

De Bruijn Graph Construction in Genome Assembly

Project Summary

- Objectives: To construct De Bruijn Graph in Genome assembly
- Scope:



Research Design : Methods and Algorithms

- The answer to the stated problem now was to find a path through the graph that traverses each edge exactly once, or in other words Eulerian trail.
- Reads are broken into smaller fragments of a specified size k.
- k-mers are identified and a de Bruijn graph with (k-1)-mers as nodes and k-mers as edges drawn as described in the text. A Eulerian path is traced through this network resulting in the reconstruction of the original genome sequence.



Research Design: Methods and Algorithms

Take all (k-1)-mers from the set of k-mers

Construct a multi-graph with nodes being k-1-mers; draw an edge between two k-1 mers only if the two k-1 mers are taken from the same read.

Graph constructed this way is guaranteed to have a Eulerian trail, follow the trail and connect the nodes to form our original sequence.

this algorithm can be used to assemble k-mer reads

Build kmers or reads from the input string

After generating the reads, debruijnize the reads to form (k-1) mers

Make node – edge map using the obtained k-1 mers

Construct an Eulerian trail using the k-1 mers as nodes by drawing an edge between them only if they are taken from the same reads

Graph constructed will have a Eulerian trail and thus print the Debruijn graph.

Follow or trace the Eulerian path and connect the nodes to get the original sequence

Results

Discussion

Conclusion

