

# Package ‘rGREAT’

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**Type** Package

**Title** Client for GREAT Analysis

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**Author** Zuguang Gu

**Depends** R (>= 3.1.2), GenomicRanges, IRanges, methods

**Imports** rjson, GetoptLong (>= 0.0.9), RCurl, utils, stats

**Suggests** testthat (>= 0.3), knitr, circlize (>= 0.4.8), rmarkdown

**VignetteBuilder** knitr

**biocViews** GeneSetEnrichment, GO, Pathways, Software, Sequencing,  
WholeGenome, GenomeAnnotation, Coverage

**Description** This package makes GREAT (Genomic Regions Enrichment of Annotations Tool) analysis automatic by constructing a HTTP POST request according to user's input and automatically retrieving results from GREAT web server.

**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*

---

## Description

Available ontology categories

## Usage

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

## Arguments

job                    a [GreatJob-class](#) instance

## 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

```
# note the `job` was generated from GREAT 3.0.0
job = readRDS(system.file("extdata", "job.rds", package = "rGREAT"))
availableCategories(job)
```

---

availableOntologies-GreatJob-method  
*All available ontology names*

---

## Description

All available ontology names

## Usage

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

## Arguments

**job** a [GreatJob-class](#) instance  
**category** one or multiple categories. All available categories can be get 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

```
# note the `job` was generated from GREAT 3.0.0  
job = readRDS(system.file("extdata", "job.rds", package = "rGREAT"))  
availableOntologies(job)  
availableOntologies(job, category = "Pathway Data")
```

---

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(job, ontology = NULL, category = "GO",  
  request_interval = 10, max_tries = 100, download_by = c("json", "tsv"),  
  verbose = TRUE)
```

## Arguments

|                  |   |
|------------------|---|
| job              | a <a href="#">GreatJob-class</a> instance   |
| 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        | maximum tries   |
| download_by      | Internally used.  |
| verbose          | Whether print messages.   |

## Details

The table contains statistics for the each term in each ontology catalogue.

Please note there is no FDR column in original tables. Users should calculate by themselves by functions such as [p.adjust](#)

## Value

The returned value is a list of data frames in which each one corresponds to result for a single ontology. 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>

**See Also**

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

**Examples**

```
# note the `job` was generated from GREAT 3.0.0
job = readRDS(system.file("extdata", "job.rds", package = "rGREAT"))
tb = getEnrichmentTables(job)
names(tb)
head(tb[[1]])
job

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

---

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:

- call `getEnrichmentTables` to get enrichment tables for selected ontologies catalogues.
- call `plotRegionGeneAssociationGraphs` to get associations between regions and genes as well as making plots.

### Author(s)

Zuguang gu <z.gu@dkfz.de>

### Examples

```
# please refer to page of `submitGreatJob`  
NULL
```

---

|   |   |
|---|---|
| plotRegionGeneAssociationGraphs-GreatJob-method | <i>Plot region-gene association figures</i> |
|---|---|

---

### Description

Plot region-gene association figures

## Usage

```
## S4 method for signature 'GreatJob'  
plotRegionGeneAssociationGraphs(job, type = 1:3, ontology = NULL,  
  termID = NULL, request_interval = 10, max_tries = 100, verbose = TRUE,  
  plot = TRUE)
```

## Arguments

|                  |  |
|------------------|--|
| job              | a <a href="#">GreatJob-class</a> instance                                |
| type             | type of plots, should be in 1, 2, 3. See details section for explanation |
| ontology         | ontology name  |
| termID           | term id which corresponds to the selected ontology                       |
| request_interval | time interval for two requests. Default is 300 seconds.                  |
| max_tries        | maximum tries  |
| verbose          | whether show message   |
| plot             | whether make plots   |

## Details

Generated figures are:

- association between regions and genes
- distribution of distance to TSS
- distribution of absolute distance to TSS

If ontology and termID 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 termID is from 'id' column in the table which is returned by [getEnrichmentTables](#).

## Value

a [GRanges](#) object. Columns in metadata are:

**gene** genes that are associated with corresponding regions

**distTSS** distance from the regions to TSS of the associated gene

The returned values corresponds to whole input regions or only regions in specified ontology term, depending on user's setting.

If there is no gene associated with the region, corresponding gene and distTSS columns will be NA.

## Author(s)

Zuguang gu <z.gu@dkfz.de>

## Examples

```
# note the `job` was generated from GREAT 3.0.0
job = readRDS(system.file("extdata", "job.rds", package = "rGREAT"))

res = plotRegionGeneAssociationGraphs(job)
res

plotRegionGeneAssociationGraphs(job, type = 1)

res = plotRegionGeneAssociationGraphs(job, ontology = "GO Molecular Function",
  termID = "GO:0004984")
res
```

---

|                |  |
|----------------|--|
| submitGreatJob | <i>Send requests to GREAT web server</i> |
|----------------|--|

---

## Description

Send requests to GREAT web server

## Usage

```
submitGreatJob(gr, bg = NULL,
  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",
  help            = TRUE)
```

## Arguments

**gr** A [GRanges](#) object or a data frame which contains at least three columns (chr, start and end). Regions for test.

**bg** A [GRanges](#) object or a data frame. Background regions if needed. Note gr should be exactly subset of bg for all columns in gr. Check <http://great.stanford.edu/help/display/GREAT/File+Formats#FileFormats-Whatshouldmybackgroundregions3F> for more explanation.



|                       |   |
|-----------------------|---|
| 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.  |
| 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             | Maximum times trying to connect to 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 explicitly specified.   |
| help                  | Whether to print help messages.   |

## Details

Note: [On Aug 19 2019 GREAT released version 4](<http://great.stanford.edu/help/display/GREAT/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 is not 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](#) class object which can be used to get results from GREAT server.

**Note**

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").**`

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**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.

**Author(s)**

Zuguang gu <z.gu@dkfz.de>

**See Also**

[GreatJob-class](#)

**Examples**

```
set.seed(123)
bed = circlize::generateRandomBed(nr = 1000, nc = 0)
job = submitGreatJob(bed, version = "3.0.0")
job

# more parameters can be set for the job
if(FALSE) { # suppress running it when building the package
  # current GREAT version is 4.0.1
  job = submitGreatJob(bed, species = "mm9")
  job = submitGreatJob(bed, bg, species = "mm9", bgChoise = "data")
  job = submitGreatJob(bed, adv_upstream = 10, adv_downstream = 2, adv_span = 2000)
  job = submitGreatJob(bed, rule = "twoClosest", adv_twoDistance = 2000)
  job = submitGreatJob(bed, rule = "oneClosest", adv_oneDistance = 2000)
}
```

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