MAX
DELBRÜCK
CENTER
BIMSB

Berlin Institute
for Medical
Systems Biology

Discovery for tomorrow's medicine

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 **Maike Sander** and the Scientific Organizing Committee

SESSION 1

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	Group photo
12:30 pm • 1:30 pm	Break (lunch on your own)
1:30 pm • 3:00 pm	Poster session

SESSION 2

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

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-Girotto**, 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

10:30 am • 11:15 am	**Manfred Claassen**, University of Tübingen, Germany Supervised learning of disease associated tissue microenvironment composition
11:15 am • 11:30 am	**Leonie Stockschläder**, 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)

FRIDAY, JUNE 7, 2024

SESSION 5

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

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

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