SnpEff Annotation and Filtration Element

Annotates and filters variations with SnpEff.

Element type: seff

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
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	**out-mode**	*string*
Input format	Select the input format of variations.	VCF	**inp-format**	*string*
Output format	Select the format of annotated output files.	VCF	**out-format**	*string*
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	**genome**	*string*
Upstream /downstream length	Upstream and downstream interval size. Eliminate any upstream and downstream effect by using 0 length.	No upstream /downstream interval (0 bases)	**updown-length**	*numeric*
Cannonical transcripts	Use only cannonical transcripts.	False	**canon**	*boolean*
HGVS nomenclature	Annotate using HGVS nomenclature.	False	**hgvs**	*boolean*
Annotate loss of function	Annotate Loss of function (LOF) and Nonsense mediated decay (NMD).	False	**lof**	*boolean*
Annotate TFBSs motifs	Annotate transcription factor binding site motifs (only available for latest GRCh37).	False	**motif**	*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*