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

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R topics documented:

getGene ................................................................. 2
getGenes ................................................................. 3
makeTxDbFromMyGene ................................................ 4
metadata ............................................................... 5
MyGene ................................................................. 5
getGene

mygene ................................................................. 6
MyGene-class ......................................................... 7
query ................................................................. 8
queryMany .......................................................... 9

Index 11

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
getGenes

Examples

```r
## 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

```r
genes(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

### 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")
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

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

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

Description

Construct a MyGene object.

Usage

`MyGene(...)`
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
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Depends: httr jsonlite Hmisc

Author(s)

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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"), 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

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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
```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)
```

### 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

```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")
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