

# Managing Parameters

When you select an *element* on the *Scene* the *Property Editor* displays detailed information about it: its 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, its 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*.

The screenshot shows a workflow with three elements: 'Input Variations File', 'Change Chromosome Notation for Variations File', and 'Annotate and Predict Effects with SnpEff'. The 'Annotate and Predict Effects with SnpEff' element is selected, and its 'Property Editor' is open on the right. The editor shows the element's name, description, and a list of parameters. Red arrows point to specific parts of the interface: 'Element description' points to the top of the Property Editor; 'Element parameters' points to the parameter list; 'Port's and slot's parameters' points to the 'Input data' section; and 'Element parameter's description' points to the detailed description of the 'Upstream/downstream length' parameter.

**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.

**Parameters**

Name	Value
Output directory	Workflow
Input format	VCF
Output format	VCF (only if VCF input)
Genome	Homo sapiens (hg19)
<b>Upstream/downstream length</b>	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):

The image shows a close-up of the 'Parameters' section, specifically the 'Dataset 1' area. It features a list of datasets, with 'FAS' currently selected. Above the list are icons for adding, deleting, and moving datasets. Red arrows and text labels identify these functions: 'Up, down, delete' points to the navigation icons; 'Add dataset' points to a green plus icon; 'Add directory' points to a folder icon; and 'Add file(s)' points to a document icon.

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.