Searching HMM Signals Using HMMER2

Task Name: hmm2-search

Searches each input sequence for the significantly similar sequence that matches to all specified profile HMM using the HMMER2 tool.

Parameters:

seq — semicolon-separated list of the input sequence files. [String, Required]

hmm — semicolon-separated list of the input HMM files. [String, Required]

out — output file with annotations. [String, Required]

name — name of the result annotations. [String, Optional, Default: “hmm_signal”]

e-val — e-value that can be used to exclude low-probability hits from the result. [Number, Optional, Default: 1e-1]

score — score based filtering which is an alternative to e-value filtering to exclude low-probability hits from the result. [Number, Optional, Default: -1000000000]

Example:

```
ugene hmm2-search --seq=CBS_seq.fa --hmm=CBS.hmm --out=CBS_hmm.gb
```