Align with MUSCLE Element

MUSCLE is public domain multiple alignment software for protein and nucleotide sequences. MUSCLE stands for MUltiple Sequence Comparison by Log-Expectation.

Parameters in GUI

Parameter	Description	Default value
Mode	Selector of preset configurations, that give you the choice of optimizing accuracy, speed, or some compromise between the two. The default favors accuracy.	MUSCLE default
Stable order	Do not rearrange aligned sequences (-stable switch of MUSCLE). Otherwise, MUSCLE re-arranges sequences so that similar sequences are adjacent in the output file. This makes the alignment easier to evaluate by eye.	True

Parameters in Workflow File

Type: muscle

Parameter	Parameter in the GUI	Type
mode	**Mode**	*numeric* Availables values are: • 0 - for MUSCLE default • 1 - for Large alignment • 2 - for Refine only
stable	**Stable order**	*boolean*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: *Input MSA*

Name in Workflow File: in-msa

Slots:

Slot In GUI	Slot in Workflow File	Type
MSA	**msa**	*msa*

And 1 *output port*:

Name in GUI: *Multiple sequence alignment*

Name in Workflow File: out-msa

Slots:

Slot In GUI	Slot in Workflow File	Type
MSA	**msa**	*msa*