Scientific Programme

The Next NGS Challenge Conference: Data Processing and Integration

14-16 May 2013, Valencia, Spain

www.thenextngschallenge.org

The Next NGS Challenge
data processing and integration

Conference Programme

8:30AM	CONFERENCE REGISTRATION	
9:15AM	CONFERENCE WELCOME	
9:30AM	Keynote #1. Janet Kelso: Sequencing ancient genomes	
10:30AM	* Ralph Vogelsang: Automated Finished Microbial Genomes and Epigenomes to Understand Infectious Diseases.	
11:00AM	Break	
11:30AM	* Francisco M. De La Vega: Toward highly accurate and fast variant and de novo mutation identification from high-throughput sequencing data by joint Bayesian family calling.	
11:50AM	* Vladimir B. Teif: Developing a Software Suite to analyze the interplay between Nucleosome arrangement, DNA Methylation and Transcription factor binding.	
12:10AM	* John William Whitaker: Interplay between DNA Sequence motifs and the Human Epigenome.	
12:30	Lunch	
2:30PM	* Morgane Thomas-Chollier: RSAT Peak- Motifs: Efficient prediction of transcription factor motifs and binding sites from Genome- Wide sequencing peaks sets.	
2:50PM	* Babette Regierer: ESFRI - Infrastructure for Systems Biology Europe - (ISBE)	
3:10PM	* Javier Santoyo: Challenges in whole exome sequencing to identify disease-causing variants in human rare diseases	
3:30PM	Break	
4:00PM	Keynote #2. Karla Neugebauer: The Role of Gene Architecture in Gene Expression	
5:00PM 7:00PM	Posters&Beers	MC Meeting SeqAhead

Thursday 16th, 2013

9:00AM	Keynote #3. Leif Andersson: How domestic animal genomics can teach human medicine and medicine and evolutionary biology
10:00AM	Keynote #4. Michele Morgante: Structural variation and the plant pan genomes
11:00AM	Break
11:30AM	* Carine Poussin: Translational Systems Biology Understanding the limits of Animals Models as Predictors of Human Biology.
11:50AM	* Kay Nieselt: Automated transcription start site prediction for comparative comparative transcriptomics using the Supergenome.
12:10AM	* Oskar Erik Karlsson: Viral Metagenomics – New applications for the broad-range detection of viromes in veterinary and public health settings.
12:30AM	Lunch
2:30PM	* Ignacio Blanquer Blanquer: Supporting NGS pilelines in the cluod.
2:50PM	* Luca Pireddu: Automated and traceable processing for large-scale high-throughput sequencing facilities.
3:10PM	* Thomas Svensson: SciLifeLab:New national infrastructures for NGS data production and applied "down stream " bioinformatics analysis in order to meet the demands of the scientific community
3:30PM	Break
4:00PM	Keynote #4. Ivo Gut: High-Throughput DNA Analysis
5:00PM 7:00PM	Posters&Beers