

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

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formatHgvs	<i>Get all HGVS IDs from Vcf object.</i>
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Description

Read in a Vcf object created by [readVcf](#) to extract all HGVS IDs for querying MyVariant.info.

Usage

```
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

<https://myvariant.info> <http://www.hgvs.org/mutnomen/recs-DNA.html>

See Also

[formatSingleHgvs](#)

Examples

```
## 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")
```

formatSingleHgvs	<i>Get Hgvs HGVS ID from chromosome, position, reference and alternate alleles.</i>
------------------	---

Description

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

Usage

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

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

<https://myvariant.info> <http://www.hgvs.org/mutnomen/recs-DNA.html>

See Also

[formatHgvs](#)

Examples

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

getVariant	<i>Return the variant object for the given HGVS id.</i>
------------	---

Description

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

Usage

```
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 <code>fields=="all"</code> , 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.

Value

returns a variant object containing the queried annotations

References

http://docs.myvariant.info/en/latest/doc/variant_annotation_service.html#get-request <http://docs.myvariant.info/en/latest/doc/parameters>

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	<i>Return the list of variant objects for the given list of HGVS ids.</i>
-------------	---

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

References

http://docs.myvariant.info/en/latest/doc/variant_annotation_service.html#batch-queries-via-post http://docs.myvariant.info/en/latest/doc/variant_annotation_service.html

See Also

[getVariants](#) [queryVariant](#) [queryVariants](#)

Examples

```
## 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, welllderly")
```

metadata

metadata

Description

Get metadata for MyVariant.info services.

Usage

```
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>

Examples

```
## Get metadata  
myvariant<-MyVariant()  
metadata(myvariant)
```

`MyVariant`*MyVariant*

Description

Construct a MyVariant object.

Usage

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

Arguments

... See help page for MyVariant-class

Value

MyVariant object

Examples

```
MyVariant()
```

`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
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Depends: httr jsonlite Hmisc

Author(s)

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

MyVariant-class	Class "MyVariant"
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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	<i>Return the query result.</i>
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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 <code>?metadata</code> .
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

http://docs.myvariant.info/en/latest/doc/variant_query_service.html#get-request http://docs.myvariant.info/en/latest/doc/variant_query_service.html#syntax

See Also

[queryVariants](#) [getVariant](#) [getVariants](#)

Examples

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

queryVariant("chr1:1-1000000")
```

queryVariants	<i>Return the batch query result.</i>
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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 <code>fields</code> , <code>size</code> as well as several other fields. <code>returnall</code> returns a list of all related data including duplicated and missing qterms. False by default. View available fields by calling <code>?metadata</code> .
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

http://docs.myvariant.info/en/latest/doc/variant_query_service.html#batch-queries-via-post <http://docs.myvariant.info/en/late>

See Also

[queryVariant](#) [getVariant](#) [getVariants](#)

Examples

```
## return the batch query result
```

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