Introduction to Python
Day One Exercises

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UNIX Exercises

1. Launch a Terminal session and navigate to your home directory with the **cd** command. Remember, there are three ways to do this:

   ```
   cd
   cd ~
   cd /path/to/home/directory/ # replace your home directory's full path
   ```

   Using the commands **cd**, **pwd**, and **ls** (and **ls -la**), examine the directory structure of your system. Spend a few minutes figuring out where different files and directories are located so that you understand your file system organization by navigating forward into sub-directories and back into parent directories and listing contents.

2. Navigate to your home directory, and perform the following tasks. After performing a task that copies, moves, or removes a file/directory, enter the command **ls** to see how things have changed.

   (a) Use the command **mkdir** to create a new directory called "blob".

   (b) Use the command **touch** to create a new file called "blerg.txt".

   (c) Use the command **echo** along with the symbol **>** to add the sentence "I'm writing to a file!" to blerg.txt.

   (d) Use the command **mv** to move this file into the directory blob. Then, enter **ls**. What do you notice?

   (e) Navigate into the directory "blob". Make a copy of blerg.txt called "blerg2.txt".

   (f) Use the command **echo** and the symbol **>** to write the line "Another sentence!" to blerg2.txt. Now use **less** to examine the contents of blerg2.txt. What do you notice?

   (g) Make a new copy of the file blerg.txt using the command **cp**, called blerg3.txt. Enter **ls**. What files now exist in this directory?

   (h) *Append* the line "Another sentence!" to blerg3.txt using **echo** and the symbol **>>**.

   (i) Navigate back to your home directory (try using the code **cd ..** for this), and use the command **rm -r** to delete the blob directory.

   (j) Use the **rm** command to delete the file blerg.txt.

3. Perform the following tasks:

   (a) Use the command **touch** to create a file "gobble.txt". Create these files in a single line of code, as in, only use **touch** once!

   (b) Use **echo** and **>** to add the line "The turkey goes gobble gobble gobble." to the file gobble.txt, and confirm that this line was correctly added using **less**.

(c) Use the command **cat** to add the contents of gobble.txt to a new file called "turkey.txt". Again, use **less** to be sure that turkey.txt contains this sentence.

4. Download the file sequences.fasta and save it to your computer. This file contains sequences from the Influenza virus PB2 gene. Navigate to the directory where this file is located, and perform the following tasks:

(a) The UNIX command **wc** stands for "word count". This command counts the number of lines, characters, and bytes in a given file. Enter the command **wc sequences.fasta** to display this information. Compare the result with the file size as displayed by **ls**. Do you see any overlapping numbers?

(b) Use **wc** with the argument **-l** to determine just the number of lines in sequences.fasta.

(c) Enter the command **head sequences.fasta** to view the top few 10 lines of this file. Consult the documentation for **head** using the command **man head**, and figure out how to specify a different number of lines. Enter **q** to exit from the man documentation, and use your new knowledge to display the first 16 lines of the file.

(d) Create a new file called "lastseqs.fasta" which contains the *last* 8 lines of sequences.fasta (hint: the command **tail**, which is basically the opposite of **head** should be useful!). For this task, *do not use* **touch**.