

Abstract

Despite active development during past years, the task of sequencing a genome still remains a challenge. Our current technologies are not able to read the whole genome in one piece. Instead, we shatter the target genome into a large amounts of small pieces that are then sequenced separately. The process of assembling these small pieces together, in order to obtain sequence of the whole genome, is painful and rsource-consuming. Multiple algorithms to solve the assembly problem were developed.

This thesis presents yet another assembly algorithm, based on the usage of de Bruijn graphs, and focusing on sequencing short genome regions. The algorithm is compared to well-known solutions in the field.