## Assignment 1

## **Re-submit Assignment**

**Due** 1 Aug by 23:59 **Points** 20 **Submitting** a file upload

Available after 30 Jul at 13:00

## Assignment 1 – Due date: Aug 1, 11.59pm

Log in to Marvin.

Write down each command line you execute to implement the following steps:

- 1. In your home directory, create a directory called "Assignment\_1".
- 2. Within Assignment 1, create two other directories called INPUT and OUTPUT.
- 3. Download the data from the following link to the INPUT directory.

## http://ssgac.org/documents/SWB\_Full.txt.gz (http://ssgac.org/documents/SWB\_Full.txt.gz)

- 4. Create a copy of SWB Full.txt.gz in the INPUT directory, name it Mydata.txt.gz
- 5. Display the first 20 lines of Mydata.txt.gz without decompressing the file.
- 6. Decompress the file.
- 7. Display how many lines (observations) there are in the data.
- 8. Display the lines containing the string "rs10830206".
- 9. Extract the first column from the data and write it into another file in the OUTPUT directory. Name the file "SNPID.txt".
- 10. In a single command line (using a pipe), extract the last 100 lines from SNPID.txt and sort them. Write the output into another file in the OUTPUT directory named "100\_SNPs.txt"
- 11. Display the following sentence: "My name is YourName".
- 12. Write your command line history into a file in the OUTPUT directory, named "History.txt".
- 13. Display the contents of "History.txt", one screen at a time.
- 14. Go into the OUTPUT directory using its relative pathname. Create a tarball (tar archive) containing the files "History.txt" and "100\_SNPs.txt", named "YourName.tar"

Congratulations! You are done with the first assignment!

Upload your answers to questions 1-13 above and the "YourName\_assignment1.tar" file to Canvas.

1 of 1 8/20/18, 9:32 PM