

# Package ‘myvariant’

September 19, 2024

**Type** Package

**Title** Accesses MyVariant.info variant query and annotation services

**Version** 1.35.0

**Date** 2015-07-10

**Author** Adam Mark

**Maintainer** Adam Mark, Chunlei Wu <cwu@scripps.edu>

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

**License** Artistic-2.0

**Depends** R (>= 3.2.1), VariantAnnotation

**Imports** htr, jsonlite, S4Vectors, Hmisc, plyr, magrittr, GenomeInfoDb

**Suggests** BiocStyle

**biocViews** VariantAnnotation, Annotation, GenomicVariation

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/myvariant>

**git\_branch** devel

**git\_last\_commit** ff9a783

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-09-18

## Contents

formatHgvs . . . . .	2
formatSingleHgvs . . . . .	2
getVariant . . . . .	3
getVariants . . . . .	4
metadata . . . . .	5
MyVariant . . . . .	6
myvariant . . . . .	6
MyVariant-class . . . . .	7
queryVariant . . . . .	8
queryVariants . . . . .	9
<b>Index</b>	<b>10</b>

---

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

---

**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 <a href="#">readVcf</a> .
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 <a href="#">MyVariant-class</a> . 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/variant_annotation_service.html#get-request) <http://docs.myvariant.info/en/latest/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

*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 <code>fields=="all"</code> , 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 <a href="#">MyVariant-class</a> . 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#batch-queries-via-post) [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#batch-queries-via-post)

## 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
Version: 0.99.0
Date: 2014-12-18
License: Artistic-2.0
Depends: httr jsonlite Hmisc
```

**Author(s)**

Adam Mark

Maintainer: Adam Mark &lt;adammark@scripps.edu&gt;

**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.as=c("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>
--------------	---------------------------------

---

### 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 <code>fields</code> , <code>size</code> 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 <a href="#">MyVariant-class</a> . 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#get-request) <http://docs.myvariant.info/en/latest/doc/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>
---------------	---------------------------------------

---

### 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. <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 <a href="#">MyVariant-class</a> . 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/latest/doc/variant_query_service.html#batch-queries-via-post) <http://docs.myvariant.info/en/>

### See Also

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

### Examples

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

# Index

## \* classes

MyVariant-class, 7

## \* 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