De Novo Transcriptome Analysis

Assembly and Differential Gene Expression in Non-Model Organisms

DATE	**October 5–7, 2016**	TIME	**8 am – 5 pm**	VENUE	**Leipzig, Germany**

Advance your research. Understand de novo transcriptome assembly and differential gene expression analysis.

The target audience is biologists or data analysts with no or little experience in analyzing RNA-Seq data.

Included in the Course

- ✓ Course materials
- ✓ Catering during the workshop
- ✓ Conference dinner
- ✓ High-performance workstations (no laptop needed)
- ✓ USB-Stick for taking home results and analysis

In a Nutshell

- Learn the essential computing skills for NGS-based assemblies
- Understand de novo assembly algorithms and NGS data formats
- Use de novo assembly tools
- Find differentially expressed transcripts by using the transcriptome assembly

Scope and Topics

This workshop focusses on the transcriptome assembly and differential gene expression in non-model organisms. While analyses of model organisms generally rely on a reference genome, studies of non-model organisms usually lack this advantage. Thus, the de novo transcriptome analysis in non-model organisms poses some unique challenges.

All workshop attendees will be enabled to perform important first tasks in de novo transcriptome assembly using short-read next-generation sequencing data and uncover differentially expressed genes themselves. The course layout has been adapted to the needs of beginners in the field of NGS bioinformatics and allows scientists with no or little background in computer science to get a first hands-on experience in this new and fast evolving research topic.

Trainers

Dr. Alexander Donath
Zoological Research Museum Alexander Koenig

Dr. Mario Fasold
CCR Bio-IT

Dr. Christian Otto
CCR Bio-IT

Enroll Today!

ecseq.com/workshops/public

Registration Fee

998 EUR (excluding VAT)
Travel expenses and accommodation are not covered by the registration fee.