

BelBI2016 Conference program

Thursday, 23.06.2016.		
Start	End	Morning session: Location - Hotel "Palace", conference hall
		Chair: Marko Djordjevic
9:00	9:35	Invited Speaker: Yuriy L. Orlov (Novosibirsk State University, Russia) <i>Comparative analysis of plant genome structure and antisense transcripts</i>
9:35	10:10	Invited Speaker: Paul Sorba (Laboratory of Theoretical Physics and CNRS, France) <i>Symmetry and Minimum Principle: a basis for the Genetic Code</i>
10:10	10:45	Invited Speaker: Konstantin Severinov (Rutgers University, USA) <i>The Influence of Copy-Number Maintenance Mechanisms of Targeted Extrachromosomal Genetic Elements on the Outcome of CRISPR-Cas Defense</i>
10:45	11:15	coffee break
		Chair: Vladimir Uversky
11:15	11:50	Invited Speaker: Bosiljka Tadić (Jozef Stefan Institute, Slovenia) <i>Algebraic Topology Analysis of Brain Graphs Emanating from Social Communications</i>
11:50	12:25	Invited Speaker: Erik Bongcam-Rudloff (Swedish University of Agricultural Sciences, Sweden) <i>Next Generation Biotechnologies, the bad and the good: a look into the future</i>
12:25	13:00	Invited Speaker: Andrea Ciliberto (IFOM-IEO, Italy) <i>Adapt or die. Investigating the molecular basis of cell variability</i>
13:00	13:30	Sponsors presentation (Genomix4Life, Pearson)
14:00	15:00	Lunch (Hotel "Palace")
		Afternoon session
		TABIS Session Hotel "Palace", Banquet hall
		Chair: Paul Sorba
		DMBI/Hi Session - Hotel "Palace", conference hall
		Chair: Noël Malod-Dognin
15:00	15:35	Invited Speaker: Branko Dragovic (Mathematical Institute Serbian SASA, Serbia) <i>Ultrametric Approach to Bioinformation Systems</i>
15:35	15:55	Natasa Misic (Lola Institute, Belgrade, Serbia) <i>Standard Genetic Code vs Vertebrate Mitochondrial Code: Nucleon Balances and p-Adic Distances</i>
15:55	16:15	Natasa Djurdjevac Conrad (Zuse Institute Berlin, Germany) <i>A new random-walk-based approach for finding co-expression modules in biological networks</i>
16:15	16:35	Ozal Mutlu (Marmara University, Istanbul, Turkey) <i>Structural Characterization of the Trypanosoma brucei CK2A1-HDAC1/HDAC2 Interactions by Molecular Modeling and Protein-Protein Docking</i>
16:35	17:10	Ana Simonovic (Institute for Biological Research, University of Belgrade, Serbia) <i>Identification of genes involved in morphogenesis in vitro in Centaurium erythraea Rafn. as a model organism</i>
		coffee break
		Richard Roettger (University of Southern Denmark, Odense, Denmark) <i>On the clustering of biomedical datasets - a data-driven perspective</i>
		Milan Vukicevic (University of Belgrade, Faculty of Organizational Sciences, Serbia) <i>White-Box Predictive Algorithms for Predicting Disease States on Gene Expression Data – From Component Based Design to Meta Learning</i>
		Chair: Yuriy L. Orlov
		Chair: Dragan Matic

BelBI2016 Conference program

17:10	17:30	<p>Tamara Dimitrova (Macedonian Academy of Sciences and Arts, Macedonia) <i>Analysis of network structural characteristics through vertex characteristics in directed networks</i></p>	<p>Dragana Dudic (University of Belgrade, Faculty of Agriculture, Serbia) <i>Mining PMMoV genotype-pathotype association rules from public databases</i></p>
17:30	17:50	<p>Balázs Szalkai (Eötvös University, Budapest, Hungary) <i>Graph Theoretical Analysis Reveals: Women's Brains Are Better Connected than Men's</i></p>	<p>Ana Jelovic (University of Belgrade, Faculty of Transport and Traffic Engineering, Serbia) <i>Filtering of repeat sequences in genomes</i></p>
17:50	18:10	<p>Balint Varga (Eötvös Loránd University, Budapest, Hungary) <i>Comparative Connectomics: Mapping the Inter-Individual Variability of Connections within the Regions of the Human Brain</i></p>	<p>Milana Grbic (Univeristy of Banja Luka, Faculty of Science and Mathematics, Bosnia and Herzegovina) <i>Improving INN strategy for classification of some prokaryotic organisms</i></p>
18:10	18:30	<p>Yair Lakretz (Tel Aviv University, Israel) <i>The perceptual structure of the phoneme manifold</i></p>	<p>Sanja Brdar (Institute for research and development of information technology in biosystem, University of Novi Sad, Serbia) <i>Non-negative Matrix Factorization for Integrative Clustering of Bioinformatics Data</i></p>
Conference Dinner			
20:00			