MyVariant.info R Client

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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 annotions.

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
```

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

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

[1] "chr1:g.10108C>T" "chr1:g.10109A>T" "chr1:g.10139A>T" "chr1:g.10150C>T"
[5] "chr1:g.10177A>C" "chr1: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"))

$max_score
NULL

$took
[1] 3

$total
[1] 0

$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 15.58943
```

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 Wellderly 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] "rs145427775" "rs55998931"  "rs199606420" "rs58108140"  "rs62635284"
 [6] "rs62635286"  "rs531730856" "rs527952245" "rs546169444" "rs201055865"
[11] "rs62635298"  "rs199856693" "rs201855936" "rs71252251"  "rs201045431"
[16] "rs201635489" "rs533630043" "rs2691315"   "rs572465511" "rs372319358"
[21] "rs11489794"  "rs113141985" "rs148220436" "rs150723783" "rs62636367"
[26] "rs62636368"  "rs199745162" "rs200658479" "rs201833382" "rs199740902"
[31] "rs200978805" "rs201535981" "rs192890528"
```

4 References

MyVariant.info help@myvariant.info