

Thursday, 1 December

Welcome

- 08:00 - 09:00 Registration (main entrance)
09:00 - 09:10 Introduction (seminar room)

Session 1: Genomics and transcriptomics

Chair: Vijay Tiwari (IMB, Mainz)

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| 09:10 - 09:40 | Philipp Bucher | EPFL, Lausanne | Core promoter elements, nucleosome architectures and transcription start site patterns across eukaryotic model organisms |
| 09:40 - 10:10 | Alexandra Henrion-Caude | Necker Hospital, Paris | Bridging the gap between human genetics, networks and attractors |
| 10:10 - 10:25 | Vladislava Milchevskaya | EMBL, Heidelberg | A tool to build up-to-date gene annotations for Affymetrix microarrays |
| 10:25 - 10:40 | Sara Fonseca Costa | University of Fribourg | Internal normalization of nascent RNA sequencing experiments to identify age-related changes of the mouse liver transcriptome |

10:40 - 11:00 *Coffee Break*

Session 2: Dynamical modelling

Chair: Denis Thieffry (ENS, Paris)

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| 11:00 - 11:30 | Laurence Calzone | Institut Curie, Paris | Mathematical modelling of the early steps of metastasis |
| 11:30 - 12:00 | Jana Wolf | MDC, Berlin | Regulation of gene expression in liver zonation |
| 12:00 - 12:15 | Emna Ben Abdallah | IRCCyN, Nantes | Learning Delays in Biological Regulatory Networks from Time Series Data |
| 12:15 - 12:30 | Flash presentations | - | 1-min presentations from selected poster presenters (no slides) |
| 12:30 - 14:30 | Lunch & Poster Session | | |

Session 3: Visualization

Chair: Jean-Fred Fontaine (JGU-IMB, Mainz)

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| 14:30 - 15:00 | Jan Aerts | Leuven University | Data Visualization for Gene Expression: Principles, Challenges and Approaches |
| 15:00 - 15:30 | Wolfgang Huber | EMBL, Heidelberg | Data-driven hypothesis weighting increases detection power in genome-scale multiple testing |
| 15:30 - 15:45 | Yayoi Natsume-Kitatani | NIBIOHN, Osaka | Integrated toxicogenomics analysis with Toxygates for inferring molecular mechanisms |
| 15:45 - 16:00 | Federico Marini | IMBEI, Mainz | Development of Applications for Interactive and Reproducible Research: a Case Study |

Session 4: 3D Chromatin

Chair: Miguel Andrade (JGU-IMB, Mainz)

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| 16:00 - 16:30 | Juanma Vaquerizas | MPI, Münster | 3D chromatin organisation and transcriptional regulation |
| 16:30 - 17:00 | Jörn Walter | Saarland University, Saarbrücken | Analysis and interpretation of DEEP Epigenomic data |

17:00 - open end *City Tour and Christmas Market*

Friday, 2 December

Session 5: Epigenomics

Chair: Miguel Andrade (JGU-IMB, Mainz)

09:00 - 09:30	Michael Stadler	FMI, Basel	More than RNA levels: What else to learn from RNA-seq data
09:30 - 09:50	Aleksandra Galitsyna	IITP RAS, Moscow	"Mirror reads" in Hi-C data
09:50 - 10:10	Junko Yamane	CiRA, Kyoto	Development of enhanced reduced representation bisulfite sequencing method for single-cell methylome analysis
10:10 - 10:30	David Fournier	University of Mainz	Histone code in higher-order chromatin folding: A hypothesis
10:30 - 11:00	<i>Coffee Break</i>		

Session 6: Cell identity

Chair: Andreas Kurtz (Charité, Berlin)

11:00 - 11:30	Wataru Fujibuchi	CiRA, Kyoto	Stem cell informatics: learning gene networks in human embryonic stem cells for predicting chemical effects on babies
11:30 - 11:50	Nancy Mah	Charité, Berlin	CellFinder's molecular database and its application to stem cell research
11:50 - 12:10	Khadija El Amrani	Charité, Berlin	A benchmark of the marker gene tool: MGFM
12:10 - 12:30	Tomoya Mori	CiRA, Kyoto	Development of 3D Tissue Reconstruction Method from Single-cell RNA-seq Data
12:30 - 13:00	Elham Azizi	MSKCC, New York	Bayesian Inference for Single-cell Clustering and Imputing
13:00 - 13:10	<i>Concluding remarks</i>		
13:10 - 14:10	<i>Lunch</i>		

Talk + discussion: 25+5 min or 17+3 min or 12+3 min