# Bioinformatic Summer School - Comparative Genomics, long-read Metagenomics and Metataxonomic Analysis 2024

The overall teaching aim of this module is to create competence in the students in terms of independently perform bioinformatic analysis on the command line. This includes comparative analysis on bacterial (meta)-genomes and metataxonomic analysis.

The course contains modules on the following 3 areas:

1. Genomic assembly and annotation.
   1. SPADES, Bakta, antiSMASH
2. Assembly of long-read metagenomes.
   1. Filtlong, metaFLYE
3. Taxonomic analysis of microbiomes.
   1. DADA2, Phyloseq

The successful student will

1. Have a working knowledge of the Linux command line
2. Be able to use suggested command line tools
3. Investigate the bioinformatic literature to find further tools relevant for the biological questions
4. Infer the biological relevance of the genetic content in bacteria
5. Infer the composition of microbiomes
6. Discuss the biological implications of phylogeny, genetic content, microbial composition and the relatedness of all the above

The workload of this course is expected to be **84 hours**, corresponding to **3 ECTS.**  The distribution of this is as follows:

* 36 hours of preparation
* 40 hours of confrontation
* 8 hours of presentation