

NR-HMM User's Guide

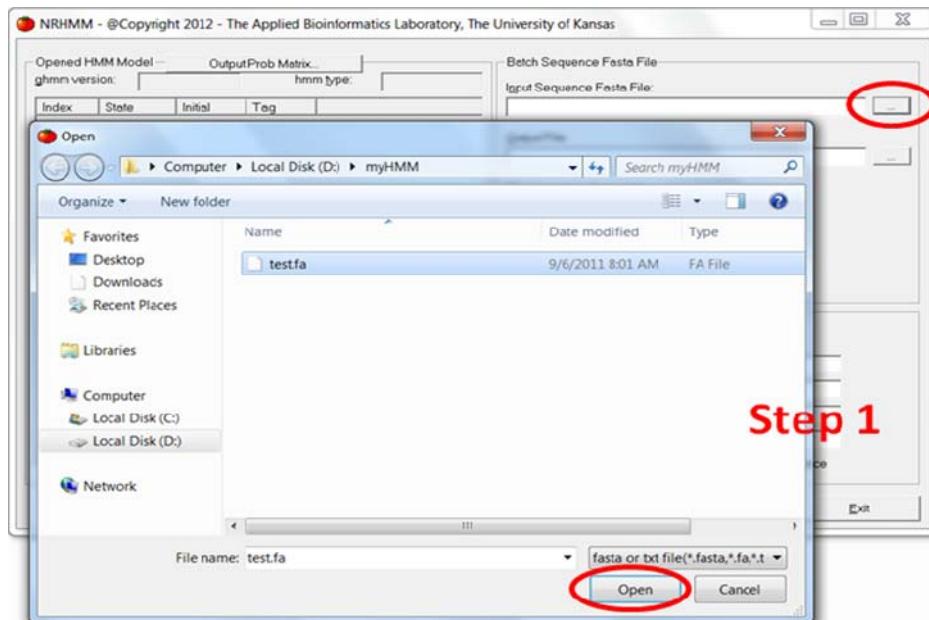
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USA

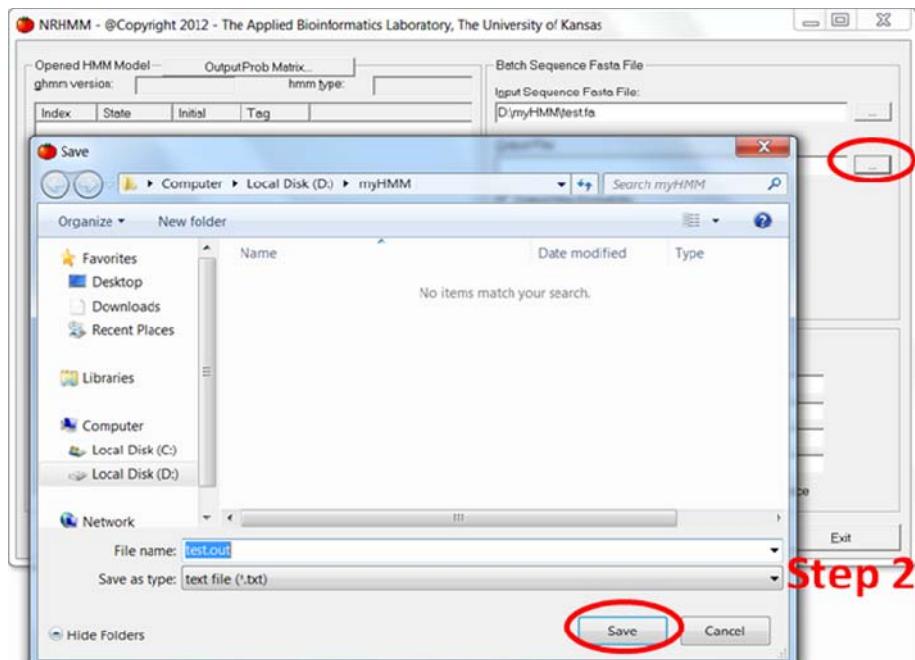
NR-HMM is a program for predicting Nuclear Receptor binding sites based on a Hidden Markov Model framework [1] and can predict variable spacing and orientation of half sites. It is created using Visual Basic (VB) and implemented on 32-bit windows system.

Part 1: Prediction of nuclear receptor binding sites

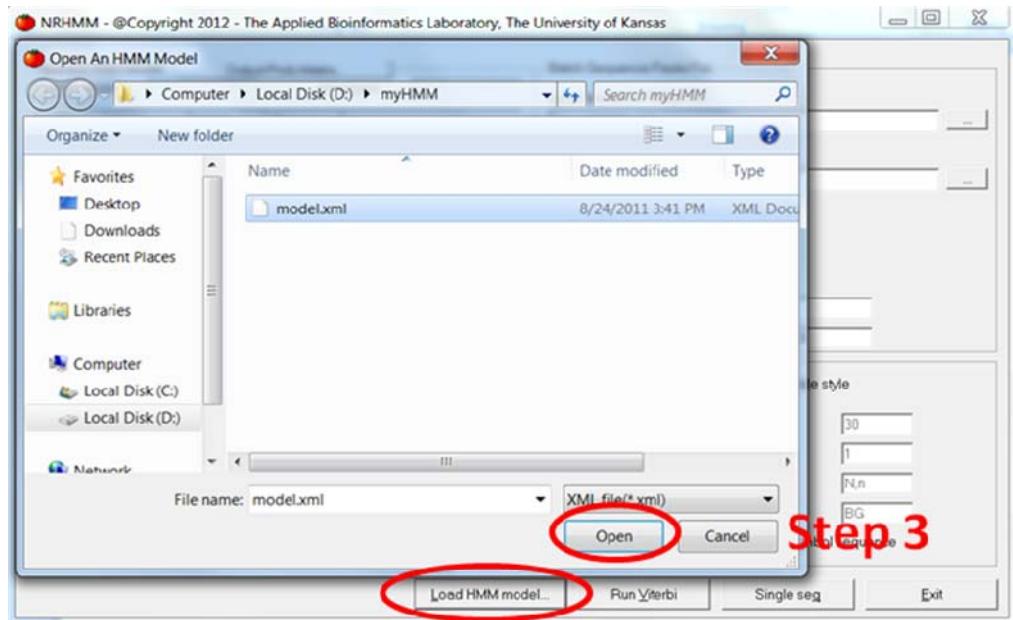
Step 1: Choose an input file containing DNA sequences in FASTA format:



Step 2: Designate an output file:

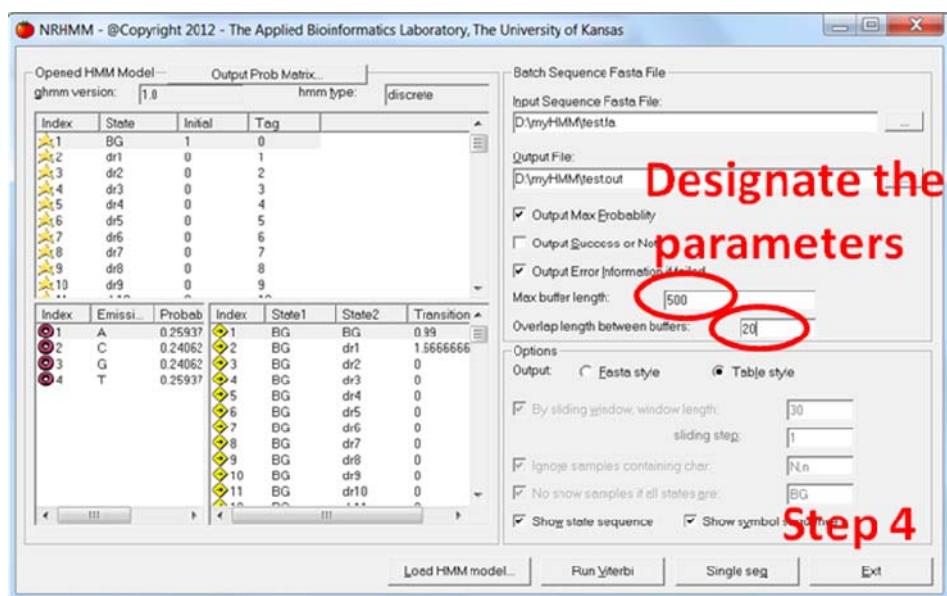


Step 3: Load the NR-HMM model model.xml:

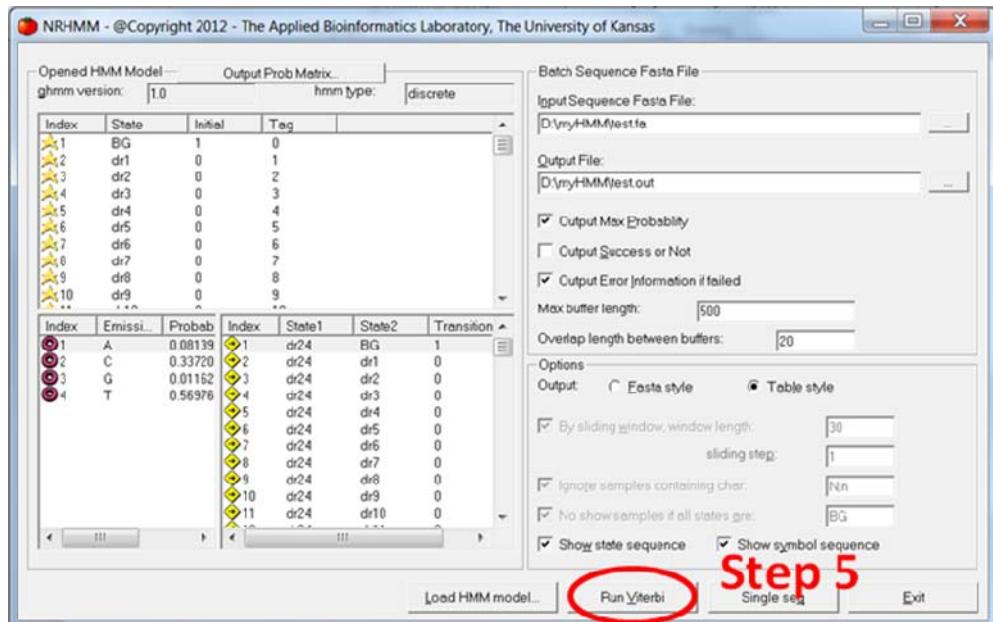


Step 4: Set parameters for predicting nuclear receptor binding sites:

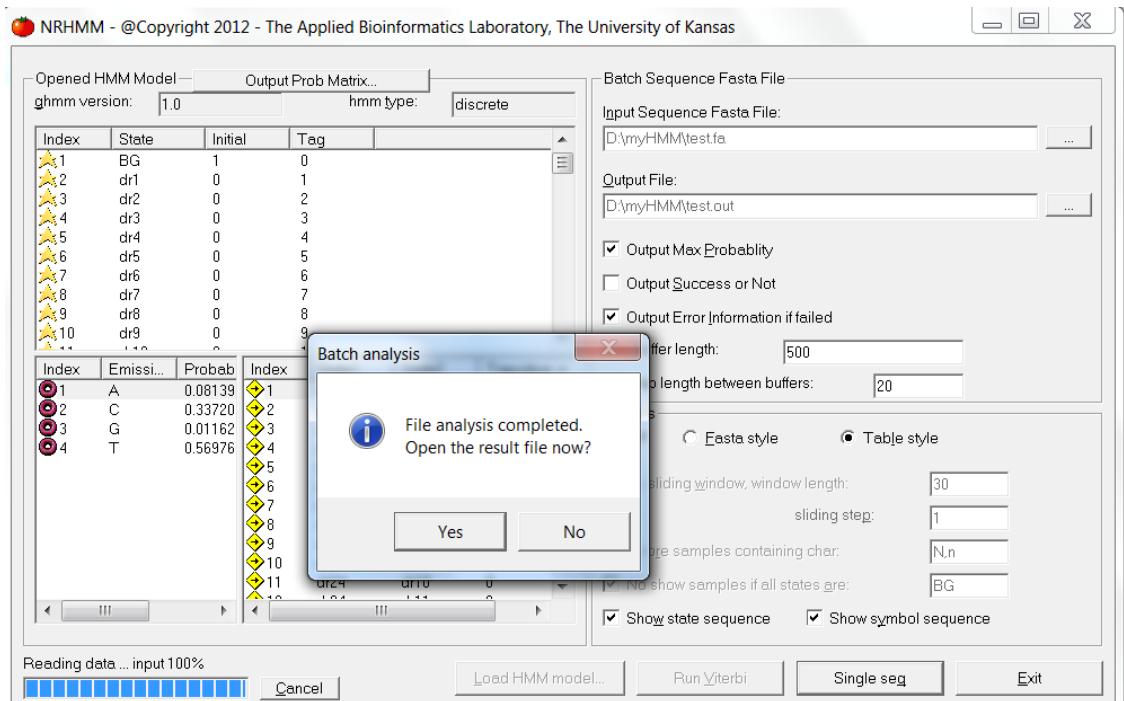
Max buffer length is the sliding window length. Overlap length between buffers is the overlap length of each two adjacent windows. For example, Max buffer length: 500; overlap length between buffer: 20.



Step 5: Run NR-HMM prediction.

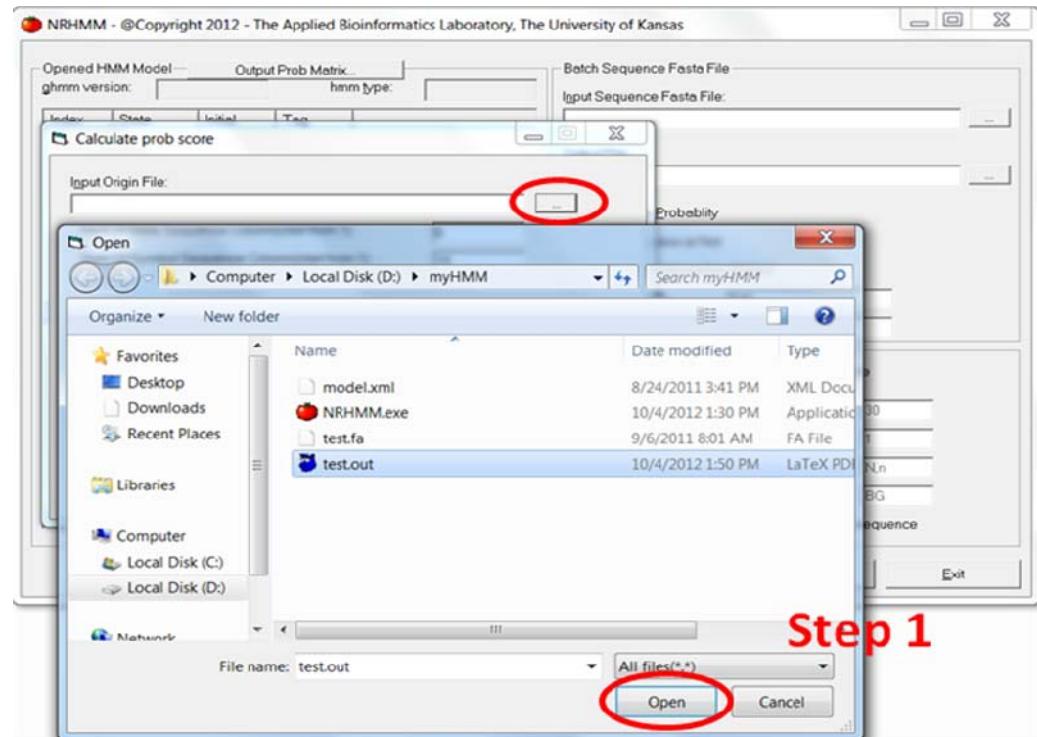


Program finished.

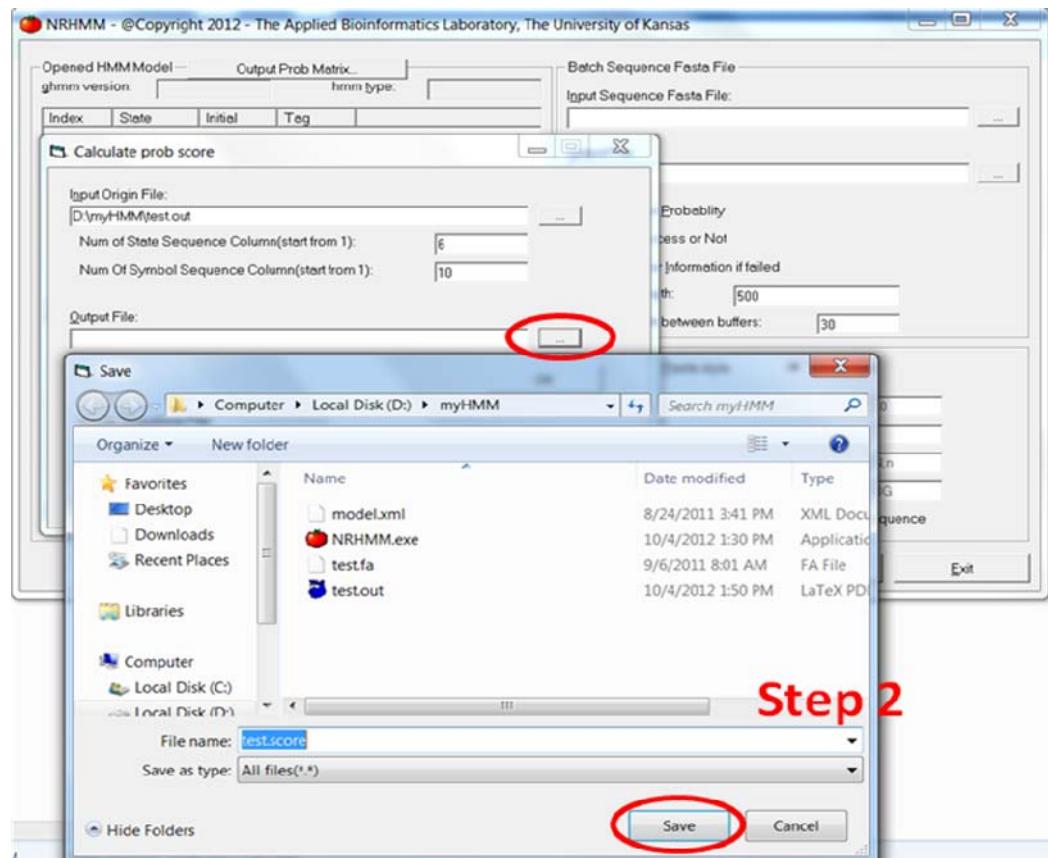


Part 2: Calculating the probability score of each predicted nuclear receptor binding site

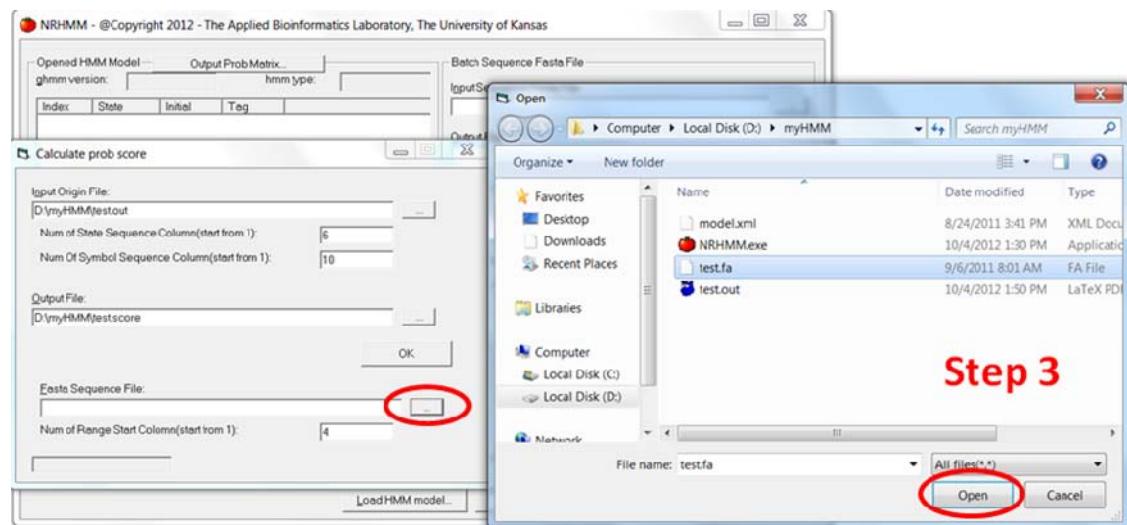
Step 1: Open an input file having predicted binding sites (generated in part 1):



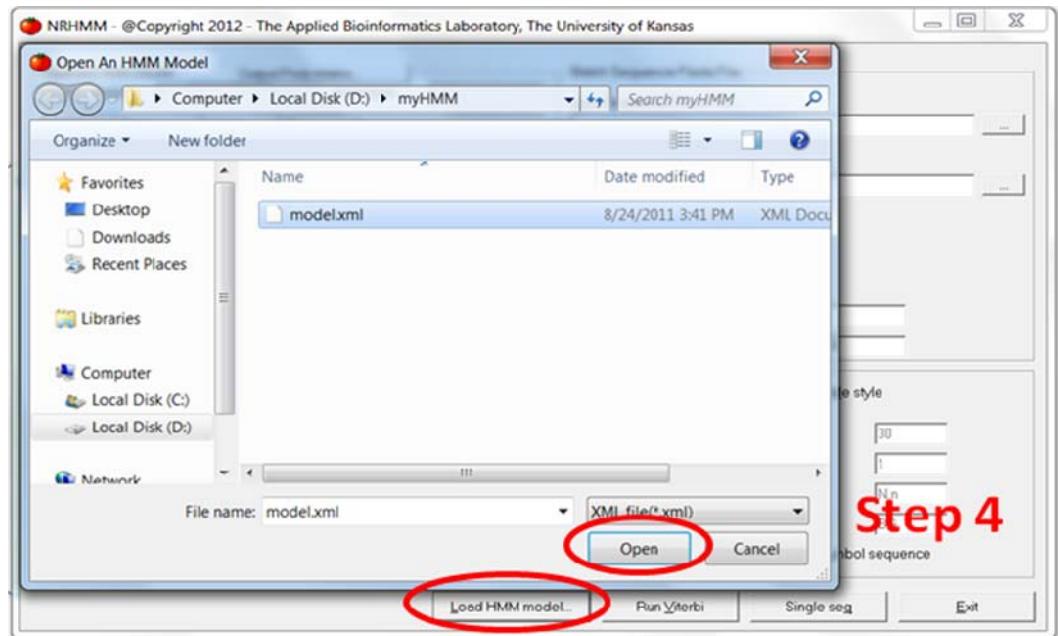
Step 2: Designate an output file for saving scores:



Step 3: Open the FASTA file having the DNA sequences used in stage 1:

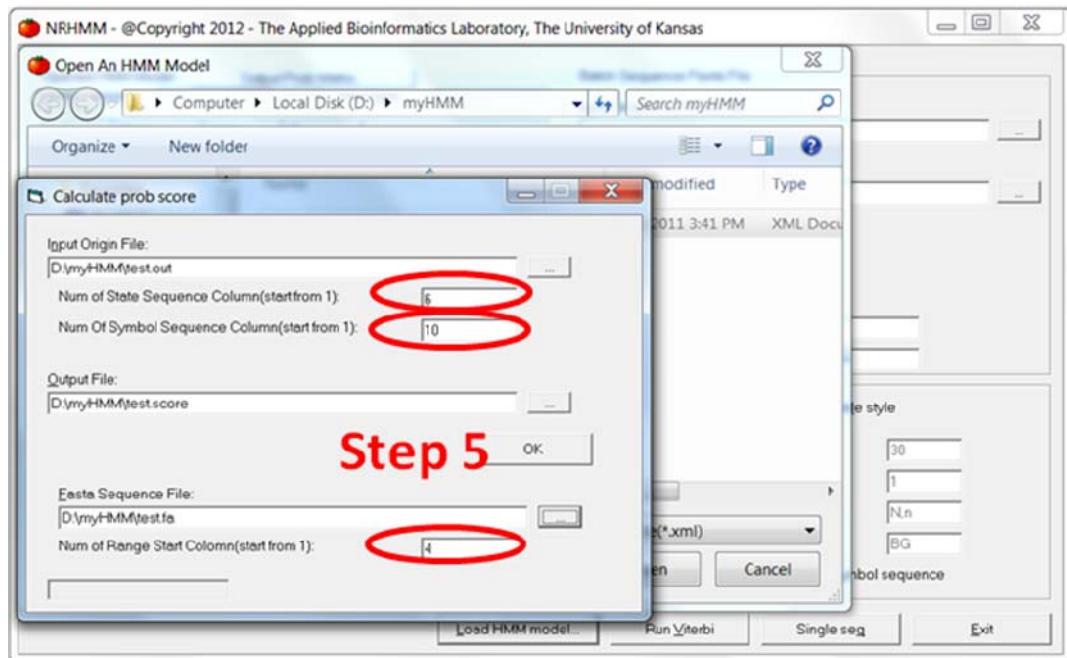


Step 4: Load the NR-HMM model model.xml:

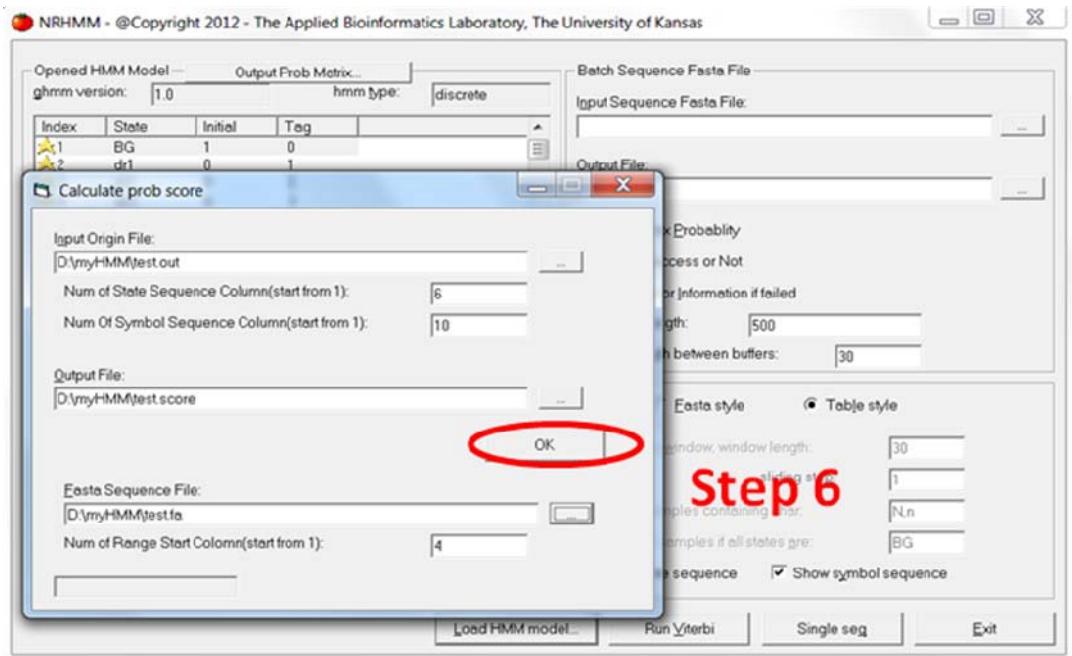


Step 5: Set Parameters for calculation of the probability score

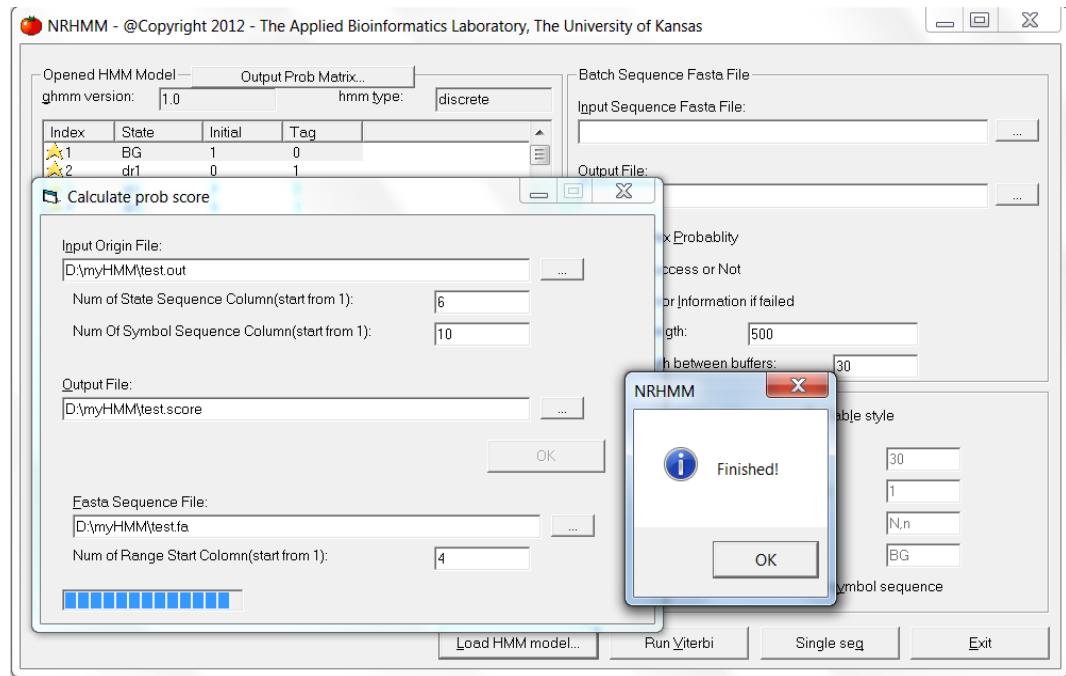
Designate the column number of State Sequence, Symbol Sequence and Range Start in the output file of part 1



Step 6: Run score calculation



Program of calculation score finished.



Reference

1. Sandelin, A. and W.W. Wasserman, *Prediction of nuclear hormone receptor response elements*. Mol Endocrinol, 2005. **19**(3): p. 595-606.