

Quiz Two

Question 1: Short Answers

- a) What approach is used to convert **RNA** to **cDNA**, and what is its application?
- b) Briefly explain the workflow of **Sanger Sequencing**.
- c) Suppose you have multiple short reads resulting from sequencing. How would you reconstruct the genome using:
- A reference genome
 - Without a reference genome
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Question 2: De Bruijn Graphs

Consider the following sequences:

ATTAC, TACAG, GATTA, ACAGA, CAGAT, TTACA, AGATT

- a) Using a **De Bruijn Eulerian graph**, find the shortest circular sequence that includes all the above sequences.
- b) Why do we use **De Bruijn Eulerian graphs** instead of Hamiltonian graphs to solve this problem?
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Question 3: Burrows-Wheeler Transform (BWT)

After applying BWT on a sequence, we obtain **CGAT\$CC**.

- a) Reconstruct the original sequence.
- b) Explain how **BWT** can be used for text compression.