

MyVariant.info R Client

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November 1, 2022

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1 Overview

MyVariant.Info is a simple-to-use REST web service to query/retrieve genetic variant annotation from an aggregation of variant annotation resources. *myvariant* is an easy-to-use R wrapper to access MyVariant.Info services and explore variant annotations.

2 Variant Annotation Service

2.1 Obtaining HGVS IDs from a VCF file.

- Use `readVcf` from the VariantAnnotation package to read a Vcf file in. The Vcf object can then be passed to `formatHgvs` to retrieve HGVS IDs. HGVS IDs are based on the GRCh38/hg19 reference genome. Support for hg38 is coming soon.

```
> file.path <- system.file("extdata", "dbsnp_mini.vcf", package="myvariant")
> vcf <- readVcf(file.path, genome="hg19")
> rowRanges(vcf)

GRanges object with 240 ranges and 5 metadata columns:
      seqnames      ranges strand | paramRangeID      REF
      <Rle>      <IRanges> <Rle> | <factor> <DNAStringSet>
rs376643643      1 10019-10020   * |      NA      TA
rs373328635      1    10055   * |      NA      T
  rs62651026      1    10108   * |      NA      C
rs376007522      1    10109   * |      NA      A
rs368469931      1    10139   * |      NA      A
  ...
rs544020171      1    17654   * |      NA      T
rs563880190      1    17694   * |      NA      C
rs574335987      1    17695   * |      NA      G
rs374995955      1    17697   * |      NA      G
rs543363182      1    17709   * |      NA      T
      ALT      QUAL      FILTER
      <DNAStringSetList> <numeric> <character>
rs376643643      T      NA      .
rs373328635      TA     NA      .
  rs62651026      T      NA      .
rs376007522      T      NA      .
rs368469931      T      NA      .
  ...
rs544020171      C      NA      .
rs563880190      T      NA      .
rs574335987      A      NA      .
rs374995955      C      NA      .
rs543363182      G      NA      .
-----
seqinfo: 1 sequence from hg19 genome; no seqlengths
```

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- You can then use `formatHgvs` to extract HGVS IDs from the Vcf object.

```
> hgvs <- formatHgvs(vcf, variant_type="snp")
> head(hgvs)

[1] "1:g.10108C>T" "1:g.10109A>T" "1:g.10139A>T" "1:g.10150C>T" "1:g.10177A>C"
[6] "1:g.10180T>C"
```

2.2 `getVariant`

- Use `getVariant`, the wrapper for GET query of `"/v1/variant/<hgvsid>"` service, to return the variant object for the given HGVS id.

```
> variant <- getVariant("chr1:g.35367G>A")
> variant[[1]]$dbnsfp$genename

NULL

> variant[[1]]$cadd$phred

[1] 3.726
```

2.3 `getVariants`

- Use `getVariants`, the wrapper for POST query of `"/v1/variant"` service, to return the list of variant objects for the given character vector of HGVS ids.

```
> getVariants(c("chr1:g.35367G>A", "chr16:g.28883241A>G"),
+             fields="cadd.consequence")

DataFrame with 2 rows and 4 columns
      query                X_id                cadd._license
  <character>          <character>          <character>
1  chr1:g.35367G>A    chr1:g.35367G>A http://bit.ly/2TIuab9
2 chr16:g.28883241A>G chr16:g.28883241A>G http://bit.ly/2TIuab9
  cadd.consequence
  <character>
1 NONCODING_CHANGE
2 NON_SYNONYMOUS
```

3 Variant Query Service

3.1 queryVariant

- `queryVariant` is a wrapper for GET query of `"/v1/query?q=<query>"` service, to return the query result. This function accepts wild card input terms and allows you to query for variants that contain a specific annotation. For example, the following query searches for the CADD phred score and consequence for all variants whose gene name (dbNSFP) is MLL2.

```
> queryVariant(q="dbnsfp.genename:MLL2", fields=c("cadd.phred", "cadd.consequence"))
$took
[1] 16

$total
[1] 0

$max_score
NULL

$hits
list()
```

- You can also use `queryVariant` to retrieve all annotations that map to a specific rsID.

```
> queryVariant(q="rs58991260", fields="dbSNP.flags")$hits
      _id  _score
1 chr1:g.218631822G>A 21.14489
```

3.2 queryVariants

- `queryVariants` is a wrapper for POST query of `"/v1/query?q=<query>"` service, to return the query result. Query terms include any available field as long as scopes are defined. The following example reads the dbSNP rsIDs from a VCF and queries for all fields. The returned DataFrame can then be easily subsetted to include, for example, those that have not been documented in the Welllderly study.

```
> rsids <- paste("rs", info(vcf)$RS, sep="")
> res <- queryVariants(q=rsids, scopes="dbSNP.rsID", fields="all")
```

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Finished

Pass `returnall=TRUE` to return lists of duplicate or missing query terms.

```
> subset(res, !is.na(wellderly.vartype))$query
```

```
[1] "rs62651026" "rs376007522" "rs368469931" "rs368469931" "rs371194064"
[6] "rs371194064" "rs201752861" "rs201752861" "rs201694901" "rs201694901"
[11] "rs201694901" "rs200279319" "rs200279319" "rs145599635" "rs148908337"
[16] "rs148908337" "rs199706086" "rs111200574" "rs111200574" "rs112155239"
[21] "rs112155239" "rs528916756" "rs565971701" "rs55998931" "rs199606420"
[26] "rs62636508" "rs537182016" "rs58108140" "rs189107123" "rs10218527"
[31] "rs540538026" "rs62635286" "rs62635286" "rs531730856" "rs548333521"
[36] "rs538791886" "rs527952245" "rs558318514" "rs574697788" "rs199896944"
[41] "rs554008981" "rs113004249" "rs546169444" "rs28503599" "rs62635297"
[46] "rs62635297" "rs201055865" "rs201327123" "rs62635298" "rs571121669"
[51] "rs533499096" "rs199856693" "rs201855936" "rs71252251" "rs71252251"
[56] "rs201045431" "rs368345873" "rs576044687" "rs201635489" "rs533630043"
[61] "rs533630043" "rs564003018" "rs374029747" "rs2691315" "rs112448831"
[66] "rs372319358" "rs541172944" "rs529651976" "rs548165136" "rs11489794"
[71] "rs113141985" "rs148220436" "rs373516660" "rs150723783" "rs62636367"
[76] "rs62636367" "rs201330479" "rs62636368" "rs201563295" "rs199745162"
[81] "rs200658479" "rs200658479" "rs201833382" "rs199740902" "rs9651250"
[86] "rs9651250" "rs200978805" "rs555297131" "rs369606208" "rs201535981"
[91] "rs200784459" "rs111588939" "rs372841554" "rs200503540" "rs192890528"
[96] "rs201578576" "rs374545136" "rs377698370" "rs201057270" "rs544020171"
[101] "rs563880190" "rs574335987" "rs543363182"
```

4 References

MyVariant.info help@myvariant.info