

Overview of **ensemblVEP** Pre Ensembl 90

Valerie Obenchain and Lori Shepherd

October 30, 2017

Contents

1	Introduction	1
2	Results as R objects	1
3	Write results to a file	4
4	Configuring runtime options	4
5	sessionInfo()	5

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 **VEPParam** object and allow a great deal of control over the content and format of the results. See the man pages for more details.

```
> ?ensemblVEP
```

```
> ?VEPParam
```

The default runtime options can be inspected by creating a **VEPParam**.

```
> param <- VEPParam(version=88)
```

```
> param
```

```
class: VEPParam88
```

```
identifier():
```

```
colocatedVariants():
```

```
dataformat():
```

```
basic():
```

```
input(1): species
```

```

cache(3): dir, dir_cache, dir_plugins
output(1): terms
filterqc(0):
database(2): host, database
advanced(1): buffer_size
version: 88
scriptPath:

```

```
> basic(param)
```

```

$verbose
[1] FALSE

```

```

$quiet
[1] FALSE

```

```

$no_progress
[1] FALSE

```

```

$config
character(0)

```

```

$everything
[1] FALSE

```

```

$fork
numeric(0)

```

Using a vcf file from VariantAnnotation as input, we query Ensembl VEP with the default runtime parameters.

```

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

```

Consequence data are parsed into the metadata columns of the GRanges. To control the type and amount of data returned see the options in output(VEPParam()).

```
> head(gr, 3)
```

GRanges object with 3 ranges and 23 metadata columns:

	seqnames	ranges	strand	Allele	
	<Rle>	<IRanges>	<Rle>	<factor>	
rs6054257	20	[14370, 14370]	*	A	
20:17330_T/A	20	[17330, 17330]	*	A	
rs6040355	20	[1110696, 1110696]	*	G	
	Consequence	IMPACT	SYMBOL	Gene	
	<factor>	<factor>	<factor>	<factor>	
rs6054257	intergenic_variant	MODIFIER	<NA>	<NA>	
20:17330_T/A	intergenic_variant	MODIFIER	<NA>	<NA>	
rs6040355	upstream_gene_variant	MODIFIER	PSMF1	ENSG00000125818	
	Feature_type	Feature	BIOTYPE	EXON	
	<factor>	<factor>	<factor>	<factor>	
rs6054257	<NA>	<NA>	<NA>	<NA>	
20:17330_T/A	<NA>	<NA>	<NA>	<NA>	
rs6040355	Transcript	ENST00000479715	processed_transcript	<NA>	
	INTRON	HGVSc	HGVSp	cDNA_position	CDS_position
	<factor>	<factor>	<factor>	<factor>	<factor>
rs6054257	<NA>	<NA>	<NA>	<NA>	<NA>
20:17330_T/A	<NA>	<NA>	<NA>	<NA>	<NA>
rs6040355	<NA>	<NA>	<NA>	<NA>	<NA>
	Protein_position	Amino_acids	Codons	Existing_variation	
	<factor>	<factor>	<factor>	<factor>	

rs6054257	<NA>	<NA>	<NA>	<NA>
20:17330_T/A	<NA>	<NA>	<NA>	<NA>
rs6040355	<NA>	<NA>	<NA>	<NA>

	DISTANCE	STRAND	FLAGS	SYMBOL_SOURCE	HGNC_ID
	<factor>	<factor>	<factor>	<factor>	<factor>
rs6054257	<NA>	<NA>	<NA>	<NA>	<NA>
20:17330_T/A	<NA>	<NA>	<NA>	<NA>	<NA>
rs6040355	2610	1	<NA>	HGNC	HGNC:9571

seqinfo: 1 sequence from genome

Next we use a vcf of structural variants as input

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

and request that a VCF object be returned by setting the *vcf* option in the *dataformat* slot to TRUE.

```
> param <- VEPParam(dataformat=c(vcf=TRUE), version=88)
```

An call to *ensemblVEP* results in an error.

```
> vcf <- ensemblVEP(fl, param)
2012-12-03 16:40:55 - Starting...
ERROR: Could not detect input file format
```

In most situations Ensembl VEP can auto-detect the input format. In this case, however, it cannot so we explicitly set the *format* option to 'vcf'.

```
> input(param)$format <- "vcf"
```

Try again.

```
> 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 0

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 0 ranges and 23 metadata columns:

seqnames	ranges	strand	Allele	Consequence	IMPACT	SYMBOL
<Rle>	<IRanges>	<Rle>	<character>	<character>	<character>	<character>
Gene	Feature_type	Feature	BIOTYPE	EXON	INTRON	
<character>	<character>	<character>	<character>	<character>	<character>	
HGVSc	HGVSp	cDNA_position	CDS_position	Protein_position		
<character>	<character>	<character>	<character>	<character>		
Amino_acids	Codons	Existing_variation	DISTANCE	STRAND		
<character>	<character>	<character>	<character>	<character>		
FLAGS	SYMBOL_SOURCE	HGNC_ID				
<character>	<character>	<character>				

seqinfo: no sequences

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: 0 1
rowRanges(vcf):
  GRanges with 5 metadata columns: paramRangeID, REF, ALT, QUAL, FILTER
info(vcf):
  DataFrame with 10 columns: BKPTID, CIEND, CIPOS, END, HOMLEN, HOMSEQ, IMPR...
info(header(vcf)):
```

	Number	Type	Description
BKPTID	.	String	ID of the assembled alternate allele in the asse...
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...
IMPRECISE	0	Flag	Imprecise structural variation
MEINFO	4	String	Mobile element info of the form NAME,START,END,P...
SVLEN	.	Integer	Difference in length between REF and ALT alleles
SVTYPE	1	String	Type of structural variant

```
geno(vcf):
  SimpleList of length 4: GT, GQ, CN, CNQ
geno(header(vcf)):
```

	Number	Type	Description
GT	1	String	Genotype
GQ	1	Float	Genotype quality
CN	1	Integer	Copy number genotype for imprecise events
CNQ	1	Float	Copy number genotype quality for imprecise events

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 in the *input* options.

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

```
> input(param)$output_file

character(0)
```

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

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

The file can be written as a *vcf* or *gvf* by setting the options in the *dataformat* 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 <- VEPParam(dataformat=c(vcf=TRUE),
+                       input=c(output_file="/path/myfile.vcf"), version=88)
> ## Write a gvf file to myfile.gvf:
> myparam <- VEPParam(dataformat=c(gvf=TRUE),
+                       input=c(output_file="/path/myfile.gvf"), version=88)
> ## Write a tab delimited file to myfile.txt:
> myparam <- VEPParam(input=c(output_file="/path/myfile.txt"), version=88)
```

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 *VEP-Param* 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 <- VEPPParam(output=c(regulatory=TRUE), version=88)
> gr <- ensemblVEP(fl, param)
```

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

```
> param <- VEPPParam(input=c(format="vcf"),
+                     output=c(terms="so"),
+                     identifiers=c(symbol=TRUE), version=88)
> gr <- ensemblVEP(fl, param)
```

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

```
> param <- VEPPParam(filterqc=c(coding_only=TRUE),
+                     colocatedVariants=c(check_existing=TRUE),
+                     identifiers=c(symbol=TRUE), version=88)
> 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 <- VEPPParam(output=c(sift="b", polyphen="p"),
                   dataformat=c(vcf=TRUE), version=88)
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	