

## Course Metagenomic Methods for Microbial Ecologists 15-19 September 2014

and

## Environmental Metagenomics Symposium

19 September 2014

NIOO, Wageningen, the Netherlands

**Date:** Course: 15-19 September 2014; Symposium: 19 September 2014.

**Location:** NIOO, Wageningen, the Netherlands (<http://www.nioo.knaw.nl>).

**Coordinators:** Bas E. Dutilh (Radboudumc & Utrecht University), Eiko Kuramae (NIOO-KNAW), Celia van Gelder (Radboudumc).

**Pre-registration:** The website will be available soon (<https://nioo.knaw.nl/en/metagenomics-course>). If you want to pre-register for the course or the symposium please contact [Barbara.vanKampen@radboudumc.nl](mailto:Barbara.vanKampen@radboudumc.nl).

**Maximum number of participants:** Course: 30; Symposium: 80.

### Description

Metagenomics has quickly become one of the most important discovery tools in microbial ecology. In this five-day course, students will get hands on experience in the analysis and treatment of metagenomic data, including preprocessing and quality filtering, data handling and submission to public archives, annotation, multivariate statistical analyses, and metagenome assembly.

On the last day of the course, we are organizing an **Environmental Metagenomics Symposium** with contributions from selected course participants, as well as international leaders in the field.

Both the course programme and the symposium programme are given below.

### Target audience

PhD students and researchers in microbial ecology. MSc students can be considered, but need a letter of reference. Basic bioinformatics knowledge is a pre-requisite. Participants will be provided with homework in preparation for the course.

## TENTATIVE COURSE PROGRAM

	Activity	Speaker / Practical Supervisor
Sep 15	Welcome	Jos Raaijmakers, (NIOO)
	Introduction	Bas E. Dutilh (Radboudumc & Utrecht University) & Eiko Kuramae (NIOO)
	Q&A, setup Linux, R, and RStudio	Dei Elurbe (Radboudumc), Manoeli Lupatini (NIOO) and Noriko Cassman (NIOO)
	Preprocessing & quality filtering using Snakemake	Mattias de Hollander (NIOO)
Sep 16	EBI metagenomics pipeline, minimum information criteria, data submission	Alex Mitchell and Peter Sterk (EBI)
Sep 17	Statistics	Paul J. McMurdie (Stanford University)
Sep 18	Assembly	Daan Speth (Radboud University Nijmegen) and Bas E. Dutilh (Radboudumc & Utrecht University)
	Course dinner	
Sep 19	Environmental Metagenomics Symposium	See programme on next page

### Registration & Information

Attending the **symposium** is **free of charge** but registration via email to [Barbara.vanKampen@radboudumc.nl](mailto:Barbara.vanKampen@radboudumc.nl) is required.

The **registration fee** for the **course week** is 350 euro. The course fee includes participation in the course, course materials, a course dinner on Thursday Sept 18, and hotel accommodation in Wageningen. Participants are asked to take care of their own travel arrangements. More details will follow on the course website (<https://nioo.knaw.nl/en/metagenomics-course>), which will be available soon. In case you are not able to pay the course fee, we will consider waiving your fee. In this case please send a letter to [Barbara.vanKampen@radboudumc.nl](mailto:Barbara.vanKampen@radboudumc.nl), stating the reason that you cannot pay the fee, and include a letter of reference.

### More information

If you need more information about the course you can contact Barbara van Kampen at [Barbara.vanKampen@radboudumc.nl](mailto:Barbara.vanKampen@radboudumc.nl).

### Support

This course is made possible by the generous support of [AllBio](https://www.allbio.nl).

# Environmental Metagenomics Symposium

19 September 2014

NIOO, Wageningen, the Netherlands

Metagenomics is a powerful tool to study the organisms in microbial communities, that has numerous applications in many areas of biomedical science. By bypassing the need for laboratory culturing, this technology can unlock the massive uncultured microbial diversity, enabling the microbial component of specific environments to be surveyed, discover new organisms, and explore the dynamic ecology of microbial populations under changing conditions. The high throughput nature of metagenomics means that huge datasets are generated, and in order to extract biological information from these data, advanced bioinformatics and statistical tools are indispensable.

This symposium will bring together renowned scientists in microbial ecology and bioinformatics, who will present their recent explorations of the microbiota of different environments. Moreover, we will welcome the presentations of several students of the metagenomics course held in the week leading up to this symposium. Together, this will be an exciting opportunity to see the latest advances in environmental metagenomics from young talents as well as established leaders in the field.

## Programme

Time	Title	Speaker / Practical Supervisor
08:30-09:00	Coffee and welcome	
09:00-09:30	Functional (meta)genomics of organohalide respiring bacteria	Hauke Smidt (WUR)
09:30-09:50		Selected course participant
09:50-10:20	Functional metagenomic analysis of lignocellulosic degradation in wood feeding beetles	Eoin Brodie (Lawrence Berkeley National Lab)
10:20-10:50	Novel methanogenic archaea revealed by integrated meta-omics	Tim Urich (University of Vienna)
10:50-11:10	Coffee break	
11:10-11:40	Title tba	Gerard Muyzer (University of Amsterdam)
11:40-12:00		Selected course participant
12:00-12:30	Title tba	Kelly Wrighton (Ohio State University)
12:30-14:00	Lunch	
14:00-14:30	How to unravel the secrets of impossible anaerobic microbes by metagenomic analysis	Mike S.M. Jetten (Radboud University)
14:30-14:50		Selected course participant
14:50-15:20	Mission accomplished? Critical evaluation of computational methods in metagenomics	Thomas Rattei (University of Vienna)
15:20-15:40	Coffee break	
15:40-16:10	Title tba	Paul J. McMurdie (Stanford University)
16:10-16:30		Selected course participant
16:30-17:00	Rhythm on the beach. Metabolic pathways in marine microbial mats	Christine Hornlein (Royal Netherlands Institute for Sea Research (NIOZ))
17:00-19:00	Drinks	