

Aligning in STAR, etc.

Basic Linux Commands as Demonstrated by C. Hoffmann on 26 March 2019	
pwd	Print working directory. Tells you where you are.
cd -	Typing this sends you back to the home directory, I believe!
cd /	This goes to the root folder.
cd ..	This goes back one directory.
tab	Use [tab] to finish the typing once you have typed enough to distinguish from others
less	Shows some of each file in the directory, no fear of editing or ruining file
head	Shows the top of the file you're talking about
cat	Opens the full file without editing incorrectly
CTRL + c	THIS KILLS THE PROCESS. ONLY USE WHEN YOU NEED TO CANCEL SOMETHING NOW.
Bash ____	Fill the underscores with a script name so the computer runs it as a bash line
mkdir	Make a directory
cp	Copy

- GTAC sends us FASTQ files (.fq) → there are scripts to change .txt files to .fq, if needed.
- Genome reference GenCode
- Each file should be copied to the home directory instead of working off a drive. Much faster.
- A shell script can do multiple files at once, instead of writing separate scripts for each file
- The drive where these files are located *currently* is "A67015BD70..."
- We use tpm for cDNA, but we do cpm for small RNA
- STAR is the aligning program. Another option is Bowtie or Bowtie2.
- Some text editors are: Emax (esoteric); Vim (old, reliable); Sublimetext (costs \$); Nano
- More alignment of one gene versus another means there's more expression
- STAR is 0-based. So if there is a 52 nt read, the computer will see the positions as 0-51.
- Yellow means command for Linux
- To run the bash script, follow:
 - **A:** For name in MAS1, MAS2, etc. ...
 - **B:** do
 - **C:** mkdir \$name
 - **D:** cd \$name
 - **E:** Call STAR...GenCode Reference...GTF file from reference directory...overhang 51...8 threads...Bash all .fq files...quantmode (either trnxt or gene level)
 - **F:** cd ..
 - **G:** done
- When done with the script, check to be sure the .bam and .sam files are in the directory that you will have created. This will show you have aligned your files properly