

# Improve Classification with WEVOTE Element

WEVOTE (WEighted VOting Taxonomic idEntification) is a metagenome shotgun sequencing DNA reads classifier based on an ensemble of other classification methods (Kraken, CLARK, etc.).

**Element type:** wevote-classify

## Parameters

Parameter	Description	Defaultvalue	Parameter in Workflow File	Type
<b>Penalty</b>	Score penalty for disagreements (-k)	2	<b>penalty</b>	<i>number</i>
<b>Number of agreed tools</b>	Specify the minimum number of tools agreed on WEVOTE decision (-a).	0	<b>number-of-agreed-tools</b>	<i>number</i>
<b>Score threshold</b>	Score threshold (-s)	0	<b>score-threshold</b>	<i>number</i>
<b>Number of threads</b>	Use multiple threads (-n).	8	<b>threads</b>	<i>number</i>
<b>Output file</b>	Specify the output text file name.	auto	<b>output-url</b>	<i>string</i>

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** Input classification CSV file:

Input a CSV file in the following format: 1) a sequence name 2) taxID from the first tool 3) taxID from the second tool 4) etc.

**Name in Workflow File:** in

**Slots:**

SlotInGUI	Slot in Workflow File	Type
<b>Input URL</b>	<b>url</b>	<i>string</i>

The element has 1 *output port*:

**Name in GUI:** WEVOTE Classification:

A map of sequence names with the associated taxonomy IDs.

**Name in Workflow File:** out

**Slots:**

SlotInGUI	Slot in Workflow File	Type
<b>Taxonomy classification data</b>	<b>tax-data</b>	<i>tax-classification</i>