Hands-on Day 1 design:

1. Linux common command
2. Linux tools install: BEDTools, samtools, BWA/bowtie
3. Try using Python code + BEDTools to simulate reads (take chr22 as a example)
   1. Generate fragment BED file using Python code
   2. Use BEDTools to extract sequences based on BED format fragment
4. Try online BLAST to figure out the alignment [optinal]
5. Generate BAM files using the BAM generated by BWA or Bowtie
6. Try IGV to visualize BAM files
   1. Create a reference by the IGV using fasta file
7. [optional] evaluate performance of different alignment tools based on the original coordinate in the BED file.