

Wednesday, 16 September					
Hours	Session	Presentation Title	Speaker	Affiliation	Chairperson
11:00 - 12:00	Registration				
12:00 - 12:10	Opening		Maciej Antczak, Tomasz Żok	Poznan University of Technology	
12:10 - 13:00	Keynote 1	How Ancient DNA Is Transforming Our Understanding of the Past	Maciej Chyleński	Adam Mickiewicz University	Aleksandra Gruca
13:00 - 14:20	Algorithms for bioinformatics and computational biology	Benchmarking Framework for Taxonomic Classifiers	Patryk Gryz	Warsaw University of Technology	Michał Dąbrowski
		Species-Level Microbiome Dynamics Distinguish Bacterial from Non-Bacterial Sinonasal Infections: Toward Precision Diagnostics	Sylvia Bożek	Sano Centre for Computational Medicine	
		UNet based Approximation of Proton Radiation Dose Distribution in the Human Body for Proton Therapy	Adam Malinowski	Poznan University of Technology	
		Investigating the Impact of Sex-Specific Reference Genomes on RNA-Seq Read Mapping	Julia Rochatka	Poznan University of Technology	
14:20: 15:10	Lunch				
15:10 - 16:30	Modelling of protein and RNA structures	When RNA Sequence Reveals Hidden Geometry	Paulina Hładki	Poznan University of Technology	Tomasz Żok
		Large-scale analysis and clustering of RNA 3D structures	Jan Pieleśiak	Poznan University of Technology	
		Analyzing Recurrent Local Protein Packing Motifs in Stable Domains and Dynamic Interfaces	Krzysztof Pysz	Wrocław University of Science and Technology	
		MD Simulations Reveal How a Tunnel Entrance Mutation Disrupts Transport in an ABCG Transporter	Aleksandra Bigos	Adam Mickiewicz University	
16:30 - 16:50	Coffe break				
16:50 - 17:40	Keynote 2	Integrative large-scale metagenomics for strain-level microbiome analysis	Edoardo Pasolli	University of Naples Federico II	Aleksandra Świercz
17:40 - 18:30	Flash poster	NATSEQ: A Nextflow pipeline for identification of natural antisense transcripts from long-read RNA-seq data	Artemi Aleshkevich	Adam Mickiewicz University	Sylvia Bożek
		Statistics for non-canonical interactions	Jan Badura	Poznan University of Technology	
		Functional clustering of low-complexity regions across RNA-binding proteins	Abdeldjalil Bouziane	Institute of Biochemistry and Biophysics PAS	
		Identification of potentially amyloidogenic peptides in gut microbiota bacterial proteins using the updated AmyLoad database	Julia Cieszko	Wrocław University of Science and Technology	
		G4Composer: A Web-Based Framework for Rapid Assembly of Complex G-Quadruplex Architectures	Dariusz Dziel	Poznan University of Technology	
		Benchmarking deep learning models for lncRNA subcellular localization prediction	Alicja Dzik	Poznan University of Technology	
		IScores: proper scoring rules for evaluating missing-value imputation methods	Krystyna Grzesiak	University of Wrocław	
		THE AMYLOGRAPH AMYLOID-ANTIBODY DATABASE: DATA ACQUISITION, CURATION, EXTRACTION FOR AMYLOID-ANTIBODY INTERACTIONS	Valentin Iglesias	Medical University of Białystok	
		SCSM: Prior-Informed Genetic Demultiplexing for Multiplexed Single-Cell Sequencing of Clinical Cohorts	Katarzyna Jurkowska	AGH University of Krakow, Leiden University Medical Centre	
		Development of conformational ensemble embedding method for flexible target diffusion based generative models	Mikołaj Kikolski	Wrocław University of Science and Technology	
		Somatic piRNA expression and their putative regulatory roles in two insect models	Krystian Komenda	Jagiellonian University	
		Investigating the Impact of Protonation-State on the Conformational Dynamics of the Glucose Facilitated Transporter (GLF)	Nitheeshkumar Kumar	Adam Mickiewicz University	
		Interface Usability Barriers for Older Adults and Their Implications for Health-Related Applications	Julia Anna Manikowska	Poznan University of Technology	
		LCR-Dataset: A Benchmark for Language Models to Analyze Functions of Low-Complexity Regions in Scientific Literature	Sylvia Morawiec	Silesian University of Technology	
		Computational analysis of sugar–Glf interactions to improve sugar transport efficiency	Abraham Muñiz-Chicharro	Adam Mickiewicz University	
		A Comparative Genomic Framework for Identifying Candidate Functional Sites in the European Bison Genome	Kamil Patan	Adam Mickiewicz University	
		FROM HEALTH TO ADENOMA TO COLORECTAL CANCER: EXPLORING GUT MICROBIOME SIGNATURES	Maja Piątek	Jagiellonian University	
		Automated and autonomous experimental setup (AAES) for long-term and multi-site behavioural experiments	Kacper Roszczak	Adam Mickiewicz University	
		Identification of double-stranded RNA molecules formed by 5'-overlapping protein-coding gene transcripts	Antoni Sawa	Adam Mickiewicz University	
		Democratising structure-based protein function prediction with metagenomic-deepFRI	Filip Schymik	AGH University of Krakow	
		LaRNAI: a web platform for RNA structure analysis	Maksim Serdakov	International Institute of Molecular Mechanisms and Machines PAS	
		TickPacket	Mariia Rutkowska	Medical University of Białystok	
		Explainable Artificial Intelligence methods for DeepVariant	Piotr Suszyński	Warsaw University of Technology	
		Secretome: finding and characterizing secreted proteins in the human gut microbiome	Alicja Wojciechowska	Alicja Wojciechowska	
		Beyond Binary ORA: Preliminary Results of Unsupervised Clustering on LLM Embeddings for Omics Data	Joanna Żyła	Silesian University of Technology	
18:30 - 20:00	Poster session + welcome reception				

Thursday, 17.09					
9:00 - 9:50	Keynote 3	Ultrafast and accurate sequence alignment and clustering of viral genomes	Sebastian Deorowicz	Silesian University of Technology	Bartosz Wilczyński
9:50 - 11:20	Modelling & proteomics	Glycine molecule radical: Predicted properties and dipeptide formation	Jarosław Synak	Poznań University of Technology	Agnieszka Rybarczyk
		Enhanced Sampling of Free-Energy Surfaces in Biomolecular Systems: Conformational and Reactive Pathways	Juan Francisco Carrascoza Mayen	Poznań University of Technology	
		Relative quantification of proteins and of post-translational modifications with shared peptides: a weight-based approach	Mateusz Staniak	University of Wrocław	
		Interpretable protein function predictions with deepFRI2	Paweł Szczerbiak	Sano Centre for Computational Medicine	
11:10 - 11:30	Coffee break				
11:30 - 12:50	Transcriptomics & proteomics	RRBS-Based Epigenomic Profiling of Type 1 Diabetes: Preliminary Data Quality Assessment and Preprocessing	Joanna Tobiasz	Silesian University of Technology	Piotr Łukasiak
		Predicting Genomic Determinants of Chromatin Compaction Using Machine Learning	Teresa Szczepińska	Warsaw University of Technology	
		Reasoning Across Expression Profiles: A Modality Fusion Architecture for Omics Interpretation	Tomasz Jetka	Ingenix.ai	
		Evolutionary-scale interpretation of protein functions in the human gut microbiome	Jakub Wojciechowski	Sano Centre for Computational Medicine	
12:50 - 13:50	Lunch				
13:50 - 14:40	Keynote 4	CASP and the Long Winding Road to Successful Computation of Protein Structure	John Moult	University of Maryland	Krzysztof Fidelis
14:40 - 16:00	Applications of bioinformatics in biology and medicine	Gene-level rare variant scoring in muscular dystrophy: comparative evaluation of GORDIAN and GenRisk	Aleksandra Suwalska	Silesian University of Technology	Tomasz Kościółek
		iFlow - Clinical NGS and PGx Data Analysis Platform	Paweł Sztromwasser	Intelliseq	
		European AI Act and biomedical data: more paperwork or more governance?	Michał Burdukiewicz	Medical University of Białystok, Vilnius University	
		Discussion about ELIXIR	Izabela Makalowska	Adam Mickiewicz University	
16:00 - 16:20	Coffee break				
16:20 - 19:00	General Assembly PTBI				
20:00	Conference dinner				

Friday, 18.09					
9:00 - 9:50	Keynote Honorary	Boruta and Beyond: Machine Learning and Information Theory for Marker Discovery	Witold Rudnicki	University of Białystok	Jacek Błazewicz
9:50 - 11:10	Systems biology	Complexity Flow Graphs: measuring adaptive complexity in coevolving systems	Mateusz Twardawa	Poznan University of Technology, Poznan Supercomputing and Networking Center	Maciej Antczak
		A Systems Approach to the Study of Complex Biological Systems Based on the Analysis of Biofilm Formation Processes in Escherichia coli	Agnieszka Rybarczyk	Poznan University of Technology	
		Recognizing Ligands in CryoEM using Deep Learning	Dariusz Brzezinski	Poznan University of Technology	
		Deep Neurosymbolic Architectures for Interpretation of Biomedical Imaging	Krzysztof Krawiec	Poznan University of Technology	
11:10 - 11:30	Coffee break				
11:30 - 13:30	Laureates	Best PhD Dissertation: Computational methods for leading-edge mass spectrometry techniques	Piotr Radziński	University of Warsaw	Joanna Żyła
		Best MSc Dissertation: Large-scale analysis of 3D chromatin structure changes affecting enhancer-promoter spatial distances in different human tissues	Nikita Kozlov	Warsaw University of Technology	
		Best MSc Dissertation: Sequencing budget allocation for inferring gene regulatory networks from single-cell data	Aleksander Jankowski	University of Warsaw	
		Best BSc Dissertation: Design and Implementation of a Machine Learning-Based System for Cytology Slide Analysis	Aleksandra Walczykbo	Wroclaw University of Science and Technology	
		Best BSc Dissertation: Automated Detection of Ki67-Positive and -Negative Cells in Immunohistochemically Stained Tissue Samples	Marcin Kuźniar	Wroclaw University of Science and Technology, CancerCenter.ai	
		HYperbolic Promoter Programming Engine: An iGEM 2026 Warsaw Project on Promoter Optimisation and de novo Design in Trichoderma atroviride	Michał Stanowski, Jakub Gieźgała	University of Warsaw	
13:30 Closing					
13:30 - 14:20	Lunch				