

# Package ‘RCAS’

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**Type** Package

**Title** RNA Centric Annotation System

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**Description** RCAS is an automated system that provides dynamic genome annotations for custom input files that contain transcriptomic regions. Such transcriptomic regions could be, for instance, peak regions detected by CLIP-Seq analysis that detect protein-RNA interactions, RNA modifications (alias the epitranscriptome), CAGE-tag locations, or any other collection of target regions at the level of the transcriptome. RCAS is designed as a reporting tool for the functional analysis of RNA-binding sites detected by high-throughput experiments. It takes as input a BED format file containing the genomic coordinates of the RNA binding sites and a GTF file that contains the genomic annotation features usually provided by publicly available databases such as Ensembl and UCSC. RCAS performs overlap operations between the genomic coordinates of the RNA binding sites and the genomic annotation features and produces in-depth annotation summaries such as the distribution of binding sites with respect to gene features (exons, introns, 5'/3' UTR regions, exon-intron boundaries, promoter regions, and whole transcripts). Moreover, by detecting the collection of targeted transcripts, RCAS can carry out functional annotation tables for enriched gene sets (annotated by the Molecular Signatures Database) and GO terms. As one of the most important questions that arise during protein-RNA interaction analysis; RCAS has a module for detecting sequence motifs enriched in the targeted regions of the transcriptome. A full interactive report in HTML format can be generated that contains interactive figures and tables that are ready for publication purposes.

**License** Artistic-2.0

**LazyData** TRUE

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---

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

queryRegions	GRanges object imported from a BED file using importBed function
targetRegions	GRanges object containing genomic coordinates of a target feature (e.g. exons)
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 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.



---

```
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 overlaps the input query regions with a target list of annotation features and calculates the coverage profile along the target regions.

### Usage

```
calculateCoverageProfileListFromTxdb(queryRegions, txdb, sampleN = 0)
```

### Arguments

queryRegions	GRanges object imported from a BED file using importBed function
txdb	A txdb object obtained by using GenomicFeatures::makeTxDb family of functions
sampleN	If set to a positive integer, targetRegions will be downsampled to sampleN regions

### Value

A list of data.frame objects consisting of two columns: 1. coverage level 2. bins. The target regions are divided into 100 equal sized bins and coverage level is summarized in a strand-specific manner using the genomation::ScoreMatrixBin function.

### Examples

```
data(gff)
data(queryRegions)
txdb <- GenomicFeatures::makeTxDbFromGRanges(gff)
df <- calculateCoverageProfileListFromTxdb(queryRegions = queryRegions,
                                           txdb = txdb,
                                           sampleN = 1000)
```

---

```
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,
gtfFilePath = "", 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
```

---

**Description**

Gene set annotations in public databases are usually geared towards human. This function is used to utilize human gene set annotations to create such gene sets for other species such as mouse, fly, and worm via orthologous relationships to human genes.

**Usage**

```
createOrthologousGeneSetList(referenceGeneSetList, refGenomeVersion = "hg19",
  targetGenomeVersion)
```

**Arguments**

referenceGeneSetList

A named list of vectors where each vector consists of a set of Entrez gene ids (for instance, returned by parseMsigdb function)

refGenomeVersion

Genome version of a reference species. (default:hg19)

targetGenomeVersion

Genome version of a target species. Available options are mm9, dm3, and ce10



**Value**

A list of vectors where each vector consists of a set of Entrez gene ids

**Examples**

```
#Recommended gene sets (with Entrez Ids) from MSIGDB database can be downloaded
#From \url{http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C2}
#Here we use built-in random gene sets to show how the function works
data(geneSets)
#Map the gene sets to a target genome (supported genomes: mm9, dm3, or ce10)
orthGeneSets <- createOrthologousGeneSetList(
  referenceGeneSetList = geneSets,
  refGenomeVersion = 'hg19',
  targetGenomeVersion = 'mm9'
)
```

---

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 <a href="#">importBed</a> 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 <a href="#">getTxdbFeaturesFromGRanges</a> or <a href="#">getTxdbFeatures</a> .
...	Other arguments passed to <a href="#">runMotifRG</a> 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	<i>extractSequences</i>
------------------	-------------------------

---

**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 <a href="#">importBed</a> 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')
```

---

geneSets	<i>Random test gene sets</i>
----------	------------------------------

---

**Description**

This dataset contains random sets of genes with Entrez ids that is designed to represent the data that can be parsed from MSIGDB database. using the parseMsigdb function.

**Usage**

```
geneSets
```

**Format**

A list of vectors, where each list element corresponds to a (randomized) gene set, where genes are represented by Entrez ids.

**Details**

Actual curated datasets must be downloaded from the MSIGDB database

**Value**

A list object

---

```
getFeatureBoundaryCoverage
      getFeatureBoundaryCoverage
```

---

**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 <code>importBed</code> 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: <code>fiveprime</code> or <code>threeprime</code> ). 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 <- GenomicFeatures::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

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
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 <- GenomicFeatures::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**

<code>bedData</code>	<code>GRangesList</code> object imported from multiple BED files using <code>importBedFiles</code> function
<code>txdbFeatures</code>	List of <code>GRanges</code> objects - outputs of <code>getTxdbFeaturesFromGRanges</code> and <code>getTxdbFeatures</code> functions
<code>sampleN</code>	(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 <- 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**

A repurposed/simplified version of the motifRG::summaryMotif function.

**Usage**

```
getMotifSummaryTable(motifResults)
```

**Arguments**

```
motifResults      Output object of runMotifRG function
```

**Value**

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

**Examples**

```

data(queryRegions)
motifResults <- runMotifRG(queryRegions = queryRegions,
                           genomeVersion = 'hg19',
                           resize = 15,
                           motifN = 1,
                           nCores = 2)
motifSummary <- getMotifSummaryTable(motifResults)

```

---

```
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 <a href="#">importBed</a> 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 <a href="#">getTxdbFeaturesFromGRanges</a> or <a href="#">getTxdbFeatures</a> .

**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 <- GenomicFeatures::makeTxDbFromGRanges(gff)
txdbFeatures <- getTxdbFeatures(txdb)
featuresTable <- getTargetedGenesTable(queryRegions = queryRegions,
                                       txdbFeatures = txdbFeatures)

## End(Not run)

```



---

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

---

**Description**

This function takes as input a txdb object from GenomicFeatures library. Then extracts the coordinates of gene features such as promoters, introns, exons, 5'/3' UTRs, and whole transcripts.

**Usage**

```
getTxdbFeatures(txdb)
```

**Arguments**

txdb                    A txdb object imported by GenomicFeatures::makeTxDb family of functions

**Value**

A list of GRanges objects

**Examples**

```
data(gff)
txdb <- GenomicFeatures::makeTxDbFromGRanges(gff)
txdbFeatures <- getTxdbFeatures(txdb)
```

---

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 importGtf function

**Value**

A list of GRanges objects

**Examples**

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

---

gff	<i>Sample GFF file imported as a GRanges object</i>
-----	---

---

**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](ftp://ftp.ensembl.org/pub/release-75/gtf/homo_sapiens/Homo_sapiens.GRCh37.75.gtf.gz)

---

importBed	<i>importBed</i>
-----------	------------------

---

**Description**

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

**Usage**

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

**Arguments**

filePath	Path to a BED file
sampleN	A positive integer value. The number of intervals in the input BED file 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.
keepStandardChr	TRUE/FALSE (default:TRUE). If set to TRUE, will convert the seqlevelsStyle to 'UCSC' and apply keepStandardChromosomes function to only keep data from the standard chromosomes
debug	TRUE/FALSE (default:TRUE). Set to FALSE to turn off messages
...	Other arguments passed to rtracklayer::import.bed 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)
```

---

importBedFiles	<i>importBedFiles</i>
----------------	-----------------------

---

**Description**

This function is a wrapper that uses RCAS::importBed() function to import BED files as a GRanges-List object

**Usage**

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

**Arguments**

filePaths	A vector of paths to one or more BED files
...	Other parameters passed to RCAS::importBed and rtracklayer::import.bed 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>&lt;filePath&gt;.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>&lt;filePath&gt;.granges.rds</code> ).
<code>overwriteObjectAsRds</code>	TRUE/FALSE (default:FALSE). If it is set to TRUE, existing .rds file ( <code>&lt;filePath&gt;.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**

A function to import gene sets downloaded from the Molecular Signatures Database (MSIGDB)

**Usage**

```
parseMsigdb(filePath)
```

**Arguments**

filePath	Path to a file containing gene sets from MSIGDB. The gene ids must be in Entrez format.
----------	---

**Value**

A list of vectors where each vector consists of a set of Entrez gene ids

**Examples**

```
#First Download gene sets (with Entrez Ids) from MSIGDB database
#from http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C2

input <- system.file('extdata', 'msigdb_test.gmt', package='RCAS')
msigDB <- parseMsigdb (filePath = input)
```



---

printMsigdbDataset	<i>Print MSIGDB Dataset to a file This function is used to print a MSIGDB dataset into a file. Mostly useful when human data is mapped to another species, and that mapping is required to run the report.</i>
--------------------	--

---

### Description

Print MSIGDB Dataset to a file This function is used to print a MSIGDB dataset into a file. Mostly useful when human data is mapped to another species, and that mapping is required to run the report.

### Usage

```
printMsigdbDataset(dataset, outputFilename)
```

### Arguments

dataset	A list of vectors containing gene sets from MSIGDB
outputFilename	A character string that denotes the output file name

### Value

A text file printed to the current directory

### Examples

```
data(geneSets)
printMsigdbDataset(geneSets, 'output.gmt')
```

---

queryGff	<i>queryGff</i>
----------	-----------------

---

### 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**

Given two biomart connections and a set of entrez gene identifiers; retrieve orthologs between mart1 and mart2 for the given list of genes

**Usage**

```
retrieveOrthologs(mart1, mart2, geneSet)
```



**Arguments**

mart1	An Ensembl biomart connection for reference species created using the <code>biomaRt::useMart()</code> function
mart2	An Ensembl biomart connection for target species created using the <code>biomaRt::useMart()</code> function
geneSet	A vector of Entrez gene ids from a reference species (should be available at the biomart object, mart1)

**Value**

A data.frame object containing a mapping of orthologouse genes from two mart objects

**Examples**

```
mart1_hg19 <- biomaRt::useMart(biomart = 'ENSEMBL_MART_ENSEMBL',
                             host = 'feb2014.archive.ensembl.org',
                             dataset = "hsapiens_gene_ensembl")
mart2_mm9 <- biomaRt::useMart(biomart = 'ENSEMBL_MART_ENSEMBL',
                             host = 'may2012.archive.ensembl.org',
                             dataset = "mmusculus_gene_ensembl")
genes <- c('2645', '5232', '5230', '5162', '5160')
orthologs <- retrieveOrthologs( mart1 = mart1_hg19,
                              mart2 = mart2_mm9,
                              geneSet = genes)
```

---

runGSEA

---

*runGSEA*


---

**Description**

This function is used to facilitate gene set enrichment analysis (GSEA) for a given set of genes

**Usage**

```
runGSEA(geneSetList, species = "human", backgroundGenes, targetedGenes)
```

**Arguments**

geneSetList	A named list of vectors where each vector consists of a set of Entrez gene ids (for instance, returned by <code>parseMsigdb</code> function)
species	A character string denoting the species under analysis. Options are 'human', 'mouse', 'fly' and 'worm'.
backgroundGenes	A vector of Ensembl gene ids that serve as background set of genes for GO term enrichment. In the context of RCAS, this should be the whole set of genes found in an input GTF file.
targetedGenes	A vector of Ensembl gene ids that serve as the set for which GSEA should be carried out. In the context of RCAS, this should be the set of genes that overlap the query regions

**Value**

A data.frame object containing enriched gene sets and associated statistics

**Examples**

```
#load test data
data(geneSets)
data(gff)
data(queryRegions)
#get all genes from the gff data
backgroundGenes <- unique(gff$gene_id)
#get genes that overlap query regions
overlaps <- queryGff(queryRegions, gff)
targetedGenes <- unique(overlaps$gene_id)
resultsGSEA <- runGSEA(geneSetList = geneSets,
                      species = 'human',
                      backgroundGenes = backgroundGenes,
                      targetedGenes = targetedGenes)
```

---

runMotifRG

*runMotifRG*


---

**Description**

This function makes use of motifRG library to carry out de novo motif discovery from input query regions

**Usage**

```
runMotifRG(queryRegions, resizeN = 0, sampleN = 0, genomeVersion,
           motifN = 5, nCores = 4)
```

**Arguments**

queryRegions	GRanges object containing coordinates of input query regions imported by the <a href="#">importBed</a> 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.
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. Available options are hg19, mm9, ce10 and dm3.
motifN	A positive integer (default:5) denoting the maximum number of motifs that should be sought by the motifRG::findMotifFgBg function
nCores	A positive integer (default:4) number of cores used for parallel execution.

**Value**

a list of objects returned by the motifRG::findMotif function

## Examples

```
data(queryRegions)
motifResults <- runMotifRG(queryRegions = queryRegions,
                           genomeVersion = 'hg19',
                           resize = 15,
                           motifN = 1,
                           nCores = 2)
```

---

runReport

*Generate a RCAS Report for a list of transcriptome-level segments*


---

## Description

This is the main report generation function for RCAS. This function can take a BED file, a GTF file and optionally an MSIGDB gene set annotation (or any text file containing annotations with the same structure as defined in MSIGDB); and use these input to run multiple RCAS functions to create a summary report regarding the annotation data that overlap the input BED file, enrichment analysis for GO terms, gene sets from MSIGDB, and motif analysis.

## Usage

```
runReport(queryFilePath = "testdata", gffFilePath = "testdata",
          msigdbFilePath = "testdata", annotationSummary = TRUE,
          goAnalysis = TRUE, msigdbAnalysis = 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
gffFilePath	A GTF format file which contains genome annotations (preferably from ENSEMBL)
msigdbFilePath	Gene set annotations for Homo sapiens from Molecular Signatures Database or any text file that has the same structure. Regardless of which species is being studied (see genomeVersion parameter), msigdbFilePath must contain annotations for human genes. The gene sets will be mapped from human to other species if genomeVersion is set to anything except human genome versions (e.g. mm9 or dm3).
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
msigdbAnalysis	TRUE/FALSE (default: TRUE) A switch to decide if RCAS should run gene set 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. Available options are hg19/hg38 (human), mm9/mm10 (mouse), ce10 (worm) and dm3 (fly).
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',
           msigdbFilePath = 'human_msigdb.gmt')

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

## End(Not run)
# To run the pipeline for species other than human
# If the msigdb module is needed, the msigdbFilePath
# must be set to the MSIGDB annotations for 'human'.
# MSIGDB datasets for other species will be calculated
# in the background using the createOrthologousMsigdbDataset
# function
## Not run:
```

```
runReport( queryFilePath = 'input.mm9.BED',
           gffFilePath = 'annotation.mm9.gtf',
           msigdbFilePath = 'msigdb.human.gmt',
           genomeVersion = 'mm9' )

## 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

<code>dbPath</code>	Path to the sqlite database generated by <code>RCAS::createDB</code>
<code>sampleTablePath</code>	A tab-separated file with two columns (no rownames) header 1: <code>sampleName</code> , header 2: <code>sampleGroup</code>
<code>outDir</code>	Path to the output directory. (default: current working directory)
<code>outFile</code>	Name of the output HTML report (by default, the base name of <code>sampleTablePath</code> value is used to create a name for the HTML report)
<code>quiet</code>	boolean value (default: <code>FALSE</code> ). If set to <code>TRUE</code> , progress bars and chunk labels will be suppressed while knitting the Rmd file.
<code>selfContained</code>	boolean value (default: <code>TRUE</code> ). 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 <code>rmarkdown::html_document</code> )

## 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**

A wrapper function to facilitate GO term enrichment analysis using topGO package

**Usage**

```
runTopGO(ontology = "BP", species = "human", backgroundGenes, targetedGenes)
```

**Arguments**

ontology	A character string denoting which type of GO ontology to use. Options are BP (biological processes), MF (molecular functions) and CC (cellular compartments).
species	A character string denoting which species is under analysis. Options are 'human', 'mouse', 'fly' and 'worm'.
backgroundGenes	A vector of Ensembl gene ids that serve as background set of genes for GO term enrichment. In the context of RCAS, this should be the whole set of genes found in an input GTF data.
targetedGenes	A vector of Ensembl gene ids that serve as the set for which GO term enrichment should be carried out. In the context of RCAS, this should be the set of genes that overlap with the query regions in an input BED file.

**Value**

A data.frame object containing enriched GO terms and associated statistics

**Examples**

```
## Not run:
#get all genes from the gff data
data(gff)
data(queryRegions)
backgroundGenes <- unique(gff$gene_id)
#get genes that overlap query regions
overlaps <- queryGff(queryRegions, gff)
targetedGenes <- unique(overlaps$gene_id)
#run TopGO
goResults = runTopGO( ontology = 'BP',
```

```

species = 'human',
backgroundGenes = backgroundGenes,
targetedGenes = targetedGenes)

## End(Not run)

```

---

```

summarizeDatabaseContent
      summarizeDatabaseContent

```

---

### Description

Given a path to an sqlite database created using RCAS::createDB function, accesses the database and provides a quick summary of available samples and number of entries of each sample in the available tables of the database.

### Usage

```
summarizeDatabaseContent(dbPath)
```

### Arguments

dbPath            Path to the sqlite database

### Value

A data.frame object

---

```

summarizeQueryRegions  summarizeQueryRegions

```

---

### Description

This function counts number of query regions that overlap with different types of gene features.

### Usage

```
summarizeQueryRegions(queryRegions, txdbFeatures)
```

### Arguments

queryRegions    GRanges object imported from a BED file using importBed function  
txdbFeatures    List of GRanges objects - outputs of getTxdbFeaturesFromGRanges and getTxdbFeatures functions

### Value

A data frame with two columns where first column holds features and second column holds corresponding counts





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