

The 19th Conference of the Hellenic Society for Computational
Biology and Bioinformatics

**17-19 October 2025, Hellenic Pasteur Institute,
Athens**

Program



Conference Program

Friday 17/10/2025

13:00 - 14:30	Registration & Poster set up (Welcome Coffee)
14:30 - 14.45	Welcome Addresses
15:00 - 16:00	Invited Talk 1 Giorgos Patrinos, Hellenic Pasteur Institute <i>"Translational tools for precision therapeutics"</i>
16:00 - 17:00	Coffee Break (Poster Session, Odd-numbered Posters)
17.00 - 18.20	Session 1 – Sequence Analysis
17:00 - 17:20	<u>Grigorios A. Moschos</u> , Konstantinos D. Tsirigos, Ioannis A. Tamposis and Pantelis G. Bagos. (Department of Computer Science and Biomedical Informatics, University of Thessaly) <i>PRED-TMSdeep: Prediction of transmembrane topology and signal peptides using deep learning.</i>
17:20 - 17:40	<u>Ioullos Konstantelos</u> , Christoforos Nikolaou and Dimitrios Stravopodis. (Biology Department, NKUA) <i>SeqRate: A Novel Approach for RNA Polymerase II Elongation Rate Estimation, Using Total RNA Sequencing datasets from Human Tissues.</i>
17:40 - 18:00	<u>Vlastimil Martinek</u> , Andrea Gariboldi, Dimosthenis Tzimotoudis, Aitor Alberdi Escudero, Edward Blake, David Cechak, Luke Cassar, Alessandro Balestrucci and Panagiotis Alexiou. (Department of Applied Biomedical Science, University of Malta). <i>Agentomics-ML: an agentic system for automated -omics machine learning model development.</i>
18:00 - 18:20	<u>Nikos Pyrgelis</u> and Nikolaos Vakirlis. (Hellenic Pasteur Institute). <i>In silico antimicrobial peptide discovery in the Animal Kingdom.</i>
18:20 - 19:00	Coffee Break (Poster Session, Odd-numbered Posters)
19:00 - 20.00	Invited Talk 2 Martin Reczko, BSRC "Alexander Fleming", Athens, Greece <i>"Transformer-Powered AI in Biomedicine: From LLMs for Question Answering to the Validation and Prediction of RNA Structures"</i>
20:00 - 22.00	Light Dinner, Pasteur Institute (Poster View, Odd-numbered Posters)

Saturday 18/10/2025

10:00 - 11:00 **Invited Talk 3**

Ivo Grosse, Institut für Informatik Martin-Luther-Universität, Halle-Wittenberg, Germany

"Hourglass Patterns in Animal and Plant Embryogenesis"

11:00 - 11:30 **Coffee Break (Poster Session, Odd-numbered Posters)**

11:30 - 13:00 **Session 2 - High-throughput biomolecular analysis**

11:30 - 11:50 Sotirios Karvelas, Spiros Kostopoulos, Ioannis S. Vlachos and Emmanouil Athanasiadis. (Department of Biomedical Engineering, University of West Attica). *Metadata-Assisted Graph Neural Networks for Spatial Transcriptomics Inference from Histopathological Images.*

11:50 - 12:10 Antonios Somarakis, Aleksandra Aljakna Khan, Yue Zhao, Amalia Sintou, Harshpreet Chandok, Brian S. White, Matthew J Mahoney, Paul Robson, Ron Korstanje and Nadia A Rosenthal. (The Jackson Laboratory for Genomic Medicine, USA). *Spatial Transcriptomics data reveal colocalization patterns among age-specific cell types in the heart.*

12:10 - 12:30 Charis Sinnis, Panagiotis Xiropotamos, Haris Manousakis, Theodore Dalamaga and Georgios K. Georgakilas. ("ATHENA" Research and Innovation Center in Information, Communication and Knowledge Technologies). *A Multi-Dimensional Strategy for Enhanced Selection of Highly Variable Genes in Single-Cell RNA-Seq Data.*

12:30 - 12:50 Christos Tzaferis, Lida Iliopoulou, Alejandro Prados, Fani Roumelioti, Vasiliki Koliaraki and George Kollias. (Biomedical Sciences Research Center "Alexander Fleming"). *Different fibroblast subtypes propel spatially defined ileal inflammation through TNFR1 signalling in murine ileitis.*

13:00 - 14:30 **Light Lunch (Poster Session, Even-numbered Posters)**

14:30 - 16:00 **Session 3 – Genome Analysis**

14:30 - 14:50 Christos Botos, Aikaterini Ntouka, Michail Loulakis and Matthieu D. Lavigne. (Institute of Molecular Biology and Biotechnology, Foundation of Research and Technology) *Computational Modeling of Transcription Dynamics Using Markov Chains and Simulation-Based Optimization.*

14:50 – 15:10 Fotis A. Baltoumas, Mateus B. Fiamenghi, Antonio Pedro Camargo, Iro N. Chasapi, Simon Roux, Artyom A. Egorov, Eleni Aplakidou, Eric Olo Ndela, Yumary M. Vasquez, I-Min A. Chen, Krishnaveni Palaniappan, T.B.K. Reddy, Supratim Mukherjee, Natalia N. Ivanova, Frederik Schulz, Tanja Woyke, Emiley A. Eloë-Fadrosh, Georgios A. Pavlopoulos and Nikos C. Kyrpides. (Biomedical Sciences Research Center "Alexander Fleming") *The Meta-Virus Resource (MetaVR): Expanding the frontiers of viral diversity with millions of*

Uncultivated Viral Genomes.

- 15:10 - 15:30** Sofia Papanikolaou, Despoina Kosmara, Dimitris Konstantopoulos, George Bertias and Christoforos Nikolaou. (Biomedical Sciences Research Center “Alexander Fleming”). *The cohesin complex member SMC1A regulates sex-biased inflammatory responses in SLE monocytes.*
- 15:30 - 15:50** Athanasia Stavropoulou, Christina Paraskeva, Anastasios Liakos, Maria Sakkou, Saara Ollila, Maria Fousteri, Christoforos Nikolaou and Vasiliki Koliarakis. (Biomedical Sciences Research Center “Alexander Fleming”). *Distinct enhancer-driven transcriptional networks shape intestinal fibroblast identities and regeneration-associated activation*
- 16:00 - 17:00** **Coffee Break (Poster Session, Even-numbered Posters)**
- 17.00 - 18.00** **Invited Talk 4**
Angelo Facchiano, Istituto di Scienze dell'Alimentazione - ISA, Avellino, Italy
"Structure-Based Bioinformatics Studies on the Health-Promoting Properties of Foods".
- 18.00 - 20.00** **HSCBB General Assembly and Elections (Open to all HSCBB members)**

Sunday 19/10/2025	
10.00 - 11.00	Invited Talk 5 Uwe Ohler, Max Delbrück Center, Berlin, Germany <i>"Dissecting regulatory networks from single cell multi omics data"</i>
11:00 - 11:30	Coffee Break (Poster Session, Even-numbered Posters)
11:30 - 13:00	Session 4 – Personalized Medicine, Systems Biology and Biodiversity
11:30 - 11:50	<u>Anargyros Skoulakis</u> , Konstantinos Daniilidis, Stefanos Digenis, Christos-Georgios Gkoutinoudis, Efthymia Petinaki and Artemis G. Hatzigeorgiou. (Hellenic Pasteur Institute). <i>Genomic Machine Learning Models for Rapid Antimicrobial Resistance Prediction in ESKAPEE Pathogens</i>
11:50 - 12:10	<u>Panagiotis Anagnostou</u> , Sotiris K. Tasoulis, Aristidis G. Vrahatis, Spiros V. Georgakopoulos and Vassilis P. Plagianakos. (Department of Computer Science and Biomedical Informatics, University of Thessaly). <i>Boosting Neural Network Performance for High Dimensional Data through Random Projections.</i>
12:10 - 12:30	<u>Vasileios Zogopoulos</u> , Ioanna Tsotra, Apostolos Malatras, Vassiliki A Iconomidou and Ioannis Michalopoulos. (Biomedical Research Foundation, Academy of Athens). <i>HGCA4.1: Updated global and tissue-specific human gene co-expression analysis based on Tabula Sapiens v2 scRNA-Seq data.</i>
12:30 - 12:50	<u>Maria Pagoni</u> , Claudia Cava, George T. Tsangaris, Fotios Siannis and Nikolaos Drakoulis. (Department of Pharmacy, NKUA) <i>Prostate cancer susceptibility in European Caucasians: A systematic review and meta-analysis.</i>
12:30 - 12:50	<u>Konstantinos Papadimitriou</u> . (Department of Food Science and Human Nutrition, Agricultural University of Athens). <i>Multi-omics Applications for the Study of Food-related Microbiomes and Microorganisms.</i>
13:00 - 14:00	Lunch Break (Poster Session, Even-numbered Posters)
14.00 - 15.00	Invited Talk 6 Elpida Fotiadou, HDIKA <i>"Advancing Healthcare: ePrescription, National Electronic Health Record, and Data-Driven Health Policy & Innovation"</i>
15:00 - 15:30	Closing Remarks, Prize Announcements and Ending of the Conference

Posters

No	Authors	Title
P1	Maria A. Gavrilou, Zoi I. Litou, Vassiliki A. Iconomidou	Unraveling the Protein Interaction Landscape in β 2-Microglobulin-Associated Amyloidosis
P2	Ioannis Charatsiaris, Panagiota I. Kontou, Pantelis G. Bagos	<i>A Bipartite Network Approach to Multifactorial Diseases: Backbone Extraction and Projection Methods for Gene-Disease Associations</i>
P3	Grigorios Karaj, Avgi E. Apostolakou, Zoi I. Litou, Vassiliki A. Iconomidou	<i>Multiple Network Alignment Across Species Identifies Conserved Mechanisms in Alzheimer's disease</i>
P4	Dimitra Panou, Alexandros C. Dimopoulos, Manolis Koubarakis, Martin Reczko	<i>LLM Farms: A Multi-Model Approach to Harness Collective Intelligence of Large Language Models for Robust Biomedical QA</i>
P5	Maria Koulouri, Sotirios Bersimis, Athanasios Sachlas	<i>Statistical Learning Approaches for Enhancing Alzheimer's Disease Diagnosis and Monitoring Using Multimodal Data: A Review</i>
P6	Elissavet Zacharopoulou, Galatea Mavromati, Maria Zioga, Anargyros Skoulakis, Filippos S Kardaras, Armen Ovsepian, Artemis G Hatzigeorgiou	<i>Integrative Sentiment Analysis of miRNA:Gene. Verified Interactions in Biomedical Literature: Leveraging BioBERT for Comprehensive Insights</i>
P7	Chrysoula P Bourtzinakou, Marios G Krokidis, Themis P Exarchos, Panagiotis Vlamos, Aristidis G Vrahatis	<i>ResearchSwarm: A Multi-Agent AI Framework for miRNA-lncRNA-cancer literature mining built on an NLP Foundation</i>
P8	Konstantinos Athanasopoulos, Nikolaos C. Athanasiadis, Stavros Chrysanthopoulos, Dennis V. Cokkinos, Ioannis Michalopoulos	<i>Estimation of the depolarization rate of the R peak in electrocardiograms</i>
P9	Konstantinos Kapelios, Panagiotis Xiropotamos, Charis Sinnis, Haris Manousaki, Theodore Dalamagas, Georgios K. Georgakilas	<i>bMinty: A Framework for Transparent and Reproducible NGS data analysis</i>
P10	Georgios A. Manios, Dionysios Kandylas, Athanasios Kylonis, Konstantina E. Vennou, Panagiota I. Kontou, Pantelis G. Bagos	<i>fastMETA: a fast and efficient tool for multivariate meta-analysis of GWAS</i>
P11	Georgios A. Manios, Panagiota I. Kontou, Pantelis G. Bagos	<i>LDSeeker: a comprehensive web tool to explore linkage disequilibrium in GWAS</i>
P12	Georgios G. Tsompanoglou, Georgios A. Manios, Dionysios Kandylas, Panagiota I. Kontou, Pantelis G. Bagos	<i>PRED-GBT: a fast and efficient tool for gene-based testing of GWAS summary statistics</i>
P13	Angeliki Atart, Evangelia E. Stasi, Georgia G. Braliou, Panagiota I. Kontou, Pantelis G. Bagos	<i>Gene-Gene Interactions: systematic review of the literature and network analysis</i>
P14	Marianthi Marouli, Sofia Papanikolaou, Christos Mantis, Despoina Tsapara, Despoina Kosmara, George Bertsias, Christoforos Nikolaou	<i>The genome architectural protein SMC1A as a nuclear sensor and mediator of the gene expression response in inflammation.</i>
P15	Despoina Voulgari, Stavros Giannoukakos, Marios Miliotis, Artemis G. Hatzigeorgiou	<i>Investigating the Genomic Context of microRNAs Lacking CLS</i>

		<i>Annotations in miRBase and MirGeneDB</i>
P16	Vasiliki Kotsira, Stefanos Digenis, Artemis G. Hatzigeorgiou	<i>sTarML: A Sequence-Based Machine Learning Framework for Predicting Bacterial sRNA–mRNA Interactions</i>
P17	Stelios Gkionis, Nikoleta Vavouraki, Irini Fundulaki, Constantine A. Stratakis, Pantelis Hatzis, Panagiotis Moulos	<i>VESTA: A Clinical Genomics Annotation Platform Tailored for the Greek Population</i>
P18	Eirini M. Tzermpou, Emilios Tassios, Nikolaos Vakirlis	<i>Examining selective pressure and motif occurrence in de novo genes of the Saccharomycotina subphylum</i>
P19	Ioannis Maris, Antonios Klonizakis, Christoforos Nikolaou	<i>Dissecting the enhancer grammar of cell trans-differentiation using multi-omics integration and Deep Learning</i>
P20	Christos Mantis, Marianthi Marouli, Sofia Papanikolaou, Christoforos Nikolaou	<i>Splicing pattern analysis of genes involved in the early development of Systemic Lupus Erythematosus</i>
P21	Epameinondas Tzagkarakis, Christoforos Nikolaou, Ioannis Iliopoulos	<i>The 3D genomic architecture of eukaryotic genomes in relation to the functional and regulatory properties of their genes</i>
P22	Pavlos Tsiartas, Maria Bousali, Magdalini Bletsas, Aristotelis C. Papageorgiou, Timokratis Karamitros	<i>Computational Reconstruction of Ancient Hepatitis B Virus Genomes from Publicly Available Human WGS Datasets</i>
P23	Natalia Tsouggou, Aleksandra Slavko, John Kapolos, Marina Papadelli, Konstantinos Papadimitriou	<i>Shotgun metagenomics and volatilomics analysis reveal producer-specific microbial and functional patterns in PDO Sfela cheese</i>
P24	Violeta Pemaj, Aleksandra Slavko, Anna Eleni Alifragki, Despoina Hatzigeorgiou, Konstantinos Valourdos, Eleftherios Drosinos, Konstantinos Papadimitriou	<i>Transcriptomic Insights into the Survival of Listeria monocytogenes in UHT Milk</i>
P25	Thodoris Daskalopoulos, Marios Miliotis, Izabella Gogaeva, Artemis G. Hatzigeorgiou	<i>Identification and Functional Characterization of Variants in microRNA Binding Regions of BRCA Patients</i>
P26	Zoi I. Litou, Geert van Geest, Sara Morsy, Fotis Psomopoulos, ELIXIR Training Platform Coordination team ,	<i>FAIR Training material: Achievements and the Road Ahead in ELIXIR</i>
P27	Maria N Chasapi, Iro N Chasapi, Eleni Aplakidou, Fotis A. Baltoumas, Evangelos Karatzas, Ioannis Iliopoulos, Dimitrios J. Stravopodis, Ioannis Z. Emiris, Aydin Buluç, Ilias Georgakopoulos-Soares, Nikos C. Kyrpides, Georgios A. Pavlopoulos	<i>metagRoot: a comprehensive database of protein families associated with plant root microbiomes</i>
P28	Zoi I. Litou, Vassiliki A. Iconomidou, ELIXIR Training Platform Coordination team	<i>ELIXIR-GR as a member of the ELIXIR Training Platform</i>
P29	Keisi Zanj, Vasileios L. Zogopoulos, Konstantinos Kyriakidis, Vasiliki A. Iconomidou, Ioannis Michalopoulos	<i>Gene expression meta-analysis of Parkinson's disease using RNA-Seq data</i>
P30	Lydia P. Kalomiris, Argyro Kalogeropoulou, Maria Papaefthimiou, Panagiota I. Kontou, Pantelis G. Bagos, Adamantini Kyriacou, Georgia G. Braliou	<i>Inulin supplementation leads to gut microbiome alterations in murine colitis: insights from a meta-analysis of 16S sequencing data</i>
P31	Dimitris Angelakis, Dimitrios-Christos Tremoulis, Timokratis Karamitros	<i>Integrative single-cell transcriptomic and epigenomic analysis of tumor</i>

		<i>adjacent lung tissue reveals smoking associated pathways in adenocarcinoma patients</i>
P32	Maria Papacheimona, Aggeliki Tsoka, Paraskevi Karousi, Julie Corraud, Guillaume Médard, Dionysios E. Raitsos, Jerome Zoidakis	<i>Impact of heat stress on the proteome of the sponge <i>Aplysina aerophoba</i></i>
P33	Marina Kornilaki, Aristeidis Leontaris, Argyro Kalogeropoulou, Panagiota I. Kontou, Pantelis G. Bagos, Adamantini Kyriacou, Georgia G. Braliou	<i>Effects of inulin in gut dysbiosis of diet-induced obesity in mouse models: a meta-analysis of metagenomics data</i>
P34	Despoina Kavalierou, Maria Adam, Panagiota Kontou, Spiros Georgakopoulos	<i>Extending Lanczos Methods for the spectral analysis of high-dimensional molecular data</i>
P35	Konstantinos Lazaros, Marios G. Krokidis, Themis P. Exarchos, Panagiotis Vlamos, Aristidis G. Vrahatis	<i>Leveraging Machine Learning for High-Dimensional Transcriptomic and Epigenetic Data in Oncology Studies</i>
P36	Margaritis Tsifintaris, Konstantinos Tegopoulos, Sonia-Vasiliki Polychronidou, Aristotelis C. Papageorgiou	<i>Biodiv-Gen: A Platform for Biodiversity Genomics Research</i>
P37	Dinesh Kumar, and Nikolaos Vakirlis	<i>Elucidating the sources of novelty in the antibiotic resistome</i>
P38	Vasiliki Dimitriadou, Vasileios L. Zogopoulos, Konstantinos Kyriakidis, Efthymia Antonopoulou, Ioannis Michalopoulos	<i>Meta-analysis of differential gene expression for Alzheimer's Disease</i>
P39	Konstantinos Apostolou-Karampelis, Maria Aslani, Aikaterini Nanou, Konstantinos Ntatsoulis, George Kollias,	<i>Restoring Native Tissue Architecture in Swiss-Roll Intestinal Samples for Spatial Transcriptomics</i>
P40	Michail Polemis, Elli Theofili, Kleon Karadimas, Aggeliki Tzoukmani, Euaggelia Maikousi, Olga Pappa, Georgia Mandilara	<i>Harnessing Bioinformatics for Public Health: Surveillance and Outbreak Investigation of Food- and Water-Borne Infections</i>
P41	Evangelia Kourtzelli, Georgios A. Manios, Panagiota I. Kontou, Pantelis G. Bagos	<i>A computational methodology to uncover unannotated transmembrane β-barrel proteins</i>
P42	Melina I. Trochalaki, Konstantina D. Vraila, Nikos C. Papandreou, Vassiliki A. Iconomidou	<i>Dual inhibitors of amyloid-β and tau aggregation in Alzheimer's disease: an in silico study</i>
P43	Evagelia Elmatzoglou, Nikolaos Nikolopoulos, Kalliopi-Dionysia Rizou, Eleni Sidiripoulou, Ioulia Sokolaki, Jerome Zoidakis, Maria Kapasa	<i>Bio-degradation of plastics in the Mediterranean region: Prediction of microbial population degradation capacity with the help of simple computational algorithms and databases.</i>
P45	Christoforos Zarkadas, Metaxia Vlassi	<i>Exploring in silico allosteric responses caused by cancer-associated amino acid changes in SR Protein Kinase 1</i>
P46	Foteini Papageorgiou, Georgios K. Georgakilas	<i>Interpretable Graph Neural Networks for Cell-Type-Specific Gene Regulatory Networks from Single-Cell Multi-Omics</i>
P47	Konstantinos Tsomakian, Electra Tsaglioti, Marianna Stagaki, Matthew Lavigne	<i>Towards Mathematical Models to predict RNA polymerase II dynamics genome-wide from chromatin and histone modifications maps</i>

P48	Konstantina Thaleia Katinioti, Emmanouil Athanasiadis, Alexandros Georgakilas	<i>Molecular insights into radiation-induced human skin injury at single cell resolution</i>
P49	Konstantinos Politof, Konstantia Moirogiorgou, Ekaterini Bei, Marios Antonakakis, Konstantinos Moulakakis, John Kakisis, Anastasios Raptis, Christos Manopoulos, Michail Zervakis	<i>Automatic Measurements of Abdominal Aortic Aneurysms</i>
P50	Emilios Tassios, Eirini M. Tzermpou, David Rinker, Chris T. Hittinger, Christoforos Nikolaou, Antonis Rokas, Nikolaos Vakirlis	<i>Origins and evolution of protein novelty across the entire budding yeast subphylum</i>
P51	Panagiotis Xiropotamos, Charis Sinnis, Haris Manousakis, Yiannis Vasilopoulos, Theodore Dalamagas, Georgios K. Georgakilas	<i>CINNAMON: An Interpretable Convolutional Neural Network Framework Revealing Regulatory Motif Insights and Transcription Factor Dynamics</i>