

Package ‘mygene’

May 25, 2024

Type Package

Title Access MyGene.Info_ services

Version 1.41.0

Date 2024-03-19

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, txdbmaker

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

Suggests BiocStyle

biocViews Annotation

git_url <https://git.bioconductor.org/packages/mygene>

git_branch devel

git_last_commit 486275d

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-05-24

Contents

| | |
|------------------------------|---|
| getGene | 2 |
| getGenes | 3 |
| makeTxDbFromMyGene | 4 |
| metadata | 5 |
| MyGene | 5 |

| | |
|--------------|-----------|
| mygene | 6 |
| MyGene-class | 7 |
| query | 8 |
| queryMany | 9 |
| Index | 11 |

| | |
|---------|-----------------------------------------------------|
| getGene | <i>Return the gene object for the given geneid.</i> |
|---------|-----------------------------------------------------|

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 <code>?metadata</code> . 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
getGene(1017)

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

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

| | |
|----------|-----------------------------------------------------------------------|
| getGenes | <i>Return the list of gene objects for the given list of geneids.</i> |
|----------|-----------------------------------------------------------------------|

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

[getGene 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"))
```

```
makeTxDbFromMyGene    makeTxDbFromMyGene
```

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://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

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

| | |
|----------|-----------------|
| metadata | <i>metadata</i> |
|----------|-----------------|

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
```

| | |
|--------|---------------|
| MyGene | <i>MyGene</i> |
|--------|---------------|

Description

Construct a MyGene object.

Usage

```
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)

Adam Mark, Chunlei Wu

Maintainer: Chunlei Wu <help@mygene.info>

References

Wu C, MacLeod I, Su AI (2013) BioGPS and MyGene.info: organizing online, gene-centric information. Nucl. Acids Res. 41(D1): D561-D565. http://mygene.info/doc/annotation_service.html
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, 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")`
 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")`
 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

Wu C, MacLeod I, Su AI (2013) BioGPS and MyGene.info: organizing online, gene-centric information. *Nucl. Acids Res.* 41(D1): D561-D565.

Examples

```
showClass("MyGene")
```

| | |
|-------|---------------------------------|
| query | <i>Return the query result.</i> |
|-------|---------------------------------|

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 <code>?metadata</code> . Also, see http://docs.mygene.info/en/latest/doc/q 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

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

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 | <i>Return the batch query result.</i> |
|-----------|---------------------------------------|

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. <code>c("reporter", "ensembl.gene", "symbol")</code> refer to <code>"http://mygene.info/doc/query_service.html#available_fields"</code> for full list of fields. |
| ... | Commonly queried fields include <code>species</code> , <code>fields</code> , <code>size</code> as well as several other fields. <code>return.all</code> returns a list of all related data including duplicated and missing qterms. <code>False</code> by default. View available fields by calling <code>?metadata</code> . Also, see <code>http://docs.mygene.info/en/latest/doc/query_service.html</code> 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/query_service.html

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

getGene, 2, 3, 8, 9

getGene,missing-method (getGene), 2

getGene,MyGene-method (getGene), 2

getGenes, 2, 3, 8, 9

getGenes,missing-method (getGenes), 3

getGenes,MyGene-method (getGenes), 3

makeTxDb, 4

makeTxDbFromMyGene, 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