90-Minute Discussion Session Plan
Lecture 2: Sequencing & k-mers

Course: BINF301 — Computational Biology
Instructor: [Enter Name]
Date: [Enter Date]

0-10 min — Warm-Up

- Icebreaker: Which sequencing technology (Sanger, Illumina, PacBio, Nanopore) are you most familiar with?

- Starter prompt: What surprised you most about differences between sequencing generations?

10-25 min — Think-Pair-Share

Prompt: Based on the lecture slides, what do you think is the main limitation of each sequencing technology (1st, 2nd, 3rd generation)?

Follow-up: How do quality scores influence downstream analysis?

25-45 min — Structured Group Discussion

Roles:

- **Summarizer:** Recap FASTA vs FASTQ formats and Phred quality scores.

- **Questioner:** Bring one question about basecalling or sequencing error models.

- **Connector:** Link k-mers to sequencing output and quality issues.

Starter question: Why do sequencing errors inflate the number of unique k-mers?

Break (15 min)

45-65 min — Applied Exercises Block

Students work collaboratively on structured exercises, see handout.

80-90 min — Reflection & Wrap-Up

- One takeaway from today?

- One question to revisit next time?