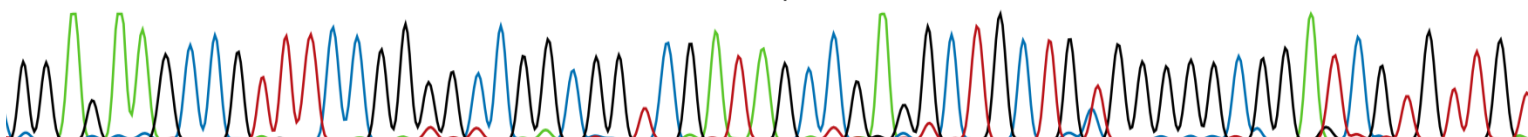


Amplicon based analysis of microbial populations

Copenhagen Feb 23th—27th 2015



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TEACHERS:

WILLIAM E HOLBEN, Department of Biological Sciences; University of Montana is a professor working with microbiomes of various habitats including animal gut and soil. He has extensive experience in designing experiments investigating microbial ecology.

MARTIN HARTMANN, Department of Microbial Ecology, Swiss Federal Research Station Agroscope, Switzerland is a senior researcher working with environmental microbiomes in agriculture, forestry, etc. Martin has extensive experience with development and use of state-of-the-art software for analyzing amplicon based microbiome data.

ANDREAS SCHRAMM, Department of Biosciences – Microbiology, University of Aarhus is a professor in microbiology with special interest in host-microbiome interactions, microbial ecology and nitrogen cycling.

LARS HESTBJERG HANSEN, Department of Microbiology, University of Aarhus is a professor investigating complex questions in microbial ecology, methods for analyzing bacterial plasmids and experimental design for Next Generation Sequencing.

MERIAN SKOUW HAUGWITZ, Center for Permafrost, University of Copenhagen is a postdoc working with soil fungi in temperate and arctic ecosystems, and has extensive knowledge of fungal community analyses.

MAREK STIBAL, Department of Environmental Chemistry, The Geological Survey of Denmark and Greenland is a scientist working with arctic microbial ecology. Marek has severe knowledge on statistical tools associated to ecology.

MICHAEL ROGGENBUCH, Institute of Biology – Microbiology, University of Copenhagen is a postdoc working with gut microbiomes from a variety of animals, and has lots of hand on experience analyzing complex microbial communities.

MADS BOLANDER, is a MSc. Student in Bioinformatics and holds a BSc in Biochemistry. Mads is a student helper at mBiolInform and at Center for Permafrost University of Copenhagen.

JACOB BÆLUM, Department of Environmental Engineering, Technical University of Denmark is senior scientist and expert in metagenomic analysis.

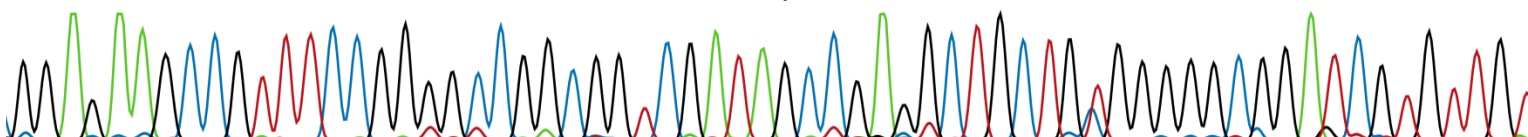
ECTS:

For PhD and MSc students the workload of the course can be converted into ECTS points. Due to the requirement of presenting the individual projects - and making sequence data available in a standardized way the workload is equivalent 42 hours of presence and 84 hours of pre and post course work. The 126 hours is then to two weeks of full time work. This is equivalent to 4.5 ECTS.

VENUE AND REGISTRATION:

The course takes place at mBiolInform at Annebergvej 16 in Brønshøj Copenhagen. Registration to courses@mbioinform.com including a short letter of motivation describing what you want to learn in relation to your project and CV. Course fee is €1100 which covers course expenses and all food and drinks during the course. The course is limited to 12 participants and registration deadline is January 20 2015.

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TENTATIVE PROGRAMME

Monday

- 9.00-10.00 Welcome, introduction of participants
- 10.00 - 11.00 Sequencing and library preparation strategies by Lars Hestbjerg Hansen, Aarhus University
- 11.00 - 12.00 Illumina presentation (Illumina) NN
- 12.00 - 13.00 Lunch
- 13.00- 14.00 Alternative library prep strategies (NEB/Kapa) NN
- 14.00 - 15.15 Establishment of computational basis for working with test dataset – download of requested packages (all freeware) Mads Bolander
- 15.15 - 17.00 Introduction to dataset, sequence dataset quality control and filtering by Jacob Bælum and Mads Bolander
- 17.00 - 20.00 Student projects and food – 6 presentations 15 min presentation and 15 min questions

Tuesday 16th September

- 9.00 - 10.10 Denoising NGS data (Illumina, 454) and curating public data repositories (Martin Hartmann)
- 10.15-10.45 Coffee break
- 10.45-12.00 OTU clustering and taxonomic classification algorithms (Martin Hartmann)
- 12.00-13.00 Lunch
- 13.00-15.00 Tutorial Part 1: Denoising, clustering, taxonomic classification (PEAR, UPARSE, MOTHUR, and other tools) – Martin Hartmann, Jacob Bælum
- 15.00-15.30 Coffee break
- 15.00-18.00 Tutorial Part 2: Basic community analysis (MOTHUR) – Martin Hartmann, Jacob Bælum
- 19.00 Dinner in town

Wednesday 17th September

- 9.00 – 10.00 Bacterial systematics based on 16S (Andreas Schramm)
- 10.00-11.00 Fungal systematics based on ITS (Merian Skouw Haugwitz)
- 11.00-12.00 Diversity measurements (Bill Holben)
- 12.00 - 13.00 Lunch
- 13.00 - 17.00 Diversity calculation, Taxonomy calculation, Tree drawing Jacob+mads
- 17.00 - 20.00 Participant projects and food– 6 presentations 15 min presentation and 15 min questions
- 19.00 Dinner (Pizza and Beer on Annebergvej 16)

Thursday 18th September

- 9.00 – 10.30 Statistics PCA plots, NMDS plots, statistical tests (Marek Stibal)
- 10.30 – 12.00 Sampling, replicate handling in bioinformatics (NN)
- 12.00 – 13.00 Lunch
- 13.00 – 17.00 PCA plots, NMDS plots, statistical tests (Marek Stibal, Jacob+Mads)
- Excursion and dinner at historic setting in Copenhagen

Friday 19th September

- 9.30 – 11.00 Network analysis (Michael Roggenbuch)
- 11.00 - 12.00 Applied study.... (evt. Bill)
- 12.00 – 13.00 Lunch
- 13.00 – 16.00 Network analysis (Michael Roggenbuch, Jacob Bælum, Mads Bolander)

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