



DNA Methylation Data Analysis Workshop

How to use bisulfite-treated sequencing to study DNA methylation

DATE November 22–25, 2016

TIME 8 am – 5 pm

VENUE Leipzig, Germany

Advance your
epigenetics research
with NGS methods.

The target audience is biologists or data analysts with no or little experience in analyzing Bisulfite-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 how bisulfite sequencing works
- Understand how bisulfite-treated reads are mapped to a reference genome
- Perform basic analyses (call methylated regions, perform basic downstream analyses)
- Use shell scripting to create reusable data pipelines
- Visualize results (ready-to-publish)

Scope and Topics

The purpose of this workshop is to get a deeper understanding of the use of bisulfite-treated DNA in order to analyze the epigenetic layer of DNA methylation. Advantages and disadvantages of the so-called 'bisulfite sequencing' and its implications on data analyses will be covered. The participants will be trained to understand bisulfite-treated NGS data, to detect potential problems/errors and finally to implement their own pipelines. After this course they will be able to analyze DNA methylation and create ready-to-publish graphics.

Trainers



Helene Kretzmer
University Leipzig



Dr. Christian Otto
CCR Bio-IT



Dr. Mario Fasold
CCR Bio-IT

Enroll Today!

ecseq.com/workshops/public

Registration Fee

1,298 EUR (excluding VAT)

Travel expenses and accommodation are not covered by the registration fee.