The 21st International Symposium on Bioinformatics Research and Application

CONFERENCE BROCHURE

AUGUST 3-5, 2025
HELSINKI, FINLAND

ISBRA 2025

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CONTENTS

About The Conference

The International Symposium on Bioinformatics Research and Applications (ISBRA) provides a forum for the exchange of ideas and results among researchers, developers, and practitioners working on all aspects of bioinformatics and computational biology and their applications. Submissions presenting original research are solicited in all areas of bioinformatics and computational biology, including the development of experimental or commercial systems. The previous ISBRA proceedings on SpringerLink is available at https://link.springer.com/conference/isbra.

Topics of interest include but are not limited to：

1) AI and machine learning methods in bioinformatics and medical informatics

2) Big data analytics in biology and medicine

3) Bioinformatics education and public engagement

4) Biomedical databases and data integration

5) Biomedical text mining and ontologies

6) Biomolecular imaging

7) Comparative genomics

8) Computational genetic epidemiology

9) Computational proteomics

10) Data mining and visualization

11) High-performance bio-computing

12) Metagenomics

13) Molecular evolution

14) Molecular modelling and simulation

15) Next-generation sequencing data analysis

16) Pattern discovery and classification

17) Population genetics

18) Software tools and applications

19) Structural biology and drug discovery

20) Systems biology

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Attendees Guide

➢ Venue

Metsätalo building, University of Helsinki City Centre Campus

Address: Unioninkatu 40, 00170 Helsinki, Finland

Meeting Room	LIVE STREAM URL	WEBINAR URL*
SALI 1 (B116)	https://video.helsinki.fi/unitube/live-stream.html?room=l15	https://helsinki.zoom.us/webinar/register/WN_HDHLokBdTDOSXeXG-QCARQ
SALI 2 (B212)	https://video.helsinki.fi/unitube/live-stream.html?room=l33	https://helsinki.zoom.us/webinar/register/WN_tAMwQtdkQq-LNH3Z4EN6fA
SALI 4 (B214)	https://video.helsinki.fi/unitube/live-stream.html?room=l32	https://helsinki.zoom.us/webinar/register/WN_u3XVn7R0T56oSGtndL5NaA
SALI 6 (B317)	https://video.helsinki.fi/unitube/live-stream.html?room=l31	https://helsinki.zoom.us/webinar/register/WN_I0EPWnkET1yiHxizprfzWw

* For on-line presenters

➢ Sign in

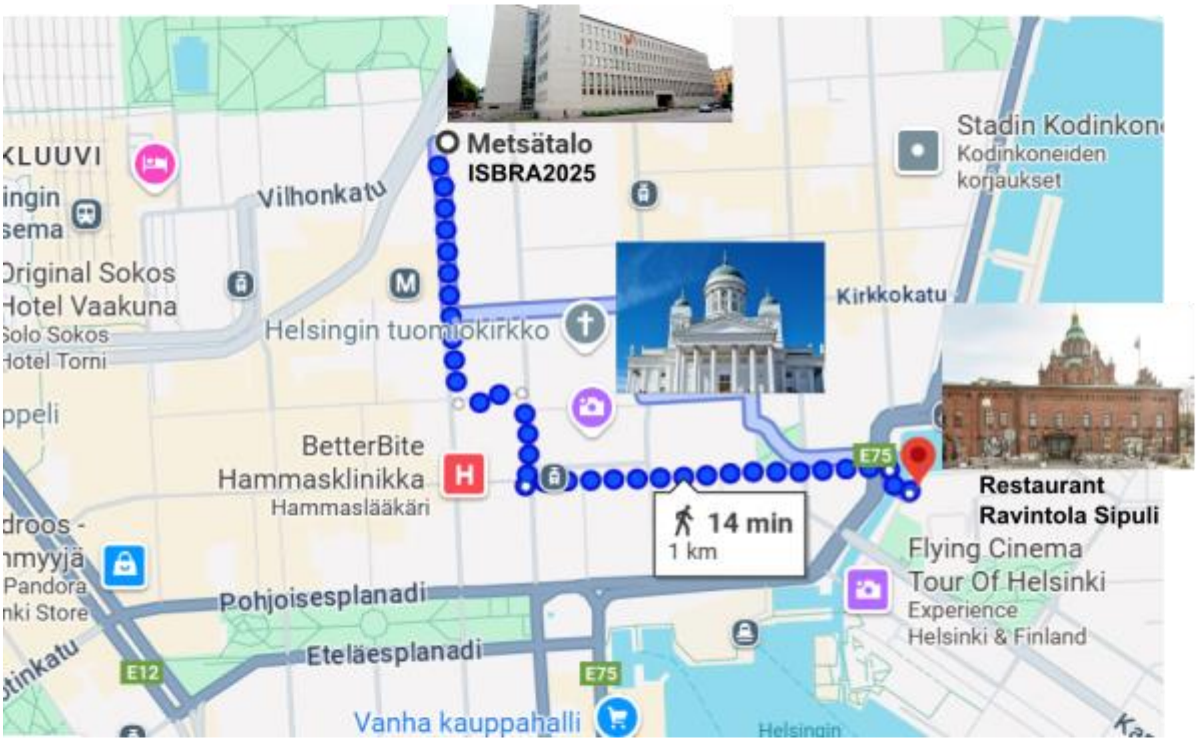
Time: August 4th 08:00 – 18:00

Location: The lobby on the first floor of Metsätalo building

➢ Dining arrangements

Date	Lunch		Dinner	
	Time	Dining Hall	Time	Dining Hall
August 4th	12:40-13:40	UniCafe Metsätalo	19:00-22:00	Ravintola Sipuli Address: Kanavaranta 7, 00170 Helsinki
August 5th	12:40-13:40	UniCafe Metsätalo		

How to get to the dinner (Ravintola Sipuli, Kanavaranta 7, 00170 Helsinki)



➢ Contact us

Conference Secretariat: isbra2025@helsinki.fi or isbra2025@confedent.fi

Schedule-at-a Glance

August 3, Sunday		
14:00-19:00	Pre-conference activities	
August 4, Monday		
08:00-09:00	Registration & Coffee	The lobby
09:00-09:10	Opening Remarks	SALI 1 (B116)
09:10-09:50	Keynote I	SALI 1 (B116)
09:50-10:30	Keynote II	SALI 1 (B116)
10:30-11:00	Coffer Break/Poster session	
11:00-12:40	Conference session I	SALI 1 (B116)
12:40-13:40	Lunch/Poster session	UniCafe
13:40-15:40	**Parallel Sessions I**	
	Session 1	SALI 1 (B116)
	Session 2*	SALI 2 (B212)
	Session 3*	SALI 4 (B214)
	Session 4*	SALI 6 (B317)
15:40-16:10	Coffer Break/Poster session	
16:10-17:50	**Parallel Sessions II**	
	Session 5	SALI 1 (B116)
	Session 6*	SALI 2 (B212)
	Session 7*	SALI 4 (B214)
	Session 8*	SALI 6 (B317)
17:50-18:30	Poster session	

19:00-22:00	Banquet	Ravintola Sipuli

August 5, Tuesday		
08:00-09:00	Registration & Coffee	The lobby
09:00-09:50	Keynote III	SALI 1 (B116)
09:50-10:30	Keynote IV	SALI 1 (B116)
10:30-11:00	Coffer Break/Poster session	
11:00-12:40	Conference session II	SALI 1 (B116)
12:40-13:40	Lunch/Poster session	UniCafe
13:40-15:40	**Parallel Sessions III**	
	Session 9	SALI 1 (B116)
	Session 10*	SALI 2 (B212)
	Session 11*	SALI 4 (B214)
	Session 12*	SALI 6 (B317)
15:40-16:10	Coffer Break/Poster session	
16:10-17:50	**Parallel Sessions IV**	
	Session 13	SALI 1 (B116)
	Session 14*	SALI 2 (B212)
	Session 15*	SALI 4 (B214)
18:00-18:10	**Closing Remarks Venue: SALI 1 (B116)**	

*: Presenters participate remotely

Agenda Monday

Time: 09:00-12:40, August 4, Monday

Place: SALI 1 (B116)

Time	Content
09:00-09:10	**Opening Remarks (Sampsa Hautaniemi)** **Meeting venue: SALI 1 (B116)**
09:10-09:50	***Keynote 1: Digital Twins for Precision Oncology*** **Presenter:** Walter Kolch
09:50-10:30	***Keynote 2: Integrative Deep Learning for Heterogeneous Biomedical Datasets*** **Presenter:** Ritambhara Singh
10:30-11:00	Coffer Break/Poster session
11:00-12:40	**Conference session I** **Meeting venue: SALI 1 (B116)** **Session chair: Jing Tang**
11:00-11:20	52: Anqi Liang, Xiujuan Lei, Ming Chen and Yi Pan ***Multi-Task Learning with Cross-Stitch for Synergistic Effect of Drug Combination Prediction***
11:20-11:40	122: Denis Skibinski, Thomas Spicher, Leonhard Sidl, Paulína Holotová, Yingjie Pan, Maximilian Faissner, Cristian A. Velandia-Huerto, Ronny Lorenz, Maria Waldl, Hua-Ting Yao and Peter F. Stadler ***Integrating High-Throughput RNA-RNA Interaction Data into RNA Secondary Structure Prediction***
11:40-12:00	131: Nicola Rizzo, Manuel Cáceres and Veli Mäkinen ***Practical colinear chaining on sequences revisited***
12:00-12:20	197: Chengbo Fu and Lu Cheng ***k-mer manifold approximation and projection for visualizing DNA sequences***
12:20-12:40	21: Ezekiel A. Adeniyi, Alexander Zelikovskiy, Murray Patterson and Akshay Juyal ***Uncovering Epistatic Interactions in SARS-CoV-2 Evolution Through Hidden Markov Models***

12:40-13:40	Lunch/Poster session	Unicafe/Lobby

Time: 13:40-15:40, August 4, Monday

Parallel Sessions I

Session 1	**Meeting venue: SALI 1 (B116)** **Session chair: Veli Mäkinen**
13:40-14:00	41: Nan Liu, Hao Jin, Xiaotian Jia and Binhai Zhu ***TF-GCNNovo: A Peptide Sequence Prediction Model Integrating Transformer and Graph Convolutional Network***
14:00-14:20	112: Xinyue Xu, Wei Peng, Wei Dai, Xiaodong Fu, Li Liu and Lijun Liu ***A Survival Prediction Model Integrating Hierarchical Pathological Image and Pathway Features***
14:20-14:40	118: Yana Hrytsenko and Tamar Sofer ***A machine learning model for predicting hypertension using gene-specific polygenic risk scores and lifestyle factors***
14:40-15:00	129: Clarence Todd, Yuan Tian, Nathaniel Osgood, Ian McQuillan and Lingling Jin ***Simulating viral evolution and immune escape reinfection dynamics using agent-based modelling***
15:00-15:20	149: Maocheng Cao, Zhelang Deng, Qiucheng Miao, Jintao Meng and Yanjie Wei ***An Efficient Parallel List Ranking Algorithm for Graph Concatenation on BSP Graph System***
15:20-15:40	159: Jian Wang, Yiding Zhang, Zhengyang Song and Ting Cheng ***BiGDC-BrainAgeNet: Enhancing EEG-Based Brain Age Prediction with Bidirectional Graph Diffusion Convolutions***
Session 2	**Meeting venue: SALI 2 (B212)** **Remote presentations only** **Session chairs: Yajun Liu/Li Shen**
13:40-14:00	11: Xingquan Xia, Guihu Zhao and Xinpan Yuan ***HCSeer: A Classification Tool for Human Genetic Variant Hot and Cold Spots Designed for PM1 and Benign Criteria in the ACMG Guideline***
14:00-14:20	14: Jianpeng Zhang, Fei Teng, Guo Chen, Changna Qian, Wenbin Chen and Xiaoshu Zhu

	ViDSG: A Hybrid Algorithm Integrating Statistical and Semantic Features via Dual-Channels for Identifying Prokaryotic and Eukaryotic Viruses
14:20-14:40	17: Shiliang Zhang, Huimin Zhu, Renyi Zhou and Min Li ***MoGE: A Benchmark for Comprehensive Evaluation of Molecular Generation Models in De Novo Drug Design***
14:40-15:00	20: Xinhang Wang, Guangming Pan, Zhen Luo, Ming Xiao, Li Yang, Mianyang Li and Le Zhang ***A Data Privacy Protection Method for Infectious Disease Prediction Models with Balanced Training Speed and Accuracy***
15:00-15:20	24: Chenhui Qin, Jingjing Zhang and Jinyan Li ***Application of streaming DNA sequencing data reading and overlap graph construction in data retrieval for DNA storage***
15:20-15:40	26: Qiu Xiao, Tuo Xiong, Xinru Zhang, Dingxi Zuo, Yide Yang and Jiancheng Zhong ***Drug repositioning with multi-source data embedding and convolutional neural network***
Session 3	**Meeting venue: SALI 4 (B214)** **Remote presentations only** **Session chairs: Yunpeng Cai/Qinhan Hou**
13:40-14:00	39: Yan Sun, Xiaohan Zhang, Junliang Shang, Qianqian Ren, Feng Li and Jin-Xing Liu ***SUIFS: A Symmetric Uncertainty based Interactive Feature Selection Method***
14:00-14:20	42: Doga Yilmaz and Emre Sefer ***Hyperbolic Deep Graph Learning for Aligning Biological Graphs at Multiple Perspectives***
14:20-14:40	44: Xuan Wang, Wenhao Tian, Zhengao Mo, Chunyi Li, Xiaohua Wan and Fa Zhang ***FSPicker: A Dual-Stream Attention Network for Multi-Scale Particle Picking in Cryo-Electron Tomography***
14:40-15:00	47: Yijin Wang, Hailin Yue, Hulin Kuang and Jianxin Wang ***SDMFF: Spatial-temporal Dual-pathway Network with Multi-scale Feature Fusion for Parkinson's Disease Diagnosis***
15:00-15:20	55: Yan Sun, Xiaoqi Tang, Linqian Zhao, Yaxuan Zhang, Junliang Shang, Feng Li and Jin-Xing Liu ***A Neighborhood Selection Learning Artificial Bee Colony Algorithm Based on Population Backtracking for Detecting Epistatic Interactions***

15:20-15:40	57: Xiaoqi Tang, Xianghan Meng, Junliang Shang, Baojuan Qin, Xin He, Yan Zhao, Daohui Ge, Feng Li and Jinxing Liu ***PDA-GTGCN: identification of piRNA-disease associations based on group feature transformation graph convolutional network***	
Session 4	**Meeting venue: SALI 6 (B317)** **Remote presentations only** **Session chair: Haochen Zhao**	
13:40-14:00	58: Jinxu Luo, Maozu Guo, Ran Duan and Jian Chen ***GFPrompt: A Gene Function-Phenotype Association Analysis Framework based on Graph Prompt Learning and Semantic Augmentation***	
14:00-14:20	61: Qiushi Liang, Shengjie Zhao, Ruo Han Wang, Yu Wei Zhang, Lingxi Chen and Shuai Cheng Li ***InfoTAD: Applying Infomap Graph Partitioning to Hi-C Contact Map***	
14:20-14:40	62: Qiao Ling, Qichang Zhao, Muhammad Habibulla Alamin, Yuqi Hong and Jianxin Wang ***Drug-Disease Associations Prediction Based on Knowledge Graph and Multimodal Fusion***	
14:40-15:00	63: Chaojin Wu, Fuhao Zhang, Pengzhen Jia, Min Zeng and Min Li ***DDLB: Using the protein language model and hierarchical architecture to improve disordered lipid-binding residues prediction***	
15:00-15:20	64: An Zeng, Zhao Guo, Dan Pan, Yiqun Zhang and Jun Liu ***EEG-TFNet: Spatiotemporal and Spectral Feature Integration for EEG-Based AD Detection***	
15:20-15:40	67: Jianyi Hu, Yongtao Zhu, Zishan Zhou, Xinqiang Wen, Ju Xiang and Xiangmao Meng ***RGMI: a multimodal graph framework with dynamic weighting for measuring disease similarity***	
15:40-16:10	**Coffee break/Poster session**	**Lobby**

Time: 16:10-17:50, August 4, Monday

Parallel Sessions II

Session 5	**Meeting venue: SALI 1 (B116)** **Session chair: Wei Peng**
16:10-16:30	29: Anyin Zhao, Zuquan Chen, Zhengyu Fang, Xiaoge Zhang and Jing Li

	Dual-Modality Representation Learning for Molecular Property Prediction
16:30-16:50	36: Jingwen Wang and Lian Liu *GDMRMD: An Ensemble Model for Predicting RNA Modification-Disease Associations*
16:50-17:10	75: Isomoiljon Muzaffarov, Xiaowen Liu, Letu Qingge, Lusheng Wang and Binhai Zhu *On Multiple Protein Scaffold Filling*
17:10-17:30	128: Po-Yu Liang and Jun Bai *E(3)-invariant diffusion model for pocket-aware peptide generation*
17:30-17:50	157: Jianxin Wang, Hongdong Li, Guihua Duan, Jin Liu and Min Li *Bioinformatics Course Reform Through Projects integrating History, Theory, and Practice*
Session 6	**Meeting venue: SALI 2 (B212)** **Remote presentations only** **Session chairs: Xiaoyang Wang/Yunxing Dai**
16:10-16:30	70: Jinhong Zhang and Jian Liu *Adaptive Fusion of Global and Local Representations for Neoantigen Retention Time Prediction through Hierarchical Sequence-Graph Hybridization*
16:30-16:50	74: Xianglong Meng, Kai Hu, Xuefeng Cui and Fa Zhang *MambaST: Hexagonal State Space Modeling for Spatial Domain Identification*
16:50-17:10	76: An Qin, Wei Lan, Feng Zhan, Ying Tan and Yiran Huang *RGNCNDDA: Predicting Potential Drug-Disease Associations via Residual Graph Normalized Convolutional Network*
17:10-17:30	77: Shuya Zhang, Xinyu Li, Xinliang Sun, Xiangmao Meng, Kongfa Hu and Tao Yang *Herb target prediction based on neural inductive matrix completion with heterogeneous graph network*
Session 7	**Meeting venue: SALI 4 (B214)** **Remote presentations only** **Session chairs: Lian Liu/Huaiwu Zhang**
16:10-16:30	85: Jiajun Chen, Renye Zhang, Bin Yang and Mengyun Yang *A Novel Sample Selection for Deep Learning Model in Computational Drug Repositioning*

16:30-16:50	87: Haoyuan Li, Haochen Zhao, Kai Zheng, Qichang Zhao, Guihua Duan and Jianxin Wang ***SGMDTI: A unified framework for drug-target interaction prediction by semantic-guided meta-path method***	
16:50-17:10	91: Minghua Xu, Kang Hu, Chao Deng, Peng Ni and Jianxin Wang ***TREPP: Tandem Repeat Expansion Pathogenicity Predicting Approach Using Stacked CatBoost Models and Multiple Features***	
17:10-17:30	92: Abdulrahman Al-Badwi, Hulin Kuang, Abdulrahman Al-Dailami and Jianxin Wang ***EMF: Enhancing Mortality Risk Prediction via Evidential Multimodal Fusion***	
Session 8	**Meeting venue: SALI 6 (B317)** **Remote presentations only** **Session chairs: Hongdong Li/Wenqing Chen**	
16:10-16:30	93: Zhenlan Liang, Ruiqing Zheng, Huayu Tao, Yuxuan Chen and Min Li ***Contrastive Learning-based Method for Single-cell Multi-omics Data Clustering***	
16:30-16:50	94: Shengkai Chen, Yuanyuan Liu, Xiaofei Mi, Ju Xiang and Dianyi Song ***Intelligent algorithms of action recognition for cardiopulmonary resuscitation based on wearable device***	
16:50-17:10	95: Baojuan Qin, Junliang Shang, Yan Zhao, Xiaohan Zhang, Feng Li and Jin-Xing Liu ***Label-guided graph contrastive learning for single-cell fusion clustering***	
17:10-17:30	98: Feng Yuan, Shenghui Liao, Ziyang Hu and Qiuyang Chen ***A Graph Convolution-Based Method for dental Image Registration***	
17:50-18:30	**Poster**	
19:00-22:00	**Banquet**	**Ravintola Sipuli**

Agenda Tuesday

Time: 09:00-12:00, August 5, Tuesday

Place: SALI 1 (B116)

Time	Content
09:00-09:10	**Opening Remarks (Matti Nykter)** **Meeting venue: SALI 1 (B116)**
09:10-09:50	***Keynote 3: Systems Biology for Cancer Reversion: A New Therapeutic Approach*** **Presenter:** Kwang-Hyun Cho
09:50-10:30	***Keynote 4: How Open and Community Approaches are Transforming Bioinformatics*** **Presenter:** Serghei Mangul
10:30-11:00	Coffer Break
11:00-12:40	**Conference session II** **Meeting venue: SALI 1 (B116)** **Session chair: Xin Lai**
11:00-11:20	51: Masahito Tsukahara and Tetsuo Shibuya ***Efficient and Accurate Approximation Algorithms for Protein Structure Alignment***
11:20-11:40	82: Huaiwu Zhang and Jing Tang ***CADS: Causal Inference for Dissecting Essential Genes to Predict Drug Synergy***
11:40-12:00	209: Ziqi Kang, Andreas Hainari, Venla Kaislo, Lina Maltrovsky, Saundarya Shah, Anastasia Lundgren, Essi Kahelin, Matilda Salko, Anni Virtanen, Ulla-Majia Haltia and Anniina Färkkilä ***Spatial mapping of tumor ecosystems reveals niches associated with immune escape in chemo-naive ovarian cancer***
12:00-12:20	148: Rwan Ahmed, Kang Jiang and Fang-Xiang Wu ***Joint Sparse Precision Matrix Estimation for Cancer Diagnosis***
12:20-12:40	86: Jihui Shi, Haochen Zhao, Guihua Duan and Jianxin Wang ***AMPGNet: Identification of Antimicrobial Peptides and Their Functional activities Based on Multimodal Fusion***

12:40-13:40	Lunch/Poster session	Unicafe/Lobby

Time: 13:40-15:40, August 5, Tuesday

Parallel Sessions III

Session 9	**Meeting venue: SALI 1 (B116)** **Session chair: Sofer Tamar**
13:40-14:00	49: Zeyu Zhong, Yan Liu, Peng Ni and Jianxin Wang ***RNA-ModCaller: A Multi Feature Fusion and Stacking Ensemble Learning Framework for Prediction of RNA Modifications***
14:00-14:20	109: Juan He, Xiaoyan Wang, Yi Pan, Zhengshan Wang, Bokai Yang, Zhiming Zhang, Tzu-Ming Liu, Yunpeng Cai, Long Chen and Ruitao Xie ***Accurate and Interpretable Wound Healing Progress Detection Based on a Task-related Knowledge Refinement Learning Method***
14:20-14:40	138: Hongyu Duan, Ziyan Li, Yixuan Wu, Bozhen Ren, Yonghua Wang, Wen Chen and Li C Xia ***EnzHier: High-Precision Enzyme Function Prediction through Multi-Scale Feature Integration and Hierarchical Contrastive Learning***
14:40-15:00	164: Zhikui Feng, Quan Zou and Hui Yang ***LGN-CAT: A Cross-Attention Deep Learning Framework for Identifying Diagnostic Biomarkers in Intrahepatic Cholangiocarcinoma***
15:00-15:20	169: Jiale Wen, Xiao Lan, Yaru Chen, Longyu Hu, Kamen Ivanov, Mingyan Xu, Jia Gu and Shifu Chen ***ACMSI: An Innovative Automated Analysis Application Utilizing Computer Vision for Accurate Microsatellite Instability Classification***
15:20-15:40	117: Nidhibahen Shah, Joyanta Basak, Sartaj Sahni and Sanguthevar Rajasekaran ***Double Metaphone Blocking: An Innovative Blocking Approach to Record Linkage***
Session 10	**Meeting venue: SALI 2 (B212)** **Remote presentations only** **Session chair: Li Shen**
13:40-14:00	99: Changfeng He, Yutao Dou, Fan Liu, Xiaoping Wang and Shaoliang Peng ***DepMambaformer: Integrating Bidirectional State Space Duality Model with Multimodal Attention for Depression Detection***

14:00-14:20	100: Saisai Ma, Xuehua Bi, Linlin Zhang, Haifeng Xu and Kai Zhao ***Prediction of High-Altitude Pulmonary Edema Based on Resampling and Ensemble Learning***
14:20-14:40	101: Chunyang Jiang, Yuanbo Guo, Linlin Zhang, Xuehua Bi and Kai Zhao ***LGFMDA: miRNA-disease association prediction with local and global feature representation learning***
14:40-15:00	103: Yang Jiao, Mingzhe Cui, Tao Chen, Ruibin Bai and Yi Pan ***TSCF-Net: A Temporal-Spectral Cross-Fusion Network for Low-channel EEG Motor Imagery Classification***
15:00-15:20	104: Jiancun Zhou, Hulin Kuang and Jianxin Wang ***HCM-Net: Hybrid CNN and Mamba Network with Multi-scale Awareness Feature Fusion for Lung Cancer Pathological Complete Response Prediction***
15:20-15:40	105: Shicheng Ma, Weiyang Liang, Kai Zhao, Xuehua Bi and Linlin Zhang ***PrePSL: A Pre-training Method for Protein Subcellular Localization Using Graph Auto-Encoder and Protein Language Model***
Session 11	**Meeting venue: SALI 4 (B214)** **Remote presentations only** **Session chair: Qinhan Hou**
13:40-14:00	107: Zhipeng Gao, Kai Zhao, Guanglei Yu, Xuehua Bi and Linlin Zhang ***MOGATFF: An Explainable Multi-Omics Prediction Model with Feature Enhancement for Genotype-Phenotype Association Analysis***
14:00-14:20	111: Bolin Chen, Zhengyu Wang, Ziyuan Li, Jianjun Zhang, Youpeng Hu, Duiyue Chen, Yuhang Li, Xinyue Hu and Zhouning Xu ***A novel weighted network control model for identifying coding and non-coding drivers in cancer***
14:20-14:40	114: Lei Chu, Hongyan Wu and Yi Pan ***Autonomous Generation of an Autism Knowledge Question-and-Answer Dataset Using Large Language Models***
14:40-15:00	119: Duo Feng, Shuaicheng Li and Yue Zhang ***Automated Prediction of Protein Pair Distances Based on Deep Learning: A Novel Approach to Protein Structure Prediction in SCOP***
15:00-15:20	123: Guangzhe Zhao, Tianyu Huang, Feihu Yan, Xueping Wang and Feng Liu ***VM-UNet++: Vision Mamba UNet with Multi-Scale Feature Fusion for Medical Image Segmentation***
15:20-15:40	127: Manjir Gurung, Kafui Efio-Akolly, Ronald Bbosa and Feng Liu

	GDCA-TransUNet for Dual-Stage Attention Enhanced Multi-Organ Segmentation in Abdominal CT Images	
Session 12	**Meeting venue: SALI 6 (B317)** **Remote presentations only** **Session chair: Huaiwu Zhang**	
13:40-14:00	144: Cheng Xu, Mingzhao Wang, Jinyan Li and Juanying Xie *Bidirectional Position-Context Feature Representation for Predicting DNA/RNA Modification Sites*	
14:00-14:20	146: Feng Deng, Yi Tang, Qinghua Fu, Lin Guo and Ying An *Optical Flow-Augmented Dual-Stream Network for Left Ventricular Ejection Fraction Prediction*	
14:20-14:40	151: Bowen Tan, Lingxi Chen, Xuedong Wang, Wenlong Jia, Yanfei Wang, Hechen Li, Shuo Yang, Guangze Pan and Shuai Cheng Li *CNAHap: a germline haplotyping method using tumor allele-specific copy number alteration*	
14:40-15:00	153: Xiang Chen, Wenfeng He, Junnan Yu and Zhaoyu Fang *scCMA:a contrastive masked autoencoder for single-cell RNA-seq embedding*	
15:00-15:20	154: Minzhu Xie, Dongze Deng and Yabin Kuang *Drug-Target Interaction Prediction via Substructure Similarity-Guided Denoising and Hierarchical Feature Fusion*	
15:20-15:40	155: Yuhe Liu, Cuixiang Lin, Xiaoqing Peng and Hongdong Li *IsoIR: a Method for Isoform-Level Intron Retention Detection*	
15:40-16:10	Coffee break	Unicafe/Lobby

Time: 16:10-17:50, August 5, Tuesday

Parallel Sessions VI

Session 13	**Meeting venue: SALI 1 (B116)** **Session chair: Xiujuan Lei**
16:10-16:30	2: Shanshan Ying, Wenqian Yan, Chongchen Pang, Liangjie Liu, Mofan Feng, Zhangli Yuan, Xin Jin, Weiping Zhu, Haoyan Chen, Xuanwen Bao, Weijia Fang,

	Mika Torhola, Klaus Förger, Henna Kujanen, Viljami Männikkö, Hao Li, Lintai Da, Yuqing Lou, Guang He, Jacek Jemielity, Joanna Kowalska and Yi Shi ***3D Genome selected circRNA in Hepatocellular Carcinoma Prediction***
16:30-16:50	68: Xiaoyang Wang, Lulu Chen and Dongmei Ai ***LDADW: An algorithm for integrating single-cell and spatial transcriptomic data based on the topic model***
16:50-17:10	80: Dong Xu, Tao Chen, Yang Jiao, Zexian Zhao, Xiaoli Liu, Lei Xie and Yi Pan ***Spindle-UMamba: A Mamba-based Attention-Unet Framework for Effective Sleep Spindle Detection***
17:10-17:30	113: Liu Yajun, Zhang Fan, Ding Yulian, Li Aimin and Fei Rong ***Identification of piRNA-disease association based on contrastive learning***
17:30-17:50	195: Reza Abbasi-Asl ***Multimillion cell self-supervised representation learning enables organ-scale tissue niche discovery***
Session 14	**Meeting venue: SALI 2 (B212)** **Remote presentations only** **Session chair: Li Shen**
16:10-16:30	158: Hoai-Nhan Tran, Nguyen-Phuc-Xuan Quynh, Haochen Zhao and Jianxin Wang ***MGPLM-PPI: A Framework for Protein–Protein Interactions based on Multiple Graph Neural Networks and Protein Language Models***
16:30-16:50	160: Haoze Du, Shumei Hou, Xiaolei Wang, Bin Sun, Dongfang Zhang, Junliang Du, Qingkai Hu, Weifeng Guo and Xianfang Wang ***CT-Semi-Net: Segmentation of infected areas in lung CT images based on attention mechanism and semi-supervised learning***
16:50-17:10	163: Yunzhi Qiu, Bo Zhang, Haohao Zhu, Changrong Min, Haifeng Liu, Tongxuan Zhang and Hongfei Lin ***Dynamic Knowledge-aware LLM for Adverse Drug Reaction Entity Recognition***
17:10-17:30	165: Yu Sheng, Yiyi Hong, Yongchang Jia and Guihua Duan ***LiteSCTransNet: Lightweight CNN-Transformer for 3D Medical Image Segmentation***
Session 15	**Meeting venue: SALI 4 (B214)** **Remote presentations only** **Session chair: Qinhan Hou**

16:10-16:30	166: Ju Huang, Ting Wang, Yumei Han, Shuo Chen, Dan Yan, Quan Zou, Hao Lin and Hui Yang ***iIHD-TADP: A Temporal-aware Transformer and Physical Examination Data-based Model for Ischemic Heart Disease Prediction***	
16:30-16:50	173: Nguyen-Phuc-Xuan Quynh, Hoai-Nhan Tran, Cheng Yan and Jianxin Wang ***EGNNMDA: A Prediction Model Based on Ensemble Graph Neural Networks for MiRNA-Disease Associations***	
16:50-17:10	177: Xiaochuan Chen, Jianqiang Zheng, Zhenni Huang, Ziqi Xu, Junye Huang, Yueyi Tan, Yanjie Wei and Huiling Zhang ***AlloPED: Leveraging Protein Language Models and Structure Features for Allosteric Site Prediction***	
17:10-17:30	181: Feng Shi, Zhanglian Lin, Xin Zeng and Jianxin Wang ***Parameterized Algorithms for the Tree Containment Problem on Multifurcating Phylogenetic Network***	
18:00-18:10	**Closing Remarks** **(Jianxin Wang)**	**SALI 1 (B116)**

Posters

18	Alex-Adrian Farcas, István-Ferenc Tóth and Alexandra Farcas	Computational Design of Polymer-Based Nanoplatforms for Advanced Gene and Drug Delivery Systems
175	Shubh Sharma, Saurav Kumar, Deepika Deepika and Vikas Kumar	GRATA: An automated in silico pipeline for Read Across Using the Transcriptomics Data
186	Serghei Mangul, Viorel Munteanu, Mihai Covasa, Mihai Dimian and Andrei Lobiuc	Predicting and Understanding Long COVID with AI and Genomics
188	Masrur Sobhan, Md Mezbahul Islam and Ananda Mondal	Lung Cancer Health Disparity Through the Lens of Explainable AI
189	Enos Kakwambi, Tuan Nguyen, Suryaveer Kapoor and Marmar Moussa	Principal Genes: A PCA-based approach to highly variable genes selection for scRNA-Seq analysis
191	Saurav Kumar, Shubh Sharma, Deepika Deepika and Vikas Kumar	BioEntityLinker: Approaching Entity Linking Through Text Compression Algorithm
192	Sriram Boddeda, Olajumoke Oladapo and Marmar Moussa	AtlasCollect: A Single Cell Data Atlas platform and Unified Platform for Datasets Collection and Integration
194	Zhesi Zhang and Xin Lai	MiREA - A Network-Based Tool for Cancer-specific miRNA-Oriented Enrichment Analysis
195	Reza Abbasi-Asl	Multimillion cell self-supervised representation learning enables organ-scale tissue niche discovery
196	Guangzhao Cheng and Lu Cheng	Raw signal segmentation for estimating RNA modification from Nanopore direct RNA sequencing data
197	Chengbo Fu and Lu Cheng	k-mer manifold approximation and projection for visualizing DNA sequences
198	Li Shen and Jing Tang	Benchmarking Computational Methods for Single-Cell Drug Response Prediction
199	Liang Zhang, Xin Lai and Zhesi Zhang	A deep learning framework for stratifying cancer patients based on their genomic and interactome profiles
200	Daria Afenteva, Alexandra Lahtinen, Sampsa Hautaniemi and Antti Häkkinen	Decoupling patient, tissue, and treatment signals from longitudinal bulk RNA-seq samples
202	Sofia Khan, Mikko Niemi and Johanna Kiiski	Identification of pharmacogene copy number variation in the Finnish population using high-throughput next generation sequencing
203	Dimitri Meistermann and Morgane Frapin	Gene Set Differential Scoring enables reliable, modular and intuitive functional enrichment
204	Samuel Leppiniemi, Daria Afenteva, Yilin Li, Guilia Micoli, Kari Lavikka, Susanna Holmström, Deborah	SegmentQTL: Identifying genetic variants influencing molecular phenotypes in copy number– driven cancers

	Boyenval, Jaana Oikkonen, Sampsa Hautaniemi and Taru Muranen	
205	Sebastian Schmidt, Jasper Krauter, Alexandru Tomescu and Ari Löytynoja	Identification of genomic template switch mutations using A* algorithm
206	Sadiksha Adhikari, Philipp Sergeev, Nemo Ikonen, Heikki Kuusanmäki, Mika Kontro, Markus Vähä-Koskela and Caroline A. Heckman	Deciphering Heterogeneity in Acute Myeloid Leukemia to Understand the Mechanisms of Disease Progression and Immune Interactions Using Single-Cell RNA-Sequencing
207	Geraldson Muluh, Tuomas Borman and Leo Lahti	miaTime: A scalable R/Bioconductor framework for longitudinal microbiome analysis
208	Tuomas Borman and Leo Lahti	Orchestrating Microbiome Analysis with Bioconductor
209	Ziqi Kang, Andreas Hainari, Venla Kaislo, Lina Maltrovsky, Saundarya Shah, Anastasia Lundgren, Essi Kahelin, Matilda Salko, Anni Virtanen, Ulla-Majia Haltia and Anniina Färkkilä	Spatial mapping of tumor ecosystems reveals niches associated with immune escape in chemo-naive ovarian cancer
210	Sara Palomino, Tatiana Belova, Ada Junquera-Mencía, Iga Niemiec, Ping-Han Hsieh, Anna Vähärautio, Marieke L. Kuijjer and Anniina Färkkilä	Unveiling the spatial regulation of chemoresistance in ovarian cancer
211	Ada Junquera, Alva Grönholm, Sara Palomino, Nika Mihailava, Lina Maltrovsky, Matilda Salko, Saundarya Shah, Zhihan Liang, Iga Niemiec, Aleksandra Shabanova, Maija Vääriskoski, Ulla-Maija Haltia and Anniina Färkkilä	Single-cell spatial proteomics reveals cell-cycle resolved tumor architecture in ovarian cancer
212	Klaudia Lewna, Pihla Kaipainen, Keerthana Ganesh, Emad Arbash, Anne Pink and Pipsa Saharinen	scRNA-seq Uncovers Novel Endothelial Subclusters and Early Inflammatory Responses in Lung Alveolar Capillaries
213	Ankita Srivastava, Joseph Saad, Philipp Sergeev, Markus Vähä-Koskela, H. Joachim Deeg, Jerald P. Radich, Kernyu Park, William Blum, Caroline Heckman and Janghee Woo	Machine Learning Network-Based Stratification Refines Prognosis and Treatment Stratification in Intermediate-Risk AML
214	Tuomas Borman	Finnish Society for Bioinformatics

Keynote Speakers

Prof. **Walter Kolch** is Director of Systems Biology Ireland (https://www.ucd.ie/sbi/) at University College Dublin and the Precision Oncology Ireland Consortium (https://www.precisiononcology.ie/). Trained as an MD he worked in experimental clinical research, pharmaceutical industry, and basic biological research. Before moving to Dublin to establish SBI he held a Chair for Molecular Cell Biology at the University of Glasgow and was a Senior Group Leader at the Beatson Institute for Cancer Research in Glasgow, Scotland. He is best known for his work in oncogene signal transduction, proteomics, systems biology, and precision medicine. He has made salient contributions to elucidating the function of the RAS-RAF pathway, and more recently to understand network wide effects of oncogenes. His current research interest focuses on understanding molecular mechanisms of malignant transformation, network mediated drug resistance in cancer, and the construction of Digital Twins for personalized cancer diagnosis and therapy. He serves on several editorial boards and scientific advisory boards and is a Fellow of the Royal Society of Edinburgh and a Member of the Royal Irish Academy.

Dr. **Ritambhara Singh** is an Associate Professor of Computer Science and Data Science and a member of the Center for Computational Molecular Biology at Brown University. Her research lab develops machine learning methods with the goals of data integration and model interpretation for biological and biomedical applications. Prior to joining Brown, she was a post-doctoral researcher in the Noble Lab at the University of Washington. She completed her Ph.D. in 2018 from the University of Virginia with Dr. Yanjun Qi as her advisor.

Ritambhara has received the NHGRI Genomic Innovator Award and Brown University’s Richard B. Salomon Faculty Research Award for developing deep learning methods to integrate and model genomics datasets. She has also received the Dean’s Award for Excellence in Teaching at Brown. She recently received the NSF CAREER award for developing integrative and explainable machine learning methods for heterogeneous health-related datasets.

Dr. **Kwang-Hyun Cho** is a Professor in the Department of Bio and Brain Engineering at Korea Advanced Institute of Science and Technology (KAIST) and a director of the Laboratory for Systems Biology and Bio-inspired Engineering (http://sbie.kaist.ac.kr). He was the recipient of IEEE/IEEK Joint Award for Young IT Engineer, National Young Scientist Award and National Engineer's Award both from the President of Korea, Walton Fellow Award from Science Foundation of Ireland, and Cheney Fellow Award from University of Leeds, U.K. He started systems biology by his own idea of combining control engineering and biological experiments from 1999 and has published over 229 papers in high-profile international journals. He has been challenging to develop innovative therapeutic approaches for reverting cancer and aging on the basis of systems biology, and co-founded biorevert, Inc. to realize these therapeutics. He is the Editor-in-Chief of IET Systems Biology (Wiley) and Encyclopedia of Systems Biology (Springer).

Dr. **Serghei Mangul** holds positions as the Director of Challenges and Benchmarking at Sage Bionetworks. He specializes in the design, development, and application of novel data-driven computational approaches to accelerate the diffusion of genomics and biomedical data into translational research and education. Dr. Mangul is a passionate advocate for promoting transparency and reproducibility in data-driven biomedical research, as well as for making bioinformatics education accessible to all. Dr. Mangul's work is dedicated to advancing the principles of reproducibility, data sharing, and software usability, with the ultimate goal of shaping a more equitable and impactful future for the field of bioinformatics. Dr. Mangul received his Ph.D. in Bioinformatics from Georgia State University and holds a B.Sc. in Applied Mathematics from Moldova State University, Chisinau, Moldova. He completed his postdoctoral training in computational genomics with Prof. Eskin at the University of California Los Angeles (UCLA). Dr. Mangul is the recipient of the prestigious National Science Foundation CAREER and Fulbright U.S. Scholar Program awards. He serves as a mentor for the NIH AIM-AHEAD Leadership Fellowship and NCATS Training Program in Advanced Data Analysis.

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