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*