

Abstract

Detailed information of the genome of the studied organism is crucial for many fields of modern research. Actual sequencing technologies are not able to read the whole DNA molecule at once therefore only fragments of the genetic information are obtained, which are not sufficiently informative on their own. The goal of the genomic-bioinformatic approach is to assemble these fragments into complete original information – genome assembly. The process of the genome assembly is demanding in terms of computational power, software equipment and expert staff. Many assemblers – programs for genome assembly are available differing in performance, size of the analyzed genome or target organism. The quality of final assembly is fully dependent on assembler and setting of inner parameters. In practice, multiple assemblies are constructed and their quality evaluated according to the technical and biological parameters. The presented thesis describes current high throughput sequencing technologies, different approaches and algorithms for genome assembly and methodology for their quality assessment. The practical part is focused on assembly and its quality assessment using Illumina data of the bird fluke *Trichobilharzia szidati*.