

MyGene.info R Client

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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 | 9 | 1017 cyclin dependent kin.. | |
| 2 | 1018 | 1018 | 4 | 1018 cyclin dependent kin.. | |
| 3 | ENSG00000148795 | 1586 | 3 | 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] 220
```

```
$total
```

```
[1] 1304
```

```
$max_score
```

```
[1] 89.11638
```

```
$hits
```

| | _id | _score | entrezgene | name | symbol | taxid |
|---|---------|----------|------------|---------------------------------|--------|-------|
| 1 | 1017 | 89.11638 | 1017 | cyclin dependent kinase 2 | CDK2 | 9606 |
| 2 | 12566 | 74.74277 | 12566 | cyclin-dependent kinase 2 | Cdk2 | 10090 |
| 3 | 5880545 | 63.97834 | 5880545 | CDK2 EDI_169580 | 370354 | |
| 4 | 362817 | 63.24388 | 362817 | cyclin dependent kinase 2 | Cdk2 | 10116 |
| 5 | 143384 | 62.32350 | 143384 | CDK2 associated cullin domain 1 | CACUL1 | 9606 |

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

```
$took
```

```
[1] 4
```

```
$total
[1] 1

$max_score
[1] 1.679133

$hits
  _id  _score entrezgene name symbol
1 780 1.679133      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 | 19.1874 | 5982 | replication factor C.. | |
| 2 | 117_at | 3310 | 18.7545 | 3310 | heat shock protein f.. | |
| 3 | 121_at | 7849 | 19.5024 | 7849 | paired box 8 | |
| 4 | 1255_g_at | 2978 | 20.0866 | 2978 | guanylate cyclase ac.. | |
| 5 | 1294_at | 100847079 | 18.8799 | 100847079 | microRNA 5193 | |
| 6 | 1294_at | 7318 | 18.8799 | 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 | 18.0289 | 220047 |
| 3 | MAST3 | NA | 23031 | 18.1422 | 23031 |
| 4 | FLOT1 | NA | 10211 | 18.4336 | 10211 |
| 5 | RPL11 | NA | 6135 | 16.7418 | 6135 |
| 6 | ZDHHC20 | NA | 253832 | 18.1827 | 253832 |
| 7 | LUC7L3 | NA | 51747 | 17.7138 | 51747 |
| 8 | SNORD49A | NA | 26800 | 22.7887 | 26800 |

| | | | | | |
|----|-------|----|-------|---------|-------|
| 9 | CTSH | NA | 1512 | 17.7504 | 1512 |
| 10 | ACOT8 | NA | 10005 | 17.7302 | 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 | 18.0403 |
| 3 | MAST3 | NA | 23031 | 18.1436 |
| 4 | FL0T1 | NA | 10211 | 18.4441 |
| 5 | RPL11 | NA | 6135 | 16.7263 |
| 6 | ZDHHC20 | NA | 253832 | 18.1871 |
| 7 | LUC7L3 | NA | 51747 | 17.7184 |
| 8 | SNORD49A | NA | 26800 | 22.7735 |
| 9 | CTSH | NA | 1512 | 17.7504 |
| 10 | ACOT8 | NA | 10005 | 17.7347 |

| | ensembl |
|----|---|
| | <list> |
| 1 | |
| 2 | ENSG00000150676 |
| 3 | ENSG00000099308 |
| 4 | ENSG00000206480, ENSG00000137312, ENSG00000236271 |
| 5 | ENSG00000142676 |
| 6 | ENSG00000180776 |
| 7 | ENSG00000108848 |
| 8 | ENSG00000277370 |
| 9 | ENSG00000103811 |
| 10 | ENSG00000101473 |

```
> out$ensembl[[4]]$gene
```

```
[1] "ENSG00000206480" "ENSG00000137312" "ENSG00000236271" "ENSG00000224740"
[5] "ENSG00000232280" "ENSG00000230143" "ENSG00000223654" "ENSG00000206379"
```

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 | 18.0502 | 220047 |
| 3 | MAST3 | NA | 23031 | 18.1422 | 23031 |
| 4 | FLOT1 | NA | 10211 | 18.4390 | 10211 |
| 5 | RPL11 | NA | 6135 | 16.7446 | 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')
>
```

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    18.0289    220047      Q8IWF9
3       MAST3       NA      23031    18.1422    23031      060307
4       FLOT1       NA     10211    18.4441    10211      075955
5       RPL11       NA      6135    16.7452     6135      P62913
6    Gm10494      TRUE        NA        NA        NA            NA
7  1007_s_at       NA  100616237    18.9973  100616237        NA
8  1007_s_at       NA       780    18.9973       780      Q08345
9   AK125780       NA  118142757    21.4483  118142757      P43080
      uniprot.TrEMBL
      <list>
1
2      H0YDV3
3  V9GYV0,A0A8V8TLL8,A0A8I5KST9,...
4      A2AB11,Q5ST80,A2AB13,...
5      Q5VVC8,Q5VVD0,A0A2R8Y447
6
7
8  A0A024RCJ0,A0A024RCL1,A0A0A0MSX3,...
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

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```
> 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  18.0496    220047    Q8IWF9
3      MAST3      NA    23031  18.1476    23031    060307
4      FLOT1      NA    10211  18.4502    10211    075955
5      RPL11      NA     6135  16.7341     6135    P62913
6    Gm10494      TRUE      NA      NA      NA      NA
7  1007_s_at      NA  100616237  18.7545  100616237      NA
8  1007_s_at      NA      780  18.7545      780    Q08345
9   AK125780      NA  118142757  21.4368  118142757    P43080
      uniprot.TrEMBL
      <list>
1
2      H0YDV3
3  V9GYV0,A0A8V8TLL8,A0A8I5KST9,...
4      A2AB11,Q5ST80,A2AB13,...
5      Q5VVC8,Q5VVD0,A0A2R8Y447
6
7
8  A0A024RCJ0,A0A024RCL1,A0A0A0MSX3,...
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., `ids` 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