Package ‘rGREAT’

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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,
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)
Description

All available ontology names of the GREAT job

Usage

```r
## 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

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

Extend TSS

Usage

\[
\text{extendTSS}(\text{gene, seqLengths = NULL, genome = NULL,}}
\]
\[
\text{gene_id_type = NULL, mode = "basalPlusExt", basal_upstream = 5000,}
\]
\[
\text{basal_downstream = 1000, extension = 1000000,}
\]
\[
\text{verbose = great_opt$verbose, .attr = list())}
\]

Arguments

- **gene**: A \texttt{GRanges} object of gene (or TSS) coordinates.
- **seqLengths**: A named vector of chromosome lengths. If it is not provided, it is taken by \texttt{seqLengths(gene)}.
- **genome**: UCSC genome can be set here, then \texttt{seqLengths} will be automatically retrieved from UCSC server.
- **gene_id_type**: Gene ID types in \texttt{gene}. You need to set this argument if you use built-in gene sets in \texttt{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.
- **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).


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, 
str = 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 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.
extendTSSFromOrgDb

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_PKG$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

```r
# no example
NULL
```

---

### Description

Get a single enrichment table from GREAT web server

#### Usage

```r
## 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

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

\textit{Get enrichment table}

\section*{Description}

Get enrichment table

\section*{Usage}

\begin{verbatim}
## S4 method for signature 'GreatObject'
getEnrichmentTable(object, min\_region\_hits = 5)
\end{verbatim}

\section*{Arguments}

\begin{itemize}
\item \textbf{object} A \texttt{GreatObject-class} object returned by \texttt{great}.
\item \textbf{min\_region\_hits} Minimal number of input regions overlapping to the geneset associated regions.
\end{itemize}

\section*{Details}

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

\section*{Value}

A data frame of enrichment results

\section*{Examples}

\begin{verbatim}
obj = readRDS(system.file("extdata", "GreatObject.rds", package = "rGREAT"))
getEnrichmentTable(obj)
\end{verbatim}

\section*{getEnrichmentTables\_dispatch}

\textit{Method dispatch page for getEnrichmentTables}

\section*{Description}

Method dispatch page for getEnrichmentTables.

\section*{Dispatch}

getEnrichmentTables can be dispatched on following classes:

\begin{itemize}
\item \texttt{getEnrichmentTables,GreatJob\_method,GreatJob\_class} class method
\item \texttt{getEnrichmentTables,GreatObject\_method,GreatObject\_class} class method
\end{itemize}
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 on-
tologies. 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

```r
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

```r
## 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

```r
# 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 gene sets from BioMart

Description
Get gene sets from BioMart

Usage
geneSetsFromBioMart(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
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**

```r
# 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.
getKEGGPathways

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

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

description

Get region-gene associations

Usage

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

Description
Get region-gene associations

Usage
```r
## 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
getTSS

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

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

\[
\text{getTSS} \quad \text{Get the internally used TSS}
\]

Description

Get the internally used TSS

Usage

```r
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

```r
# There is no example
NULL
```
Perform GREAT analysis

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 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.
tss_source
Source of TSS. See "TSS" section.
bioMart_dataset
The value should be in BioMartG0GeneSets::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.
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 Binominal 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 between 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: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: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

```r
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-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 between regions and genes.
- `shinyReport,GreatJob-method` to view the results by a shiny application.

**Author(s)**

Zuguang gu <z.gu@dkfz.de>

**Examples**

```r
# 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 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

```r
# 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 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

```r
# no example
NULL
```

Description

Plot region-gene associations

Usage

```r
## 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

```r
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")
```

Description

Plot region-gene associations

Usage

```r
## 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

```r
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
**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**

```r
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 chromosome length.

Examples

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

---

**read_gmt**

*Read gmt gene sets file*

**Description**

Read gmt gene sets file

**Usage**

```r
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 'EN-TREZ/SYMBOL/ENSEMBL/REFSEQ'.

- **to**
  - Gene ID type that you want to convert to. Value can only take values in 'EN-TREZ/SYMBOL/ENSEMBL/REFSEQ'.

- **orgdb**
  - The name of an OrgDb database.

**Value**

A named list of vectors.

**Examples**

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

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

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

Arguments

- `object` The GreatJob object returned by `submitGreatJob`.

Value

A shiny app object.

Examples

```r
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

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

object The GreatObject object returned by great.

Value

A shiny app object.

Examples

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

Description

Perform online GREAT analysis

Usage

```r
submitGreatJob(gr, bg = NULL,
    gr_is_zero_based = FALSE,
    species = "hg19",
    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".
submitGreatJob

gr_is_zero_based
  Are start positions in gr zero-based?

species
  Species. "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.

includeCuratedRegDoms
  Whether to include curated regulatory domains, see https://great-help.atlassian.net/wiki/spaces/GREAT/pages/655443/Association+Rules#AssociationRules-CuratedRegulatoryDomains.

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 automatically 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 species = "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).


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

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

# 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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