Package ‘mygene’

March 4, 2024

Type Package

Title Access MyGene.Info_ services

Version 1.38.0

Date 2014-04-18

Author Adam Mark, Ryan Thompson, Cyrus Afrasiabi, Chunlei Wu

Maintainer Adam Mark, Cyrus Afrasiabi, Chunlei Wu <cwu@scripps.edu>

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

git_url https://git.bioconductor.org/packages/mygene
git_branch RELEASE_3_18
git_last_commit f4ab791
git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-03-03

R topics documented:

<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>getGene</td>
<td>2</td>
</tr>
<tr>
<td>getGenes</td>
<td>3</td>
</tr>
<tr>
<td>makeTxDbFromMyGene</td>
<td>4</td>
</tr>
<tr>
<td>metadata</td>
<td>5</td>
</tr>
<tr>
<td>MyGene</td>
<td>5</td>
</tr>
</tbody>
</table>
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

genes query queryMany
**getGenes**

Examples

```r
## return the gene object for the given gene id
getGene(1017)

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

## all fields
getGene(1017, fields="all")
```

### Description

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

### Usage

```r
genes <- getGenes(geneids = 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

`getGene` `queryMany`
Examples

```r
## 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

```r
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://docs.mygene.info/en/latest/doc/data.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

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

Get metadata for MyGene.info services.

Usage

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

MyGene(...)
Arguments

See help page for MyGene-class

Value

MyGene object

Examples

MyGene()

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)

Adam Mark, Chunlei Wu
Maintainer: Chunlei Wu <help@mygene.info>

References

**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, version=version, verbose=TRUE, debug=FALSE)`.

**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"))`: 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)

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

## 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

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

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.
... Commonly queried fields include species, fields, size as well as several other fields. returnall 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

## 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")
Index

* classes
  MyGene-class, 7
* package
  mygene, 6

gene, 2, 3, 8, 9
getGene, 2, 3, 8, 9
getGene,missing-method (getGene), 2
getGene,MyGene-method (getGene), 2
gene, 2, 3, 8, 9
gene,missing-method (gene), 3
gene,MyGene-method (gene), 3

cTxDb, 4
cTxDbFromMyGene, 4
metadata, 5
metadata,MyGene-method (metadata), 5
MyGene, 5
mygene, 6
MyGene-class, 7

query, 2, 3, 8, 9
query,missing-method (query), 8
query,MyGene-method (query), 8
queryMany, 2, 3, 8, 9
queryMany,missing-method (queryMany), 9
queryMany,MyGene-method (queryMany), 9