



Monday 14th September 2015

8:00	Registration and welcome
SESSION 1. Multi-omics data	
9:00-10:00	Keynote lecture <i>Lennart Martens</i> . Dig deep and dig greedily: what we awaken in omics data analyses.
10:00-10:30	STATegra talk <i>Sonia Tarazona</i> . Useful tools for the analysis of multi-omic data
10:30-11:00	COFFEE BREAK
11:00-11:30	STATegra talk <i>David Gomez-Cabrero</i> . Multi-omics clustering: understanding a system through functional modules
11:30-12:00	STATegra talk <i>Johan Westernhuis</i> . Low level data fusion of hetero ~omics data sets
12:00-12:30	Contributed talk <i>Wiktor Jurkowski</i> . Omics data integration via biology driven penalised regression
12:30-13:00	Contributed talk <i>Costas Bouyioukos</i> . Multivariate analysis of the interplay between genome architecture and gene expression
13:00-14:30	LUNCH & POSTERS
SESSION 2 . Integrated network analysis	
14:30-15:00	Contributed talk <i>Animesh Acharjee</i> . Integration of metabolomics, lipidomics and clinical data by random forest
15:30-16:00	STATegra talk <i>Theo Reijmers</i> . From Data Fusion towards Network-based data integration
15:30-16:00	Contributed talk <i>Lisette J.A. Kogelman</i> . Gene co-expression networks within and across tissues in morbidly obese individuals
16:00-16:30	COFFEE BREAK
16:30-17:00	STATegra talk <i>Venkateshan Kannan</i> . Tracing the evolution of network transitions between distinct steady states from the integration of omics data
17:00-17:30	STATegra talk <i>Ana Conesa</i> . Comparison of temporal gene expression profiles with other omics to understand gene expression regulation

Tuesday 15th September

SESSION 3. Regulation of Gene expression		
9:00-10:00	Keynote lecture	Jason Ernst. Computational Methods for Large-scale Detection and Dissection of Human Regulatory Element
10:00-10:30	STATegra talk	Sonia Tarazona. IntegrRa: An omics integration pipeline to find gene expression regulatory programs and assess the effect of regulators
10:30-11:00 COFFEE BREAK		
11:00-11:30	STATegra talk	David Gomez-Cabrero. Regulatory mechanisms in chromatin domains and loops
11:30-12:00	Contributed talk	Eric Triplett. Integrating DNA methylation and gene expression data to understand the role of epigenetics in the development of the soybean-Bradyrhizobium N2-fixing symbiosis
12:00-12:30	Contributed talk	Stefano de Petris. INSPECT: a computational tool to infer mRNA synthesis, processing and degradation dynamics from RNA and 4SU-seq time course
12:30-13:00	STATegra talk	Ricardo Ramirez. High-resolution epigenomic analysis of human myeloid differentiation reveals temporal and lineage-specific patterns of transcriptional regulation
13:00-14:30 LUNCH & POSTERS		
SESSION 4. Integrative pathway analysis.		
14:30-15:00	STATegra talk	Rafael Hernandez. Paintomics 3.0: Integrated visualization of multi omics data on KEGG pathways
15:00-15:30	Contributed talk	Andrej Blejec. Animated graphics in R to reveal temporal dynamics of time course data
15:30-16:00	Contributed talk	Eugenia Galeota. Ontology-based annotations and semantic relations in large scale (epi)genomics data
16:00-16:30 COFFEE BREAK		
16:30-17:00	STATegra talk	Patricia Sebastian. Integrated Path signal propagation analysis to link transcriptional regulation to metabolic changes
17:00-17:30	Contributed talk	Abel Folch-Fortuny. Chemometric approaches for systems biology
17:30-18:00	Contributed talk	Ugur Sezerman. Identification of methylation affected pathways in cancer
21:00 CONFERENCE DINNER		

*Gala Dinner (Conference Dinner) will take place in Restaurante Gran Azul, Avenida Aragón, 10 46021 Valencia. More info: http://smodia2015.cipf.es/?page_id=501

Wednesday 16th September

SESSION 5. Integrative disease models		
9:00-10:00	Keynote lecture	Martin Morgan. R / Bioconductor: Challenges and Rewards from Integrative Analysis of High-Throughput Genomic Data
10:00-10:30	STATegra talk	Vincenzo Lagani. Integrative analysis of publicly available genomic and transcriptomic data: a case study in Acute Lymphoblastic Leukemia
10:30-11:00 COFFEE BREAK		
11:00-11:30	Contributed talk	Narsis A. Kiani. Phenotypic omic signature of Multiple Sclerosis
11:30-12:00	STATegra talk	Gilad Silberberg. Reconstructing DNase-seq regulatory networks by improved transcription-factor binding prediction
12:00-12:30	Contributed talk	Javier de las Rivas. Identification of expression patterns in the progression of disease stages by integration of transcriptomics data
12:30-14:00 LUNCH		

SMODIA2015 "Statistical Methods for Omics Data Integration and Analysis 2015" Valencia, Spain



PRINCIPE FELIPE
CENTRO DE INVESTIGACION