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