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 <= this E-value threshold in output (hmmsearch-domE option).	1e+1
Filter by Low Score	Reports domains >= this score cutoff in output (hmmsearch-domT 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 (hmmsearch-domZ 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	Туре
key	Annotate As	string
min-len	Min Length	string
max-len	Max Length	string
hmm-profile	Profile HMM	string
use-e-val	Use E-value	boolean
e-val	Filter by High E-value	numeric
score	Filter by Low Score	numeric
do-max	Max	boolean
msv-filter-threshold	MSV Filter Threshold	numeric
viterbi-filter-threshold	Viterbi Filter Threshold	numeric
forward-filter-threshold	Forward Filter Threshold	numeric
no-bias-filter	No Bias Filter	boolean
no-score-corrections	No Null2	boolean
seqs-num	Number of Sequences	numeric
random-generator-seed	Seed	numeric