# Assignment #3

## Objective

Bash is a *shell*. When you open a UNIX/Linux terminal and type commands you are using a “shell”. For example, when you type ‘ls’ or ‘cp’ or ‘mkdir’ the shell recognizes those commands and executes them for you. It turns out the shell is much more powerful than just interpreting your command-line instructions, it is also a programming language. Bash is quite different from Python, R or other languages, but it has some of the same structures (such as if statements, loops and functions). In this assignment we will learn a bit of Bash programming as it will be necessary for launching jobs on a Unix-based high-performance computing (HPC) infrastructure as well as for scientific workflow construction.

## Due

Before 9am on Tuesday April 9th.

## Tasks

Read the following:

Vi Text Editor at Ryan’s Tutorials: <https://ryanstutorials.net/linuxtutorial/vi.php>. You will use the vi text editor to create Bash scripts later for high-performance computing.

Bash Scripting tutorial at Ryan’s Tutorials: <https://ryanstutorials.net/bash-scripting-tutorial/>. Be sure to read each of the following sections:

1. Introduction
2. What is a Bash Script
3. Variables
4. Input
5. Arithmetic
6. If Statements
7. Loops
8. Functions

With your new BASH knowledge, write a small script that does the following.

1. Using vi, create a file named SRA\_IDs.txt. Here you will add the run IDs for several NCBI Sequence Read Archive (SRA) IDs. These IDS correspond to unique DNA/RNA sequenced data sets. For example: <https://www.ncbi.nlm.nih.gov/sra/?term=SRR2931286>. Inside of this file, add the following IDs, each on a separate line:   
     
   SRR2931286

SRR2931270

SRR2931473

SRR2931500

SRR2931514

SRR2931513

SRR2931318

1. Using what you learned about “Command substitution” use the ‘cat’ command to put these IDs into a variable named SRAs.
2. Loop over the SRAs and create a new directory that has the same name as the SRA. But, if the directory already exists, don’t create it. To test if the directory already exists use the “Test” conditionals you learned about in the tutorial.
3. Run your script and make sure it creates a directory for each SRA ID in the file.
4. Run your script again and make sure it doesn’t complain that the directories already exist.

***Do not spend excessive time on this*** if you can’t get it or run out of time. Do your best, ask questions, and turn in what you are able to accomplish.

You are allowed to work together via Slack: ask questions to try to solve the problem and help others*. Do not post a full solution on Slack.*

Full credit will be awarded for either of the following cases:

1. A correct solution that generates proper output
2. A partial solution but documented interactions in a Word file listing any efforts you made to work with others that include:

* Questions you asked on Slack
* Responses you gave to others on Slack
* Solutions you found that were already posted on Slack and tagged by you with a thumbs up (or other emoji)

Partial credit will be awarded If you have attempted the assignment and turned in a solution but it does not work and you *do not* have documented interactions on Slack. Remember there is a 5-point per day penalty for each day late.

**What to Turn in**

Please send your completed Bash script and SRA\_IDs.txt file to Dr. Ficklin via Slack.