

ReadMe: for Comp 7850 Project

S.M. Al Mamun

December 30, 2010

1 Parallel Program

Three files are used as the main source code, named as `phylo.c`, `phylo-handler.c` and `phylo.h`. For compilation, I used:

Step 1: `mpicc phylo.c phylo-handler.c -o phylo`

All the datasets are stored in a directory names files. They are named as `ATP.txt`, `ACT.txt` and `p450.phylip`. Then a sample myjob file description for helium may be as the following:

Step 2: `mpirun -np 10 phylo -i ../files/ATP.txt` [I used in this way]

2 Serial Program

Quicktree program can be run by running quicktree which is located inside the bin directory. I ran this program with editing the main program with measuring the execution time. Compilation can be done as follows:

quicktrees -in m ../../files/ATP.txt [For more info, quicktree -h can be used]