**To Do List**

* LOOK INTO CUTAPAPTS/GENOME MAPPING
* Read around process of epigenetic modification – absolute basics
  + Enzymes involved in modification – different types of modifications
  + Disease linkages and use in treatment/diagnosis
* Read around WGBS and TBS
  + FastQC (DONE) + BowTie (DONE) + hiSAT2 (spliced aligner) + SamTools + Cutadapt + Fastq-screen (maps to multiple genomes quickly for quality control) + multiqc (generates HTML report of multiple tools – produces graphics from pipeline) + TopHat + CrossBow + Cufflinks + myRNA
  + TBS – TABSAT
  + RNASeq, ChipSeq, HMEDip-Seq
  + Mapping
  + Quality Control
  + ID’ing different type of modifications
* Learn GIT version control
* Get an external hard drive