

# HMM2 Build Element

Builds a HMM profile from a multiple sequence alignment. The HMM profile is a statistical model which captures position-specific information about how conserved each column of the alignment is, and which residues are likely.

## Parameters in GUI

Parameter	Description	Default value
<b>Profile name</b>	Descriptive name of the HMM profile.	
<b>HMM strategy</b>	Specifies the kind of alignments you want to allow.	hmmls
<b>Calibrate profile</b>	Enables/disables optional profile calibration. An empirical HMM calibration costs time but it only has to be done once per model, and can greatly increase the sensitivity of a database search.	True
<b>Parallel calibration</b>	Number of parallel threads that the calibration will run in.	1
<b>Standard deviation</b>	Standard deviation of the synthetic sequence length. A positive number. Note that the Gaussian is left-truncated so that no sequences have lengths.	200.0
<b>Fixed length of samples</b>	Fixes the length of the random sequences to, where is a positive (and reasonably sized) integer. The default is instead to generate sequences with a variety of different lengths, controlled by a Gaussian (normal) distribution.	0
<b>Mean length of samples</b>	Mean length of the synthetic sequences, positive real number.	325
<b>Number of samples</b>	Number of synthetic sequences. If is less than about 1000, the fit to the EVD may fail Higher numbers of will give better determined EVD parameters. The default is 5000; it was empirically chosen as a tradeoff between accuracy and computation time.	5000
<b>Random seed</b>	The random seed, where is a positive integer. The default is to use time() to generate a different seed for each run, which means that two different runs of hmmcalibrate on the same HMM will give slightly different results. You can use this option to generate reproducible results for different hmmcalibrate runs on the same HMM.	0

## Parameters in Workflow File

Type: hmm2-build

Parameter	Parameter in the GUI	Type
<b>profile-name</b>	<b>Profile name</b>	<i>string</i>
<b>strategy</b>	<b>HMM strategy</b>	<i>numeric</i>  Available values are: <ul style="list-style-type: none"><li>• 0 - for hmms</li><li>• 1 - for hmmls</li><li>• 2 - for hmmsfs</li><li>• 3 - for hmmsw</li></ul>
<b>calibrate</b>	<b>Calibrate profile</b>	<i>boolean</i>
<b>calibration-threads</b>	<b>Parallel calibration</b>	<i>numeric</i>
<b>deviation</b>	<b>Standard deviation</b>	<i>numeric</i>
<b>fix-samples-length</b>	<b>Fixed length of samples</b>	<i>numeric</i>
<b>mean-samples-length</b>	<b>Mean length of samples</b>	<i>numeric</i>
<b>samples-num</b>	<b>Number of samples</b>	<i>numeric</i>
<b>seed</b>	<b>Random seed</b>	<i>numeric</i>

## 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	<i>msa</i>

And 1 *output port*:

**Name in GUI:** *HMM profile*

**Name in Workflow File:** out-hmm2

Slots:

Slot In GUI	Slot in Workflow File	Type
HMM profile	hmm2-profile	<i>hmm2-profile</i>