

SnpEff Annotation and Filtration Element

Annotates and filters variations with SnpEff.

Parameters in GUI

Parameter	Description	Default value
Output directory	Select an output directory. Custom - specify the output directory in the 'Custom directory' parameter. Workflow - internal workflow directory. Input file - the directory of the input file.	Input file
Input format	Select the input format of variations.	VCF
Output format	Select the format of annotated output files.	VCF
Genome	Select the target genome from the list of SnpEff databases. Genome data will be downloaded if it is not found. The list of databases depends on the SnpEff external tool version.	Homo sapiens
Upstream /downstream length	Upstream and downstream interval size. Eliminate any upstream and downstream effect by using 0 length.	No upstream /downstream interval (0 bases)
Cannonical transcripts	Use only canonical transcripts.	False
HGVS nomenclature	Annotate using HGVS nomenclature.	False
Annotate loss of function	Annotate Loss of function (LOF) and Nonsense mediated decay (NMD).	False
Annotate TFBSs motifs	Annotate transcription factor binding site motifs (only available for latest GRCh37).	False

Parameters in Workflow File

Type: seff

Parameter	Parameter in the GUI	Type
out-mode	Output directory	string
inp-format	Input format	string
out-format	Output format	string
genome	Genome	string
updown-length	Upstream/downstream length	numeric
canon	Cannonical transcripts	boolean
hgvs	HGVS nomenclature	boolean
lof	Annotate loss of function	boolean
motif	Annotate TFBSs motifs	boolean

Input/Output Ports

The element has 1 *input port*.

Name in GUI: Variations

Name in Workflow File: in-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source url	url	string

And 1 *output port*.

Name in GUI: Annotated variations

Name in Workflow File: out-file

Slots:

Slot In GUI	Slot in Workflow File	Type
Source url	url	<i>variation</i>