

- 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](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`  
All the following tasks **MUST** be done using Linux commands as learned in **class**.  
When you execute the `.sh` file the following will be execute by the `.sh` file:
  - a - Display program two Starting
  - b - Write the name of the file just created with all its attributes into a file called stats.txt
  - c - Change the access rights as follows: `chmod 755 yourLastNameFirstNameInitialPgm2.sh`
  - d - Again, write the name of the file just created with all its attributes 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 and outfile file name geneAmts.txt
  - j - Display contents in geneAmts.txt
  - j - Count the amount of the word "**gene**" 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 **3** lines of the file merged.txt
  - m - display program two ended