

7th NGS Symposium

14th April – 16th April 2026

Tuesday 14th April		
	12:00 – 12:30	Arrival and Coffee
Opening session	12:30 – 12:40	Lars Feuerbach <i>Welcome and Overview</i>
	12:40 – 13:15	Lars Feuerbach <i>Characterizing telomeres by single-cell and long-read sequencing</i>
	13:15 – 13:40	David Wissel <i>Benchmarking long-read RNA-seq for transcript quantification across modalities, methods, and sequencing depths</i>
	13:40 – 14:05	Mathias Boulanger <i>Molecular co-accessibility identifies coordinated regulation between distant cis-regulatory elements</i>
	14:05 – 14:30	Break
Single molecule & Single cell	14:30 – 14:55	Philippe Hupé <i>Deployment practices with nextflow and apptainer for production-ready bioinformatics pipelines: example at the Institut Curie</i>
	14:55 – 15:20	Michela Palamin <i>ChromSMF: integrated profiling of histone modifications, protein-DNA interactions and DNA methylation on multi-kilobase DNA molecules</i>
	15:20 – 15:45	Mark Hartmann <i>sciGMT-seq: A single-cell multi-omics framework for simultaneous profiling of immunophenotype, genotype, methylome, and transcriptome</i>
	15:45 – 16:10	Break
Spatial-omics	16:10 – 16:35	Martin Emons <i>Quantification and multi-sample comparison of spatial omics data using spatial statistics</i>
	16:35 – 17:00	Rémi Montagne <i>Through spatial transcriptomics and proteomics data analysis</i>
	17:00 – 17:25	Gianni Zanardelli <i>Spatio temporal regulation of cell cycle states in tumor microenvironments using spatial transcriptomics</i>
	TBA	Pub Crawl or restaurant visit

Please note that the program is susceptible to change and will be continuously updated

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Wednesday 15th April		
Epigenomics & TFs	9:30 – 9:55	Martina Capriati <i>Essential genes are dominantly activated by single transcription factors</i>
	9:55 – 10:20	Lukas Burger <i>Using deep learning to infer the chromatin sensitivity of transcription factors from ChIP-seq data</i>
	10:20 – 10:45	Yahia Hadj-Arab <i>Neuronal epigenetic plasticity in polyaddictions</i>
Break		
AI & ML	11:05 – 11:30	Ilia Kats <i>MOFA-FLEX: One factor model to rule them all</i>
	11:30 – 11:55	Ferdinand Popp <i>ML-guided TMM diagnostics in precision oncology programs</i>
	11:55 – 12:20	Emma Engel / Oscar Gonzales Velasco <i>Machine Learning Approaches to Infer the Primary Site from Cancers of Unknown Primary (CUP) Using Spatial Transcriptomics</i>
Cancer & Precision medicine	12:20 – 12:45	Maximilian Schöning <i>Rapid Multi-Omics Leukemia Diagnostics using Nanopore-Sequencing</i>
	Lunch break	
	14:00 – 14:25	Robert Autry <i>INFORM Bioinformatics: From Impact to Innovation through Collaboration and Data Sharing</i>
	14:25 – 14:50	Kendra Maaß <i>Liquid biopsy in early diagnosis, therapy monitoring and surveillance</i>
	14:50 – 15:15	Frank Westermann <i>TBA</i>
	15:15 – 16:00	Priya Chudasama <i>ALternative architecture of chromosomal-instable sarcoma</i>
Break		
	16:30	<i>Panel discussion „Genomics in the Clouds“</i>

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Thursday 16th April		
Frameworks & Workflows	9:00 – 9:25	Charlotte Sonesson <i>A computational framework for representation and analysis of single molecule genomics data</i>
	9:25 – 9:50	Daniel Hübschmann <i>Assessment of cellular interactions at ultra-high throughput</i>
	9:50 – 10:15	Wolfgang Maier <i>Reproducible data analysis integrated with research data management with Galaxy</i>
	10:15 – 10:40	Jan Eufinger <i>The German Human Genome-Phenome Archive (GHGA): A national resource for the reuse of human Omics data</i>
	10:40 – 11:00	Break
Latest breakthroughs	11:00 – 11:25	Anne Friedrich <i>A thousand near telomere-to-telomere yeast genome assemblies help to decipher the genotype-phenotype relationship</i>
	11:25 – 11:50	Daria Doncevic <i>PELICAN: Conditional Wasserstein Adversarial Learning Enables Unpaired and Batch-Integrated Translation Across Single-Cell Modalities.</i>
	11:50 – 12:15	Juan Caballero Perez <i>Early experiences with AVITI sequencing technology</i>
	12:15 – 12:30	Break
	12:30 – 12:55	Cihan Erkut <i>Integrative analysis of the TBXT-driven transcriptome and proteome in chordoma</i>
Keynote	12:55 – 13:40	Tobias Rausch <i>Discovery of structural variants with long-read genomics</i>

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