Annotate variations with SNPToolbox Element

Assess damage effect and find intersected genes with SNPToolbox algorithms.

Parameters in GUI

Parameter	Description	Default value
Database path	Path to SNPToolbox database with sequences, features and damage effect data.	

Parameters in Workflow File

Type: SNPToolbox-id

Parameter	Parameter in the GUI	Type
db_path	**Database path**	*string*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Input variations

Name in Workflow File: in-variations

Slots:

Slot In GUI	Slot in Workflow File	Type
Variation track	**variation-track**	*variation*

And 1 *output port*:

Name in GUI: Output variations

Name in Workflow File: out-variations