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.

Parameters in GUI

Parameter	Description	Default value
Gap extension penalty	The penalty for extending a gap.	8.52
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
Terminal gap penalty	The penalty to extend gaps from the N/C terminal of protein or 5'/3' terminal of nucleotide sequences.	4.42
Bonus score	A bonus score that is added to each pair of aligned residues.	0.02

Parameters in Workflow File

Type: kalign

Parameter	Parameter in the GUI	Type
gap-ext-penalty	**Gap extension penalty**	*numeric*
gap-open-penalty	**Gap open penalty**	*numeric*
terminal-gap-penalty	**Terminal gap penalty**	*numeric*
bonus-score	**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*