

Sunday, 17th June

EARLY REGISTRATION, Hotel Palace (Toplicin venac 23), Hotel Lobby, 17.00-20.00 h

Monday, 18th June

start	end		start	end	COST CA15120 Session / Banquet Hall, Hotel Palace
9.00	12.00	REGISTRATION University of Belgrade Rectorate (Studentski trg 1), Lobby			
10.00	14.00	OPENING CEREMONY Congress Hall of the University of Belgrade Rectorate, (Studentski trg 1)	9.00	14.00	COST CA15120 WG Meeting, OpenMultiMed
14.00	15.00	LUNCH*			
TABIS Session/ Conference Hall, Hotel Palace			COST CA15120 Session / Banquet Hall, Hotel Palace		
15.00	15.25	Marsili - Relevance	15.00	16.15	COST CA15120 WG Meeting, OpenMultiMed
15.25	15.50	de Brevern - Analysis of allosteric effect of pathologic variants at the light of local protein conformations			
15.50	16.15	Tadic - Why Human Brain Networks are Hyperbolic			
16.15	16.45	Coffee break			
TABIS Session / Conference Hall, Hotel Palace			COST CA15120 Session / Banquet Hall, Hotel Palace		
16.45	17.10	Fimmel - On Dichotomy Classes and Bijections of the Genetic Code	16.45	17.00	Introduction by the STSM Committee
17.10	17.35	Struengmann - Circular Codes in the Genetic Information	17.00	17.20	Demirkol - Characterization of novel risk predictors in colorectal cancer
17.35	18.00	Kozyrev - Biology is a constructive physics	17.20	17.40	Lazareva -Network-constrained bi-clustering of patients and multi-scale omics data
			17.40	18.00	Vilor - Independent Multifactorial Association algorithm to assess genetic and neuroimaging features associated with neurodevelopmental domains

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

Tuesday, 19th June

start	end				
8.00	9.00	REGISTRATION, Hotel Palace			
PLENARY LECTURES / Conference Hall, Hotel Palace					
9.00	9.30	Severinov - Maintenance of plasmid DNA at conditions of countering CRISPR-Cas interference			
9.30	10.00	Baumbach - Network-based disease classification and de novo endophenotyping			
10.00	10.30	Stres -The rare layers of significance			
10.30	11.00	Coffee break			
MORNING SESSION / Conference Hall, Hotel Palace		COST CA15120 Session / Banquet Hall, Hotel Palace			
11.00	11.25	11.00 14.00 MC Meeting COST CA15120, OpenMultiMed			
11.25	11.50				Vilar - Inference and prediction in molecular biological systems
11.50	12.15				Ciliberto - Cells proliferating under constant checkpoint activation: adaptation, refractory state and memory
12.15	12.35				Studholme - Comparative genomics of a recently emerging epidemic on banana in Sub-Saharan Africa.
12.35	13.05				Vlahovicek - Predicting Disease from Gut Microbiota Codon Usage Profiles
12.35	13.05	Pojksic - Digital reconstruction of partial DNA profiles of human skeletal remains			
13.05	14.00	POSTER SESSION 1 / Conference Hall, Hotel Palace			
		1.P1 – Saveljic - 3D Simulation of Inflammatory Process in Coronary Arteries 1.P2 – Nikolic - Geometry Optimization of Nitinol Stent Design based on FEA Topology Optimisation 1.P3 – Vulovic - Numerical Simulation of Blood Flow and Plaque Progression in Right Femoral Artery Bypass Patient-Specific Case 1.P4 – Nikolic - Modelling of Monocytes Behaviour inside the Bioreactor 1.P5 – Djorovic - Parametric Modelling and Computational Examination of Bicuspid Aortic Valve 1.P6 – Grbic - Conditional Random Fields based approach for classification of the reactants in some metabolic reactions 1.P7 – Stankovic - Binding of metal ions and water molecules to nucleic bases 1.P8 – Milanovic - Inactivation of free radical species with selected triazoles 1.P9 – Avdović - Molecular docking study on the interaction of human procalcitonin with 3-(1-(2-mercaptoethylamino)ethylidene)-chroman-2,4-dion 1.P10– Doric - PalFin: A Software Tool to Identify Specific Palindrome Motifs in mtDNA			
14.00	15.00	LUNCH*			
Bioinformatics and Data Mining of Biological Data (BiDMBD) – Oral presentation / Conference Hall, Hotel Palace		COST CA15120 Session / Banquet Hall, Hotel Palace			
15.00	15.15	Djordjevic - A Kolmogorov-Smirnov based approach for predicting bacterial transcription targets	15.00	15.15	Lautizi - Extracting survival-relevant subnetworks from multi-scale omics data with KeyPathwayMiner
15.15	15.30	Guzina - Predicting CRISPR/Cas associated small RNAs and their role in bacterial virulence	15.15	15.35	Brdar - Clustering and classification of human microbiome data: evaluating impact of different settings in bioinformatics workflows
15.30	15.40	Chervontceva - The role of mRNA secondary structure in the control of translation and mRNA degradation in E. coli	15.35	15.55	Belik -Modelling Hospital Infection Spread in the Polish Regional Healthcare Network
15.40	15.50	Krause - Establishing Benchmark Criteria for Single Chromosome Bacterial Genome Assembly	15.55	16.15	Casas Guijarro - 3D reconstruction of cerebral reactive oxygen species formation as a gold standard for future in vivo molecular imaging approaches
15.50	16.00	Rodic - Investigating the role of key features in CRISPR-Cas system regulation			

16.00	16.15	DISCUSSION			
16.15	16.45		Coffee break		
16.45	17.15	Sponsor Session 1 / Conference Hall Sarah Nema, QIAGEN - QIAGEN Bioinformatics - The journey so far	16.45	17.15	MC Meeting COST CA15120, OpenMultiMed
Bioinformatics and Data Mining of Biological Data (BiDMBD) – Oral presentation / Conference Hall, Hotel Palace			Bioinformatics and Data Mining of Biological Data (BiDMBD) / BI – Oral presentation / Banquet Hall, Hotel Palace		
17.15	17.40	Savic-Pavicevic - Identifying modifiers of somatic instability and age at onset in myotonic dystrophy type 1 by modeling genetic data	17.15	17.40	Exarchos - New concepts for the stratification of patients with carotid artery disease: Multiscale modelling and big data analytics
17.35	17.45	Vukovic - Higher-order genetic interactions in prostate cancer and benign prostatic hyperplasia			
17.45	17.55	Nikolic - GARLIC: A Bioinformatic Toolkit for Etiologically Connecting Diseases and Cell Type-Specific Regulatory Maps	17.40	17.50	Radovic - Application of Machine Learning Algorithms to Detect Coronary Artery Disease using Genomic Data
17.55	18.05	List - Genome-wide endogenous RNA networks highlight novel biomarkers in cancer	17.50	18.00	Isailovic - Numerical simulation of stent deployment procedure in patient specific coronary artery
18.05	18.15	Kosvyra - Developing an Integrated Genomic Profile for Cancer Patients Utilizing NGS Data	18.00	18.10	Simic - Application of multiscale smeared finite element model for modelling of mass transport in capillary systems and biological tissue
18.15	18.25	Marjanovic - Bioinformatics pipeline used for Next Generation Sequencing analysis of predictive markers in hematological malignancies	18.10	18.20	Andjelkovic Cirkovic - Prediction of Pharmacological Treatment for Patients with Coronary Artery Disease
18.25	18.35	DISCUSSION	18.20	18.30	DISCUSSION

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Wednesday, 20th June 2018

start	end				
8.00	9.00	REGISTRATION, Hotel Palace			
PLENARY LECTURES – COST BM1405 Session / Conference Hall, , Hotel Palace					
9.00	9.10	Introduction			
9.10	9.40	Rost – Implications of dark proteome for precision medicine			
9.40	10.05	Tosatto – Computational resources for the study of intrinsically disordered proteins			
10.05	10.30	Ventura - Combining structural aggregation propensity and stability predictions to re-design protein solubility			
10.30	11.00	Coffee break			
COST BM1405 Session / Conference Hall, Hotel Palace			Bioinformatics and Data Mining of Biological Data (BiDMBD) / Banquet Hall, Hotel Palace		
11.00	11.30	Bateman - Pfam: 20 years of classifying protein repeat families	11.40	12.05	Grzybowski - Genetic portrait of Central- and Eastern European populations
11.30	11.55	Tompa - Phase separation in ALS demonstrates the role of RNA binding and low-complexity regions in collective protein functions			
11.55	12.20	Galzitskaya - Influence of homo-repeats on the aggregation properties of proteins from 122 proteomes and codon usage in DNA	12.05	12.30	Kovacevic-Grujicic - Insights into the mitochondrial gene pool of Serbian population: phylogenetic and phylogeographic analysis
12.20	12.45	Mitic - Disorder predictors precision and accuracy - a computer science view	12.30	12.40	Kacprowski - Circulating miRNAs as Potential Liver-Related Biomarkers
12.45	13.00	Session wrap-up and informal discussions	12.40	12.50	Babenko R - FTO haplotyping underlines high obesity risk for European populations
			12.50	13.00	DISCUSSION
13.00	14.00	POSTER SESSION 2 / Conference Hall, Hotel Palace			
		2.P1 – Popovic - Video-based extraction of movement artifacts in electrogastrography signal 2.P2 – Milicevic - Muscle model with net of fibers used for modelling cell migration 2.P3 – Vulovic - Finite Element Analysis of the Modified Hip Implant Surface 2.P4 – Ferouka - Discrete simulation of electrospinning jet's evolution 2.P5 – Marovac - Classification of proteins into COG categories based on n-gram patterns 2.P6 – Zivanovic - Optimization of Electrochemical Parameters for Detection of microRNA: Computer Simulation and Experimental Study 2.P7 – Sustersic - Numerical simulation of electrospinning using PAK and ANSYS software 2.P8 – Jovanovic - Subtle transcriptomic signals in circulation after myocardial infarction might indicate the ventricular remodeling outcome 2.P9 – Djukic - Parallelization of software for stent deployment inside artery 2.P10– Anic - Neural Networks Implemented on Aorta with Abdominal Aneurism			
14.00	15.00	LUNCH*			
15.00	16.30	ROUND TABLE: Experience, Challenges and Networking			
16.30	16.45	Coffee break			
16.45	17.15	Sponsor Session 2 / Conference Hall Alexander Kirpiy, Vivogen - Ion Torrent™ bioinformatics environment GALA DINNER to be announced			

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Thursday, 21st June

start	end				
8.00	9.00	REGISTRATION, Hotel Palace			
PLENARY LECTURES / Conference Hall, Hotel Palace					
9.00	9.30	Gelfand - From computer to a test tube. How comparative genomics informs molecular biology			
9.30	10.00	Milosavljevic - ClinGen Allele and Evidence Registries catalyze the emergence of an open ecosystem of data and knowledge about genetic variants in humans			
10.00	10.30	Brusic - Classification of Blood Cell Subtypes using Single Cell Gene Expression Data			
10.30	11.00	Coffee break & Meet the expert Sponsor Session (Alexander Kirpiy, Vivogen), TV Hall			
MORNING SESSION / Conference Hall, Hotel Palace			Bioinformatics and Data Mining of Biological Data (BiDMBD) / Banquet Hall, Hotel Palace		
11.00	11.25	Przulj - Mining the Integrated Connectedness of Biomedical Systems	11.40	12.05	Banovic-Djeri - Bioinformatics in plant genetics from molecular biologists point of view
11.25	11.50	Mamitsuka - Data-Integrative Machine Learning for Bioinformatics			
11.50	12.15	Hong-Yu OU - Identification of type II toxin-antitoxin loci in bacterial genome	12.05	12.30	Ivanova - Sequencing and annotation of resurrection plant <i>Haberlea rhodopensis</i> cp and mt genomes.
12.15	12.35	Stanojevic - Use of phylogenetics in the study of viral genomes	12.30	12.40	Paunovic - ragp: An R toolbox for mining plant Hydroxyproline rich glycoproteins
12.35	13.05	Starcevic - Semantic Ion Vectors - deep learning applied to mass spectrometer	12.40	12.50	Yadav - Characterization of cellular metabolic response in abiotic stress-induced growth in Arabidopsis thaliana utilizing data mining
			12.50	13.00	DISCUSSION
13.05	14.00	POSTER SESSION 3 / Conference Hall, Hotel Palace			
3.P1 – Pavlovic - Positional Biases of the Experimentally Characterized T-cell Epitopes 3.P2 – Trifunovic - Determination of hTERT promoter methylation status using methylation specific PCR 3.P3 – Gemovic - Function Annotation Algorithm Based on Sequence Spectral Features: Evaluation on Human Transcription Factors 3.P4 – Sumonja - Exploring the usefulness of graph properties in protein protein interaction predictions 3.P5 – Zelic - Development Of Anatomically Correct Human Mandible Finite Element Model From CT-Scans 3.P6 – Zukic - FINDbase: worldwide database for clinically relevant genomic variation allele frequencies 3.P7 – Dragicevic - Review of (effective) data collection methods for data-driven personalized medicine 3.P8 – Kotur - Population pharmacogenomic aspect of glucocorticoids response in Serbian population 3.P9 - Mitic Potkrajac - Risk prediction of bladder cancer progression from gene expression data 3.P10- Davidovic S - Phylogenetic analysis of putative Balkan specific mtDNA lineages					
14.00	15.00	LUNCH*			
FREE TIME / EXCURSION to be announced					

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Friday, 22nd June

start	end				
PLENARY LECTURES / Conference Hall, Hotel Palace					
9.00	9.30	Dragovich - p-Adic Genetic Code			
9.30	10.00	Petoukhov - The New Wide Class of Symmetries in Long DNA-Texts. Elements of Quantum-Information Genetics			
10.00	10.30	Volkov - The Mechanisms of DNA Genetic Information Deactivation in Ion Cancer Therapy			
10.30	11.00	Coffee break			
MORNING SESSION / Conference Hall, Hotel Palace					
11.00	11.25	Martins - Spectral signature of gene family trees			
11.25	11.50	Orlov - Analysis of Differential Alternative Splicing and Gene Networks by RNA-seq Data in Brain Areas of Laboratory Rats			
11.50	12.15	Hofestadt - PNlib-Shell: Modeling and Simulation of biological networks based on Petri nets			
12.15	12.40	Zukic - Bioinformatics strategy for rare disease diagnostics in the era of next-generation sequencing			
POSTER SESSION 4 / Conference Hall, Hotel Palace					
13.00	14.00	4.P1 – Blagojevic - Defining dynamical property observables which ensure efficient restriction-modification systems establishment in bacterial host 4.P2 – Tasic - Application of bioinformatics in the identification of autohtonous bacterial strains of Vranjska Banja thermal springs based on different methods 4.P3 – Malkov - Correlation of intrinsically disordered protein regions content with environmental characteristic in Archaea and Bacteria 4.P4 – Loncar-Turukalo - Improving Clustering Performance in Microbiome Studies 4.P5 – Katic - Motor Imagery Classification using H2O Machine Learning Platform 4.P6 – Jelovic - RepeatPlus - program for finding repeats in nucleic acids and proteins 4.P7 – Menon - Insilico identification of Transcription End Sites in Human Genome 4.P8 – Maljkovic - Analysis of Amino Acid Interactions Based on Geometric Distances 4.P9 – Bjelica - Unobtrusive Human Activity Recognition 4.P10– Vrecl - Combined in silico and experimental approach to identify the peptide mimetic of the nanobody that stabilize functional conformational state of the beta2 adrenergic receptor (β 2AR)			
14.00	15.00	LUNCH*			
Biomedical Informatics / Conference Hall, Hotel Palace			TABIS / Banquet Hall, Hotel Palace		
15.00	15.10	Perovic - Prediction of Human Phenotype Ontology Terms For Intrinsically Disordered Proteins	15.00	15.25	Babenko V - Brain regions transcriptome analysis in mouse chronic stress model
15.10	15.20	Davidovic R - DiNGO: stand-alone application for GO and HPO term enrichment	15.25	15.35	Dushanov - Effect of mutant NMDA receptors on oscillations in a model of hippocampus
15.20	15.30	Vinterhalter - Bioinformatics analysis of correlation between protein function and intrinsic disorder	15.35	15.45	Misic - Arithmetical Regularities Inside the Standard Genetic Code as a Clue for the Investigation of Natural Biocomputing
15.30	15.40	Oros - MALDI-TOF/TOF and diagnosis of bacterial UTIs	15.45	15.55	Graovac - Investigating interplay of intracellular regulation and population dynamics in a bacterial restriction-modification system
15.40	15.50	Milosevic - Information extraction from tables: case studies on extracting demographic information from tables in clinical trial literature and drug-drug interactions from tables in drug labels	15.55	16.05	Păuna - Reduction method for reaction-diffusion equations from biology

15.50	16.00	Milovanovic - Numerical approach for determination of virtual functional assessment index in coronary arteries	16.05	16.15	DISCUSSION
16.00	16.15	DISCUSSION			
16.15	16.45	Coffee break			
16.45	17.15	CLOSING CEREMONY			
17.15	18.00	SERBIAN SOCIETY FOR BIOINFORMATICS AND COMPUTATIONAL BIOLOGY MEETING			

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