

# 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