guildifyR

February 1, 2018

`get.species.info` *Get info on available species and tissues*

Description

Get info on available species and tissues

Usage

```
get.species.info()
```

Value

result List containing available species tax ids and names for tissue-specific networks

Examples

```
result = get.species.info()
```

`GifyResult` *Read/use only class*

Description

Read/use only class

Usage

```
GifyResult(score.table, function.table, drug.table, enrichment.cutoff, job.id,
  job.id2)
```

`query` *Get protein/gene info associated with the query keywords*

Description

Get protein/gene info associated with the query keywords

Usage

```
query(keywords, species = "9606", tissue = "All", whitespaces.as.and = T)
```

Arguments

`keywords` Text containing description of a phenotype or list of genes (seperated by ;)

`species` Species tax identifier (9606: human, 10090: mouse, etc., see get.species.info method)

`whitespaces.as.and` Treat whitespaces as ANDs in querying (quotes the keywords)

`tissues` Tissue identifier (All, brain, liver, etc., see get.species.info method)

Value

result.table Data frame containing list of matching proteins/genes and their description

Examples

```
result.table = query("alzheimer", species="10090", tissue="All")
```

`retrieve.job` *Retrieve results using job id*

Description

Retrieve results using job id

Usage

```
retrieve.job(job.id, n.top = NULL, fetch.files = F, output.dir = ".")
```

Arguments

`job.id` Job id

`n.top` Number of top proteins to retrieve. If NULL top functionally enriched proteins are provided (upto 500 proteins)

`fetch.files` Flag to fetch result files from server and save them locally in output.dir

`output.dir` Directory to save the ranking, function, subnetwork and drug info files fetched from the server

Value

result List containing scores of top-ranking proteins, functions enriched among top-ranking proteins, drugs targeting top-ranking proteins, top-ranking subnetwork cutoff

Examples

```
result = retrieve.job(job.id)
getSlots(class(result))
head(scores(result))
```

retrieve.overlap *Retrieve overlap between two results using two job ids*

Description

Retrieve overlap between two results using two job ids

Usage

```
retrieve.overlap(job.id1, job.id2, fetch.files = F, output.dir = "./")
```

Arguments

`job.id1`	Job id 1
`job.id2`	Job id 2
`fetch.files`	Flag to fetch result files from server and save them locally in output.dir
`output.dir`	Directory to save the ranking, function, subnetwork and drug info files fetched from the server

Value

result List containing scores of common top-ranking proteins, common functions enriched among top-ranking proteins, drugs targeting common top-ranking proteins (Note that the number of top-ranking proteins and common functions are limited to 500)

Examples

```
result = retrieve.overlap(job.id1, job.id2)
getSlots(class(result))
head(scores(result))
```

submit.job *Submit job using the guildifyR query result table*

Description

Submit job using the guildifyR query result table

Usage

```
submit.job(result.table, species, tissue, scoring.options = list(netcombo =
  T))
```

Arguments

`scoring.options`
Prioritization method options (default NetCombo)

`query.table` Data frame contaning information from guildifyR query (user entitiy info, network info, source etc...)

Value

job id

Examples

```
species="10090"
tissue="All"
result.table = query("alzheimer", species)
#Diamond
scoring.options = list(diamond=T)
#NetScore
scoring.options = list(netscore=T, repetitionSelector=3, iterationSelector=2)
#NetZcore
scoring.options = list(netzcore=T, repetitionZelector=3)
#NetShort
scoring.options = list(netshort=T)
#NetCombo
scoring.options = list(netcombo=T)
job.id = submit.job(result.table, species, tissue, scoring.options)
```

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