

# Overview of **ensemblVEP** Pre Ensembl 90

Valerie Obenchain and Lori Shepherd

October 26, 2021

## Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>Results as R objects</b>	<b>1</b>
<b>3</b>	<b>Write results to a file</b>	<b>6</b>
<b>4</b>	<b>Configuring runtime options</b>	<b>7</b>
<b>5</b>	<b>sessionInfo()</b>	<b>8</b>

## 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 R objects 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](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 R objects (**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(0):
```

```
colocatedVariants(0):
```

```
dataformat(0):
```

```
basic(0):
```

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

```

cache(3): dir, dir_cache, dir_plugins
output(1): terms
filterqc(0):
database(1): 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
	<factor>	<factor>	<factor>	<factor>
rs6054257	<NA>	<NA>	<NA>	<NA>
20:17330_T/A	<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 6

```
[[1]] -|intergenic_variant|MODIFIER|
[[2]] deletion|intron_variant&non_coding_transcript_variant&feature_truncatio...
[[3]] deletion|intergenic_variant|MODIFIER|
[[4]] insertion|intron_variant&feature_elongation|MODIFIER|SETD5|ENSG00000168...
[[5]] duplication|upstream_gene_variant|MODIFIER|RAF1|ENSG00000132155|Transcr...
[[6]] duplication|intron_variant&non_coding_transcript_variant&feature_elonga...
```

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
		<Rle>
1:2827693_CCGTGGATGCGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		1
	2:321682_T/<DEL>	2
	2:321682_T/<DEL>	2
		ranges
		<IRanges>
1:2827693_CCGTGGATGCGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C	2827693-2827762	
	2:321682_T/<DEL>	321682
	2:321682_T/<DEL>	321682

		strand
		<Rle>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		*
	2:321682_T/<DEL>	*
	2:321682_T/<DEL>	*
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		
	2:321682_T/<DEL>	
	2:321682_T/<DEL>	
		VCFRowID
		<integer>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		2
	2:321682_T/<DEL>	3
	2:321682_T/<DEL>	3
		Allele
		<character>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		-
	2:321682_T/<DEL>	deletion
	2:321682_T/<DEL>	deletion
		Consequence
		<character>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		intergenic_variant
	2:321682_T/<DEL>	intron_variant&non_c..
	2:321682_T/<DEL>	intron_variant&non_c..
		IMPACT
		<character>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		MODIFIER
	2:321682_T/<DEL>	MODIFIER
	2:321682_T/<DEL>	MODIFIER
		SYMBOL
		<character>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	LINC01865
	2:321682_T/<DEL>	LINC01865
		Gene
		<character>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	ENSG00000233684
	2:321682_T/<DEL>	ENSG00000233684
		Feature_type
		<character>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	Transcript
	2:321682_T/<DEL>	Transcript
		Feature
		<character>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	ENST00000430529
	2:321682_T/<DEL>	ENST00000436808
		BIOTYPE
		<character>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	lncRNA
	2:321682_T/<DEL>	lncRNA
		EXON
		<character>
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>

	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	INTRON	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	1/1
	2:321682_T/<DEL>	1/3
	HGVSc	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	HGVSp	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	cDNA_position	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	CDS_position	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	Protein_position	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	Amino_acids	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	Codons	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	Existing_variation	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	DISTANCE	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	<NA>
	2:321682_T/<DEL>	<NA>
	STRAND	
	<character>	
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C		<NA>
	2:321682_T/<DEL>	1
	2:321682_T/<DEL>	1
	FLAGS	

```

1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C
2:321682_T/<DEL>
2:321682_T/<DEL>
SYMBOL_SOURCE
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C
2:321682_T/<DEL>
2:321682_T/<DEL>
HGNC_ID
1:2827693_CCGTGGATGCGGGGACCCGCATCCCCTCTCCCTTCACAGCTGAGTGACCCACATCCCCTCTCCCCTCGCA/C
2:321682_T/<DEL>
2:321682_T/<DEL>
HGNC:52684
HGNC:52684

```

```

-----
seqinfo: 4 sequences 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: 28 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):
  List 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 <- VEPPParam(dataformat=c(vcf=TRUE),
+                       input=c(output_file="/path/myfile.vcf"), version=88)
> ## Write a gvf file to myfile.gvf:
> myparam <- VEPPParam(dataformat=c(gvf=TRUE),
+                       input=c(output_file="/path/myfile.gvf"), version=88)
> ## Write a tab delimited file to myfile.txt:
> myparam <- VEPPParam(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](http://uswest.ensembl.org/info/docs/tools/vep/script/vep_options.html) Below are examples of how to configure the runtime options in the *VEPParam* 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 4.1.1 Patched (2021-08-22 r80813)
```

```
Platform: x86_64-apple-darwin17.0 (64-bit)
```

```
Running under: macOS Mojave 10.14.6
```

```
Matrix products: default
```

```
BLAS: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.0.dylib
```

```
LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
```

```
locale:
```

```
[1] C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
attached base packages:
```

```
[1] stats4      stats      graphics  grDevices  utils      datasets  methods
```

```
[8] base
```

```
other attached packages:
```

```
[1] ensemblVEP_1.36.0      VariantAnnotation_1.40.0  
[3] Rsamtools_2.10.0       Biostrings_2.62.0  
[5] XVector_0.34.0         SummarizedExperiment_1.24.0  
[7] Biobase_2.54.0         MatrixGenerics_1.6.0  
[9] matrixStats_0.61.0     GenomicRanges_1.46.0  
[11] GenomeInfoDb_1.30.0    IRanges_2.28.0  
[13] S4Vectors_0.32.0      BiocGenerics_0.40.0
```

```
loaded via a namespace (and not attached):
```

```
[1] Rcpp_1.0.7              lattice_0.20-45         prettyunits_1.1.1  
[4] png_0.1-7              assertthat_0.2.1       digest_0.6.28  
[7] utf8_1.2.2             BiocFileCache_2.2.0    R6_2.5.1  
[10] RSQLite_2.2.8          httr_1.4.2            pillar_1.6.4  
[13] zlibbioc_1.40.0        rlang_0.4.12          GenomicFeatures_1.46.0  
[16] progress_1.2.2         curl_4.3.2            rstudioapi_0.13  
[19] blob_1.2.2             Matrix_1.3-4          BiocParallel_1.28.0  
[22] stringr_1.4.0          RCurl_1.98-1.5        bit_4.0.4  
[25] biomaRt_2.50.0         DelayedArray_0.20.0    rtracklayer_1.54.0  
[28] compiler_4.1.1         pkgconfig_2.0.3       tidyselect_1.1.1  
[31] KEGGREST_1.34.0        tibble_3.1.5          GenomeInfoDbData_1.2.7  
[34] XML_3.99-0.8           fansi_0.5.0           crayon_1.4.1  
[37] dplyr_1.0.7            dbplyr_2.1.1          GenomicAlignments_1.30.0  
[40] bitops_1.0-7           rappdirs_0.3.3        grid_4.1.1  
[43] lifecycle_1.0.1       DBI_1.1.1             magrittr_2.0.1  
[46] stringi_1.7.5          cachem_1.0.6          xml2_1.3.2  
[49] ellipsis_0.3.2         filelock_1.0.2        vctrs_0.3.8  
[52] generics_0.1.1         rjson_0.2.20          restfulr_0.0.13  
[55] tools_4.1.1           bit64_4.0.5           BSgenome_1.62.0  
[58] glue_1.4.2            purrr_0.3.4           hms_1.1.1  
[61] yaml_2.2.1            parallel_4.1.1        fastmap_1.1.0  
[64] AnnotationDbi_1.56.0   memoise_2.0.0         BiocIO_1.4.0
```