

Quiz ONE

Question 1: Alignment

a) Provide an algorithm to find the global alignment between two circular DNA sequences (**m2no**) by linearizing each sequence.

Note: The sequences should be linearized by cutting at any arbitrary point. The best alignment among all possible cut points is considered optimal.

b) In some cases, two candidate sequences might exist:

- One sequence is significantly smaller than the other.
- The smaller sequence appears as part of the larger sequence (with potential differences caused by mutations such as **insertion, deletion, or substitution**).

The goal is to find the position in the larger sequence that most closely matches the smaller sequence. Use a **semi-global alignment** approach to solve this problem.

Question 2: Multiple Sequence Alignment

Suppose at a stage of a heuristic **MSA algorithm**, the following two alignments are available:

Alignment 1:

```
- GGAT- -  
AGC-TAC  
--CAGAC
```

Alignment 2:

```
TGAC  
-CAC
```

Align these two sequences.

Note: In cases of equal scores, prioritize the alignment with the higher total score.

Short Answer Questions

- a) What are **non-coding RNAs**? Provide an example of a functional RNA.
 - b) Explain the advantages of **DNA splicing**.
 - c) If the genome is identical in all cells of an organism, why do cells differ in function (e.g., eye cells vs. blood cells)?
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Optional Questions for Revision:

- a) What methods can identify the **origin of replication**?
- b) What are the two primary differences between prokaryotic and eukaryotic cells?
- c) Why is the number of possible codons greater than the number of amino acids?