Align with ClustalW Element

Aligns multiple sequence alignments (MSAs) supplied with ClustalW.

ClustalW is a general-purpose multiple sequence alignment program for DNA or proteins. Visit http://www.clustal.org/ to learn more about it.

> Clustal is used as an external tool from UGENE and it must be installed on your system. To learn more about the external tools, please, read the main UGENE User Manual.

Element type: clustalw

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Weight matrix	For proteins, it is a scoring table which describes the similarity of each amino acid to each other. For DNA it is the scores assigned to matches and mismatches.	default	**matrix**	*numeric* Available values are: • 0 - for IUB • 1 - for ClustalW • 2 - for BLOSUM • 3 - for PAM • 4 - for GONNET • 5 - for ID • -1 - for default matrix
End gaps	The penalty for closing a gap.	False	**close-gap-penalty**	*boolean*
Gap distance	The gap separation penalty. Tries to decrease the chances of gaps being too close to each other.	4.42	**gap-distance**	*numeric*
Gap extension penalty	The penalty for extending a gap.	8.52	**gap-ext-penalty**	*numeric*
Gap open penalty	The penalty for opening a gap.	53.90	**gap-open-penalty**	*numeric*
Hydrophilic gaps off	Hydrophilic gap penalties are used to increase the chances of a gap within a run (5 or more residues) of hydrophilic amino acids.	False	**no-hydrophilic-gaps**	*boolean*
Residue-specific gaps off	Residue-specific penalties are amino specific gap penalties that reduce or increase the gap opening penalties at each position in the alignment.	False	**no-residue-specific-gaps**	*boolean*
Iteration type	Alignment improvement iteration type.	None	**iteration-type**	*numeric* Available values are: • 0 - for None • 1 - for Tree • 2 - for Alignment
Number of iterations	The maximum number of iterations to perform.	3	**iterations-max-num**	*numeric*
Tool path (required)	Path to the ClustalW tool. The default path can be set in the UGENE Application Settings.	default	**path**	*string*
Temporary directory	Directory to store temporary files.	default	**temp-dir**	*string*

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: *ClustalW result MSA*

Name in Workflow File: out-msa

Slots:

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