

# 2022 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2022)

The conference schedule is based on USA PST Time  
December 6-7, 2022  
Las Vegas, NV, USA.

## December 6: 8:40-9:00am, Opening Ceremony

### Chairs:

Donald Adjero, [donald.adjero@mail.wvu.edu](mailto:donald.adjero@mail.wvu.edu)

Qi Long, [qlong@pennmedicine.upenn.edu](mailto:qlong@pennmedicine.upenn.edu)

Xinghua Mindy Shi, [mindyshi@temple.edu](mailto:mindyshi@temple.edu)

Srinivas Aluru, [aluru@cc.gatech.edu](mailto:aluru@cc.gatech.edu)

Giri Narasimhan, [giri@cs.fiu.edu](mailto:giri@cs.fiu.edu)

Xiaohua Tony Hu, [xh29@drexel.edu](mailto:xh29@drexel.edu)

Time & Location: 8:35-9am, Augustus 6

Registration Desk Hours: Dec 5: 3:00-7:00PM

Dec 6 8:00AM- 5:00PM

Dec 7: 8:00-2PM

Location - Registration Desk is next to Emperor's Ballroom on Emperors Level

Time	December 6	December 7
Keynote Sessions (9-10am)	Keynote Talk: Dr. Dan Gusfield, <a href="mailto:gusfield@cs.ucdavis.edu">gusfield@cs.ucdavis.edu</a> Chair: Donald Adjero, <a href="mailto:donald.adjero@mail.wvu.edu">donald.adjero@mail.wvu.edu</a> <u>Location:</u> Augustus 6	Keynote Talk: Dr. Marylyn Ritchie, <a href="mailto:marylyn@pennmedicine.upenn.edu">marylyn@pennmedicine.upenn.edu</a> Chair: Qi Long, <a href="mailto:qlong@pennmedicine.upenn.edu">qlong@pennmedicine.upenn.edu</a> <u>Location:</u> Augustus 6
Coffee Break (10:00-10:30am)	Coffee	

<p><b>Morning Sessions</b> (10:30am-12:00pm)</p>	<p>Session 1: Molecular Structure, Function and Evolution (1) (Emperors Ballroom I) Session 2: Computational and Systems Biology; Cheminformatics and pharmacogenomics (1) (Emperors Ballroom II) Session 3: Next Generation Sequencing and High-throughput Methods (1) (Messina) Session 5: Cross-Cutting Computational Methods and Bioinformatics of Disease (2) (Pisa)</p>	<p>Session 7: Cross-Cutting Computational Methods and Bioinformatics of Disease (4) (Emperors Ballroom I) Session 13: Biomedical and Health Informatics (6) (Emperors Ballroom II) Session 14: Biomedical and Health Informatics (7) (Messina) Session 15: Biomedical and Health Informatics (8) (Pisa)</p>
<p><b>9-12:30pm Workshop</b></p>	<p>Workshop: “Network Science and Artificial Intelligence for Biomedicine &amp; Health informatics” (Anzio)  Workshop: “Biomedical Informatics Applications in Translational Research and Rare Diseases” (Modena)  Workshop: “The 6<sup>th</sup> Workshop on Computational Methods for the Immune System Function (CMISF 2022)” (Livorno)  Workshop: “The 13<sup>th</sup> Integrative Data Analysis in Systems Biology (IDASB 2022)” (Capri)  Workshop: “Computational Structural Bioinformatics Workshop (CSBW)” (Neopolitan 2)</p>	<p>Workshop: “3<sup>rd</sup> International Workshop on High Performance Computing Methods and Interdisciplinary Applications for Fighting the COVID-19 Pandemic (HPC4COVID-19)” + Workshop: “Foundations of Network Analysis” (Palermo)  Workshop: “Sixth Edition of Workshop of Processes and Algorithms for Healthcare and Life Quality Improvement (CBPBL)” (Anzio)  Workshop: “Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics (MABM2022)” (Modena)  Workshop: “Workshop on Long Non-Coding RNAs: Mechanism, Function, and Computational Analysis (BIBM-LncRNA)” (Trevi)  Workshop: “CBEAS-Computational Microbial Biofilm Engineering and Applications workshop” (Turin)</p>
<p><b>9-12:30pm Online Workshop</b> (no physical meeting rooms)</p>	<p>Workshop: “The 9<sup>th</sup> International Workshop on High Performance Computing on Bioinformatics”  Workshop: “Artificial Intelligence Techniques for BioMedicine and HealthCare”  Workshop: “Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics (MABM2022)”  Workshop: “The 3<sup>rd</sup> International Workshop on Machine Learning for EEG Signal Processing (MLESP 2022)”</p>	<p>“The 6<sup>th</sup> International Workshop on Deep Learning in Bioinformatics, Biomedicine, and Healthcare Informatics (DLB2H 2022)”</p>

10am-5pm	Poster Display (Augustus 5)	Poster Display (Augustus 5)
Lunch Break	Lunch (12:15pm – 2pm) Location: Augustus 6	Lunch (12:15pm-2pm) Funding Agency Panel (12-2pm) Location: Augustus 6
Afternoon Sessions I (2pm-3:30pm)	<p>Session 6: Cross-Cutting Computational Methods and Bioinformatics of Disease (3) (Emperors Ballroom I)</p> <p>Session 8: Biomedical and Health Informatics (1) (Emperors Ballroom II)</p> <p>Session 9: Biomedical and Health Informatics (2) (Messina)</p> <p>Session 10: Biomedical and Health Informatics (3) (Pisa)</p> <p>Workshop: “4<sup>th</sup> IEEE Workshop on High Performance Computing, Big Data Analytics, and Integration for Multi-Omics Biomedical Data (HPC-BOD)” (Palemo)</p> <p>Workshop: “Artificial Intelligence Techniques for BioMedicine and HealthCare” (Anzio)</p> <p>Workshop: “3rdAI&amp;BdvsPandemics (Artificial Intelligence &amp; Big Data vs Pandemics)” (Modena)</p> <p>Workshop: “Computational Structural Bioinformatics Workshop (CSBW)” (Neopolitan 2)</p> <p>Workshop: “Data mining from genomic variants and its application to genome-wide analysis 2022 (Data mining from genomic variants and its application to genome-wide analysis 2022)” (Livorno)</p>	<p>Workshop: “13<sup>th</sup> International Workshop on High Performance Bioinformatics and Biomedicine (HiBB-2022)” (Messina)</p> <p>Workshop: “3<sup>rd</sup> International Workshop on High Performance Computing Methods and Interdisciplinary Applications for Fighting the COVID-19 Pandemic (HPC4COVID-19)” + Workshop: “Foundations of Network Analysis” (Palermo)</p> <p>Workshop: “Computational methods to characterize genomic variants using high-throughput sequencing data” (Pisa)</p> <p>Workshop: “Sixth Edition of Workshop of Processes and Algorithms for Healthcare and Life Quality Improvement (CBPBL)” (Anzio)</p> <p>Workshop: “Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics (MABM2022)” (Modena)</p> <p>Workshop: “Workshop on Long Non-Coding RNAs: Mechanism, Function, and Computational Analysis (BIBM-LncRNA)” (Trevi)</p> <p>Workshop: “The 3<sup>rd</sup> RroBin Workshop: Reproducibility, Robustness and Validation in Biomedical Data Analysis (RroBin 2022)” (Emperors Ballroom II)</p> <p>Workshop: “CBEAS-Computational Microbial Biofilm Engineering and Applications workshop” (Turin)</p>

	Workshop: “Network Science and Artificial Intelligence for Biomedicine & Health informatics.” (Capri)	
Coffee Break (3:30-4:00pm)	Coffee	
Afternoon Sessions II (4pm-6pm)	<p>Session 4: Cross-Cutting Computational Methods and Bioinformatics of Disease (1) (Emperors Ballroom I)</p> <p>Session 11: Biomedical and Health Informatics (4) (Emperors Ballroom II)</p> <p>Session 12: Biomedical and Health Informatics (5) (Messina)</p> <p>Workshop: “4<sup>th</sup> IEEE Workshop on High Performance Computing, Big Data Analytics, and Integration for Multi-Omics Biomedical Data (HPC-BOD)” (Palemo)</p> <p>Workshop: “Artificial Intelligence Techniques for BioMedicine and HealthCare” (Anzio)</p> <p>Workshop: “3<sup>rd</sup>AI&amp;BdvsPandemics (Artificial Intelligence &amp; Big Data vs Pandemics)” (Modena)</p> <p>Workshop: “Computational Structural Bioinformatics Workshop (CSBW)” (Neopolitan 2)</p> <p>Workshop: “Data mining from genomic variants and its application to genome-wide analysis 2022 (Data mining from genomic variants and its application to genome-wide analysis 2022)” (Livorno)</p> <p>Workshop: “Network Science and Artificial Intelligence for Biomedicine &amp; Health informatics.” (Capri)</p>	<p>Workshop: “13<sup>th</sup> International Workshop on High Performance Bioinformatics and Biomedicine (HiBB-2022)” (Messina)</p> <p>Workshop: “3<sup>rd</sup> International Workshop on High Performance Computing Methods and Interdisciplinary Applications for Fighting the COVID-19 Pandemic (HPC4COVID-19)” + Workshop: “Foundations of Network Analysis” (Palermo)</p> <p>Workshop: “Sixth Edition of Workshop of Processes and Algorithms for Healthcare and Life Quality Improvement (CBPBL)” (Anzio)</p> <p>Workshop: “Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics (MABM2022)” (Modena)</p> <p>Workshop: “Workshop on Long Non-Coding RNAs: Mechanism, Function, and Computational Analysis (BIBM-LncRNA)” (Trevi)</p> <p>Workshop: “CBEAS-Computational Microbial Biofilm Engineering and Applications workshop” (Turin)</p>

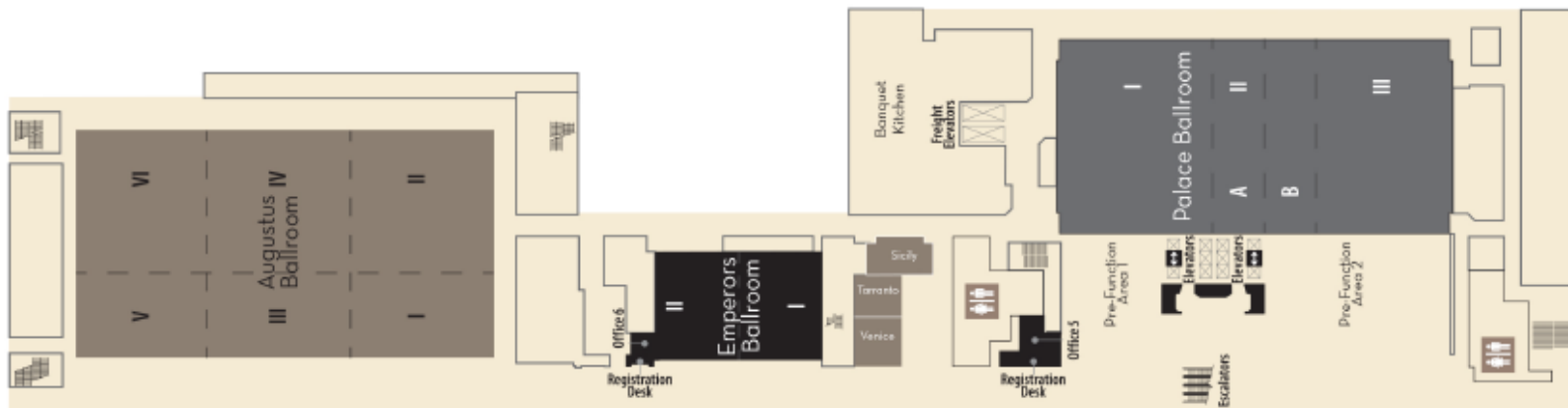
Afternoon Session Online 2-6pm	Workshop: "Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics (MABM2022)"	"The 6th International Workshop on Deep Learning in Bioinformatics, Biomedicine, and Healthcare Informatics (DLB2H 2022)"
Keynote Sessions (7:30- 8:30pm)	Keynote Talk: Dr. Amarda Shehu, <a href="mailto:ashehu@gmu.edu">ashehu@gmu.edu</a> Chair: Mindy Shi, <a href="mailto:mindyshi@temple.edu">mindyshi@temple.edu</a>  Location: Augustus 6	
	Banquet (7-9pm) Augustus 6	

## Wifi Information

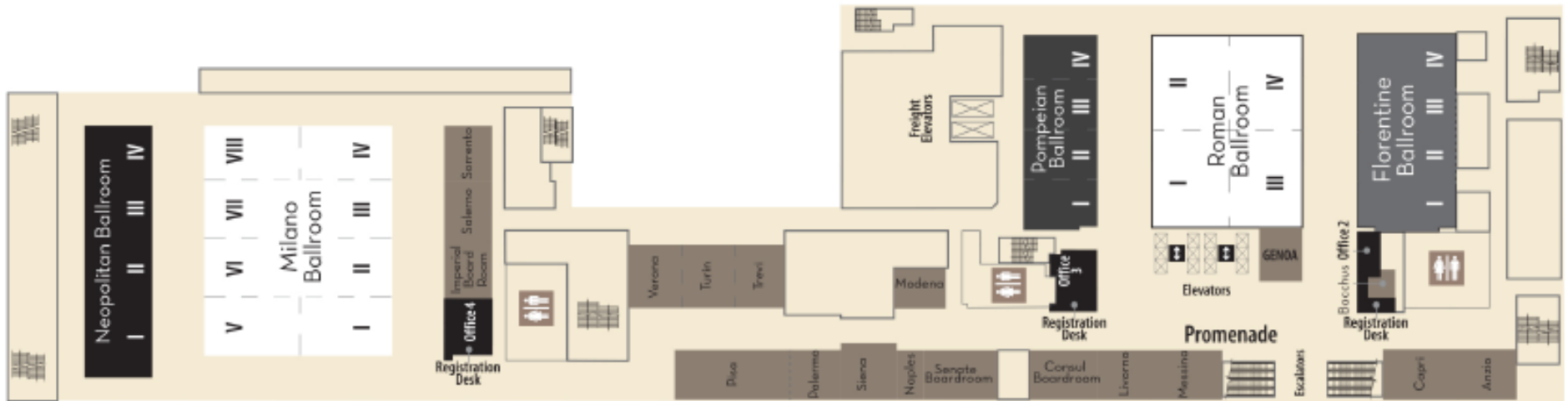
Network – IEEE Conference  
Password – BIBM2022

## Floor Plan

### EMPERORS LEVEL



## PROMENADE LEVEL



## December 6: Morning Sessions (10:30am-12:00pm)

### Session 1: Molecular Structure, Function and Evolution (1)

Chair: Dr. Jun-Tao Guo, University of North Carolina at Charlotte

Email: [jguo4@uncc.edu](mailto:jguo4@uncc.edu)

R	B450 "ST-ChIP: Accurate prediction of spatiotemporal ChIP-seq data with recurrent neural networks" Tong Liu and Zheng Wang
R	B733 "A NEW PHYLOGENY-DRIVEN RANDOM FOREST-BASED CLASSIFICATION APPROACH FOR FUNCTIONAL METAGENOMICS" Jyotsna Talreja Wassen, Haiying Wang, and Huiru Zheng
S	B730 "GCL-GO: A novel sequence-based hierarchy-aware method for protein function prediction" Kyudam Choi, Yurim Lee, and Cheongwon Kim
S	B937 "Protein-Protein Interaction Network Analysis Reveals Distinct Patterns of Antibiotic Resistance Genes" Nazifa Ahmed Mousi, Connor Brown, Peter Vikesland, Amy Pruden, and Liqing Zhang
S	B983 "The Combined Focal Cross Entropy and Dice Loss Function for Segmentation of Protein Secondary Structures from Cryo-EM 3D Density maps" Yongcheng Mu, Jiangwen Sun, and Jing He

### Session 2: Computational and Systems Biology; Cheminformatics and pharmacogenomics (1)

Chair: Dr. Tony Hu, Drexel University

Email: [xh29@drexel.edu](mailto:xh29@drexel.edu)

R	B878 "Multi-View Brain Network Analysis with Cross-View Missing Network Generation" Gongxu Luo, Chenyang Li, Hejie Cui, Lichao Sun, Lifang He, and Carl Yang
S	B383 "MicroCellClust 2: a hybrid approach for multivariate rare cell mining in large-scale single-cell data" Alexander Gerniers and Pierre Dupont
S	B877 "Computational learning of small RNA regulation in pancreatic cancer progression" Roland Madadjim and Juan Cui
R	B461 "Molecular Property Prediction based on Bimodal Supervised Contrastive Learning" Yan Sun, Mohaiminul Islam, Ehsan Zahedi, M'elaine Kuenemann, Hassan Chou, and Pingzhao Hu
R	B516 "PandoraRL: DQN and Graph Convolution based ligand pose learning for SARS-COV1 Mprotease" Justin Jose, Ujjaini Alam, Divye Singh, Nidhi Jatana, and Pooja Arora
R	B604 "MoleHD: Efficient Drug Discovery using Brain Inspired Hyperdimensional Computing" Dongning Ma, Rahul Thapa, and Xun Jiao

### Session 3: Next Generation Sequencing and High-throughput Methods (1)

Chair: Dr. Xuan Guo, University of North Texas

Email: [xuan.guo@unt.edu](mailto:xuan.guo@unt.edu)

R	B900 "ranscriptomics" Carlos Soto, Darshan Bryner, Audrey Dalgarno, Nicola Neretti, and Anuj Srivastava
S	B407 "SNEP-DB: An integrated database to associate genomic and pathological aspects of psychiatric disorders" Ohhyeon Kwon, Maree J Webster, Sanghyeon Kim, and Doheon Lee
S	B721 "Analysis of correlative radiomic signatures with genetic intratumoral heterogeneity in breast cancer" Jiyun Hong, Ga Ram Kim, You Jin Ku, Eunwoo Choi, Young Han Lee, and Sangwoo Kim
S	B931 "IDIA: An Integrative Signal Extractor for Data-Independent Acquisition Proteomics" Jiancheng Li, Chongle Pan, and Xuan Guo
S	B945 "FineFDR: Fine-grained Taxonomy-specific False Discovery Rates Control in Metaproteomics" Shengze Wang, Shichao Feng, Chongle Pan, and Xuan Guo



Session 5: Cross-Cutting Computational Methods and Bioinformatics of Disease (2)

Chair: Dr. Shaolei Teng, Howard University

Email: [shaolei.teng@howard.edu](mailto:shaolei.teng@howard.edu)

R	B610 "Patient Similarity Learning with Selective Forgetting" Wei Qian, Chenxu Zhao, Huajie Shao, Minghan Chen, Fei Wang, and Mengdi Huai
R	B870 "Preference Matrix Guided Sparse Canonical Correlation Analysis for Genetic Study of Quantitative Traits in Alzheimer's Disease" Jiahang Sha, Jingxuan Bao, Kefei Liu, Shu Yang, Zixuan Wen, Yuhan Cui, Junhao Wen, Christos Davatzikos, Jason Moore, Andrew Saykin, Qi Long, and Li Shen
S	B400 "Gene expression-based classification of benign and malignant canine mammary tumors" In Seok Yang, Byung-Joon Seung, Yoo-Jin Ha, Jung-Hyang Sur, and Sangwoo Kim
S	B607 "ReactClass: Cross-Modal Supervision for Subword-Guided Reactant Entity Classification" Xuan Wang, Vivian Hu, Minhao Jiang, Yu Zhang, Jinfeng Xiao, Danielle Loving, Heng Ji, Martin Burke, and Jiawei Han
S	B614 "Cost-effective Vaccine Provisioning using Coalitional Game Theory" Satyaki Roy, Ahmad Al Musawi, and Preetam Ghosh

December 6: Afternoon Sessions I (2pm-3:30pm)

Session 6: Cross-Cutting Computational Methods and Bioinformatics of Disease (3)

Chair: Dr. Zhiyu Wan, Vanderbilt University Medical Center

Email: [zhiyu.wan.1@vumc.org](mailto:zhiyu.wan.1@vumc.org)

R	B883 "Tensor-Based Multi-Modal Multi-Target Regression for Alzheimer's Disease Prediction" Jun Yu, Benjamin Zalatan, Yong Chen, Li Shen, and Lifang He
S	B853 "KANALYZER: an accurate and rapid method to identify discriminative k-mer variations in genomic sequences" Dylan Lebatteux, Hugo Soudeyans, Isabelle Boucoiran, Soren Gantt, and Abdoulaye Baniré Diallo
S	B891 "Bi-directional Ranking of Forward and Reverse Strand Suffixes with Application to Memory Efficient Reference Genome Indexing" Arghya Kusum Das, Oguzhan Kulekci, and Sharma Thankachan
S	B899 "Information retrieval in single cell chromatin analysis using TF-IDF transformation methods" Mehrdad Zandigohar and Yang Dai
S	B946 "Robust identification of critical states and temporal tissue-specific biomarkers during disease development through ensemble learning and analysis" Qiong Cheng

Session 8: Biomedical and Health Informatics (1)

Chair: Dr. Alejandro Martin-Gomez, Johns Hopkins University

Email: [alejandro.martin@jhu.edu](mailto:alejandro.martin@jhu.edu)

R	B612 "Causal Discovery in Biological Data Using Directed Topological Overlap Matrix" Borzou Alipourfard and Jean Gao
R	B618 "AccSleepNet: An Axis-Aware Hybrid Deep Fusion Model for Sleep Stage Classification Using Wrist-Worn Accelerometer Data" Guanjie Huang, Ye Yuan, Guohong Cao, and Fenglong Ma
R	B638 "KIT-LSTM: Knowledge-guided Time-aware LSTM for Continuous Clinical Risk Prediction" Lucas Jing Liu, Victor Ortiz-Soriano, Javier A. Neyra, and Jin Chen

S	B388 "Multimodal Analysis Uncovers Links between Grey Matter Volume and both Low- and High-frequency Dynamic Connectivity States in Schizophrenia" Marlena Duda, Ashkan Faghiri, and Vince Calhoun
S	B436 "Evaluation of sparsity metrics and evolutionary algorithms applied for normalization of H&E histological images" Thaína Tosta, Paulo de Faria, Leandro Neves, Alessandro Martins, Chetna Kaushal, and Marcelo do Nascimento

Session 9: Biomedical and Health Informatics (2)

Chair: Dr. Donald Adjero, West Virginia University

Email: [donald.adjero@mail.wvu.edu](mailto:donald.adjero@mail.wvu.edu)

R	B526 "Document-level DDI relation extraction with document-entity embedding" Mingliang Dou, Jijun Tang, and Fei Guo
R	B653 "PolaViz Reveals Microglia Polarization at Single Cell Level in Alzheimer's Disease" Chenyu Zhang and Dong-Guk Shin
R	B738 "Hierarchical Categorical Generative Modeling for Multi-omics Cancer Subtyping" Ziwei Yang, Lingwei Zhu, Chen Li, Zheng Chen, Naoki Ono, MD Altaf-Ul-Amin, and Shigehiko Kanaya
S	B463 "Region Extraction with Deep Cascaded Neural Architecture for Preserving Image Intensities" Muhammad Zubair Khan and Yugyung Lee
S	B574 "Evaluation of personalized treatment goals on engagement of SMI patients with an mHealth app" Lorenzo James, Jordi van Heugten, Pieter Van Gorp, Raoul Nuijten, Barbara Montagne, Muriel Hagenaars, and Lily Frank

Session 10: Biomedical and Health Informatics (3)

Chair: Dr. Mihail Popescu, University of Missouri

Email: [popescum@missouri.edu](mailto:popescum@missouri.edu)

R	B759 "Automatic Sleep Staging via Frequency-Wise Spiking Neural Networks" Haohui Jia, Ziwei Yang, Pei Gao, Man Wu, Chen Li, Yirong Kan, and Renyuan Zhang
R	B813 "Consistency of Graph Theoretical Measurements of Alzheimer's Disease Fiber Density Connectomes Across Multiple Parcellation Scales" Frederick Xu, Sumita Garai, Duy Duong-Tran, Andrew Saykin, Yize Zhao, and Li Shen
R	B855 "AUTOMED: Automated Medical Risk Predictive Modeling on Electronic Health Records" Suhan Cui, Jiaqi Wang, Xinning Gui, Ting Wang, and Fenglong Ma
S	B603 "Beat-by-Beat Classification of ECG Signals Using Machine Learning Algorithms to Detect PVC Beats for Real-time Predictive Cardiac Health Monitoring" I Hua Tsai and Bashir Morshed
S	B649 "MedAttacker: Exploring Black-Box Adversarial Attacks on Risk Prediction Models in Healthcare" Muchao Ye, Junyu Luo, Guanjie Zheng, Cao Xiao, Houping Xiao, Ting Wang, and Fenglong Ma

December 6: Afternoon Sessions II (4pm-6pm)

Session 4: Cross-Cutting Computational Methods and Bioinformatics of Disease (1)

Chair: Dr. Mindy Shi, Temple University

Email: [mindyshi@temple.edu](mailto:mindyshi@temple.edu)

R	B277 "LDAGSO: Predicting lncRNA-Disease Associations from Graph Sequences and Disease Ontology via Deep Learning techniques" Norah Saeed Awn, Yiming Li, Baoying Zhao, Min Zeng, and Min Li
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R	B343 "Predicting Lymph Node Metastasis and Distant Metastasis using Differential Correlations of miRNAs and Their Target RNAs in Cancer" Seokwoo Lee, Myounghoon Cho, Wook Lee, Byungkyu Park, and Kyungsook Han
S	B325 "Positive Feature Values Prioritized Hierarchical Dependency Constrained Averaged One-dependence Estimators for Gene Ontology Feature Spaces" Cen Wan
S	B354 "Improving the Timeliness of Early Prediction Models for Sepsis through Utility Optimization" Anastasios Lamproudis, Aron Henriksson, John Karlsson Valik, and Pontus Naucner
S	B387 "An agent-based multi-level model to study the spread of antimicrobial-resistant gonorrhoea" Paola Stolfi, Davide Vergni, Rik Oldenkamp, Constance Schultz, Emiliano Mancini, and Filippo Castiglione
S	B389 "Machine Learning Algorithms in Gene Editing" Kaluad Sanyour and Wooyoung Kim

#### Session 11: Biomedical and Health Informatics (4)

Chair: Dr. Nansu Zong, Mayo Clinic

Email: [Zong.Nansu@mayo.edu](mailto:Zong.Nansu@mayo.edu)

R	B247 "Explainability-guided Mathematical Model-Based Segmentation of Transrectal Ultrasound Images for Prostate Brachytherapy" Tao Peng, Yiyun Wu, Jing Zhao, Bo Zhang, Jin Wang, and Jing Cai
R	B295 "End-to-End Deep Learning for Stress Recognition Using Remote Photoplethysmography" Kai Zhou, Markus Schinle, Sascha Weimar, Marius Gerdes, Simon Stock, and Wilhelm Stork
S	B231 "An Embedded Machine Learning Model for Early Detection and Intervention of High-Risk Intensive Care Unit Readmission Patients" Lu He, Haifeng Wang, Mandana Rezaeiahari, and Chun-An Chou
S	B238 "Development of an EEG-based Brain-Controlled System for a Virtual Prosthetic Hand" Neil Joshua Limbaga, Kevin Luis Mallari, Nathan Richward Yeung, and Jose Claro Monje
S	B251 "Federated Learning for Chronic Obstructive Pulmonary Disease Classification with Partial Personalized Attention Mechanism" Yiqing Shen, Baiyun Liu, Ruize Yu, Yudong Wang, Shaokang Wang, Jiangfen Wu, and Weidao Chen
S	B372 "Machine Learning Algorithm to Predict Cardiac Output Using Arterial Pressure Waveform Analysis" Ke Liao, Armagan Elibol, Wei Xiao, Cenyu Liao, Wei Wang, and Nak Young Chong

#### Session 12: Biomedical and Health Informatics (5)

Chair: Dr. Huiru (Jane) Zheng, Ulster University

Email: [h.zheng@ulster.ac.uk](mailto:h.zheng@ulster.ac.uk)

R	B874 "Weakly Unpaired Image Translation from Hematoxylin and Eosin Staining Image to Immunohistochemistry Staining Image" Kuan Huang, Yifei Cheng, Qiang Gao, and Bing Zhang
R	B884 "Using Optimal Transport to Improve Spherical Harmonic Quantification of Complex Biological Shapes" Zexuan Wang, Wenxi Yang, Katharine Ryan, Sumita Garai, Benjamin Auerbach, and Li Shen
R	B907 "Individualized seizure cluster prediction using machine learning and ambulatory intracranial EEG" Krishnakant Saboo, Yurui Cao, Vaclav Kremen, Vladimir Sladky, Nicholas Gregg, Paul Arnold, Philippa Karoly, Dean Freestone, Mark Cook, Gregory Worrell, and Ravishankar Iyer

S	B887 "ExG signal feature selection using hyperdimensional computing encoding" Una Pale, Tomas Teijeiro, and David Atienza
S	B889 "Local Naïve Bayes for Predicting Evolution of COVID-19 Patients on Self Organizing Maps" Carlos Arias-Alcaide, Cristina Soguero-Ruiz, Paloma Santos-Alvarez, José Felipe Varona Arche, and Inmaculada Mora-Jiménez
S	B905 "Subpopulation Analysis in Causal Inference: A Healthcare Case Study" Georgios Mavroudeas, Nafis Neehal, Jason Kuruzovich, Kristin P. Bennett, and Malik Magdon-Ismail

## December 7: Morning Sessions (10:30am-11:30am)

Session 7: Cross-Cutting Computational Methods and Bioinformatics of Disease (4)

Chair: Dr. Daniele Pala, University of Pennsylvania

Email: [daniele.pala@penntmedicine.upenn.edu](mailto:daniele.pala@penntmedicine.upenn.edu)

R	B950 "Cell-type Deconvolution and Age Estimation Using DNA Methylation Reveals NK Cell Deficiency in the Hepatocellular Carcinoma Microenvironment" Sidharth Jain, Megan Barefoot, Rency Varghese, and Habtom Ressim
S	B953 "A Data-Driven Approach for the Analysis of Behavioral Disorders With a Focus on Classification and Severity Estimation" RAMA KRISHNA THELAGATHOTI and Hesham H. ALI
S	B990 "OCT-guided Robotic Subretinal Needle Injections: A Deep Learning-Based Registration Approach" Kristina Mach, Shuwen Wei, Ji Woong Kim, Alejandro Martin-Gomez, Peiyao Zhang, Jin U. Kang, Ali Nasser, Peter Gehlbach, Nassir Navab, and Iulian Iordachita
S	B994 "A Multi-Omics Classifier For Prediction Of Treatment Response In Prostate Cancer Patients" Itunuoluwa Isewon, Emmanuel Alagbe, Jelili Oyelade, and Solomon Rotimi
S	B1049 "A continuous glucose monitoring measurements forecasting approach via sporadic blood glucose monitoring" Yuting Xing, Hangting Ye, Xiaoyu Zhang, Wei Cao, Shun Zheng, Jiang Bian, and Yike Guo

Session 13: Biomedical and Health Informatics (6)

Chair: Dr. Margaret Varga, University of Oxford

Email: [margaret.varga@biology.ox.ac.uk](mailto:margaret.varga@biology.ox.ac.uk)

R	B865 "Deep Learning Based Parametrization of Diffeomorphic Image Registration for the Application of Cardiac Image Segmentation" Amenah Sheikhjafari, Deepa Krishnaswamy, Michelle Noga, Nilanjan Ray, and Kumaradevan Punithakumar
R	B375 "MHSnet: Multi-head and Spatial Attention Network with False-Positive Reduction for Lung Nodule Detection", Juanyun Mai, Minghao Wang, Jiayin Zheng, Yanbo Shao, Zhaoqi Diao, Xinliang Fu, Yulong Chen, Jianyu Xiao, Jian You, Airu Yin, Yang Yang, Xiangcheng Qiu, Jinsheng Tao, Bo Wang, and Hua Ji
S	B665 "OSA-CCNN: Obstructive Sleep Apnea Detection Based on a Composite Deep Convolution Neural Network Model using Single-Lead ECG signal" Yu Zhou, Yinxian He, and Kyungtae Kang
S	B673 "A Deep Active Learning Framework with Information Guided Label Generation for Medical Image Segmentation" Kuan Huang, Jianhua Huang, Weichen Wang, Meng Xu, and Feifei Liu

S	B873 "UDA-CT: A General Framework for CT Image Standardization" Md Selim, Jie Zhang, Baowei Fei, Matthew Lewis, Guo-Qiang Zhang, and Jin Chen
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Session 14: Biomedical and Health Informatics (7)

Chair: Dr. Jiangwen Sun, Old Dominion University

Email: [jsun@odu.edu](mailto:jsun@odu.edu)

R	B926 "A Latent Space Model for HLA Compatibility Networks in Kidney Transplantation" Zhipeng Huang and Kevin Xu
R	B1020 "Unsupervised extraction, labelling and clustering of segments from clinical notes" Petr Zelina, Jana Halámková, and Vít Nováček
S	B913 "Unsupervised Feature Clustering Improves Contrastive Representation Learning for Medical Image Segmentation" Yejia Zhang, Xinrong Hu, Nishchal Sapkota, Yiyu Shi, and Danny Chen
S	B924 "Highly Scalable Task Grouping for Deep Multi-Task Learning in Prediction of Epigenetic Events" Mohammad Shiri and Jiangwen Sun

Session 15: Biomedical and Health Informatics (8)

Chair: Golrokh Mirzaei, Ohio State University

Email: [mirzaei.4@osu.edu](mailto:mirzaei.4@osu.edu)

R	B1040 "Privacy-Preserving Publishing of Individual-Level Pandemic Data Based on a Game Theoretic Model" Abinitha Gourabathina, Zhiyu Wan, James Brown, Chao Yan, and Bradley Malin
S	B943 "Keep Your Friends Close & Enemies Closer: Debiasing Contrastive Learning with Spatial Priors in 3D Radiology Images" Yejia Zhang, Pengfei Gu, Nishchal Sapkota, Yaopeng Peng, Hao Zheng, and Danny Chen
S	B998 "Peripheral Arterial Stiffness Response to Heptanal Odor and its Relation to Subjective Evaluation" Songzhi Chen, Zu Soh, Takafumi Sasaoka, Yuu Minematsu, Hikaru Momose, Takahiide Nozawa, and Toshio Tsuji
S	B1046 "Deep learning-based restraining of histopathological images" Ozdemir Cetin, Mingzhi Chen, Paul Ziegler, Peter Wild, and Heinz Koepl

## **Workshop Program Schedule**

## Network Science and Artificial Intelligence for Biomedicine & Health Informatics

*Workshop Chair:: Pietro Hiram Guzzi, Manuela Petti, Swarup Roy, Paolo Tieri*

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Time	Title	Presenter/Author
8.30-8.40	<b>Opening remarks</b>	
8.40-9.00	S01202 Clique Network-Based Statistics for Detecting Altered Topological Structures in the Brain Network	Ziliang Zhang, Yunxiang Ge, and Weibei Dou
9.00-9.20	S01207 DruSiLa: An integrated disease similarity-based approach for drug repurposing	Pratuat Amatya, Paola Stolfi, Flavio Lombardi, and Paolo Tieri
9.20-9.40	S01206 K-Mer Fingerprinting with RNN to predict MICs for <i>K. pneumoniae</i>	Cory Kromer-Edwards, Mariana Castanheira, and Suely Oliveira
9.40-10.00	S01208 Heterogeneous Graph Sparsification for Efficient Representation Learning	Chandan Chunduru, Chunjiang Zhu, Blake Gaines, and Jinbo Bi
10.00-10.30	<b>Coffee Break</b>	
10.30-10.50	B324 Single-Cell Topological Simplicial Analysis Reveals Higher-Order Cellular Complexity	Baihan Lin
10.50-11.10	S01211 Differential co-expression network analysis to investigate sexual dimorphism in colon cancer	Caterina Alfano, Lorenzo Farina, and Manuela Petti
11.10-11.30	B848 Arrhythmia Classification Using CGAN-Augmented ECG Signals	Edmond Adib, Fatemeh Afghah, and John J. Prevost
11.30-11.50	B918 Network based Identification of Dementia Onsets Using Structural MRI Signatures	Abdulyekeen Adebisi, Venkateswarlu Gonuguntla, Ho-Won Lee, Myong-Hun Hahm, and Kalyana Veluvolu
11.50-12.10	S01210 A novel framework based on network embedding for the simulation and analysis of disease progression	Francesco Chiodo, Mario Torchia, Enza Messina, Elisabetta Fersini, Tommaso Mazza, and Pietro Hiram Guzzi
12.10-12.30	B1011 Private Federated Framework for Health Data	Tanzir Ul Islam, Noman Mohammed, and Dima Alhadidi
12.30-14.00	<b>Lunch break</b>	
14.00-14.20	S01205 PROCONSUL: PRObabilistic exploration of CONnectivity Significance patterns for disease modULe discovery	Riccardo De Luca, Marco Carfora, Gonzalo Blanco, Andrea Mastropietro, Manuela Petti, and Paolo Tieri
14.20-14.40	S01214 Effective Subject Representation based on Multi-omics Disease Networks using Graph Embedding	Sundous Hussein, Thao Vu, Katerina Kechis, Russel Bowler, Leslie Lange, and Farnoush Banaei-Kashani
14.40-15.00	S01203 ClassAphasia: An Ensemble Machine Learning Network to Improve Aphasia Diagnosis and Determine Severity	Jagadeepam Maddipatla
15.00-15.20	B415 A Novel Joint Drug-drug Interaction Relationship Extraction Framework based on Implicit Relationships and Entity Alignment	Biao Duan, Jing Peng, and Yi Zhang
15.30-16.00	<b>Coffee Break</b>	
16.00-16.20	B842 A knowledge graph embedding-based method for predicting the synergistic effects of drug combinations	Peng Zhang and Shikui Tu,
16.20-16.40	B952 GraMDTA: Multimodal Graph Neural Networks for Predicting Drug-Target Associations	Jaswanth Yella, Sudhir Ghandikota, and Anil Jegga
16.40-17.00	B972 Effective Subjects Representation based on Multi-omics Disease Networks Using Graph Embeddings	Sundous Hussein, Thao Vu, Katerina Kechris, Russell Bowler, Leslie Lange, and Farnoush Banaei-Kashani,
17.00-17.20	S01204 NOMA-DB: a framework for management and analysis of ageing-related gene-expression data	Pietro Hiram Guzzi, Ugo Lomoio, Rocco Scicchitano, and Pierangelo Veltri,
17.20-17.40	S01213 Identification of cancer biomarkers for multi-class diagnostics through machine learning and network analysis applied to RNAseq data of Tumor-Educated Platelets	Ali Toccaceli and Manuela Petti
17.40-18.00	B230 A Gene Similarity Algorithm Based on Autocorrelation of Diseases and Phenotypes	Jinlian Du, Xiaolin Du, and Hang Su

18.00-18.15	<b>Closing Remarks</b>
19.00-21.00	<b>Banquet</b>

<b>The 3<sup>rd</sup> International Workshop on Machine Learning for EEG Signal Processing (MLESP 2022)</b> December 6 <sup>th</sup> , 2022 (9am – 1pm) <i>Workshop Chair: Larbi Boubchir, larbi.boubchir@univ-paris8.fr</i>		
<b>Time</b>	<b>Title</b>	<b>Presenter/Authors</b>
<b>8:50-9:00</b>	<b>Opening Workshop</b>	
<b>9:00-9:20</b>	<b>S02203:</b> A Framework to Evaluate Independent Component Analysis applied to EEG signal: testing on the Picard algorithm	Gwenevere Frank, Scott Makeig, and Arnaud Delorme
<b>9:20-9:40</b>	<b>S02201:</b> Electroencephalography-Neurofeedback for Decoding and Modulating Human Emotions	Sara Alzahmi, Bashayer Alyammahi, Maitha Alyammahi, Mariam Alshamsi, and Abdelkader Belkacem
<b>9:40-10:00</b>	<b>S02202:</b> Secure Password Using EEG-based Brain Print System: Unlock Smartphone Password Using Brain-Computer Interface Technology	Mazna Alhemeiri, Abdelkader Belkacem, Zuwaina Alkhyeli, Ayesha Alshehhi, Khalil AlBalushi, Salma Aldhanhani, and Fatima AlNuaimi
<b>10:00-10:20</b>	<b>S02208:</b> Prediction Models for Epilepsy Detection on the EEG Signal	Dalila Cherifi, Hichem Zenati, Mohamed Amine Ouchene, Mohammed Abdenacer Merbouti, Dyhia Ibrahim et al.
<b>10:20-10:40</b>	<b>S02204:</b> Electroencephalogram Emotion Recognition Based on Individual Frontal Asymmetry Hypothesis	Gang Cao, Liying Yang, and Pei Ni
<b>10:40-11:00</b>	<b>S02206:</b> Markov Guided Spatio-Temporal Networks for Brain Image Classification	Yupei Zhang, Yunan Xu, Rui An, Yuxin Li, Shuhui Liu, and Xuequn Shang
<b>11:00-11:20</b>	<b>S02207:</b> A Multi-stream Deep Learning Model for EEG-based Depression Identification	Hao Wu and Jiyao Liu
<b>11:20-11:40</b>	<b>S02211:</b> CR-GAT: Consistency Regularization Enhanced Graph Attention Network for Semi-supervised EEG Emotion Recognition	Jiyao Liu, Hao Wu, and Li Zhang
<b>11:40-12:00</b>	<b>S02212:</b> REEG-BTCNet: A Novel Framework for EEG-based Motor Imagery Classification	Jiyao Liu and Huifu Li
<b>12:00-12:20</b>	<b>B503:</b> A Multidimensional Feature Extraction Method Based on MSTBN and EEMD-WPT for Emotion Recognition from EEG Signals	Shilin Zhang and Qingchen Zhang
<b>12:42-12:40</b>	<b>B699:</b> Multimodal Emotion Recognition from EEG and Facial Expressions	Yong Zhang, Shuai Wang, and Yidie Zhang



12:40-13:00	Closing Remarks
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\* The workshop schedule is based on Pacific Standard Time.

<b>13<sup>th</sup> International Workshop on High Performance Bioinformatics and Biomedicine (HiBB-2022)</b> <i>Workshop Chairs: <u>Mario Cannataro, Giuseppe Agapito, Marianna Milano</u></i> <i>Thursday, December 7, 2022</i> <b>The workshop schedule is based on USA PST Time</b> <b>Room: Messina</b>		
Time	High Performance Bioinformatics and Biomedicine (HiBB-2022)	Presenter/Author
2:00pm-2:20pm	<b>S04201</b> Predicting LncRNA-Disease Associations Based on LncRNA-MiRNA-Disease Multilayer Association Network and Bipartite Network Recommendation	Guo-Zheng Zhang, Shu-Zhen Li, Xu-Ran Dou, Junliang Shang, Qian-Qian Ren, and Ying-Lian Gao,
2:20pm-2:40pm	<b>S04205</b> Serverless computing for RNA-Seq data analysis	Pietro Cinaglia, José Luis Vazquez-Poletti, and Mario Cannataro
2:40pm-3:00pm	<b>S04203</b> A Review of Deep Learning Methods for Multi-omics Integration in Precision Medicine	Shaza Zaghlool and Omneya Attallah
3:00pm-3:20pm	<b>S04204</b> Understanding Performance Portability of Bioinformatics Applications in SYCL on an NVIDIA GPU	Zheming Jin, Jeffrey S. Vetter
3:20pm-3:40pm	<b>S04206</b> A Machine-Learning Approach for Predicting Depression Through Demographic and Socioeconomic Features	Joseph Sun, Rory Liao, Mikhail Shalaginov, and Tingying Helen Zeng
<b>Coffee Break</b>	<b>Coffee Break (3:40pm-4:00pm)</b>	
4:00pm-4:20pm	<b>S04207</b> Edge-based Deep Learning in Medicine: Classification of ECG signals	Luca Barillaro, Giuseppe Agapito, and Mario Cannataro
4:20pm-4:40pm	<b>B497</b> Domain Adaptation for Medical Image Classification without Source Data	Chuan Zhou, Wei Zhang, Hang Chen, and Leiting Chen
4.40pm-5.00pm	<b>B510</b> Few-shot Learning Framework Based on Adaptive Subspace for Skin Disease Classification	Chuan Zhou, Mengqi Sun, Leiting Chen, Anping Cai, and Jiahao Fang
5:00pm-5:20pm	<b>B1015</b> A Feature Weighted Tracking Method for 3D Neutrophils in Time lapse Microscopy	Chen Li, Wilson Yiu, Wanbin Hu, Lu Cao, and Fons Verbeek
5:20pm-5:40pm	<b>B1047</b> Approximate Minimum Homology Basis for 3D Image and Its Application in Medical Image Segmentation	Jisui Huang, Na Lei, Ke Chen, Yuxue Ren, Zhenchang Wang, and Yuanyuan Shang
5.40pm-6.00pm	<b>B396</b> Automatic Detection of Fractionation in the QRS-Complex and its Effects on All-cause Mortality and Ischemic Heart Disease	Patrick Liston, Andreas Ellegaard, Kirstine Banke, and Emma Bertelsen
6:00pm-6:20pm	<b>B499</b> A Multimodal Attention-Based Framework for Accurate and Interpretable Health Risk Prediction	Yuxi Liu, Richard Leibbrandt, Campbell Thompson, and Shaowen Qin
	<b>Closing Remarks</b>	

**3<sup>rd</sup> International Workshop on High Performance Computing Methods and Interdisciplinary Applications for Fighting the COVID-19 Pandemic (HPC4COVID-19)**

*Workshop Chairs: Mario Cannataro, Giuseppe Agapito, Mauro Castelli,  
Riccardo Dondi, Rodrigo Weber dos Santos, Italo Francesco Zoppis*

*held jointly with*

**1st International Workshop on Foundation of Network Analysis**

*Workshop Chairs: Marianna Milano and Giuseppe Agapito*

*Thursday, December 7, 2022*

*The workshop schedule is based on USA PST Time*

*Room: Palermo*

Time	High Performance Computing Methods and Interdisciplinary Applications for Fighting the COVID-19 Pandemic	Presenter/Author
9:00am-9:20am	<b>S05201</b> Identifying Variability in U.S. COVID-19 Response Through Temporal Partial Ordering Detection	Jon Rogers, Ramazan Aygun, and Letha Etzkorn
9:20am-9:40am	<b>S05204</b> COVID-19 Impact on Mental Health Analysis based on Reddit Comments	Justin Chen, Kevin Qi, Aaron Zhang, Mikhail Shalaginov, and Tingying Helen Zeng
9:40am-10:00am	<b>S05202</b> S-PDB: Analysis and Classification of SARS-CoV-2 Spike Protein Structures	M. Saqib Nawaz, Philippe Fournier-Viger, and Yulin He
<b>Coffee Break</b>	<b>Coffee Break (10-00:30am)</b>	
10:30am-10:50am	<b>B318</b> KEP-1.0: An Automatic Pipeline to Assist a Rapid Learning of COVID-19 Publications	Jingyi Shi, Ghodsieh Ghanbari, and Chao Xia
10:50am-11:10am	<b>B704</b> Multi-MedVit: a deep learning approach for the diagnosis of COVID-19 with the CT images	Yunjie Cai, Zeqi Zheng, Shanling Nie, Yue Guo, Ruijie Zhang, and Hai Yang
11:10am-11:30am	<b>B755</b> An Improved COVID-19 Segmentation Model Based on Mask R-CNN	Hui Ding, Rui Liu, Junwei Cai, Xin Li, and Yuanyuan Shang
11:30am-11:50am	<b>B973</b> Identification of potential inhibitors of severe acute respiratory syndrome coronavirus 2 envelope protein ion channel activity using machine learning techniques	Wency Suo and Xikun Liu
11:50am-12:10am	<b>B1024</b> TLU-Net: Transfer Learning Framework using U-Net Convolutional Neural Networks for CT-based Lungs and COVID-19 Segmentation	Ahmed Albishri, Syed Jawad Hussain Shah, and Yugyung Lee
	<b>Concluding Remarks</b>	
<b>Lunch Break</b>	<b>Lunch (12:30-2pm)</b>	
Time	Foundation of Network Analysis	Presenter/Author
2:00pm-2:20pm	<b>B1041</b> Alignment of Dynamic Networks based on Temporal Embeddings	Pietro Cinaglia and Mario Cannataro
2:20pm-2:40pm	<b>S11201</b> TC-6mA-Pred: Prediction of DNA N6-methyladenine sites using CNN with transformer	Zeeshan Abbas, Mobeen Ur Rehman, and Kil To Chong
2:40pm-3:00pm	<b>S11203</b> Checking for non-Euclidean latent geometry of biological networks	Paola Lecca and Angela Re
3:00pm-3:20pm	<b>S11202</b> Identification of Human RNA m5C sites using CapsuleNet Architecture	Mobeen Ur Rehman, Zeeshan Abbas, and Kil To Chong
3:20pm-3:40pm	<b>S11204</b> Computing Minimal Models Networks of Gene Regulatory Networks	Guy Karlebach and Peter N Robinson
	<b>Closing Remarks</b>	
<b>Coffee Break</b>	<b>Coffee Break (3:40pm-4:00pm)</b>	

## 4th IEEE Workshop on High Performance Computing, Big Data Analytics, and Integration for Multi-Omics Biomedical Data (HPC-BOD 2022)

*Workshop Chairs: Fahad Saeed (FIU), Serdar Bozdag (UNT)*

*fsaeed@fiu.edu, Serdar.Bozdag@unt.edu*

Time	Title	Presenter/Author
2:00 pm – 2:10 pm	<b>Opening Remarks - Fahad Saeed</b>	
2:10 pm – 2:30pm	S08203 - Comprehensive analysis of gene expression profiles to radiation exposure reveals molecular signatures of low-dose radiation response	Xihaier Luo, Sean McCorkle, Gilchan Park, Vanessa Lopez-Marrero, Shinjae Yoo, Edward Dougherty, Xiaoning Qian, Francis Alexander, and Byung-Jun Yoon
2:30 pm – 2:50pm	B600 - Shallow Sparse Autoencoder Based Epileptic Seizure Prediction	Gul Hameed Khan, Nadeem Ahmad Khan, Muhammad Awais Bin Altaf
2:50 pm – 3:10 pm	S08201 - Identification of Cross-feeding Metabolism Reveals Oral-Microbiome Modulated Host Behavior	Suganya Chandrababu and Dhundy Bastola
3:10 pm – 3:30 pm	B834 - Crescent: A GPU-based Targeted Nanopore Sequence Selector	Tong Li, Xueqi Li, Yewen Li, Ruibao Song, and Xun Wang
3:30 pm – 4:00 pm	<b>Coffee Break</b>	
4:00 pm – 4:20 pm	S08205 - Comparison of deep and shallow graph representation learning algorithms for detecting modules in molecular networks	Zhiwei Song, Brittany Baur, and Sushmita Roy
4:20 pm – 4:40 pm	B915 - Personalized Semantic Annotation Recommendations on Biomedical Content through an Expanded Socio-technical Approach	Asim Abbas, Nadeem Iqbal, and Syed Ahmad Chan Bukhari
4:40 pm – 5:00 pm	B506 - PNF: a novel method based on connectivity and similarity for data integration and cancer subtyping	Shihao Zhang, Fenghui Liu, Feng Wang, Lin Qi, and Yun Tie
5:00 pm – 5:20 pm	S08207 - Deep Learning Based MS2 Feature Detection for Data-independent Shotgun Proteomics	Jonathan He, Olivia Liu, and Xuan Guo
5:20 pm – 5:30 pm	<b>Closing Remarks – Serdar Bozdag</b>	

## Biological ontologies and knowledge bases

*Workshop Chairs: Yongtian Wang, Jin Chen, Jiajie Peng*

*jiajiepeng@nwpu.edu.cn, chenjin@gmail.com*

Time	Title	Presenter/Author
1:30 pm-1: 50 pm	S09201 “The Regulation Networks of Chinese Medicines Against Rheumatoid Arthritis with Syndrome of Deficiency of Liver and Kidney” Guang Zheng	Guang Zheng
1:50 am-2:10 am	S09202 “Identification of the expression, prognostic value and cancer immunity of Gasdermin E based on multi-omics data, machine learning and gene ontology” Shizheng Qiu, Ying Zhang, and Yang Hu	Shizheng Qiu
2:10 am-2:30 am	S09203 “MTOR hypermethylation may associate with the susceptibility and survival of lung adenocarcinoma patients infected with SARS-Cov-2 based on multi-omics data and machine learning” Yu Guo, Minghao Li, Yang Hu, and Tianyi Zang	Yu Guo
2:30 am-2:50 am	S09204 “CircRNA-Disease Association Prediction based on Heterogeneous Graph Representation” Xinmeng Liu, Yuhe Zhang, Yewei Shen, Xuequn Shang, and Yongtian Wang	Xinmeng Liu
	<b>Break (5min)</b>	
2:55 pm-3:15 pm	S09206 “The regulatory network analysis of single-cell RNA-seq and single-cell ATAC-seq data using differential equation models with perturbations” Ming Cao, Hang Mi, and Qinke Peng	Ming Cao
3:15 pm-3:35 pm	S09208 “Hypergraph-based Gene Ontology Embedding for Disease Gene Prediction” Tao Wang, Hengbo Xu, Ranye Zhang, Yifu Xiao, Jiajie Peng, and Xuequn Shang	Tao Wang
3:35 pm-3:55 pm	S09209 “Exploring genetic mechanisms underlying EEG endophenotypes via summary-data-based Mendelian randomization” Jing Chen, Pengfei Zhu, and Tao Wang	Jing Chen
3:55 pm-4:15 pm	B447 “An Ontology for the Social Determinants of Health Domain”	Navya Martin Kollapally

	Navya Martin Kollapally, Yan Chen, Julia Xu, and James Geller	
	<b>Closing Remarks</b>	

### The 3rd International Workshop on Deep Learning Techniques for Bioinformatics and Biomedicine

*Workshop Chairs: Fuquan Zhang*  
*zfq@mju.edu.cn, zfq@mju.edu.cn*

Time	Title	Presenter/Author
8:00-8:10	Workshop Introduction	Fuquan Zhang
8:10-8:30	S10201: Fusion Learning of Multimodal Neuroimaging with Weighted Graph AutoEncoder	Gen Shi
8:30-8:50	S10204: A Deep Convolutional Neural Network For Early Diagnosis of Alzheimer's Disease	Maximus Liu
8:50-9:10	S10205: Intelligent Recognition of Data Matrix Code for Rack-Tube System	Jinjia Lin
9:10-9:30	S10206: 5G-Enabled and Mobility Supported ICN Routing based on Ant Swarm Behavior	Jianhui Lv
9:30-9:50	S10213: Efficient Biomedical Ontology Meta-matching Based on Interpolation Model Based Hybrid Evolutionary Algorithm	Xingsi Xue
10:10-10:30	S10218: PAMS-DP: Building a Unified Open PAMS Human Movement Data Platform	Mengfei Tang
10:30-10:50	S10222: Deep Transfer Learning with Graph Neural Network for Sensor-Based Human Activity Recognition	Tianzheng Liao
10:50-11:10	S10227: A Pupil Segmentation Framework with Masked Image Modeling Enhanced Swin-Transformer	Yongde Guo
11:10-11:30	S10228: A Rehabilitation activity Monitoring method based on Shallow-CNN	Sisi Wu
11:30-11:50	S10229: EEG emotion recognition via Identity based Multi-gate Mixture-of-Experts network	Liyang Yang
11:50-12:10	B416: Accurate Real-time Polyp Detection in Videos from Concatenation of Latent Features Extracted from Consecutive Frames	Hemin Ali Qadir
12:10-12:30	B602: Combining a Boundary Detection module with the BiLSTM-CRF model improves Human Phenotype entity recognition	Jiayi Li and Jing Peng
12:30-12:50	B637: Lesion-Aware Contrastive Learning Framework for Medical Image Classification	Yu Tang
12:50-13:10	B1028: A Co-adaptive Dual Learning Framework for Entity and Relation Extraction in Chinese Medical Texts	Weiyan Zhang
	<b>Closing Remarks</b>	

### The 9th International Workshop on High Performance Computing on Bioinformatics

*Workshop Chairs: Che-Lun Hung*  
*clhung@nycu.edu.tw*

Time	Title	Presenter/Author
9:00~9:25	S12201 COVID-19 Impact on Mental Health Analysis based on Reddit Comments	Justin Chen, Kevin Qi, Aaron Zhang, Mikhail Shalaginov, and Tingying Helen Zeng
9:25~9:50	S12202 Class Activation Mapping Enhanced AlexNet Convolutional Neural Networks for Early Diagnosis of Alzheimer's Disease	william Xu, Tingying Helen Zeng, and Mikhail Shalaginov
9:50~10:15	B494 Multi-scale Label Attention Network based on Abductive Causal Graph for Disease Diagnosis	Haotian Wang, Yi Guan, Linjiang Ma, Xin Li, Jing Xie, Yi Lin, and Jingchi Jiang
10:15~10:40	B517 Disease Gene Prediction using Type 2 Fuzzy Model with Network based Method	SURABHI MISHRA, RAVI SHANKER, OSHIN MISRA, and MAHUA BHATTACHARYA
10:40~11:05	B545 A GPU-based approach for detecting genome-wide SNP-SNP interactions of quantitative trait in ANDI cohorts	Qiushi Zhang, Hongwei Liu, Lang Ao, Hong Liang, and Dandan Chen
11:05~11:30	B599 Causal Coupled Mechanisms: A Control Method with Cooperation and Competition for Complex System	Xuehui Yu, Jingchi Jiang, Xinmiao Yu, Xue Li, and Yi Guan

11:30~11:55	B970 Identification of Cross-feeding Metabolism Reveals Oral-Microbiome Modulated Host Behavior	Suganya Chandrababu and Dhundy Bastola
	Closing Remarks	

<b>Workshop in Artificial Intelligence Techniques for BioMedicine and HealthCare AIBH@BIBM2022 December 6, 2022 Workshop Chairs: Ester Zumpano, Pierangelo Veltri, Luciano Caroprese Ester Zumpano &lt;e.zumpano@dimes.unical.it&gt;</b>		
Time	Title	Presenter/Author
<b>8:30</b>	<b>Workshop Introduction</b>	
	<b>Session 1 (online) Chair: Ester Zumpano/Luciano Caroprese</b>	
8:30	<b>B394</b> <i>Fuzzy kernel-free support vector machine and applications in medicine</i>	Ai-bing Ji, Bo-wen Wei, and Ye Ji
8:45	<b>B885</b> <i>A Low Cost EDA-based Stress Detection Using Machine Learning</i>	Elahe Hosseini, Ruijie Fang, Ruoyu Zhang, Anna Parentea, Sally Hang, Setareh Rafatirad, Camelia Hostinar, Mahdi Orooji, and Houman Homayoun
9:00	<b>B1033</b> <i>TsERL: Two-stage Enhancement of Radical and Lexicon for Chinese Medical Named Entity Recognition</i>	Donglin Yang, Huifan Yang, and Bin Wu
9:15	<b>B963</b> <i>Towards Generalized ML Model in Automated Physiological Arousal Computing: A Transfer Learning-Based Domain Generalization Approach</i>	Ruijie Fang, Ruoyu Zhang, Elahe Hosseini, Anna Parentea, Sally Hang, Setareh Rafatirad, Camelia Hostinar, Mahdi Orooji, and Houman Homayoun,
9:30	<b>S13204</b> <i>Modeling a Fine-Tuned Deep Convolutional Neural Network for Diagnosis of Kidney Diseases from CT Images</i>	Sohaib Asif, Wenhui Yi, Jinhai Si, Qurrat ul Ain, Yueyang Yi, and Jin Hou
9:45	<b>S13212</b> <i>Visual Concurrent Analysis of Gait Patterns among Healthy Young, Old Adults, and Patients with Parkinson's Disease</i>	Tuan Pham
10:00	<b>B258</b> <i>How Well Apply Multimodal Mixup and Simple MLPs Backbone to Medical Visual Question Answering?</i>	Lei Liu and Xiangdong Su
10:15	<b>B964</b> <i>Prevent Over-fitting and Redundancy in Physiological Signal Analyses for Stress Detection</i>	Ruijie Fang, Ruoyu Zhang, Elahe Hosseini, Sally Hang, Anna Parentea, Setareh Rafatirad, Camelia Hostinar, Mahdi Orooji, and Houman Homayoun,
10:30	<b>B540</b> <i>Detecting Mild Cognitive Impairment in Alzheimer's Disease using Speech Acoustics Only: A Two-Stage Deep Metric Learning Approach</i>	Chen Qian, Jingkai Di, and Jiyun Li
10:45	<b>B606</b> <i>Modeling Alzheimer's Disease Progression via Amalgamated Magnitude-Direction Brain Structure Variation Quantification and Tensor Multi-task Learning</i>	Yu Zhang, Vitaveska Lanfranchi, Xulong Wang, Menghui Zhou, and Po Yang

11:00	<b>B839</b> <i>Smart Diet Management through Food Image and Cooking Recipe Analysis</i>	<b>Zeynep Hakguder</b> and Juan Cui
11:15	<b>S13211</b> <i>A Hybrid Model for Depression Detection With Transformer and Bi-directional Long Short-Term Memory</i>	Yazhou Zhang, Yu He, Lu Rong, and Yijie Ding
11:30	<b>B867</b> <i>Real-time Control of UGV Robot in Gazebo Simulator using P300-based Brain-Computer Interface</i>	Fatima Al Nuaimi, Jamal Zeddoug, and Abdelkader Belkacem
11:45	<b>S13210</b> <i>CBFV Waveform Pattern Analysis in Ultrasound-based Noninvasive ICP Monitoring</i>	Miaomiao Wei, Corey Thibeault, Robert Hamilton, and Fabien Scalzo
12:00	<b>S13205</b> <i>The Chinese Medicines Reduce Osteoporosis Caused by Therapy of Glucocorticoids</i>	Guang Zheng
12:15	<b>B246</b> <i>Effect of arsenic trioxide on human ventricular myocytes: a model study</i>	Yacong Li, Jun Liu, Runlan Wan, Lei Ma, and Henggui Zhang
12:30	<b>B563</b> <i>RESurv: A Deep Survival Analysis Model to Reveal Population Heterogeneity by Individual Risk</i>	Qiguang Zheng, Qifan Shen, Xin Su, Kuo Yang, Zixin Shu, and Xuezhong Zhou
<b>Lunch</b>		
<b>14:00 – 14:45</b>	<b>Session 2 (in-person) Chair: Ester Zumpano</b>	
14:00	<b>B930</b> Machine Learning Models to Classify Normal and Fibrotic Mouse Liver Model using Dielectric Properties	<b>Poulami Samaddar</b> , Poushali Samadder, Bhavana Baraskar, Priyanka Anvekar, Shalil Khanal, Sunil Gaddam, Sayan Roy, Dipankar Mitra, Enis Kostallari, and Shivaram Arunachalam
14:15	<b>S13209</b> <i>Low Data Image Analysis with a Generative Adversarial Network: A Case Study on Women Pelvic MRI Scans</i>	Sabino Ramirez, Mathias Brieu, and <b>Negin Forouzesh</b>
14:30	<b>S13213</b> <i>A machine-learning based tool for bioimages managing and annotation</i>	<b>Raffaele Giancotti</b> , Ugo Lomoio, Pierangelo Veltri, Pietro Hiram Guzzi, and Patrizia Vizza
<b>14:45 – 15:30</b>	<b>Session 3 (in-person) Chair: Negin Forouzesh</b>	
14:45	<b>S13208</b> Automatic Image Segmentation of Monocytes and Index Computation Using Deep Learning	<b>Luis A. Pena Marquez</b> and Subhajit Chakrabarty
15:00	<b>B478</b> A substrig replacement approach for identifying missing IS-A relations in SNOMED CT	<b>Xubing Hao</b> , Rashmie Abeysinghe, Jay Shi, and Licong Cui
15:15	<b>B646</b> <i>Wavelet-based Spectral Analysis For Protein Conformation Selection and Prediction Using AI in Drug Discovery Applications</i>	Shivangi Gupta, <b>Vineetha Menon</b> , and Jerome Baudr
<b>15:30 - 16:00</b>	<b>Coffee Break</b>	
<b>16:00 - 17:00</b>	<b>Session 3 (in-person) Chair: Poulami Samaddar</b>	
16:00	<b>B211</b> <i>An assistant decision-making method for rare diseases based on RNNs model</i>	<b>Qi Li</b> , Ming Jiang, and Changtian Ying
16:15	<b>B793</b> <i>Mediation Analysis and Mixed-Effects Models for the Identification of Stage-specific Imaging Genetics Patterns in Alzheimer's Disease</i>	<b>Daniele Pala</b> , Brian Lee, Xia Ning, Dokyoon Kim, and Li Shen

16:30	<b>B1029</b> <i>Multimodal Learning for Predicting Mortality in Patients with Pulmonary Arterial Hypertension</i>	Mohammad Naimul Islam Suvon, Prasun Chandra Tripathi, Samer Alabed, Andrew James Swift, and <u>Haiping Lu</u> ,
<b>16:45</b>	<b>Closing Remarks- Ester Zumpano</b>	

<b>Workshop in</b> <b>Artificial Intelligence &amp; Big Data vs Pandemics</b> <b>AI&amp;BDvsPandemics@BIBM2022</b> <b>December 6, 2022</b> <b>WorkshopChairs: Ester Zumpano, Elio Masciari, Andrea Tagarelli, Eugenio Vocaturo</b> <b>Ester Zumpano &lt;e.zumpano@dimes.unical.it&gt;</b>		
Time	Title	Presenter/Author
<b>14:00</b>	<b>Workshop Introduction</b>	
	<b>Session 1 (hybrid)</b>	
<b>14:00</b>	<b>S14201</b> <i>Social Media Mining and Analysis to support authorities in COVID-19 pandemic preparedness</i>	Carmela Comito
<b>14:15</b>	<b>S14203</b> <i>Prompt Learning for Multi-modal COVID-19 Diagnosis</i>	Yang Yu, Lu Rong, Mengyao Wang, Min Huang, Yazhou Zhang, and Yijie Ding
<b>14:30</b>	<b>S14206</b> <i>Development of Machine Learning Regression Model for COVID-19 Drug Target Prediction</i>	Alexandra Zamitalo, Qingtong Xie, Mayar Allam, Phinu Philip, Wenqi Shi, Felipe Giuste, Benoit Marteau, Mio Murakoso, and May Dongmei Wang
<b>14:45</b>	<b>S14202</b> <i>Covid-19 impact on health information technology: the rapid rise of e-Health and Big Data driven innovation of healthcare processes</i>	Arianna Anniciello, Simona Fioretto, Elio Masciari, and Enea Vincenzo Napolitano
<b>15:00</b>	<b>B595</b> <i>Evolution Of SARS-CoV-2 In The Presence Of Vaccines</i>	Vishwajeet Marathe and Changhui Yann
<b>15:15</b>	<b>B596</b> <i>Face Age Predictions by combining Local and Global Facial Features</i>	Kaiyan Chen, Xiangjun Dong, and Weiyang Chen
<b>15:30</b>	<b>B939</b> <i>Health Informatics on Big COVID-19 Epidemiological Data</i>	Carson Leung, Nguyen Duy Thong Tran, and Christine Zhang
<b>16:00</b>	<b>B530</b> <i>Prompt Learning for Multi-modal COVID-19 DiagnosisAnalyzing historical diagnosis code data from NIH N3C and RECOVER Programs using deep learning to determine risk factors for Long Covidsis</i>	Saurav Sengupta, Johanna Loomba, Suchetha Sharma, and Donald Brown
<b>16:15</b>	<b>S14205</b> <i>Fake News Detection on COVID 19 tweets via Supervised Learning Approach</i>	Maria Cevallos, Matteo De Biase, Eugenio Vocaturo, and Ester Zumpano
<b>16:30</b>	<b>Closing Remarks</b>	



## The 13th Workshop on Integrative Data Analysis in Systems Biology (IDASB 2022)

*Workshop Chairs: Huiru (Jane) Zheng, Zhongming Zhao, Min Xiao*

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*The schedule is based on USA PST Time*

Time	Title	Presenter/Author
8:15 – 8:20	Workshop Opening	
8:20 – 8:40	<b>MOCSC: a multi-omics data-based framework for cancer subtype classification (B362)</b>	Yuanling Ma and Jinting Guan (China)
8:40 – 9:00	<b>Identification of cancer driver modules by combining network functional and topology information (S15201)</b>	Xin Chu, Feng Li, Hongyu Duan, Junliang Shang, Juan Wang, and Jin-Xing Liu
9:00 – 9:20	<b>Detection of Chronic Kidney Disease Using Neuro-Fuzzy Rule-based Classifier (B876)</b>	Arnab Hazra, Supantha Das, Suharta Banerjee, Soumadip Ghosh, Saurav Mallik, Ayan Mukherji, Aimin Li, and Zhongming Zhao
9:20 – 9:40	<b>Loci2Tissue: Ranking tissues by the e3xpression of disease-associated genes reveals insights of the underlying mechanisms of complex diseases and traits (S15202)</b>	Boqi Wang, Catherine Zhang, Steven Qiu, Brian Hu, Daniel Lu, Nicole Xu, Yongsheng Bai, and Zhaohui Qin
9:40 – 10:00	<b>Systems biology approach for analysis of mobile genetic elements in chicken gut microbiome (S15203)</b>	Jana Schwarzerová, Michal Zeman, Ivan Rychlík, Wolfram Weckwerth, Ivo Provazník, Monika Dolejšká, and Darina Čejková
10-10:30	Coffee Break	
10:30 – 10:50	<b>Grid-Search Integrated Optimized Support Vector Machine Model for Breast Cancer Detection (B605)</b>	Partho Ghose, Selina Sharmin, Loveleen Gaur, and Zhongming Zhao (USA)
10:50 – 11:10	<b>Prioritizing Intellectual Disability Candidate Genes and Understanding Family Diseases Using Machine Learning (S15204)</b>	James Yang and Yongsheng Bai
11:10 – 11:30	<b>Identification of Cross-feeding Metabolism Reveals Oral-Microbiome Modulated Host Behavior(S15205)</b>	Suganya Chandrababu and Dhundy Bastola
11:30 – 11:50	<b>A Single-Cell-Resolution Quantitative Metric of Similarity to a Target Cell Type for scRNA-seq Data (S15206)</b>	Zuolin Cheng, Songtao Wei, and Guoqiang Yu
11:50 – 12:10	<b>Spreading of Monkeypox Infections Dictated by the Diffusion Equation The Case of Central Europe (B711)</b>	Huber Nieto-Chaupis
12:10 – 12:30	<b>Visual Analytics Exploration of PubMLST Meningitis Genomic Data (B611)</b>	<b>Margaret Varga</b> , Keith Jolley, James Bray, Holly Bratcher, Odile Harrison, and Martin Maiden
	Closing Remarks	

## Sixth Workshop on Processes and Algorithms for Healthcare and Life Quality Improvement

*Workshop Chairs: Pierangelo Veltri and Patrizia Vizza*

*[pveltri@univcamerino.it](mailto:pveltri@univcamerino.it), [pvizza@univcamerino.it](mailto:pvizza@univcamerino.it)*

Time	Title	Presenter/Author
10.25	Introduction to 6th Edition	Pierangelo Veltri
10.30	<b>S16206: A Dataset for Falling Risk Assessment of the Elderly using Wearable Plantar Pressure.</b>	Guohua Hu, Jianxiu Jin, Zhen Song, Shibin Wu, Lin Shu, Junan Xie, Jianlin Ou, Zhuoming Chen, and Xiangmin Xu
10.45	<b>B245: Effect of cell coupling between pacemaker cells on the biological pacemaker in cardiac tissue model.</b>	Yacong Li, Qince Li, Kuanquan Wang, Lei Ma, and Henggui Zhang
11.00	<b>B490: A Portable System of Mental Fatigue Detection and Mitigation based on Physiological Signal</b>	Chao Wu, Fuze Tian, Qiuxia Shi, QinLin Zhao, and Bin Hu
11.15	<b>B629: An evolutionary prototype of a self-care application for type 2 diabetes</b>	Kosala Maduwantha, Sajani Mayadunne, Vishwa Gunathilake, Kosala Disanayake, Chaturangika Kahandawaarachchi,



		Dharshana Kasthurirathna, and Priyamali Jayasekera
11.30	<b>B662:</b> Dynamic Physical Activity Routine creation using Machine learning and Optimization Methods	Kosala Maduwantha, Sajani Mayadunne, Kosala Disanayake, Vishwa Gunathilake, Chathurangika Kahandawarachchi, and Dharshana Kasthurirathna
11.45	<b>B736:</b> Association rule analysis for fetal heart rate pattern of late FGR	Liyan Zhong, Shiyao Huang, Xia Li, Guiqing liu, Qinqun Chen, Xiaomu Luo, Yuexing Hao, Jiaming Hong, and Hang Wei
12.00	<b>S16208:</b> Application of DTW Algorithm in Behavior	kai Wang, Xiaoyun Jia, Erhu Wang, and Jingyi Wu
12.15	<b>S16210:</b> On the use of the analysis for EEG functional connectivity networks in epilepsy	Barbara Puccio, Patrizia Vizza, and Pierangelo Veltri
12.30 – 14.00	<b>Lunch</b>	
14.00	<b>B908:</b> Quantum Algorithm for the Simulation of Squamous Cell Lung Carcinoma tested through IBM Quantum Composer	Akshita Tiwari
14.15	<b>B894:</b> Psychosis iREACH: Reach for Psychosis Treatment using Artificial Intelligence	Jonathan Lee, Sarah Kopelovich, Sunny Cheng, and Dong Si
14.30	<b>S16204:</b> Identification of Social and Racial Disparities in Risk of HIV Infection in Florida using Causal AI Methods	Mattia Prosperi, Jie Xu, Jingchuan Guo, Jiang Bian, Wei-Han Chen, Shantrel Canidate, Simone Marini, and Mo Wang
14.45	<b>B812:</b> Passive Monitoring of Physiological Precursors of Stress Leveraging Smartwatch Data	Shayan Fazeli, Lionel Levine, Baharan Mirzasoleiman, Bitra Zadeh, Tara Peris, and Majid Sarrafzadeh
15.00	<b>B613:</b> Pan-Tompkins++: A Robust Approach to Detect R-peaks in ECG Signals	Md Niaz Imtiaz and Naimul Khan
15.15	<b>S16207:</b> Mobile Application for Measuring Pectus Excavatum Treatment Progress	brian Sanders, Nahom Kidane, Yuzhong Shen, and Robert Kelly
15.30	<b>S16201:</b> A Machine-Learning Approach for Predicting Depression Through Demographic and Socioeconomic Features	Joseph Sun, Rory Liao, Mikhail Y Shalaginov, and Tingying Helen Zeng
15.45 – 16.00	<b>Coffee break</b>	
16.00	<b>S16202:</b> ClassAphasia: An Ensemble Machine Learning Network to Improve Aphasia Diagnosis and Determine Severity	Jagadeepam Maddipatla
16.15	<b>S16203:</b> An interleaved hardware-accelerated k-mer parser	Franco Milicchio, Marco Oliva, and Mattia Prosperi
16.30	<b>S16205:</b> Transmission cluster characteristics of global, regional, and lineage-specific SARS-CoV-2 phylogenies	Mattia Prosperi, Brittany Rife, Simone Marini, and Marco Salemi
16.45	<b>S16209:</b> Glucose Metabolism Evaluation by using cardiac PET images	Patrizia Vizza, Giuseppe Tradigo, Pietro Hiram Guzzi, Elena Succurro, Giuseppe Lucio Cascini, and Pierangelo Veltri
17.00	<b>S16211:</b> Medical image fusion: a proposed methodology for treatment evaluation	Patrizia Vizza, Claudia Barrese, Luigi Marafioti, Giuseppe Lucio Cascini, and Pierangelo Veltri
17.15	<b>Closing Remarks</b>	

## Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics (MABM2022)

Online Session on Tuesday, December 6<sup>th</sup>, 2022, Pacific Standard Time

Chair: Dr. Haiying Wang

Time (PST Time)	Title	Presenter/Author
8:55 – 9:00	Opening Remarks	
9:00 – 9:15	<b>B567:</b> Prediction Algorithm of DNA Sites Based on Weighted Feature Matrix	Zhendong Liu, Xi Chen, Dongyan Li, Xinrong Lv, Leyi Wei, and Qionghai Dai

9:15 – 9:30	<b>B549:</b> Predicting Algorithm of Transcription Factor Binding Sites Based on Weighted Multi-Grained Scanning	Zhendong Liu, Dongyan Li, Xi Chen, Xinrong Lv, Daming Zhu, and Qionghai Dai
9:30 – 9:45	<b>B483:</b> CFC: a Cascade Forest approach to discover Cancer driver genes using multi-omics data	Lei Zhang, Yijing Yang, Zhe Wang, Dongdong Li, Jingping Liu, and Hai Yang
9:45 – 10:00	<b>B1014:</b> Unsupervised continual learning of single-cell clustering based on novelty detection and memory replay	Peng Ke, Shuke Xiang, Zhongnan Zhang, and Zhen He
10:00 – 10:30	<b>Coffee Break</b>	
10:30 – 10:45	<b>B464:</b> Identification of linear epitope with Multiple Sequence Representation Learning Network	Yan Liu and Zheng Liu
10:45 – 11:00	<b>B630:</b> A Multi-Graph Laplacian Regularized Low-Rank Representation method for cancer sample clustering with integrated TCGA data	Juan Wang, Li -Hong Wang, Tian-Jing Qiao, and Sha-Sha Yuan
11:00 – 11:15	<b>B715:</b> KtreeGRN: A Method of Gene Regulatory Network Construction Based on k-tree Sampling and Decomposition	Zongheng Cai, Jimeng Lei, Junli Deng, and Jianxiao Liu
11:15 – 11:30	<b>B749:</b> Structure Regularized Attentive Network for Automatic Femoral Head Necrosis Diagnosis and Localization	Lingfeng Li, Huaiwei Cong, Gangming Zhao, Junran Peng, Zheng Zhang, and Jinpeng Li
11:30 – 11:45	<b>B777:</b> Towards DDIs Identification by Knowledge Graph with BiRW and Back Aggregation	Zhuang Yin, Xiaoli Lin, and Xiaolong Zhang
11:45 – 12:00	<b>B828:</b> Graph Neural Networks for Z-DNA prediction in Genomes	Artem Voytetskiy, Alan Herbert, and Maria Poptsova
12:15 – 12:30	<b>B608:</b> On functional annotation with gene co-expression networks	Vladimír Kunc and Jiri Klema
12:30 – 14:00	<b>Lunch Break</b>	
14:00 – 14:15	<b>B448:</b> A Hybrid Feature Selection Method Based on Binary Differential Evolution and Feature Subset Correlation for Microarray Data	Weidong Xie, Wei Li, Yushan Fang, Yuhuan Chi, and Kun Yu
14:15 – 14:30	<b>B376:</b> scARMF: Association Rule Mining-based feature selection Framework for Single-Cell transcriptomics data	Dibyendu Seal, Vivek Das, and Rajat De
14:30 – 14:45	<b>B401:</b> Dual-branch body and boundary supervision network for ultrasound image segmentation	Wentao Liao, Guoping Xu, Xinglong Wu, Xuan Zhang, Xinwei He, and Chang Li
14:45 – 15:00	<b>B977:</b> Selective ensemble learning for cross-muscle ALS disease identification with EMG signal	Xujian Wang, Shenghua Teng, Chenxu Hao, Yan Liu, Ji He, Shuo Zhang, and Dongsheng Fan
15:00 – 15:15	<b>B373:</b> Multimodal Emotion Recognition Using CNN-SVM and Data Augmentation	Gengyuan Guo, Xiangwei Zheng, Pengzhi Gao, and Cun Ji
15:15 – 15:30	<b>S18205:</b> Determining and Validating Population Differences in Magnetic Resonance Angiography Using Sparse Representation	Steve Mendoza, Fabien Scalzo, and Aichi Chien
15:30 – 16:00	<b>Coffee Break</b>	
16:00 – 16:15	<b>B568:</b> A Deep Reinforcement Computation Model for Sepsis Treatment	Hang Yu and Qingchen Zhang
16:15 – 16:30	<b>B275:</b> Predicting The Likelihood of Patients Developing Sepsis Based on Compound Ensemble Learning	Liang Zhao, Rui Lin, Zhuo Liu, and Hong Yuan
16:30 – 16:45pm	<b>B263:</b> KSMDb: A classification method in imbalanced COVID dataset based on KmeansSMOTE and DeBERT	Rong Zhu, Hua-Hui Gao, Jun-Liang Shang, and Ling-Yun Dai
16:45 – 17:00pm	<b>B1058:</b> Curriculum Contrastive Learning for COVID-19 FAQ Retrieval	Leilei Zhang and Junfei Liu
Closing Remarks (Day 1 – Online Session)		

## Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics (MABM2022)

*Wednesday, December 7<sup>th</sup>, 2022, Las Vegas, Pacific Standard Time*

*Chair: Dr. Haiying Wang/Prof. Huiru(Jane) Zheng*

Time (PST Time)	Title	Presenter/Author
8:55 – 9:00	Opening Remarks	
9:00 – 9:20	<b>S18208:</b> Explainable Machine Learning to Identify Patient-specific Biomarkers for Lung Cancer	Masrur Sobhan and Ananda Mondal
9:20 – 9:40	<b>S18206:</b> An Autoencoder Based Bioinformatics Framework for Predicting Prognosis of Breast Cancer Patients	Raihanul Bari Tanvir, Masrur Sobhan, and Ananda Mondal
9:40 – 10:00	<b>B966:</b> Unseen Epitope-TCR Interaction Prediction based on Amino Acid Physicochemical Properties	Rawshon Raha, Yulian Ding, Qiang Liu, and Fang-Xiang Wu
10:00 – 10:30	<b>Coffee Break</b>	
10:30 – 10:50	<b>S18203:</b> Sequential pattern detection for identifying courses of treatment and anomalous claim behaviour in medical insurance	James Kemp, Christopher Barker, Norm Good, and Michael Bain
10:50 – 11:10	<b>B925:</b> Using Twitter Data Analysis to Understand the Perceptions, Awareness, and Barriers to the Wide Use of Pre-Exposure Prophylaxis in the United States	Arslan Erdengasileng, Shubo Tian, Sara Green, Sylvie Naar, and Zhe He
11:10 – 11:30	<b>S18204:</b> Detection of Parkinson's Disease from a 5-second Walking with Smart Insoles: A Statistical and Machine Learning Approach	Luigi D'Arco, Haiying Wang, and Huiru Zheng
11:30 – 11:50	<b>B452:</b> Vital Measurements of Hospitalized COVID-19 Patients as a Predictor of Long COVID: An EHR-based Cohort Study from the RECOVER Program in N3C	Sihang Jiang, Johanna Loomba, Suchetha Sharma, and Donald Brown
11:50 – 12:10	<b>B969:</b> Transfer Learning Pre-training Dataset and Fine-tuning Effect Analysis on Cancer Histopathology Images	Koushik Howlader and Lu Liu
12:10 – 12:30	<b>S18202:</b> Efficient Classification of Very High Resolution Histopathological Images	Mohammad Iqbal Nouyed, Gianfranco Doretto, and Donald Adjeroh
12:30 – 14:00	<b>Lunch Break</b>	
14:00 – 14:20	<b>B652:</b> Depth Encoding for Neonatal Patient Segmentation	Yasmina Souley Dosso, Kim Greenwood, JoAnn Harrold, and James Green
14:20 – 14:40	<b>B590:</b> Utilizing deep learning to automatically screen for osteoporosis from dental panoramic radiographs	Rajaram Anantharaman, Anwika Bhandary, Raveesh Nandakumar, Rajesh Kumar R, and Pranav Vajapeyam
14:40 – 15:00	<b>B593:</b> Multi-task Learning with Consistent Prediction for Efficient Breast Ultrasound Tumor Detection	Kaiwen Yang, Aiga Suzuki, Jiaxing Ye, Hirokazu Nosato, Ayumi Izumori, and Hidenori Sakanashi
15:00 – 15:20	<b>B725:</b> Determination of Neuron Activation States Facilitated by Artificial Intelligence	Ana Topasna, Eric Xie, Sammy Park, Sophia Huang, Xiaowei Wu, and Hehuang Xie
15:30 – 16:00	<b>Coffee Break</b>	
16:00 – 16:20	<b>B921:</b> Multiclass Classification of Nonalcoholic Steatohepatitis Mouse Models Using Dielectric Properties as Disease Biomarker	Poulami Samaddar, Keerthy Gopalakrishnan, Priyanka Anvekar, Poushali Samadder, Ivone Cristina Igreja E Sa, Rachel Bayer, Sunil Gaddam, Dipankar Mitra, Sayan Roy, Petra Hirsova, and Shivaram Arunachalam
16:20 – 16:40	<b>B869:</b> Multi-armed bandit approach for multi-omics data integration	Aditya Raj and Golrokh Mirzaei
<b>Closing Remarks (Day 2)</b>		

<b>Workshop Title: Biomedical Informatics Applications in Translational Research and Rare Diseases</b> <i>Workshop Chairs: Qian Zhu &amp; Yanji Xu</i> <i>qian.zhu@nih.gov, yanji.xu@nih.gov</i>			
Time	Paper ID	Title	Presenter/Author
9:00 – 9:10am		Opening Remarks	Qian Zhu
9:10 – 9:25am	S19202	Identifying Missing IS-A Relations in Orphanet Rare Disease Ontology	Maryamsadat Mohtashamian
9:25 – 9:40am	S19206	Integrative Rare Disease Profile Creation via NormMap to Advance Rare Disease Research	Devon Leadman
9:40 – 9:55am	S19204	Integrated bioinformatics analysis identifies hub genes and pathways involved in the metastasis of synovial sarcoma	Helin Feng
9:55 – 10:10am	B901	Investigating stagnant clinical outcomes after fecal microbiome transplant in autism spectrum disorder	Caleb Pecka
10:10 – 10:30am		<b>Coffee Break</b>	
10:30 – 10:45am	S19201	ClassAphasia: An Ensemble Machine Learning Network to Improve Aphasia Diagnosis and Determine Severity	Jagadeepam Maddipatla
10:45 – 11:00am	S19205	Semantic Annotation of NIH Funding Data for Supporting Rare Disease Research	Qian Zhu
11:00 – 11:15am	B868	Multimodal feature learning framework for disease biomarker discovery	Sudhir Ghandikota
11:15 – 11:30am	S19203	Network pharmacology-based prediction of underlying mechanisms of Glycyrrhiza uralensis Fisch and Anglica sinensis (Oliv.) Diels in the treatment of breast cancer	Zhangying Feng
11:30 – 11:50am		<b>Coffee Break</b>	
11:50 – 12:05pm	B655	Hybrid Modified League Championship Algorithm and its Applications in Compartmental Pharmacokinetic-Pharmacodynamic Data Analysis	Shyam Sundar Das
12:05 – 12:20pm	B922	Sublanguage Characteristics of Clinical Documents	Sungrim Moon
12:20 – 12:30pm		<b>Closing Remarks</b>	

<b>Computational Structural Bioinformatics Workshop (CSBW 2022)</b> <i>Workshop Chairs: Bruna Jacobson and Chinwe Ekenna</i>		
Time	Title	Presenter/Author
8:45 am	Welcome	Bruna Jacobson, Chinwe Ekenna
9:00 am	<b>Keynote: “Machine learning and molecular simulation for the design of finely tuned drugs”</b>	Ron Dror
10:00 am	<b>Coffee Break</b>	
10:30 am	S22202: <i>“Equivariant Encoding based GVAE (EqEn-GVAE) for Protein Tertiary Structure Generation”</i>	Taseef Rahman, Fardina Fathmiul Alam, and Amarda Shehu
10:45 am	S22206: <i>“Exhaustive In-silico Simulation of Single Amino Acid Insertion and Deletion Mutations”</i>	Alistair Turcan, Grant Chou, Liliu Martin, Theo Miller, Dylan Thompson, and Filip Jagodzinski
11:00 am	B338: <i>“Property-Controllable Generation of Quaternary Ammonium Compounds”</i>	Bo Pan, Yinkai Wang, Xuanyang Lin, Muran Qin, Yuanqi Du, Shiva Ghaemi, Aowei Ding, Shiyu Wang, Saleh Alkhalifa, Kevin Minbiole, William M. Wuest, Ashley Petersen, Austin Leitgeb, Amarda Shehu, and Liang Zhao
11:15 am	S22203: <i>“Generation and Characterization of Quaternary Ammonium Compounds via Deep Learning”</i>	Yinkai Wang, Shiva Ghaemi, Aowei Ding, Yuanqi Du, Bo Pan, Muran Qin, Xuanyang Lin, Ashley Ann Petersen, Austin Leitgeb, Saleh Alkhalifa, Kevin Minbiole, William Wuest, Liang Zhao, and Amarda Shehu

11:30 am	S22209: <i>"Molecular Descriptors Property Prediction via a Natural Language Processing Approach"</i>	Tuan Tran and Chinwe Ekenna
11:45 am	B983: <b>Invited talk:</b> <i>"The Combined Focal Cross Entropy and Dice Loss Function for Segmentation of Protein Secondary Structures from Cryo-EM 3D Density maps"</i>	Yongcheng Mu, Jiangwen Sun, and Jing He
12:00 pm	<b>Keynote talk</b>	Brian Chen
12:30 pm	<b>Lunch</b>	
2:00 pm	S22204: <i>"Refinement of AlphaFold2 Models against Experimental Cryo-EM Density Maps at 4-6Å Resolution"</i>	Maytha Alshammari, Jing He, and Willy Wriggers
2:15 pm	B371: <i>"Unsupervised Heterogeneous Cryo-EM Projection Image Classification Using Autoencoder"</i>	Xiangwen Wang, Yonggang Lu, Jianwei Li, and Zequn Zhang
2:30 pm	S22205: <i>"Tracing Randomly Oriented Filaments in Simulated Actin Network Tomograms"</i>	Salim Sazzed, Peter Scheible, Jing He, and Willy Wriggers
2:45 pm	S22210: <i>"Calculating the Binding Entropy of Host-Guest Systems with Physics-Guided Neural Networks"</i>	Alles Rebel, Ali Risheh, Negin Massoudian, and Negin Forouzes
3:00pm	B949: <i>"A geometric and topological analysis of the binding behavior of Intrinsically Disordered Proteins"</i>	Aakriti Upadhyay and Chinwe Ekenna
3:15pm	B521: <i>"In silico Screening, Docking, and Redesigning of Traditional Chinese Medicinal Compounds Against Streptococcus pneumoniae Glycosyl Hydrolase GHIP and Peptidoglycan Hydrolase LytB"</i>	Vince Busania, Denice Millen Canilao, Marla Endriga, and Enrique Jose Frio
3:30 pm	<b>Coffee Break</b>	
4:00 pm	<b>Panel Discussion: Future Research and Careers in Computational Structural Bioinformatics</b>	Jing He, Filip Jagodzinski
4:40 pm	S22207: <i>"Computational analysis of Receptor-Binding Domains of SARS-CoV-2 to reveal the mechanism of immune escape"</i>	Mengxu Zhu, Kongyan Li, and Hong Yan
5:05pm	B739: <i>"Docking-based Multi-objective Molecular Optimization Pipeline using Structure-constrained Genetic Algorithm"</i>	Yurim Lee, Kyudam Choi, and Cheongwon Kim
5:20 pm	S22208: <i>"An Efficient Voxel-Based Deep Learning Approach for Ligand Binding Site Detection"</i>	Jingbo Liang and Bruna Jacobson
5:35 pm	<b>Closing Remarks</b>	

<b>The 6th Workshop on Computational Methods for the Immune System Function (CMISF 2022)</b> Workshop Chairs: <b>Ping Zhang</b> , Francesco Pappalardo, Marzio Pennisi, Giulia Russo <a href="mailto:p.zhang@griffith.edu.au">p.zhang@griffith.edu.au</a> , <a href="mailto:francesco.pappalardo@unict.it">francesco.pappalardo@unict.it</a> , <a href="mailto:marzio.pennisi@uniupo.it">marzio.pennisi@uniupo.it</a> , <a href="mailto:giulia.russo@unict.it">giulia.russo@unict.it</a>		
Time	Title	Presenter/Author
9:00-9:20	<b>S23207: Cutaneous Leishmaniasis: discovering new effective therapies using the Universal Immune System Simulator</b>	Valentina Di Salvatore
9:20-9:40	<b>S23206: Genetic algorithm application for the prediction of potential SARS-CoV-2 new variant of concern</b>	Avisa Maleki
9:40-10:00	<b>S23202: The performance of UMAP plus linkage compared with Daura-Clustering of molecular dynamics of the PD-1 checkpoint receptor</b>	Wolfgang Schreiner
10-10:30	<b>Coffee Break</b>	
10:30-10:50	<b>S23203: UISS-GPU: Accelerated In-Silico Tuberculosis Vaccine Trials Using FLAME GPU</b>	Paul Richmond
10:50-11:10	<b>B1021: Modeling Internalization and Expelling of Nanoparticles of Tumorial Cells Through Electrodynamics and Diffusion Equation</b>	Huber Nieto-Chaupis

11:10-11:30	<b><i>S23205: Ectopic Heartbeat Detection from ECG Signals using Deep Convolutional Neural Networks</i></b>	Ping Zhang
11:30-11:50	<b><i>S23204: Using Multiple Factor Analysis to Determine the Dietary Risk Factors for Alzheimer's Disease</i></b>	Tahera Ahmed
11:50-12:10	<b><i>S23201: Identification of Cross-feeding Metabolism Reveals Oral-Microbiome Modulated Host Behavior</i></b>	Suganya Chandrababu
12:10 – 12:15	<b>Closing Remarks</b>	

<b>RRoBin 2022</b> <i>WorkshopChairs:</i> <i>Hesham Ali, hali@unomaha.edu</i>		
<b>Time</b>	<b>Title</b>	<b>Presenter/Author</b>
2:00 – 2:20 pm (PST)	B1063 “Refinement of Biological Regulatory Graphs using Functional Enrichment”	Jeffrey Page, Matthew Morris, Gary Skuse, and Gordon Broderick
2:25 – 2:45 pm (PST)	<a href="#">S24201</a> “Comprehensive Assessment of OCR Tools for Gene Name Recognition in Biological Pathway Figures”	Stuart Aldrich, Micheal Arowolo, Fei He, Mihail Popescu, and Dong Xu
	<b>Closing Remarks</b>	

<b>Computational methods to characterize genomic variants using high-throughput sequencing data</b> <i>WorkshopChairs: Xin Maizie Zhou, Eric Lu Zhang, Ryan Matthew Layer, Zechen Chong, Xian Fan Mallory</i> <b>Tuesday, December 7, 2022</b> <i>The workshop schedule is based on USA PST Time</i> <b>Room: Pisa</b>		
<b>Time</b>	<b>Title</b>	<b>Presenter/Author</b>
2:00pm-2:20pm	<b>B556</b> High-resolution sample size enrichment of single-cell multi-modal low-throughput Patch-seq datasets	Lorenzo Martini, Roberta Bardini, Alessandro Savino, and Stefano Di Carlo
2:20pm-2:40pm	<b>B320</b> Haplotype-phasing of long-read HiFi data to enhance structural variant detection through a Skip-Gram model	Can Luo, Parth Datar, Yichen Henry Liu, and Xin Zhou
2:40pm-3:00pm	<b>B244</b> Reliable tumor evolution estimates using bulk sequencing data	Jared Huzar, Madelyn Shenoy, Maxwell Sanderford, Sudhir Kumar, and Sayaka Miura
3:00pm-3:20pm	<b>B985</b> Targeted Next generation Sequencing Reveals the Genetic Mechanism of Chinese Marfan syndrome Cohort with Ocular Manifestation	Dongming Han, Wei Li, Ziwei Wang, Sicheng Guo, Jiayu Gao, and Jiankang Li
	<b>Closing Remarks</b>	

<b>The 6th International Workshop on Deep Learning in Bioinformatics, Biomedicine, and Healthcare Informatics</b> <i>WorkshopChairs: Jung Hun Oh</i>		
<b>Time (Wed)</b>	<b>Title</b>	<b>Presenter/Author</b>

9:25-9:30 am	<b>Opening Remarks</b>	
9:30-9:50	<b>S21203: Exploration of protein sequence embeddings for protein-ligand binding site detection</b>	David Hoksza
9:50-10:10	<b>S21204: Predicting transcription factor binding sites by dual-stream multiple instance learning network</b>	Ruqun Song
10:10-10:30	<b>S21205: Extraction of Gene Regulatory Relation Using BioBERT</b>	Clement Essien
10:30-10:50	<b>B257: scSASSL: Self-attention semi-supervised learning with deep generative models to automatically identify cell types</b>	Hongyu Duan
10:50-11:10	<b>B487: Prediction for the Number of Standard Terminologies from Chinese EHR</b>	Qi Ye
11:10-11:30	<b>B947: Contrastive Self-Supervised Learning on Crohn's Disease Detection</b>	Jing Xing
11:30-11:50	<b>B999: Disease Risk Prediction via Heterogeneous Graph Attention Networks</b>	Zhe Qu
	<b>Coffee Break</b>	
1:00-1:20 pm	<b>S21207: Defensive Adversarial Training for Enhancing Robustness of ECG based User Identification</b>	Hongbi Jeong
1:20-1:40	<b>B333: Multi-View Representation Learning for Multi-Instance Learning with Applications to Medical Image Classification</b>	Lu Zhao
1:40-2:00	<b>B384: Impact of Concatenation of Digital Craniocaudal Mammography Images on a Deep-Learning Breast-Density Classifier Using Inception-V3 and ViT</b>	Conrad Testagrose
2:00-2:20	<b>B403: AdapSQA: Adaptive ECG Signal Quality Assessment Model for Inter-Patient Paradigm using Unsupervised Domain Adaptation</b>	Hui Li
2:20-2:40	<b>B420: Deep Multi-Instance Learning with Adaptive Recurrent Pooling for Medical Image Classification</b>	Yi Ding
2:40-3:00	<b>B347: Using Label-text Correlation and Deviation Punishment for Fine-grained Suicide Risk Detection in Social Media</b>	Zepeng Li
3:00-3:05	<b>Closing Remarks</b>	

## BIBM 2022 Posters at Las Vegas

Poster ID	Accept Posters
P206	Mingjia Ma, Ian Hou, Jeslyn Gao, Chang Li, Yongsheng Bai, and Xiaoming Liu, <i>A Bioinformatics Pipeline for the identification of disease-causing variants in humans that can change protein structure</i>
P207	Younghoon Kim, <i>Developing global gene regulatory network inference method for investigating disease genes using High-Performance Computing resources</i>
P208	Itsuki Hirahata, Laijun Yang, Ken'ichi Yano, and Katsuhiko Torii, <i>Standing Support Robot for Recovery of Lower Limb Function and Evaluation of Caregiver's Burden by Measuring Biological Signals</i>
P209	Geervani Koneti, Mastan Vali Shaik, Shyam Sundar Das, and Narayanan Ramamurthi, <i>Parallelized Population Based Exhaustive Replacement Method for Reproducible Features Selection and Its Applications in Drug Discovery</i>
P210	Lei Jiang, Yuexu Jiang, Cankun Wang, Clement Essien, Juexin Wang, Anjun Ma, Qin Ma, and Dong Xu, <i>Machine learning development environment for single-cell sequencing data analyses</i>

P212	Rizwan Qureshi, Tanvir Alam, and Jia Wu, <i>Drug response prediction model for lung cancer patients using biophysical simulation and machine learning</i>
P213	Jin Hee Kim, Thi Mai Nguyen, Hoang Long Le, Kyu-Baek Hwang, and Yun-Chul Hong, <i>Prediction of Hypertension Using DNA Methylome-Based Machine Learning Models</i>
P214	Geervani Koneti, Shyam Sundar Das, Jyotsna Bahl, Prithish Ranjan, and Narayanan Ramamurthi, <i>Discovering the Knowledge in Unstructured Early Drug Development Data Using NLP and Advanced Analytics</i>
P215	Sagar Patel, Chathurani Ranathunge, Lubna Pinky, Julius Nyalwidhe, John Semmes, Robert Armstrong, and Donald Combs, <i>PROMOR App: A web application for label-free quantification (LFQ) proteomics data analysis and predictive modeling</i>
P216	Thi Thuy Duong Vu and Jaehee Jung, <i>Gene Ontology based Protein Functional Annotation using Pretrained Embeddings</i>
P217	Abdurrahman Elbasir, Ying Ye, Daniel Schäffer, Jayamanna Wickramasinghe, Xue Hao, Paul Lieberman, Quaid Morris, Rugang Zhang, Alejandro Schäffer, and Noam Auslander, <i>Characterizing the Landscape of Viral Expression in Cancer by Deep Learning</i>
P220	Yejin Kan, Dongyeon Kim, and Gangman Yi, <i>A Novel Gap-Filling Method Based on Hybrid Read Information Analysis</i>
P221	Qiushi Chen, Rory Liao, Mikhail Shalaginov, and Tingying Helen Zeng, <i>Scoliosis Detection with Convolutional Neural Networks</i>
P224	Vivian Liu, Mikhail Shalaginov, Rory Liao, and Tingying Helen Zeng, <i>A Deep Convolutional Neural Network for Diagnosis of Diabetic Retinopathy</i>
P226	Pietro Hiram Guzzi, Francesca Cortese, Gaia Chiara Mannino, Elisabetta Pedace, Francesco Andreozzi, and Veltri Pierangelo, <i>A network-based analysis of genes related to comorbidities in diabetes.</i>
P227	Qi Zhang, Jianhang Zhou, and Bob Zhang, <i>Multi-feature representation for fatty liver disease detection with breath sample analysis</i>
P229	Emma Chen, Rory Liao, Mikhail Y. Shalaginov, and Tingying Helen Zeng, <i>Real-time Detection of Acute Lymphoblastic Leukemia Cells Using Deep Learning</i>
P232	Matthew Smith-Erb, Ziyun Guang, and Layla Oesper, <i>Deriving consensus tumor trees using integer linear programming</i>
P233	Inseung Hwang, Jaeyeon Jang, Kwangsoo Kim, Hye-Yeong Jo, Sang Cheol Kim, and Inuk Jung, <i>Measuring single-cell level gene expression stability and variability in healthy and severe COVID-19 patients using Kullback–Leibler divergence</i>
P234	Tu Tu, Jing Zhang, Yue Wang, Hui Jin, and Megan He, <i>MULABS: Multi-Task Learning with Attention-Based Scoring for Click-Through Rate Prediction on Sparse Data in Healthcare Real-World Scenarios</i>
P235	Yibo Chen, Dong Xu, and Mihail Popescu, <i>Integration of Gene Regulatory Pathways Found in the Literature in a Graph Database</i>
P239	zhenggui xiang, <i>Risk Prediction on the Elderly' Check-out from a Continuing Care Retirement Community</i>
P240	Saki Maruko, Zu Soh, Shin Wakitani, Masayuki Yoshida, and Toshio Tsuji, <i>Estimating the Swimming Positions of Zebrafish: A Spatial Distribution Model of Ventilatory Signals</i>
P242	Hakdong Kim, Taeheul Jun, Byung Gyu Chae, Hyun-Eui Kim, MinSung Yoon, and Cheongwon Kim, <i>Deep learning-based 3D refractive index generation for live blood cell</i>
P248	Kentaro Kaneko, Songzhi Chen, Zu Soh, Takafumi Sasaoka, Yuu Minematsu, Hikaru Momose, Takahide Nozawa, and Toshio Tsuji, <i>Autonomic Nervous Response to <math>\gamma</math>-Undecalactone Odor and its Relation to Subjective Evaluation</i>
P249	Ivana Sixtová, Tomáš Skopal, David Hoksza, Jakub Matějlik, and Tomáš Uher, <i>Machine and human interpretable patient visualizations</i>
P250	Quan Mai, Ukash Nakarmi, and Miaoqing Huang, <i>BrainVGAE: End-to-End Graph Neural Networks for Noisy fMRI Dataset</i>
P251	Cecilia Ehrlichman and Layla Oesper, <i>Combining Distance Measures on Tumor Evolutionary Trees</i>
P252	Anish Salvi, Raj Shah, Luke Higgins, and Prahlad G. Menon, <i>Vision Transformers for AI-Driven Classification of Peripheral Artery Disease from Maximum Intensity Projections of Runoff CT Angiograms</i>
P253	Anish Salvi, Ender Finol, and Prahlad G. Menon, <i>3D Segmentation of Abdominal Aortic Aneurysm Walls from CT Angiograms</i>
P254	Quoc Nguyen and Layla Oesper, <i>An Approach to Relax the Infinite Sites Assumption in Tumor Phylogeny Distance Measures</i>
P259	Chérubin Mugisha and Incheon Paik, <i>Optimization of Biomedical Language Model with Optuna and a Sentencepiece Tokenization for NER</i>
P262	Fatemeh Shah-Mohammadi and Joseph Finkelstein, <i>Using NLP for Differential Diagnosis of Chronic Obstructive Pulmonary Disease Exacerbation</i>
P264	Shafayat Ahmed, Muhit Islam Emon, Nazifa Ahmed Mouri, and Liqing Zhang, <i>LM-ARG: Identification &amp; classification of antibiotic resistance genes leveraging pre-trained protein language models</i>



P268	Younghoon Kim, <i>Classification of multiple cancer types from transcriptome profiles using convolutional neural networks</i>
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