Classification Report Element

Based on the input taxonomy classification data the element generates a detailed report and saves it in a tab-delimited text format.

Parameters in GUI

Parameter	Description	Defaultvalue
Output file	Specify the output text file name.	
All taxa	By default, taxa with no sequences (reads or contigs) assigned are not included into the output. This option specifies to include all taxa. This may be useful when an output from several samples is compared. Set "Sort by" to "Tax ID" in this case.	False
Sort by	It is possible to sort rows in the output file in two ways: • by the number of reads, covered by the clade rooted at the taxon(i.e. "clade_num" for this taxID) • by taxIDs The second option may be useful when an output from different samples is compared.	Tax ID

Parameters in Workflow File

Type: classification-report

Parameter	Parameter in the GUI	Type
output-url	**Output file**	*string*
all-taxa	**All taxa**	*bool*
sort-by	**Sort by**	*string*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Input taxonomy data

Name in Workflow File: in

Slots:

SlotInGUI	Slot in Workflow File	Type
Taxonomy classification data	**tax-data**	*tax-classification*