Assignment #5

Due: 11:59pm, Wednesday, Nov 8, 2017

1. In previous homework, you implemented python programs to report "Reverse Complement" of your sequence with or without Biopython. Now, let's merge the two programs and give options for users to select which method will be used to report reverse complement. In addition, you should upgrade the program to allow getting an input file (not multiple files) from the user. In summary,
    a. Use Python optparse (https://docs.python.org/2/library/optparse.html) to get options from user.
    b. The program runs the Biopython reverse complement method by default, but should have an option to run your own reverse complement method.
    c. If there is no argument, then ask "Type your DNA sequence : " as previous and print out the reverse complement of the string. If you provide the DAN sequence file as an argument, the program should generate the output file that contains reverse complements of the file.
    d. The Input file and output file requirements:
        i. Multi lines of DNA sequences are allowed as an input.
        ii. Allow to get Fasta file
            1. If the input is FASTA file, then add "`(reverse)`" at the end of the ID line in the output file.
    e. The output filename requirements:
        i. Default is "input_base_filename_reverse.extension"
        ii. If user provides an output filename, then use it

2. Run "Spades" for the genome assembly of lab.
    a. Run quast of the assembly.
    b. Compare the results with Velvet.

    Extra credit: optimize the Velvet or Spades, and then get the best (based on N50) result as possible.