Part 1: Use fastq-dump, fastqc, and trimmomatic to process your short-read files

1. Convert your file from the SRA format to fastq format. At the end of this process, you should have two files, a forward-read file and a reverse-read file.
   a. The module is `ncbi-sra`
   b. The command is `fastq-dump`
   c. The arguments you want are `--split-e` and `--split-spot`
2. Use fastqc to check the quality of your fastq files.
   a. The module is fastqc
   b. The command is fastqc
3. Use Trimmomatic to trim your files.
   a. The module is trimmomatic
   b. The command is trimmomatic followed by the arguments
   c. See http://www.usadellab.org/cms/?page=trimmomatic
   d. Do not type "java -jar" or "-0.39.jar". In other words, the first argument after trimmomatic should be PE.
   e. Make sure the TruSeq3-PE-2.fa file is in your folder and make sure you use this filename after ILLUMINACLIP. This tells trimmomatic that the adapter sequences are in this file.
   f. You may want to direct the trimmomatic output to a file using ">"
   g. You should write a script with your trimmomatic command so you have a record of it
4. Use fastqc to check the quality of your trimmed files.
   a. Are there any remaining issues?
      i. If so, discuss these with your group to decide whether you should trim the files more aggressively
5. Prepare to use hisat2 and stringtie to map your reads against your genome (in class and homework).
   a. Consult the hisat2 manual online: http://daehwankimlab.github.io/hisat2/
      i. Discuss with your group what hisat2 does and why you need it
      ii. Discuss with your group the commands you will need to use for hisat2
      iii. If the manual by itself doesn't clear it up, use Google to find other sources of information – hisat2 is very widely used
      iv. What arguments will you need to provide hisat2 for it to run successfully?
   b. Consult the stringtie manual online: https://ccb.jhu.edu/software/stringtie/index.shtml?t=manual
      i. Discuss with your group why you need the services of stringtie
      ii. What commands do you need to run and what arguments do they take?
      iii. Is there something you have to do to the hisat2 output before you feed it into stringtie?
   c. Homework: Everyone independently take the quiz on Canvas. This quiz is due Tuesday at 10 am.