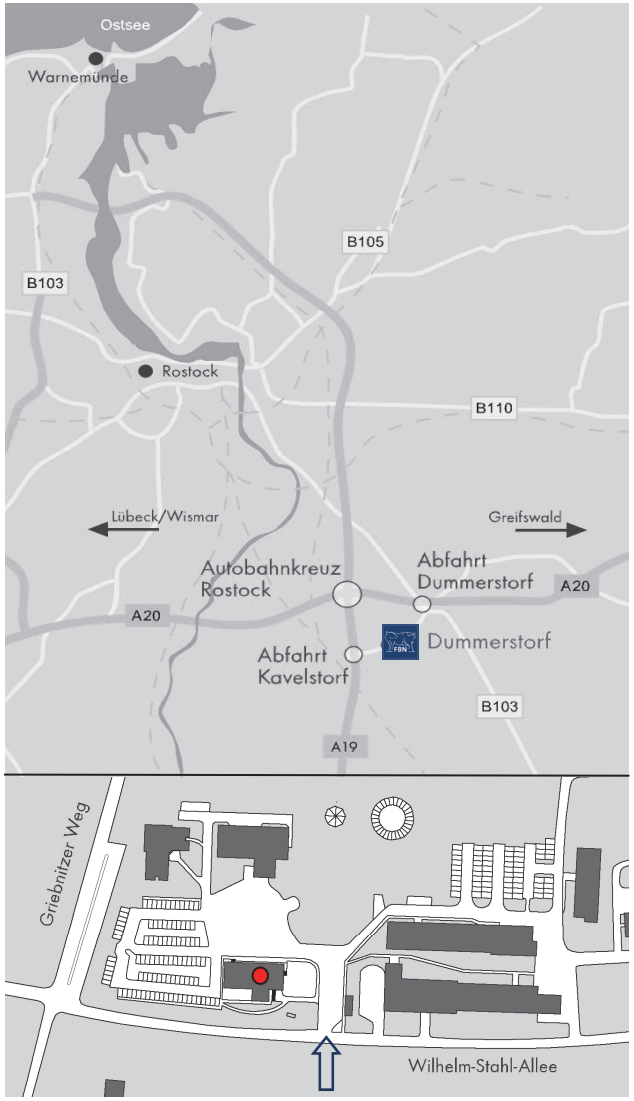
Next Generation Sequencing in Mecklenburg -Vorpommern (NGS-MV):

The goal of the NGS-MV initiative is to highlight existing resources and infrastructure with respect to this high current and future impact technology, as well as to exchange experiences and to stimulate collaborations within the state. Therefore, the initiative is based on current projects at universities and research institutes in Mecklenburg-Vorpommern. The great complexity of the NGS technology will increasingly require an interplay between areas such as genetics, bioinformatics, microbiology or systems biology, all areas which are already themselves established within the state.

The workshop should furthermore enable an exchange of expertise from the different subject areas and broaden the horizons to stimulate new research ideas. Therefore, we invite all interested parties to actively participate in the workshop. We especially would like to invite young scientists to an intensive seminar with their own contributions in the subject area of NGS applied to pro- and eukaryotes.

Georg Fuellen
Andreas Kuss
Israel Barrantes
Christian Junghanß
Christa Kühn
Pål Westermark
Hugo Murua Escobar
Mohamed Hamed

Leibniz Association



Leibniz Institute for Farm Animal Biology
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Workshop
Next-Generation-Sequencing (NGS)

Leibniz Institute for Farm Animal Biology
Monday, 8. Oktober 2018

Universitätsmedizin Rostock
BioCon Valley®
Universität Rostock
Traditio et Innovatio
FBN

Program

Monday, 8.Oktober 2018

8:00 Registration (Convention Center)

9:10 - 9:15
Welcome **Prof. Dr. K. Wimmers**
Head of FBN Dummerstorf

9:15 - 9:45
Keynote 1: **Jan Gorodkin** (Center for non-coding RNA in Technology and Health, Kopenhagen/Dänemark)
„Assessment and prediction of CRISPR-Cas9 on/off-targets"

9:45 - 10:30
Contributed talks
Höper, Dirk: "*Improved library preparation for Ion Torrent sequencing using custom-made Y-adapters"*
Murua Escobar, Hugo: "*TBA"*
Wolfien, Markus: "*Structured Analysis and Integration of RNA-Seq Experiments: de.STAIR"*

10:30 - 11:15
Coffee break, Posters, Networking

11:15 - 11:45
Keynote 2: **Sebastian Kadener** (Brandeis University, Waltham/USA)
„From single cells to whole transcriptomes: How NGS allows us to understand the functions of circular RNAs in the brain"

11:45 - 12:30
Contributed talks:
Berthold, Anne: *„The path to ChIP-Seq: opti mization of ChIP assays for bovine udder cell mo dels"*
Brodhagen, Johanna: *„Evaluation of a method for depletion of highly expressed transcripts for transcriptome analysis of pathogen-infected and non infected udder quarters"*
Nath, Neetika: *„Detection of Radiation-induced Alteration in the Exome of the Human Gingiva Fibroblast"*

12:30 - 14:15
Lunch, Posters, Networking, Group Foto

14:15 - 14:45
Keynote 3: **Bernd Timmermann** (Max-Planck-Institute for Molecular Genetics, Berlin)
"A decade of Next Generation Sequencing at the Max Planck Sequencing Core Facility: Technolgies, Applications and Projects"

14:45 - 15:30
Contributed talks:
Hoff, Katharina: **"***Increasing accuracy of fully automated gene prediction with transcriptome data"*
Hamed, Mohamed: **"***Machine learning applica tions of NGS data"*
Fuellen, Georg: **"***TBA"*

15:30 - 16:15
Coffee break, Poster, Networking

16:15 - 16:45
Keynote 4: **Thomas Werner** (Internal Medicine-Nephrology Division, University of Michigan)
„NGS and other High-Throughput technology in Medi cine: Lost in translation or the promised land?"

16:45 - 17:30
Contributed talks:
Thiesen, Hans-Jürgen: *„Comparative validation of whole genome data generated by the NGS techno logy platform initially offered by complete genomics versus the updated platform offered by BGI in Hong kong"*
De los Rios Perez: *„Identification of SNPs in RNA-Seq samples in rainbow trout (Oncorhynchus mykiss)"*

17:30 Farewell

Next Generation Sequencing

The introduction of next generation sequencing (NGS) technology enables the cost-efficient and comparably fast sequencing of genomes and transcriptomes of pro- and eukaryotes. In addition, NGS allows for comparative analysis of many genomes/transcriptomes with respect to chromosomal alterations, mutations, or differences in transcriptional activity. Furthermore, NGS opens up new possibilities for virological, microbiological, or pathological diagnostics.
During the last years, the cost per NGS-equenced megabase has continuously fallen, which has facilitated its use in a broad range of applications. However, this increased use comes with requirements of assembly, annotation, and data analysis, which posits large challenges and requires interdisciplinary expertise.

Registering

The workshop takes place at the Leibniz Institute for Farm Animal Biology. The conference office is found at the entrance. The conference fee is 20,- EUR. This includes participation, lunch and pause meals, and working materials.

Link: https://sites.google.com/site/nexgenseqmv/

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