Genome Assembly

High Throughput Sequencing

Example applications:
- Sequencing a genome (DNA)
- Sequencing a transcriptome and gene expression studies (RNA)
- ChIP (chromatin immunoprecipitation)

Example platforms:
- 454
- Illumina
- SOLiD

Sequencing Output

- Hundreds of millions of sequencing reads, each ~100 nts in length
- We need to re-assemble the genome from these sequencing reads
Assembly

GGCTAG

>GGCAGGC
>GGCTAGGG
>TAGGGCA

Assembly

GGCTAAGG

>GGCAGGC
>GGCTAGGG
>TAGGGCA

Assembly

GGCTAGGCAG

>GGCAGGC
>GGCTAGGG
>TAGGGCA

Assembly

GGCTAGGCAGGGC

>GGCAGGC
>GGCTAGGG
>TAGGGCA
**Challenges**

- Repeats
- Sequencing errors

**Implementation**

deBruijn graph can be implemented with a hash table

- Each entry in hash table corresponds to an edge in the graph (each key is a $k$-mer and each value is the number of occurrences of the $k$-mer).
- Nodes are stored implicitly.

**Assembly corresponds to Euler path through graph**

- Genome sequence starts with any $k$-mer (edge in the graph)
- Repeatedly extend genome sequence **forward**, one nucleotide at a time, until no further extensions are possible
  - The genome sequence is extended and a nucleotide added to its end if there exists a nucleotide (A, C, G, or T) that can be added to the end of the $k$-1 final nucleotides of the genome sequence to form a $k$-mer that is an edge in the graph.
  - If there are multiple individual nucleotides that can be added to the final $k$-1 nucleotides in the genome sequence to form $k$-mer edges in the graph, then the nucleotide resulting in the $k$-mer edge with the largest number of occurrences is chosen.
  - Each time the genome sequence is extended by a nucleotide, the corresponding $k$-mer edge is removed from the graph.

- Repeatedly extend genome sequence **backward**, one nucleotide at a time, until no further extensions are possible
  - The genome sequence is extended and a nucleotide added to its front if there exists a nucleotide (A, C, G, or T) that can be added to the front of the $k$-1 first nucleotides of the genome sequence to form a $k$-mer that is an edge in the graph.
  - If there are multiple individual nucleotides that can be prepended to the first $k$-1 nucleotides in the genome sequence to form $k$-mer edges in the graph, then the nucleotide resulting in the $k$-mer edge with the largest number of occurrences is chosen.
  - Each time the genome sequence is extended by a nucleotide, the corresponding $k$-mer edge is removed from the graph.