

Searching Sequence Using HMM Profile (HMM3 Search)

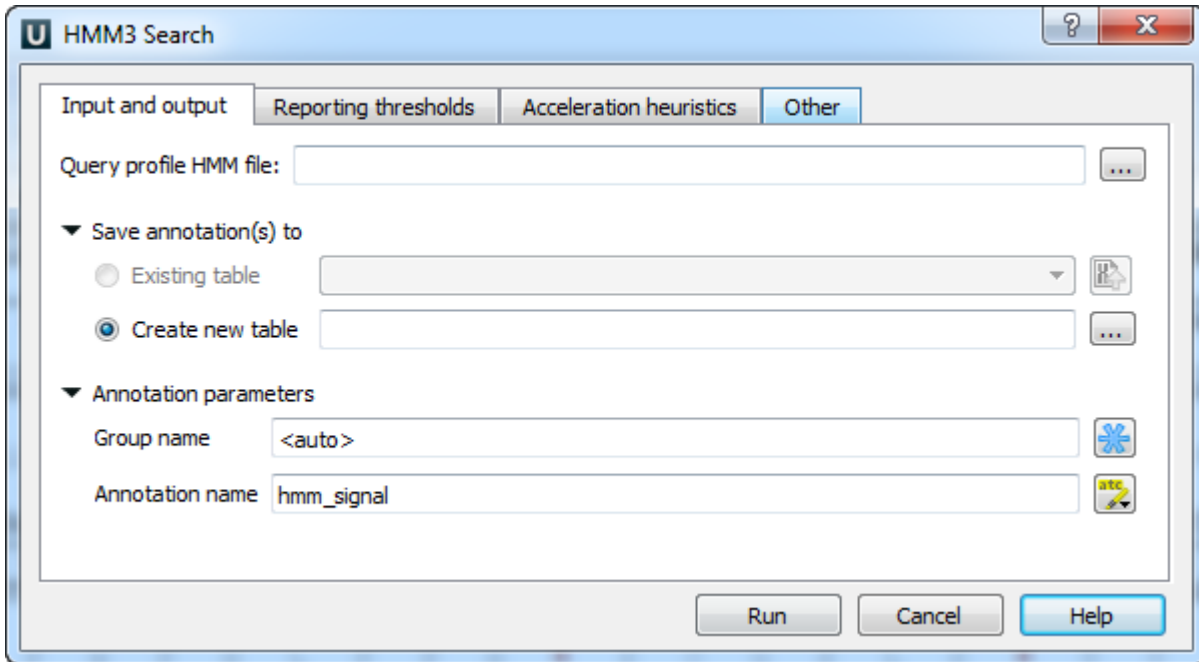
The *HMM3 search* tool reads a HMM profile from a file and searches a sequence for significantly similar sequence matches.

The sequence must be selected in the *Project View* or there must be an active *Sequence View* window opened.

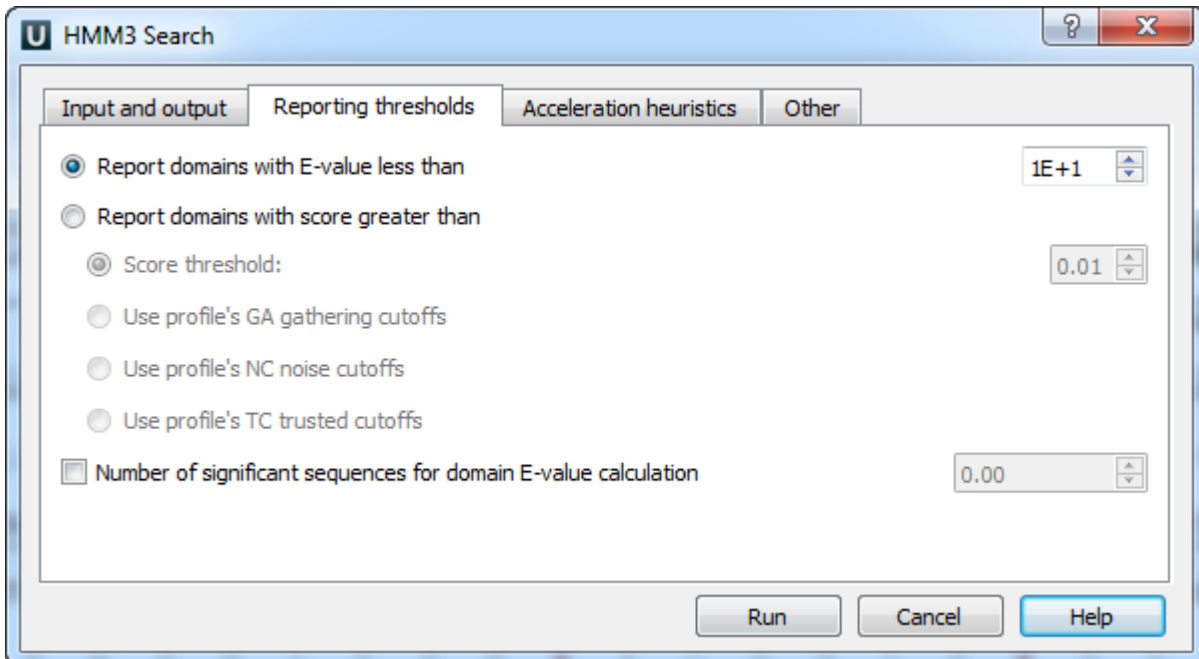
If the selected sequence is nucleic and profile HMM is built from amino alignment, the sequence will be automatically translated and searched in all possible frames (6 totally).

If a profile HMM is built for nucleic alignment, the search is performed for both strands (direct and complement).

The *HMM3 search* accepts the HMMER2 HMM profiles (amino only) as a backward compatibility feature. An interesting post about using the HMMER2 models with the HMMER3 is available on the [Sean Eddy's blog](#).



For example, reporting thresholds options can be configured using the dialog:



The search results are stored as sequence annotations in the Genbank file format.

gi|2136280|pir||I38344 titin - human

Annotations [MyDocument_3.gb] *

Name	Value
hmm_signal (0, 24024)	
hmm_signal	6594..6679
hmm_signal	6695..6781
hmm_signal	6796..6882
hmm_signal	6992..7076
hmm_signal	7092..7177
Accuracy per residue	9.76351e-01
Bias	3.53754e-02
Conditional e-value	5.96204e-17
Envelope of domain location	7091...7177
HMM model	fn3 Accession number in PFAM database: PF00041
HMM region	1...87
Independent e-value	1.89874e-17
Score	49.864132
hmm_signal	7288..7372
hmm_signal	7387..7473

! The *HMM3* search works only with files that contain a single HMM model.