

Next Generation Sequencing Workshop – Programme

Friday, 28th May

- 8:00 – 9:00 **Registration**
- 9:00 **Welcome** Andreas Ziegler
- 9:15 – 10:30 **Basics: Technology and biology** Chair: Eberhard Schwinger
Next Generation Technologies – Basics and applications Michael L. Metzker
- 10:30 – 11:00 *Coffee Break*
- 11:00 – 2:30 **The data: Preprocessing and quality control (Part 1)**
11:00 1000 Genomes, a large data problem: Ensuring data quality and consistency Laura Clarke
- 12:00 – 1:30 *Lunch*
- 1:30 – 2:30 **The data: Preprocessing and quality control (Part 2)** Chair: Jeanette Erdmann
SeqTrim: Sequence preprocessing in next-generation sequencing era M. Gonzalo Claros Díaz
- 2:30 – 3:00 *Coffee Break*
- 3:00 – 4:00 **The data: Statistical analyses (Part 1)**
Study designs for the analysis of complex traits and testing for rare variants associations: Application to the analysis of sequence data Suzanne M. Leal
- 4:00 – 4:30 *Coffee Break*
- 4:30 – 6:30 *Guided city tour*
- 6:30 *Dinner at the „Kartoffelkeller“*

Saturday, 29th May

- 9:00 – 10:00 **The data: Statistical analyses (Part 2)** Chair: Andreas Ziegler
The Weighted-Sum Method: Identifying rare disease-associated mutations Bo E. Madsen
- 10:00 – 10:30 *Coffee Break*
- 10:30 – 11:30 **The data: Statistical analyses (Part 3)**
Rare variant analysis in large-scale association and sequencing studies Eleftheria Zeggini
- 11:30 – 1:00 *Lunch*
- 1:00 – 2:00 **Applications (Part 1)** Chair: Inke R. König
The emerging pathogen mycobacterium uclerans: Reductive evolution and clonal complexes Gerd Pluschke
- 2:00 – 2:30 *Coffee Break*
- 2:30 – 3:30 **Applications (Part 2)**
NGS as tool for discovery disease related differences in circulating nucleic acids (CNA) Ekkehard Schütz
- 3:30 – 3:35 **Adjourn** Andreas Ziegler