

# Variation Annotation with SnpEff

SnpEff is a variant annotation and effect prediction tool. It annotates and predicts the effects of genetic variants (such as amino acid changes).

A typical SnpEff use case would be:

- Input: The inputs are predicted variants (SNPs, insertions, deletions and MNPs). The input file is usually obtained as a result of a sequencing experiment, and it is usually in variant call format (VCF).
- Output: SnpEff analyzes the input variants. It annotates the variants and calculates the effects they produce on known genes (e.g. amino acid changes).



## How to Use This Sample

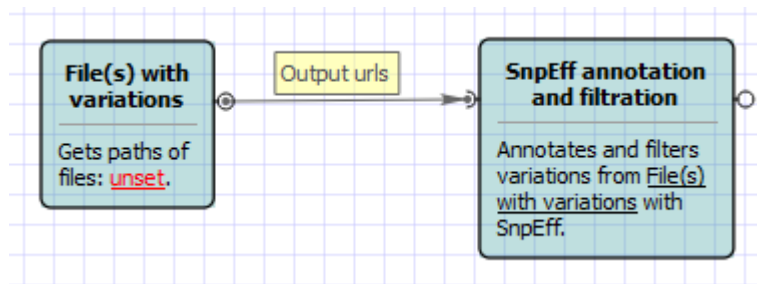
If you haven't used the workflow samples in UGENE before, look at the "[How to Use Sample Workflows](#)" section of the documentation.

## Workflow Sample Location

The workflow sample "Variation Annotation with SnpEff" can be found in the "NGS" section of the Workflow Designer samples.

## Workflow Image

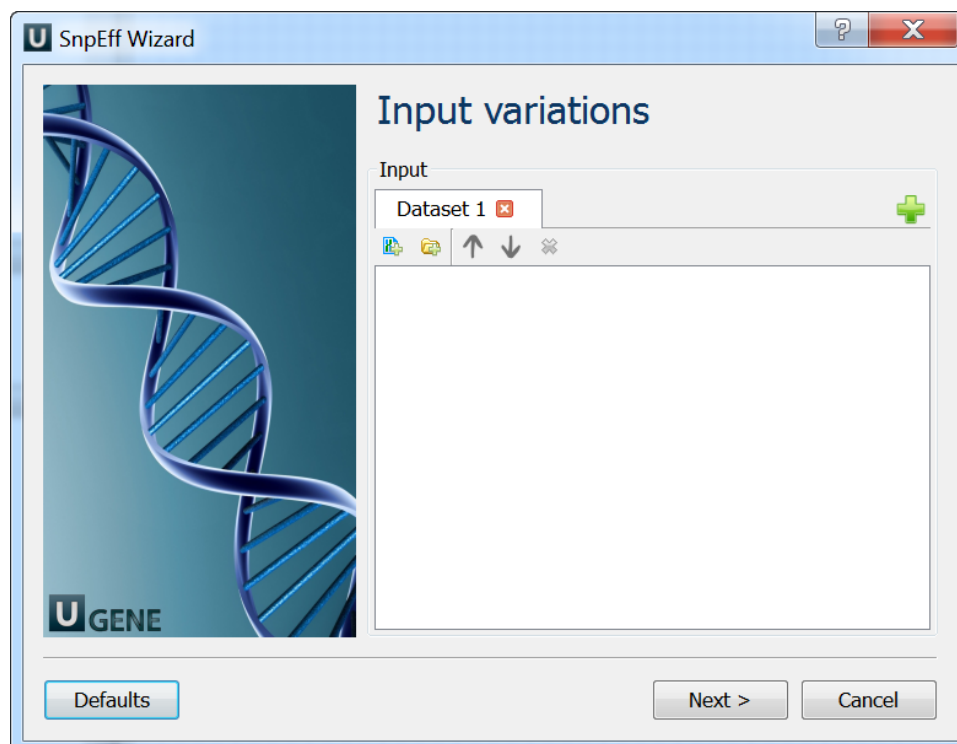
The opened workflow looks as follows:



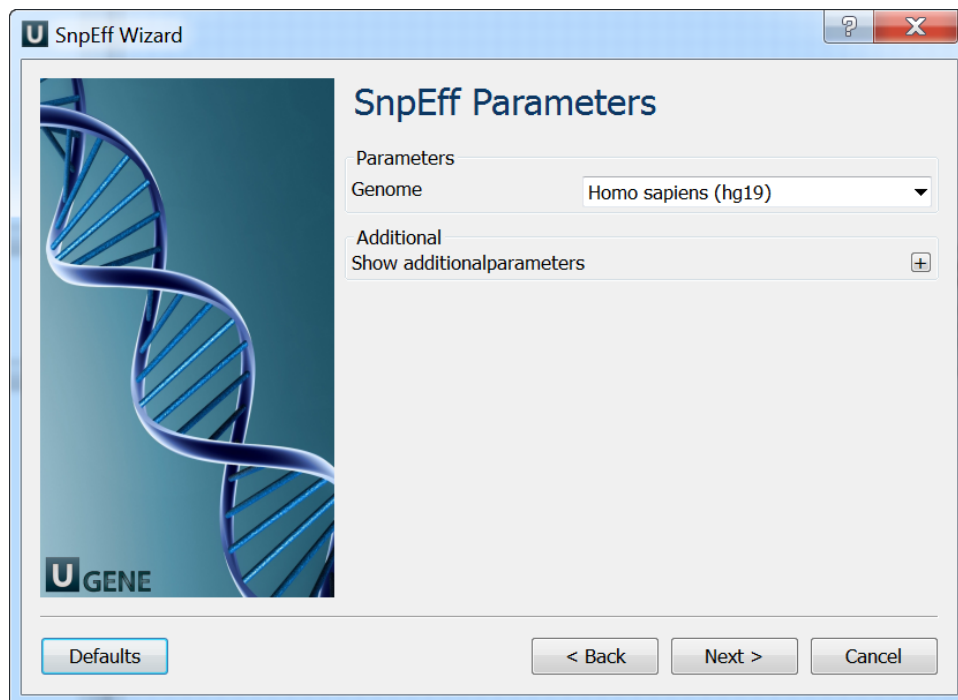
## Workflow Wizard

The wizard has 3 pages.

1. Input Variations: On this page you must input variations file(s).



2. SnpEff Parameters: On this page you can modify SnpEff parameters.



3. Output: On this page you need input output parameters.

