

HMM3 Algorithm Element

Searches a sequence for significantly similar sequence matches with one or more profile HMM and saves the results as annotations.

The search is performed using HMMER3 `hmmsearch` tool integrated into UGENE.

Parameters in GUI

General parameters:

Parameter	Description	Default value
Annotate As	Name of the result annotations.	hmm_signal
Profile HMM	Semicolon-separated list of input HMM files.	You must specify a value!
Min Length	Minimum length of a result region.	30
Max Length	Maximum length of a result region.	5000

Parameters controlling reporting threshold:

Reporting thresholds controls which hits are reported.

Parameter	Description	Default value
Use E-value	Filter by E-value if true. Otherwise, filters by score.	True
Filter by High E-value	Reports domains \leq this E-value threshold in output (<code>hmmsearch-domE</code> option).	1e+1
Filter by Low Score	Reports domains \geq this score cutoff in output (<code>hmmsearch-domT</code> option).	0.01

Parameters controlling the acceleration pipeline:

HMMER3 searches are accelerated in a three-step filter pipeline: the MSV filter, the Viterbi filter, and the Forward filter. The first filter is the fastest and most approximate; the last is the full Forward scoring algorithm. There is also a bias filter step between MSV and Viterbi.

Parameter	Description	Default value
Max	Turns off all acceleration heuristic filters. This increases sensitivity somewhat, at a large cost in speed.	False
MSV Filter Threshold	P-value threshold for the MSV filter step.	0.02
Viterbi Filter Threshold	P-value threshold for the Viterbi filter step.	0.001
Forward Filter Threshold	P-value threshold for the Forward filter step.	1e-5
No Bias Filter	Turns off composition bias filter. This increases sensitivity somewhat, but can come at a high cost in speed.	False

Other parameters:

Parameter	Description	Default value
No Null2	Turns off the null2 score corrections for biased composition.	False
Number of Sequences	Specifies number of significant sequences. It is used for domain E-value calculations (<code>hmmsearch-domZ</code> option).	1 (i.e. one input sequence)
Seed	Random number seed. The default is to use a fixed seed(42), so that results are exactly reproducible. Any other positive integer will give different (but also reproducible) results. A choice of 0 uses a randomly chosen seed.	42

Parameters in Schema File

Type: hmm3

Parameter	Parameter in the GUI	Type
key	Annotate As	<i>string</i>
min-len	Min Length	<i>string</i>
max-len	Max Length	<i>string</i>
hmm-profile	Profile HMM	<i>string</i>
use-e-val	Use E-value	<i>boolean</i>
e-val	Filter by High E-value	<i>numeric</i>
score	Filter by Low Score	<i>numeric</i>
do-max	Max	<i>boolean</i>
msv-filter-threshold	MSV Filter Threshold	<i>numeric</i>
viterbi-filter-threshold	Viterbi Filter Threshold	<i>numeric</i>
forward-filter-threshold	Forward Filter Threshold	<i>numeric</i>
no-bias-filter	No Bias Filter	<i>boolean</i>
no-score-corrections	No Null2	<i>boolean</i>
seqs-num	Number of Sequences	<i>numeric</i>
random-generator-seed	Seed	<i>numeric</i>