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**

```r
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](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**


**See Also**

- `getGenes` query `queryMany`

**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")
```
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

```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://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

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

**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**

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

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

---

**MyGene**

**Description**

Construct a MyGene object.

**Usage**

MyGene(...)

**Arguments**

- `...` : See help page for MyGene-class
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, ...
query

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: htr 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(terms, 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 aTxDb object from transcript annotations

Author(s)

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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)
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

### 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)
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.

... 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"
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