The following Is the overall idea what I would like to do on the final project. Details of README file, instruction , and user guildline will be accompanying with the program.

As a wet-lab biologist, I am always intrigued by how to make a python program could help aligning sequencing data into the reference genome. Bowtie is one of the existing tools for conducting such an alignment. Instead of using existing data or genome, I would like to take a further step by stimulate random reads and a random genome to do the alignment (.random). I will also implement an assignment learnt from previous classes that setting >50% CG content for stimulated reads so as to mimic some model plant genomes. The proposed program will allow users to input files for reads and the reference genome, parameters such as stringent mismatch allow etc.. The ultimate output inform the users where the reads aligned and how many mismatches are found.