

Sequencing of DNA from microbial communities enables, besides taxonomic profiling, study of intrapopulation genetic variability. Its description is a result of a computational analysis of sequencing data. This thesis investigates what bioinformatics tools are available for *de novo* detection of intrapopulation variability in metagenomic data and how these tools function algorithmically. It provides a perspective for tool performance validation, and for that, it begins by discussing sequencing methods of platforms Illumina, PacBio and Oxford Nanopore Technologies, aiming at their limitations, and it continues with describing computational reconstruction of genomic sequences. Beyond the review of tools and benchmarks, it attempts to provide conceptual view on approaches to the study of variability based on metagenomic data.