

## NGS Symposium 2013

### Day 1 – 18. April 2013 - Lectures

Großer Seminarraum des ATV (Room A0.106) – Building behind DKFZ main building

Im Neuheimer Feld 280, 69120 Heidelberg

Session	Time	Speaker	Institute	Title
	10.00			Welcome address
NGS Plattformen	10.15	Nora Rieber	DKFZ	An introduction into NGS sequencing
	10.45	Volker Endris	Universität Heidelberg	Targeted resequencing with Ion Torrent
	Break			
NGS Applications	11.30	Lars Feuerbach	DKFZ	Calling point mutations in cancer genomes
	12.00	Naveed Ishaque	DKFZ	ChIP-Seq: Applications and quality control
	12.30	Prakash Balasubramanian	DKFZ	One in a billion – Searching viral DNA in NGS cancer data
	Lunch			
Biases and Pitfalls	14.00	Fidel Ramirez	MPI Immunology & Epigenetics	Understanding and correcting the GC bias from high throughput sequencing data
	14.30	Barbara Hutter	DKFZ	Common pitfalls in the NGS Jungle
	15.00	Simone Röh	MPI Psychiatrie	An overview of pitfalls in quantitative accuracy of high throughput sequencing
	Break			
Epigenome Tools	16.00	Fabian Müller	MPI Informatik	Comprehensive Analysis of DNA methylation data using RnBeads
	16.30	Matthias Bieg	DKFZ	AsmHunter – Finding allele-specific methylation in methyl-seq data
	17.00	Felipe Albrecht	MPI Informatik	The EpiExplorer – High level analysis of epigenome data

### Day 2 – 19. April 2013 – Moderated discussions

Seminarraum - Gästehaus Berliner Strasse 38, 69120 Heidelberg

Time	Moderator	Topic
9.30	Michael Heinold	Bioinformatical solutions for high-throughput of high-throughput sequencing projects
10.00	Barbara Hutter	Where sequencers and aligners fail – Strategies for excluding biased genome regions
11.00	Natalie Jäger	The non-coding challenge – Analyzing mutations outside of protein-coding genes
12.00	Lars Feuerbach	Integrated analysis – Combining Genome-seq, RNA-seq, Methyl-seq and ChIP-seq data
13.00	Qi Wang	Hot topics, tools and resources

Locations:

