

Package ‘RCAS’

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Type Package

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Description RCAS is an R/Bioconductor package designed as a generic reporting tool for the functional analysis of transcriptome-wide regions of interest detected by high-throughput experiments. Such transcriptomic regions could be, for instance, signal peaks detected by CLIP-Seq analysis for protein-RNA interaction sites, RNA modification sites (alias the epitranscriptome), CAGE-tag locations, or any other collection of query regions at the level of the transcriptome. RCAS produces in-depth annotation summaries and coverage profiles based on the distribution of the query regions with respect to transcript features (exons, introns, 5'/3' UTR regions, exon-intron boundaries, promoter regions). Moreover, RCAS can carry out functional enrichment analyses and discriminative motif discovery.

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Contents

| | |
|--|----|
| calculateCoverageProfile | 3 |
| calculateCoverageProfileFromTxdb | 4 |
| calculateCoverageProfileList | 4 |
| calculateCoverageProfileListFromTxdb | 5 |
| checkSeqDb | 5 |
| createControlRegions | 6 |
| createDB | 6 |
| createOrthologousGeneSetList | 8 |
| deleteSampleDataFromDB | 8 |
| discoverFeatureSpecificMotifs | 9 |
| extractSequences | 10 |
| findDifferentialMotifs | 10 |
| findEnrichedFunctions | 11 |
| generateKmers | 12 |
| getFeatureBoundaryCoverage | 12 |
| getFeatureBoundaryCoverageBin | 13 |
| getFeatureBoundaryCoverageMulti | 14 |
| getIntervalOverlapMatrix | 15 |
| getMotifSummaryTable | 16 |
| getPWM | 17 |
| getTargetedGenesTable | 17 |
| getTxdbFeatures | 18 |
| getTxdbFeaturesFromGRanges | 18 |
| gff | 19 |
| importBed | 19 |
| importBedFiles | 20 |
| importGtf | 21 |
| parseMsigdb | 22 |
| plotFeatureBoundaryCoverage | 22 |
| printMsigdbDataset | 23 |
| queryGff | 23 |
| queryRegions | 24 |
| retrieveOrthologs | 24 |
| runGSEA | 25 |
| runMotifDiscovery | 25 |
| runMotifRG | 26 |
| runReport | 26 |
| runReportMetaAnalysis | 28 |
| runTopGO | 29 |
| summarizeDatabaseContent | 30 |
| summarizeQueryRegions | 30 |

| | |
|---|-----------|
| <i>calculateCoverageProfile</i> | 3 |
| <i>summarizeQueryRegionsMulti</i> | 31 |
| Index | 32 |

`calculateCoverageProfile`
calculateCoverageProfile

Description

This function checks overlaps between input query regions and annotation features, and then calculates coverage profile along target regions.

Usage

```
calculateCoverageProfile(
  queryRegions,
  targetRegions,
  sampleN = 0,
  bin.num = 100,
  bin.op = "mean",
  strand.aware = TRUE
)
```

Arguments

| | |
|----------------------------|---|
| <code>queryRegions</code> | GRanges object imported from a BED file using <code>importBed</code> function |
| <code>targetRegions</code> | GRanges object containing genomic coordinates of a target feature (e.g. exons) |
| <code>sampleN</code> | If set to a positive integer, <code>targetRegions</code> will be downsampled to <code>sampleN</code> regions |
| <code>bin.num</code> | Positive integer value (default: 100) to determine how many bins the <code>targetRegions</code> should be split into (See <code>genomation::ScoreMatrixBin</code>) |
| <code>bin.op</code> | The operation to apply for each bin: 'min', 'max', or 'mean' (default: mean). (See <code>genomation::ScoreMatrixBin</code>) |
| <code>strand.aware</code> | TRUE/FALSE (default: TRUE) The strands of target regions are considered. |

Value

A `ScoreMatrix` object returned by `genomation::ScoreMatrixBin` function. Target regions are divided into 100 equal sized bins and coverage level is calculated in a strand-specific manner.

Examples

```
data(gff)
data(queryRegions)
txdbFeatures <- getTxdbFeaturesFromGRanges(gffData = gff)
df <- calculateCoverageProfile(queryRegions = queryRegions,
                             targetRegions = txdbFeatures$exons,
                             sampleN = 1000)
```

```
calculateCoverageProfileFromTxdb
    calculateCoverageProfileFromTxdb
```

Description

This function is deprecated. Use ?calculateCoverageProfile instead.

Usage

```
calculateCoverageProfileFromTxdb()
```

```
calculateCoverageProfileList
    calculateCoverageProfileList
```

Description

This function checks overlaps between input query regions and a target list of annotation features, and then calculates the coverage profile along the target regions.

Usage

```
calculateCoverageProfileList(
  queryRegions,
  targetRegionsList,
  sampleN = 0,
  bin.num = 100,
  bin.op = "mean",
  strand.aware = TRUE
)
```

Arguments

| | |
|-------------------|--|
| queryRegions | GRanges object imported from a BED file using importBed function |
| targetRegionsList | A list of GRanges objects containing genomic coordinates of target features (e.g. transcripts, exons, introns) |
| sampleN | If set to a positive integer, targetRegions will be downsampled to sampleN regions |
| bin.num | Positive integer value (default: 100) to determine how many bins the targetRegions should be split into (See genomation::ScoreMatrixBin) |
| bin.op | The operation to apply for each bin: 'min', 'max', or 'mean' (default: mean). (See genomation::ScoreMatrixBin) |
| strand.aware | TRUE/FALSE (default: TRUE) The strands of target regions are considered. |

Value

A data.frame consisting of four columns: 1. bins level 2. meanCoverage 3. standardError 4. feature
Target regions are divided into 100 equal sized bins and coverage level is summarized in a strand-specific manner using the `genomation::ScoreMatrixBin` function. For each bin, mean coverage score and the standard error of the mean coverage score is calculated (`plotrix::std.error`)

Examples

```
data(gff)
data(queryRegions)
txdbFeatures <- getTxdbFeaturesFromGRanges(gffData = gff)
dfList <- calculateCoverageProfileList(queryRegions = queryRegions,
                                     targetRegionsList = txdbFeatures,
                                     sampleN = 1000)
```

```
calculateCoverageProfileListFromTxdb
      calculateCoverageProfileListFromTxdb
```

Description

This function is deprecated. Use `?calculateCoverageProfileList` instead.

Usage

```
calculateCoverageProfileListFromTxdb()
```

```
checkSeqDb      checkSeqDb
```

Description

Given a string that denotes a genome version (e.g. hg19) returns the BSgenome object matching the genome version that are available in `BSgenome::available.genomes()`

Usage

```
checkSeqDb(genomeVersion)
```

Arguments

`genomeVersion` String that denotes genome version. To unambiguously select a BSgenome object, provide a string that matches the end of the available genomes at: `BSgenome::available.genomes()`

Value

Returns a BSgenome object that uniquely matches the genomeVersion.

Examples

```
checkSeqDb('hg19')
```

createControlRegions *createControlRegions*

Description

Given a GRanges object of query regions, create a background set of peaks that have the same length distribution based on the flanking regions of the peaks.

Usage

```
createControlRegions(queryRegions)
```

Arguments

queryRegions GRanges object containing coordinates of input query regions imported by the [importBed](#) function.

Value

GRanges object that contains the same number of regions as query regions

Examples

```
data(queryRegions)
controlRegions <- createControlRegions(queryRegions = queryRegions)
```

createDB

createDB

Description

Creates an sqlite database consisting of various tables of data obtained from processed BED files

Usage

```
createDB(
  dbPath = file.path(getwd(), "rcasDB.sqlite"),
  projDataFile,
  gtffFilePath = "",
  update = FALSE,
  genomeVersion,
  annotationSummary = TRUE,
  coverageProfiles = TRUE,
  motifAnalysis = TRUE,
  nodeN = 1
)
```

Arguments

| | |
|-------------------|---|
| dbPath | Path to the sqlite database file (could be an existing file or a new file path to be created at the given path) |
| projDataFile | A file consisting of meta-data about the input samples. Must minimally consist of two columns: 1. sampleName (name of the sample) 2. bedFilePath (full path to the location of the BED file containing data for the sample) |
| gtfFilePath | Path to the GTF file (preferably downloaded from the Ensembl database) that contains genome annotations |
| update | TRUE/FALSE (default: FALSE) whether an existing database should be updated |
| genomeVersion | A character string to denote for which genome version the analysis is being done. Available options are hg19/hg38 (human), mm9/mm10 (mouse), ce10 (worm) and dm3 (fly). |
| annotationSummary | TRUE/FALSE (default:TRUE) whether annotation summary module should be run |
| coverageProfiles | TRUE/FALSE (default: TRUE) whether coverage profiles module should be run |
| motifAnalysis | TRUE/FALSE (default: TRUE) whether motif discovery module should be run |
| nodeN | Number of cpus to use for parallel processing (default: 1) |

Value

Path to an SQLiteConnection object created by RSQLite package

Examples

```
FUS_path <- system.file("extdata", "FUS_Nakaya2013c_hg19.bed",
package='RCAS')

FMR1_path <- system.file("extdata",
"FMR1_Ascano2012a_hg19.bed", package='RCAS')

projData <- data.frame('sampleName' = c('FUS', 'FMR1'),
'bedFilePath' = c(FUS_path,FMR1_path), stringsAsFactors = FALSE)

write.table(projData, 'myProjDataFile.tsv', sep = '\t', quote =FALSE,
row.names = FALSE)

gtfFilePath <- system.file("extdata",
"hg19.sample.gtf", package='RCAS')

createDB(dbPath = 'hg19.RCASDB.sqlite',
projDataFile = './myProjDataFile.tsv',
gtfFilePath = gtfFilePath,
genomeVersion = 'hg19',
motifAnalysis = FALSE,
coverageProfiles = FALSE)

#Note: to add new data to an existing database, set update = TRUE
```

createOrthologousGeneSetList

createOrthologousMsigdbDataset This function is deprecated. For functional enrichment analysis, use findEnrichedFunctions.

Description

createOrthologousMsigdbDataset This function is deprecated. For functional enrichment analysis, use findEnrichedFunctions.

Usage

```
createOrthologousGeneSetList()
```

deleteSampleDataFromDB

deleteSampleDataFromDB

Description

Given a list of sample names, the function deletes all datasets calculated for the given samples from the database.

Usage

```
deleteSampleDataFromDB(dbPath, sampleNames)
```

Arguments

| | |
|-------------|---|
| dbPath | Path to the sqlite database |
| sampleNames | The names of the samples for which all relevant datasets should be deleted from the database. Tip: Use RSQLite::dbReadTable function to read the table 'processedSamples' to see which samples are available in the database. |

Value

SQLiteConnection object with updated contents in the dbPath

```
discoverFeatureSpecificMotifs  
    discoverFeatureSpecificMotifs
```

Description

This function groups query regions based on their overlap with different transcript features and generates a table of top enriched motif and matching patterns for each given transcript feature type along with some other motif discovery related statistics.

Usage

```
discoverFeatureSpecificMotifs(queryRegions, txdbFeatures, ...)
```

Arguments

| | |
|--------------|--|
| queryRegions | GRanges object containing coordinates of input query regions imported by the importBed function |
| txdbFeatures | A list of GRanges objects where each GRanges object corresponds to the genomic coordinates of gene features such as promoters, introns, exons, 5'/3' UTRs and whole transcripts. This list of GRanges objects are obtained by the function getTxdbFeaturesFromGRanges or getTxdbFeatures . |
| ... | Other arguments passed to runMotifRG function. Important arguments are 'genomeVersion' and motifN. If motifN is bigger than 1, then multiple motifs will be found but only the top motif will be plotted. |

Value

A data.frame object

Examples

```
## Not run:  
data(gff)  
data(queryRegions)  
txdbFeatures <- getTxdbFeaturesFromGRanges(gffData = gff)  
discoverFeatureSpecificMotifs(queryRegions = queryRegions,  
    genomeVersion = 'hg19', txdbFeatures = txdbFeatures,  
    motifN = 1, nCores = 1)  
## End(Not run)
```

extractSequences *extractSequences*

Description

Given a GRanges object and a genome version (hg19, mm9, ce10 or dm3), this function extracts the DNA sequences for all genomic regions found in an input object.

Usage

```
extractSequences(queryRegions, genomeVersion)
```

Arguments

queryRegions GRanges object containing coordinates of input query regions imported by the [importBed](#) function

genomeVersion A character string to denote the BS genome library required to extract sequences. Available options are hg19, mm9, ce10 and dm3.

Value

DNASTringSet object will be returned

Examples

```
data(queryRegions)
sequences <- extractSequences(queryRegions = queryRegions,
                             genomeVersion = 'hg19')
```

findDifferentialMotifs
Find Differential Motifs

Description

Find Differential Motifs

Usage

```
findDifferentialMotifs(  
  querySeqs,  
  controlSeqs,  
  motifWidth = 6,  
  motifN = 1,  
  nCores = 1,  
  maxMismatch = 1  
)
```

Arguments

| | |
|-------------|--|
| querySeqs | A DNASTringSet object that is the regions of interest. |
| controlSeqs | A DNASTrintSet object that serve as the control |
| motifWidth | A Positive integer (default: 6) for the generated k-mers. Warning: we recommend using values below 10 as the computation gets exponentially difficult as the motif width is increased. |
| motifN | A positive integer (default:1) denoting the maximum number of motifs that should be returned by the findDifferentialMotifs function |
| nCores | A positive integer (default:1) number of cores used for parallel execution. |
| maxMismatch | A positive integer (default: 1) - maximum number of mismatches to allow when searching for k-mer matches in sequences. |

Examples

```

data(queryRegions)

# get query and control sequences
querySeqs <- extractSequences(queryRegions[1:500], 'hg19')
controlRegions <- createControlRegions(queryRegions[1:500])
controlSeqs <- extractSequences(controlRegions, 'hg19')

#run motif discovery
motifResults <- findDifferentialMotifs(querySeqs = querySeqs,
                                     controlSeqs = controlSeqs,
                                     motifWidth = 5,
                                     motifN = 1,
                                     maxMismatch = 0,
                                     nCores = 1)

#summarize motif results
getMotifSummaryTable(motifResults)

```

findEnrichedFunctions *findEnrichedFunctions*

Description

Find enriched functional terms among the genes that overlap the regions of interest.

Usage

```
findEnrichedFunctions(targetGenes, species, ...)
```

Arguments

| | |
|-------------|---|
| targetGenes | Vector of Ensembl gene ids or gene names |
| species | First letter of genus + species name: e.g. hsapiens |
| ... | Other arguments to be passed to gprofiler2::gost |

Details

This function is basically a call to `gprofiler2::gost` function. It is here to serve as a replacement for other deprecated functional enrichment functions.

Examples

```
data(gff)
data(queryRegions)

overlaps <- queryGff(queryRegions, gff)
res <- findEnrichedFunctions(unique(overlaps$gene_id), 'hsapiens')
```

| | |
|---------------|------------------------|
| generateKmers | <i>Generate K-mers</i> |
|---------------|------------------------|

Description

Given a list of characters, generates all possible fixed length strings

Usage

```
generateKmers(k, letters = c("A", "C", "G", "T"))
```

Arguments

| | |
|---------|---|
| k | The length of the strings to be generated |
| letters | A character vector |

Value

Vector of strings

Examples

```
generateKmers(3, c('A', 'C', 'G'))
```

| | |
|----------------------------|-----------------------------------|
| getFeatureBoundaryCoverage | <i>getFeatureBoundaryCoverage</i> |
|----------------------------|-----------------------------------|

Description

This function extracts the flanking regions of 5' and 3' boundaries of a given set of genomic features and computes the per-base coverage of query regions across these boundaries.

Usage

```
getFeatureBoundaryCoverage(
  queryRegions,
  featureCoords,
  flankSize = 500,
  boundaryType,
  sampleN = 0
)
```

Arguments

| | |
|---------------|---|
| queryRegions | GRanges object imported from a BED file using importBed function |
| featureCoords | GRanges object containing the target feature coordinates |
| flankSize | Positive integer that determines the number of base pairs to extract around a given genomic feature boundary |
| boundaryType | (Options: fiveprime or threeprime). Denotes which side of the feature's boundary is to be profiled. |
| sampleN | A positive integer value less than the total number of feature coordinates that determines whether the target feature coordinates should be randomly down-sampled. If set to 0, no downsampling will happen. If |

Value

a data frame containin three columns. 1. fivePrime: Coverage at 5' end of features 2. threePrime: Coverage at 3' end of features; 3. bases: distance (in bp) to the boundary

Examples

```
data(queryRegions)
data(gff)
txdb <- txdbmaker::makeTxDbFromGRanges(gff)
transcriptCoords <- GenomicFeatures::transcripts(txdb)
transcriptEndCoverage <- getFeatureBoundaryCoverage (
  queryRegions = queryRegions,
  featureCoords = transcriptCoords,
  flankSize = 100,
  boundaryType = 'threeprime',
  sampleN = 1000)
```

```
getFeatureBoundaryCoverageBin
```

```
getFeatureBoundaryCoverageBin
```

Description

This function extracts the flanking regions of 5' and 3' boundaries of a given set of genomic features, splits them into 100 equally sized bins and computes the per-bin coverage of query regions across these boundaries.

Usage

```
getFeatureBoundaryCoverageBin(
  queryRegions,
  featureCoords,
  flankSize = 50,
  sampleN = 0
)
```

Arguments

| | |
|----------------------------|---|
| <code>queryRegions</code> | GRanges object imported from a BED file using <code>importBed</code> function |
| <code>featureCoords</code> | GRanges object containing the target feature coordinates |
| <code>flankSize</code> | Positive integer that determines the number of base pairs to extract around a given genomic feature boundary |
| <code>sampleN</code> | A positive integer value less than the total number of feature coordinates that determines whether the target feature coordinates should be randomly down-sampled. If set to 0, no downsampling will happen. If |

Value

a data frame containin three columns. 1. `fivePrime`: Coverage at 5' end of features 2. `threePrime`: Coverage at 3' end of features; 3. `bases`: distance (in bp) to the boundary

Examples

```
data(queryRegions)
data(gff)
txdb <- txdbmaker::makeTxDbFromGRanges(gff)
transcriptCoords <- GenomicFeatures::transcripts(txdb)
transcriptEndCoverageBin <- getFeatureBoundaryCoverageBin (
  queryRegions = queryRegions,
  featureCoords = transcriptCoords,
  flankSize = 100,
  sampleN = 1000)
```

```
getFeatureBoundaryCoverageMulti
  getFeatureBoundaryCoverageMulti
```

Description

This function is a wrapper function to run `RCAS::getFeatureBoundaryCoverage` multiple times, which is useful to get coverage signals across different kinds of transcript features for a given list of bed files imported as a `GRangesList` object.

Usage

```
getFeatureBoundaryCoverageMulti(bedData, txdbFeatures, sampleN = 10000)
```

Arguments

| | |
|--------------|---|
| bedData | GRangesList object imported from multiple BED files using importBedFiles function |
| txdbFeatures | List of GRanges objects - outputs of getTxdbFeaturesFromGRanges and getTxdbFeatures functions |
| sampleN | (default=10000) Positive integer value that is used to randomly down-sample the target feature coordinates to improve the runtime. Set to 0 to avoid down-sampling. |

Value

A data.frame object with coverage data at three prime and five prime boundaries of a list of transcript features

Examples

```
data(gff)
data(queryRegions)
queryRegionsList <- GenomicRanges::GRangesList(queryRegions, queryRegions)
names(queryRegionsList) <- c('q1', 'q2')
txdbFeatures <- getTxdbFeaturesFromGRanges(gffData = gff)
getFeatureBoundaryCoverageMulti(queryRegionsList, txdbFeatures, sampleN = 500)
```

```
getIntervalOverlapMatrix
      getIntervalOverlapMatrix
```

Description

This function is used to obtain a binary matrix of overlaps between a list of GRanges objects (GRangesList object) and a target GRanges object. The resulting matrix has N rows where N is the number of intervals in the target GRanges object and M columns where M is the number GRanges objects in the query GRangesList object.

Usage

```
getIntervalOverlapMatrix(
  queryRegionsList,
  targetRegions,
  targetRegionNames = NULL,
  nodeN = 1
)
```

Arguments

| | |
|------------------|----------------------|
| queryRegionsList | A GRangesList object |
| targetRegions | A GRanges object |

`targetRegionNames` Optional vector of names to be used as rownames in the resulting matrix. The vector indices must correspond to the intervals in `targetRegions` object.

`nodeN` Positive integer value to use one or more cpus for parallel computation (default: 1)

Value

A binary matrix object consisting of number of rows equal to the number of intervals in `targetRegions` object, and number of columns equal to the number of GRanges objects available in the `queryRegionsList` object.

Examples

```
data(gff)
input1 <- system.file("extdata", "testfile.bed", package='RCAS')
input2 <- system.file("extdata", "testfile2.bed", package='RCAS')
bedData <- RCAS::importBedFiles(filePaths = c(input1, input2))
M <- RCAS::getIntervalOverlapMatrix(
  queryRegionsList = bedData,
  targetRegions = gff[gff$type == 'gene',][1:100],
  targetRegionNames = gff[gff$type == 'gene',][1:100]$gene_name)
```

`getMotifSummaryTable` *getMotifSummaryTable*

Description

Get summary stats for top discovered motifs

Usage

```
getMotifSummaryTable(motifResults)
```

Arguments

`motifResults` Output object of `runMotifDiscovery` function

Value

A data.frame object containing summary statistics about the discovered motifs

Examples

```
data(queryRegions)
motifResults <- runMotifDiscovery(queryRegions = queryRegions[1:1000],
                                genomeVersion = 'hg19',
                                resize = 15,
                                motifN = 1,
                                maxMismatch = 1,
                                nCores = 2)
motifSummary <- getMotifSummaryTable(motifResults)
```

```
getPWM          getPWM
```

Description

Given a vector of strings of equal width, generate a position-specific weight matrix based on the frequency of occurrence of the unique letters found in the sequences.

Usage

```
getPWM(sequences, letters = c("A", "C", "G", "T"))
```

Arguments

sequences vector of strings of equal widths.
 letters vector of characters to consider as the an alphabet

Value

A matrix of position-specific-weights.

Examples

```
sequences = c("GGAGAG", "GAAGAA", "TGAGAA", "GGAGAA", "GAAGAA")
getPWM(sequences)
```

```
getTargetedGenesTable  getTargetedGenesTable
```

Description

This function provides a list of genes which are targeted by query regions and their corresponding numbers from an input BED file. Then, the hits are categorized by the gene features such as promoters, introns, exons, 5'/3' UTRs and whole transcripts.

Usage

```
getTargetedGenesTable(queryRegions, txdbFeatures)
```

Arguments

queryRegions GRanges object containing coordinates of input query regions imported by the [importBed](#) function
 txdbFeatures A list of GRanges objects where each GRanges object corresponds to the genomic coordinates of gene features such as promoters, introns, exons, 5'/3' UTRs and whole transcripts. This list of GRanges objects are obtained by the function [getTxdbFeaturesFromGRanges](#) or [getTxdbFeatures](#).

Value

A data.frame object where rows correspond to genes and columns correspond to gene features

Examples

```
data(gff)
data(queryRegions)
txdbFeatures <- getTxdbFeaturesFromGRanges(gffData = gff)
featuresTable <- getTargetedGenesTable(queryRegions = queryRegions,
                                       txdbFeatures = txdbFeatures)

#or
## Not run:
txdb <- txdbmaker::makeTxDbFromGRanges(gff)
txdbFeatures <- getTxdbFeatures(txdb)
featuresTable <- getTargetedGenesTable(queryRegions = queryRegions,
                                       txdbFeatures = txdbFeatures)

## End(Not run)
```

| | |
|-----------------|------------------------|
| getTxdbFeatures | <i>getTxdbFeatures</i> |
|-----------------|------------------------|

Description

This function is deprecated. Use *getTxdbFeaturesFromGRanges* instead.

Usage

```
getTxdbFeatures()
```

| | |
|----------------------------|-----------------------------------|
| getTxdbFeaturesFromGRanges | <i>getTxdbFeaturesFromGRanges</i> |
|----------------------------|-----------------------------------|

Description

This function takes as input a GRanges object that contains GTF file contents (e.g from the output of *importGtf* function). Then extracts the coordinates of gene features such as promoters, introns, exons, 5'/3' UTRs and whole transcripts.

Usage

```
getTxdbFeaturesFromGRanges(gffData)
```

Arguments

| | |
|---------|--|
| gffData | A GRanges object imported by <i>importGtf</i> function |
|---------|--|

Value

A list of GRanges objects

Examples

```
data(gff)
txdbFeatures <- getTxdbFeaturesFromGRanges(gffData = gff)
```

gff

Sample GFF file imported as a GRanges object

Description

This dataset contains genomic annotation data from Ensembl version 75 for Homo sapiens downloaded from Ensembl. The GFF file is imported via the `importGtf` function and a subset of the data is selected by choosing features found on 'chr1'.

Usage

gff

Format

GRanges object with 238010 ranges and 16 metadata columns

Value

A GRanges object

Source

ftp://ftp.ensembl.org/pub/release-75/gtf/homo_sapiens/Homo_sapiens.GRCh37.75.gtf.gz

importBed

importBed

Description

This function uses `rtracklayer::import.bed()` function to import BED files

Usage

```
importBed(filePath, sampleN = 0, keepStandardChr = TRUE, debug = TRUE, ...)
```

Arguments

| | |
|------------------------------|---|
| <code>filePath</code> | Path to a BED file |
| <code>sampleN</code> | A positive integer value. The number of intervals in the input BED file are randomly downsampled to include intervals as many as <code>sampleN</code> . The input will be downsampled only if this value is larger than zero and less than the total number of input intervals. |
| <code>keepStandardChr</code> | TRUE/FALSE (default:TRUE). If set to TRUE, will convert the <code>seqlevelsStyle</code> to 'UCSC' and apply <code>keepStandardChromosomes</code> function to only keep data from the standard chromosomes |
| <code>debug</code> | TRUE/FALSE (default:TRUE). Set to FALSE to turn off messages |
| <code>...</code> | Other arguments passed to <code>rtracklayer::import.bed</code> function |

Value

A `GRanges` object containing the coordinates of the intervals from an input BED file

Examples

```
input <- system.file("extdata", "testfile.bed", package='RCAS')
importBed(filePath = input, keepStandardChr = TRUE)
```

| | |
|-----------------------------|-----------------------|
| <code>importBedFiles</code> | <i>importBedFiles</i> |
|-----------------------------|-----------------------|

Description

This function is a wrapper that uses `RCAS::importBed()` function to import BED files as a `GRangesList` object

Usage

```
importBedFiles(filePaths, ...)
```

Arguments

| | |
|------------------------|---|
| <code>filePaths</code> | A vector of paths to one or more BED files |
| <code>...</code> | Other parameters passed to <code>RCAS::importBed</code> and <code>rtracklayer::import.bed</code> function |

Value

A `GRangesList` object containing the coordinates of the intervals from multiple input BED files

Examples

```
input1 <- system.file("extdata", "testfile.bed", package='RCAS')
input2 <- system.file("extdata", "testfile2.bed", package='RCAS')
bedData <- importBedFiles(filePaths = c(input1, input2),
  keepStandardChr = TRUE)
# when importing multiple bed files with different column names, it
# is required to pass the common column names to be parsed from the
# bed files
bedData <- importBedFiles(filePaths = c(input1, input2),
  colnames = c('chrom', 'start', 'end', 'strand'))
```

importGtf

*importGtf***Description**

This function uses `rtracklayer::import.gff()` function to import genome annotation data from an Ensembl gtf file

Usage

```
importGtf(
  filePath,
  saveObjectAsRds = TRUE,
  readFromRds = TRUE,
  overwriteObjectAsRds = FALSE,
  keepStandardChr = TRUE,
  ...
)
```

Arguments

| | |
|-----------------------------------|---|
| <code>filePath</code> | Path to a GTF file |
| <code>saveObjectAsRds</code> | TRUE/FALSE (default:TRUE). If it is set to TRUE, a GRanges object will be created and saved in RDS format (<code><filePath>.granges.rds</code>) so that importing can re-use this .rds file in next run. |
| <code>readFromRds</code> | TRUE/FALSE (default:TRUE). If it is set to TRUE, annotation data will be imported from previously generated .rds file (<code><filePath>.granges.rds</code>). |
| <code>overwriteObjectAsRds</code> | TRUE/FALSE (default:FALSE). If it is set to TRUE, existing .rds file (<code><filePath>.granges.rds</code>) will be overwritten. |
| <code>keepStandardChr</code> | TRUE/FALSE (default:TRUE). If it is set to TRUE, <code>seqlevelsStyle</code> will be converted to 'UCSC' and <code>keepStandardChromosomes</code> function will be applied to only keep data from the standard chromosomes. |
| <code>...</code> | Other arguments passed to <code>rtracklayer::import.gff</code> function |

Value

A GRanges object containing the coordinates of the annotated genomic features in an input GTF file

Examples

```

#import the data and write it into a .rds file
## Not run:
importGtf(filePath='./Ensembl75.hg19.gtf')

## End(Not run)
#import the data but don't save it as RDS
## Not run:
importGtf(filePath='./Ensembl75.hg19.gtf', saveObjectAsRds = FALSE)

## End(Not run)
#import the data and overwrite the previously generated
## Not run:
importGtf(filePath='./Ensembl75.hg19.gtf', overwriteObjectAsRds = TRUE)

## End(Not run)

```

parseMsigdb

parseMsigdb

Description

This function is deprecated. For functional enrichment analysis, use `findEnrichedFunctions`.

Usage

```
parseMsigdb()
```

plotFeatureBoundaryCoverage

plotFeatureBoundaryCoverage

Description

This function is used to create interactive plots displaying 5' and 3' end coverage profiles of given transcript features.

Usage

```
plotFeatureBoundaryCoverage(cvgF, cvgT, featureName)
```

Arguments

| | |
|-------------|--|
| cvgF | data.frame object containing 'fiveprime' coverage data returned by <code>getFeatureBoundaryCoverage</code> function |
| cvgT | data.frame object containing 'threeprime' coverage data returned by <code>getFeatureBoundaryCoverage</code> function |
| featureName | character object. This is used to label the axes (e.g. transcripts, exons) |

Value

a plotly htmlwidget is returned

Examples

```
data(queryRegions)
data(gff)
txdb <- txdbmaker::makeTxDbFromGRanges(gff)
transcriptCoords <- GenomicFeatures::transcripts(txdb)
cvgF <- getFeatureBoundaryCoverage (queryRegions = queryRegions,
                                   featureCoords = transcriptCoords,
                                   flankSize = 100,
                                   boundaryType = 'fiveprime',
                                   sampleN = 1000)

cvgT <- getFeatureBoundaryCoverage (queryRegions = queryRegions,
                                   featureCoords = transcriptCoords,
                                   flankSize = 100,
                                   boundaryType = 'threeprime',
                                   sampleN = 1000)

p <- plotFeatureBoundaryCoverage(cvgF = cvgF,
                                cvgT = cvgT,
                                featureName = 'transcript')
```

printMsigdbDataset *Print MSIGDB Dataset to a file*

Description

This function is deprecated. For functional enrichment analysis, use findEnrichedFunctions.

Usage

```
printMsigdbDataset()
```

queryGff *queryGff*

Description

This function checks overlaps between the regions in input query and in reference. Input query should be in BED format and reference should be in GFF format. Both data are imported as GRanges object.

Usage

```
queryGff(queryRegions, gffData)
```

Arguments

queryRegions GRanges object imported from a BED file using importBed function
 gffData GRanges object imported from a GTF file using importGtf function

Value

a GRanges object (a subset of input gff) with an additional column 'overlappingQuery' that contains the coordinates of query regions that overlap the target annotation features

Examples

```
data(queryRegions)
data(gff)
overlaps <- queryGff(queryRegions = queryRegions, gffData = gff)
```

| | |
|--------------|---|
| queryRegions | <i>Sample BED file imported as a GRanges object</i> |
|--------------|---|

Description

This dataset contains a randomly selected sample of human LIN28A protein binding sites detected by HITS-CLIP analysis downloaded from DoRina database (LIN28A HITS-CLIP hESCs (Wilbert 2012)). The BED file is imported via the importBed function and a subset of the data is selected by randomly choosing 10000 regions.

Usage

```
queryRegions
```

Format

GRanges object with 10000 ranges and 2 metadata columns

Value

A GRanges object

Source

<http://dorina.mdc-berlin.de/regulators>

| | |
|-------------------|--------------------------|
| retrieveOrthologs | <i>retrieveOrthologs</i> |
|-------------------|--------------------------|

Description

This function is deprecated. For functional enrichment analysis, use findEnrichedFunctions.

Usage

```
retrieveOrthologs()
```

runGSEA

runGSEA

Description

This function is deprecated. For functional enrichment analysis, use `findEnrichedFunctions`.

Usage

```
runGSEA()
```

runMotifDiscovery

runMotifDiscovery

Description

This function builds a random forest classifier to find the top most discriminative motifs in the query regions compared to the background. The background sequences are automatically generated based on the query regions. First, k-mers of a fixed length are generated. The query and control sequences are searched for k-mers allowing for mismatches. A random forest model is trained to find the most discriminative motifs.

Usage

```
runMotifDiscovery(
  queryRegions,
  resizeN = 0,
  motifWidth = 6,
  sampleN = 0,
  genomeVersion,
  maxMismatch = 1,
  motifN = 5,
  nCores = 1
)
```

Arguments

| | |
|---------------|--|
| queryRegions | GRanges object containing coordinates of input query regions imported by the importBed function |
| resizeN | Integer value (default: 0) to resize query regions if they are shorter than the value of resize. Set to 0 to disable resize. |
| motifWidth | A Positive integer (default: 6) for the generated k-mers. Warning: we recommend using values below 10 as the computation gets exponentially difficult as the motif width is increased. |
| sampleN | A positive integer value. The queryRegions are randomly downsampled to include intervals as many as sampleN. The input will be downsampled only if this value is larger than zero and less than the total number of input intervals. |
| genomeVersion | A character string to denote the BS genome library required to extract sequences. Example: 'hg19' |

| | |
|-------------|---|
| maxMismatch | A positive integer (default: 1) - maximum number of mismatches to allow when searching for k-mer matches in sequences. |
| motifN | A positive integer (default:5) denoting the maximum number of motifs that should be returned by the findDifferentialMotifs function |
| nCores | A positive integer (default:1) number of cores used for parallel execution. |

Value

A list of four objects: k-mer count matrices for query and background and lists of string matches for the top discriminating motifs (motifN).

Examples

```
data(queryRegions)
motifResults <- runMotifDiscovery(queryRegions = queryRegions[1:1000],
                                genomeVersion = 'hg19',
                                motifWidth = 6,
                                resize = 15,
                                motifN = 1,
                                maxMismatch = 1,
                                nCores = 1)
```

| | |
|------------|--------------------|
| runMotifRG | <i>run motifRG</i> |
|------------|--------------------|

Description

run motifRG

Usage

runMotifRG()

| | |
|-----------|--|
| runReport | <i>Generate a RCAS Report for a list of transcriptome-level segments</i> |
|-----------|--|

Description

This is the main report generation function for RCAS. This function takes a BED file, a GTF file to create a summary report regarding the annotation data that overlap the input BED file, enrichment analysis for functional terms, and motif analysis.

Usage

```
runReport(
  queryFilePath = "testdata",
  gfffFilePath = "testdata",
  annotationSummary = TRUE,
  goAnalysis = TRUE,
  motifAnalysis = TRUE,
  genomeVersion = "hg19",
  outDir = getwd(),
  printProcessedTables = FALSE,
  sampleN = 0,
  quiet = FALSE,
  selfContained = TRUE
)
```

Arguments

| | |
|----------------------|--|
| queryFilePath | a BED format file which contains genomic coordinates of protein-RNA binding sites |
| gfffFilePath | A GTF format file which contains genome annotations (preferably from ENSEMBL) |
| annotationSummary | TRUE/FALSE (default: TRUE) A switch to decide if RCAS should provide annotation summaries from overlap operations |
| goAnalysis | TRUE/FALSE (default: TRUE) A switch to decide if RCAS should run GO term enrichment analysis |
| motifAnalysis | TRUE/FALSE (default: TRUE) A switch to decide if RCAS should run motif analysis |
| genomeVersion | A character string to denote for which genome version the analysis is being done. |
| outDir | Path to the output directory. (default: current working directory) |
| printProcessedTables | boolean value (default: FALSE). If set to TRUE, raw data tables that are used for plots/tables will be printed to text files. |
| sampleN | integer value (default: 0). A parameter to determine if the input query regions should be downsampled to a smaller size in order to make report generation quicker. When set to 0, downsampling won't be done. To activate the sampling a positive integer value that is smaller than the total number of query regions should be given. |
| quiet | boolean value (default: FALSE). If set to TRUE, progress bars and chunk labels will be suppressed while knitting the Rmd file. |
| selfContained | boolean value (default: TRUE). By default, the generated html file will be self-contained, which means that all figures and tables will be embedded in a single html file with no external dependencies (See rmarkdown::html_document) |

Value

An html generated using rmarkdown/knitr/pandoc that contains interactive figures, tables, and text that provide an overview of the experiment

Examples

```

#Default run will generate a report using built-in test data for hg19 genome.
## Not run:
runReport()

## End(Not run)

#A custom run for human
## Not run:
runReport( queryFilePath = 'input.BED',
           gffFilePath = 'annotation.gtf',
           genomeVersion = 'hg19')

## End(Not run)
# To turn off certain modules of the report
## Not run:
runReport( queryFilePath = 'input.BED',
           gffFilePath = 'annotation.gtf',
           motifAnalysis = FALSE,
           goAnalysis = FALSE )

## End(Not run)

```

```
runReportMetaAnalysis runReportMetaAnalysis
```

Description

Generate a stand-alone HTML report with interactive figures and tables from a pre-calculated RCAS database (using RCAS::createDB) to compare multiple samples.

Usage

```

runReportMetaAnalysis(
  dbPath = "RCAS.sqlite",
  sampleTablePath,
  outDir = getwd(),
  outFile = NULL,
  quiet = FALSE,
  selfContained = TRUE
)

```

Arguments

| | |
|-----------------|--|
| dbPath | Path to the sqlite database generated by RCAS::createDB |
| sampleTablePath | A tab-separated file with two columns (no rownames) header 1: sampleName, header 2: sampleGroup |
| outDir | Path to the output directory. (default: current working directory) |
| outFile | Name of the output HTML report (by default, the base name of sampleTablePath value is used to create a name for the HTML report) |

- `quiet` boolean value (default: FALSE). If set to TRUE, progress bars and chunk labels will be suppressed while knitting the Rmd file.
- `selfContained` boolean value (default: TRUE). By default, the generated html file will be self-contained, which means that all figures and tables will be embedded in a single html file with no external dependencies (See `rmarkdown::html_document`)

Value

An html generated using `rmarkdown/knitr/pandoc` that contains interactive figures, tables, and text that provide an overview of the experiment

Examples

```
dbPath <- system.file("extdata", "hg19.RCASDB.sqlite",
  package='RCAS')

#Hint: use RCAS::summarizeDatabaseContent to see which samples have processed
#data in the database.
summarizeDatabaseContent(dbPath = dbPath)

#Create a data table for samples and their groups sampleGroup field is used
#to group replicates of #the same sample into one group in visualizations.
#Any arbitrary name can be used for sampleGroup field. However, entries in
#the sampleName field must be available in the queried database
sampleData <- data.frame('sampleName' = c('FUS', 'FMR1'),
  'sampleGroup' = c('FUS', 'FMR1'), stringsAsFactors = FALSE)
write.table(sampleData, 'sampleDataTable.tsv', sep = '\t',
  quote =FALSE, row.names = FALSE)
#Use the generated database to run a report
runReportMetaAnalysis(dbPath = 'hg19.RCASDB.sqlite',
  sampleTablePath = 'sampleDataTable.tsv')
```

runTopGO

runTopGO

Description

This function is deprecated. Use `findEnrichedFunctions` instead.

Usage

```
runTopGO()
```


Index

* datasets

- gff, [19](#)
- queryRegions, [24](#)

- calculateCoverageProfile, [3](#)
- calculateCoverageProfileFromTxdb, [4](#)
- calculateCoverageProfileList, [4](#)
- calculateCoverageProfileListFromTxdb, [5](#)
- checkSeqDb, [5](#)
- createControlRegions, [6](#)
- createDB, [6](#)
- createOrthologousGeneSetList, [8](#)

- deleteSampleDataFromDB, [8](#)
- discoverFeatureSpecificMotifs, [9](#)

- extractSequences, [10](#)

- findDifferentialMotifs, [10](#)
- findEnrichedFunctions, [11](#)

- generateKmers, [12](#)
- getFeatureBoundaryCoverage, [12](#)
- getFeatureBoundaryCoverageBin, [13](#)
- getFeatureBoundaryCoverageMulti, [14](#)
- getIntervalOverlapMatrix, [15](#)
- getMotifSummaryTable, [16](#)
- getPWM, [17](#)
- getTargetedGenesTable, [17](#)
- getTxdbFeatures, [9](#), [17](#), [18](#)
- getTxdbFeaturesFromGRanges, [9](#), [17](#), [18](#)
- gff, [19](#)

- importBed, [6](#), [9](#), [10](#), [17](#), [19](#), [25](#)
- importBedFiles, [20](#)
- importGtf, [21](#)

- parseMsigdb, [22](#)
- plotFeatureBoundaryCoverage, [22](#)
- printMsigdbDataset, [23](#)

- queryGff, [23](#)
- queryRegions, [24](#)

- retrieveOrthologs, [24](#)

- runGSEA, [25](#)
- runMotifDiscovery, [25](#)
- runMotifRG, [9](#), [26](#)
- runReport, [26](#)
- runReportMetaAnalysis, [28](#)
- runTopGO, [29](#)

- summarizeDatabaseContent, [30](#)
- summarizeQueryRegions, [30](#)
- summarizeQueryRegionsMulti, [31](#)