

# Package ‘myvariant’

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**Type** Package

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

**Version** 1.24.0

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

**Suggests** BiocStyle

**biocViews** VariantAnnotation, Annotation, GenomicVariation

**NeedsCompilation** no

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

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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 <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")
```

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

### 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 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 <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/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>
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---

### 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 <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](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")
```

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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)
```

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`MyVariant`*MyVariant*

---

**Description**

Construct a MyVariant object.

**Usage**

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

**Arguments**

... See help page for MyVariant-class

**Value**

MyVariant object

**Examples**

```
MyVariant()
```

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`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>


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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, verbose=TRUE)`**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.batch=TRUE)`: Return the batch query result.**Author(s)**

Adam Mark



**References**

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

**Examples**

```
showClass("MyVariant")
```

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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 <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/variant\\_query\\_service.html#syntax](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")
```

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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 <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/late>

### See Also

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

### Examples

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

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