Before using python script to run MUSCLE multiple sequence alignment on sequence files, make sure you already download MUSCLE from http://www.drive5.com/muscle/, with correct executable file match to your operating system. <muscle3.8.31_i86linux64> in this directory is used on Linux server.

<run_MSA.py> is use to run real sequence files with filename <all_seqs_with_latin_names$genenames.fasta> which is generated from my data retrieval program; <sun_sim_seq_MSA.py> is use to run simulated sequence files with filename start with 'sim_'. The only difference in these two script is the name of fasta files in a directory. If you would like to run MUSCLE on different kinds of file names, you can simply change the if statement in script.

You can run these two script from terminal with the following command:
    'python run_MSA.py <latinname_seqfiles_dir_path> <MSA_program_exe_path>'
    'python run_sim_MSA.py <simulated_seqfiles_dir_path> <MSA_program_exe_path>'

Following are the detailed screenshots:

```
[xiao@esc3055m-hp-moses run_MSA_testing]$ python run_MSA.py /home/xiao/run_MSA_testing/example_real_seqfiles/ /home/xiao/run_MSA_testing/muscle3.8.31_i86linux64

MUSCLE v3.8.31 by Robert C. Edgar

http://www.drive5.com/muscle
This software is donated to the public domain.
Please cite: Edgar, R.C. Nucleic Acids Res 32(5), 1792-97.

all_seqs_with_latin_names$A1BG 22 seqs, max length 548, avg  length 498
00:00:00     10 MB(1%)  Iter   1  100.00%  K-mer dist pass 1
00:00:00     10 MB(1%)  Iter   1  100.00%  K-mer dist pass 2
00:00:00     19 MB(1%)  Iter   1  100.00%  Align node
00:00:00     19 MB(1%)  Iter   1  100.00%  Root alignment
00:00:01     19 MB(1%)  Iter   2  100.00%  Refine tree
00:00:01     19 MB(1%)  Iter   2  100.00%  Root alignment
00:00:01     19 MB(1%)  Iter   2  100.00%  Root alignment
00:00:01     19 MB(1%)  Iter   3  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter   4  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter   5  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter   6  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter   7  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter   8  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter   9  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  10  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  11  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  12  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  13  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  14  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  15  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  16  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  17  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  17  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  18  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  19  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  20  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  21  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  21  100.00%  Refine biparts
00:00:01     19 MB(1%)  Iter  22  100.00%  Refine biparts
```

```
[xiao@esc3055m-hp-moses run_MSA_testing]$ python run_sim_seq_MSA.py /home/xiao/run_MSA_testing/example_simulated_seqfiles/ /home/xiao/run_MSA_testing/muscle3.8.31_i86linux64

MUSCLE v3.8.31 by Robert C. Edgar

http://www.drive5.com/muscle
This software is donated to the public domain.
Please cite: Edgar, R.C. Nucleic Acids Res 32(5), 1792-97.

sim_1185_CDKN1A_idr_4_filter01_ 36 seqs, max length 81, avg  length 80
00:00:00     10 MB(1%)  Iter   1  100.00%  K-mer dist pass 1
00:00:00     10 MB(1%)  Iter   1  100.00%  K-mer dist pass 2
00:00:00     14 MB(1%)  Iter   1  100.00%  Align node
00:00:00     14 MB(1%)  Iter   1  100.00%  Root alignment
00:00:00     14 MB(1%)  Iter   2  100.00%  Refine tree
00:00:00     14 MB(1%)  Iter   2  100.00%  Root alignment
00:00:00     14 MB(1%)  Iter   2  100.00%  Root alignment
00:00:00     14 MB(1%)  Iter   3  100.00%  Refine biparts
00:00:00     14 MB(1%)  Iter   4  100.00%  Refine biparts
00:00:00     14 MB(1%)  Iter   5  100.00%  Refine biparts
```

For further questions, send me an email:
xiaow.wang@mail.utoronto.ca