Package ‘myvariant’

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Type Package

Title Accesses MyVariant.info variant query and annotation services

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Description MyVariant.info is a comprehensive aggregation of variant annotation resources. myvariant is a wrapper for querying MyVariant.info services

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Depends R (>= 3.2.1), VariantAnnotation

Imports httr, jsonlite, S4Vectors, Hmisc, plyr, magrittr, GenomeInfoDb

Suggests BiocStyle

biocViews VariantAnnotation, Annotation, GenomicVariation

NeedsCompilation no

R topics documented:

formatHgvs ................................................................. 2
formatSingleHgvs .................................................... 2
getVariant ............................................................. 3
getVariants ............................................................. 4
metadata ................................................................. 5
MyVariant ............................................................... 6
myvariant .............................................................. 6
MyVariant-class ....................................................... 7
queryVariant .......................................................... 8
queryVariants .......................................................... 9

Index 10
**formatHgvs**

*Get all HGVS IDs from Vcf object.*

**Description**

Read in a Vcf object created by `readVcf` to extract all HGVS IDs for querying MyVariant.info.

**Usage**

```r
formatHgvs(vcf, variant_type = c("snp", "insertion", "deletion"))
```

**Arguments**

- **vcf**: Vcf object created by `readVcf`.
- **variant_type**: Type of variant HGVS IDs to retrieve from Vcf object. Default c("snp", "insertion", "deletion")

**Value**

vector

**References**


**See Also**

`formatSingleHgvs`

**Examples**

```r
## return HGVS IDs for all snps in a Vcf
file.path <- system.file("extdata", "dbsnp_mini.vcf", package="myvariant")
vcf <- readVcf(file.path, genome="hg19")
hgvs <- formatHgvs(vcf, variant_type="snp")
```

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**formatSingleHgvs**

*Get Hgvs HGVS ID from chromosome, position, reference and alternate alleles.*

**Description**

Create a single HGVS ID for a variant from chromosome, position, reference and alternate alleles.

**Usage**

```r
formatSingleHgvs(chrom, pos, ref, alt, mutant_type=FALSE)
```

**Arguments**

- **chrom**: Chromosome location.
- **pos**: Position.
- **ref**: Reference allele.
- **alt**: Alternate allele.
- **mutant_type**: Mutant type. Default FALSE

**Value**

HGVS ID as a string

**Examples**

```r
## return HGVS ID from chromosome, position, and alleles
chrom <- "1"
pos <- 1
ref <- "T"
alt <- "C"
mutant_type <- FALSE
hgvs_id <- formatSingleHgvs(chrom, pos, ref, alt, mutant_type)
```
getVariant

Arguments

- **chrom**: Chromosome.
- **pos**: Position of the variant on the reference genome (hg19).
- **ref**: Reference allele.
- **alt**: Alternate allele.
- **mutant_type**: Logical indicating whether to return the type of mutation along with the HGVS ID.

Value

returns a string

References


See Also

formatHgvs

Examples

```r
## return HGVS ID for a variant
formatSingleHgvs(1, 35367, "G", "A")
```

getVariant

Return the variant object for the given HGVS id.

Description

This is a wrapper for GET query of "/variant/<hgvsid>" service.

Usage

```r
getVariant(hgvsid, fields=NULL,
           ...,
           return.as=c("records", "text"),
           myvariant)
```

Arguments

- **hgvsid**: HGVS id
- **fields**: Fields to return, a list of a comma-sep string. If fields=="all", all available fields are returned.
- **...**: 
- **return.as**: "records" (list), "text" (JSON).
- **myvariant**: A MyVariant object that describes how to connect to data resources. See MyVariant-class. If missing, default object will be used that accesses the main MyVariant.info portal. Default is recommended.
getVariants

Value
returns a variant object containing the queried annotations

References

See Also
getVariants queryVariant queryVariants

Examples
## return the variant object for the given HGVS id
getVariant("chr7:g.55241707G>T")

## customize fields
getVariant("chr7:g.55241707G>T",
    fields=c("dbnsfp.cadd.phred", "dbnsfp.polyphen2"),
    return.as="text")

getVariants
Return the list of variant objects for the given list of HGVS ids.

description
This is a wrapper for POST query of "/variant" service.

Usage
getVariants(hgvsids, fields=NULL, verbose=NULL, ...
    return.as=c("DataFrame", "records", "text"), myvariant)

Arguments
hgvsids A vector, list, or comm-sep string HGVS ids
fields A vector of fields to return. If fields=="all", all available fields are returned.
verbose A logical turning on or off process status messages. Default = TRUE.
... return.as "DataFrame" (default), "records" (list), "text" (JSON).
myvariant A MyVariant object that describes how to connect to data resources. See MyVariant-class.

If missing, default object will be used that accesses the main MyVariant.info portal. Default is recommended.

Value
returns a variant object (DataFrame, list, or JSON text) containing the queried annotations
**metadata**

**References**


**See Also**

`getVariants` `queryVariant` `queryVariants`

**Examples**

```r
## given a list of HGVS ids
vars <- c('chr1:g.866422C>T',
          'chr1:g.876664G>A',
          'chr1:g.69635G>C',
          'chr1:g.69869T>A',
          'chr1:g.881918G>A',
          'chr1:g.865625G>A',
          'chr1:g.879368C>A',
          'chr1:g.889226C>T',
          'chr1:g.879492C>G',
          'chr1:g.879423T>G',
          'chr1:g.881602C>T',
          'chr1:g.879115C>G',
          'chr1:g.69892T>C',
          'chr1:g.879381C>T',
          'chr1:g.878330C>G')

## Return the list of variant object for the given list of HGVS ids.
df <- getVariants(vars, fields="dbsnp, wellderly")
```

---

**Description**

Get metadata for MyVariant.info services.

**Usage**

```r
metadata(x, ...)
```

**Arguments**

- `x` MyVariant object
- `...` MyVariant object slot parameters

**Value**

returns the metadata including available databases and number of documents.

**References**

http://myvariant.info/v1/metadata
## Get metadata

```r
myvariant <- MyVariant()
metadata(myvariant)
```

### Description

Construct a MyVariant object.

### Usage

```r
MyVariant(...)  
```

### Arguments

... 

See help page for MyVariant-class

### Value

MyVariant object

### Examples

```r
MyVariant()
```

---

## Access MyVariant.info variant annotation services

### Description

MyVariant.Info provides REST web services to query/retrieve variant annotations. myvariant is an easy-to-use R wrapper to access MyVariant.info services.

### Details

- **Package**: myvariant
- **Type**: Package
- **Version**: 0.99.0
- **Date**: 2014-12-18
- **License**: Artistic-2.0
- **Depends**: httr jsonlite Hmisc
MyVariant-class

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References

https://github.com/Network-of-BioThings/myvariant.info/wiki

MyVariant-class

Class "MyVariant"

Description

R Client to access MyVariant.Info annotation services

Objects from the Class

Objects can be created by calls of the form MyVariant(base.url="http://myvariant.info/v1", delay=1, step=1000, version=version, verbose=TRUE, debug=FALSE).

Slots

base.url: "http://myvariant.info/v1". 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

getVariant(hgvsid, fields=NULL, ..., return.as=c("records", "text")): Return the variant object for the given hgvsid
getVariants(hgvsids, fields=NULL, ..., return.as=c("DataFrame", "records", "text")): Return the list of variant object for the given list of hgvsids.
queryVariant(q, fields=NULL, ..., return.as=c("DataFrame", "records", "text")): Return the query result.
queryVariants(qterms, scopes=NULL, fields=NULL, ..., return.as=c("DataFrame", "records", "text")): Return the batch query result.

Author(s)

Adam Mark

References

https://github.com/Network-of-BioThings/myvariant.info/wiki

Examples

showClass("MyVariant")
queryVariant  

Return the query result.

Description

This is a wrapper for GET query of "/query?q=<query>" service.

Usage

queryVariant(q, ..., return.as=c("DataFrame", "records", "text"),
myvariant)

Arguments

q  
query term(s).

...  
Commonly queried fields include fields, size as well as several other fields. View available fields by calling ?metadata.

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

myvariant  
A MyVariant object that describes how to connect to data resources. See MyVariant-class. If missing, default object will be used that accesses the main MyVariant.info portal. Default is recommended.

Value

returns a variant object (DataFrame, list, or JSON text) containing the queried annotations

References


See Also

queryVariants getVariant getVariants

Examples

## return the query result
queryVariant("dbnsfp.variantname:BRCA2")

queryVariant("chr1:1-1000000")
queryVariants

queryVariants  Return the batch query result.

Description
This is a wrapper for POST query of "/query" service.

Usage
queryVariants(qterms, scopes=NULL, ..., return.as=c("DataFrame", "records", "text"), myvariant)

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.
- ...: Commonly queried fields include 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.
- return.as: "DataFrame" (default), "records" (list), "text" (JSON).
- myvariant: A MyVariant object that describes how to connect to data resources. See MyVariant-class. If missing, default object will be used that accesses the main MyVariant.info portal. Default is recommended.

Value
returns a variant object (DataFrame, list, or JSON text) containing the queried annotations

References

See Also
queryVariant getVariant getVariants

Examples
## return the batch query result
Index

*Topic **classes**
  MyVariant-class, 7

*Topic **package**
  myvariant, 6

formatHgvs, 2, 3
formatSingleHgvs, 2, 2

getVariant, 3, 8, 9
getVariant, missing-method (getVariant), 3
getVariant, MyVariant-method
  (getVariant), 3
getVariants, 4, 4, 5, 8, 9
getVariants, missing-method
  (getVariants), 4
getVariants, MyVariant-method
  (getVariants), 4

metadata, 5
metadata, MyVariant-method (metadata), 5
MyVariant, 6
myvariant, 6
MyVariant-class, 7

queryVariant, 4, 5, 8, 9
queryVariant, missing-method
  (queryVariant), 8
queryVariant, MyVariant-method
  (queryVariant), 8
queryVariants, 4, 5, 8, 9
queryVariants, missing-method
  (queryVariants), 9
queryVariants, MyVariant-method
  (queryVariants), 9

readVcf, 2