# Genome assembly paradigms 

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## Recap

- A simple greedy algorithm can solve the assembly problem reasonably well.
- The greedy algorithm gets stuck in repeats - graph based approaches may address this problem


## Genome assembly paradigms

- Greedy algorithm
- easy to implement
- relatively efficient
- but... can make mistakes because it is greedy (only takes into account local information)
- How can you "reason" about repeats?
- Graph theory can help: 2 paradigms
- Overlap-Layout-Consensus: nodes=reads, edges= reads overlap
- deBruijn/repeat graph: nodes $=k$-mers, edges $=k+1$-mers (extracted from the reads).
- Both translate into: find a constrained path within a graph


## Overlap-layout-consensus

- Essentially an extension/refinement of the greedy approach
- Given the set of reads, what can we infer about the genome?

- All reads (nodes) must be used exactly once
- Algorithm?


## Overlap Layout Consensus

- Build a graph
- Traverse it such that each node is seen exactly once

- Hamiltonian path/cycle - NP-hard


## De Bruijn graph (Eulerian) formulation

Inspiration: sequencing by hybridization

|  | AAAA |
| :---: | :---: |
| $\because: 8:: 8: 8:$ | AAAC |
| : $: 8: 8: 8: 8:$ | AAAG |
| : $: 8: 8: 8: 8$ | AAAT |
| $\because: \because: 8: 8:$ | AACA |
| : $\because: 80: 8: 8$ | AACG |
| $\because: \because: 8: 8: \%$ | AACT |
| $: \because: \geq: 8: 8:$ | AAGA |

AACAGTAGCTAGATG
AACA TAGC AGAT
ACAG AGCT GATG CAGT GCTA
AGTA CTAG
GTAG TAGA
probes - all possible k-mers

## De Bruijn graph formulation

 ACCTAGATTGAGGTCG

- (segment of) read = pair of k-mers overlapping by k-1 bp = edge
- Need to use all k+1-mers in the genome (the reads), i.e., all edges


## de Bruijn graph

- Traverse a graph such as each edge is visited

- Exactly once - Eulerian path/cycle
- At least once (but least amount necessary) - Postman/route inspection path/cycle
- Both can be solved efficiently


## Aside: graph traversals

- Hamiltonian path: visit every single node of a graph EXACTLY once (NP-hard)
- Eulerian path: visit every edge of a graph EXACTLY once (polynomial time)
- Postman/route inspection: find the shortest path in a graph that visits all the edges (i.e. Eulerian path where you allow a minimum number of edges to be reused)
- Note: a Hamiltonian path or an Eulerian path are not guaranteed to exist. A postman path can always be constructed


## Eulerian circuit

## The 7 bridges of Koenigsburg


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