

MyVariant.info R Client

Adam Mark, Chunlei Wu

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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 genename (dbNSFP) is MLL2.

```
> queryVariant(q="dbnsfp.genename:MLL2", fields=c("cadd.phred", "cadd.consequence"))

$took
[1] 9

$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 21.26964
```

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")
```

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