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:

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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")
```

---

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)
```
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

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

## 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.879492G>',
  '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")

## 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
### Description

Construct a MyVariant object.

### Usage

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

### Arguments

... 

See help page for MyVariant-class

### Value

MyVariant object

### Examples

```r
MyVariant()
```

---

### Description

Access MyVariant.info variant annotation services

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

Author(s)
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References
https://github.com/Network-of-BioThings/myvariant.info/wiki

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

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 
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
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