

# Package ‘rGREAT’

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**Type** Package

**Title** Client for GREAT Analysis

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

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

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

**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

**git\_url** <https://git.bioconductor.org/packages/rGREAT>

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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**

```
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 <a href="#">GreatJob-class</a> instance
category	one or multiple categories. All available categories can be get by <a href="#">availableCategories</a>

**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", "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 = 30, max_tries = 100)
```

**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

**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**

```
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-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:

- 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  
*Plot region-gene association figures*

---

**Description**

Plot region-gene association figures

**Usage**

```
## S4 method for signature 'GreatJob'
plotRegionGeneAssociationGraphs(job, type = 1:3, ontology = NULL,
  termID = NULL, request_interval = 30, max_tries = 100)
```

**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

**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**

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

op = par("mfrow")
par(mfrow = c(1, 3))
res = plotRegionGeneAssociationGraphs(job)
res

par(mfrow = c(1, 1))
plotRegionGeneAssociationGraphs(job, type = 1)

par(mfrow = c(1, 3))
res = plotRegionGeneAssociationGraphs(job, ontology = "GO Molecular Function",
  termID = "GO:0004984")
res

par(mfrow = op)
```

---

submitGreatJob

*Send requests to GREAT web server*

---

**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 = 300,
max_tries = 10,
version = "default",
base_url = "http://great.stanford.edu/public/cgi-bin")

```

## Arguments

gr	A <a href="#">GRanges</a> object or a data frame which contains at least three columns (chr, start and end). Regions for test.
bg	A <a href="#">GRanges</a> object or a data frame. Background regions if needed. Note gr should be exactly subset of bg for all columns in gr. Check <a href="http://great.stanford.edu/help/display/GREAT/File+Formats#FileFormats-Whatshouldmybackground">http://great.stanford.edu/help/display/GREAT/File+Formats#FileFormats-Whatshouldmybackground</a> <a href="#">3F</a> for more explanation.
species	Species. "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 "3.0.0", "2.0.2". Shorten version numbers can also be used, such as using "3" or "3.0" is same as "3.0.0".
base_url	the url of cgi-bin path, only used when explicitly specified.

## Details

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.

When `bg` is set, some pre-processing is applied before submitting to GREAT server for the reason that GREAT needs `gr` should be exactly subsets of `bg`, which means for any region in `gr`, there must be a region in `bg` which is exactly the same. Taking following example:

for `gr`:

```
chr1 200 300
chr1 250 400
```

for `bg`:

```
chr1 100 250
chr1 300 500
chr1 400 600
```

They will be transformed as: for `gr`:

```
chr1 200 250
chr1 300 400
```

for `bg`:

```
chr1 100 199
chr1 200 250
chr1 300 400
chr1 401 600
```

### Author(s)

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### See Also

[GreatJob-class](#)

### Examples

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

# more parameters can be set for the job
## Not run:
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)

## End(Not run)
```

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