

### Wednesday, 15.09

Hours	Session	Presentation title	Speaker	Chairperson
09:00-09:10	Welcome			Marta Szachniuk, Witold Rudnicki
09:10-09:50	Keynote speaker	Assessing conservation of Alternative Splicing with Evolutionary Splicing Graphs	Hugues Richard	Aleksandra Świercz
09:50-10:00	Questions to keynote speaker			
10:00-10:10	Break			
10:10-11:30	Genome assembly and structural variant detection	Algorithm for DNA sequence assembly by quantum annealing	Katarzyna Nałęcz-Charkiewicz	Aleksandra Świercz
		A pipeline for resolving complex constitutional rearrangements using long reads sequencing technology	Barbara Poszowiecka	
		Near-complete de novo assembly of non-reference Arabidopsis thaliana accession on the basis of only nanopore sequencing data reveals structural variation and strong synteny	Anastasiia Satyr	
		Automatized consensus identification and comparative analysis of structural variants using Illumina and Oxford Nanopore sequencing in selected human families	Mateusz Chiliński	
11:30-11:40	Break			
11:40-13:20	Machine learning	Predicting pathogenic potentials of novel viruses, bacteria and fungi directly from NGS reads	Jakub Bartoszewicz	Michał Dramiński
		Automating Secondary Structure Assignment of Proteins using Neural Networks	Mohammad Saqib	
		Exploring the microbiome protein structure space using simulations and deep learning	Paweł Szczerbiak	
		Functional annotation of microbial genomes and metagenomes using deep learning-based method (DeepFRI)	Mary Maranga	
		The quest for mediator paths	Miron Kurska	
13:20-13:30	Break			
13:30-14:50	Network biology	Systems approach to study relations between SARS-CoV-2 infection and essential hypertension	Kaja Gutowska	Małgorzata Perycz
		MultiNet: A diffusion based approach to assign directionality in protein interactions using a consensus of eight protein interaction datasets	Kaustav Sengupta	
		Trapalyzer: A PartSeg plugin for the semi-automatic quantification of Neutrophil Extracellular Traps in fluorescence microscopic images	Grzegorz Bokota	
		The Clade Displacement Index: detecting Horizontal Gene Transfers in unrooted gene trees	Michał Ciach	
14:50-15:30	Lunch break			
15:30-16:30	Poster session	Impact of Copy Number Variation on gene expression (Room 1)	Magda Mielczarek	Maciej Antczak
		The robustness of the chaos game representation to mutations and its application in free-alignment methods (Room 2)	Adrian Kania	
		Enhancing the time of de novo assembly by matching genomic data (Room 3)	Artur Laskowski	
		Impact of DNA methylation on expression of rheumatoid arthritis related genes (Room 4)	Aleksandra Gabriela Biliska	
		Interpretable deep learning for phage life cycle prediction (Room 5)	Melania Nowicka	
		To reuse or not to reuse: Effect of flowcell reuse on sequencing efficiency on subsequent runs and identification of key environmental microbiomes. (Room 6)	Dedan Githae	
		Optical map assembly algorithms (Room 7)	Konrad Bratosiewicz	
		Identification of heat stress responsive transcripts in Sprague-Dawley rats using mixed linear models (Room 8)	Krzysztof Kotlarz	
		Bioinformatic modelling of SARS-CoV-2 pandemic with a focus on country-specific dynamics (Room 9)	Jakub Liu	
		RNA World simulation using partial differential equations (Room 10)	Jarosław Synak	
16:30-16:40	Break			
16:40-17:20	Social event	Scientific speed dating		Aleksander Jankowski
17:20-17:30	Break			
>17:30	Social event	Imaginary research projects		Aleksander Jankowski

**Thursday, 16.09**

Hours	Session	Presentation title	Speaker	Chairperson
08:30-9:50	RNA structure and function	Identification and characteristics of lncRNAs in Polish Landrace boars	Bartłomiej Hofman	Tomasz Żok
		Novel database for quadruplexes... and more - ONQUADRO	Joanna Miśkiewicz	
		fingeRNAt - a novel tool for high-throughput analysis of nucleic acid-ligand interactions	Natalia Szulc	
		Activity prediction of small molecules toward RNA targets using interaction fingerprints and machine learning	Filip Stefaniak	
09:50-10:00	Break			
10:00-10:30	Honorary member	From SBH to the Genomic Map of Poland	Jacek Błażewicz	Piotr Łukasiak
10:30-10:40	Questions to honorary member			
10:40-10:50	Break			
10:50-12:00	Sequencing methodologies and their application in clinical health	The role of DNA methylation in the regulation of the expression of TGF- $\beta$ pathway related genes	Michał J. Dąbrowski	Bartosz Wojtaś
		Basecalling with joint raw and event data sequence-to-sequence processing	Adam Napieralski	
		Investigation of the influence of selection at the amino acid level on the synonymous codon usage in alternative genetic codes	Konrad Pawlak	
12:00-12:10	Break			
12:10-13:10	Poster session	LCRAnnotationsDB: Dataset containing functional information about low complexity fragments in proteins (Room 11)	Joanna Ziemska-Legięcka	Marta Jordanowska
		Masserstein extended: dealing with noise in mass spectra (Room 12)	Barbara Domżał	
		ABG Assistant-Towards an Understanding of Complex Acid-Base Disorders (Room 13)	Łukasz Gutowski	
		MASSTERMIND: Accurate Monoisotopic Mass Determination Based On Isotopic Envelope (Room 14)	Piotr Radziński	
		Alignstein: a novel LC-MS alignment algorithm based on Wasserstein distance (Room 15)	Grzegorz Skoraczyński	
		Multi-agent model of cancer hypoxia adaptation (Room 16)	Mateusz Twardawa	
		Predicting gut microbiota fluctuations in time using vector autoregressive model (Room 17)	Zuzanna Karwowska	
		ViralCounter: An automated algorithm that allows to count the number of viruses in cells (Room 18)	Dagmara Błaszczuk	
		Urine cytology with the infrared hyperspectral spectroscopy – exemplary steps of the chemometric analysis (Room 19)	Monika Kujdowicz	
13:10-14:00	Poster session in rooms			Aleksandra Świercz, Marta Jordanowska
14:00-14:20	Break			
14:20-15:00	Keynote speaker	Age- and sex-dependent effect of low dose radiation on the T-cell repertoire in mice and humans	Joanna Polańska	Aleksandra Gruca
15:00-15:10	Questions to keynote speaker			
15:10-16:00	Lunch break			
>16:00	General Assembly of the Polish Bioinformatics Society			

**Friday, 17.09**

Hours	Session	Presentation title	Speaker	Chairperson
08:30-09:50	Gene expression and genome organization	Discovery of gene expression levels specific for various brain cells and significant in Alzheimer disease based on single cell data	Mateusz Jakiel	Agnieszka Rybarczyk
		Gene expression variation in the context of Topologically Associating Domains	Patrycja Rosa	
		Discovering novel alternative splicing events in mouse genome	Agata Muszyńska	
		New tool for detection of polyadenylation in RNA-seq data	Lidia Lipińska-Zubrycka	
09:50-10:00	Break			
10:00-10:40	Keynote speaker	Deciphering 3D genome organization with probabilistic models	Noam Kaplan	Aleksander Jankowski
10:40-10:50	Questions to keynote speaker			
10:50-11:00	Break			
11:00-12:00	Laureates	Comparison of whole genome alignment methods	Agata Gruszyńska	Paweł Górecki
		Determination of sets of substrings of nucleotide sequences in genome sequencing data	Marek Kokot	
		Quantitative Methods to Describe Information Flow in Biochemical Signalling Pathways	Tomasz Jetka	
12:00-12:15	Break			
12:15-12:45	Honorary member	Shining Light on Proteins (and Students)	Wiesław Nowak	Łukasz Peplowski
12:45-12:55	Questions to honorary member			
12:55-13:15	Break			
13:15-13:45	Awards and closing remarks			Michał J. Dąbrowski