Analysis of next generation sequencing data

March 11-15, 2019

Large Seminar Room F6,
Leibniz Centre for Tropical Marine Research (ZMT) GmbH
Fahrenheitstraße 6, 28359 Bremen, Germany

Instructors:	Christiane Hassenrück, TBA
Course description:	The course will cover the basics of planning next generation sequencing studies and bioinformatic sequence analysis. Starting with sampling and experimental design, we will discuss different sequencing approaches and platforms, various bioinformatic tools for sequence processing, available reference databases, data archiving, statistical data analysis, and data visualization. The course consists of lectures, guided tutorials, as well as extended hands-on sessions, where the participants have the opportunity to analyze their own data (assisted coding). The lectures and tutorials will include a strong interactive component. The practical sessions will focus on the analysis of amplicon sequencing data.
Target group:	PhDs and early postdocs, but B.Sc./M.Sc. students and senior scientists are equally welcome. Although the course is primarily intended for people who have recently started working with sequencing data or are planning to do so in the near future, everyone who is interested in the topic can apply. Basic knowledge of R is an advantage.
Application:	The number of participants is limited to **15**. Please register until **10.02.2019** on: https://forms.leibniz-zmt.de/Wordpress/?page_id=211 Briefly state your background and experience, and include a short justification why you want to participate, as well as your expectations for the course.
Credit:	This course is offered as part of the ZMT academy. You will receive a certificate of attendance for attending at least 80% of the sessions of the course (excluding assisted coding and Q &A sessions).

Preparation: You will work in groups during the practical sessions. Each group should have access to a laptop that is either powerful enough to run the analyses locally (linux, >4-8GB RAM) or has access to a server cluster. A list of programs to install will be distributed after the application deadline. To avoid technical issues, please make an appointment with Christiane Hassenrück if you have issues with the program installation.

Preliminary schedule:

MON 11	09:00 - 12:00	**Lecture: Planning sequencing studies** - Sampling and experimental design, power analysis - Choosing your sequencing target - Amplicon vs. shotgun sequencing - Sequencing platforms - Requirements for data analysis (computing facilities) - Data archiving
	12:00 - 14:00	**Lunch break**
	14:00 - 17:00	**Lecture: Amplicon sequencing studies (metabarcoding)** - Primer selection - Programs for sequence pre-processing - OTU clustering vs. denoising approaches - Chimera detection - Taxonomic classification - Reference databases
TUE 12	09:00 - 12:00	**Practical: Introduction to the linux command line** - ZMT computing resources - Navigating your file system - Reading and modifying text files - Setting up your working environment - Work load manager
	12:00 - 14:00	**Lunch break**
	14:00 - 17:00	**Guided tutorial: amplicon sequence analysis (pipeline 1)** - Primer design (ecoPrimer, ecoPCR) - Obitools or swarm (TBD)

WED 13	09:00 - 12:00	**Guided tutorial: amplicon sequence analysis (pipeline 2)** - DADA2 (in R)
	12:00 - 14:00	**Lunch break**
	14:00 - 17:00	**Analyze your own data**
THU 14	09:00 - 12:00	**Lecture: Multivariate statistics and data visualization (in R)** - Diversity concepts - Alpha diversity indices and rarefaction curves - Beta diversity and ordination methods - Compositionality - Hypothesis testing (permanova, redundancy analysis, differential OTU abundance, random forests) - Co-occurrence networks - Data visualization
	12:00 - 14:00	**Lunch break**
	14:00 - 17:00	**Analyze your own data**
FRI 15	09:00 - 12:00	**Q & A session: open questions**
	12:00 - 14:00	**Lunch break**
	14:00 - 17:00	**Analyze your own data**