Solution

Data Structures and Algorithms

Quiz1 (Fall 2022)

Total Marks: 20 Maximum Time Allowed: 30 mins

Instructions:

- This is a **closed book** exam.
- All necessary working must be clearly shown to receive full credit.
- No calculators or programming devices allowed.
- If you are asked to write an algorithm, it means you can write it in **pseudocode** form.
- Do not use the space for answer outside the provided space.

Question No.1 [CLO2][7 marks]

Finding the median of a sorted array A is easy: simply return the middle element. But what if you are given two sorted arrays A and B of size m and n respectively, and you want to find the median of all the numbers in A and B instead of finding the median separately of both A and B? You may assume that elements of A and B are disjoint.

1. Give an algorithm running in $\Theta(m+n)$ time. (3 point(s)) (Hint: You can use the concepts discussed in first two weeks)

Merge the two sorted arrays (which takes O(m+n) time) and find the median using linear time selection.

2. If m = n i.e. number of elements in both arrays are equal, give an algorithm that runs in $\Theta(\lg n)$ time. (4 point(s)) Pick the median m1 for A and median m2 for B. If m1 = m2, return m1. If m1 > m2, remove the second half of A and the first half of B. Then we get two subarrays with size n/2. Repeat until both arrays are smaller than a constant. m1 < m2 is symmetric.

Question No.2 [CLO2][6 marks]

1. Given a polynomial in n of degree d; p(n), how would you represent it asymptotically.(1 point(s))

 $p(n) = \sum_{i=0}^d a^i n^i = O(n^d)$

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- 2. What do you mean by randomized algorithm? (1 point(s))
 - a particular problem. Often, we shall assume that all inputs of a given size are equally likely. In practice, this assumption may be violated, but we can sometimes use a *randomized algorithm*, which makes random choices, to allow a probabilistic analysis and yield an *expected* running time. We explore randomized algorithms
- 3. What was the purpose of Human Genome Project? (Just one line.) (1 point(s))

 The Human Genome Project has made great progress toward the goals of identifying all the 100,000 genes in human DNA, determining the sequences of the 3 billion chemical base pairs that make up human DNA, storing this information in databases, and developing tools for data analysis.
- 4. What is the smallest value of n such that an algorithm whose running time is $100n^2$ runs faster than an algorithm whose running time is 2^n on the same machine? (1.5 point(s))

 Calculate value for n = 1, 2, 3, --- for both functions. Value is n = 15
- 5. What is the criteria to say that the an algorithm A is efficient than another algorithm B? (1.5 point(s))

Question No.3 [CLO2][7 marks]

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Code	Code Analysis of each line(3 point(s))
for i = 1 to n	$c_1(n+1)$
for j = i to n	$c_2 \sum_{i=1}^n n - i + 2$
print(j)	$c_3 \sum_{i=1}^n n - i + 1$
z = 1	$c_4 \sum_{i=1}^n n - i + 1$
while z > n	$c_5 \sum_{i=1}^n n - i + 1$
print(z)	$c_{6}(0)$
Sum of complexity of each line and detailed calculati	ions (3 point(s))
Add all these entities, we will get equation of the form	$m an^2 + bn + c$

Final result in form of Asym	<pre>ptotic Notation(1 point(s)):</pre>	$O(n^2)$

Space for Rough work