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. Wor kflow - 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 cannonical 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**	*variation*