**Post Assignment**

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**Q6) Port MPI-HMMER application on PARAM SHAVAK and compare time with serial and parallel**

**Solution: Step to Port MPI-HMMER application**

**1. wget** [**https://software.intel.com/sites/default/files/managed/ca/03/hmmer-2.3.2-MPI-0.92.tar.gz**](https://software.intel.com/sites/default/files/managed/ca/03/hmmer-2.3.2-MPI-0.92.tar.gz)

**2. tar -xvf hmmer-2.3.2-MPI-0.92.tar.gz**

**3.cd hmmer-2.3.2-MPI-0.92**

**4.mkdir build**

**5.export CC=mpicc**

**6. ./configure --prefix=/home/param2/LIB/hmmer-2.3.2-MPI-0.92/build/ --enable-mpi**

**7. make**

**8. make install**

**[root@shavakmuj hmmer-2.3.2-MPI-0.92]# cd build/bin/**

**[root@shavakmuj bin]# ls**

hmmalign hmmcalibrate hmmemit hmmindex hmmsearch

hmmbuild hmmconvert hmmfetch hmmpfam

**[root@shavakmuj ~]# cd Alam**

**[root@shavakmuj Alam]# cd hmmer-2.3.2-MPI-0.92**

**[root@shavakmuj hmmer-2.3.2-MPI-0.92]# cd tutorial/**

**[root@shavakmuj tutorial]# hmmbuild test1.hmm fn3.sto**

hmmbuild - build a hidden Markov model from an alignment

HMMER 2.3.2 (Oct 2003)

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Alignment file: fn3.sto

File format: Stockholm

Search algorithm configuration: Multiple domain (hmmls)

Model construction strategy: MAP (gapmax hint: 0.50)

Null model used: (default)

Prior used: (default)

Sequence weighting method: G/S/C tree weights

New HMM file: test1.hmm

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Alignment: fn3

Number of sequences: 108

Number of columns: 119

Determining effective sequence number ... done. [108]

Weighting sequences heuristically ... done.

Constructing model architecture ... done.

Converting counts to probabilities ... done.

Setting model name, etc. ... done. [fn3]

Constructed a profile HMM (length 84)

Average score: 67.54 bits

Minimum score: 27.53 bits

Maximum score: 105.77 bits

Std. deviation: 17.07 bits

Finalizing model configuration ... done.

Saving model to file ... done.

//

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**[root@shavakmuj tutorial]# hmmsearch test1.hmm globins630.fa**

hmmsearch - search a sequence database with a profile HMM

HMMER 2.3.2 (Oct 2003)

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HMM file: test1.hmm [fn3]

Sequence database: globins630.fa

per-sequence score cutoff: [none]

per-domain score cutoff: [none]

per-sequence Eval cutoff: <= 10

per-domain Eval cutoff: [none]

- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Query HMM: fn3

Accession: PF00041

Description: Fibronectin type III domain

[No calibration for HMM; E-values are upper bounds]

Scores for complete sequences (score includes all domains):

Sequence Description Score E-value N

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[no hits above thresholds]

Parsed for domains:

Sequence Domain seq-f seq-t hmm-f hmm-t score E-value

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[no hits above thresholds]

Alignments of top-scoring domains:

[no hits above thresholds]

Histogram of all scores:

score obs exp (one = represents 1 sequences)

----- --- ---

-69 4 -|====

-68 3 -|===

-67 5 -|=====

-66 7 -|=======

-65 14 -|==============

-64 25 -|=========================

-63 23 -|=======================

-62 32 -|================================

-61 35 -|===================================

-60 33 -|=================================

-59 35 -|===================================

-58 37 -|=====================================

-57 35 -|===================================

-56 24 -|========================

-55 32 -|================================

-54 41 -|=========================================

-53 27 -|===========================

-52 29 -|=============================

-51 35 -|===================================

-50 24 -|========================

-49 18 -|==================

-48 24 -|========================

-47 26 -|==========================

-46 12 -|============

-45 11 -|===========

-44 12 -|============

-43 4 -|====

-42 3 -|===

-41 2 -|==

-40 7 -|=======

-39 2 -|==

-38 2 -|==

-37 1 -|=

-36 2 -|==

-35 0 -|

-34 0 -|

> -33 4 -|====

% No statistical fit available

Total sequences searched: 630

Whole sequence top hits:

tophits\_s report:

Total hits: 10

Satisfying E cutoff: 0

Total memory: 20K

Domain top hits:

tophits\_s report:

Total hits: 10

Satisfying E cutoff: 10

Total memory: 25K

Total Time = 0.088840

[root@shavakmuj tutorial]#