

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 the UGENE software interface. On the left, a workflow is visible with three elements: 'Input Variations File', 'Change Chromosome Notation for Variations File', and 'Annotate and Predict Effects with SnpEff'. On the right, the 'Property Editor' for the selected element is open. It contains several sections: 'Element description', 'Parameters' (a table of element settings), 'Input data' (a table of input port slots), 'Output data' (a table of output port slots), and a detailed description for the selected 'Upstream/downstream length' parameter.

Element description

Element parameters

Port's and slot's parameters

Element parameter's description

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

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

Dataset name (by Input Variations File)
Source URL (by Input Variations File)
Produced URL (by Change Chrom... 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):

This close-up shows the 'Dataset 1' list in the 'Parameters' section. It contains a list of datasets, with 'FAS' currently selected. Above the list are icons for adding files, directories, and datasets, and buttons for moving (up/down) and deleting items.

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.