

## **Focus on Soils and Water Application form for funding of courses and other activities**

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**Date of application:** 21 11 2024

**Title of activity:** Multi-omics analyses of the microbial community

**Type of activity** course

### **Background and aim**

**-Give a short background and general aims of the activity-Include a short motivation for why you think it fits with the objectives of the research school-Provide information on availability of similar courses**

Background and general aim:

In the last couple of decades, metagenomics approaches have completely updated our view on microbial diversity and bypassed limitations of cultivation methods. These metagenomic studies unearthed a remarkable bacterial and archaeal diversity from different ecosystems and revealed novel microbial and viral lineages. These findings have completely revolutionized our view on the tree of life. Metagenomics has become an exciting approach to push the frontiers of our understanding of microbial life.

As we are moving forward, we have questions about activity and interaction of microbes, which cannot be answered by relying only on metagenomics. In addition to understanding the diversity of microbes in each environment, we want to know what they are doing and how their metabolites are contributing to ecosystem functioning and elemental cycling. So it is inevitable that we need to combine methods to not only look into their genomes but also explore the genes they transcribe, proteins they synthesis and metabolites they generate.

Now is the prime time for multi-omics analyses, meaning using a combination of different high throughput omics approaches, to get a more comprehensive understanding of the ecosystem and its microbiome.

The main challenge in the way for these analyses is the effective combination of these omics methods in a multi-omics perspective that will enable us to answer a specific question. This course will start by providing a basic understanding of potential and limitations of different high throughput omics methods and then enable students to use this knowledge for building a proper multi-omics perspective fitting their biological question. We will also have a specific focus on gene annotation since genes are the key for allowing us to integrate and connect different omics approaches. This course will familiarize students with different analyses approaches and proper gene annotation methods. Students will learn to design multi-omics studies and identify the appropriate analyses method for different multi-omics datasets and questions.

Alignment with the objectives of the research school:

Microbes are a major component of aquatic and terrestrial ecosystems. High throughput omics approaches have completely revolutionized our understanding of microbial diversity. These methods are becoming an indispensable component of comprehensive studies of the ecosystem for understanding the diversity and function of microbes. Additionally, these methods are an exciting target for next generation monitoring approaches using environmental DNA. That is why understanding these methods, their advantages and disadvantages, and how to combine them for mechanistic understanding of the environmental microbiome is necessary for students of this research school.

Availability of similar courses:

In the list of provided and planned courses of the Focus on Soils and Water research school a course focusing on omics methods is missing. Additionally at SLU level there are courses focusing on analyses of high throughput RNA sequencing which is not encompassing metatranscriptome analyses, the course molecular methods in microbial ecology touches upon aspects of environmental omics methods but does not provide a view on combination of omics methods for answering more complex questions. Covering state-of-the-art environmental omics methods and advantages/disadvantages in combining them in a multi-omics approach is unique to this course. Additionally, by focusing on gene annotation this course is providing needed insight into challenges we are facing in understanding microbial metabolism and physiology from their genome which is not covered in other courses.

## **General structure**

### **-Type of activities, e.g. lectures, computer exercises, seminar discussions?**

The course will include a mix of synchronous lectures, interactive activities in smaller groups, hands-on data analyses sessions, and asynchronous sessions in form of flipped classroom and literature review plus demonstration laboratory aspects.

The course design will enable participants to follow the course material at their own pace and to discuss among peers in order to deepen their understanding of the topic and the methods.

**Week 1** will contain active teaching sessions followed by extensive and directed literature review and preparatory exercises for the rest of the week. Instructors will be available for questions and guidance.

**Week 2** will contain active teaching and exercises every day of the week.

## **Learning targets**

### **Aims of this course:**

- Familiarize the participants with different high throughput omics methods including metagenomics, metatranscriptomics, single cell genomics and transcriptomics

- Discuss how these methods can be efficiently integrated in a multi-omics study for answering our biological questions
- Introduce participants to different approaches for analyzing multi-omics datasets
- Discuss advantages and disadvantages of different multi-omics integration designs and analyses approaches in addressing aims and objectives of different studies
- Focus on gene annotation as a key for integrating different omics methods
- Use gene-based perspective to combine different omics methods and identify the challenges
- Improve participant critical thinking in designing experiments and sampling campaigns employing a combination of different omics approaches
- improve participants understanding of the limitations of integrating different omics approaches
- enable student to design their own studies by integrating appropriate omics methods
- enable student to design their analyses steps to answer their biological questions

### **Corresponding Learning Outcomes:**

- Define different high throughput omics methods
- Understand the potential and limitations of different high throughput omics methods
- Integrate different omics methods in an effective way to answer their own biological question
- Summaries different annotation tools and databases and understand their advantages and disadvantages
- Understand analyses steps for metagenomes
- Understand analyses steps for metatranscriptomes
- Understand analyses steps for single cell genomics
- List limitations of each omics method

### **Time plan**

#### **-Include a rough total time plan for the activity**

This course is preliminarily planned for March 3 to 14, 2025

### **Organizers**

#### **-Main organizer, assistants, suggested invited speakers**

Dr. Maliheh Mehrshad (main organizer)

Prof. Stefan Bertilsson (assistant organizer)

Dr. Moritz buck (lecturer)

Dr. Fernando Puente Sanchez (lecturer)

Dr. Claudia Bergin (lecturer)

Prof. Sarahi Garcia (invited lecturer)

Dr. Samuel Miravet-Verde (invited lecturer)

Prof. Yin Chen (invited lecturer- online)

Dr. JP Balmonte (invited lecturer-online)

In the process of finalizing more local and invited speakers for lectures in the course

**Participants** -Expected number of students: 20

**Credits (course activities only)** -Expected number of ETC for PhD students: 3

**Examination (course activities only)**

**-Describe examination activities**

The grading scale **pass/fail** will be used for this course. The course examination will be based on attendance and active participation in discussion sessions. Students will be requested at the beginning of the course to prepare a short presentation about how they will or plan to use environmental omics or multi-omics methods in their thesis work and what are their questions/concerns regarding integrating these methods in their research. We will revisit this at the end of the course and update their plans and assess its feasibility based on what they have learned in the course. In another course activity students will be presented with a research question/hypothesis. They will then be divided in groups of 2 students and discuss how they will address this question/hypothesis by applying multi-omics approach, they will also design the analysis steps and envisioned results in a two page written proposal.

**Additional funding** -Do you plan to apply for funding from other sources? no

**Additional comments**

**Send your application together with the budget sheet to  
Maria.Kahlert@slu.se**