Bioinformatics in Torun 2026

Thursday, June 18th
Venue: Institute of Physics, Nicolaus Copernicus University, Grudzadzka 5 Street, Torun

12:00 – 1:20 pm	Registration
12:00 – 1:20 pm	**Lunch** *(included in registration fee)*
1:25 – 1:30 pm	Conference opening / Welcome – Wiesław Nowak

Session I: Artificial Intelligence, AlphaFold Breakthroughs and Perspectives

1:30 – 2:15 pm	Wladek Minor, University of Virginia, Charlottesville, USA; **Opening lecture** *Powering Drug Discovery with Structural Insight*
2:15 – 2:45 pm	Aleksandra Świercz, Institute of Computing Science, Poznan University of Technology, Poland *Genomics for Poland (G4PL): building a national genomic infrastructure for precision medicine and European integration*
2:45 – 3:30 pm	Jan Kosinski, European Molecular Biology Laboratory (EMBL) Hamburg, Germany; Internet *Combining AI and experiment*
3:30 – 4:00 pm	Artur Meller, University of California, San Francisco, USA; Internet *Predicting Locations of Cryptic Pockets from Single Protein Structures Using the PocketMiner Graph Neural Network*
4:00 – 4:30 pm	**Coffee break**

Session II: Nucleic Acid Mysteries

4:30 – 5:00 pm	Marta Szachniuk, Institute of Computing Science, Poznan University of Technology, Poland *The SpaceTetrado odyssey: into the quadruplex galaxy*
5:00 – 5:30 pm	Nithin Chandran, Warsaw University, Poland *Advances and Bottlenecks in RNA 3D Structure Modeling*
5:30 – 5:50 pm	Marcin Magnus, Harvard University, USA & University of Warsaw, Poland *OpenRNAFold: an end-to-end approach for RNA 3D structure Prediction*
5:50 – 7:00 pm	**Poster session & Coffee break**

Session III: Nucleic Acid Mysteries Recognitions

7:00 – 7:15 pm	Michał K. Białobrzewski, Institute of Physics, Polish Academy of Sciences , Warsaw, Poland *RNA Recognition Motif, but Not for RNA: The GW182 SD RRM Controls Liquid-liquid Phase Separation and CNOT1 Recognition*
7:15 – 7:30 pm	Tomasz Chady, Department of Mathematical Statistics and Data Analysis, Faculty of Mathematics and Computer Science, Adam Mickiewicz University, Poznan, Poland *Machine learning guided eccDNA prediction based on gene locus data, as a PU learning problem*
7:30 – 7:45 pm	Kunal Shewani, The International Institute of Molecular Mechanisms and Machines Polish Academy of Sciences, Warsaw, Poland *R3BIND: Decoding protein-nucleic acid recognition through 3D structural template*
8:15 – 9:30 pm	**Conference Evening with Pierogi (beer and chat session) at “Pierogarnia Stary Torun” restaurant,** Most Pauliński 2/10 street, Torun (included in the registration fee)

Friday, June 19th
Venue: Institute of Physics, Nicolaus Copernicus University, Grudzadzka 5 Street, Torun

Session IV: Proteins’ Modeling

9:00 – 9:30 am	Krzysztof Kuczera, University of Kansas, Lawrence, USA *Computational Design and Optimization of Blood-Brain Barrier Modulating Peptides*
9:30 – 10:00 am	Edward O’Brien, Director of NSF NCEM, Penn State University, University Park, USA *A novel, widespread class of protein misfolding is associated with aging and disease*
10:00 – 10:15 am	Przemysław Miszta, Warsaw University, Poland *Comparative molecular-dynamics study of dibenzoylmethane and emodepside in BK potassium channels (6V38, 7PXH)*
10:15 – 10:30 am	Karolina Mikulska-Rumińska, Nicolaus Copernicus University, Poland *Computational Modeling of Proteins Involved in Regulating Cell Fate*
10:30 – 11:00 am	**Coffee break**

Session V: Genomics and AI	
11:00 – 11:15 am	Magda Mielczarek, Wroclaw University of Environmental and Life Sciences, Poland *Exploring the genomic landscape of Neolithic human populations*
11:15 – 11:30 am	Sylwia Bożek, Sano Centre for Computational Personalized Medicine, Krakow, Poland *Longitudinal analysis of sinonasal microbiome in chronic rhinosinusitis*
11:30 – 11:50 am	Chandra Pareek, Nicolaus Copernicus University in Toruń, Poland *From genes to lifestyle changes: multiomics analysis of pigs' liver transcriptome in context to modern lifestyle diseases*
11:50 – 12:15 am	Witold Rudnicki, University of Białystok, Poland *Applications of Machine Learning methods to datasets with small number of samples*
12:15 – 1:00 pm	Wlodzislaw Duch, Nicolaus Copernicus University in Torun, Poland; Keynote *Harnessing Artificial Intelligence*
1:05 – 1:15 pm	**Conference photo**
1:15 – 3:00 pm	**Lunch** *(included in registration fee)*
Session VI: Dynamical aspects of proteins	
3:00 – 3:30 pm	Marten Vos, *LOB, Ecole Polytechnique, Institut polytechnique de Paris, Palaiseau, France* *Dynamics and mechanism of photoreactions in flavo-enzymes*
3:30 – 4:00 pm	Sebastian Kmiecik, Faculty of Chemistry, University of Warsaw, Poland *CABS-flex 3.0: Web Server and Standalone Workflows for Protein Flexibility and Peptide Modeling*
4:00 – 4:20 pm	Aleksandra Gruca, Silesian Technical University, Gliwice, Poland *Unmasking the Data: Dedicated Methods for LCR Analysis and Annotation Transfer*
4:20 – 4:40 pm	Paweł Rubach, SGH Warsaw School of Economics, Centre for New Technologies, University of Warsaw *From Sequence to a Knot - using Large Language Models to Predict the Existence of a Knot in a Protein Directly from its Sequence*
4:40 -5:00 pm	**Coffee break**
Session VII: Advancements in Computational Structural Biology	
5:00 – 5:10 pm	Konrad Gorzelańczyk, Poznań University of Technology, Poland *PROTO-NOOS: Orchestrating Open-Access Bioinformatics for Seamless Drug Discovery*
5:10 – 5:20 pm	Urszula Orzeł, University of Coimbra, Portugal *Epitope-driven molecular docking and structural characterization of B10 camelid antibody against SARS-CoV-2 virus*
5:20 – 5:30 pm	Piotr Śmieja, University of Warsaw, Poland *An Automated Pipeline Combining Hidden Markov Models, Structural Alignment, and Keyword Mining for Systematic Identification and Classification of Cytochrome P450s in the Protein Data Bank*
5:30 – 5:45 pm	Jakub Jakowiecki, University of Warsaw, Warsaw, Poland *Molecular dynamics simulations reveal dimerization-dependent rearrangement of the tyrosine toggle switch in the histamine H4 receptor*
5:45 – 6:15 pm	Jarosław Meller, University of Cincinnati, USA**;** **Keynote;** Internet *Accelerating Drug Discovery and Repurposing by Combining Transcriptional Signature Connectivity with Docking and Large Language Models*
6:30 – 7:30 pm	**Free sightseeing tour in English**
7:30 – 9:30 pm	**Social Gathering: Beer & Chat (Venue TBC, self-funded)**
Saturday, June 20th Venue: Institute of Physics, Nicolaus Copernicus University, Grudzadzka 5 Street, Torun	
8:30 – 1:00 pm	**Coffee break**
8:30 – 10:30 am	**Workshop 1:** ***Mastering RAG: customizing Large Language Models for bioinformatics.*** ***Mgr Piotr Ablewski, Nicolaus Copernicus University in Torun***
	Workshop 2: ***Biomolecular systems visualization with Blender (Part I - for beginners).*** ***Dr Jakub Jaszewski, Faculty of Fine Arts, Nicolaus Copernicus University in Torun,***
10:45 – 12:45 pm	**Workshop 3:** ***From raw sequencing data to biological insight: genome-wide detection, functional annotation and prioritization of genetic variants from DNA-seq (NGS) data.*** ***Dr Magda Mielczarek, UP Wrocław***
	Workshop 4: ***Biomolecular systems visualization with Blender (Part II - for advanced users).*** ***Dr Jakub Jaszewski, Faculty of Fine Arts, Nicolaus Copernicus University in Torun***