

- Go into your virtual machine and load up Fedora
- Create a folder called : program2
- Move to your program2 folder
- Download into the program2 folder this file:
http://users.cis.fiu.edu/~mrobi002/downloads/pseudomonas_aeruginosa/pa01nov2006/NC_002516.gbk

1 - Using the linux terminal commands

- 0 - Create a linux Script file called yourLastNameFirstNameInitialPgm2.sh
In the first line of this file write: `#!/bin/bash`
- a - Display program two Starting
- b - Display the name of the file just created with all its attributes and output that information into a file called stats.txt
- c - Change the access rights as follows:
`chmod 755 yourLastNameFirstNameInitialPgm2.sh`
- d - Display the name of the file just created with all its attributes and append that information into a file called stats.txt
- e - Create a directory called dna
- f - Find out how many words, lines/row/records, and how many bytes are in the NC_002516.gbk file. Write that information to a file called dnaCount.txt to be written into the dna folder.
- g - Using the cat command display the contents of the dnaCount.txt file and write its output to a to a file named dnaCount2.txt, in the current directory
- h - Using the cat command merge the following files: dnaCount.txt, NC_002516.gbk, dnaCount2.txt into a new file called merged.txt in the dna folder.
- i - Find out all locations of the word gene in the NC_002516.gbk file and create an outfile file name geneAmts.txt
- j - Display contents in geneAmts.txt
- j - Count the amount of genes in the geneAmts.txt file and merge it to the merged.txt file
- k - Display the last lines of the file merged.txt
- l - Display the first lines of the file merged.txt
- m - display program two ended