Package ‘hiAnnotator’

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Title Functions for annotating GRanges objects
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Description hiAnnotator contains set of functions which allow users to
annotate a GRanges object with custom set of annotations. The
basic philosophy of this package is to take two GRanges
objects (query & subject) with common set of seqnames (i.e.
chromosomes) and return associated annotation per seqnames and rows
from the query matching seqnames and rows from the subject (i.e.
genes or cpg islands). The package comes with three types of annotation
functions which calculates if a position from query is: within a feature,
near a feature, or count features in defined window sizes. Moreover, each
function is equipped with parallel backend to utilize the foreach package.
In addition, the package is equipped with wrapper functions, which finds
appropriate columns needed to make a GRanges object from a
common data frame.

Depends GenomicRanges, R (>= 2.10)
Imports foreach, iterators, rtracklayer, dplyr, BSgenome, ggplot2,
scales
License GPL (>= 2)
VignetteBuilder knitr
Suggests knitr, doParallel, testthat, BiocGenerics
biocViews Software, Annotation
LazyLoad yes
RoxygenNote 5.0.1
NeedsCompilation no

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cleanColname

Description

Function to clean the supplied string from punctuations and spaces so it can be used as column headings.

Usage

cleanColname(x, description = NULL)

Arguments

x  
string or a vector to be cleaned.

description  
OPTIONAL string identifying the purpose of the supplied string in x to be displayed in the cleaning message. This triggers a message.

Value

cleaned string or a vector.

See Also

getFeatureCounts, makeGRanges, getNearestFeature, getSitesInFeature.

Examples

cleanColname("HIV-test")
cleanColname("HIV*test")
cleanColname("HIV-test","myAlias")
**doAnnotation**

Annotate a GRanges object using one of annotation functions.

**Description**

This is a wrapper function which calls one of following functions depending on annotType parameter: `getFeatureCounts`, `getFeatureCountsBig`, `getNearestFeature`, `get2NearestFeature`, `getSitesInFeature`

**Usage**

```r
doAnnotation(annotType = NULL, ..., postProcessFun = NULL,
              postProcessFunArgs = list())
```

**Arguments**

- `annotType`: one of following: within, nearest, twoNearest, counts, countsBig.
- `...`: Additional parameters to be passed to the respective annotation function.
- `postProcessFun`: function to call on the resulting object for any post processing steps.
- `postProcessFunArgs`: additional arguments for postProcessFun as a list.

**Value**

a GRanges object with new annotation columns appended at the end of sites.rd.

**See Also**

- `makeGRanges`, `getFeatureCounts`, `getFeatureCountsBig`, `getNearestFeature`, `get2NearestFeature`, `getSitesInFeature`.

**Examples**

```r
# Convert a dataframe to GRanges object
data(sites)
alldata.rd <- makeGRanges(sites,soloStart=TRUE)
data(genes)
genes.rd <- makeGRanges(genes)

doAnnotation(annotType="within",alldata.rd,genes.rd,"InGene",asBool=TRUE)
## Not run:
doAnnotation(annotType="counts",alldata.rd,genes.rd,"NumOfGene")
doAnnotation(annotType="nearest",alldata.rd,genes.rd,"NearestGene")
doAnnotation(annotType="countsBig",alldata.rd,genes.rd,"ChipSeqCounts")
geneCheck <- function(x,wanted) { x$isWantedGene <- x$InGene %in% wanted;
return(x) }
doAnnotation(annotType="within",alldata.rd,genes.rd,"InGene",
              postProcessFun=geneCheck,
              postProcessFunArgs=list("wanted"=c("FOXJ3","SEPT9","RPTOR"))
)
## End(Not run)
```
### genes

**Sample RefSeq genes annotation**

**Description**

A sample annotation containing collection of genes from RefSeq database in the human genome mapped to UCSC freeze hg18. See UCSC table description page for the details regarding the column headings.

**Format**

A data frame with 33965 rows and 9 variables

**Source**

http://genome.ucsc.edu/cgi-bin/hgTables?db=hg18&hgta_table=refGene&hgta_doSchema=describe+table+schema

---

### get2NearestFeature

Get two nearest upstream and downstream annotation boundary for a position range.

**Description**

Given a query object, the function retrieves the two nearest feature upstream and downstream along with their properties from a subject and then appends them as new columns within the query object. When used in genomic context, the function can be used to retrieve two nearest gene upstream and downstream of the genomic position of interest.

**Usage**

```r
get2NearestFeature(sites.rd, features.rd, colnam = NULL, side = "either", feature.colnam = NULL, relativeTo = "subject")
```

**Arguments**

- **sites.rd**
  - GRanges object to be used as the query.
- **features.rd**
  - GRanges object to be used as the subject or the annotation table.
- **colnam**
  - column name to be added to sites.rd for the newly calculated annotation...serves a core!
- **side**
  - boundary of annotation to use to calculate the nearest distance. Options are '5p', '3p', 'either' (default), or 'midpoint'.
- **feature.colnam**
  - column name from features.rd to be used for retrieving the nearest feature name. By default this is NULL assuming that features.rd has a column that includes the word 'name' somewhere in it.
- **relativeTo**
  - calculate distance relative to query or subject. Default is 'subject'. See documentation of `getNearestFeature` for more information.
getFeatureCounts

Value

a GRanges object with new annotation columns appended at the end of sites.rd.

Note

• When side='midpoint', the distance to nearest feature is calculated by (start+stop)/2.
• For cases where a position is at the edge and there are no feature up/down stream since it would fall off the chromosome, the function simply returns 'NA'.
• If there are multiple locations where a query falls into, the function arbitrarily chooses one to serve as the nearest feature, then reports 2 upstream & downstream feature. That may occasionally yield features which are the same upstream and downstream, which is commonly encountered when studying spliced genes or phenomena related to it.
• If strand information doesn’t exist, then everything is defaults to ‘+’ orientation (5’ -> 3’)
• If parallel=TRUE, then be sure to have a parallel backend registered before running the function. One can use any of the following libraries compatible with foreach: doMC, doSMP, doSNOW, doMPI, doParallel. For example: library(doMC); registerDoMC(2)

See Also

getNearestFeature, makeGRanges, getFeatureCounts, getSitesInFeature.

Examples

```r
# Convert a dataframe to GRanges object
data(sites)
alldata.rd <- makeGRanges(sites, soloStart=TRUE)

data(genes)
genesis.rd <- makeGRanges(genes)

nearestGenes <- get2NearestFeature(alldata.rd, genesis.rd, "NearestGene")

## Not run:
nearestGenes <- get2NearestFeature(alldata.rd, genesis.rd, "NearestGene", side="5p")
nearestGenes <- get2NearestFeature(alldata.rd, genesis.rd, "NearestGene", side="3p")

## End(Not run)
```

getFeatureCounts

Get counts of annotation within a defined window around each query range or positions.

Description

Given a query object and window size(s), the function finds all the rows in subject which are <= window size/2 distance away. If weights are assigned to each positions in the subject, then tallied counts are multiplied accordingly. For large annotations, use getFeatureCountsBig.
getFeatureCounts

Usage

getFeatureCounts(sites.rd, features.rd, colnam = NULL, chromSizes = NULL,
widths = c(1000, 10000, 1e+06), weightsColname = NULL,
doInChunks = FALSE, chunkSize = 10000, parallel = FALSE)

Arguments

sites.rd   GRanges object to be used as the query.
features.rd GRanges object to be used as the subject or the annotation table.
colnam   column name to be added to sites.rd for the newly calculated annotation...serves as a prefix to windows sizes!
chromSizes named vector of chromosome/seqnames sizes to be used for testing if a position is off the mappable region. DEPRECATED and will be removed in future release.
widths   a named/numeric vector of window sizes to be used for casting a net around each position. Default: c(1000,10000,1000000).
weightsColname if defined, weigh each row from features.rd when tallying up the counts.
doInChunks break up sites.rd into small pieces of chunkSize to perform the calculations. Default is FALSE. Useful if you are expecting to find great deal of overlap between sites.rd and features.rd.
chunkSize number of rows to use per chunk of sites.rd. Default to 10000. Only used if doInChunks=TRUE.
parallel use parallel backend to perform calculation with foreach. Defaults to FALSE. If no parallel backend is registered, then a serial version of foreach is ran using registerDoSEQ.

Value

a GRanges object with new annotation columns appended at the end of sites.rd. There will be a column for each width defined in widths parameter. If widths was a named vector i.e. c("100bp"=100,"1K"=1000), then the colname parameter will be pasted together with width name else default name will be generated by the function.

Note

• If parallel=TRUE, then be sure to have a parallel backend registered before running the function. One can use any of the following libraries compatible with foreach: doMC, doSMP, doSNOW, doMPI. For example: library(doMC); registerDoMC(2)

See Also

makeGRanges, getNearestFeature, getSitesInFeature, getFeatureCountsBig.

Examples

# Convert a dataframe to GRanges object
data(sites)
alldata.rd <- makeGRanges(sites,soloStart=TRUE)

data(genes)
genes.rd <- makeGRanges(genes)
getFeatureCountsBig

```r
geneCounts <- getFeatureCounts(alldata.rd,genes.rd,"NumOfGene")
## Not run:
geneCounts <- getFeatureCounts(alldata.rd,genes.rd,"NumOfGene",
doInChunks=TRUE, chunkSize=200)
geneCounts  
## Parallel version of getFeatureCounts
# geneCounts <- getFeatureCounts(alldata.rd,genes.rd,"NumOfGene",
# parallel=TRUE)
# geneCounts

## End(Not run)
```

---

getFeatureCountsBig  
Get counts of annotation within a defined window around each query range/position for large annotation objects spanning greater than 1 billion rows.

Description

Given a query object and window size(s), the function finds all the rows in subject which are \( \leq \) window size/2 distance away. Note that here counting is done using midpoint of the ranges in query instead of start-stop boundaries. The counts will differ slightly when compared to `getFeatureCounts`.

Usage

```r
getFeatureCountsBig(sites.rd, features.rd, colnam = NULL, widths = c(1000, 10000, 1e+06))
```

Arguments

- `sites.rd`  
  GRanges object to be used as the query.
- `features.rd`  
  GRanges object to be used as the subject or the annotation table.
- `colnam`  
  column name to be added to sites.rd for the newly calculated annotation...serves as a prefix to windows sizes!
- `widths`  
  a named/numeric vector of window sizes to be used for casting a net around each position. Default: `c(1000,10000,1000000)`

Value

a GRanges object with new annotation columns appended at the end of sites.rd. There will be a column for each width defined in widths parameter. If widths was a named vector i.e. `c("100bp"=100,"1K"=1000)`, then the colname parameter will be pasted together with width name else default name will be generated by the function.

See Also

`makeGRanges, getNearestFeature, getSitesInFeature, getFeatureCounts`. 
getLowestDists

Get the lowest biological distance from the 5' or 3' boundaries of query and subject.

Description

Given a query and subject with indices from nearest, calculate the shortest biological distance to either boundaries of the query and subject. This is a helper function utilized in getNearestFeature, get2NearestFeature

Usage

getLowestDists(query = NULL, subject = NULL, res.nrst = NULL, side = "either", relativeTo = "subject")

Arguments

query GRanges object to be used as the query which holds data for 'queryHits' attribute of res.nrst.
subject GRanges object to be used as the subject which holds data for 'subjectHits' attribute of res.nrst.
res.nrst a dataframe of nearest indices as returned by nearest.
side boundary of subject/annotation to use to calculate the nearest distance. Options are '5p','3p', or the default 'either'.
relativeTo calculate distance relative to query or subject. Default is 'subject'. See documentation of getNearestFeature for more information.

Value

res.nrst with lowest distances appended at the end.

Note

for cases where a query has multiple nearest neighbors or overlaps with >1 subjects, the function will choose the subject with the lowest absolute distance.
getNearestFeature

See Also

gGetNearestFeature, get2NearestFeature.

Examples

query <- GRanges("A", IRanges(c(1, 5, 12, 20), width=1),
        strand=c("-","+","-","+"))
subject <- GRanges("A", IRanges(c(1,5,10,15,21), width=8:4),
        strand=c("+","+","-","-","-"))
res <- as.data.frame(nearest(query, subject, select="all",
        ignore.strand=TRUE))
res <- getLowestDists(query, subject, res, "either", "query")

---

getNearestFeature Get nearest annotation boundary for a position range.

Description

Given a query object, the function retrieves the nearest feature and its properties from a subject and
then appends them as new columns within the query object. When used in genomic context, the
function can be used to retrieve the nearest gene 5’ or 3’ end relative to genomic position of interest.

Usage

getNearestFeature(sites.rd, features.rd, colnam = NULL, side = "either",
        feature.colnam = NULL, dists.only = FALSE, parallel = FALSE,
        relativeTo = "subject")

Arguments

- **sites.rd**: GRanges object to be used as the query.
- **features.rd**: GRanges object to be used as the subject or the annotation table.
- **colnam**: column name to be added to sites.rd for the newly calculated annotation...serves
  a core!
- **side**: boundary of annotation to use to calculate the nearest distance. Options are
  '5p','3p','either'(default), or 'midpoint'.
- **feature.colnam**: column name from features.rd to be used for retrieving the nearest feature name.
  By default this is NULL assuming that features.rd has a column that includes the
  word ‘name’ somewhere in it.
- **dists.only**: flag to return distances only. If this is TRUE, then ‘feature.colnam’ is not re-
  quired and only distance to the nearest feature will be returned. By default this
  is FALSE.
- **parallel**: use parallel backend to perform calculation with foreach. Defaults to FALSE.
  If no parallel backend is registered, then a serial version of foreach is ran using
  registerDoSEQ.
- **relativeTo**: calculate distance relative to query or subject. Default is ‘subject’. This essentially
  means whether to use query or subject as the anchor point to get distance from!
Value

a GRanges object with new annotation columns appended at the end of sites.rd.

Note

• When side='midpoint', the distance to nearest feature is calculated by (start+stop)/2.
• If strand information doesn’t exist, then everything is defaulted to ‘+’ orientation (5' -> 3’)
• If parallel=TRUE, then be sure to have a parallel backend registered before running the function. One can use any of the following libraries compatible with foreach: doMC, doSMP, doSNOW, doMPI, doParallel. For example: library(doMC); registerDoMC(2)
• When relativeTo="subject", the biological distance is relative to subject, meaning, the function reports the distance to query from subject (i.e. an integration site is upstream or downstream from a gene). When relativeTo="query", the distance is from the point of view of query or an integration site (i.e. gene is upstream or downstream from an integration site).

See Also

makeGRanges, getFeatureCounts, getSitesInFeature, get2NearestFeature.

Examples

# Convert a dataframe to GRanges object
data(sites)
alldata.rd <- makeGRanges(sites,soloStart=TRUE)
data(genes)
genes.rd <- makeGRanges(genes)

nearestGenes <- getNearestFeature(alldata.rd,genes.rd,"NearestGene")
nearnestGenes <- getNearestFeature(alldata.rd,genes.rd,"NearestGene", side="5p")
nearcestGenes
## Not run:
nearrestGenes <- getNearestFeature(alldata.rd,genes.rd,"NearestGene", side="3p")
nearrestGenes
## Parallel version of getNearestFeature
nearestGenes <- getNearestFeature(alldata.rd,genes.rd,"NearestGene", parallel=TRUE)
nearrestGenes
## End(Not run)

getRelevantCol

Find the column index of interest given the potential choices.
**Description**

The function finds relevant column(s) of interest from a vector of column names derived from a dataframe. If no usable column is found, the function spits out a relevant error or returns the index of the usable column(s). This is an assistant function called by functions listed in the see also section.

**Usage**

```r
getRelevantCol(col.names, col.options, col.type = NULL, multiple.ok = FALSE)
```

**Arguments**

- `col.names`: column names from a dataframe
- `col.options`: potential column names or partial names that may exist in `col.names`
- `col.type`: type of column information the function is searching for, used in construction of error messages. Default is `NULL`.
- `multiple.ok`: if multiple matches are found then return indices, else spit an error out. Default is `TRUE`.

**Value**

the index of usable column(s) or an error if no applicable column is found.

**See Also**

`makeGRanges`, `getNearestFeature`, `getSitesInFeature`.

**Examples**

```r
data(sites)
names(sites)
getRelevantCol(names(sites),c("chr","chromosome","tname","seqnames",
"chrom","contig"),"seqnames")
getRelevantCol(names(sites),c("ort","orientation","strand"),"strand")
```

---

**getSitesInFeature**

Find overlapping positions/ranges that match between the query and subject.

**Description**

When used in genomic context, the function annotates genomic positions of interest with information like if they were in a gene or cpg island or whatever annotation that was supplied in the subject.

**Usage**

```r
getSitesInFeature(sites.rd, features.rd, colnam = NULL, asBool = FALSE,
feature.colnam = NULL, parallel = FALSE, allSubjectCols = FALSE,
overlapType = "any")
```
getSitesInFeature

Arguments

- **sites.rd**
  - GRanges object to be used as the query.

- **features.rd**
  - GRanges object to be used as the subject or the annotation table.

- **colnam**
  - column name to be added to sites.rd for the newly calculated annotation...serves a core! If allSubjectCols=TRUE, then this is used as a prefix to all metadata column.

- **asBool**
  - Flag indicating whether to return results as TRUE/FALSE or the property of an overlapping feature..namely feature name and orientation if available. Defaults to FALSE.

- **feature.colnam**
  - column name from features.rd to be used for retrieving the feature name. By default this is NULL assuming that features.rd has a column that includes the word 'name' somewhere in it. Not required if asBool=TRUE or allSubjectCols=TRUE

- **parallel**
  - use parallel backend to perform calculation with foreach. Defaults to FALSE. Not applicable when asBool=T. If no parallel backend is registered, then a serial version of foreach is ran using registerDoSEQ.

- **allSubjectCols**
  - Flag indicating whether to return all annotations or metadata columns from features.rd. Defaults to FALSE.

- **overlapType**
  - see findOverlaps. Defaults to 'any'

Value

- a GRanges object with new annotation columns appended at the end of sites.rd.

Note

- If parallel=TRUE, then be sure to have a parallel backend registered before running the function. One can use any of the following libraries compatible with foreach: doMC, doSMP, doSNOW, doMPI. For example: library(doMC); registerDoMC(2)

See Also

- makeGRanges, getFeatureCounts, getNearestFeature.

Examples

```r
# Convert a dataframe to GRanges object
data(sites)
alldata.rd <- makeGRanges(sites,soloStart=TRUE)
data(genes)
genrows.rd <- makeGRanges(genes)

InGenes <- getSitesInFeature(alldata.rd,genes.rd,"InGene")
InGenes
## Not run:
InGenes <- getSitesInFeature(alldata.rd,genes.rd,"InGene",asBool=TRUE)
InGenes
## Parallel version of getSitesInFeature
InGenes <- getSitesInFeature(alldata.rd,genes.rd,"InGene",asBool=TRUE, parallel=TRUE)
InGenes
```
getUCSCtable

```
InGenes <- getSitesInFeature(alldata.rd, genes.rd, "InGene",
allSubjectCols=TRUE, parallel=TRUE)
InGenes

## End(Not run)
```

getUCSCtable

Obtain a UCSC annotation table given the table & track name.

Description

Obtain a UCSC annotation table given the table & track name.

Usage

```
getUCSCtable(tableName, trackName, bsession = NULL, freeze = "hg18", ...)
```

Arguments

- `tableName`: Name of the annotation table as it appears on UCSC browser.
- `trackName`: Name of the track annotation table as it appears in UCSC browser.
- `bsession`: UCSC session object returned by `makeUCSCsession` or `browserSession`. If left NULL the function will call `makeUCSCsession` with the provided freeze to initiate a session.
- `freeze`: one of following: hg18, mm8, rheM, etc. Default is hg18.
- `...`: Arguments to be passed to `ucscTableQuery`.

Value

a dataframe containing the annotation data.

See Also

`makeUCSCsession`, `getNearestFeature`, `getSitesInFeature`.

Examples

```
## Not run:
refflat <- getUCSCtable("refFlat","RefSeq Genes")
## same as above ##
refflat <- getUCSCtable("refFlat","RefSeq Genes",
bsession=session,freeze="hg18")

## End(Not run)
```
getWindowLabel  Generate a window size label.

Description

Function to generate aesthetically pleasing window size label given an integer. This is one of the helper function used in `getFeatureCounts` & `getFeatureCountsBig`.

Usage

```r
getWindowLabel(x)
```

Arguments

- `x` vector of integers to generate the labels for.

Value

a character vector of length(x) which has x normalized and suffixed by bp, Kb, Mb, or Gb depending on respective interval sizes.

See Also

`getFeatureCounts`, `makeGRanges`, `getNearestFeature`, `getSitesInFeature`.

Examples

```r
getWindowLabel(c(0, 1e7, 1e3, 1e6, 2e9))
```

hiAnnotator  Annotating GRanges objects with hiAnnotator.

Description

hiAnnotator contains set of functions which allow users to annotate a GRanges object with custom set of annotations. The basic philosophy of this package is to take two GRanges objects (query & subject) with common set of seqnames (i.e. chromosomes) and return associated annotation per seqnames and rows from the query matching seqnames and rows from the subject (i.e. genes or cpg islands). The package comes with three types of annotation functions which calculates if a position from query is: within a feature, near a feature, or count features in defined window sizes. Moreover, one can utilize parallel backend for each annotation function to utilize the foreach package. In addition, the package is equipped with wrapper functions, which finds appropriate columns needed to make a GRanges object from a common dataframe.

Author(s)

Nirav V Malani
makeChunks  

Description

Breaks two GRanges objects into chunks of N size.

Usage

makeChunks(sites.rd, features.rd, chunkSize = NULL)

Arguments

- sites.rd: a GRanges object.
- features.rd: a GRanges object.
- chunkSize: number of rows to use per chunk of query. Default to length(sites.rd)/detectCores() or length(query)/getDoParWorkers() depending on parallel backend registered.

Value

a list of GRanges objects where each element is of length 2 representing query & subject chunks.

See Also

makeGRanges, doAnnotation, getNearestFeature, getSitesInFeature, getFeatureCounts.

Examples

data(sites)
data(genes)
sites <- makeGRanges(sites, soloStart=TRUE)
genes <- makeGRanges(genes)
makeChunks(sites, genes)

makeGRanges  

Description

Make a sorted GRanges object from a dataframe.

Description

The function converts a dataframe into a GRanges object without too much hassle of renaming column names. The function finds column names that sound like seqname, chromosome, start, stop, position, etc and puts them in respective slots to facilitate the conversion of a dataframe to a GRanges object. If more than one column that sounds like start, stop, or position is present, the function will use the first match as the representative. It is recommended to run this function before utilizing any other annotation functions since it will sort the object by chromosome and position for copying annotations back to their respective rows confidently.
makeGRanges

Usage

makeGRanges(x, freeze = NULL, positionsOnly = FALSE, soloStart = FALSE, chromCol = NULL, strandCol = NULL, startCol = NULL, stopCol = NULL, keepFactors = FALSE)

Arguments

x dataframe to be converted into a GRanges object
freeze UCSC genome version of the data in x. Default is NULL. This parameter is generally used to populate seqinfo slot of GRanges objects.
positionsOnly boolean flag indicating to return only position based data or everything from the dataframe. Defaults to FALSE.
soloStart flag denoting whether only one position based column is available. In other words, only starts are present and no stops. Default=FALSE.
chromCol use the defined column name for seqname/chromosome based data from the dataframe. Defaults to NULL.
strandCol use the defined column name for strand or orientation from the dataframe. Defaults to NULL.
startCol use the defined column name for start coordinate from the dataframe. Defaults to NULL.
stopCol use the defined column name for stop coordinate from the dataframe. Defaults to NULL and not required if soloStart=TRUE.
keepFactors keep vectors/columns stored as factors? Defaults to FALSE

Value

a GRanges object converted from x.

See Also

getNearestFeature, getFeatureCounts, getSitesInFeature.

Examples

# Convert a dataframe to GRanges object
data(genes)
makeGRanges(genes, soloStart=TRUE)
makeGRanges(genes)
#makeGRanges(genes, freeze="hg18", soloStart=TRUE)
#makeGRanges(genes, freeze="hg18")
**makeUCSCsession**

Initiate UCSC genome browser session given the freeze argument.

**Description**

Initiate UCSC genome browser session given the freeze argument.

**Usage**

```r
makeUCSCsession(freeze = "hg18")
```

**Arguments**

- **freeze**
  - one of following: hg18, mm8, rheM, etc. Default is hg18.

**Value**

browser session object compatible with rtracklayer functions.

**See Also**

- getUCSCtable, makeGRanges, getNearestFeature, getSitesInFeature

**Examples**

```r
## Not run:
session <- makeUCSCsession()
geno <- genomic(session)
session <- makeUCSCsession("mm8")
geno <- genomic(session)
## End(Not run)
```

---

**plotdisFeature**

Plot distance distribution to a feature boundary.

**Description**

Given a dataframe of samples and distance based annotation, the function calculates the distribution of data in or around the given annotation. From genomic point of view, the function can be used to identify distribution of data around genomic features like gene TSS, CpG island, etc.

**Usage**

```r
plotdisFeature(dat = NULL, grouping = NULL, annotCol = NULL,
               breaks = NULL, discreteBins = TRUE, geom = "bar", stacked = FALSE,
               typeRatio = FALSE, printPlotData = FALSE)
```
### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>dat</code></td>
<td>a dataframe/GRanges with required columns to make the plot.</td>
</tr>
<tr>
<td><code>grouping</code></td>
<td>name of the column grouping the data or denoting the samples</td>
</tr>
<tr>
<td><code>annotCol</code></td>
<td>name of the column holding the distance to feature data. This can also be boolean data in which case plot will be in/out of feature.</td>
</tr>
<tr>
<td><code>breaks</code></td>
<td>intervals by which to break up the distance data. Default is seq(-1e5,1e5,5e3). Not required if ‘annotCol’ is of type boolean.</td>
</tr>
<tr>
<td><code>discreteBins</code></td>
<td>whether to plot continuous variable supplied in annotCol as a discrete axis. This conserves plotting area, thus default is TRUE.</td>
</tr>
<tr>
<td><code>geom</code></td>
<td>plot distribution using bars or lines? Default is 'bar'. One can use 'line' as well when there are many groups.</td>
</tr>
<tr>
<td><code>stacked</code></td>
<td>make a stacked plot? Only applies when geom is 'bar'. Default is FALSE.</td>
</tr>
<tr>
<td><code>typeRatio</code></td>
<td>whether to plot data as ratio of experimental to controls. Default is FALSE. Enabling this requires a column in 'dat' called &quot;type&quot; with two values &quot;expr&quot; for experimental and &quot;ctrl&quot; for control. This column subdivides data within each group. Enabling this transforms the data into plotting distribution of ratios of experimental/controls around feature of interest.</td>
</tr>
</tbody>
</table>

### Value

ggplot2 plot and/or table of summarized plot data.

### See Also

`makeGRanges`, `getNearestFeature`, `getSitesInFeature`, `getFeatureCounts`

### Examples

```r
# Convert a dataframe to GRanges object
data(sites)
data(sites.ctrl)
sites$type <- "expr"
sites <- rbind(sites,sites.ctrl)
alldata.rd <- makeGRanges(sites,soloStart=TRUE)
data(genes)
genes.rd <- makeGRanges(genes)

res <- doAnnotation(annotType="within", alldata.rd, genes.rd, "InGene", asBool=TRUE)
plotdisFeature(res, "virus", "InGene")
plotdisFeature(res, "virus", "InGene", typeRatio=TRUE)

## Not run:
res <- doAnnotation(annotType="nearest", res, genes.rd, "NearestGene", side="5p")
plotdisFeature(res, "virus", "X5pNearestGeneDist")
plotdisFeature(res, "virus", "X5pNearestGeneDist", typeRatio=TRUE)

## End(Not run)
```
**sites**  
*Sample Retrovirus Integration Sites data*

**Description**  
A sample dataset containing collection of unique HIV & MLV integration sites in the human genome mapped to UCSC freeze hg18 from PMID: 12805549.

**Format**  
A data frame with 1303 rows and 5 variables

**Details**  
- Sequence. Name of the DNA sequence which was aligned to the host genome. This is also a unique ID.
- Position. The genomic coordinate of the integration site.
- Chr. The chromosome of the integration site.
- Ort. The orientation or strand of the integration site.
- virus. Name of the virus used for the experiment and a given sequencing clone.

**Source**  

---

**sites.ctrl**  
*Controls for Sample Retrovirus Integration Sites data*

**Description**  
Controls for a sample dataset containing collection of unique HIV & MLV integration sites in the human genome mapped to UCSC freeze hg18 from PMID: 12805549. Each row represents three controls per integration site in sites object.

**Format**  
A data frame with 3909 rows and 6 variables

**Details**  
- Sequence. Name of the DNA sequence which was aligned to the host genome. There should be three control sites per experimental site from the "sites" dataset.
- Position. The genomic coordinate of the integration site.
- Chr. The chromosome of the integration site.
- Ort. The orientation or strand of the integration site.
- virus. Name of the virus used for the experiment and a given sequencing clone.
- type. Column denoting whether the data is control
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