Determine the hexanucleotide frequencies of a metagenomic sample

Purpose: to determine the hexanucleotide frequencies of a metagenomic sample
Source code: hexa.cpp
Example input file #1: test_out.txt
Additional input file #2: six_mer.txt

Example output file: hexa_freq_test.txt

Instructions:
1) Compile source code to app called "hexa" using the line command:

      g++ hexa.cpp -o hexa

2) Run the "hexa" program by invoking the following line command:

      ./hexa test_out.txt six_mer.txt hexa_freq_test.txt