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

17:10	17:30		**Tamara Dimitrova** (Macedonian Academy of Sciences and Arts, Macedonia) *Analysis of network structural characteristics through vertex characteristics in directed networks*	**Dragana Dudic** (University of Belgrade, Faculty of Agriculture, Serbia) *Mining PMMoV genotype-pathotype association rules from public databases*
17:30	17:50		**Balázs Szalkai** (Eötvös University, Budapest, Hungary) *Graph Theoretical Analysis Reveals: Women's Brains Are Better Connected than Men's*	**Ana Jelovic** (University of Belgrade, Faculty of Transport and Traffic Engineering, Serbia) *Filtering of repeat sequences in genomes*
17:50	18:10		**Balint Varga** (Eötvös Loránd University, Budapest, Hungary) *Comparative Connectomics: Mapping the Inter-Individual Variability of Connections within the Regions of the Human Brain*	**Milana Grbic** (Univeristy of Banja Luka, Faculty of Science and Mathematics, Bosnia and Herzegovina) *Improving 1NN strategy for classification of some prokaryotic organisms*
18:10	18:30		**Yair Lakretz** (Tel Aviv University, Israel) *The perceptual structure of the phoneme manifold*	**Sanja Brdar** (Institute for research and development of information technology in biosystem, University of Novi Sad, Serbia) *Non-negative Matrix Factorization for Integrative Clustering of Bioinformatics Data*
20:00			Conference Dinner	