Abstract

The cost of sequencing has fallen almost ten thousand times over the past ten years due to the development of second and third generation sequencers. Sequencing and assembling the whole genome sequence of an organism is thus becoming a more affordable tool which can be utilized in many fields of science. On the way to the complete DNA sequence of an organism, multiple important decisions have to be made. These are crucial for the successful assembly of high-quality whole genome sequence and regard sample preparation, choice of sequencing technique and choice of an appropriate approach to whole genome assembly. This bachelor thesis describes various methods which can be utilized in individual steps of the process and aspects to consider while making the decisions.

Keywords: next generation sequencing, third generation sequencing, whole genome sequencing, *de novo* assembly, genome assembly algorithms