**Coding Tasks**

Write a program for each of the following:

1. Recursively find all FASTQ files in a directory and report each file name and the percent of sequences in that file that are greater than 30 nucleotides long.
2. Given a FASTA file with DNA sequences, find 10 most frequent sequences and return the sequence and their counts in the file.
3. Given a chromosome and coordinates, write a program for looking up its annotation. Keep in mind you'll be doing this annotation millions of times.

* Input:
  + Tab-delimited file: Chr<tab>Position
  + GTF formatted file with genome annotations.
* Output:
  + Annotated file of gene name that input position overlaps.
* Hint: Most of the sequence reads come from a small portion of the genome. Try to use this information to improve performance, if possible.

NOTE:

* Keep in mind; we will use the results of these tasks to assess your ability. This is a chance for you to show off your programming skills and style.
* A Python solution is ideal, as our code-base is primarily in Python.
* Sample input files have been provided for each task.
* Make sure you understand the file formats (FASTQ, FASTA, GTF) to perform these tasks correctly.
* Please make sure each task can run on the command line.
* In the spirit of assessing your programming abilities, please avoid using 3rd-party tools to solve these problems (parsers and formatters excluded).