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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/

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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 assigined 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 great 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 extendTSS.

Value

A GRanges object with one meta column 'gene_id'.

Examples

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

---

extendTSSFromOrgDb *Extend TSS*

Description

Extend TSS

Usage

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

Arguments

orgdb	Name of "org.*" packages from Bioconductor. All supported OrgDb packages are in rGREAT:::BIOC_ANNO_PKGS$orgdb.
verbose	Whether to print messages.
...	All pass to extendTSS.

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 rGREAT:::BIOC_ANNO_PKGS$txdb. Note short genome version can also be used here such as "hg19" or "hg19.knownGene".
verbose	Whether to print messages.
...	All pass to extendTSS.

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 GreatJob-class object returned by submitGreatJob.
ontology	A single ontology names. Valid values are in availableOntologies.
...	All pass to getEnrichmentTables,GreatJob-method.

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,GreatJob-method, GreatJob-class class method
- getEnrichmentTables,GreatObject-method, GreatObject-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 `GreatJob-class` object returned by `submitGreatJob`.
`ontology`	Ontology names. Valid values are in `availableOntologies`. `ontology` is prior to `category` argument.
`category`	Pre-defined ontology categories. One category can contain more than one ontologies. Valid values are in `availableCategories`
`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 envoked 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 GreatObject-class object returned by great.
...	All passed to getEnrichmentTable,GreatObject-method.

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

genome	UCSC genome, such as "hg19".
seqnames	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

dataset	Name of the dataset.
ontology	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 GRanges 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 `GreatJob-class` object returned by `submitGreatJob`.
`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

object	A GreatObject-class object returned by great.
term_id	Term ID.
by_middle_points	Whether the distances are calculated from the middle points of input regions?
use_symbols	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 *Get the internally used TSS*

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 *Perform GREAT analysis*

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

gr	A GRanges 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 getTSS to see the format of internal TSS regions.
gene_sets	A single string of defautly 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.
tss_source	Source of TSS. See "TSS" section.
biomart_dataset	The value should be in BioMartGOGeneSets::supportedOrganisms.
min_gene_set_size	Minimal size of gene sets.
mode	The mode to extend genes. Value should be one of 'basalPlusExt', 'twoClosest' and 'oneClosest'. See extendTSS for details.
extend_from	Should the gene be extended only from its TSS or the complete gene?

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.

extended_tss If your organism is not defaultly supported, you can first prepare one by extendTSSFromDataFrame or extendTSS, and set the object to this argument. Please see more examples in the vignette.

background Background regions. The value can also be a vector of chromosome names.

exclude Regions that are excluded from analysis such as gap regions (which can be get by getGapFromUCSC). 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.

cores Number of cores to use.

verbose 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 pacakge.

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")
}
```

---

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`	Pllease ignore.
`ADD`	Please ignore.

Details

There are following parameters:

`verbose` Whether to show messages.

Examples

```
great_opt
```

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 *Class to store and retrieve GREAT results*

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 bewteen 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` *Constructor method for GreatObject class*

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 bewteen 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
```

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

Description

Plot region-gene associations

Usage

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

Arguments

object	A GreatJob-class object returned by submitGreatJob.
...	All passed to plotRegionGeneAssociations,GreatJob-method.

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,GreatJob-method`, `GreatJob-class` class method
- `plotRegionGeneAssociations,GreatObject-method`, `GreatObject-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 `GreatJob-class` object returned by `submitGreatJob`.
`ontology`	A single ontology names. Valid values are in `availableOntologies`.
`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 `GreatObject-class` object returned by `great`.
`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 GreatJob-class object returned by submitGreatJob.
ontology	A single ontology names. Valid values are in availableOntologies.
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 GreatObject-class object returned by great.
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 chromsome 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 `BioMartGOGeneSets::supportedOrganisms`.
nr	Number of regions.
...	Pass to `randomRegions`.

Details

The number of regions per chromosome is proportional to the chromsome 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("https://data.broadinstitute.org/gsea-msigdb/msigdb/release/2025.1.Hs/h.all.v2025.1.Hs.entrez.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,GreatObject-method`, `GreatObject-class` class method
- `shinyReport,GreatJob-method`, `GreatJob-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

gr	A GRanges object or a data frame which contains at least three columns (chr, start and end).
bg	Not supported any more. See explanations in section "When_background_regions_are_set".
gr_is_zero_based	Are start positions in gr zero-based?
genome	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.
species	The same as genome but it will be deprecated soon.
includeCuratedRegDoms	Whether to include curated regulatory domains, see https://great-help.atlassian.net/wiki/spaces/GREAT/pages/655443/Association+Rules#AssociationRules-CuratedRegulat .
rule	How to associate genomic regions to genes. See 'Details' section.
adv_upstream	Unit: kb, only used when rule is basalPlusExt.
adv_downstream	Unit: kb, only used when rule is basalPlusExt.
adv_span	Unit: kb, only used when rule is basalPlusExt.
adv_twoDistance	Unit: kb, only used when rule is twoClosest.
adv_oneDistance	Unit: kb, only used when rule is oneClosest.
request_interval	Time interval for two requests. Default is 300 seconds.
max_tries	Maximal times for aotumatically reconnecting GREAT web server.
version	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 retreive the result tables.
- 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.

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 contigency 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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