

**Thursday, 21<sup>st</sup> June**

start	end				
8.00	9.00	<b>REGISTRATION, Hotel Palace</b>			
<b>PLENARY LECTURES / Conference Hall, Hotel Palace</b> <b>Chair Leonardo de Oliveira Martins</b>					
9.00	9.30	<b>Prof. Mikhail Gelfand</b> – From computer to a test tube. How comparative genomics informs molecular biology <i>Institute for Information Transmission Problems, Russia</i>			
9.30	10.00	<b>Prof. Aleksandar Milosavljevic</b> – ClinGen Allele and Evidence Registries catalyze the emergence of an open ecosystem of data and knowledge about genetic variants in humans <i>Computational and Integrative Biomedical Research Center, Baylor College of Medicine, USA</i>			
10.00	10.30	<b>Prof. Vladimir Brusic</b> – Classification of Blood Cell Subtypes using Single Cell Gene Expression Data <i>Faculty of Science and Engineering, University of Nottingham, China</i>			
10.30	11.00	<b>Coffee break &amp;</b> <b>Meet the expert Sponsor Session (Alexander Kirpiy, Vivogen), TV Hall</b>			
<b>MORNING SESSION / Conference Hall, Hotel Palace</b> <b>Chair Prof. Aleksandar Milosavljevic</b>			<b>Bioinformatics and Data Mining of Biological Data (BiDMBD) /</b> <b>Banquet Hall, Hotel Palace</b> <b>Chair Dr. Bojana Banovic Djeri</b>		
11.00	11.25	<b>Prof. Natasa Przulj</b> – Mining the Integrated Connectedness of Biomedical Systems <i>Department of Computer Science, University College London, United Kingdom</i>	11.40	12.05	<b>Dr. Banovic-Djeri</b> - Bioinformatics in plant genetics from molecular biologists point of view
11.25	11.50	<b>Prof. Hiroshi Mamitsuka</b> – Data-Integrative Machine Learning for Bioinformatics <i>Bioinformatics Center, Institute for Chemical Research, Japan</i>			
11.50	12.15	<b>Prof. Hong-Yu OU</b> – Identification of type II toxin-antitoxin loci in bacterial genome <i>Shanghai Jiao Tong University, China</i>	12.05	12.30	<b>Dr. Zdravka Ivanova</b> - Sequencing and annotation of resurrection plant <i>Haberlearhodopensiscp</i> and mt genomes.
12.15	12.35	<b>Prof. Maja Stanojevic</b> – Use of phylogenetics in the study of viral genomes <i>Faculty of Medicine, University of Belgrade, Serbia</i>	12.30	12.40	<b>Danijela Paunovic</b> - ragp: An R toolbox for mining plant Hydroxyproline rich glycoproteins
12.35	13.05	<b>Prof. Antonio Starcevic</b> – Semantic Ion Vectors - deep learning applied to mass spectrometer <i>Faculty of Food Technology and Biotechnology, University of Zagreb, Croatia</i>	12.40	12.50	<b>Dr. Brijesh Singh Yadav</b> - Characterization of cellular metabolic response in abiotic stress-induced growth in <i>Arabidopsis thaliana</i> utilizing data mining
			12.50	13.00	<b>DISCUSSION</b>

13.05	14.00	<b>POSTER SESSION 3 / Conference Hall, Hotel Palace</b> <b>Dr. Lidija Djokic</b>
		<p>3.P1 – <b>Pavlovic</b>- Positional Biases of the Experimentally Characterized T-cell Epitopes</p> <p>3.P2 – <b>Trifunovic</b> - Determination of hTERT promoter methylation status using methylation specific PCR</p> <p>3.P3 – <b>Gemovic</b> - Function Annotation Algorithm Based on Sequence Spectral Features: Evaluation on Human Transcription Factors</p> <p>3.P4 – <b>Sumonja</b> - Exploring the usefulness of graph properties in protein protein interaction predictions</p> <p>3.P5 – <b>Zelic</b> - Development Of Anatomically Correct Human Mandible Finite Element Model From CT-Scans</p> <p>3.P6 – <b>Zukic</b> - FINDbase: worldwide database for clinically relevant genomic variation allele frequencies</p> <p>3.P7 – <b>Dragicevic</b> - Review of (effective) data collection methods for data-driven personalized medicine</p> <p>3.P8 – <b>Kotur</b> - Population pharmacogenomic aspect of glucocorticoids response in Serbian population</p> <p>3.P9 - <b>MiticPotkrajac</b> - Risk prediction of bladder cancer progression from gene expression data</p> <p>3.P10- <b>Davidovic S</b> - Phylogenetic analysis of putative Balkan specific mtDNA lineages</p>
14.00	15.00	<b>LUNCH*</b>
<b>FREE TIME / EXCURSION to be announced</b>		

\* Lunch will start every day at 13.30 and end at 15.30