Align with Kalign Element

Aligns multiple sequence alignments (MSAs) supplied with Kalign. Kalign is a fast and accurate multiple sequence alignment tool. The original version of the tool can be found onhttp://msa.sbc.su.se.

Element type: kalign

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Gap extension penalty	The penalty for extending a gap.	8.52	**gap-ext-penalty**	*numeric*
Gap open penalty	The penalty for opening/closing a gap. Half the value will be subtracted from the alignment score when opening, and half when closing a gap.	54.90	**gap-open-penalty**	*numeric*
Terminal gap penalty	The penalty to extend gaps from the N/C terminal of protein or 5'/3' terminal of nucleotide sequences.	4.42	**terminal-gap-penalty**	*numeric*
Bonus score	A bonus score that is added to each pair of aligned residues.	0.02	**bonus-score**	*numeric*

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: *Kalign result MSA*

Name in Workflow File: out-msa

Slots:

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