Package ‘mygene’

April 4, 2024

Type Package
Title Access MyGene.Info_ services
Version 1.38.0
Date 2014-04-18
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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
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 2024-04-03

R topics documented:

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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

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")
```

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
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

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**

```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
```

---

**Description**

Construct a MyGene object.

**Usage**

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

---
**Arguments**

... See help page for MyGene-class

**Value**

MyGene object

**Examples**

MyGene()

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**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**

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**References**

http://mygene.info/doc/query_service.html
**MyGene-class**

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**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**
  
  `getGene(geneid, fields = c("symbol", "name", "taxid", "entrezgene"), ..., return.as=c("records", "text"))`  
  
  Return the gene object for the given geneid.

- **getGenes**
  
  `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**
  
  `query(q, fields=c("name", "symbol", "taxid", "entrezgene"), ..., return.as=c("DataFrame", "records", "text"))`  
  
  Return the query result.

- **queryMany**
  
  `queryMany(qterms, scopes=NULL, fields=c("name", "symbol", "taxid", "entrezgene"), ..., return.as=c("DataFrame", "records", "text"))`  
  
  Return the batch query result.

- **metadata**
  
  `metadata(x, ...)`: Get metadata for MyGene.info services.

- **makeTxDbFromMyGene**
  
  `makeTxDbFromMyGene(gene.list, scopes, species, returnall=FALSE)`: Make a TxDb 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)

Arguments

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