

MyGene.info R Client

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Contents

1	Overview	2
2	Gene Annotation Service	2
2.1	<code>getGene</code>	2
2.2	<code>getGenes</code>	2
3	Gene Query Service	3
3.1	<code>query</code>	3
3.2	<code>queryMany</code>	4
4	<code>makeTxDbFromMyGene</code>	5
5	Tutorial, ID mapping	6
5.1	Mapping gene symbols to Entrez gene ids	6
5.2	Mapping gene symbols to Ensembl gene ids	7
5.3	When an input has no matching gene	8
5.4	When input ids are not just symbols	8
5.5	When an input id has multiple matching genes	10
5.6	Can I convert a very large list of ids?	11
6	References	11

1 Overview

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.

2 Gene Annotation Service

2.1 `getGene`

- Use `getGene`, the wrapper for GET query of `"/gene/<geneid>"` service, to return the gene object for the given geneid.

```
> gene <- getGene("1017", fields="all")
> length(gene)

[1] 1

> gene["name"]

[[1]]
NULL

> gene["taxid"]

[[1]]
NULL

> gene["uniprot"]

[[1]]
NULL

> gene["refseq"]

[[1]]
NULL
```

2.2 `getGenes`

- Use `getGenes`, the wrapper for POST query of `"/gene"` service, to return the list of gene objects for the given character vector of geneids.

```
> getGenes(c("1017", "1018", "ENSG00000148795"))

DataFrame with 3 rows and 7 columns
```

	query	_id	X_version	entrezgene	name
	<character>	<character>	<integer>	<character>	<character>
1	1017	1017	2	1017 cyclin dependent kin..	
2	1018	1018	2	1018 cyclin dependent kin..	
3	ENSG00000148795	1586	2	1586 cytochrome P450 fami..	

	symbol	taxid
	<character>	<integer>
1	CDK2	9606
2	CDK3	9606
3	CYP17A1	9606

3 Gene Query Service

3.1 query

- Use `query`, a wrapper for GET query of `"/query?q=<query>"` service, to return the query result.

```
> query(q="cdk2", size=5)

$took
[1] 41

$total
[1] 2290

$max_score
[1] 139.2689

$hits
```

	_id	_score	entrezgene	name	symbol
1	1017	139.26892	1017 cyclin dependent kinase 2	CDK2	
2	12566	116.80619	12566 cyclin dependent kinase 2	Cdk2	
3	362817	98.83601	362817 cyclin dependent kinase 2	Cdk2	
4	115557556	89.85092	115557556 cyclin dependent kinase 2	cdk2	
5	ENSHHUG00000015903	89.85092	<NA> cyclin dependent kinase 2	cdk2	

```
  taxid
1  9606
2 10090
3 10116
4  8049
```

```
5 62062
```

```
> query(q="NM_013993")

$took
[1] 5

$total
[1] 1

$max_score
[1] 1.696116

$hits
  _id  _score entrezgene                                name symbol
1 780 1.696116      780 discoidin domain receptor tyrosine kinase 1  DDR1
  taxid
1 9606
```

3.2 queryMany

- Use `queryMany`, a wrapper for POST query of `"/query"` service, to return the batch query result.

```
> queryMany(c('1053_at', '117_at', '121_at', '1255_g_at', '1294_at'),
+           scopes="reporter", species="human")

Finished
Pass returnall=TRUE to return lists of duplicate or missing query terms.
DataFrame with 6 rows and 7 columns
```

	query	_id	X_score	entrezgene	name
	<character>	<character>	<numeric>	<character>	<character>
1	1053_at	5982	19.1620	5982	replication factor C..
2	117_at	3310	19.1669	3310	heat shock protein f..
3	121_at	7849	19.1772	7849	paired box 8
4	1255_g_at	2978	19.1620	2978	guanylate cyclase ac..
5	1294_at	100847079	18.4952	100847079	microRNA 5193
6	1294_at	7318	18.4952	7318	ubiquitin like modif..

```
  symbol  taxid
  <character> <integer>
1    RFC2    9606
2   HSPA6    9606
```

3	PAX8	9606
4	GUCA1A	9606
5	MIR5193	9606
6	UBA7	9606

4 makeTxDbFromMyGene

TxDb is a container for storing transcript annotations. `makeTxDbFromMyGene` allows the user to make a TxDb object in the Genomic Features package from a mygene "exons" query using a default mygene object.

```
> xli <- c('CCDC83',
+         'MAST3',
+         'RPL11',
+         'ZDHHC20',
+         'LUC7L3',
+         'SNORD49A',
+         'CTSH',
+         'ACOT8')
> txdb <- makeTxDbFromMyGene(xli,
+                             scopes="symbol", species="human")
> transcripts(txdb)
```

GRanges object with 17 ranges and 2 metadata columns:

	seqnames	ranges	strand	tx_id	tx_name
	<Rle>	<IRanges>	<Rle>	<integer>	<character>
[1]	11	85855382-85920013	+	1	NM_001286159
[2]	11	85855382-85920013	+	2	NM_173556
[3]	19	18097777-18151686	+	3	NM_015016
[4]	1	23691805-23696835	+	4	NM_000975
[5]	1	23691778-23696426	+	5	NM_001199802
...
[13]	17	50719602-50756215	+	13	NM_016424
[14]	17	16440035-16440106	+	14	NR_002744
[15]	15	78921749-78945098	-	15	NM_001319137
[16]	15	78921059-78945046	-	16	NM_004390
[17]	20	45841720-45857392	-	17	NM_005469

seqinfo: 7 sequences from an unspecified genome; no seqlengths

`makeTxDbFromMyGene` invokes either the `query` or `queryMany` method and passes the response to construct a `TxDb` object. See `?TxDb` for methods to utilize and access transcript annotations.

5 Tutorial, ID mapping

ID mapping is a very common, often not fun, task for every bioinformatician. Supposedly you have a list of gene symbols or reporter ids from an upstream analysis, and then your next analysis requires to use gene ids (e.g. Entrez gene ids or Ensembl gene ids). So you want to convert that list of gene symbols or reporter ids to corresponding gene ids.

Here we want to show you how to do ID mapping quickly and easily.

5.1 Mapping gene symbols to Entrez gene ids

Suppose `xli` is a list of gene symbols you want to convert to entrez gene ids:

```
> xli <- c('DDX26B',
+         'CCDC83',
+         'MAST3',
+         'FLOT1',
+         'RPL11',
+         'ZDHHC20',
+         'LUC7L3',
+         'SNORD49A',
+         'CTSH',
+         'ACOT8')
```

You can then call `queryMany` method, telling it your input is `symbol`, and you want `entrezgene` (Entrez gene ids) back.

```
> queryMany(xli, scopes="symbol", fields="entrezgene", species="human")
```

Finished

Pass `returnall=TRUE` to return lists of duplicate or missing query terms.

DataFrame with 10 rows and 5 columns

	query	notfound	_id	X_score	entrezgene
	<character>	<logical>	<character>	<numeric>	<character>
1	DDX26B	TRUE	NA	NA	NA
2	CCDC83	NA	220047	17.9453	220047
3	MAST3	NA	23031	18.1793	23031
4	FLOT1	NA	10211	18.4348	10211

5	RPL11	NA	6135	16.4053	6135
6	ZDHHC20	NA	253832	18.1872	253832
7	LUC7L3	NA	51747	17.5998	51747
8	SNORD49A	NA	26800	23.3170	26800
9	CTSH	NA	1512	16.8719	1512
10	ACOT8	NA	10005	17.5946	10005

5.2 Mapping gene symbols to Ensembl gene ids

Now if you want Ensembl gene ids back:

```
> out <- queryMany(xli, scopes="symbol", fields="ensembl.gene", species="human")
```

Finished

Pass returnall=TRUE to return lists of duplicate or missing query terms.

```
> out
```

DataFrame with 10 rows and 5 columns

	query	notfound	_id	X_score	
	<character>	<logical>	<character>	<numeric>	
1	DDX26B	TRUE	NA	NA	
2	CCDC83	NA	220047	17.9462	
3	MAST3	NA	23031	18.1810	
4	FL0T1	NA	10211	18.4317	
5	RPL11	NA	6135	16.4052	
6	ZDHHC20	NA	253832	18.1871	
7	LUC7L3	NA	51747	17.6019	
8	SNORD49A	NA	26800	23.3167	
9	CTSH	NA	1512	16.8719	
10	ACOT8	NA	10005	17.5938	
					ensembl
					<list>
1					
2					ENSG000000150676
3					ENSG000000099308
4					ENSG000000232280, ENSG000000223654, ENSG000000236271
5					ENSG000000142676
6					ENSG000000180776
7					ENSG000000108848
8					ENSG000000277370
9					ENSG000000103811
10					ENSG000000101473

```
> out$ensembl[[4]]$gene
[1] "ENSG00000232280" "ENSG00000223654" "ENSG00000236271" "ENSG00000224740"
[5] "ENSG00000206480" "ENSG00000206379" "ENSG00000230143" "ENSG00000137312"
```

5.3 When an input has no matching gene

In case that an input id has no matching gene, you will be notified from the output. The returned list for this query term contains `notfound` value as `True`.

```
> xli <- c('DDX26B',
+         'CCDC83',
+         'MAST3',
+         'FLOT1',
+         'RPL11',
+         'Gm10494')
> queryMany(xli, scopes="symbol", fields="entrezgene", species="human")
```

Finished

Pass `returnall=TRUE` to return lists of duplicate or missing query terms.

DataFrame with 6 rows and 5 columns

	query	notfound	_id	X_score	entrezgene
	<character>	<logical>	<character>	<numeric>	<character>
1	DDX26B	TRUE	NA	NA	NA
2	CCDC83	NA	220047	17.9459	220047
3	MAST3	NA	23031	18.1790	23031
4	FLOT1	NA	10211	18.4320	10211
5	RPL11	NA	6135	16.4056	6135
6	Gm10494	TRUE	NA	NA	NA

5.4 When input ids are not just symbols

```
> xli <- c('DDX26B',
+         'CCDC83',
+         'MAST3',
+         'FLOT1',
+         'RPL11',
+         'Gm10494',
+         '1007_s_at',
+         'AK125780')
>
```


MyGene.info R Client

Above id list contains symbols, reporters and accession numbers, and supposedly we want to get back both Entrez gene ids and uniprot ids. Parameters `scopes`, `fields`, `species` are all flexible enough to support multiple values, either a list or a comma-separated string:

```
> out <- queryMany(xli, scopes=c("symbol", "reporter", "accession"),
+                  fields=c("entrezgene", "uniprot"), species="human")
```

Finished

Pass `returnall=TRUE` to return lists of duplicate or missing query terms.

```
> out
```

DataFrame with 9 rows and 7 columns

	query	notfound	_id	X_score	entrezgene	uniprot.Swiss.Prot
	<character>	<logical>	<character>	<numeric>	<character>	<character>
1	DDX26B	TRUE	NA	NA	NA	NA
2	CCDC83	NA	220047	17.9457	220047	Q8IWF9
3	MAST3	NA	23031	18.1793	23031	060307
4	FL0T1	NA	10211	18.4342	10211	075955
5	RPL11	NA	6135	16.4053	6135	P62913
6	Gm10494	TRUE	NA	NA	NA	NA
7	1007_s_at	NA	100616237	18.4954	100616237	NA
8	1007_s_at	NA	780	18.4954	780	Q08345
9	AK125780	NA	118142757	22.0353	118142757	P43080

uniprot.TrEMBL

<list>

```
1
2
3 A0A8I5KST9, A0A8V8TLL8, A0A8V8TMW0, ...
4 A2AB11, Q5ST80, A2AB12, ...
5 A0A2R8Y447, Q5VVD0, Q5VVC8
6
7
8 A0A0A0MSX3, A0A024RCQ1, Q96T62, ...
9 A0A7I2V6E2, B2R9P6
```

```
> out$uniprot.Swiss.Prot[[5]]
```

```
[1] "P62913"
```

5.5 When an input id has multiple matching genes

From the previous result, you may have noticed that query term `1007_s_at` matches two genes. In that case, you will be notified from the output, and the returned result will include both matching genes.

By passing `returnall=TRUE`, you will get both duplicate or missing query terms

```
> queryMany(xli, scopes=c("symbol", "reporter", "accession"),
+           fields=c("entrezgene", "uniprot"), species='human', returnall=TRUE)
```

Finished

\$response

DataFrame with 9 rows and 7 columns

	query	notfound	_id	X_score	entrezgene	uniprot.Swiss.Prot
	<character>	<logical>	<character>	<numeric>	<character>	<character>
1	DDX26B	TRUE	NA	NA	NA	NA
2	CCDC83	NA	220047	17.9457	220047	Q8IWF9
3	MAST3	NA	23031	18.1789	23031	060307
4	FL0T1	NA	10211	18.4348	10211	075955
5	RPL11	NA	6135	16.4056	6135	P62913
6	Gm10494	TRUE	NA	NA	NA	NA
7	1007_s_at	NA	100616237	18.4952	100616237	NA
8	1007_s_at	NA	780	18.4952	780	Q08345
9	AK125780	NA	118142757	22.0109	118142757	P43080

uniprot.TrEMBL
<list>

```
1
2
3 A0A8I5KST9,A0A8V8TLL8,A0A8V8TMW0,...
4 A2AB11,Q5ST80,A2AB12,...
5 A0A2R8Y447,Q5VVD0,Q5VVC8
6
7
8 A0A0A0MSX3,A0A024RCQ1,Q96T62,...
9 A0A7I2V6E2,B2R9P6
```

\$duplicates

```
X1007_s_at
1      2
```

\$missing

```
[1] "DDX26B" "Gm10494"
```

The returned result above contains `out` for mapping output, `missing` for missing query terms (a list), and `dup` for query terms with multiple matches (including the number of matches).

5.6 Can I convert a very large list of ids?

Yes, you can. If you pass an id list (i.e., `xli` above) larger than 1000 ids, we will do the id mapping in-batch with 1000 ids at a time, and then concatenate the results all together for you. So, from the user-end, it's exactly the same as passing a shorter list. You don't need to worry about saturating our backend servers. Large lists, however, may take a while longer to query, so please wait patiently.

6 References

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