

# Autumn School

## 1<sup>st</sup> day: 22<sup>nd</sup> September

8<sup>45</sup> - 9<sup>00</sup>

Welcome and NGS-CN Introduction

**Andreas Dahl**  
DcGC, Dresden

9<sup>00</sup> - 10<sup>00</sup>

An overview of NGS Sequencing technologies  
The Vision of Roche Genomics

**Bernd Timmermann**  
Roche, Scientific  
Director Genomics

10<sup>00</sup> - 11<sup>00</sup>

Introduction into NGS  
with Illumina Instruments

**Maria Lange/Asija Diag**  
Illumina Inc

11<sup>00</sup> - 12<sup>00</sup>

Long Read NGS  
using Oxford Nanopore Technologies (ONT)

**Björn Usadel,**  
WGGC Düsseldorf

12<sup>00</sup> - 13<sup>00</sup>

**Lunch break**

13<sup>00</sup> - 14<sup>00</sup>

Long Read Sequencing with PacBio

**Kerstin Becker**  
WGGC Cologne

14<sup>00</sup> - 15<sup>00</sup>

Single cell technologies at hand &  
possible applications in bio- and medical fields

**Neha Mishra**  
**Joana Bernardes**  
IKMB Kiel

15<sup>00</sup> - 15<sup>30</sup>

**Coffee break**

15<sup>30</sup> - 16<sup>15</sup>

Nucleosome landscape of eukaryotic genomes  
Use case of modification calling  
in long-read sequencing data

**Felix Müller-Planitz**  
TU Dresden

16<sup>15</sup> - 17<sup>00</sup>

COVID-19: NGS in viral diagnostics  
and host genetics research

**Kerstin Ludwig**  
WGGC Bonn

17<sup>00</sup> - 17<sup>30</sup>

GHGA - FAIR principles  
and the importance of Metadata

**Anandhi Iyappan**  
EMBL Heidelberg

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## 2<sup>nd</sup> day: 23<sup>rd</sup> September

9 <sup>00</sup> - 10 <sup>45</sup>	<b>RNA-Seq and Differential Gene Expression Analysis</b>	<b>Heiko Schoof</b> WGCG Bonn
10 <sup>45</sup> - 11 <sup>00</sup>	<b>Coffee break</b>	
11 <sup>00</sup> - 12 <sup>30</sup>	<b>Experimental Planning and Statistical analysis of NGS experiments</b>	<b>Nicolas Casadei</b> NCCT Tübingen
12 <sup>30</sup> - 13 <sup>30</sup>	<b>Lunch break</b>	
13 <sup>30</sup> - 15 <sup>00</sup>	<b>Single Cell Data Analysis</b>	<b>Katrin Sameith Fabian Rost</b> DcGC, Dresden
15 <sup>00</sup> - 15 <sup>30</sup>	<b>Coffee break</b>	
15 <sup>30</sup> - 16 <sup>30</sup>	<b>Creating chromosome-scale assemblies from Long- and Short-read sequencing data</b>	<b>Martin Pippel Tom Brown</b> MPI-CBG Dresden
16 <sup>30</sup> - 17 <sup>30</sup>	<b>Exome Analysis and Variant Calling for precision medicine</b>	<b>Tzung-Chieh Hsieh Meghna Ahuja Bhasin</b> WGCG Bonn
17 <sup>30</sup> - 18 <sup>00</sup>	<b>Closing remarks and feedback</b>	<b>Andreas Dahl</b> DcGC, Dresden

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DRESDEN  
concept



genome  
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C COMPETENCE  
C CENTRE FOR  
G GENOMIC  
A ANALYSIS KIEL



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WEST GERMAN  
GENOME CENTER