

NGS Symposium 2014



Thursday, 10 July 2014

9:00 Arrival @ MPI-IE's lounge (Stübeweg 51, 79108 Freiburg im Breisgau)

Session I: Galaxy

10:00 - 11:30

Björn Grüning	University of Freiburg	Freiburg	The Galaxy universe
Hans-Rudolf Hotz	FMI	Basel	Using Galaxy for NGS analysis in a collaborative environment
Stephanie Le Gras	IGBMC	Strasbourg	GalaxEast - an open and powerful Galaxy instance for Integrative Omics data analysis

coffee break @ lounge

Session II: DNA methylation analysis

12:00 - 13:00

Lukas Burger	FMI	Basel	Sequence determinants of DNA methylation in mammalian genomes
Lars Feuerbach	DKFZ	Heidelberg	Comparing methylome data from MCIP-seq and Illumina 450k arrays

lunch break @ canteen (1st floor)

Session III: Hi-C analysis

14:00 - 15:30

Thomas Sexton	IGBMC	Strasbourg	A pipeline to study Hi-C (genome-wide chromosome conformation capture) datasets
Aleksandra Pekowska	EMBL	Heidelberg	Restriction fragment resolution analysis of Hi-C data
Fidel Ramirez	MPI-IE	Freiburg	Genome assembly using Hi-C

coffee break @ lounge

Session IV: Assorted gems

14:00 - 15:30

TBA			
Gnana Prakash Balasubramanian	DKFZ	Heidelberg	Detection of pathogen integration sites in cancer
Thomas Manke	MPI-IE	Freiburg	Challenges of setting up a bioinformatics unit

Session V: Geteiltes Leid - share your expertise!

17:30 - 18:00

BBQ @ Seepark - 6:10 departure of the bus #24!

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coffee from 9:30 @ lounge

Session V: Generating & Analyzing ChIP-seq reference sets

10:00 - 11:30

Ulrike Bönisch	MPI-IE	Freiburg	Strategies for size selection during library preparation
Andreas Richter	MPI-IE	Freiburg	DEEP insights from generating reference epigenomes
Felipe Albrecht	MPI-Inf	Saarbrücken	DeepBlue, epigenomic data server
Hinrich Gronemeyer	IGBMC	Strasbourg	Assessing quality standards for ChIP-seq and related massive parallel sequencing-generated datasets