



AI'S ADVENTURES IN GENOMICS

17TH BERLIN
SUMMER MEETING
6-7 JUNE 2024

THURSDAY, JUNE 6, 2024

9:15 am • 10:00 am	Registration & coffee
10:00 am • 10:15 am	Welcome address by Maïke Sander, Nikolaus Rajewsky and Dagmar Kainmüller

SESSION 1

Chair: **Dagmar Kainmüller**

10:15 am • 11:00 am	Julien Gagneur , TU Munich, Germany DNA language model interpretation reveals functional elements and their context
11:00 am • 11:15 am	Pia Keukeleire , Universitätsklinikum Schleswig-Holstein, University of Lübeck, Germany Uncovering preferential binding between putative promoters and enhancers using a combined capture Hi-C MPRA experiment
11:15 am • 11:30 am	Alexander Rakowski , Hasso Plattner Institute for Digital Engineering, Potsdam, Germany Deep-learning Powered GWAS on T1-weighted Brain MRI Data
11:30 am • 12:15 am	Andreas Keller , HIPS, Saarbrücken, Germany Cell by Cell: Using AI for Charting the Single Cell Landscape in Alzheimer's Disease and Aging
12:15 pm • 12:30 pm 12:30 pm • 1:30 pm	Group photo Break (lunch on your own)
1:30 pm • 3:00 pm	Poster session

SESSION 2

Chair: **Uwe Ohler**

3:00 pm • 3:45 pm	Rebekka Burkholz , CISPA, Saarbrücken, Germany Scaling up gene regulatory models to fight underspecification
3:45 pm • 4:00 pm	Utkarsh M. Mahamune , Amsterdam UMC, The Netherlands Systematic evaluation of robustness to cell type mismatch of deconvolution
4:00 pm • 4:15 pm	Daniel León Perinán , MDC-BIMSB, Berlin, Germany Solving the biases of 2D spatial transcriptomics with generative AI
4:15 pm • 5:00 pm	Joshua Welch , University of Michigan, Ann Arbor, USA Mapping cell fate transition in time and space using single-cell multi-omics

FRIDAY, JUNE 7, 2024

SESSION 3

Chair: **Markus Mittnenzweig**

9:00 am • 9:45 am

Florian Büttner, Goethe University Frankfurt/DKFZ, Germany
Interpretable integration of multi-modal data via Bayesian machine learning

9:45 am • 10:00 am

Miquel Anglada-Giroto, CRG, Barcelona, Spain
Disentangling the splicing factor programs underlying complex molecular phenotypes

10:00 am • 10:15 am

Artür Manukyan, MDC-BIMSB, Berlin, Germany
VoltRon: A Spatial Omics Analysis Platform for Multi-Resolution and Multi-omics Integration using Image Registration

10:15 am • 10:30 am

Coffee & refreshments

SESSION 4

Chair: **Dagmar Kainmüller**

10:30 am • 11:15 am

Manfred Claassen, University of Tübingen, Germany
tba

11:15 am • 11:30 am

Leonie Stockscläder, BIH at Charité – Universitätsmedizin Berlin, Germany
Exploring Tumorigenesis through Meta-Analysis of the Human Somatic Mutational Landscape

11:30 am • 11:45 pm

Adam Streck, ICCB, Cologne, Germany
Feature extraction and validation from genomic copy number profiles in cancer

11:45 am • 12:30 pm

Katharina Schmid, LMU Munich, Germany
Identifying copy number variations in single-cell data

12:30 pm • 1:30 pm

Break (lunch on your own)

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SESSION 5

Chair: **Nikolaus Rajewsky**

1:30 pm • 2:15 pm

Ewa Szczurek, Helmholtz Munich, Germany/University of Warsaw, Poland
Generative AI for antimicrobial peptide discovery

2:15 pm • 2:30 pm

Lisa Barros de Andrade e Sousa, Helmholtz Munich, Germany
Oligo Designer Toolsuite – lightweight development of custom oligo design pipelines

2:30 pm • 3:15 pm

Georg Seelig, University of Washington, Seattle, USA
Machine-learning guided sequence design for mRNA and gene therapy applications

3:15 pm • 3:30 pm

Coffee & refreshments

SESSION 6

Chair: **Uwe Ohler**

3:30 pm • 4:15 pm

Liana Lareau, UC Berkeley, USA
Deep learning and deep sequencing for mRNA design

4:15 pm • 5:00 pm

Vikram Agarwal, Sanofi, Waltham, USA
Predicting the translation efficiency of messenger RNA in mammalian cells

5:00 pm

Closing remarks
