

# Seq-Spotlight on Campus 2018

Thursday, September 27<sup>th</sup>  
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](http://www.seq-spotlight.de)



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



## Hear

introductions to  
selected techniques

**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



## Ask

questions you never  
had the chance to ask



## Meet

operators & expert users  
from on-campus facilities



## See

current applications  
of sequencing

# Poster Session

- 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**  
Thomas Walzthoeni, Mattias Heinig. Bioinformatics Core Facility, Epigenetic Gene Regulation, Institute of Computational Biology, Helmholtz Zentrum Munich
- 4. Rare disease in children solved by Next Generation Sequencing**  
Meino Rohlf. 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 Leukämie Labor (MLL), Munich
- 13. DNA Metabarcoding – Molecular Biodiversity assessment & Biomonitoring 2.0**  
Jérôme Morinière. Marita Sacher, Advanced Identification Methods (AIM), Munich
- 14. High-throughput, full-length, single-cell RNA sequencing**  
Nico Dunkel, Andrew Farmer. Takara Bio Europe
- 15. An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics**  
Ilias Angelidis et al., Schiller lab, Comprehensive Pneumology Center, Helmholtz Zentrum Munich; German Center for Lung Research
- 16. Single cell analysis of lung injury and repair**  
Maximilian Strunz 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**  
Christoph Mayr 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 mcSCR-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. Combinatorial chromatin state calling and genome segmentation using ChIP-seq data**  
Akshaya Ramakrishnan. Colomé-Tatché lab, Computational Epigenomics, Institute of Computational Biology, Helmholtz Zentrum Munich
- 36. Genome-wide two-step RNA splicing kinetics in human cells**  
Leonhard Wachutka. Gagneur lab. Computational Biology, Informatics, TU Munich
- 37. Multi-omics approaches for rare disease research**  
Vicente Yopez. Gagneur lab. Computational Biology, Informatics, TU Munich
- 38. GenoGAM: genome-wide generalized additive models for ChIP-seq analysis**  
Julien Gagneur. Computational Biology, Informatics, TU Munich
- 39. Kipoi: accelerating the community exchange and reuse of predictive models for regulatory genomics**  
Ziga Avsec. Gagneur lab. Computational Biology, Informatics, TU Munich

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Rooms – Poster Session  
N01.014-N01.016

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### 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

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of biochemistry

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