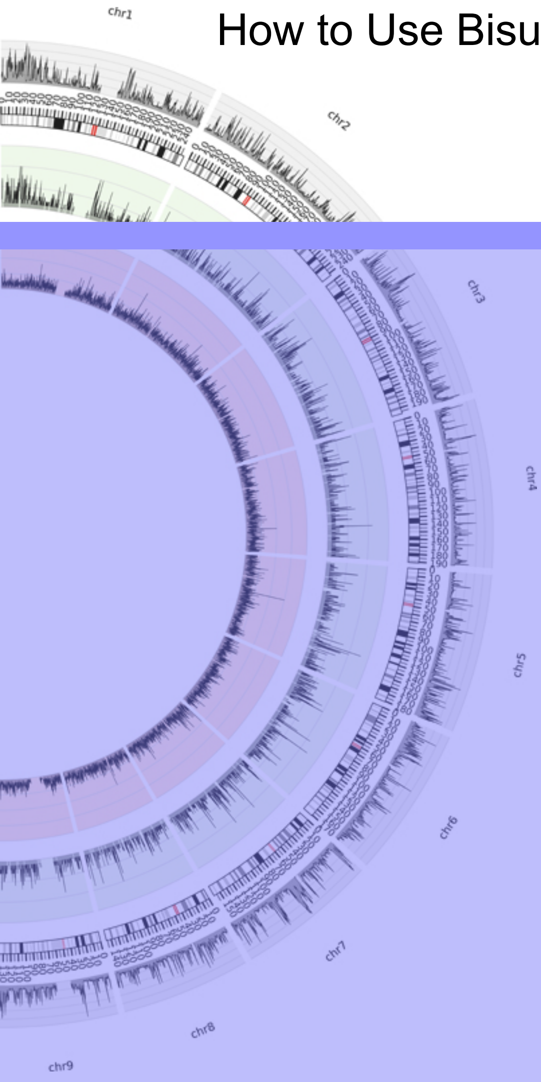
DNA Methylation Analysis

ECSEQ BIOINFORMATICS

How to Use Bisulfite-Treated Sequencing to Find Methylated Regions

Workshop



20th - 21st October 2014
9:00 am - 18:00pm
Leipzig, Germany

Join this hands-on workshop taught by experts in the field. Learn how to analyze bisulfite sequencing experiment 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
- Interprete the results and extract scientific valuable findings

ENROLL TODAY

1. Visit www.ecseq.com/training.html
2. Choose from our list of upcoming workshops **‘DNA Methylation Analysis‘**
3. Click ‘Register‘

Workshop Cost:

industry rate:	850EUR
early-bird:	750EUR
academic rate:	600 EUR
early-bird:	500 EUR

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

Course materials, conference dinner and catering included!

SPEAKERS

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

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