

# 90-Minute Discussion Session Plan

## Lecture 2: Sequencing & k-mers

**Course:** BINF301 — Computational Biology

**Instructor:** Tom Michoel

**Date:** 19/01/2026

**Created with Copilot**

### 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?