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.
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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**

<table>
<thead>
<tr>
<th>Function</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>getGene</td>
<td>Return the gene object for the given geneid.</td>
</tr>
</tbody>
</table>

**Description**

This is a wrapper for GET query of "/gene/<geneid>" service.

**Usage**

```r
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
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
genes <- 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 ?metad 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

```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")
```
**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

```r
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)

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References

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", "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('DDX26', '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