

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*.

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):

Parameters

Dataset 1 X

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.