Seq-Spotlight on Campus 2018
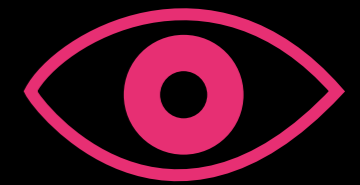
Hear

introductions to selected techniques

Ask

questions you never had the chance to ask

Meet

operators & expert users from on-campus facilities

See

current applications of sequencing

Thursday, September 27th
13:00 - 18:00

Small Lecture Hall, N02.040

LMU Biomedical Center (BMC)
Großhanderner Str. 9
Planegg-Martinsried

An informal symposium for junior scientists interested in cutting edge high-throughput sequencing techniques

www.seq-spotlight.de

HiC RNA-seq
Genomes Analysis Data
ATAC-seq
Illumina
Multivariate
Experimental
sequencing High-throughput 3rd-generation Resequencing Single-cell Sequencing
Nanopore
ChIP-seq design
All-you-can-seq

13:00 - 13:15 **Welcome and introduction**
Wolfgang Enard, Anthropology and Human Genomics, LMU Biocenter

13:15 - 13:45 **Insights in short and long read high throughput sequencing of nucleic acids**
Helmut Blum, LAFUGA Genomics Unit, LMU Gene Center

13:45 - 14:15 **Genomic approaches in natural populations**
Jochen Wolf, Evolutionary Biology, LMU Biocenter

14:15 - 14:45 **RNA-seq: Quantifying transcriptomes of (single) cells**
Wolfgang Enard, Anthropology and Human Genomics, LMU Biocenter

14:45 - 15:45 **Break and poster session**

15:45 - 16:15 **Mapping the functional state of the genome**
Tobias Straub, Core Facility Bioinformatics, LMU BMC

16:15 - 16:45 **Measuring epimutation rates in *Arabidopsis thaliana***
Maria Colomé Tatché, Computational Epigenomics, ICB, Helmholtz Zentrum München

16:45 - 17:15 **Cracking the gene regulatory code using multi-omics data**
Julien Gagneur, Computational Biology, TUM

17:15 - 18:00 **Happy Hour and poster session**

◢ Poster Session

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Rooms – Poster Session
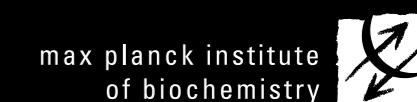**N01.014-N01.016**

LMU Biomedical Center
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Planegg-Martinsried

Organizers

IRTG-SFB 1064 Chromatin Dynamics
IRTG-SFB 1243 Cancer Evolution
IMPRS for Molecular Life Sciences
IRTG-SFB 914 Leukocyte Trafficking
IRTG-SFB 1054 Cell-Fate Decisions in Immune Systems
QBM Graduate School of Quantitative Biosciences Munich
LSM Graduate School of Life Science Munich
Research School Lung Biology and Disease

Contributors

Supported by:

1. **Munich Sequencing Alliance: state-of-the-art NGS at scale**
   Elisabeth Graf, Barbara Schormair. Munich Sequencing Alliance, Helmholtz Zentrum, TU Munich, LMU Munich, MPI for Psychiatry

2. **NGS @ MPI of Biochemistry**
   Marja Driessen, MPI of Biochemistry Sequencing Facility, Munich

3. **Bioinformatics Core Facility @HMGU**
   Mattias Heinig. Genetic and Epigenetic Gene Regulation, Institute of Computational Biology, Helmholtz Zentrum Munich

4. **Rare disease in children solved by Next Generation Sequencing**
   Meino Rohlfs. Dr.von Hauner'sche Sequencing Facility, LMU Munich

5. **Genomics Service Unit at the Biocenter: Enabling Nucleic Acid Research**
   Andreas Brachmann. Genomics Unit, Biocenter, LMU Munich

6. **Genome-wide capture of methylation by Nanopore long reads sequencing**
   Alexander Graf et al., LAFUGA Sequencing Facility, Gene Center, LMU Munich

7. **Different approaches to study transcriptomes by high throughput sequencing**
   Julia Phillippou-Massier et al., LAFUGA Sequencing Facility, Gene Center, LMU Munich

8. **Using SMRT technology to map the genome-wide distribution of Base**
   Benedikt Brink. Siegel lab, Molecular Parasitology, BMC, LMU Munich

9. **moreThan-SEQ: what comes before and after sequencing?**
   Tobias Straub. Bioinformatics Core Facility, BMC, LMU Munich

10. **MNase-based Sequencing Methods for Studying Chromatin**
    Tamas Schauer. Bioinformatics Core Facility, BMC, LMU Munich

11. **Genome-wide measurement of local nucleosome array regularity and spacing by nanopore sequencing**
    Sandro Baldi. Becker lab. Molecular Biology, Biomedical Center Munich, LMU Munich

12. **Next generation sequencing in hematological diagnostics and research: present and future**
    Stephan Hutter. Münchner Leukämielabor (MLL), Munich

13. **DNA Metabarcoding – Molecular Biodiversity assessment & Biomonitoring 2.0**
    Jérôme Moriniere. Marita Sacher, Advanced Identification Methods (AIM), Munich

14. **High-throughput, full-length, single-cell RNA sequencing**
    Sylvia Simon, Harald Berninger. Takara Bio Europe

15. **An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics**
    Maximillian Strunz et al., Schiller lab, Comprehensive Pneumology Center, Helmholtz Zentrum Munich; German Center for Lung Research

16. **Single cell analysis of lung injury and repair**
    Christoph Mayr et al., Schiller lab, Comprehensive Pneumology Center, Helmholtz Zentrum Munich; German Center for Lung Research

17. **Single cell sequencing reveals mesenchymal cell heterogeneity in mouse and human lungs**
    Meshal Ansari, Ilias Angelidis et al., Schiller lab, Comprehensive Pneumology Center, Helmholtz Zentrum Munich; German Center for Lung Research

18. **Deep sequencing approaches to study post-transcriptional regulation in pathogenic bacteria**
    Nikolai Peschek. Pappenfort lab, Microbiology, Biocenter, LMU Munich

19. **Multiplex bisulfite sequencing for accurate and cost-effective determination of genomic DNA methylation**
    Martin Groth. Institute of Biochemical Plant Pathology (BIOP), Helmholtz Zentrum Munich

20. **ATAC-seq for chromatin accessibility analysis in plants**
    Groth lab, Institute of Biochemical Plant Pathology (BIOP), Helmholtz Zentrum Munich

21. **Cancer genome analysis and genome-scale screening applications in mice**
    Roland Rad. TranslaTUM, Med II, Klinikum rechts der Isar, TU Munich

22. **Using TOMO-seq to map spatial gene expression in the mouse olfactory epithelium**
    Mayra Ruiz, Antonio Scialdone. Institute of Epigenetics and Stem Cells, Helmholtz Zentrum Munich

23. **Assembly and phase of extreme long haploid-like subtelomeres in the parasite *Trypanosoma brucei* combining SMRT sequencing and Hi-C data**
    Raúl Cosentino. Siegel lab, Molecular Parasitology, BMC, LMU Munich

24. **Methods to determine absolute nucleosome occupancy**
    Elisa Oberbeckmann. Korber lab, Molecular Biology, BMC, LMU Munich

25. **Sensitive and quantitative sequencing of cellular barcodes and genotypes**
    Daniel Richter. Enard lab, Human Genomics, Biocenter, LMU Munich

26. **zUMIs - A fast and flexible pipeline to process RNA sequencing data with UMIs**
    Ines Hellmann. Enard lab, Human Genomics, Biocenter, LMU Munich

27. **Sensitive and powerful single-cell RNA sequencing using mcSCRB-seq**
    Johannes Bagnoli. Enard lab, Human Genomics, Biocenter, LMU Munich

28. **powsimR: Power analysis for bulk and single cell RNA-seq experiments**
    Beate Vieth. Enard lab, Human Genomics, Biocenter, LMU Munich

29. **So, you want to sequence a reference genome?**
    Joshua Penalba. Wolf lab, Evolutionary Biology, Biocenter, LMU Munich

30. **Biological determinants of the distribution of fitness effects (DFE) of new mutations in corvids**
    Fidel Botero. Wolf lab, Evolutionary Biology, Biocenter, LMU Munich

31. **The Genomics of Adaptive Divergence with Gene Flow by Means of Experimental Evolution**
    Sergio Tusso. Wolf lab, Evolutionary Biology, Biocenter, LMU Munich

32. **Using ATAC-seq to uncover sex-biased gene expression regulation**
    Ana Catalan. Wolf lab, Evolutionary Biology, Biocenter, LMU Munich

33. **episcanpy: a single cell epigenomics analysis pipeline**
    Anna Danese. Colomé-Tatché lab, Computational Epigenomics, Institute of Computational Biology, Helmholtz Zentrum Munich

34. **Epimutation rates in *A. thaliana***
    Johanna Denkena. Colomé-Tatché lab, Computational Epigenomics, Institute of Computational Biology, Helmholtz Zentrum Munich

35. **Genome segmentation using convolutional neural networks**
    Akshaya Ramakrishnan. Colomé-Tatché lab, Computational Epigenomics, Institute of Computational Biology, Helmholtz Zentrum Munich

36. **Study of RNA metabolism with TT-seq**
    Gagneur lab. Computational Biology, Informatics, TU Munich

37. **RNA-seq for pinpointing the causes of rare diseases**
    Gagneur lab. Computational Biology, Informatics, TU Munich

38. **GenoGAM: genome-wide generalized additive models for ChIP-seq analysis**
    Gagneur lab. Computational Biology, Informatics, TU Munich

39. **Kipoi: accelerating the community exchange and reuse of predictive models for regulatory genomics**
    Gagneur lab. Computational Biology, Informatics, TU Munich