



# Next-Generation Sequencing Data Analysis: A Practical Introduction

Quality Control, Read Mapping, Visualization and Differential Expression Analysis

DATE June 29 - July 1, 2016

TIME 9 am – 5 pm

VENUE Munich, Germany

Advance your research. Understand NGS and analyze sequenced data yourself.

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 Nutshel

- Learn the essential computing skills for NGS bioinformatics
- Understand NGS technology, algorithms and data formats
- Use bioinformatics tools for handling sequencing data
- · Perform first downstream analyses and find differentially expressed gene

### Scope and Topics

The purpose of this workshop is to get a deeper understanding in Next-Generation Sequencing (NGS) with a special focus on bioinformatics issues. Advantages and disadvantages of current sequencing technologies and their implications on data analysis will be discovered. The participants will be trained on understanding their own NGS data, finding potential problems/errors therein and finally perform their first downstream analysis (differential gene expression). In the course we will use a reallife RNA-seq dataset from the current market leader illumina.

All workshop attendees will be enabled to perform important first tasks of NGS data analysis 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. David Langenberge ecSeq Bioinformatics



Dr. Mario Fasold CCR Bio-IT

## Enroll Today!

ecseq.com/workshops/public

Registration Fee 898 EUR (excluding VAT)

Travel expenses and accommodation are not