



Figure 1 illustrates the methodological workflow of present thesis. In the first step, the microbial community (mono-eukaryotic community with co-isolated prokaryotes) is sequenced with Oxford Nanopore and Illumina. In the raw sequencing data, we can detect 16S rDNA (Barrnap) and use it to generate phylogenetic trees (RAXML, Iqtree). The raw data from Oxford Nanopore is complemented by Illumina data (NextPolish) and assembled (MetaFlye). The assembled metagenomes are used as input for binning (Maxbin2, Metabat2, DAS Tool). The quality of the resulting bins is checked with BUSCO and CheckM. For each bin we perform a structural and functional annotation (Prodigal, RAST, KEGG). Based on the results of the functional annotation, I try to identify possible interactions between the protists and their associated prokaryotic community).