

Succinct Data Structures for Genome Assembly and Pan-Genomics

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Abstract

The de Bruijn graph lies at the heart of many processes in modern bioinformatics, and almost always both the size of the graph and the time required to construct it are serious bottlenecks in practice. This talk will describe different succinct representations of the de Bruijn graph that alleviate these bottlenecks in two important applications, namely genome assembly, and the study of variations between individuals from the same species (pan genomics).

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