

# Package ‘rGREAT’

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**Enhances** BioMartGOGeneSets, UniProtKeywords

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**Description** GREAT (Genomic Regions Enrichment of Annotations Tool) is a type of functional enrichment analysis directly performed on genomic regions. This package implements the GREAT algorithm (the local GREAT analysis), also it supports directly interacting with the GREAT web service (the online GREAT analysis). Both analysis can be viewed by a Shiny application. rGREAT by default supports more than 600 organisms and a large number of gene set collections, as well as self-provided gene sets and organisms from users. Additionally, it implements a general method for dealing with background regions.

**URL** <https://github.com/jokergoo/rGREAT>,  
<http://great.stanford.edu/public/html/>

**License** MIT + file LICENSE

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---

*availableCategories-GreatJob-method*  
*Available ontology categories of the GREAT job*

---

### **Description**

Available ontology categories of the GREAT job

### **Usage**

```
## S4 method for signature 'GreatJob'  
availableCategories(object)
```

### **Arguments**

object           A [GreatJob-class](#) object returned by `submitGreatJob`.

### **Details**

The values of the supported categories sometime change. You should run the function to get the real-time values. The meaning of categories returned is quite self-explained by the name.

### **Value**

The returned value is a vector of categories.

### **Author(s)**

Zuguang gu <z.gu@dkfz.de>

### **Examples**

```
job = readRDS(system.file("extdata", "GreatJob.rds", package = "rGREAT"))  
availableCategories(job)
```

---

*availableOntologies-GreatJob-method*  
*All available ontology names of the GREAT job*

---

### **Description**

All available ontology names of the GREAT job

### **Usage**

```
## S4 method for signature 'GreatJob'  
availableOntologies(object, category = NULL)
```

**Arguments**

object            A [GreatJob-class](#) object returned by [submitGreatJob](#).  
category         one or multiple categories. All available categories can be got by [availableCategories](#).

**Details**

The values of the supported ontologies sometime change. You should run the function to get the real-time values. The meaning of ontology returned is quite self-explained by the name.

**Value**

The returned values is a vector of ontologies.

**Author(s)**

Zuguang gu <z.gu@dkfz.de>

**Examples**

```
job = readRDS(system.file("extdata", "GreatJob.rds", package = "rGREAT"))
availableOntologies(job)
```

---

extendTSS

*Extend TSS*

---

**Description**

Extend TSS

**Usage**

```
extendTSS(gene, seqlengths = NULL, genome = NULL,
          gene_id_type = NULL, mode = "basalPlusExt", extend_from = c("TSS", "gene"),
          basal_upstream = 5000, basal_downstream = 1000, extension = 1000000,
          verbose = great_opt$verbose, .attr = list())
```

**Arguments**

gene            A [GRanges](#) object of gene (or TSS) coordinates.  
extend\_from     Should the gene be extended only from its TSS or the complete gene?  
seqlengths     A named vector of chromosome lengths. If it is not provided, it is taken by `seqlengths(gene)`.  
genome         UCSC genome can be set here, then `seqlengths` will be automatically retrieved from UCSC server.  
gene\_id\_type   Gene ID types in gene. You need to set this argument if you use built-in gene sets in [great](#) so that genes can be correctly mapped. The value can only be one of "SYMBOL", "ENTREZ", "ENSEMBL" and "REFSEQ".  
mode            The mode to extend TSS. Value should be one of 'basalPlusExt', 'twoClosest' and 'oneClosest'. See "Details" section.

basal_upstream	In 'basalPlusExt' mode, number of base pairs extending to the upstream of TSS to form the basal domains.
basal_downstream	In 'basalPlusExt' mode, number of base pairs extending to the downstream of TSS to form the basal domains.
extension	Extensions from the basal domains. The value can also be a vector of length two which corresponds to extension to upstream and downstream respectively.
verbose	Whether to print messages.
.attr	Only used internally.

### Details

Following are general explanations of the three modes for extending TSS:

**basalPlusExt** 1. TSS are extended into basal domains (e.g. by upstream 5kb, downstream 1kb);  
2. basal domains are sorted by their genomic coordinates; 3. each basal domain is extended to its both sides until it reaches the next TSS's basal domain or it reaches the maximal extension (e.g. 1000kb).

**twoClosest** 1. TSS are sorted by their genomic coordinates; 2. each TSS is extended to its both sides until it reaches the next TSS or it reaches the maximal extension (e.g. 1000kb).

**oneClosest** 1. TSS are sorted by their genomic coordinates; 2. each TSS is extended to its both sides until it reaches the middle point of itself and the next TSS or it reaches the maximal extension (e.g. 1000kb).

The official explanation is at <https://great-help.atlassian.net/wiki/spaces/GREAT/pages/655443/Association+Rules>.

### Value

A [GRanges](#) object with one meta column 'gene\_id'.

### Examples

```
# There is no example
NULL
```

---

```
extendTSSFromDataFrame
```

*Extend TSS*

---

### Description

Extend TSS

### Usage

```
extendTSSFromDataFrame(df, seqlengths, genome = NULL,
  strand = NULL, gene_id = NULL,
  gene_id_type = NULL, verbose = great_opt$verbose, ...)
```

**Arguments**

df	A bed-like data frame where the first three columns should be chromosomes, start positions, end positions. It does not matter whether regions correspond to genes or TSS.
seqlengths	A named vector of chromosome lengths.
genome	UCSC genome can be set here, then seqlengths will be automatically retrieved from UCSC server.
strand	The strand information can be provided in df as a column named "strand" or as a column with "+"/"-/*", or the strand information can be provided as a vector and be assigned to this argument.
gene_id	The gene ID information can be provided in df as a column named "gene_id", or it can be provided as a vector and be assigned to this argument.
gene_id_type	Gene ID types in df. You need to set this argument if you use built-in gene sets in <a href="#">great</a> so that genes can be correctly mapped. The value can only be one of "SYMBOL", "ENTREZ", "ENSEMBL" and "REFSEQ".
verbose	Whether to print messages.
...	All pass to <a href="#">extendTSS</a> .

**Value**

A [GRanges](#) object with one meta column 'gene\_id'.

**Examples**

```
# There is no example
NULL
```

---

extendTSSFromOrgDb	<i>Extend TSS</i>
--------------------	-------------------

---

**Description**

Extend TSS

**Usage**

```
extendTSSFromOrgDb(orgdb, verbose = great_opt$verbose, ...)
```

**Arguments**

orgdb	Name of "org.*" packages from Bioconductor. All supported OrgDb packages are in <code>rGREAT:::BIOC_ANNO_PKGS\$orgdb</code> .
verbose	Whether to print messages.
...	All pass to <a href="#">extendTSS</a> .

**Value**

A [GRanges](#) object with one meta column 'gene\_id'.

**Examples**

```
if(FALSE) {
  extendTSSFromOrgDb("Org.Hs.eg.db")
  extendTSSFromOrgDb("hg19")
}
```

---

extendTSSFromTxDb      *Extend TSS*

---

**Description**

Extend TSS

**Usage**

```
extendTSSFromTxDb(txdb, verbose = great_opt$verbose, ...)
```

**Arguments**

txdb	Name of "TxDb.*" packages from Bioconductor. All supported TxDb packages are in <code>rGREAT:::BIOC_ANNO_PKGS\$txdb</code> . Note short genome version can also be used here such as "hg19" or "hg19.knownGene".
verbose	Whether to print messages.
...	All pass to <a href="#">extendTSS</a> .

**Value**

A [GRanges](#) object with one meta column 'gene\_id'.

**Examples**

```
if(FALSE) {
  extendTSSFromTxDb("TxDb.Hsapiens.UCSC.hg19.knownGene")
  extendTSSFromTxDb("hg19")
}
```

---

getEnrichmentTable-dispatch  
*Method dispatch page for getEnrichmentTable*

---

**Description**

Method dispatch page for getEnrichmentTable.

**Dispatch**

getEnrichmentTable can be dispatched on following classes:

- [getEnrichmentTable,GreatJob-method](#), [GreatJob-class](#) class method
- [getEnrichmentTable,GreatObject-method](#), [GreatObject-class](#) class method

**Examples**

```
# no example
NULL
```

---

getEnrichmentTable-GreatJob-method

*Get a single enrichment table from GREAT web server*

---

**Description**

Get a single enrichment table from GREAT web server

**Usage**

```
## S4 method for signature 'GreatJob'
getEnrichmentTable(object, ontology, ...)
```

**Arguments**

object	A <a href="#">GreatJob-class</a> object returned by <a href="#">submitGreatJob</a> .
ontology	A single ontology names. Valid values are in <a href="#">availableOntologies</a> .
...	All pass to <a href="#">getEnrichmentTables, GreatJob-method</a> .

**Value**

A data frame of the enrichment results for a single ontology.

**Examples**

```
job = readRDS(system.file("extdata", "GreatJob.rds", package = "rGREAT"))
tb = getEnrichmentTable(job, ontology = "GO Molecular Function")
head(tb)
```

---

getEnrichmentTable-GreatObject-method

*Get enrichment table*

---

**Description**

Get enrichment table

**Usage**

```
## S4 method for signature 'GreatObject'
getEnrichmentTable(object, min_region_hits = 5)
```

**Arguments**

- object            A [GreatObject-class](#) object returned by [great](#).
- min\_region\_hits            Minimal number of input regions overlapping to the geneset associated regions.

**Details**

Note: adjusted p-values are re-calculated based on min\_region\_hits.

**Value**

A data frame of enrichment results

**Examples**

```
obj = readRDS(system.file("extdata", "GreatObject.rds", package = "rGREAT"))
getEnrichmentTable(obj)
```

---

getEnrichmentTables-dispatch

*Method dispatch page for getEnrichmentTables*

---

**Description**

Method dispatch page for getEnrichmentTables.

**Dispatch**

getEnrichmentTables can be dispatched on following classes:

- [getEnrichmentTables,GreatObject-method](#), [GreatObject-class](#) class method
- [getEnrichmentTables,GreatJob-method](#), [GreatJob-class](#) class method

**Examples**

```
# no example
NULL
```

---

getEnrichmentTables-GreatJob-method

*Get enrichment tables from GREAT web server*

---

## Description

Get enrichment tables from GREAT web server

## Usage

```
## S4 method for signature 'GreatJob'  
getEnrichmentTables(object, ontology = NULL, category = "GO",  
  request_interval = 10, max_tries = 100, download_by = c("json", "tsv"),  
  verbose = TRUE)
```

## Arguments

object	A <a href="#">GreatJob-class</a> object returned by <a href="#">submitGreatJob</a> .
ontology	Ontology names. Valid values are in <a href="#">availableOntologies</a> . ontology is prior to category argument.
category	Pre-defined ontology categories. One category can contain more than one ontologies. Valid values are in <a href="#">availableCategories</a>
request_interval	Time interval for two requests. Default is 300 seconds.
max_tries	Maximal times for automatically reconnecting GREAT web server.
download_by	Internally used. The complete enrichment table is provided as json data on the website, but there is no information of gene-region association. By setting download_by = 'tsv', another URL from GREAT will be invoked which also contains detailed information of which genes are associated with each input region, but due to the size of the output, only top 500 terms will be returned. So if you do not really want the gene-region association column, take the default value of this argument. The columns that contain statistics are identical.
verbose	Whether to print messages.

## Value

The structure of the data frames are same as the tables available on GREAT website.

## See

[availableOntologies](#), [availableCategories](#)

## Author(s)

Zuguang gu <z.gu@dkfz.de>

**Examples**

```
job = readRDS(system.file("extdata", "GreatJob.rds", package = "rGREAT"))
tbl = getEnrichmentTables(job)
names(tbl)
head(tbl[[1]])
job

tbl = getEnrichmentTables(job, ontology = "GO Molecular Function")
tbl = getEnrichmentTables(job, category = "GO")
```

---

getEnrichmentTables-GreatObject-method  
*Get enrichment table*

---

**Description**

Get enrichment table

**Usage**

```
## S4 method for signature 'GreatObject'
getEnrichmentTables(object, ...)
```

**Arguments**

object	A <a href="#">GreatObject-class</a> object returned by <a href="#">great</a> .
...	All passed to <a href="#">getEnrichmentTable,GreatObject-method</a> .

**Details**

Please use [getEnrichmentTable,GreatObject-method](#) directly.

**Value**

A data frame of enrichment results

**Examples**

```
# There is no example
NULL
```

---

`getGapFromUCSC`                      *Get gap regions from UCSC*

---

**Description**

Get gap regions from UCSC

**Usage**

```
getGapFromUCSC(genome, seqnames = NULL)
```

**Arguments**

<code>genome</code>	UCSC genome, such as "hg19".
<code>seqnames</code>	A vector of chromosome names.

**Value**

A [GRanges](#) object.

**Examples**

```
getGapFromUCSC("hg19")
```

---

`getGeneSetsFromBioMart`  
*Get GO gene sets from BioMart*

---

**Description**

Get GO gene sets from BioMart

**Usage**

```
getGeneSetsFromBioMart(dataset, ontology = "bp")
```

**Arguments**

<code>dataset</code>	Name of the dataset.
<code>ontology</code>	Value should be bp, mf or cc.

**Details**

GO gene sets are from `BioMartGOGeneSets::getBioMartGOGeneSets`.

**Value**

A list of vectors where each vector contains Ensembl IDs annotated to a GO term.

### Examples

```
# There is no example  
NULL
```

---

getGeneSetsFromOrgDb *Get GO gene sets from OrgDb object*

---

### Description

Get GO gene sets from OrgDb object

### Usage

```
getGeneSetsFromOrgDb(orgdb, ontology = "BP")
```

### Arguments

orgdb	An OrgDb object.
ontology	Value should be bp, mf or cc.

### Value

A list of vectors where each vector contains Entrez IDs annotated to a GO term.

### Examples

```
# There is no example  
NULL
```

---

getGenesFromGencode *Get Gencode genes*

---

### Description

Get Gencode genes

### Usage

```
getGenesFromGencode(version)
```

### Arguments

version	Gencode version, e.g. v19 for human, vM21 for mouse.
---------	--

### Details

Only the protein coding genes.

**Value**

A [GRanges](#) object.

**Examples**

```
# There is no example
NULL
```

---

getGenomeDataFromNCBI *Get genome data from NCBI*

---

**Description**

Get genome data from NCBI

**Usage**

```
getGenomeDataFromNCBI(refseq_assembly_accession, return_granges = FALSE)
```

**Arguments**

**refseq\_assembly\_accession** The RefSeq accession number for the assembly, such as "GCF\_000001405.40" for human.

**return\_granges** If the assembly is already on chromosome level, it will directly construct a GRanges object where "chromosomes" are only used and chromosome lengths are corrected fitted in its seqlengths.

**Details**

Only protein coding genes are used.

**Value**

If return\_granges is set to FALSE, it returns a list of two data frames:

**genome** A data frame of several columns.

**gene** A data frame for genes. The first column contains the RefSeq accession numbers of the corresponding contigs. If the genome is assembled on the chromosome level, the first column corresponds to chromosomes. The contig names can be converted to other names with the information in the genome data frame.

**Examples**

```
if(FALSE) {
  getGenomeDataFromNCBI("GCF_000001405.40", return_granges = TRUE)
  getGenomeDataFromNCBI("GCF_000001405.40")
}
```

---

getGREATDefaultTSS      *Get built-in TSS from GREAT*

---

**Description**

Get built-in TSS from GREAT

**Usage**

```
getGREATDefaultTSS(genome)
```

**Arguments**

genome                      Only support "hg19", "hg38", "mm10", "mm9". Files are downloaded from <https://great-help.atlassian.net/wiki/spaces/GREAT/pages/655445/Genes> .

**Value**

A [GRanges](#) object.

**Examples**

```
# There is no example  
NULL
```

---

getKEGGGenome              *Get the corresponding assembly id for a kegg organism*

---

**Description**

Get the corresponding assembly id for a kegg organism

**Usage**

```
getKEGGGenome(organism)
```

**Arguments**

organism                    The organism code on KEGG.

**Value**

The Refseq access ID for the genome.

**Examples**

```
# There is no example  
NULL
```

---

getKEGGPathways      *Get KEGG pathway gene sets*

---

**Description**

Get KEGG pathway gene sets

**Usage**

```
getKEGGPathways(organism, as_table = FALSE)
```

**Arguments**

organism      The organism code on KEGG.  
as\_table      Whether to return the gene sets as a two-column table.

**Value**

A list of a data frame, depends on the value of as\_table.

**Examples**

```
# There is no example  
NULL
```

---

getRefSeqGenesFromUCSC  
*Get RefSeq genes from UCSC*

---

**Description**

Get RefSeq genes from UCSC

**Usage**

```
getRefSeqGenesFromUCSC(genome, subset = c("RefSeqSelect", "RefSeqCurated"))
```

**Arguments**

genome      UCSC genome, such as "hg19".  
subset      Subset of RefSeq genes. See <https://genome.ucsc.edu/cgi-bin/hgTrackUi?db=hg38&g=refSeqComposite>.

**Value**

A [GenomicRanges](#) object.

**Examples**

```
# There is no example
NULL
```

---

```
getRegionGeneAssociations-dispatch
    Method dispatch page for getRegionGeneAssociations
```

---

**Description**

Method dispatch page for getRegionGeneAssociations.

**Dispatch**

getRegionGeneAssociations can be dispatched on following classes:

- [getRegionGeneAssociations, GreatObject-method, GreatObject-class](#) class method
- [getRegionGeneAssociations, GreatJob-method, GreatJob-class](#) class method

**Examples**

```
# no example
NULL
```

---

```
getRegionGeneAssociations-GreatJob-method
    Get region-gene associations
```

---

**Description**

Get region-gene associations

**Usage**

```
## S4 method for signature 'GreatJob'
getRegionGeneAssociations(object, ontology = NULL, term_id = NULL,
    request_interval = 10, max_tries = 100, verbose = great_opt$verbose)
```

**Arguments**

object	A <a href="#">GreatJob-class</a> object returned by <a href="#">submitGreatJob</a> .
ontology	ontology name
term_id	Term id in the selected ontology.
request_interval	Time interval for two requests. Default is 300 seconds.
max_tries	Maximal times for automatically reconnecting GREAT web server.
verbose	Whether to show messages.

**Value**

A [GRanges](#) object. Please the two meta columns are in formats of `CharacterList` and `IntegerList` because a region may associate to multiple genes.

Please note, the distance is from the middle points of input regions to TSS.

**Author(s)**

Zuguang gu <z.gu@dkfz.de>

**Examples**

```
job = readRDS(system.file("extdata", "GreatJob.rds", package = "rGREAT"))
gr = getRegionGeneAssociations(job)
gr
```

---

getRegionGeneAssociations-GreatObject-method  
*Get region-gene associations*

---

**Description**

Get region-gene associations

**Usage**

```
## S4 method for signature 'GreatObject'
getRegionGeneAssociations(object, term_id = NULL, by_middle_points = FALSE,
  use_symbols = TRUE)
```

**Arguments**

<code>object</code>	A <a href="#">GreatObject-class</a> object returned by <a href="#">great</a> .
<code>term_id</code>	Term ID.
<code>by_middle_points</code>	Whether the distances are calculated from the middle points of input regions?
<code>use_symbols</code>	Whether to use gene symbols

**Value**

A [GRanges](#) object. Please the two meta columns are in formats of `CharacterList` and `IntegerList` because a region may associate to multiple genes.

**Examples**

```
obj = readRDS(system.file("extdata", "GreatObject.rds", package = "rGREAT"))
getRegionGeneAssociations(obj)
```

---

getTSS	<i>Get the internally used TSS</i>
--------	------------------------------------

---

**Description**

Get the internally used TSS

**Usage**

```
getTSS(tss_source, biomart_dataset = NULL)
```

**Arguments**

tss\_source      The same format as in [great](#).  
biomart\_dataset      The same format as in [great](#).

**Value**

A [GRanges](#) object.

**Examples**

```
# There is no example  
NULL
```

---

great	<i>Perform GREAT analysis</i>
-------	-------------------------------

---

**Description**

Perform GREAT analysis

**Usage**

```
great(gr, gene_sets, tss_source, biomart_dataset = NULL,  
      min_gene_set_size = 5, mode = "basalPlusExt", extend_from = c("TSS", "gene"),  
      basal_upstream = 5000, basal_downstream = 1000, extension = 1000000,  
      extended_tss = NULL, background = NULL, exclude = "gap",  
      cores = 1, verbose = great_opt$verbose)
```

## Arguments

<code>gr</code>	A <a href="#">GRanges</a> object. This is the input regions. It is important to keep consistent for the chromosome names of the input regions and the internal TSS regions. Use <a href="#">getTSS</a> to see the format of internal TSS regions.
<code>gene_sets</code>	A single string of defaultly supported gene sets collections (see the full list in "Genesets" section), or a named list of vectors where each vector correspond to a gene set.
<code>tss_source</code>	Source of TSS. See "TSS" section.
<code>biomart_dataset</code>	The value should be in <code>BioMartG0GeneSets::supportedOrganisms</code> .
<code>min_gene_set_size</code>	Minimal size of gene sets.
<code>mode</code>	The mode to extend genes. Value should be one of 'basalPlusExt', 'twoClosest' and 'oneClosest'. See <a href="#">extendTSS</a> for details.
<code>extend_from</code>	Should the gene be extended only from its TSS or the complete gene?
<code>basal_upstream</code>	In 'basalPlusExt' mode, number of base pairs extending to the upstream of TSS to form the basal domains.
<code>basal_downstream</code>	In 'basalPlusExt' mode, number of base pairs extending to the downstream of TSS to form the basal domains.
<code>extension</code>	Extensions from the basal domains.
<code>extended_tss</code>	If your organism is not defaultly supported, you can first prepare one by <a href="#">extendTSSFromDataFrame</a> or <a href="#">extendTSS</a> , and set the object to this argument. Please see more examples in the vignette.
<code>background</code>	Background regions. The value can also be a vector of chromosome names.
<code>exclude</code>	Regions that are excluded from analysis such as gap regions (which can be get by <a href="#">getGapFromUCSC</a> ). The value can also be a vector of chromosome names. It also allows a special character value "gap" so that gap regions for corresponding organism will be removed from the analysis.
<code>cores</code>	Number of cores to use.
<code>verbose</code>	Whether to print messages.

## Details

When `background` or `exclude` is set, the analysis is restricted in the background regions, still by using Binomial method. Note this is different from the original GREAT method which uses Fisher's exact test if background regions is set. See [submitGreatJob](#) for explanations.

By default, gap regions are excluded from the analysis.

## Value

A [GreatObject-class](#) object. The following methods can be applied on it:

- [getEnrichmentTable, GreatObject-method](#) to retrieve the result table.
- [getRegionGeneAssociations, GreatObject-method](#) to get the associations between input regions and genes.
- [plotRegionGeneAssociations, GreatObject-method](#) to plot the associations bewteen input regions and genes.
- [shinyReport, GreatObject-method](#) to view the results by a shiny application.

## Tss

rGREAT supports TSS from many organisms. The value of `tss_source` should be encoded in a special format:

- Name of TxDb.\* packages. Supported packages are in `rGREAT:::BIOC_ANNO_PKGS$txdb`.
- Genome version of the organism, e.g. "hg19". Then the corresponding TxDb will be used.
- In a format of `RefSeqCurated:$genome` where `$genome` is the genome version of an organism, such as hg19. RefSeqCurated subset will be used.
- In a format of `RefSeqSelect:$genome` where `$genome` is the genome version of an organism, such as hg19. RefSeqSelect subset will be used.
- In a format of `Gencode_v$version` where `$version` is gencode version, such as 19 (for human) or M21 for mouse. Gencode protein coding genes will be used.
- In a format of `GREAT:$genome`, where `$genome` can only be mm9, mm10, hg19, hg38. The TSS from GREAT will be used.

## Genesets

rGREAT supports the following built-in GO gene sets for all organisms (note "GO:" can be omitted):

**"GO:BP"**: Biological Process, from GO.db package.

**"GO:CC"**: Cellular Component, from GO.db package.

**"GO:MP"**: Molecular Function, from GO.db package.

rGREAT also supports built-in gene sets collections from MSigDB (note this is only for human, "msigdb:" can be omitted):

**"msigdb:H"** Hallmark gene sets.

**"msigdb:C1"** Positional gene sets.

**"msigdb:C2"** Curated gene sets.

**"msigdb:C2:CGP"** C2 subcategory: chemical and genetic perturbations gene sets.

**"msigdb:C2:CP"** C2 subcategory: canonical pathways gene sets.

**"msigdb:C2:CP:BIOCARTA"** C2 subcategory: BioCarta subset of CP.

**"msigdb:C2:CP:KEGG"** C2 subcategory: KEGG subset of CP.

**"msigdb:C2:CP:PID"** C2 subcategory: PID subset of CP.

**"msigdb:C2:CP:REACTOME"** C2 subcategory: REACTOME subset of CP.

**"msigdb:C2:CP:WIKIPATHWAYS"** C2 subcategory: WIKIPATHWAYS subset of CP.

**"msigdb:C3"** Regulatory target gene sets.

**"msigdb:C3:MIR:MIRDB"** miRDB of microRNA targets gene sets.

**"msigdb:C3:MIR:MIR\_LEGACY"** MIR\_Legacy of MIRDB.

**"msigdb:C3:TFT:GTRD"** GTRD transcription factor targets gene sets.

**"msigdb:C3:TFT:TFT\_LEGACY"** TFT\_Legacy.

**"msigdb:C4"** Computational gene sets.

**"msigdb:C4:CGN"** C4 subcategory: cancer gene neighborhoods gene sets.

**"msigdb:C4:CM"** C4 subcategory: cancer modules gene sets.

**"msigdb:C5"** Ontology gene sets.

"**msigdb:C5:GO:BP**" C5 subcategory: BP subset.  
 "**msigdb:C5:GO:CC**" C5 subcategory: CC subset.  
 "**msigdb:C5:GO:MF**" C5 subcategory: MF subset.  
 "**msigdb:C5:HPO**" C5 subcategory: human phenotype ontology gene sets.  
 "**msigdb:C6**" Oncogenic signature gene sets.  
 "**msigdb:C7**" Immunologic signature gene sets.  
 "**msigdb:C7:IMMUNESIGDB**" ImmuneSigDB subset of C7.  
 "**msigdb:C7:VAX**" C7 subcategory: vaccine response gene sets.  
 "**msigdb:C8**" Cell type signature gene sets.

If the defaultly supported TxDb is used, Entrez gene ID is always used as the main gene ID. If you provide a self-defined gene\_sets or extended\_tss, you need to make sure they two have the same gene ID types.

## Biomart

rGREAT supports a large number of organisms of which the information is retrieved from Ensembl BioMart. The name of a BioMart dataset can be assigned to argument biomart\_dataset. All supported organisms can be found with BioMartGOGeneSets::supportedOrganisms.

## Examples

```
if(FALSE) {
  gr = randomRegions(genome = "hg19")
  res = great(gr, "MSigDB:H", "txdb:hg19")
  res = great(gr, "MSigDB:H", "TxDb.Hsapiens.UCSC.hg19.knownGene")
  res = great(gr, "MSigDB:H", "RefSeq:hg19")
  res = great(gr, "MSigDB:H", "GREAT:hg19")
  res = great(gr, "MSigDB:H", "Gencode_v19")
  res = great(gr, "GO:BP", "hsapiens_gene_ensembl")
}
```

---

GreatJob

*Constructor method for GreatJob class*

---

## Description

Constructor method for GreatJob class

## Usage

```
GreatJob(...)
```

## Arguments

... arguments.

## Details

There is no public constructor method for the [GreatJob-class](#).

**Value**

No value is returned.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```
# There is no example
NULL
```

---

GreatJob-class	<i>Class to store and retrieve GREAT results</i>
----------------	--

---

**Description**

Class to store and retrieve GREAT results

**Details**

After submitting request to GREAT server, the generated results will be available on GREAT server for some time. The GreatJob-class is defined to store parameters that user has set and result tables what were retrieved from GREAT server.

**Constructor**

Users don't need to construct by hand, [submitGreatJob](#) is used to generate a GreatJob-class instance.

**Workflow**

After submitting request to GREAT server, users can perform following steps:

- [getEnrichmentTables, GreatJob-method](#) to get enrichment tables for selected ontologies catalogues.
- [plotRegionGeneAssociations, GreatJob-method](#) to plot associations between regions and genes
- [getRegionGeneAssociations, GreatJob-method](#) to get a [GRanges](#) object which contains associations between regions and genes.
- [shinyReport, GreatJob-method](#) to view the results by a shiny application.

**Author(s)**

Zuguang gu <z.gu@dkfz.de>

**Examples**

```
# There is no example
NULL
```

---

GreatObject	<i>Constructor method for GreatObject class</i>
-------------	---

---

### Description

Constructor method for GreatObject class

### Usage

```
GreatObject(...)
```

### Arguments

... arguments.

### Details

There are following methods that can be applied on [GreatObject-class](#) object:

- [getEnrichmentTable,GreatObject-method](#) to retrieve the result table.
- [getRegionGeneAssociations,GreatObject-method](#) to get the associations between input regions and genes.
- [plotRegionGeneAssociations,GreatObject-method](#) to plot the associations between input regions and genes.
- [shinyReport,GreatObject-method](#) to view the results by a shiny application.

### Value

No value is returned.

### Author(s)

Zuguang Gu <z.gu@dkfz.de>

### Examples

```
# There is no example  
NULL
```

---

GreatObject-class      *Class for local GREAT analysis*

---

**Description**

Class for local GREAT analysis

**Details**

`great` returns A `GreatObject-class` object.

**Examples**

```
# There is no example
NULL
```

---

great\_opt                      *Global parameters for rGREAT*

---

**Description**

Global parameters for rGREAT

**Usage**

```
great_opt(..., RESET = FALSE, READ.ONLY = NULL, LOCAL = FALSE, ADD = FALSE)
```

**Arguments**

...	Arguments for the parameters, see "details" section
RESET	Reset to default values.
READ.ONLY	Please ignore.
LOCAL	Please ignore.
ADD	Please ignore.

**Details**

There are following parameters:

`verbose` Whether to show messages.

**Examples**

```
great_opt
```

---

```
plotRegionGeneAssociationGraphs-GreatJob-method
    Plot region-gene associations
```

---

**Description**

Plot region-gene associations

**Usage**

```
## S4 method for signature 'GreatJob'
plotRegionGeneAssociationGraphs(object, ...)
```

**Arguments**

object	A <a href="#">GreatJob-class</a> object returned by <a href="#">submitGreatJob</a> .
...	All passed to <a href="#">plotRegionGeneAssociations, GreatJob-method</a> .

**Details**

This function will be removed in the future, please use [plotRegionGeneAssociations, GreatJob-method](#) instead.

**Examples**

```
# There is no example
NULL
```

---

```
plotRegionGeneAssociations-dispatch
    Method dispatch page for plotRegionGeneAssociations
```

---

**Description**

Method dispatch page for plotRegionGeneAssociations.

**Dispatch**

plotRegionGeneAssociations can be dispatched on following classes:

- [plotRegionGeneAssociations, GreatObject-method, GreatObject-class](#) class method
- [plotRegionGeneAssociations, GreatJob-method, GreatJob-class](#) class method

**Examples**

```
# no example
NULL
```

---

plotRegionGeneAssociations-GreatJob-method  
*Plot region-gene associations*

---

## Description

Plot region-gene associations

## Usage

```
## S4 method for signature 'GreatJob'  
plotRegionGeneAssociations(object, ontology = NULL, term_id = NULL, which_plot = 1:3,  
  request_interval = 10, max_tries = 100, verbose = great_opt$verbose)
```

## Arguments

object	A <a href="#">GreatJob-class</a> object returned by <a href="#">submitGreatJob</a> .
ontology	A single ontology names. Valid values are in <a href="#">availableOntologies</a> .
term_id	Term id in the selected ontology
which_plot	Which plots to draw? The value should be in 1, 2, 3. See "Details" section for explanation.
request_interval	Time interval for two requests. Default is 300 seconds.
max_tries	Maximal times for automatically reconnecting GREAT web server.
verbose	Whether to show messages.

## Details

There are following figures:

- Association between regions and genes (`which_plot = 1`).
- Distribution of distance to TSS (`which_plot = 2`).
- Distribution of absolute distance to TSS (`which_plot = 3`).

If ontology and term\_id are set, only regions and genes corresponding to selected ontology term will be used. Valid value for ontology is in [availableOntologies](#) and valid value for term\_id is from 'id' column in the table which is returned by [getEnrichmentTables](#).

## Author(s)

Zuguang gu <z.gu@dkfz.de>

## Examples

```
job = readRDS(system.file("extdata", "GreatJob.rds", package = "rGREAT"))  
  
plotRegionGeneAssociations(job)  
plotRegionGeneAssociations(job, which_plot = 1)  
# Do not use other term_id for this example, or you need to generate a new `job` object.  
plotRegionGeneAssociations(job, ontology = "GO Molecular Function",  
  term_id = "GO:0004984")
```

---

plotRegionGeneAssociations-GreatObject-method  
*Plot region-gene associations*

---

**Description**

Plot region-gene associations

**Usage**

```
## S4 method for signature 'GreatObject'
plotRegionGeneAssociations(object, term_id = NULL, which_plot = 1:3)
```

**Arguments**

object	A <a href="#">GreatObject-class</a> object returned by <a href="#">great</a> .
term_id	Term ID.
which_plot	Which plots to draw? The value should be in 1, 2, 3. See "Details" section for explanation.

**Details**

There are following figures:

- Association between regions and genes (which\_plot = 1).
- Distribution of distance to TSS (which\_plot = 2).
- Distribution of absolute distance to TSS (which\_plot = 3).

**Examples**

```
obj = readRDS(system.file("extdata", "GreatObject.rds", package = "rGREAT"))
plotRegionGeneAssociations(obj)
```

---

plotVolcano-dispatch *Method dispatch page for plotVolcano*

---

**Description**

Method dispatch page for plotVolcano.

**Dispatch**

plotVolcano can be dispatched on following classes:

- [plotVolcano,GreatObject-method](#), [GreatObject-class](#) class method
- [plotVolcano,GreatJob-method](#), [GreatJob-class](#) class method

## Examples

```
# no example
NULL
```

---

```
plotVolcano-GreatJob-method
      Make volcano plot
```

---

## Description

Make volcano plot

## Usage

```
## S4 method for signature 'GreatJob'
plotVolcano(object, ontology, min_region_hits = 5,
            x_values = c("fold_enrichment", "z-score"),
            y_values = c("p_value", "p_adjust"),
            main = NULL)
```

## Arguments

object	A <a href="#">GreatJob-class</a> object returned by <a href="#">submitGreatJob</a> .
ontology	A single ontology names. Valid values are in <a href="#">availableOntologies</a> .
min_region_hits	Minimal number of input regions overlapping to the geneset associated regions.
x_values	Which values for the x-axis.
y_values	Which values for the y-axis.
main	Title of the plot.

## Details

Since the enrichment is an over-representation test, it is only the half volcano.

## Examples

```
# There is no example
NULL
```

---

plotVolcano-GreatObject-method  
*Make volcano plot*

---

**Description**

Make volcano plot

**Usage**

```
## S4 method for signature 'GreatObject'
plotVolcano(object, min_region_hits = 5,
             x_values = c("fold_enrichment", "z-score"),
             y_values = c("p_value", "p_adjust"),
             main = NULL)
```

**Arguments**

object	A <a href="#">GreatObject-class</a> object returned by <a href="#">great</a> .
min_region_hits	Minimal number of input regions overlapping to the geneset associated regions.
x_values	Which values for the x-axis.
y_values	Which values for the y-axis.
main	Title of the plot.

**Details**

Since the enrichment is an over-representation test, it is only the half volcano.

**Examples**

```
# There is no example
NULL
```

---

randomRegions      *Generate random regions*

---

**Description**

Generate random regions

**Usage**

```
randomRegions(genome = NULL, nr = 1000, seqlengths = NULL,
              width_fun = function(n) runif(n, min = 1000, max = 10000))
```

**Arguments**

genome	UCSC genome version, e.g. "hg19".
nr	Number of regions.
seqlengths	Alternatively, you can also specify a named vector of seqlengths (chromosome lengths).
width_fun	A function which defines the distribution of region widths.

**Details**

The number of regions per chromosome is proportional to the chromosome length.

**Examples**

```
gr = randomRegions(genome = "hg19")
quantile(width(gr))
```

---

```
randomRegionsFromBioMartGenome
```

*Generate random regions from a BioMart genome*

---

**Description**

Generate random regions from a BioMart genome

**Usage**

```
randomRegionsFromBioMartGenome(biomart_dataset, nr = 1000, ...)
```

**Arguments**

biomart_dataset	A BioMart dataset. Values should be in <code>BioMartGOGeneSets::supportedOrganisms</code> .
nr	Number of regions.
...	Pass to <code>randomRegions</code> .

**Details**

The number of regions per chromosome is proportional to the chromosome length.

**Examples**

```
if(FALSE) {
  # Giant panda
  gr = randomRegionsFromBioMartGenome("amelanoleuca_gene_ensembl")
}
```

---

read\_gmt *Read gmt gene sets file*

---

**Description**

Read gmt gene sets file

**Usage**

```
read_gmt(x, from = NULL, to = NULL, orgdb = NULL)
```

**Arguments**

x	The file name of a .gmt file.
from	Gene ID type in the original gmt file. Value can only take values in 'ENTREZ/SYMBOL/ENSEMBL/REFSEQ'.
to	Gene ID type that you want to convert to. Value can only take values in 'ENTREZ/SYMBOL/ENSEMBL/REFSEQ'.
orgdb	The name of an OrgDb database.

**Value**

A named list of vectors.

**Examples**

```
read_gmt(url("http://dsigdb.tanlab.org/Downloads/D2_LINCS.gmt"))
```

---

reduce\_by\_start\_and\_end  
*Reduce by start and end*

---

**Description**

Reduce by start and end

**Usage**

```
reduce_by_start_and_end(s, e)
```

**Arguments**

s	Start positions. Sorted.
e	End positions. Sorted.

**Details**

Only internally used.

**Value**

Sum of total widths of the reduced regions.

**Examples**

```
# There is no example
NULL
```

---

shinyReport-dispatch *Method dispatch page for shinyReport*

---

**Description**

Method dispatch page for shinyReport.

**Dispatch**

shinyReport can be dispatched on following classes:

- [shinyReport, GreatJob-method, GreatJob-class](#) class method
- [shinyReport, GreatObject-method, GreatObject-class](#) class method

**Examples**

```
# no example
NULL
```

---

shinyReport-GreatJob-method  
*Shiny app on the GreatJob object*

---

**Description**

Shiny app on the GreatJob object

**Usage**

```
## S4 method for signature 'GreatJob'
shinyReport(object)
```

**Arguments**

object            The GreatJob object returned by [submitGreatJob](#).

**Value**

A shiny app object.

**Examples**

```
if(FALSE) {  
  # pseudo code  
  job = submitGreatJob(...)  
  shinyReport(job)  
}
```

---

shinyReport-GreatObject-method

*Shiny app on the GreatObject object*

---

**Description**

Shiny app on the GreatObject object

**Usage**

```
## S4 method for signature 'GreatObject'  
shinyReport(object)
```

**Arguments**

object            The GreatObject object returned by [great](#).

**Value**

A shiny app object.

**Examples**

```
if(FALSE) {  
  # pseudo code  
  obj = great(...)  
  shinyReport(obj)  
}
```

---

submitGreatJob

*Perform online GREAT analysis*

---

**Description**

Perform online GREAT analysis

**Usage**

```
submitGreatJob(gr, bg = NULL,
  gr_is_zero_based = FALSE,
  species = "hg19",
  genome = species,
  includeCuratedRegDoms = TRUE,
  rule = c("basalPlusExt", "twoClosest", "oneClosest"),
  adv_upstream = 5.0,
  adv_downstream = 1.0,
  adv_span = 1000.0,
  adv_twoDistance = 1000.0,
  adv_oneDistance = 1000.0,
  request_interval = 60,
  max_tries = 10,
  version = DEFAULT_VERSION,
  base_url = "http://great.stanford.edu/public/cgi-bin",
  use_name_column = FALSE,
  verbose = help, help = great_opt$verbose)
```

**Arguments**

<code>gr</code>	A <a href="#">GRanges</a> object or a data frame which contains at least three columns (chr, start and end).
<code>bg</code>	Not supported any more. See explanations in section "When_background_regions_are_set".
<code>gr_is_zero_based</code>	Are start positions in <code>gr</code> zero-based?
<code>genome</code>	Genome. "hg38", "hg19", "mm10", "mm9" are supported in GREAT version 4.x.x, "hg19", "mm10", "mm9", "danRer7" are supported in GREAT version 3.x.x and "hg19", "hg18", "mm9", "danRer7" are supported in GREAT version 2.x.x.
<code>species</code>	The same as <code>genome</code> but it will be deprecated soon.
<code>includeCuratedRegDoms</code>	Whether to include curated regulatory domains, see <a href="https://great-help.atlassian.net/wiki/spaces/GREAT/pages/655443/Association+Rules#AssociationRules-CuratedReg">https://great-help.atlassian.net/wiki/spaces/GREAT/pages/655443/Association+Rules#AssociationRules-CuratedReg</a> .
<code>rule</code>	How to associate genomic regions to genes. See 'Details' section.
<code>adv_upstream</code>	Unit: kb, only used when rule is <code>basalPlusExt</code> .
<code>adv_downstream</code>	Unit: kb, only used when rule is <code>basalPlusExt</code> .
<code>adv_span</code>	Unit: kb, only used when rule is <code>basalPlusExt</code> .
<code>adv_twoDistance</code>	Unit: kb, only used when rule is <code>twoClosest</code> .
<code>adv_oneDistance</code>	Unit: kb, only used when rule is <code>oneClosest</code> .
<code>request_interval</code>	Time interval for two requests. Default is 300 seconds.
<code>max_tries</code>	Maximal times for automatically reconnecting GREAT web server.
<code>version</code>	Version of GREAT. The value should be "4.0.4", "3.0.0", "2.0.2". Shorten version numbers can also be used, such as using "4" or "4.0" is same as "4.0.4".

base_url	the url of cgi-bin path, only used when it is explicitly specified.
use_name_column	If the input is a data frame, whether to use the fourth column as the "names" of regions?
verbose	Whether to print help messages.
help	Whether to print help messages. This argument will be replaced by verbose in future versions.

## Details

Note: On Aug 19 2019 GREAT released version 4(<https://great-help.atlassian.net/wiki/spaces/GREAT/pages/655442/Version+History>) where it supports hg38 genome and removes some ontologies such pathways. `submitGreatJob` still takes hg19 as default. hg38 can be specified by the genome = "hg38" argument. To use the older versions such as 3.0.0, specify as `submitGreatJob(..., version = "3.0.0")`.

Note it does not use the standard GREAT API. This function directly send data to GREAT web server by HTTP POST.

Following text is copied from GREAT web site (<http://great.stanford.edu/public/html/>)

Explanation of rule and settings with names started with 'adv\_' (advanced settings):

**basalPlusExt** Mode 'Basal plus extension'. Gene regulatory domain definition: Each gene is assigned a basal regulatory domain of a minimum distance upstream and downstream of the TSS (regardless of other nearby genes, controlled by `adv_upstream` and `adv_downstream` argument). The gene regulatory domain is extended in both directions to the nearest gene's basal domain but no more than the maximum extension in one direction (controlled by `adv_span`).

**twoClosest** Mode 'Two nearest genes'. Gene regulatory domain definition: Each gene is assigned a regulatory domain that extends in both directions to the nearest gene's TSS (controlled by `adv_twoDistance`) but no more than the maximum extension in one direction.

**oneClosest** Mode 'Single nearest gene'. Gene regulatory domain definition: Each gene is assigned a regulatory domain that extends in both directions to the midpoint between the gene's TSS and the nearest gene's TSS (controlled by `adv_oneDistance`) but no more than the maximum extension in one direction.

## Value

A `GreatJob-class` object which can be used to get results from GREAT server. The following methods can be applied on it:

- `getEnrichmentTables, GreatObject-method` to retrieve the result tables.
- `getRegionGeneAssociations, GreatObject-method` to get the associations between input regions and genes.
- `plotRegionGeneAssociations, GreatObject-method` to plot the associations between input regions and genes.
- `shinyReport, GreatObject-method` to view the results by a shiny application.

## When\_background\_regions\_are\_set

Note when `bg` argument is set to a list of background regions, GREAT uses a completely different test!

When `bg` is set, `gr` should be exactly subset of `bg`. For example, let's say a background region list contains five regions: [1, 10], [15, 23], [34, 38], [40, 49], [54, 63], `gr` can only be a subset of the five regions, which means `gr` can take [15, 23], [40, 49], but it cannot take [16, 20], [39, 51]. In this setting, regions are taken as single units and Fisher's exact test is applied for calculating the enrichment (by testing number of regions in the 2x2 contingency table).

Check <https://great-help.atlassian.net/wiki/spaces/GREAT/pages/655452/File+Formats#FileFormats-Whatshouldmybackgroundregionsfilecontain?> for more explanations.

Please note from rGREAT 1.99.0, setting `bg` is not supported any more and this argument will be removed in the future. You can either directly use GREAT website or use other Bioconductor packages such as "LOLA" to perform the Fisher's exact test-based analysis.

If you want to restrict the input regions to background regions (by intersections) and still to apply Binomial test there, please consider to use local GREAT by [great](#).

### Author(s)

Zuguang gu <z.gu@dkfz.de>

### See Also

[great](#) for the local implementation of GREAT algorithm.

### Examples

```
set.seed(123)
gr = randomRegions(nr = 1000, genome = "hg19")
job = submitGreatJob(gr)
job

# more parameters can be set for the job
if(FALSE) { # suppress running it when building the package
  # current GREAT version is 4.0.4
  job = submitGreatJob(gr, genome = "hg19")
  job = submitGreatJob(gr, adv_upstream = 10, adv_downstream = 2, adv_span = 2000)
  job = submitGreatJob(gr, rule = "twoClosest", adv_twoDistance = 2000)
  job = submitGreatJob(gr, rule = "oneClosest", adv_oneDistance = 2000)
}
```

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