Lecture 3: Genome Assembly
Student Handout & In-Class Exercises

Course: BINF301 — Computational Biology
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Date: 21/01/2026
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1. Overview

This handout summarizes core ideas:

- What genome assembly is and why it is difficult.
- Two graph-based strategies: Overlap-Layout-Consensus (OLC) and De Bruijn Graphs (DBG).
- Complexity considerations.
- Handling errors and graph imperfections.

2. Genome Assembly Basics

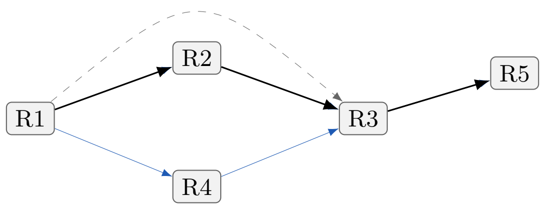
Definition & Challenges

Genome assembly combines sequencing reads into longer contiguous sequences (*contigs*). Key challenges:

- Repeats introduce ambiguity (multiple valid traversals).
- Sequencing errors introduce false paths/edges.
- Data volume drives graph size and cost.

3. Overlap-Layout-Consensus (OLC)

Idea. Reads are *nodes*; overlaps are *edges*. Reconstructing the genome corresponds (ideally) to a **(directed) Hamiltonian path** (visit each node/read once).



OLC sketch: nodes are reads (R1–R5), edges show overlaps. Dashed edge indicates a *transitive* overlap (can be removed). Solid black edges show assembled contig. Blue edges show alternative branching path (due to repeat or errors) that cannot be resolved directly by Hamiltonian path finding. Alignment of R2 and R4 could be used to collapse nodes and resolve the path.

Why transitive reduction? Removing transitive edges simplifies the graph and reduces ambiguity.

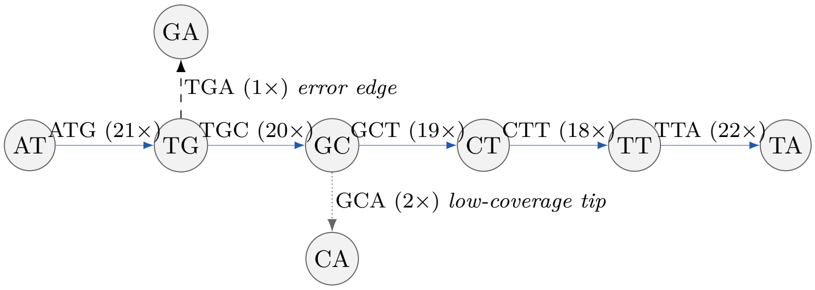
4. De Bruijn Graphs (DBG)

Idea. Nodes are $(k-1)$-mers; edges are k-mers. Reconstruction corresponds to an **Eulerian path** (visit each edge once). Under perfect sequencing (each genomic k-mer present exactly once), the graph is Eulerian.

DBG sketch: nodes are $(k-1)$-mers, edges are k-mers; traversal uses each *edge* exactly once (Eulerian).

5. Non-perfect Sequencing in DBG (errors/repeats)

Errors, missing/duplicated k-mers create tips, bubbles, or spurious branches.



Non-perfect DBG. Top chain: high-frequency true k-mers (18–22×). Dashed branch: *TGA* (1×) is a sequencing error → novel, unsupported k-mer. Dotted tip: *GCA* (2×) may be real but insufficiently sampled → low-coverage artifact.

6. Complexity (OLC vs DBG)

OLC. Building overlap graphs can be $O(N^2)$ in reads; graph can be large (especially for short reads). **DBG.** Construction scales with number of k-mers ($\approx O(N)$); more memory-efficient for high read counts, but sacrifices long-read continuity.

7. In-Class Exercises

Exercise 1 — Understanding OLC Overlap Graphs

Using OLC diagrams:

- Identify nodes vs edges.
- Find transitive edges (and say why to remove them).

Exercise 2 — Hamiltonian vs Eulerian

Reads: `ACTTTCTTCTGG`.

- In OLC: visit each *read* once (Hamiltonian).
- In DBG: traverse each *edge* once (Eulerian).
- Why is one NP-hard and the other linear-time?

Exercise 3 — DBG Error Scenario

Genome: `ATGCTTA` Reads ($k = 3$): `ATG, TGC, GCT, CTT, TTA, TGA` (TGA erroneous)

Tasks:

- Build the 3-mer DBG (nodes=2-mers; edges=3-mers).
- Identify the inconsistent edge.
- Explain coverage-based pruning.

Exercise 4 — Choosing OLC vs DBG

- Why OLC for long reads and DBG for short reads?