

# Overview of ensemblVEP

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## 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. 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:

*variant\_effect\_predictor.pl*

## 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()
```

```
> param
```

```
class: VEPParam77
```

```
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: 77
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 with 3 ranges and 13 metadata columns:

seqnames	ranges	strand	Allele	Gene
<Rle>	<IRanges>	<Rle>	<factor>	<factor>
rs58108140	1 [10583, 10583]	*	A	ENSG00000223972
rs58108140	1 [10583, 10583]	*	A	ENSG00000227232
rs58108140	1 [10583, 10583]	*	A	ENSG00000223972
Feature	Feature_type	Consequence	cdna_position	
<factor>	<factor>	<factor>	<factor>	
rs58108140	ENST00000456328	Transcript	upstream_gene_variant	<NA>
rs58108140	ENST00000488147	Transcript	downstream_gene_variant	<NA>
rs58108140	ENST00000450305	Transcript	upstream_gene_variant	<NA>
CDS_position	Protein_position	Amino_acids	Codons	
<factor>	<factor>	<factor>	<factor>	
rs58108140	<NA>	<NA>	<NA>	<NA>
rs58108140	<NA>	<NA>	<NA>	<NA>
rs58108140	<NA>	<NA>	<NA>	<NA>
Existing_variation	DISTANCE	STRAND		
<factor>	<factor>	<factor>		
rs58108140	<NA>	1286	1	
rs58108140	<NA>	3821	-1	
rs58108140	<NA>	1427	1	

---

seqlengths:

```

1
NA

```

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))
```

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 5
[[1]] deletion|ENSG00000233684|ENST00000430529|Transcript|intron_variant&non...
[[2]] -||||intergenic_variant|||||||
[[3]] insertion|ENSG00000168137|ENST00000468208|Transcript|intron_variant&non...
[[4]] duplication|ENSG00000132155|ENST00000423275|Transcript|upstream_gene_va...
[[5]] -||||intergenic_variant|||||||
```

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 with 3 ranges and 14 metadata columns:

	seqnames	ranges	strand	VCFRowID
	<Rle>	<IRanges>	<Rle>	<integer>
	2:321682_T/<DEL>	2 [ 321682, 321682]	*	3
	2:321682_T/<DEL>	2 [ 321682, 321682]	*	3
	2:14477084_C/<DEL:ME:ALU>	2 [14477084, 14477084]	*	4
	Allele	Gene	Feature	
	<factor>	<factor>	<factor>	
	2:321682_T/<DEL>	deletion	ENSG00000233684	ENST00000430529
	2:321682_T/<DEL>	deletion	ENSG00000233684	ENST00000436808
	2:14477084_C/<DEL:ME:ALU>	-	<NA>	<NA>
	Feature_type			
	<factor>			
	2:321682_T/<DEL>	Transcript		
	2:321682_T/<DEL>	Transcript		
	2:14477084_C/<DEL:ME:ALU>	<NA>		
			Consequence	
			<factor>	
	2:321682_T/<DEL>	intron_variant&non_coding_transcript_variant&feature_truncation		
	2:321682_T/<DEL>	intron_variant&non_coding_transcript_variant&feature_truncation		
	2:14477084_C/<DEL:ME:ALU>	intergenic_variant		
		cDNA_position	CDS_position	Protein_position

```

                <factor>      <factor>      <factor>
2:321682_T/<DEL>      <NA>      <NA>      <NA>
2:321682_T/<DEL>      <NA>      <NA>      <NA>
2:14477084_C/<DEL:ME:ALU>      <NA>      <NA>      <NA>
      Amino_acids    Codons Existing_variation DISTANCE
      <factor> <factor>      <factor> <factor>
2:321682_T/<DEL>      <NA>      <NA>      <NA>      <NA>
2:321682_T/<DEL>      <NA>      <NA>      <NA>      <NA>
2:14477084_C/<DEL:ME:ALU>      <NA>      <NA>      <NA>      <NA>
      STRAND
      <factor>
2:321682_T/<DEL>      1
2:321682_T/<DEL>      1
2:14477084_C/<DEL:ME:ALU>      <NA>
---
seqlengths:
  2  3  4
NA NA NA

```

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: 22 1
rowData(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 ass...
CIEND       2      Integer Confidence interval around END for imprecise va...
CIPOS       2      Integer Confidence interval around POS for imprecise va...
END         1      Integer End position of the variant described in this r...
HOMLEN      .      Integer Length of base pair identical micro-homology at...
HOMSEQ      .      String  Sequence of base pair identical micro-homology ...
IMPRECISE   0      Flag    Imprecise structural variation
MEINFO      4      String  Mobile element info of the form NAME,START,END,...
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"))
> ## Write a gvf file to myfile.gvf:
> myparam <- VEPParam(dataformat=c(gvf=TRUE),
+                      input=c(output_file="/path/myfile.gvf"))
> ## Write a tab delimited file to myfile.txt:
> myparam <- VEPParam(input=c(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](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 <- VEPParam(output=c(regulatory=TRUE))
> gr <- ensemblVEP(fl, param)
```

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

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

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

```
> param <- VEPParam(filterqc=c(coding_only=TRUE),
+                   colocatedVariants=c(check_existing=TRUE),
+                   identifiers=c(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 <- VEPParam(output=c(sift="b", polyphen="p"),
                  dataformat=c(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 3.1.1 (2014-07-10)

Platform: x86\_64-apple-darwin13.1.0 (64-bit)

locale:

[1] C/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8

attached base packages:

[1] parallel stats graphics grDevices utils datasets methods

[8] base

other attached packages:

[1] ensemblVEP_1.4.4	VariantAnnotation_1.10.5	Rsamtools_1.16.1
[4] Biostrings_2.32.1	XVector_0.4.0	GenomicRanges_1.16.4
[7] GenomeInfoDb_1.0.2	IRanges_1.22.10	BiocGenerics_0.10.0

loaded via a namespace (and not attached):

[1] AnnotationDbi_1.26.1	BBmisc_1.7	BSgenome_1.32.0
[4] BatchJobs_1.4	Biobase_2.24.0	BiocParallel_0.6.1
[7] DBI_0.3.1	GenomicAlignments_1.0.6	GenomicFeatures_1.16.3
[10] RCurl_1.95-4.3	RSQLite_0.11.4	XML_3.98-1.1
[13] base64enc_0.1-2	biomaRt_2.20.0	bitops_1.0-6
[16] brew_1.0-6	checkmate_1.4	codetools_0.2-9
[19] digest_0.6.4	fail_1.2	foreach_1.4.2
[22] iterators_1.0.7	rtracklayer_1.24.2	sendmailR_1.2-1
[25] stats4_3.1.1	stringr_0.6.2	tools_3.1.1
[28] zlibbioc_1.10.0		