

# 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
<b>Matrix type</b> (required)	Dinucleic matrices are more detailed, while mononucleic one is more useful for small input data sets.	Mononucleic	<b>type</b>	<i>boolean</i>  Available values are: <ul style="list-style-type: none"><li>• true - for Dinucleic</li><li>• false - for Mononucleic</li></ul>
<b>Weight algorithm</b>	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	<b>weight-algorithm</b>	<i>string</i>  Available values are: <ul style="list-style-type: none"><li>• Berg and von Hippel</li><li>• Log-odds</li><li>• Match</li><li>• NLG</li></ul>

## 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	<i>wmatrix</i>