COSC581 - Algorithms
Spring 2023
Homework #4

Due: Monday, 02/20/2023, 5PM.

1. Data structures review -
    a. Describe the difference between the binary search tree property and the min-heap property.

    b. Can a stack be implemented using a queue? If so, describe how.

    c. Can dictionaries/maps be implemented using a hash table? If so, describe why.

2. Dynamic Programming -

DNA sequences are made up of four different amino acids: Adenine, Cytosine, Guanine, and Thymine (denoted A, C, G, T respectively). We can tell the basic genetic differences between two organisms by measuring the distance between their respective DNA strands. One method for measuring this is called global alignment. When we produce a global alignment, we weight our decisions based on the number of matches, mismatches and gaps. For example:

s1 = AGCTTTGAA, s2 = AGGTTGGCAA

AG--CTTTG----AA
AGG--TT--GGCAA

In this example, we weighed match=1, gap=0, and mismatch=-1, for a global alignment score equal to 7 (7 matches - green, 5 gaps - black, 0 mismatches - red).

For your homework, you need to show the full dynamic programming table for aligning the sequences: s1=GCTTACGTGACG, and s2=GCTATCGCGACC. Use match=2, gap=-1, and mismatch=-1. Show all your work.

***Please note that in sequence alignment a λ is prepended to the beginning of each sequence.*

	λ	G	C	T	T	A	C	G	T	G	A	C	G
λ													
G													
C													
T													
A													
T													
C													
G													
C													
G													
A													
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C													