

ASSIGNMENT 1: Due Date: 07-February-2023

Criteria for evaluation

- Commenting of code
 - The code file you have submitted needs to be executable and satisfy all the test cases.
 - A clear and comprehensive explanation of your problem-solving approach.
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Question 1.

Find the time complexity of the following pseudo-code.

1.1. Code Snippet 1

```
1 int a = 0 , b = 0;
2 for ( i = 0; i < N ; i ++ ) {
3   a = a + rand () ;
4 }
5 for ( j = 0; j < M ; j ++ ) {
6   b = b + rand () ;
7 }
```

1.2. Code snippet 2

```
1 int l , t , k = 0;
2 for ( l = n / 2; l <= n ; l ++ ) {
3   for ( t = 2; t <= n ; t = t * 2 ) {
4     k = k + n / 2;
5   }
6 }
```

1.3. Code snippet 3

```
1 int a = 0 , i = N ;
2 while ( i > 0 ) {
3   a += i ;
4   i /= 2;
5 }
```

Question 2.

Given an array of numbers, find the GCD of the array elements (Hint: Use the Euclidean algorithm discussed in the lecture)

- Example Input
 - arr[] = {1, 2, 3}
- Output:
 - 1

- Example Explanation
 - The GCD of three or more numbers equals the product of the prime factors common to all the numbers.

Question 3.

The biological challenge we will work on for this homework is Restriction Mapping. For a more detailed explanation of the methods, please see this link: <https://www.ncbi.nlm.nih.gov/books/NBK21116/#A6269>

What we have: A collection of Sequences of varying lengths from different parts of, let's say, a chromosome. What we want to do: Determine which two sequences span the entire chromosome. We want the two fragments to overlap a little but not too much because it would be a waste of resources.

Restriction enzymes can cut/digest at specific sites. In normal applications, multiple restriction enzymes are used, separately and in combination, to cut DNA into smaller pieces. The pieces of DNA are then run on a gel that separates the fragments based on size.

The figure below shows the result of running the fragments in the gel.

Develop an algorithm that will allow you to assemble the sequence based on the fragments provided so we know how they are related (how they overlap). After determining the relationship of the sequences, determine which two sequences span the entire chromosome.

Size	Seq1		Seq2		Seq3		Seq4		Seq5		Seq6
200											
150											
100											
75											
60											
50											

How to read this image: Sequence 1 has four DNA fragments, 150, 100, 75, and 60 bp long. If a fragment size is shared between different sequences, it represents the same region from the chromosome.