Overview of ensemblVEP

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Contents

1 Introduction

Ensembl provides the facility to predict functional consequences of known and unknown variants using the Variant Effect Predictor (VEP). The ensemblVEP package wraps Ensembl VEP and returns the results as Robjects or a file on disk. To use this package the Ensembl VEP perl script must be installed in your path. See the package README for details.

NOTE: As of Ensembl version 88 the VEP script has been renamed from variant_effect_predictor.pl to vep. The ensemblVEP package code and documentation have been updated to reflect this change.
Downloads: `http://uswest.ensembl.org/info/docs/tools/vep/index.html`
Complete documentation for runtime options: `http://uswest.ensembl.org/info/docs/tools/vep/script/vep_options.html`
To test that Ensembl VEP is properly installed, enter the name of the script from the command line:

vep

2 Results as R objects

```
> library(ensemblVEP)
```

The `ensemblVEP` function can return variant consequences from Ensembl VEP as Robjects (`GRanges` or `VCF`) or write them to a file. The default behavior returns a `GRanges`. Runtime options are stored in a `VEPFlags` object and allow a great deal of control over the content and format of the results. See the man pages for more details.

```
> ?ensemblVEP
> ?VEPFlags
```

The default runtime options can be inspected by creating a `VEPFlags`.

```
> param <- VEPFlags()
> param
```

```
class: VEPFlags
flags(2): host, database
version: 90
scriptPath:
```

```
> flags(param)
```

```
$host
[1] "useastdb.ensembl.org"

$database
[1] TRUE

$vcf
[1] FALSE
```

Using a vcf file from VariantAnnotation as input, we query Ensembl VEP with the default runtime parameters. Consequence data are parsed into the metadata columns of the GRanges. To control the type and amount of data returned see the output options at http://uswest.ensembl.org/info/docs/tools/vep/script/vep_options.html.

```
> fl <- system.file("extdata", "gl_chr1.vcf", package="VariantAnnotation")
> gr <- ensemblVEP(fl)
> head(gr, 3)

GRanges object with 3 ranges and 23 metadata columns:
             seqnames         ranges strand |      Allele
                <Rle>      <IRanges>  <Rle> | <character>
  rs58108140        1 [10583, 10583]      * |           A
  rs58108140        1 [10583, 10583]      * |           A
  rs58108140        1 [10583, 10583]      * |           A
                      Consequence      IMPACT      SYMBOL            Gene
                      <character> <character> <character>     <character>
  rs58108140   upstream_gene_variant    MODIFIER     DDX11L1 ENSG00000223972
  rs58108140   upstream_gene_variant    MODIFIER     DDX11L1 ENSG00000223972
  rs58108140 downstream_gene_variant    MODIFIER      WASH7P ENSG00000227232
             Feature_type         Feature                         BIOTYPE
              <character>     <character>                       <character>
  rs58108140   Transcript ENST00000450305 transcribed_unprocessed_pseudogene
  rs58108140   Transcript ENST00000456328               processed_transcript
  rs58108140   Transcript ENST00000488147             unprocessed_pseudogene
                   EXON      INTRON       HGVSc       HGVSp cDNA_position
             <character> <character> <character> <character>   <character>
  rs58108140        <NA>        <NA>        <NA>        <NA>          <NA>
  rs58108140        <NA>        <NA>        <NA>        <NA>          <NA>
  rs58108140        <NA>        <NA>        <NA>        <NA>          <NA>
             CDS_position Protein_position Amino_acids      Codons
              <character>      <character> <character> <character>
  rs58108140         <NA>             <NA>        <NA>        <NA>
  rs58108140         <NA>             <NA>        <NA>        <NA>
  rs58108140         <NA>             <NA>        <NA>        <NA>
             Existing_variation    DISTANCE      STRAND       FLAGS
                    <character> <character> <character> <character>
  rs58108140               <NA>        1427           1        <NA>
  rs58108140               <NA>        1286           1        <NA>
  rs58108140               <NA>        3821          -1        <NA>
             SYMBOL_SOURCE     HGNC_ID
               <character> <character>
  rs58108140          HGNC  HGNC:37102
  rs58108140          HGNC  HGNC:37102
  rs58108140          HGNC  HGNC:38034
  -------
  seqinfo: 1 sequence from  genome; no seqlengths
```

Next we request that a VCF object be returned by setting the *vcf* option in the *flags* slot to TRUE.

```
> param <- VEPFlags(flags=list(vcf=TRUE))
> vep <- ensemblVEP(fl, param)
```

Success! When a `VCF` is returned, consequence data are included as an unparsed INFO column labeled *CSQ*.

```
> info(vep)$CSQ
```

```
CharacterList of length 3
[[1]] A|upstream_gene_variant|MODIFIER|DDX11L1|ENSG00000223972|Transcript|ENS...
[[2]] T|non_coding_transcript_exon_variant|MODIFIER|DDX11L1|ENSG00000223972|T...
[[3]] T|downstream_gene_variant|MODIFIER|FAM138A|ENSG00000237613|Transcript|E...
```

The `parseCSQToGRanges` function parses these data into a `GRanges`. When the rownames of the original VCF are provided as `VCFRowID` a metadata column of the same name is included in the output.

```
> vcf <- readVcf(fl, "hg19")
> csq <- parseCSQToGRanges(vep, VCFRowID=rownames(vcf))
> head(csq, 3)
```

```
GRanges object with 3 ranges and 24 metadata columns:
             seqnames         ranges strand |  VCFRowID      Allele
                <Rle>      <IRanges>  <Rle> | <integer> <character>
  rs58108140        1 [10583, 10583]      * |         1           A
  rs58108140        1 [10583, 10583]      * |         1           A
  rs58108140        1 [10583, 10583]      * |         1           A
                       Consequence      IMPACT      SYMBOL            Gene
                       <character> <character> <character>     <character>
  rs58108140   upstream_gene_variant    MODIFIER     DDX11L1 ENSG00000223972
  rs58108140   upstream_gene_variant    MODIFIER     DDX11L1 ENSG00000223972
  rs58108140 downstream_gene_variant    MODIFIER      WASH7P ENSG00000227232
             Feature_type         Feature                          BIOTYPE
              <character>     <character>                        <character>
  rs58108140   Transcript ENST00000450305 transcribed_unprocessed_pseudogene
  rs58108140   Transcript ENST00000456328               processed_transcript
  rs58108140   Transcript ENST00000488147             unprocessed_pseudogene
                   EXON      INTRON       HGVSc       HGVSp cDNA_position
             <character> <character> <character> <character>   <character>
  rs58108140        <NA>        <NA>        <NA>        <NA>          <NA>
  rs58108140        <NA>        <NA>        <NA>        <NA>          <NA>
  rs58108140        <NA>        <NA>        <NA>        <NA>          <NA>
             CDS_position Protein_position Amino_acids      Codons
              <character>      <character> <character> <character>
  rs58108140         <NA>             <NA>        <NA>        <NA>
  rs58108140         <NA>             <NA>        <NA>        <NA>
  rs58108140         <NA>             <NA>        <NA>        <NA>
             Existing_variation    DISTANCE      STRAND       FLAGS
                    <character> <character> <character> <character>
  rs58108140               <NA>        1427           1        <NA>
  rs58108140               <NA>        1286           1        <NA>
  rs58108140               <NA>        3821          -1        <NA>
             SYMBOL_SOURCE     HGNC_ID
               <character> <character>
  rs58108140          HGNC  HGNC:37102
  rs58108140          HGNC  HGNC:37102
  rs58108140          HGNC  HGNC:38034
  -------
  seqinfo: 1 sequence from  genome; no seqlengths
```

The `VCFRowID` columns maps the expanded *CSQ* data back to the rows in the *VCF* object. This index can be used to subset the original VCF.

```
> vcf[csq$"VCFRowID"]
```

```
class: CollapsedVCF
dim: 13 85
rowRanges(vcf):
  GRanges with 5 metadata columns: paramRangeID, REF, ALT, QUAL, FILTER
info(vcf):
  DataFrame with 22 columns: LDAF, AVGPOST, RSQ, ERATE, THETA, CIEND, CIPOS,...
info(header(vcf)):
             Number Type    Description
   LDAF      1      Float   MLE Allele Frequency Accounting for LD
   AVGPOST   1      Float   Average posterior probability from MaCH/Thunder
   RSQ       1      Float   Genotype imputation quality from MaCH/Thunder
   ERATE     1      Float   Per-marker Mutation rate from MaCH/Thunder
   THETA     1      Float   Per-marker Transition rate from MaCH/Thunder
   CIEND     2      Integer Confidence interval around END for imprecise var...
   CIPOS     2      Integer Confidence interval around POS for imprecise var...
   END       1      Integer End position of the variant described in this re...
   HOMLEN    .      Integer Length of base pair identical micro-homology at ...
   HOMSEQ    .      String  Sequence of base pair identical micro-homology a...
   SVLEN     1      Integer Difference in length between REF and ALT alleles
   SVTYPE    1      String  Type of structural variant
   AC        .      Integer Alternate Allele Count
   AN        1      Integer Total Allele Count
   AA        1      String  Ancestral Allele, ftp://ftp.1000genomes.ebi.ac.u...
   AF        1      Float   Global Allele Frequency based on AC/AN
   AMR_AF    1      Float   Allele Frequency for samples from AMR based on A...
   ASN_AF    1      Float   Allele Frequency for samples from ASN based on A...
   AFR_AF    1      Float   Allele Frequency for samples from AFR based on A...
   EUR_AF    1      Float   Allele Frequency for samples from EUR based on A...
   VT        1      String  indicates what type of variant the line represents
   SNPSOURCE .      String  indicates if a snp was called when analysing the...
geno(vcf):
  SimpleList of length 3: GT, DS, GL
geno(header(vcf)):
      Number Type   Description
   GT 1      String Genotype
   DS 1      Float  Genotype dosage from MaCH/Thunder
   GL .      Float  Genotype Likelihoods
```

3 Write results to a file

In the previous section we saw Ensembl VEP results returned as R objects in the workspace. Alternatively, these results can be written directly to a file. The flag that controls how the data are returned is the *output_file* flag.

When *output_file* is NULL (default), the results are returned as either a *GRanges* or *VCF* object.

```
> flags(param)$output_file
```

```
NULL
```

To write results directly to a file, specify a file name for the *output_file* flag.

```
> flags(param)$output_file <- "/mypath/myfile"
```

The file can be written as a *vcf* or *gvf* by setting the options of the slot to TRUE. If neither of *vcf* or *gvf* are TRUE the file is written out as tab delimited.

```
> ## Write a vcf file to myfile.vcf:
> myparam <- VEPFlags(flags=list(vcf=TRUE,
+                          output_file="/path/myfile.vcf"))
> ## Write a gvf file to myfile.gvf:
> myparam <- VEPFlags(flags=list(gvf=TRUE,
```

```
+                          output_file="/path/myfile.gvf"))
> ## Write a tab delimited file to myfile.txt:
> myparam <- VEPFlags(flags=list(output_file="/path/myfile.txt"))
```

4 Configuring runtime options

The Ensembl VEP web page has complete descriptions of all runtime options. `http://uswest.ensembl.org/info/docs/tools/vep/script/vep_options.html` Below are examples of how to configure the runtime options in the *VEPFlags* for specific situations. Investigate the differences in results using a sample file from VariantAnnotation.

```
> fl <- system.file("extdata", "ex2.vcf", package="VariantAnnotation")
```

- Add regulatory region consequences:

```
> param <- VEPFlags(flags=list(regulatory=TRUE))
> gr <- ensemblVEP(fl, param)
```

- Specify input file format as VCF, add HGNC gene identifiers, output SO consequence terms:

```
> param <- VEPFlags(flag=list(format="vcf",
+                         terms="SO",
+                         symbol=TRUE))
> gr <- ensemblVEP(fl, param)
```

- Check for co-located variants, output only coding sequence consequences, output HGVS names:

```
> param <- VEPFlags(flags=list(coding_only=TRUE,
+                         check_existing=TRUE,
+                         symbol=TRUE))
> gr <- ensemblVEP(fl, param)
```

- Add SIFT score and prediction, PolyPhen prediction only, output results as `VCF`:

```
fl <- system.file("extdata", "chr22.vcf.gz", package="VariantAnnotation")
param <- VEPFlags(flags=list(sift="b", polyphen="p",
                  vcf=TRUE))
vcf <- ensemblVEP(fl, param)
csq <- parseCSQToGRanges(vcf)

> head(levels(mcols(csq)$SIFT))
[1] "deleterious(0.01)" "deleterious(0.02)" "deleterious(0.03)"
[4] "deleterious(0.04)" "deleterious(0.05)" "deleterious(0)"

> levels(mcols(csq)$PolyPhen)
[1] "benign"            "possibly_damaging" "probably_damaging"
[4] "unknown"
```

5 sessionInfo()

```
> sessionInfo()

R version 3.4.2 (2017-09-28)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.3 LTS

Matrix products: default
BLAS: /home/biocbuild/bbs-3.6-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.6-bioc/R/lib/libRlapack.so

locale:
```

```
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8        LC_COLLATE=C
 [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
 [9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] stats4    parallel  stats     graphics  grDevices utils     datasets
[8] methods   base

other attached packages:
 [1] ensemblVEP_1.20.0          VariantAnnotation_1.24.0
 [3] Rsamtools_1.30.0           Biostrings_2.46.0
 [5] XVector_0.18.0             SummarizedExperiment_1.8.0
 [7] DelayedArray_0.4.0         matrixStats_0.52.2
 [9] Biobase_2.38.0             GenomicRanges_1.30.0
[11] GenomeInfoDb_1.14.0        IRanges_2.12.0
[13] S4Vectors_0.16.0           BiocGenerics_0.24.0

loaded via a namespace (and not attached):
 [1] Rcpp_0.12.13             compiler_3.4.2           prettyunits_1.0.2
 [4] GenomicFeatures_1.30.0   bitops_1.0-6             tools_3.4.2
 [7] zlibbioc_1.24.0          progress_1.1.2           biomaRt_2.34.0
[10] digest_0.6.12            bit_1.1-12               BSgenome_1.46.0
[13] RSQLite_2.0              memoise_1.1.0            tibble_1.3.4
[16] lattice_0.20-35          rlang_0.1.2              Matrix_1.2-11
[19] DBI_0.7                  GenomeInfoDbData_0.99.1  rtracklayer_1.38.0
[22] stringr_1.2.0            bit64_0.9-7              grid_3.4.2
[25] R6_2.2.2                 AnnotationDbi_1.40.0     XML_3.98-1.9
[28] RMySQL_0.10.13           BiocParallel_1.12.0      magrittr_1.5
[31] blob_1.1.0               GenomicAlignments_1.14.0 assertthat_0.2.0
[34] stringi_1.1.5            RCurl_1.95-4.8
```