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 main UGENE User Manual.

Parameters in GUI

Parameter	Description	Default value
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
End gaps	The penalty for closing a gap.	False
Gap distance	The gap separation penalty. Tries to decrease the chances of gaps being too close to each other.	4.42
Gap extension penalty	The penalty for extending a gap.	8.52
Gap open penalty	The penalty for opening a gap.	53.90
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
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
Iteration type	Alignment improvement iteration type.	None
Number of iterations	The maximum number of iterations to perform.	3
Tool path (required)	Path to the ClustalW tool. The default path can be set in the UGENE Application Settings.	default
Temporary directory	Directory to store temporary files.	default

Parameters in Workflow File

Type: clustalw

Parameter	Parameter in the GUI	Type
matrix	**Weight 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
close-gap-penalty	**End gaps**	*boolean*
gap-distance	**Gap distance**	*numeric*
gap-ext-penalty	**Gap extension penalty**	*numeric*
gap-open-penalty	**Gap open penalty**	*numeric*

no-hydrophilic-gaps	**Hydrophilic gaps off**	*boolean*
no-residue-specific-gaps	**Residue-specific gaps off**	*boolean*
iteration-type	**Iteration type**	*numeric* Available values are: • 0 - for None • 1 - for Tree • 2 - for Alignment
iterations-max-num	**Number of iterations**	*numeric*
path	**Tool path**	*string*
temp-dir	**Temporary directory**	*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*