

DNA Methylation Data Analysis

How to Use Bisulfite-Treated Sequencing
to Find Methylated Regions

15th - 17th December 2015
8:00 am - 5:00 pm
Leipzig, Germany

Join this hands-on workshop taught by experts in the field. Learn how to analyze bisulfite sequencing experiments and how to visualize the results, ready for publication.

SCOPE AND TOPICS

- Discuss the method of bisulfite sequencing
- Understand the advantages and limitations of bisulfite sequencing analyses
- Use bioinformatics software and tools to undertake analysis of NGS data
- Learn how to visualize genome-wide methylation for publications
- Interpret the results and extract scientific valuable findings

ENROLL TODAY

- Visit www.ecseq.com/workshops/public
- Choose from our upcoming events **'DNA Methylation Data Analysis'**
- Click **'register now'**

Workshop Cost:

998 EUR (without VAT)

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

Course materials, conference dinner and catering included!

Trainers

- Helene Kretzmer (Universität Leipzig)
Expert in analyzing and interpreting bisulfite-treated NGS experiments
- Christian Otto (CCR Bio-IT)
Developer of segemehl, a software suite for mapping bisulfite-treated sequencing data
- David Langenberger (ecSeq Bioinformatics)
Expert in NGS data analysis
- Mario Fasold (ecSeq Bioinformatics)
Expert in NGS data analysis