ECSEQ BIOINFORMATICS

DNA Variant Calling Workshop

How to call genomic variations and uncover their effects

DATE **September 21–23, 2016** **TIME** **9 am – 5 pm** **VENUE** **Berlin, Germany**

Advance your research and uncover genomic variations and their effects.

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

Included in the Course

- ✔ Course materials
- ✔ Catering during the workshop
- ✔ Conference dinner
- ✔ High-performance workstations (no laptop needed)

In a Nutshell

- Understand NGS technologies, data formats and algorithms
- Learn essential computing skills for NGS bioinformatics
- Use bioinformatics tools to predict variants
- Uncover the effects of relevant variants

Scope and Topics

The purpose of this workshop is to predict single nucleotide variations (SNVs) using Next-Generation Sequencing (NGS). Advantages and disadvantages of current tools and their implications on downstream analyses will be discovered. The participants will be trained on analyzing their own NGS data, finding potential SNVs therein and finally perform downstream analyses including the prediction of variant effects, analyses of affected pathways, associations of detected SNPs to diseases, etc. In the course we will use a real-life DNA-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. Jörg Linde
Hans Knöll Institute

Dr. Rina Ahmed
CCR Bio-IT

Dr. Mario Fasold
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.

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