# Improve Classification with WEVOTE

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

## Parameters in GUI

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

## Parameters in Workflow File
**Type:** wevote-classify

| Parameter | Parameter in the GUI | Type |
|---|---|---|
| **penalty** | **Penalty** | *number* |
| **number-of-agreed-tools** | **Number of agreed tools** | *number* |
| **score-threshold** | **Score threshold** | *number* |
| **threads** | **Number of threads** | *number* |
| **output-url** | **Output file** | *string* |

## 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** | *string* |

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** | *tax-classification* |