



# DNA Methylation Data Analysis Workshop

How to use bisulfite-treated sequencing to study DNA methylation

**DATE** November 29 – December 1, 2017

**TIME** 9 am – 5 pm

**VENUE** Berlin, 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

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[ecseq.com/workshops/public](http://ecseq.com/workshops/public)

### Registration Fee

998 EUR (excluding VAT)

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