Package ‘mygene’

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Type Package

Title Access MyGene.Info_ services

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Description MyGene.Info_ provides simple-to-use REST web services to query/retrieve gene annotation data. It's designed with simplicity and performance emphasized. *mygene*, is an easy-to-use R wrapper to access MyGene.Info_ services.

License Artistic-2.0

Depends R (>= 3.2.1), GenomicFeatures,

Imports httr (>= 0.3), jsonlite (>= 0.9.7), S4Vectors, Hmisc, sqldf, plyr

Suggests BiocStyle

biocViews Annotation

NeedsCompilation no

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getGene

Return the gene object for the given geneid.

Description

This is a wrapper for GET query of "/gene/<geneid>" service.

Usage

getGene(geneid, fields = c("symbol", "name", "taxid", "entrezgene"),
     ..., return.as=c("records", "text"), mygene)

Arguments

geneid  Entrez/ensembl gene id
fields  Fields to return, a list of a comma-sep string. If fields="all", all available fields
        are returned.
...     Includes species as well as several other fields. View available fields by calling
        ?metadata. Also, see http://docs.mygene.info/en/latest/doc/annotation_service.html
        for complete argument details and syntax.
return.as  "records" (list), "text" (JSON).
mygene  A MyGene object that describes how to connect to data resources. See MyGene-class.
        If missing, default object will be used that accesses the main MyGene.info portal. Default is recommended.

Value

returns a gene object containing the queried annotations

References

Ref: http://docs.mygene.info/en/latest/doc/annotation_service.html

See Also

getGenes query queryMany

Examples

## return the gene object for the given gene id
gene(1017)

## customize fields
gene(1017, fields=c("name", "symbol", "refseq"), return.as="text")

## all fields
gene(1017, fields="all")
getGenes

Return the list of gene objects for the given list of geneids.

Description

This is a wrapper for POST query of "/gene" service.

Usage

getGenes(geneids, fields = c("symbol", "name", "taxid", "entrezgene"), ..., return.as=c("DataFrame", "records", "text"), mygene)

Arguments

geneids A vector, list, or comm-sep string entrez/ensembl gene ids
fields A vector of fields to return. If fields="all", all available fields are returned.
... Includes species as well as several other fields. View available fields by calling ?metadata. Also, see http://docs.mygene.info/en/latest/doc/annotation_service.html for complete argument details and syntax.
return.as "DataFrame" (default), "records" (list), "text" (JSON).
mygene A MyGene object that describes how to connect to data resources. See MyGene-class. If missing, default object will be used that accesses the main MyGene.info portal. Default is recommended.

Value

returns a gene object (DataFrame, list, or JSON text) containing the queried annotations

References

Ref: http://docs.mygene.info/en/latest/doc/annotation_service.html

See Also

gene query queryMany

Examples

## Return the list of gene object for the given list of gene ids.
getGenes(c(1017,1018))

## mix types of gene ids
getGenes(c(1017,1018,"ENSG00000148795"))
Description

makeTxDbFromMyGene allows the user to make a TxDb object in the Genomic Features package from a mygene "exons" query using a default MyGene object.

Usage

makeTxDbFromMyGene(gene.list, scopes, species, returnall=FALSE)

Arguments

gene.list: A list, vector, or comma-separated string of query terms.

scopes: Type of types of identifiers, either a list, vector, or a comma-separated fields to specify type of input qterms, e.g. c("reporter", "ensembl.gene", "symbol") refer to "http://mygene.info/doc/query_service.html#available_fields" for full list of fields.

species: Names or taxonomy ids

returnall: Logical, if TRUE, return list of genes without exons annotations. False by Default.

Details

makeTxDbFromMyGene invokes either the query or queryMany method and passes the response to construct a TxDb object. See ?TxDb for utilizing transcript annotations.

Value

returns TxDb object

See Also

makeTxDb

Examples

xli <- c("DDX26B", "CCDC83", "MAST3", "RPL11")
txdb <- makeTxDbFromMyGene(xli, scopes="symbol", species="human")
**Description**

Get metadata for MyGene.info services.

**Usage**

```r
metadata(x, 
```

**Arguments**

- `x`: MyGene object
- `...`: MyGene object slot parameters

**Value**

returns the metadata including available fields, genome assemblies, sources, statistics, taxonomy, and timestamp

**References**

http://mygene.info/v2/metadata

**Examples**

```
## Get metadata
mygene<-MyGene()
metadata(mygene)

## get available fields to return
metadata(mygene)$available_fields
```

**Description**

Construct a MyGene object.

**Usage**

```r
MyGene(...) 
```

**Arguments**

- `...`: See help page for MyGene-class
Value

MyGene object

Examples

MyGene()


mygene Access MyGene.info annotation services

Description

MyGene.Info provides simple-to-use REST web services to query/retrieve gene annotation data. It's designed with simplicity and performance emphasized. *mygene* is an easy-to-use R wrapper to access MyGene.info services.

Details

Package: mygene
Type: Package
Version: 0.99.0
Date: 2014-04-18
License: BSD
Depends: httr jsonlite Hmisc

Author(s)

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References

Wu C, MacLeod I, Su AI (2013) BioGPS and MyGene.info: organizing online, gene-centric infor-
http://mygene.info/doc/query_service.html


MyGene-class Class "MyGene"

Description

R Client to access MyGene.Info annotation services

Objects from the Class

Objects can be created by calls of the form MyGene(base.url="http://mygene.info/v2", delay=1, step=1000, ...
Slots

base.url: "http://mygene.info/v2". Object of class "character"
delay: Sleep time between batch retrieval. Object of class "numeric"
step: Batch limit. Object of class "numeric"
version: httr package version. Object of class "character"
verbose: Object of class "logical"
debug: Object of class "logical"

Methods

getGene(geneid, fields = c("symbol", "name", "taxid", "entrezgene"), ..., return.as=c("records", "text"),
Return the gene object for the given geneid
getGenes(geneids, fields = c("symbol", "name", "taxid", "entrezgene"), ..., return.as=c("DataFrame", "records", "text"),
Return the list of gene object for the given list of geneids.
query(q, fields=c("name", "symbol", "taxid", "entrezgene"), ..., return.as=c("DataFrame", "records", "text"),
Return the query result.
queryMany(qterms, scopes=NULL, fields=c("name", "symbol", "taxid", "entrezgene"), ..., return.as=c("DataFrame", "records", "text"), returnall=FALSE,
Return the batch query result.
metadata(x, ...): Get metadata for MyGene.info services.
makeTxDbFromMyGene(gene.list, scopes, species, returnall=FALSE): Make a TxDb object from transcript annotations

Author(s)

Adam Mark, Chunlei Wu, Ryan Thompson

References


Examples

showClass("MyGene")

---

query Return the query result.

Description

This is a wrapper for GET query of "/query?q=<query>" service.

Usage

query(q, ..., return.as=c("DataFrame", "records", "text"), mygene)
queryMany

Arguments

- **q**
  - query term(s), see query syntax at http://mygene.info/doc/query_service.html#query-syntax

... Commonly queried fields include **species**, **fields**, **size** as well as several other fields. View available fields by calling `?metadata`. Also, see http://docs.mygene.info/en/latest/doc/query_service.html for complete argument details and syntax.

- **return.as**
  - "DataFrame" (default), "records" (list), or "text" (JSON).

- **mygene**
  - A MyGene object that describes how to connect to data resources. See `MyGene-class`. If missing, default object will be used that accesses the main MyGene.info portal. Default is recommended.

Value

returns a gene object (DataFrame, list, or JSON text) containing the queried annotations

References


See Also

queryMany getGene getGenes

Examples

```r
## return the query result
query("cdk2", size=5)

query("reporter:1000_at")

query("symbol:cdk2", return.as="text")

query(q="cyclin-dependent kinase", fields="uniprot")
```

---

**queryMany**

*Return the batch query result.*

Description

This is a wrapper for POST query of "/query" service.

Usage

```r
queryMany(qterms, scopes=NULL, ..., return.as=c("DataFrame", "records", "text"), mygene)
```
**queryMany**

**Arguments**

- **qterms**
  A vector or list, or string of comma-separated query terms

- **scopes**
  Type of types of identifiers, either a list or a comma-separated fields to specify type of input qterms, e.g. `c("reporter", "ensembl.gene", "symbol")` refer to "http://mygene.info/doc/query_service.html#available_fields" for full list of fields.

- **return.all**
  Returns a list of all related data including duplicated and missing qterms. False by default. View available fields by calling `?metadata`. Also, see http://docs.mygene.info/en/latest/doc/query_service.html for complete argument details and syntax.

- **return.as**
  "DataFrame" (default), "records" (list), "text" (JSON).

- **mygene**
  A MyGene object that describes how to connect to data resources. See MyGene-class. If missing, default object will be used that accesses the main MyGene.info portal. Default is recommended.

**Value**

returns a gene object (DataFrame, list, or JSON text) containing the queried annotations

**References**


**See Also**

query getGene getGenes

**Examples**

```r
## return the batch query result
queryMany(c("1053_at", "117_at", "121_at"), scopes="reporter", fields="ensembl.gene", species="human", return.as="records")

queryMany(c("1053_at", "117_at", "121_at"), scopes="reporter", species=9606)

queryMany(c("DDX26B", "CCDC83", "MAST3", "FLOT1"), scopes="symbol", fields="entrezgene", species="human")
```
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