

Abstract :

- The Problem is De Bruijn graphs Consume Large memory.
- We have a solution to reduce this complexity by compacting paths with single vertices
- On the other hand, this way has a problem because it requires the graph to be in the memory.
- Bifrost features is a parallel and algorithm which saves the memory ,also.
- Our Parallel algorithm enable the direct construction of the compacted graphs.
- Bifrost has some added features such as indexing, editing, querying and the graph coloring method.

Introduction :

- De Bruijn graph is an abstract data structure used in computational biology as a tool for genome assembly.
- Since 2008, the de Bruijn graph genome assemblers range have been released.
- De Bruijn graph-based methods are nonetheless used to assemble and correct long reads.
- De Bruijn graphs have found widespread by solving a variety of problems such as de novo transcriptome assembly, variant calling, short read compression, short read correction, long read correction, and short read mapping to name a few.
- There is a colored de Bruijn graph which is a variant of the de Bruijn graph.
- The colored de Bruijn graph keeps track of the source of each vertex in the graph.
- The initial application was for assembly, genotyping, pan-genomics, variant calling, and transcript quantification methods.