

# Improve Classification with WEVOTE

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

## Parameters in GUI

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

# Parameters in Workflow File

Type: wevote-classify

Parameter	Parameter in the GUI	Type
penalty	Penalty	<i>number</i>
number-of-agreed-tools	Number of agreed tools	<i>number</i>
score-threshold	Score threshold	<i>number</i>
threads	Number of threads	<i>number</i>
output-url	Output file	<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
Input URL	url	<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
Taxonomy classification data	tax-data	<i>tax-classification</i>