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.

Element type: hmm2-build

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Profile name	Descriptive name of the HMM profile.		**profile-name**	*string*
HMM strategy	Specifies the kind of alignments you want to allow.	hmmls	**strategy**	*numeric* Available values are: • 0 - for hmms • 1 - for hmmls • 2 - for hmmfs • 3 - for hmmsw
Calibrate profile	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	**calibrate**	*boolean*
Parallel calibration	Number of parallel threads that the calibration will run in.	1	**calibration-threads**	*numeric*
Standard deviation	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	**deviation**	*numeric*
Fixed length of samples	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	**fix-samples-length**	*numeric*
Mean length of samples	Mean length of the synthetic sequences, positive real number.	325	**mean-samples-length**	*numeric*
Number of samples	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	**samples-num**	*numeric*
Random seed	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	**seed**	*numeric*

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: *HMM profile*

Name in Workflow File: out-hmm2

Slots:

Slot In GUI	Slot in Workflow File	Type
HMM profile	**hmm2-profile**	*hmm2-profile*