## Name of the subject: METAGENOMICS OF MICROBIAL COMMUNITIES

Teacher(s): Dr. Ivica Tamaš

Status of the subject: Elective

Number of ECTS points: 15

Condition: A prior consultation with the subject teacher.

### Goal of the subject

A detailed outline of the principles of metagenome analysis of the microbial communities including a bioinformatic analysis of the sequences on the basis of seuqence similarities . Laboratory aspects such as DNA extraction from the environmental samples, primers design, samples preparaton for Nest Generation Sequencing, description of the existing NGS platforms (Illumina, PacBio, IonTorrent, etc.)

#### **Outcome of the subject**

Gaining a knowledge about the latest trends in microbial ecology using molecular techniques and Next Generation Sequencing.

# Content of the subject

Theoretical lectures

Methodology of samples preparation from a variety of environments. Bioinformatic analysis of the sequnces using different bioinformatic tools.

Practical lectures

Bioinformatic analysis of the chosen sequences from the publica data basis (https://www.ncbi.nlm.nih.gov/bioproject?term=metagenomes).

### **Recommended literature**

De Bruijin F. J. (2011): Handbook of Molecular Microbial Ecology I. John Wiley & sons, Inc. Hoboken, New Jersey

2. De Bruijin F. J. (2011): Handbook of Molecular Microbial Ecology II Metagenomics in Different Habitats, Wiley-Blackwell

Ian L. Pepper, Charles P. Gerba, Terry J. Gentry (2014): Environmental Microbiology, third edition, Academic Press, San Diego

### Methods of delivering lectures

Consultations with the subject teacher, computer classes (a variety of bio

informatic tools currently used for sequence analysis), individual computer work from home.

### Evaluation of knowledge (maximum number of points 100)

Assignment - up to 30, Seminar up to 30, Project Presentation of scientific work up to 10. Oral exam up to 30 points