Bachelor of Technology Partnership
McMaster University Engineering
MOHAWK COLLEGE

C++ Programming – SFWR TECH 3PR3
Structures & File I/O

Assignment 3

1. Ocean wave measurement and analysis is important in Tsunami warning systems. Wave steepness is the ratio of wave height (WH) to wave length (WL) and is an indicator of wave stability. When wave steepness exceeds a 1/7 ratio the wave becomes unstable and begins to break.

   A file called wave.txt contains data for ocean waves. Each line in the data file contains time and wave height measurements as follows:

   year, month, day, hour, minute, wave height (metres), wave length (metres)

   The values are separated by one or more space characters.

   Create a program that will create a structure to store one record of wave data. Create a single-dimensional array of structures to store all wave data. There will be a maximum of 50 records in a data file, but there could be fewer than 50 records. Make sure your program can accommodate an unknown number of records, to a maximum of 50 records.

   The program will read the wave data, storing one record in each structure in the single-dimensional array. After reading the data and storing all data in the array, perform the following:

   Output to a file the data for all waves that exceed the 1/7 steepness ratio. Include the steepness ratio for each wave in the output.

   Output to the console the average steepness for each year (2010 – 2012), and the data for the steepest wave for each year.

2. Consider a strand of deoxyribose nucleic acid (DNA) with a length of 100 nucleotides (nt's), in which the sugar is called deoxyribose, and the only four choices for nucleobases are molecules called adenine (A), cytosine (C), guanine (G), and thymine (T). You can read more about DNA here (https://en.wikipedia.org/wiki/DNA).

An experiment was performed on 80 DNA strands that generated a series of numbers ranging between 1 and 4 in its output, where 1 refers to adenine, 2 to cytosine, 3 to guanine and 4 to thymine. The output of the experiment is recorded in a text file called “*data.txt*”; attached to the problem. It is required to decode the data from this file into proper DNA strands expressed in ACGT sequences. It is also required to calculate the number of nucleotides of each of the four nucleobases in each DNA strand. Finally, you need to convert some of the DNA strands to RNA (Ribonucleic Acid) strands based on certain conditions.

Write a C++ program to perform the task required while making use of the following:

a) A structure called “**DNAnt**” has 5 elements with the first 4 each storing the number of each of the four nucleobases in a DNA strand and the fifth is a c-string storing the DNA strand.
b) A function called “***data2DNA***” that reads the “data.txt” file, decodes the data stored in it and converts it into proper DNA strands. The function should write the results into a new text file called “*DNA.txt*”.
Example: 4 2 1 4 3 3 … is decoded to TCATGG…
c) A function called “***countDNAnt***” that accepts a c-string representing a DNA strand and its output is a **DNAnt** structure containing the number of A, C, G & T symbols in this strand.
d) An array of structures to store all 80 DNA structures called “**allDNA**” in main.
e) A void function called “***DNAtoRNA***” that accepts the DNA array of structures. For each DNA with more than 25 ‘T’ symbols, the function will replace all ‘T’s with ‘U’s, then write the modified sequence into a new file called “*RNA.txt*”.
Example: TCATGG… is converted to UCAUGG…

The main will display a table showing the counts of A, C, G & T of all 80 DNA strands.

Note: - Indicate the units for all I/O values required from- or provided to- the user.

Create a Word .doc file that contains the source code and a screen captures of the console window as the program is running, for all C++ programs. Save this file as *YourName_Assignment_1.doc* and upload and submit to the appropriate AVENUE lab assignment drop-box.