

Managing Parameters

When you select an [element](#) on the [Scene](#) the [Property Editor](#) displays detailed information about it: it's name, description, parameters, [input](#) and [output](#) ports, etc. To change the name of the element displayed on the Scene edit the *Element name* value.

All the parameters available for the element are displayed in the *Parameters* area. Some parameters must have a value, they are displayed in bold. Notice, that when you select a parameter, it's description is shown below. To modify a value click on it. Depending on the parameter's type you may be required to either input a value or browse for a file(s). Also you can configure slots of a connected input port by selecting different (matching) data available through the dataflow. More advanced users can use their own scripts to set a parameter's value, read chapter [Using Script to Set Parameter Value](#) to learn more. The image below shows the *Property Editor*.

Element description

Element parameters

Port's and slot's parameters

Element parameter's description

Property Editor

Element name: Annotate and Predict Effects with SnpEff

SnpEff annotation and filtration : Annotates and filters variations with SnpEff.

To configure the parameters of the element go to "Parameters" area below.

Name	Value
Output directory	Workflow
Input format	VCF
Output format	VCF (only if VCF input)
Genome	Homo sapiens (hg19)
Upstream/downstream length	No upstream/downstream (0 bases)
Canonical transcripts	False
HGVs nomenclature	False
Annotate Loss of function	False
Annotate TFBSs motifs	False

Input data

Slots	Data source
Source URL	Produced URL (by Chan... for Variations File)

Output data

Dataset name (by Input Variations File)
Source URL (by Input Variations File)
Produced URL (by Change Chrom...Notation for Variations File)
Source URL (by Annotate and Predict Effects with SnpEff)

Upstream/downstream length : Upstream and downstream interval size. Eliminate any upstream and downstream effect by using 0 length

For [Data Readers](#) you can manipulate with file(s) or directory(ies) with a help of dataset(s):

Up, down, delete

Add dataset

Add directory

Add file(s)

Also, to remove files from dataset you can select it and press the *Delete* button.

For [Data Writers](#), if the *Output file* parameter is empty, UGENE will generate output files names automatically. You can use the *Output file suffix* parameter to manipulate it.