

Bioinformatics for Human Health and Disease

November 7 - 9, 2016, Heidelberg

List of Posters

Poster-Nr.	Poster Title	Presenting Author
1	Overview of familial cancer variant prioritization pipeline (FCVPP) and its application	Kumar, Dr. Abhishek
2	Harmonizing Standardization Processes for Model and Data Exchange in Systems Biology	Golebiewski, Martin
3	PAA: an R/Bioconductor package for biomarker discovery with protein microarrays	Turewicz, Michael
4	Trading service against metadata in Systems Biology Data and Model Management	Müller, Dr. Wolfgang
5	SEMS and de.NBI-SysBio: Two projects working towards improved model management and result reproducibility	Henkel, Ron
6	Predicting the influence of combination therapies in signaling networks	Sitte, Maren
7	GenomeCRISPR - a database for high-throughput CRISPR/Cas9 screens	Heigwer, Florian
8	Imglib2 - generic image processing and visualization	Pietzsch, Dr. Tobias
9	The de.NBI-GCBN Service Centre – A Crop BioGreenformatics Network	Schmutzer, Dr. Thomas
10	Drug Discovery enhancing Systems	Leonov, Dr. Hadas
11	NBI-SysBio: de.NBI-node serving the Systems Biology Cycle	Rey, Dr. Maja
12	GenomeRNAi: A Phenotype Database for Large-scale RNAi Screens	Rauscher, Benedikt
13	Butler: A Framework for Large Scale Data Analysis on the Cloud	Yakneen, Sergei
14	Simplifying the publication of Bioconductor workflows with BiocWorkflowTools	Smith, Dr. Mike
15	Allele-specific copy number estimation from sequencing - ACEseq	Kleinheinz, Kortine
16	Mutational signatures of B-cell lymphomas	Huebschmann, Dr. Daniel
17	Web-based image analysis workflows for large-scale high-content cellular phenotyping	Wollmann, Thomas
18	Roddy: A framework for developing and managing cluster based scientific workflows	Heinold, Michael Christian
19	OTP: An automation platform for managing next generation sequencing	Zipprich, Gideon
20	Prototyping the HD-HuB Cloud in Heidelberg	Prinz, Manuel Alexander
21	de.NBI - German Network for Bioinformatics Infrastructure	Dammann-Kalinowski, Dr. Tanja
22	The MGX Framework for Metagenome Analysis	Jaenicke, Sebastian
23	Bioinformatics Services for Medical Microbial Genome Research of the de.NBI BiGi Center at Justus-Liebig-University Gießen	Goesmann, Prof. Alexander
24	RCAS: The RNA Centric Annotation System	Yusuf, Dr. Dilmurat
25	“Bioinformatics Training Platform at the Heidelberg Center for Human Bioinformatics”	Sharan, Dr. Malvika
26	The MetaProteomeAnalyzer software provides a complete workflow for analysis of metaproteomic data in microbiome research	Benndorf, Dr. Dirk
27	Comprehensive Molecular Diagnostics in Swiss Clinics	Toussaint, Dr. Nora
28	Semantic technologies for disease modeling of neurodegenerative diseases	Schaaf, Sebastian
29	Benchmarking of NGS Data Generation and Processing	Buchhalter, Ivo
30	OpenMS: Efficient tools and workflows for computational mass spectrometry	Sachsenberg, Timo
31	Uncovering the clinical genomics of AL Amyloidosis through omics tools	Meziane, Iman
32	Service Center 'Bioinformatics for Proteomics' - Partner MPC Bochum	Uszkoreit, Julian
33	Computational analysis of clinical microbiome studies	Zeller, Georg
34	Efficiency and the quality of methylation calls of RRBS and WGBS pipelines	Assenov, Yassen
35	Service platforms and tools for computational lipidomics	Kopczynski, Dominik