

# 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><br><br>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><br><br>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> |