

Searching Sequence Using HMM Profile

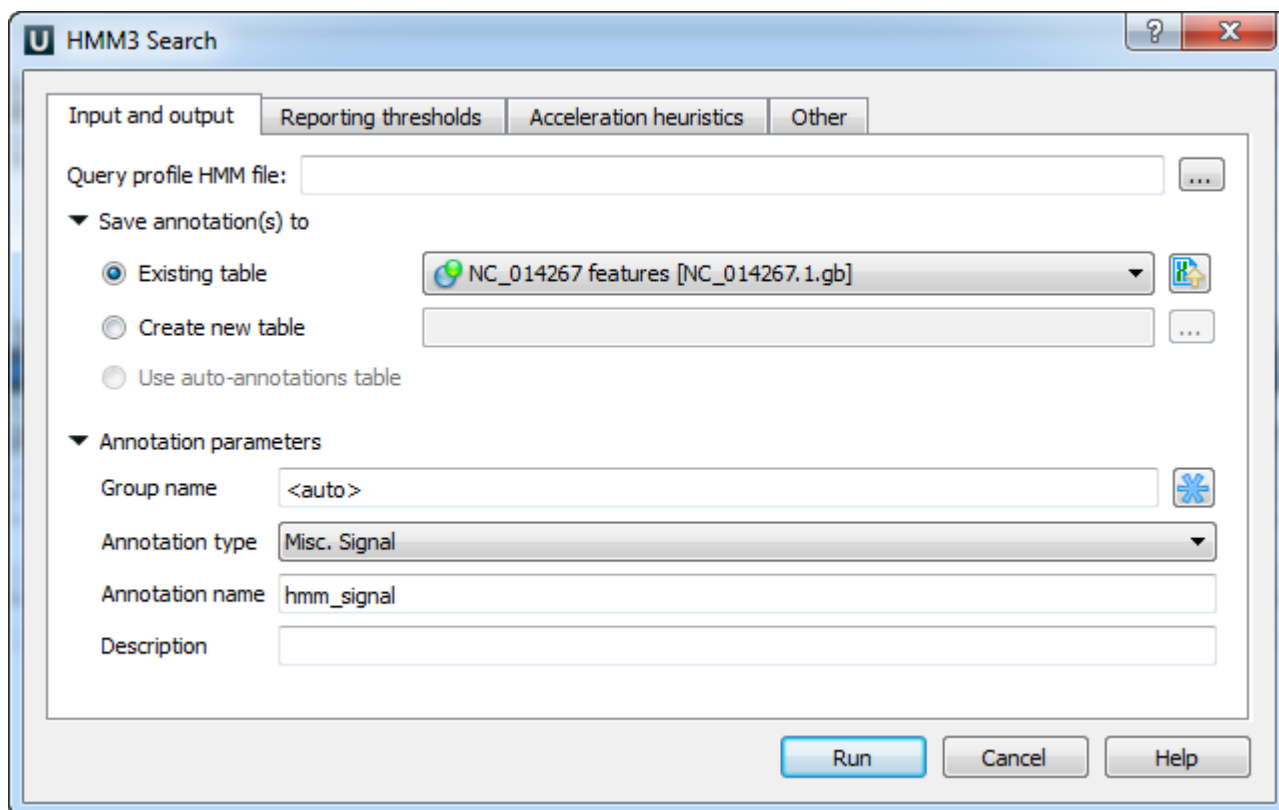
The *HMM3 search* tool reads a HMM profile from a file and searches a sequence for significantly similar sequence matches.

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

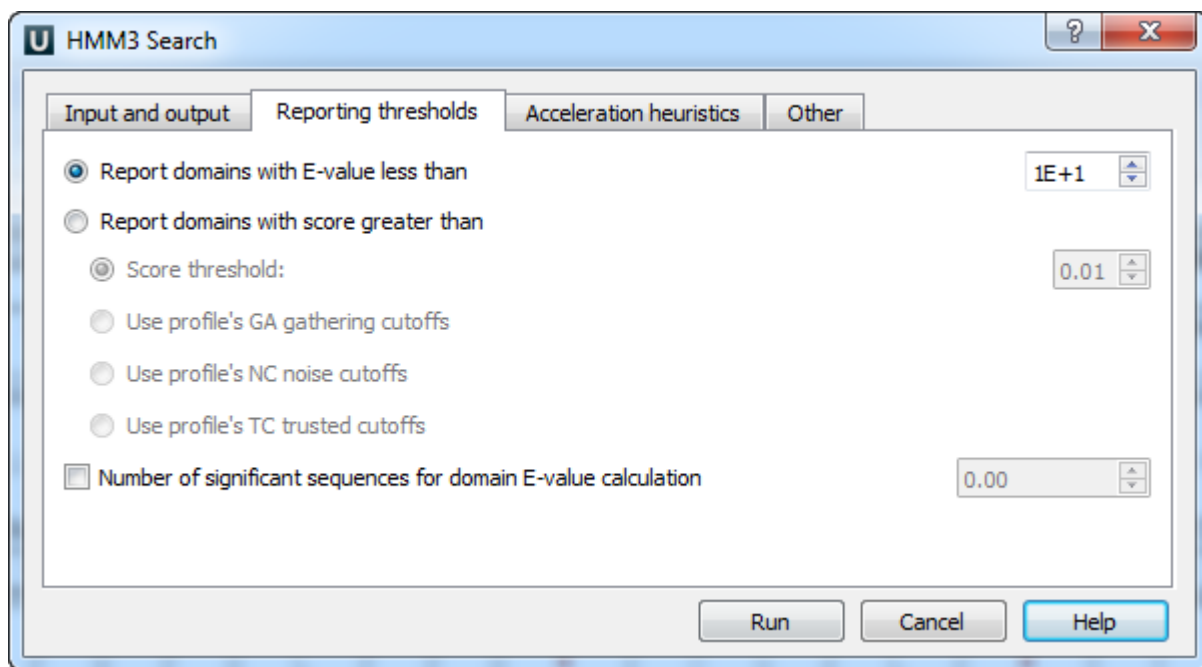
If the selected sequence is nucleic and profile HMM is built from amino alignment, the sequence will be automatically translated and searched in all possible frames (6 totally).

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

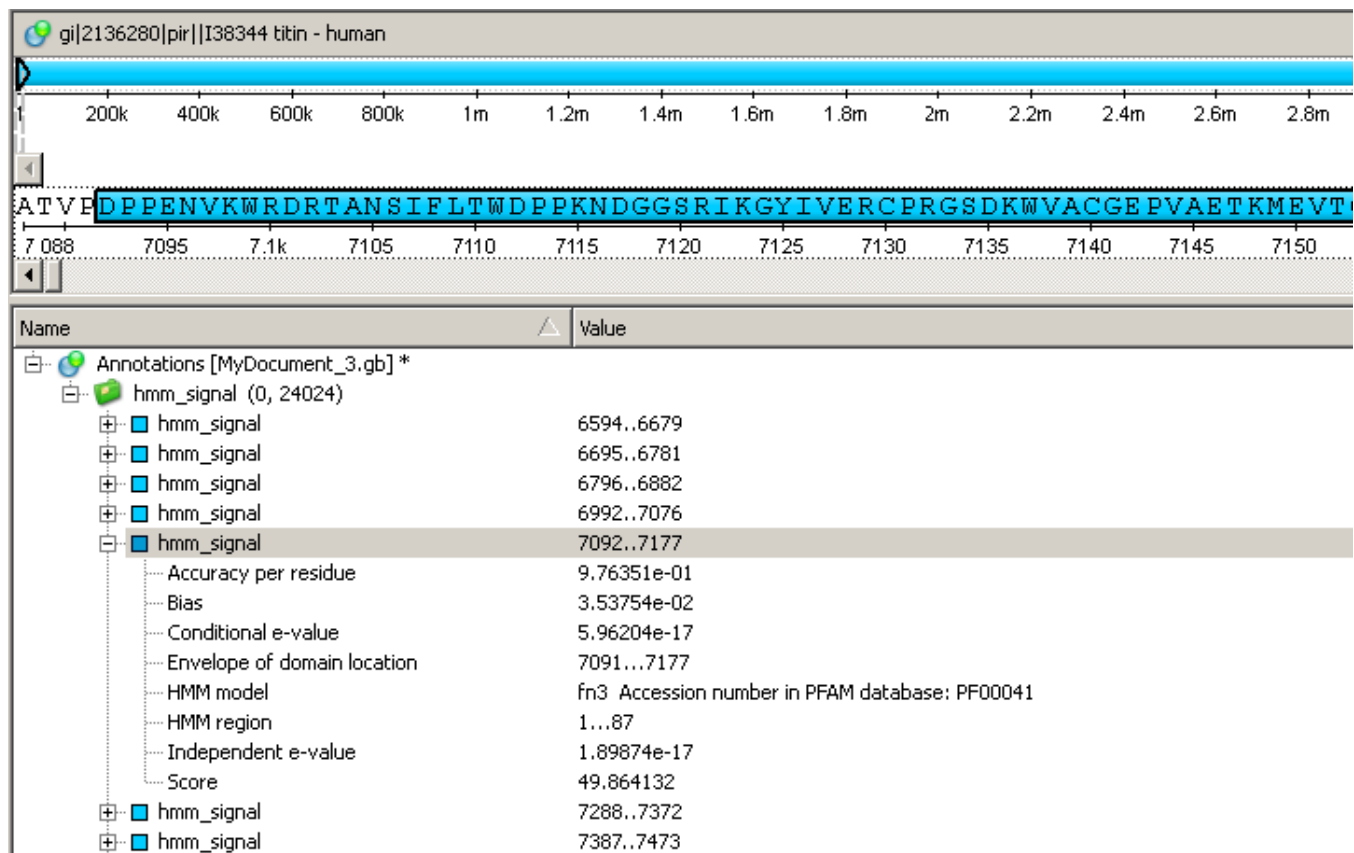
The *HMM3 search* accepts the HMMER2 HMM profiles (amino only) as a backward compatibility feature. An interesting post about using the HMMER2 models with the HMMER3 is available on the [Sean Eddy's blog](#).



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



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



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