Indraprastha Institute of Information Technology Delhi (IIITD)
Department of Computational Biotechnology

BIO213 − Introduction to Quantitative Biology

ASSIGNMENT-1 (October 02, 2025)

Instructions:

1. Assignment can be hand written or typed, should be submitted as a PDF file.
2. Submissions after **October 10, 2025** will not be entertained.

De Bruijn Graphs in Fragment Assembly

In class, we discussed the use of De Bruijn graphs for fragment assembly in genome sequencing. We reviewed how this approach works and examined the challenges and limitations associated with the algorithm. Despite these challenges, De Bruijn graph–based methods remain state-of-the-art and are widely used in modern genome assembly pipelines.

Tasks to do:

1. Revisit the concepts discussed in class and summarize the key problems and limitations of De Bruijn graph−based assembly that we covered.   **(5 marks)**

2. Explore and identify the solutions or improvements that have been proposed and integrated into present-day genome assembly tools to overcome these challenges.   **(15 marks)**

3. Provide examples of at least two current genome assemblers (e.g., Velvet, SOAPdenovo, SPAdes, etc.) and explain how they implement these improvements.   **(10 marks)**