

ISBRA 2022 Program

Monday, November 14th, 2022

7:00pm-
9:00pm **Reception**

Tuesday, November 15th, 2022

9:00am-
10:00am **Plenary Session Room: TBA**
Chair: TBA

Session 1:

Keynote Talk

Talk Title

*Eugene Koonin, National Center for Biotechnology Information,
National Institutes of Health*

10:00am-
10:20am **Coffee Break**

10:20am-
12:20pm **Parallel Sessions**

Session 2A:

**Evolution, Ecology, Comparative
Genomics**

Room:

Chair:

10:20am-
10:40am BLASTphylo - an Interactive Web Tool
for Taxonomic and Phylogenetic
Analysis of Genes, *Susanne Zabel,
Jennifer Müller, Friedrich Götz and Kay
Nieselt*

10:40am-
11:00am A Clonal Evolution Simulator for
Planning Somatic Evolution Studies,
*Arjun Srivatsa, Haoyun Lei and Russell
Schwartz*

11:00am-
11:20am Transposition Distance Considering
Intergenic Regions for Unbalanced
Genomes, *Alexsandro Oliveira*

Session 2B:

**Machine Learning: Medical
Records/Data, Protein Domains**

Room:

Chair:

Automatic ICD Coding based on Multi-
granularity Feature Fusion, *Ying Yu, Han
Jiang, Junwen Duan and Jianxin Wang*

Fusing Label Relations for Chinese EMR
Named Entity Recognition with Machine
Reading Comprehension, *Shuyue Liu,
Junwen Duan, Feng Gong, Hailin Yue
and Jianxin Wang*

Effectively Training MRI Reconstruction
Network via Sequentially Using
Undersampled k-Space Data with Very

	<i>Alexandrino, Andre Rodrigues Oliveira, Geraldine Jean, Guillaume Fertin, Ulisses Dias and Zaroni Dias</i>	<i>Low Frequency Gaps, Tian-Yi Xing, Xiao-Xin Li, Zhi-Jie Chen, Xi-Yu Zheng and Fan Zhang</i>
11:20am-11:40pm	Interactions between culturable bacteria are predicted by individual species' growth, <i>Jonathan Friedman and Einat Nestor</i>	Research on the prediction method of disease classification based on imaging features, <i>Yu Sheng, Shengyi Yang, Huirong Hu and Guihua Duan</i>
11:40am-12:00pm	Using variable-order Markov models to improve metagenomics binning and genome taxonomic classification, <i>Leibovich Or, Yochai Meir and Itai Sharon</i>	NIDN: Medical Code Assignment via Note-Code Interaction Denoising Network, <i>Xiaobo Li, Yijia Zhang, Xingwang Li, Jian Wang and Mingyu Lu</i>
12:00pm-12:20pm	Revisiting SVDQuartets: Performance under Real Life Values and Improvements, <i>Shay Hakim and Sagi Snir</i>	GNN-Dom: an unsupervised method for protein domain partition via protein contact map, <i>Wang Lei and Yan Wang</i>
12:20pm-2:00pm	Lunch Break	
2:00pm-3:00pm	Plenary Session Room:	
	Chair:	
	Session 3:	
	Keynote Talk	
	Talk Title	
	<i>Tamar Friedlander, Faculty of Agriculture, Hebrew University of Jerusalem</i>	
3:00pm-3:20pm	Coffee Break	
3:20pm-5:40pm	Parallel Sessions	
	Session 4A:	Session 4B:
	Cancer, SARS-CoV-2	Networks, Machine Learning
	Room:	Room:
	Chair:	Chair:
3:20pm-3:40pm	Tumor type-specific survival associations of transcriptomic-weighted codon usage and tRNA abundance, <i>Douglas Meyer, Haim Bar, Anton Komar, Ryan Hunt, Michael DiCuccio and Chava Kimchi-Sarfaty</i>	STgcor: A Distribution-based Correlation Measurement Method for Spatial Transcriptome Data, <i>Xiaoshu Zhu, Liyuan Pang, Wei Lan, Shuang Meng and Xiaoqing Peng</i>
3:40pm-4:00pm	A Network-Based Voting Method for Identification and Prioritization of Personalized Cancer Driver Genes, <i>Han Li, Feng Li, Junliang Shang, Xikui Liu and Yan Li</i>	An SMT-based Framework for Reasoning about Discrete Biological Models, <i>Boyan Yordanov, Sara-Jane Dunn, Colin Gravill, Hillel Kugler and Christoph M. Wintersteiger</i>

4:00pm-4:20pm	A Tensor Robust Model Based on Enhanced Tensor Nuclear Norm and Low-Rank Constraint for Multi-view Cancer Genomics Data, <i>Qian Qiao, Sha-Sha Yuan, J. Shang and Jin-Xing Liu</i>	Power and limitations of hybrid system models for gene regulatory networks, <i>Juris Viksna, Kārlis Čerāns, Lelde Lace and Gatis Melkus</i>
4:20pm-4:40pm	Efficient Distance-Based Reconstruction of Large-Scale Single-Cell Phylogenies from Copy Number Data, <i>Samson Weiner and Mukul S. Bansal</i>	Graph Random Forest: A graph embedded algorithm for identifying highly connected important features, <i>Leqi Tian and Tianwei Yu</i>
4:40pm-5:00pm	Evaluating the Robustness of ML Models in SARS-CoV-2 Genome Sequences Generated Using TGS Technology, <i>Bikram Sahoo, Sarwan Ali, Pin-Yu Chen, Murray Patterson and Alex Zelikovsky</i>	Simulating Spiking Neural Networks based on SW26010pro, <i>Zhichao Wang, Xuelei Li, Yi Pan and Yanjie Wei</i>
5:00pm-5:20pm	t-SNE Highlights Phylogenetic and Temporal Patterns of SARS-CoV-2 Spike and Nucleocapsid Protein Evolution, <i>Gaik Tamazian, Andrey Komissarov, Dmitry Kobak, Dmitry Polyakov, Evgeny Andronov, Sergei Nechaev, Sergey Kryzhevich, Yuri Porozov and Eugene Stepanov</i>	A methodology for classifying tissue-specific metabolic and inflammatory receptor functions applied to subcutaneous and visceral adipose, <i>Judith Somekh and Gur Arye</i>
5:20pm-5:40pm	A rigorous benchmarking of methods for SARS-CoV-2 lineage quantification in wastewater, <i>Viorel Munteanu, Nitesh Kumar Sharma, Bohdan Tyshchenko, Alina Frolova, Serghei Knyazev and Serghei Mangul</i>	Deep learning-enhanced MHC-II presentation prediction and peptidome deconvolution, <i>Juntao Deng and Min Liu</i>
6:00pm-8:00pm	Banquet	

Wednesday, November 16th, 2022

9:00am-10:00am	Plenary Session Room: TBA Chair: TBA	
	Session 5: Keynote Talk Talk Title <i>Mona Singh, Professor of Computer Science, Princeton University</i>	
10:00am-10:20am	Coffee Break	
10:20am-12:20pm	Parallel Sessions	
	Session 5A: Clustering, Sequence Analysis Room: Chair:	Session 5B: Privacy, PPI, Pathways Room: Chair:
10:20am-10:40am	Entropy Based Clustering of Viral Sequences, <i>Akshay Juyal, Mark Grinshpon, Daniel Novikov, Roya Hosseini and Alex Zelikovsky</i>	Private Epigenetic PaceMaker Detector using Homomorphic Encryption, <i>Meir Goldenberg, Adi Akavia and Sagi Snir</i>
10:40am-11:00am	FEED: a feature extraction method based on gene expression decomposition for single-cell clustering, <i>Chao Zhang, Yunpei Xu, Lu He, Tao Zhang and Hongdong Li</i>	MPCDDI: A Secure Multiparty Computation-based Deep Learning Framework for Drug-drug Interaction Predictions, <i>Xia Xiao, Shaoliang Peng, Shengyun Liu and Xiaoqi Wang</i>
11:00am-11:20am	ARGLRR: An Adjusted Random Walk Graph Regularization Sparse Low-rank Representation Method for Single-cell RNA-sequencing Data Clustering, <i>Zhen-Chang Wang, Jin-Xing Liu, Jun-Liang Shang, Ling-Yun Dai, Chun-Hou Zheng and Juan Wang</i>	EMRShareChain: A Privacy-Preserving EMR Sharing System Model Based on the Consortium Blockchain, <i>Xinglong Zhang, Peng Xi, Wenjuan Liu and Shaoliang Peng</i>
11:20am-11:40pm	An Efficient and User-friendly Software for PCR Primer Design for Detection of Highly Variable Bacteria, <i>Dongzheng Hu, Wubin Qu, Fan Tong, Xiangwen Zheng, Jiangyu Li and Dongsheng Zhao</i>	Estimating enzyme expression and metabolic pathway activity in mice, <i>Filipp Rondel, Roya Hosseini, Hafsa Farooq and Alex Zelikovsky</i>

11:40am-12:00pm	Optimal sequence alignment to ED-strings, <i>Njagi Moses Mwaniki and Nadia Pisanti</i>	Heterogeneous PPI network representation learning for protein complex identification, <i>Peixuan Zhou, Yijia Zhang, Fei Chen, Kuo Pang and Mingyu Lu</i>
12:00pm-12:20pm	An Algorithm to Calculate the p-value of the Monge-Elkan Distance, <i>Petr Ryšavý and Filip Železný</i>	Gaussian-enhanced Representation Model for Extracting Protein-Protein Interactions Affected by Mutations, <i>Da Liu, Yijia Zhang, Ming Yang, Fei Chen and Mingyu Lu</i>
12:20pm-2:00pm	Lunch Break	

2:00pm-3:00pm	Plenary Session Room:	
	Chair:	
	Session 6:	
	Keynote Talk	
	Talk Title	
	<i>Michal Linial, Professor of Biochemistry and Bioinformatics, Hebrew University of Jerusalem</i>	
3:00pm-3:20pm	Coffee Break	

3:20pm-5:20pm	Parallel Sessions	
	Session 7A:	Session 7B:
	Human Disease 1	RNA, Viral Transmission/Genomics
	Room:	Room:
	Chair:	Chair:
3:20pm-3:40pm	A multi-view perspective on predicting human diseases based on gut microbiome features, <i>Efrat Muller, Itamar Shiryen and Elhanan Borenstein</i>	Predict CircRNA-disease Associations Based on Random Walk with Restart, Principal Component Analysis and Random Forest, <i>Qiang Luo and Minzhu Xie</i>
3:40pm-4:00pm	Multi-atlas Representations based on Transformer for Autism Spectrum Disorders Diagnosis, <i>Jianchun Zhu, Jin Liu, Junbin Mao, Yu Sheng and Yi Pan</i>	Distance Profiles of Optimal RNA Foldings, <i>Jinyi Liu, Isabel Duan, Santi Santichaivekin and Ran Libeskind-Hadas</i>
4:00pm-4:20pm	M-US-EMRs: A Multi-Modal Data Fusion Method of Ultrasonic Images and Electronic Medical Records Used for Screening of Coronary Heart Disease, <i>Bokai Yang, Yingnan Zuo, Shunxiang Yang, G. Deng, S. Zhu and Yunpeng Cai</i>	A Locality-Constrained Linear Coding-Based Ensemble Learning Framework for Predicting Potentially Disease-Associated MiRNAs, <i>Yi Shen, Ying-Lian Gao, Juan Wang, Bo-Xin Guan and Jin-Xing Liu</i>

4:20pm-4:40pm	Machine Learning based biomarker discovery for chronic kidney disease–mineral and bone disorder (CKD-MBD), <i>Xiang Shao, Yukuan Lou, Weixin Kong, Yutin Li, Qianpan Liu and Suhua Zhang</i>	Global profiling and annotation of templated isomiRs dynamics across <i>Caenorhabditis elegans</i> development, <i>Ganesh Panzade, Li Li, Shilpa Hebbar, Isana Veksler-Lublinsky and Anna Zinovyeva</i>
4:40pm-5:00pm	TDCOSR: A multimodality fusion framework for association analysis between genes and ROIs of Alzheimer's disease, <i>Qi Zou, Yan Sun, Feng Li, Juan Wang, Jin-Xing Liu and Junliang Shang</i>	Unlocking capacities of genomics for the COVID-19 response and future pandemics, <i>Serghei Mangul and Alex Zelikovsky</i>
5:00pm-5:20pm	Policy-based Hypertension Monitoring using Formal Runtime Verification Monitors, <i>Abhinandan Panda, Srinivas Pinisetty and Partha Roop</i>	Inference of viral transmission networks under structural constraints, <i>Kiril Kuzmin, Sagi Snir, Yury Khudyakov and Pavel Skums</i>
6:00pm-8:00pm	ISBRA 2022 Organizer Dinner	

Thursday, November 17th, 2022

9:00am-10:00am	Plenary Session Room: TBA Chair: TBA	
	Session 8: Keynote Talk Talk Title <i>Abraham B Korol, Professor, Institute of Evolution, University of Haifa</i>	
10:00am-10:20am	Coffee Break	
10:20am-11:40am	Parallel Sessions	
	Session 9A: Human Disease 2 Room: Chair: Applying machine learning and leave-pair-out cross-validation to a clinical and steroidomics dataset to find predictors for preeclampsia, <i>Alexander Biehl</i>	Session 9B: Drug Interaction/Association Room: Chair: MLMVFE: A Machine Learning Approach Based on Multi-View Features Extraction for Drug-Disease Associations Prediction, <i>Ying Wang, Ying-Lian Gao, Juan Wang, Junliang Shang and Jin-Xing Liu</i>
10:20am-10:40am		
10:40am-11:00am	MMLN: Leveraging Domain Knowledge for Multimodal Diagnosis, <i>Haodi Zhang, Chenyu Xu, Peirou Liang, Ke Duan, Hao Ren, Weibin Cheng and Kaishun Wu</i>	Mixed expert Model For Drug-Target Interaction Prediction, <i>Honghui Lian, Zhi Zeng, Xiang Li, Huan Wang, Guodong Li and Ziwen Cui</i>
11:00am-11:20am	Transfer Learning for Semi-Supervised 3D Left Atrium Segmentation through Dual-Task Consistency Framework, <i>Jiahao Chen, Ruohan Lin, Xiaobin Lan, Rongxing Wang, Xipeng Pan and Yanju Zhang</i>	Prediction of Drug-disease Relationship on Heterogeneous Networks Based on Graph Convolution, <i>Jiancheng Zhong, Pan Cui, Zuohang Qu, Qiu Xiao and Yihong Zhu</i>
11:20am-11:40am	2D Photogrammetry Image of Adolescent Idiopathic Scoliosis Screening Using Deep Learning, <i>Zhenda Xu, Jiazi Ouyang, Qiang Gao, Aiqian Gan, Qihua Zhou, Jiahao Hu and Song Guo</i>	A Multimodal Data Fusion-based Deep Learning Approach for Drug-Drug Interaction Prediction, <i>An Huang, Xiaolan Xie, Xiaoqi Wang and Shaoliang Peng</i>
11:40am-12:00pm	Closing Remarks	
12:00 pm-7:00pm	Lunch Break + Excursion	