DNA Methylation Data Analysis Workshop
How to use bisulfite-treated sequencing to study DNA methylation

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

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

DATE  November 22–25, 2016  TIME  8 am – 5 pm  VENUE  Leipzig, Germany

Enroll Today!
ecseq.com/workshops/public

Registration Fee
1,298 EUR (excluding VAT)
Travel expenses and accommodation are not covered by the registration fee.