Build Weight Matrix Element

Builds a weight matrix. Weight matrices are used for probabilistic recognition of transcription factor binding sites.

Element type: wmatrix-build

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Matrix type (required)	Dinucleic matrices are more detailed, while mononucleic one is more useful for small input data sets.	Mononucleic	**type**	*boolean* Available values are: • true - for Dinucleic • false - for Mononucleic
Weight algorithm	Different weight algorithms use different functions to build weight matrices. It allows us to get better precision on different data sets. Log-odds, NLG, and Match algorithms are sensitive to input matrices with zero values, so some of them may not work on those matrices.	Berg and Von Hippel	**weight-algorithm**	*string* Available values are: • Berg and von Hippel • Log-odds • Match • NLG

Input/Output Ports

The element has 1 *input port*:

Name in GUI: *Input alignment*

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: *Weight matrix*

Name in Workflow File: out-wmatrix

Slots:

Slot In GUI	Slot in Workflow File	Type
Weight matrix	**wmatrix**	*wmatrix*