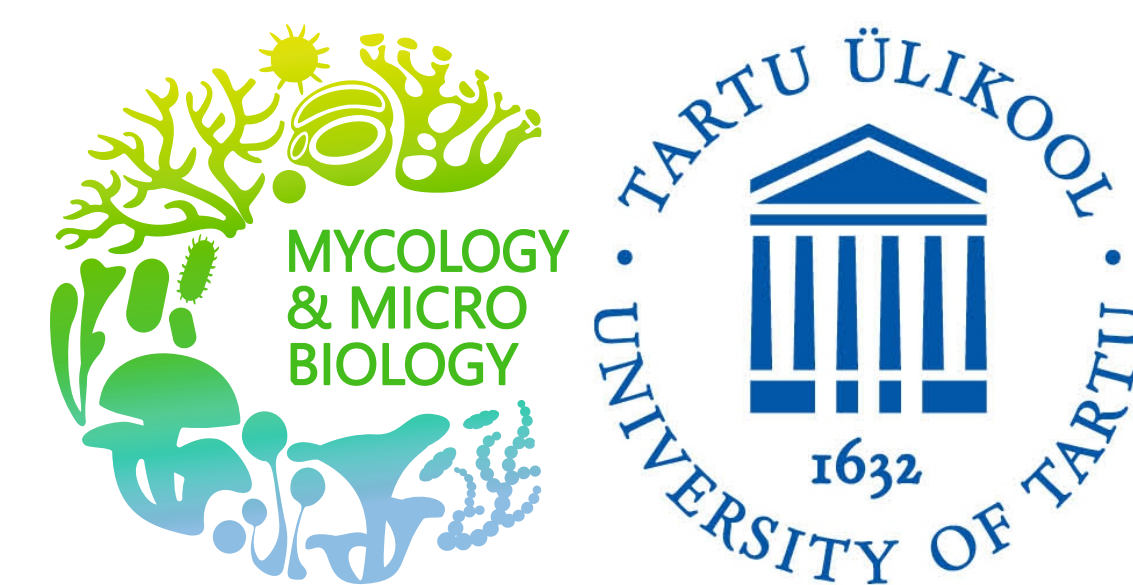


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<https://github.com/vmikk/NextITS>



The most widely used genetic markers for metabarcoding of fungal communities are rRNA ITS1 and ITS2 sub-regions of internal transcribed spacer. Unlike 18S or 28S genes, the ITS region is more variable in fungi, and thus, used for taxonomic identification. High-throughput metabarcoding has greatly improved our understanding of the ecology of fungal communities. However, second-generation sequencing methods allow analysis only of short amplicons providing limited taxonomic and phylogenetic resolution for species assignment.

Here, we present NextITS, a Nextflow-based pipeline for analyzing full-length ITS sequences (ITS1-5.8S-ITS2) obtained using the Pacific Biosciences (PacBio) third-generation sequencing platform.

