Running FASTA programs using an Apple Mac

The following is a series of steps that should allow you to run the fasta programs on a Mac computer.

Using FASTA on MacOS

We're going to be installing and using the program from the Unix command line. To get started, run Terminal from the Finder. It is located under:

/Applications/Utilities/Terminal.app

Run it. You'll probably want to keep that application on your dock. If so, right click on the Terminal app icon on your dock after you have started it. Under options, select "Keep in Dock."

Type: pwd

This shows us our current working directory. In the terminal window let's create a directory where we'll store the FASTA application files and our amino acid sequence files.

mkdir FASTA

Change your working directory to the directory you've just created.

cd FASTA

For grins type pwd again.

pwd

The command interpreter (we call it a shell in Unix) prints your current directory.

Now we're going to download a compressed tar (tape archive) of the FASTA program. We're going to do this from the command line because we can. Type the following all in one line (the line is broken here by the word processor):

curl -o fasta-36.3.8i-macosuniv.tar.gz
https://fasta.bioch.virginia.edu/wrpearson/fasta/CURRENT/fasta-36.3.8i-macosuniv.tar.gz

Look at the contents of our current working directory:

ls

You should see a single file: fasta-36.3.8i-maxosuniv.tar.gz

Now we need to uncompress and un-archive the contents of the file we just downloaded. We're going to do that with a single command line.

tar xzf fasta-36.3.8i-macosuniv.tar.gz

Now have a look at your current directory:

ls

You should see the tar.gz file and another file which is a directory of the FASTA distribution. If you run "ls -l" you should see a bunch of attributes about the files -- their type (notice the d signifying that it is a directory), who can read or write, who owns the files, when they were created, etc.

Do an "ls fasta-36.3.8i". You will see a lot of files and directories. There is a README file. You might want to read it. You could do that with TextEdit, or Microsoft Word, but those are big and slow. Just use the Unix file pager more.

more fasta-36.3.8i/README

We can use curl to retrieve some test sequences from my website.

curl -o Abies.aa https://schulte.faculty.unlv.edu/BIO480/Abies.aa
curl -o Chenia.aa https://schulte.faculty.unlv.edu/BIO480/Chenia.aa

Repeat the above process for the other four amino acid files as listed in the lab exercise.

Assuming the files are in our current directory, we can try a run of the program. In the README it told us that the compiled executable binaries were stored under bin. So here is how we could do a test run:

fasta-36.3.8i/bin/fasta36 -O abieschenia.txt Abies.aa Chenia.aa

By convention -<something> signifies a command line option is given to the running program. In this case, it tells the fasta36 program to write its output to a file named abieschenia.txt. Have a look at the output file with more.

more abieschenia.txt