

**Bioinformtics for Microbiology
-course and practicals-**

Dr. Peter HANTZ, Eötvös University Budapest and Fibervar Llc., Klausenburg

Sampling, sample conservation

Sequencing methods: Sanger / Illumina / Nanopore

Linux Basics, R and AI copilots

File formats for DNA and Protein

Metabarcoding, Amplicon sequencing (16S, 18S, ITS)

DADA2 pipeline, Silva and Unite databases

Assembly: longer sequences from reads, Sequence Alignments

Annotation: what did we get

BLAST, Biological databases

Metabolic Functions, KEGG database of metabolic pathways

Phylogenetic Trees