Bioinformatics Workshop Exercise Handout #1

Day 1, AM: BASH

Directory Operations Exercise:

1. Open your command prompt.
2. Print your current directory.
3. Move to a directory where you want to add files (for example, within Documents).
4. Make a new directory named 'GWAS_Course'.

File Operations Exercise:

1. Move to the 'GWAS_Course' directory.
   Create the file 'polkadots.txt' using cat > polkadots.txt
3. Type 'hello'. This will be appended to the file's first line.
4. Press Control D to return to the command prompt.
5. List the files in the directory.
6. Read and edit 'polkadots.txt' and type 'goodbye' on the second line.
7. Save and exit. (Control X → Y → Enter).
8. Move up one directory and create the directory 'Practice'.
9. Copy 'polkadots.txt' to this directory.
10. Within 'Practice', move 'polkadots.txt' to 'stripes.txt'.
11. Print the last 10 lines of 'stripes.txt'.
12. Move up to the parent directory that contains both 'GWAS_Course' and 'Practice'.
13. Remove 'Practice' directory.

Bash Script Exercise:

1. Move to the 'GWAS_Course' directory.
2. Create the file 'patterns.sh'.
3. Determine the path to bash.
4. Within the file, add the Shebang and tell the script to use the bash shell in the first line.
5. On line three, type 'cp polkadots.txt paisley.txt'.
6. Save and exit file.
7. Make the script executable.
8. Run the script.
9. List the files to make sure it worked. You should have two files in the directory: 'polkadots.txt' and 'paisley.txt'.

Grep Exercise:

1. Produce a file 'an.txt' with the following text on separate lines: ant, anteater, dinosaur, and, andover, cranium, antebellum, argyle, andes.
2. Count the number of words in the text file.
3. Count the number of characters in the text file.
4. Use grep to print every line that contains the string 'an' in the file.

For Loop Exercise:

1. Navigate to the ‘GWAS_Course’ directory.
2. Make a file called ‘stripes.txt’.
3. Produce a script that runs through all text files in the directory and prints their names as output.

Piping Exercise:

1. Create a command that contains two pipe operators and counts the number of text files in the directory ‘GWAS_Course’.