**Homework Day 5**

Authors: Daniel Ramírez, 2022

Samuel Hunter, 2023

Hope Townsend, 2024

**Everyone**

1. Watch Day 6 videos
2. Install R (https://rweb.crmda.ku.edu/cran/)) and R-studio (<https://www.rstudio.com/products/rstudio/download/>)

**If you took more than two hours to do the Assessment:**

1. Create a directory to hold your bash script
2. Create the startings of a bash script (*Hint*: use vim and add the heading needed to tell your computer that it is a bash script)
3. In the bash script print out the words “Hello world!”. Run the script to check it worked!
4. Now let’s practice using variables. Let’s say we want the script to say “Hello” to any person we want. **Using bash variables**, have the script print “Hello Ethan!” and “Hello Eric!” by using the bash variable NAME.
5. Now edit this script to become a SBATCH script
   1. Create an error and output directory (again we usually name this e\_and\_o)
   2. Add the SBATCH required headings to the bash script to make it SBATCH. Use nodes=1, ntasks=1, and time is 1 minute, and mem=1gb. Don’t forget to change the paths to the output and error!
6. Now annotate each step of **day05/scripts/d5-fastq-to-tdf.sbatch** with what the different parameter options mean for the following commands: (Examples of what a good annotation might look like is on lines 192-194)
   1. hisat2 (line 52)
   2. samtools view (line 63 & 69)
   3. samtools index (line 77)
   4. genomeCoverageBed (line 153)
7. *If you’re still struggling with Bash Variables (like ${}),* go through**day05/scripts/d5-fastq-to-tdf.sbatch** and write out what each of the bash variables equals on each line.
8. What does “|” do? Find an example of where this is used.

**If you want to challenge yourself:**

How do you have to edit the script **d5-fastq-to-tdf.sbatch and runloopfastqtotdf.sh** for the scripts to run on datasets sequenced as single-end reads?