simulated data matrix with rows representing genomic locations and columns representing samples.
- **design** Design matrix with rows representing samples and columns representing covariates.
- **chr** A character vector with the chromosomes of each location.
- **pos** A numeric vector representing the chromosomal position.
- **cluster** A vector representing the cluster of each locations
- **n1** Number of samples in cluster 1
- **n2** Number of samples in cluster 2

**Author(s)**

Martin J. Aryee

**Examples**

```r
dat <- dummyData()
names(dat)
head(dat$pos)
```
getSegments

Segment a vector into positive, zero, and negative regions

description
Given two cutoffs, L and U, this function divides a numerical vector into contiguous parts that are above U, between L and U, and below L.

usage
getSegments(x, f = NULL, cutoff = quantile(abs(x), 0.99),
  assumeSorted = FALSE, verbose = FALSE)

arguments
x  A numeric vector.
f  A factor used to pre-divide x into pieces. Each piece is then segmented based on the cutoff. Setting this to NULL says that there is no pre-division. Often, clusterMaker is used to define this factor.
cutoff  a numeric vector of length either 1 or 2. If length is 1, U (see details) will be cutoff and L will be -cutoff. Otherwise it specifies L and U. The function will furthermore always use the minimum of cutoff for L and the maximum for U.
assumeSorted  This is a statement that the function may assume that the vector f is sorted. Allowing the function to make this assumption may increase the speed of the function slightly.
verbose  Should the function be verbose?

details
This function is used to find the indexes of the ‘bumps’ in functions such as bumphunter.
x is a numeric vector, which is converted into three levels depending on whether x>=U (‘up’), L<x<U (‘zero’) or x<=L (‘down’), with L and U coming from cutoff. We assume that adjacent entries in x are next to each other in some sense. Segments, consisting of consecutive indices into x (ie. values between 1 and length(x)), are formed such that all indices in the same segment belong to the same level of f and have the same discretized value of x.

In other words, we can use getSegments to find runs of x belonging to the same level of f and with all of the values of x either above U, between L and U, or below L.

value
A list with three components, each a list of indices. Each component of these lists represents a segment and this segment is represented by a vector of indices into the original vectors x and f.
upIndex:  a list with each entry an index of contiguous values in the same segment. These segments have values of x above U.
dnIndex:  a list with each entry an index of contiguous values in the same segment. These segments have values of x below L.
zeroIndex: a list with each entry an index of contiguous values in the same segment. These segments have values of x between L and U.
locfitByCluster

Author(s)
Rafael A Irizarry and Kasper Daniel Hansen

See Also
clusterMaker

Examples

x <- 1:100
y <- sin(8*pi*x/100)
chr <- rep(1, length(x))
indexes <- getSegments(y, chr, cutoff=0.8)
plot(x, y, type="n")
for(i in 1:3){
  ind <- indexes[[i]]
  for(j in seq(along=ind)) {
    k <- ind[[j]]
    text(x[k], y[k], j, col=i)
  }
}
abline(h=c(-0.8,0.8))

locfitByCluster

Apply local regression smoothing to values within each spatially-defined cluster.

Description
Local regression smoothing with a gaussian kernel, is applied independently to each cluster of genomic locations. Locations within the same cluster are close together to warrant smoothing across neighbouring locations.

Usage
locfitByCluster(y, x = NULL, cluster, weights = NULL, minNum = 7, bpSpan = 1000, minInSpan = 0, verbose = TRUE)

Arguments

y A vector or matrix of values to be smoothed. If a matrix, each column represents a sample.

x The genomic location of the values in y

cluster A vector indicating clusters of locations. A cluster is typically defined as a region that is small enough that it makes sense to smooth across neighbouring locations. Smoothing will only be applied within a cluster, not across locations from different clusters.

weights weights used by the locfit smoother

minNum Clusters with fewer than minNum locations will not be smoothed

bpSpan The span used when locfit smoothing. (Expressed in base pairs.)

minInSpan Only smooth the region if there are at least this many locations in the span.

verbose Boolean. Should progress be reported?
Details

This function is typically called by smoother, which is in turn called by bumphunter.

Value

fitted  
The smoothed data values
smoothed  
A boolean vector indicating whether a given position was smoothed
smoother  
always set to ‘locfit’.

Author(s)

Rafael A. Irizarry and Kasper D. Hansen

See Also

smoother, runmedByCluster, loessByCluster

Examples

dat <- dummyData()
smoothed <- locfitByCluster(y=dat$mat[,1], cluster=dat$cluster, bpSpan = 1000,
                          minNum=7, minInSpan=5)

loessByCluster  
Apply loess smoothing to values within each spatially-defined cluster.

Description

Loess smoothing is applied independently to each cluster of genomic locations. Locations within the same cluster are close together to warrant smoothing across neighbouring locations.

Usage

loessByCluster(y, x = NULL, cluster, weights = NULL, bpSpan = 1000,
               minNum = 7, minInSpan = 5, maxSpan = 1, verbose = TRUE)

Arguments

y  
A vector or matrix of values to be smoothed. If a matrix, each column represents a sample.
x  
The genomic location of the values in y
cluster  
A vector indicating clusters of locations. A cluster is typically defined as a region that is small enough that it makes sense to smooth across neighbouring locations. Smoothing will only be applied within a cluster, not across locations from different clusters.
weights  
weights used by the loess smoother
bpSpan  
The span used when loess smoothing. (Expressed in base pairs.)
minNum  
Clusters with fewer than minNum locations will not be smoothed
minInSpan  
Only smooth the region if there are at least this many locations in the span.
maxSpan  
The maximum span. Spans greater than this value will be capped.
verbose  
Boolean. Should progress be reported?
matchGenes

Details

This function is typically called by smoother, which is in turn called by bumphunter.

Value

- fitted: The smoothed data values
- smoothed: A boolean vector indicating whether a given position was smoothed
- smoother: always set to ‘loess’.

Author(s)

Rafael A. Irizarry

See Also

smoother, runmedByCluster, locfitByCluster

Examples

dat <- dummyData()
smoothed <- loessByCluster(y=dat$mat[,1], cluster=dat$cluster, bpSpan = 1000, minNum=7, minInSpan=5, maxSpan=1)

matchGenes

Find and annotate closest genes to genomic regions

Description

Find and annotate closest genes to genomic regions

Usage

matchGenes(x, subject, type = c("any", "fiveprime"), promoterDist = 2500, skipExons = FALSE, verbose = TRUE)

Arguments

- x: An IRanges or GenomicRanges object, or a data.frame with columns for start, end, and, optionally, chr or seqnames.
- subject: An GenomicRanges object containing transcripts or genes that have been annotated by the function annotateTranscripts.
- promoterDist: Anything within this distance to the transcription start site (TSE) will be considered a promoter.
- type: Should the distance be computed to any part of the transcript or the five prime end.
- skipExons: Should the annotation of exons be skipped. Skipping this part makes the code slightly faster.
- verbose: logical value. If 'TRUE', it writes out some messages indicating progress. If 'FALSE' nothing should be printed.
**matchGenes**

**Details**

This function runs nearest and then annotates the relationship between the region and the transcript/gene that is closest. Many details are provided on this relationship as described in the next section.

**Value**

A data frame with one row for each query and with columns `c("name", "annotation", "description", "region", "distance", "subregion", "insideDistance", "exonnumber", "nexons", "UTR", "strand", "geneL", "codingL", "Entrez", "subjectHits")`. The first column is the gene nearest the query, by virtue of it owning the transcript determined (or chosen by nearest) to be nearest the query. Note that the nearest gene to a given query, in column 3, may not be unique and we arbitrarily chose one as done by default by nearest.

The "distance" column is the distance from the query to the 5' end of the nearest transcript, so may be different from the distance computed by nearest to that transcript, as a range.

- **name**: Symbol of nearest gene
- **annotation**: RefSeq ID
- **description**: a factor with levels `c("upstream", "promoter", "overlaps 5'", "inside intron", "inside exon", "covers exon(s)", "overlaps exon upstream", "overlaps exon downstream", "overlaps two exons", "close to 3'", "downstream", "covers")`
- **region**: a factor with levels `c("upstream", "promoter", "overlaps 5'", "inside", "overlaps 3'", "close to 3'", "downstream", "covers")`
- **distance**: distance before 5' end of gene
- **subregion**: a factor with levels `c("inside intron", "inside exon", "covers exon(s)", "overlaps exon upstream", "overlaps exon downstream", "overlaps two exons")`
- **insideDistance**: distance past 5' end of gene
- **exonnumber**: which exon
- **nexons**: number of exons
- **UTR**: a factor with levels `c("inside transcription region", "5' UTR", "overlaps 5' UTR", "3'UTR", "overlaps 3' UTR", "covers transcription region")`
- **strand**: "+" or "-"
- **geneL**: the gene length
- **codingL**: the coding length
- **Entrez**: Entrez ID of closest gene
- **subjectHits**: Index in subject of hit

**Author(s)**

Harris Jaffee, Peter Murakami and Rafael A. Irizarry

**See Also**

annotateNearest, annotateTranscripts

**Examples**

```r
## Not run:
islands=makeGRangesFromDataFrame(read.delim("http://rafalab.jhsph.edu/CGI/model-based-cpg-islands-hg19.txt")[,1:100,])
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
genes <- annotateTranscripts(TxDb.Hsapiens.UCSC.hg19.knownGene)
tab<- matchGenes(islands,genes)
## End(Not run)
```
regionFinder

Find non-zero regions in vector

Description

Find regions for which a numeric vector is above (or below) predefined thresholds.

Usage

regionFinder(x, chr, pos, cluster = NULL, y = x, summary = mean,  
      ind = seq(along = x), order = TRUE, oneTable = TRUE,  
      maxGap = 300, cutoff=quantile(abs(x), 0.99),  
      assumeSorted = FALSE, verbose = TRUE)

Arguments

- **x**: A numeric vector.
- **chr**: A character vector with the chromosomes of each location.
- **pos**: A numeric vector representing the genomic location.
- **cluster**: The clusters of locations that are to be analyzed together. In the case of microarrays, the cluster is many times supplied by the manufacturer. If not available the function `clusterMaker` can be used.
- **y**: A numeric vector with same length as `x` containing values to be averaged for the region summary. See details for more.
- **summary**: The function to be used to construct a summary of the `y` values for each region.
- **ind**: an optional vector specifying a subset of observations to be used when finding regions.
- **order**: if `TRUE` then the resulting tables are ordered based on area of each region. Area is defined as the absolute value of the summarized `y` times the number of features in the regions.
- **oneTable**: if `TRUE` only one results table is returned. Otherwise, two tables are returned: one for the regions with positive values and one for the negative values.
- **maxGap**: If cluster is not provided this number will be used to define clusters via the `clusterMaker` function.
- **cutoff**: This argument is passed to `getSegments`. It represents the upper (and optionally the lower) cutoff for `x`.
- **assumeSorted**: This argument is passed to `getSegments` and `clusterMaker`.
- **verbose**: Should the function be verbose?

Details

This function is used in the final steps of `bumphunter`. While bumphunter does many things, such as regression and permutation, `regionFinder` simply finds regions that are above a certain threshold (using `getSegments`) and summarizes them. The regions are found based on `x` and the summarized values are based on `y` (which by default equals `x`). The summary is used for the ranking so one might, for example, use t-tests to find regions but summarize using effect sizes.
runmedByCluster

Value
If `oneTable` is FALSE it returns two tables otherwise it returns one table. The rows of the table are regions. Information on the regions is included in the columns.

Author(s)
Rafael A Irizarry

See Also
`bumphunter` for the main usage of this function, `clusterMaker` for the typical input to the `cluster` argument and `getSegments` for a function used within `regionFinder`.

Examples
```r
x <- seq(1:1000)
y <- sin(8*pi*x/1000) + rnorm(1000, 0, 0.2)
chr <- rep(c(1,2), each=length(x)/2)
tab <- regionFinder(y, chr, x, cutoff=0.8)
print(tab[tab$L>10,])
```

runmedByCluster
Apply running median smoothing to values within each spatially-defined cluster

Description
Running median smoothing is applied independently to each cluster of genomic locations. Locations within the same cluster are close together to warrant smoothing across neighbouring locations.

Usage
```r
runmedByCluster(y, x = NULL, cluster, weights = NULL, k = 5,
endrule = "constant", verbose = TRUE)
```

Arguments
- `y` A vector or matrix of values to be smoothed. If a matrix, each column represents a sample.
- `x` The genomic location of the values in `y`.
- `cluster` A vector indicating clusters of locations. A cluster is typically defined as a region that is small enough that it makes sense to smooth across neighbouring locations. Smoothing will only be applied within a cluster, not across locations from different clusters.
- `weights` weights used by the smoother.
- `k` integer width of median window; must be odd. See `runmed`
- `endrule` character string indicating how the values at the beginning and the end (of the data) should be treated. See `runmed`.
- `verbose` Boolean. Should progress be reported?
**smoother**

### Details

This function is typically called by `smoother`, which is in turn called by `bumphunter`.

### Value

- **fitted**: The smoothed data values
- **smoothed**: A boolean vector indicating whether a given position was smoothed
- **spans**: The span used by the loess smoother. One per cluster.
- **clusterL**: The number of locations in each cluster.
- **smoother**: always set to ‘runmed’.

### Author(s)

Rafael A. Irizarry

### See Also

`smoother`, `loessByCluster`. Also see `runmed`.

### Examples

```r
dat <- dummyData()
smoothed <- runmedByCluster(y=dat$mat[,1], cluster=dat$cluster, k=5, endrule="constant")
```

---

### Description

Apply smoothing to values typically representing the difference between two populations across genomic regions.

### Usage

```r
smoother(y, x = NULL, cluster, weights = NULL, smoothFunction, verbose = TRUE, ...)
```

### Arguments

- **y**: A vector or matrix of values to be smoothed. If a matrix, each column represents a sample.
- **x**: The genomic location of the values in y
- **cluster**: A vector indicating clusters of locations. A cluster is typically defined as a region that is small enough that it makes sense to smooth across neighbouring locations. Smoothing will only be applied within a cluster, not across locations from different clusters
- **weights**: weights used by the smoother.
- **smoothFunction**: A function to be used for smoothing the estimate of the genomic profile. Two functions are provided by the package: `loessByCluster` and `runmedByCluster`.
- **verbose**: Boolean. Should progress be reported?
- **...**: Further arguments to be passed to `smoothFunction`
Details

This function is typically called by bumhunter prior to identifying candidate bump regions. Smoothing is carried out within regions defined by the cluster argument.

Value

- `fitted`: The smoothed data values
- `smoothed`: A boolean vector indicating whether a given position was smoothed
- `spans`: The span used by the loess smoother. One per cluster.
- `clusterL`: The number of locations in each cluster.
- `smoother`: The name of the smoother used

Author(s)

Rafael A. Irizarry and Martin J. Aryee

See Also

loessByCluster, runmedByCluster

Examples

```r
dat <- dummyData()

# Enable parallelization
require(doParallel)
registerDoParallel(cores = 2)

## loessByCluster
smoothed <- smoother(y=dat$mat[,1], cluster=dat$cluster, smoothFunction=loessByCluster,
                     bpSpan = 1000, minNum=7, minInSpan=5, maxSpan=1)

## runmedByCluster
smoothed <- smoother(y=dat$mat[,1], cluster=dat$cluster, smoothFunction=runmedByCluster,
                     k=5, endrule="constant")

# cleanup, for Windows
bumhunter:::foreachCleanup()
```

Description

Example data

Format

A list with three components.

- `txdb`  Has a TxDb example.
- `org`  has an Org DB example.
- `transcripts`  has example transcripts output.
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