

Package: BioThingsClient.R (via r-universe)

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Type Package

Title BioThings Client
(<https://github.com/biothings/BioThingsClient.R>)

Description This is a unified R client for all ``BioThings APIs" (more at <http://biothings.io>). BioThings APIs are a collection of high-performance APIs for variety of aggregated entity-type specific annotations, such as genes, variants, chemicals, drugs etc. (so called ``BioThings"). It also provides a SDK (BioThings SDK) for users to build their own BioThings API for any biological entity types. This client provides a generic R library for existing BioThings APIs as well as the new BioThings APIs will be created in the future, either by us or users.

Version 0.99.1

Author Thomas Johnson <thomascjohnson@gmail.com>

Maintainer Thomas Johnson <thomascjohnson@gmail.com>

Depends R (>= 3.4)

License Apache License 2.0

LazyData true

Imports jsonlite, magrittr, methods, Hmisc, stats, utils, http

Suggests testthat, knitr, rmarkdown

Roxygen list(wrap = FALSE)

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'metadata.R' 'query.R'

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biothings_clients	<i>BioThings API Client Configuration</i>
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Description

This is a list that contains configuration information for each Biothings API:

Usage

`biothings_clients`

Format

An object of class `list` of length 4.

Details

BioThings APIs:

- **MyGene**
- **MyVariant**
- **MyTaxon**
- **MyChem**

To integrate a new API into the package, be sure to update this in addition to generating the associated methods from `getThing` and `getThings`.

BioThingsClient-class *BioThingsClient*

Description

An S4 Class to access BioThings APIs.

BioThings APIs:

- **MyGene**
- **MyVariant**
- **MyTaxon**
- **MyChem ...**

Value

An S4 class object of the class Biothings.

Slots

`client` A client configuration list.
`version` The version of the BioThings package.
`verbose` logical.
`debug` logical.

Examples

```
biothings <- BioThingsClient("gene")
slot(biothings, "verbose") <- FALSE # default is TRUE
biothings
```

<code>btFields</code>	<i>btFields</i>
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Description

Get field metadata information from BioThings API field metadata endpoints

Usage

```
btFields(biothings, ...)
```

S4 method for signature 'BioThingsClient'

```
btFields(biothings, ...)
```

S4 method for signature 'character'

```
btFields(biothings, ...)
```

Arguments

biothings A BioThings class object
 ... Additional API parameters. See API documentation.

Value

A list of results from the metadata fields endpoint

Examples

```
fields <- btFields("gene")
head(fields)
```

btGet	<i>Get items from BioThings APIs</i>
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Description

Use gene, taxon, variant, chemical and other IDs to get annotation information from BioThings APIs.

Usage

```
btGet(biothings, ids, fields, ..., return.as = "records")

## S4 method for signature 'BioThingsClient'
btGet(biothings, ids, fields, ...,
      return.as = "records")

## S4 method for signature 'character'
btGet(biothings, ids, fields, ...,
      return.as = "records")

## S4 method for signature 'missing'
btGet(biothings, ids, fields, ..., return.as = "records")
```

Arguments

biothings BioThings object or character .
 ids character.
 fields Specify fields to receive from API
 ... Other parameters to pass to API
 return.as character.

Value

The API response in the form of the provided argument return.as

Examples

```
#Equivalent:  
  
btGet("gene", "1017", fields = c("symbol","name","taxid","entrezgene"),  
      return.as = "text")
```

btMetadata	<i>btMetadata</i>
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Description

Get metadata information from BioThings API metadata endpoints

Usage

```
btMetadata(biothings, ...)  
  
## S4 method for signature 'BioThingsClient'  
btMetadata(biothings, ...)  
  
## S4 method for signature 'character'  
btMetadata(biothings, ...)
```

Arguments

biothings	A BioThings class object
...	Additional API parameters. See API documentation.

Value

A list of results from the metadata endpoint

Examples

```
metadata <- btMetadata("gene")  
head(metadata)
```

 btQuery

btQuery

Description

Retrieve results from the query endpoint of BioThings APIs

Usage

```
btQuery(biothings, q, ..., fetch_all = FALSE, scopes, return.as = "records")

## S4 method for signature 'BioThingsClient'
btQuery(biothings, q, ..., fetch_all = FALSE,
        scopes, return.as = "records")

## S4 method for signature 'missing'
btQuery(biothings, q, ..., fetch_all = FALSE, scopes,
        return.as = "records")

## S4 method for signature 'character'
btQuery(biothings, q, ..., fetch_all = FALSE, scopes,
        return.as = "records")
```

Arguments

biothings	An S4 class BioThings object
q	A query string
...	Any parameters to pass to API
fetch_all	This returns a list of <code>_all_</code> results for a query, regardless of <code>return.as</code> . See the API documentation.
scopes	One or more fields (separated by comma) as the search "scopes"
return.as	Type of return value

Value

Returns the API result as the provided `return.as` type

Examples

```
btQuery("gene", q = "NM_013993")
gene_client <- BioThingsClient("gene")
btQuery(gene_client, "NM_013993")
```

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* datasets

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