60-Minute Discussion Session Plan
Lecture 5: Repeats

Course: BINF301 – Computational Biology
Instructor: Tom Michoel
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0-5 min – Warm-Up

Warm-up prompt:

'Did any of the genome-size figures or TE diagrams stand out or raise questions?"

Instructor note. Goal: get students comfortable speaking early; activate recall from key ideas on Slides 3–6 and 10–12 (C-value variation, what counts as repetitive DNA). Encourage brief answers rather than deep explanations at this stage.

5–20 min – Guided Concept Walkthrough

Purpose: Establish shared conceptual grounding before deeper discussion.

Topics:

- The C-value paradox and genome-size variability (Slides 3–6).
- Types of repetitive DNA: tandem vs. interspersed, autonomy, replication mode (Slides 10–12).
- Transposable elements: LTR, LINE, SINE, DNA transposons (Slides 14–22).
- Genome evolution impacts: structural variation, plasticity, HTT (Slides 25–28).
- Why repeat detection is difficult (degeneration, partial copies, divergent families; Slides 32–39).

Guiding prompts:

- "Why can genome size vary so widely between similar organisms?"
- "How would you explain the difference between LINEs and SINEs to a beginner?"
- "What features help us identify whether a TE is autonomous?"
- "Why do degenerate repeats cause trouble for computational tools?"

Instructor note. Keep the walkthrough brisk. Anchor students by pointing to major diagrams: e.g., C-value plots, TE life-cycle schematics, classification tables, and the TE propagation mechanisms on Slides 17–21. Clarify autonomy vs. non-autonomy and replication intermediates.

20–40 min – Open Reflection & Deep Dive

Discussion prompts:

- "Which classification dimension (mechanism, structure, autonomy) is hardest for you?"
- "Why does repeat degeneration complicate family classification?"
- "How do LINEs and SINEs co-evolve? Why do SINEs depend on LINE machinery?"
- "Which detection approach (alignment-based, k-mer–based, HMM-based) best handles highly degenerate repeats?"

- "How do repeats affect genome assembly, annotation, and error-prone regions?"

Instructor note. Use this block to unify biological and computational angles. Encourage reasoning rather than fact recall. For example: degeneration → lower sequence identity → clustering ambiguity; TE co-evolution → shared machinery but different autonomy; HMMs (RED) handle weak signals better than strict k-mer frequency.

40–55 min – Assignment

Work on the Portfolio Assignment Genomics, task data retrieval.

55–60 min – Wrap-Up

Closing prompt:

"What remains confusing about how repeat detection tools differentiate families?"

Instructor note. Collect a quick diagnostic of students' comprehension. These answers help target the next lecture (e.g., more depth on TE evolution, or practical lab work on RepeatMasker/RepeatModeler).