2020 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)

The conference schedule is based on Korea Seoul Time. A few days before the event, every registered participant will receive a login instruction email to access the virtual conference platform

Conference and Workshop Schedule at a Glance

	Dec. 16	Dec. 17	Dec. 18	Dec. 19
Keynote Sessions		Keynote Talk	Keynote Talk:	Keynote Talk:
Morning Sessions	Workshops	Sessions 1-5 Workshops	Sessions 16-20 Workshops	Sessions 30-34 Posters
	Lunch Break			*End of Conference*
Afternoon Sessions 1	Workshops	Sessions 6-10 Workshops	Sessions 21-24 Workshops	
Afternoon Sessions 2	Workshops	Sessions 11-15 Workshops	Sessions 25-29 Workshops	

Time Zone

Time	Korea	China	India	Western Europe	US Eastern	US Central
Keynote Sessions	9:00am – 10:00am	8:00am – 9:00am	5:30am – 6:30am	1:00am – 2:00am	7:00pm – 8:00pm (-1 day)	6:00pm – 7:00pm (-1 day)
Morning Session	10:00am – 12:30pm	9:00am – 11:30am	6:30am – 9:00am	2:00am – 5:30am	8:00pm – 10:30pm (-1 day)	7:00pm – 9:30pm (-1 day)
Lunch Break	12:30pm – 1:30pm	11:30am – 12:30pm				
Afternoon Session 1	1:30pm – 4:00pm	12:30pm – 3:00pm	10:00am – 12:30pm	5:30am – 8:00am	11:30pm – 2:00am (-1 day)	10:30pm – 1:00am (-1 day)
Afternoon Session 2	4:00pm – 6:30pm	3:00pm – 5:30pm	12:30pm – 3:00pm	8:00am – 10:30am	2:00am – 4:30am	1:00am – 3:30am

Conference Schedule

Time (KST)	December 17	December 18	December 19
Keynote Sessions 9:00am – 10:00am	**Keynote Talk**: Dr. Doheon Lee	**Keynote Talk**: Dr. Eva Lee	**Keynote Talk**: Dr. Luonan Chen
Morning Sessions 10:00am – 12:30pm	**Session 1**: Structure, Function, and Evolution (1) **Session 2**: Machine Learning and Modelling for Biomedicine (1) **Session 3**: AI and Machine Learning for Health Informatics (1) **Session 4**: Biomedical Image Analysis (1) **Session 5**: Healthcare Systems (1)	**Session 16**: Computational Systems Biology (1) **Session 17**: Machine Learning and Modelling for Biomedicine (4) **Session 18**: AI and Machine Learning for Health Informatics (4) **Session 19**: Biomedical Image Analysis (4) **Session 20**: Biomedical Text Mining and Ontologies (1)	**Session 30**: Sequencing and High-throughput Methods (2) **Session 31**: Machine Learning and Modelling for Biomedicine (7) **Session 32**: AI and Machine Learning for Health Informatics (7) **Session 33**: Biomedical Image Analysis (7) **Session 34**: Healthcare Systems (2)
12:30pm – 1:30pm	Lunch Break		***End of Conference***
Afternoon Sessions 1 1:30pm – 4:00pm	**Session 6**: Structure, Function, and Evolution (2) **Session 7**: Machine Learning and Modelling for Biomedicine (2) **Session 8**: AI and Machine Learning for Health Informatics (2) **Session 9**: Biomedical Image Analysis (2) **Session 10**: Biomedical Signal Analysis (1)	**Session 21**: Computational Systems Biology (2) **Session 22**: Machine Learning and Modelling for Biomedicine (5) **Session 23**: AI and Machine Learning for Health Informatics (5) **Session 24**: Biomedical Image Analysis (5)	
Afternoon Sessions 2 4:00pm – 6:30pm.	**Session 11**: Structure, Function, and Evolution (3) **Session 12**: Machine Learning and Modelling for Biomedicine (3) **Session 13**: AI and Machine Learning for Health Informatics (3) **Session 14**: Biomedical Image Analysis (3) **Session 15**: Biomedical Signal Analysis (2)	**Session 25**: Sequencing and High-throughput Methods (1) **Session 26**: Machine Learning and Modelling for Biomedicine (6) **Session 27**: AI and Machine Learning for Health Informatics (6) **Session 28**: Biomedical Image Analysis (6) **Session 29**: Biomedical Text Mining and Ontologies (2)	

Keynote Lectures

December 17	December 18	December 19
Accelerating Drug Discovery with an AI-Based Virtual Human System CODA	*Modeling and Evaluating Intervention Options and Strategies for COVID-19 Containment: A Biological-Behavioral-Logistics Computation Decision Framework*	*Network Biomarker for Quantifying Regular State of a Biological System, and Dynamic Network Biomarker for Quantifying Critical State of a Biological System*
		
Dr. Doheon Lee Director of Bio-Synergy Research Center and Professor, Department of Bio and Brain Engineering Korea Advanced Institute of Science and Technology, Korea	**Dr. Eva Lee** Virginia C. and Joseph C. Mello Chair and Professor, H. Milton Stewart School of Industrial and Systems Engineering, Georgia Tech, USA	**Dr. Luonan Chen** Professor, Executive Director, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, China

12/17: Keynote Lecture

Accelerating Drug Discovery with an AI-Based Virtual Human System CODA

Doheon Lee, Professor, Department of Bio and Brain Engineering, Korea Advanced Institute of Science and Technology and Director of Bio-Synergy National Research Center, Korea

Abstract: Formidable complexity of systemic human physiology often give rises of unintended effects of therapeutic compounds during the drug development processes or even after the drug approvals. Though the beneficial unintended effects could lead opportunities of repositioning drugs, the harmful effects might put critical hurdles against successful drug development. We have been developing a virtual human system, CODA, which can explore functional effects of therapeutic compounds in the systemic level. CODA integrates three types of physiological knowledge from public structured databases, literature, and in-house experiments into a unified format of physiological interactions. More than ten public databases including KEGG, GO, and CTD have been transformed; around 25 million PUBMED abstracts have been text-mined; and more than 5,000 in-house novel findings have been incorporated. We have also developed two types of analysis on the CODA knowledge repository. Given therapeutic compounds of interest, CODA can identify possible phenotypic effects in the systemic level. When therapeutic compounds and their observed functional effects are given, CODA can enumerate possible effect paths encompassing molecular, functional, and disease level interactions. We have been testing CODA by applying it to various tasks including drug repositioning, drug-drug interactions, and side effect prediction with known benchmark datasets. Though we are enriching CODA with more knowledge sources and more sophisticated analysis techniques, the current version is already providing unique analysis capabilities and one of the most comprehensive information for drug discovery.

Prof. Doheon Lee is Professor in the Department of Bio and Brain Engineering, Korea Advanced Institute of Science and Technology and Director of Bio-Synergy National Research Center, Korea. He also serves as the President of Korean Society for Bioinformatics. Doheon Lee received the B.S., M.S., and Ph.D. degrees in computer science from Korea Advanced Institute of Science and Technology (KAIST), Korea, in 1990, 1992, and 1995, respectively. He was a visiting professor of Stanford University, Indiana University, Translational Genomics Research Institute (TGEN) and Univ. of Texas at Austin, USA. Currently, he is a professor in Department of Bio and Brain Engineering, KAIST, and the director of Bio-Synergy Research Center (BSRC), a Korean national project where over 30 principal investigators are collaborating for natural product bioinformatics and systems biology. He was an Associate Editor for ACM Transactions on Internet Technology for nine years. He is also serving Scientific Reports, International Journal of Data Mining in Bioinformatics, and Healthcare Informatics Research as an Editorial Board Member. He is a co-founder of ACM International Workshop on Data and Text Mining for Biomedical Informatics. He has published over 200 academic papers in bioinformatics, medical informatics, neuroinformatics, and data mining.

12/18: Keynote Lecture

Modeling and Evaluating Intervention Options and Strategies for COVID-19 Containment: A Biological-Behavioral-Logistics Computation Decision Framework

Eva Lee, Virginia C. and Joseph C. Mello Chair and Professor, H. Milton Stewart School of Industrial and Systems Engineering, Georgia Tech, USA

Abstract: SARs, bird flu, H1N1, Ebola crisis in W. Africa, Zika and current SARS-CoV-2 underscore the critical importance of emergency response and medical preparedness. Such needs are wide-spread as globalization and air transportation facilitate rapid disease spread across the world. Computational modeling of infectious disease outbreaks and epidemics offer insights in propagation patterns and facilitate policy makers to synthesize potential interventions. Current models include inclined decay with an exponential adjustment, SEIR (susceptible, exposed, infectious, recovered) compartmental model, discrete time stochastic processes, and transmission tree. While many of these models incorporate contact tracing to predict spread pattern, key elements on optimal usage of scarce resources and effective and efficient process performance (e.g., diagnostics and screening, non-pharmaceutical interventions, trained personnel/robots for treatment, decontamination) have not been included. This is particularly critical in the fight of COVID-19 containment due to lack of testing kits and the prevalence of asymptomatic transmission, and the long period of hospitalization required by severely sick patients. This work focuses on designing a system computational decision modeling framework that simultaneously i) captures disease spread characteristics, ii) incorporates day-to-day hospital and home care processes and resource usage, iii) explores non-pharmaceutical intervention, social and human behavior and iv) allows for system optimization to minimize infection and mortality under time and labor constraints.

Prof. Eva Lee is the Chair and Professor in H. Milton Stewart School of Industrial and Systems Engineering at Georgia Tech, also serves as the Director of the Center for Operations Research in Medicine and HealthCare. She is also a Senior Research Professor at the Atlanta VA Medical Center. Dr. Lee works in the area of mathematical programming and large-scale computational algorithms with a primary emphasis on medical/healthcare decision analysis and logistics operations management. She tackles challenging problems in health systems and biomedicine through systems modeling, algorithm and software design, and decision theory analysis. Specific research areas include health risk prediction, early disease prediction and diagnosis, optimal treatment strategies and drug delivery, healthcare outcome analysis and treatment prediction, public health and medical preparedness, large-scale healthcare/medical decision analysis and quality improvement. Dr. Lee's research in logistics focuses on large-scale optimization and algorithmic advances for optimal operations planning and resource allocation. She has developed decision support systems for inventory control; large-scale truck dispatching, scheduling, and transportation logistics; telecommunications; portfolio investment; and emergency treatment response and facility layout and planning. Dr. Lee was awarded a NSF/NATO postdoctoral fellowship on Scientific Computing, and a postdoctoral fellowship from Konrad-Zuse-Zentrum Informationstechnik Berlin in 1995 for Parallel Computation. In 1996, she received the NSF Presidential Young Investigator Award for research on integer programming and parallel algorithms and their applications to medical diagnosis and cancer treatment. She was the first OR/IE recipient for the prestigious Whitaker Foundation Biomedical Grant for Young Investigators, awarded for her work on a novel approach for combining biological imaging and optimal treatment design for prostate cancer. In 2004, she was selected as one of the Extraordinary Women Engineers. In 2005, she received the INFORMS Pierskalla award for research excellence in HealthCare and Management Science for her work on emergency response and planning, large-scale prophylaxis dispensing, and resource allocation for bioterrorism and infectious disease outbreaks. In 2006, she was chosen by the American Mathematical Society as the representative mathematician to speak and discuss individually with congressional leaders about her research advances in the medical and healthcare domain, and about the importance of mathematics in scientific advances. Together, Lee and Dr. Marco Zaider from Memorial Sloan-Kettering Cancer Center were named winners of the 2007 Franz Edelman award for their work on using operations research to advance cancer therapeutics. Lee has received seven patents for innovative medical systems and devices. Her research has been featured and discussed in numerous news media articles, including articles in the New York Times, London Times, Urology Times, Atlanta Business Chronicle, and Homeland Security IAIP Directorate Daily Report. Her cancer research was featured in a TV science news segment for Discoveries and Breakthroughs, Inside Science, Curing Prostate Cancer, broadcast by television stations nationwide.

12/19: Keynote Lecture

Network Biomarker for Quantifying Regular State of a Biological System, and Dynamic Network Biomarker for Quantifying Critical State of a Biological System

Luonan Chen, Professor, Executive Director, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, China

Abstract: We defined two new types of biomarkers to quantify the states of biological systems based on network, in contrast to the traditional molecular biomarkers. Network biomarker is constructed to quantify regular state of a biological system, while dynamic network biomarker is to quantify the critical state or tipping point of a biological system. (1) Network biomarker (NB) is a subnetwork or network module, which is composed of a number of associations or regulations between molecules (or variables), rather than simply a number of molecules. Those associations (the second-order statistics) in the module are formed collectively as a biomarker, thus robustly and accurately quantifying the regular state of a biological system, completely different from the concentrations or densities of conventional molecular biomarkers (the first-order statistics). (2) Dynamic network biomarker (DNB) is a subnetwork or module, and is also composed of a number of associations or regulations between molecules but with three statistical conditions (in terms of variances and covariances), which are actually a number of strongly and collectively fluctuated molecules in the network. Theoretically, DNB is able to quantify the critical state or the tipping point of a biological system, thereby serving as a general early-warning signal to indicate an imminent state transition. A number of real datas are provided to validate the effectiveness of NB and DNB.

Prof. Luonan Chen received BS degree in the Electrical Engineering, from Huazhong University of Science and Technology, and the M.E. and Ph.D. degrees in the electrical engineering, from Tohoku University, Sendai, Japan, in 1988 and 1991, respectively. From 1997, he was an associate professor of the Osaka Sangyo University, Osaka, Japan, and then a full Professor. Since 2010, he has been a professor and executive director at Key Laboratory of Systems Biology, Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences. He was the founding director of Institute of Systems Biology, Shanghai University. He was elected as the founding president of Computational Systems Biology Society of OR China, and Chair of Technical Committee of Systems Biology at IEEE SMC Society.In recent years, he published over 350 journal papers and two monographs (books) in the area of bioinformatics, nonlinear dynamics and machine learning.

12/17: Invited Talk

Identification of functional modules controlling tumor-stroma communication signals by multi-dimensional genomic and epigenomic analysis

Tae-Young Roh, Professor, Department of Life Sciences and Division of Integrative Biosciences and Biotechnology, POSTECH, Korea

Abstract: The tumor microenviroment forms a dynamic milieu of non-cancerous cells interacting with cancer cells, which plays an important role in inducing the cancer heterogeneity, progression, and metastasis. It is well known that epigenetic mechanisms are involved in the developing of these cells. Epigenetics refers to as an alteration of gene expression program without changes in DNA sequence. During the tumor progression, many groups have been explored the interaction between cancer and stroma cells by examining gene expression profiles but simple comparison of gene expression patterns might not be enough to explain the principles of biological system. Here we extensively analyzed the functional modules responsible for tumor-stroma communications by multi-dimensional genomic and epigenomic approaches such as Exome-Seq, RNA-Seq, ChIP-Seq, ATAC-Seq, and single cell RNA-Seq using bladder tumors and assembloids as a model. The assembloids were constructed by assembling tissue stem cells and stromal components establishing tumor microenvironment. From the single cell RNA-Seq result, the cellular components were matured distinctively by confirming specific marker genes' expression for each cluster by a Wilcoxon rank sum test with Bonferroni correction. Also the functional epigenetic modules were identified by differential changes in chromatin structures (ATAC-Seq) and transcription factor occupancy with histone modification alterations (ChIP-Seq). Our result shows a good example that the multi-omics comparative analysis could reveal that dynamic signaling feedback communication between tumor and stroma under the control of epigenetic dynamics.

Prof. Tae-Young Roh received Ph.D degree in Biochemistry from Department of Chemistry, Seoul National University, Korea in 2002. He trained as a Visiting and Research Fellow at the National Institutes of Health, USA. Since 2008, he has served as an assistant and currently associate professor of Pohang University of Science and Technology (POSTECH), Korea. He published about 70 scientific papers and articles in the field of genomics, epigenomics, bioinformatics, and etc. He is a founder of SysGenLab Inc. providing genomic services such as sequencing, biomarker finding, and bioinformatic analysis. He is a Board Member of Korea Genome Organization (KOGO), Korea Organoid Society (KOS), and Korean Society of Biochemistry and Molecular Biology (KSBMB).

12/19: Invited Talk

Use cases of big data and deep learning for large-scale biomedical applications using supercomputers.

Seung-Jong Park, Professor, Department of Computer Science, Louisiana State University, USA

Abstract: This talk will discuss about diverse use-cases based on big data and deep learning technologies for large scale bioinformatics applications especially for whole genome de novo assembly and error corrections. The talk will discuss about a distributed assembler that achieves both scalability and memory efficiency by using partitioned de Bruijn graphs, enhancing the memory-to-disk swapping, and reducing the network communication in the HPC cluster.

Then the talk presents a use-case of Deep Learning to the automated detection and diagnosis of breast cancer using mammogram images using advanced deep learning techniques and then demonstrates the effectiveness of the proposed method on detection of suspicious areas and further diagnosis as benign or malignant compared to related works.

Dr. Seung-Jong (Jay) Park is the Dr. Fred H. Fenn Memorial Professor of the School of Electrical Engineering & Computer Science and jointly appointed with the Center for Computation Technology at Louisiana State University. He received his Ph.D. from The School of Electrical and Computer Engineering at Georgia Institute of Technology, 2004. He has performed interdisciplinary research projects including (1) big data & deep learning research including developing software frameworks for large-scale science applications and (2) cyberinfrastructure development using cloud computing and high-performance computing. Those projects have been supported by federal and state funding programs including NSF CC-NIE, NSF MRI, NSF IBSS, NSF GENI, NASA Geohealth, NIH LBRN programs, etc. He has published more than 70 papers in major journals and conferences (e.g., IEEE Tran. on Mobile Computing, ACM MobiHoc, IEEE Bigdata, IEEE BIBM, IEEE IPDPS, IEEE ICDCS, ACM BCB, MICCAI, IEEE Cloud, IEEE ICPADS, IEEE ICCCN, IEEE LCN, IEEE ICC, IEEE Globecom, EDBT/ICDT, etc.)

12/17: Morning Sessions

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

(Session Chair: Marcel Turcotte)

R	B326 "Decoy Selection in Protein Structure Determination via Symmetric Non-negative Matrix Factorization" Kazi Lutful Kabir, Gopinath Chennupati, Raviteja Vangara, Hristo Djidjev, Boian Alexandrov, and Amarda Shehu
R	B357 "Protein Decoy Generation via Adaptive Stochastic Optimization for Protein Structure Determination" Ahmed Bin Zaman, Toki Tahmid Inan, and Amarda Shehu
R	B572 "Assessing the Use of Secondary Structure Fingerprints and Deep Learning to Classify RNA Sequences" Kevin Sutanto and Marcel Turcotte
S	B695 "Phylogenetic Manifold Regularization: A semi-supervised approach to predict transcription factor binding sites" Faizy Ahsan, Alexandre Drouin, François Laviolette, Doina Precup, and Mathieu Blanchette
R	B259 "Protein Ensemble Learning with Atrous Spatial Pyramid Networks for Secondary Structure Prediction" Yuzhi Guo, Jiaxiang Wu, Hehuan Ma, Sheng Wang, and Junzhou Huang
S	B419 "WeightAln: Weighted Homologous Alignment for Protein Structure Property Prediction" Yuzhi Guo, Jiaxiang Wu, Hehuan Ma, Jinyu Yang, Xinliang Zhu, and Junzhou Huang
S	B223 "α-MOP: Molecule Optimization with α-divergence" Tianfan Fu, Cao Xiao, Lucas Glass, and Jimeng Sun

Session 2: Machine Learning and Modelling for Biomedicine (1)

(Session Chair: Chen Li)

R	B556 "A Novel Algorithm for Training Hidden Markov Models with Positive and Negative Examples" Jiefu Li, Jung-Youn Lee, and Li Liao
R	B690 "Analysis of Meta-Learning Approaches for TCGA Pan-cancer Datasets" Jingyuan Chou, Stefan Bekiranov, Chongzhi Zang, Mengdi Huai, and Aidong Zhang
S	B734 "Learning A Lower Bound on Direct Causal Influences From Marginal Independencies" Borzou Alipourfard and Jean Gao
R	B293 "Multi-task Based Few-Shot Learning for Disease Similarity Measurement" Jianliang Gao, Ling Tian, Yuxin Liu, Jianxin Wang, Zhao Li, and Xiaohua Hu
R	B391 "Symptom and Pathology Report Generation for Ophthalmic Diseases in Fundus Images" Yang Wen, Leiting Chen, Lifeng Qiao, Deng Yu, Siying Dai, Junjing Chen, and Chuan Zhou
S	B203 "A multi-task learning method for analyzing microbiota as cancer immunotherapy signal" Changzhi Jiang, Yousi Fu, Shuting Jin, Xiangrong Liu, Baishan Fang, and Xiangxiang Zeng
S	B250 "CLUE: Personalized Hospital Readmission Prediction Against Data Insufficiency under Imbalanced-Data Environment" Qianwen Meng, Lizhen Cui, Guoxian Yu, Han Yu, Wei Guo, and Hui Li

Session 3: AI, Machine Learning for Health Informatics (1)

(Session Chair: Guoxian Yu)

R	B730 "Artifact Detection in Invasive Blood Pressure Data using Forecasting Methods and Machine Learning" Mengqi Wu, Paula Branco, Janny Xuechen Ke, and David B. MacDonald
R	B682 "Imputing Growth Snapshot Similarity in Early Childhood Development: A Tensor Decomposition Approach" Jennifer Schnur, Ryan Karl, Angelica Garcia-Martinez, Meng Jiang, and Nitesh Chawla
R	B271 "Predicting Prescriptions via DSCA-Dual Sequences with Cross Attention Network" Wu Lee, Yuliang Shi, Lin Cheng, Yongqing Zheng, and Zhongmin Yan
R	B366 "Spatial--temporal Joint Optimization Network on Covariance Manifolds of Electroencephalography for Fatigue Detection" Xiaowei Zhang, Dawei Lu, Jian Shen, Jin Gao, Xiao Huang, and Manxi Wu
S	B266 "Evaluating the relative value of care interventions based on clinical pathway variation detection and propensity score" Haifeng Xu, Jianfei Pang, Xi Yang, Hui Yan, Shan Nan, and Dongsheng Zhao
S	B335 "A Graph-boosted Framework for Adverse Drug Event Detection on Twitter" Chen Shen, Hongfei Lin, Zhiheng Li, Yonghe Chu, Zhengguang Li, and Zhihao Yang
S	B401 "Chinese Word Segmentation in Electronic Medical Record Text via Graph Neural Network-Bidirectional LSTM-CRF Model" Jinlian Du, Wei Mi, and Xiaolin Du

Session 4: Biomedical Image Analysis (1)

(Session Chair: Hua Wang)

S	B677 "Enhancing Automated COVID-19 Chest X-ray Diagnosis by Image-to-Image GAN Translation" Zhaohui Liang, Jimmy Xiangji Huang, Jun Li, and Stephen Chan
R	B513 "Unlabeled Data Guided Semi-supervised Histopathology Image Segmentation" Hongxiao Wang, Hao Zheng, Jianxu Chen, Lin Yang, Yizhe Zhang, and Danny Chen
S	B724 "Detailed Investigation of Lumen-Based Tomographic Co-Registration" Abhishek Karmakar, Max Olender, Farhad Rikhtegar Nezami, David Marlevi, Evan Shlofmitz, Richard Shlofmitz, and Elazer Edelman
S	B418 "Learning Semi-Supervised Enrichment of Longitudinal Imaging-Genetic Data for Improved Prediction of Cognitive Decline" Hoon Seo, Lodewijk Brand, and Hua Wang
R	B287 "Flow-Mixup: Classifying Multi-labeled Medical Images with Corrupted Labels" Jintai Chen, Hongyun Yu, Ruiwei Feng, Danny Chen, and Jian Wu
R	B295 "Constrained Multi-scale Dense Connections for Accurate Biomedical Image Segmentation" Jiawei Zhang, Yanchun Zhang, Shanfeng Zhu, and Xiaowei Xu
S	B445 "Deep Multi-Instance Learning with Induced Self-Attention for Medical Image Classification" Zhenliang Li, Liming Yuan, Haixia Xu, Rui Cheng, and Xianbin Wen

Session 5: Healthcare Systems (1)

(Session Chair: Seungyoon Nam)

	Invited Talk: Dr. Tae-Young Roh “Identification of functional modules controlling tumor-stroma communication signals by multi-dimensional genomic and epigenomic analysis”
S	B581 "Identifying prognostic subgroups of luminal-A breast cancer using a deep autoencoder" Seunghyun Wang and Doheon Lee
S	B383 "GSSMD: A new standardized effect size measure to improve robustness and interpretability in biological applications" Seongyong Park, Shujaat Khan, Muhammad Moinuddin, and Ubaid M. Al-Saggaf
S	B763 "Coded Dynamic Consent framework using Blockchain for Healthcare Information Exchange" Ah Ra Lee, Min Gyu Kim, Kyung Jae Won, Il Kon Kim, and Eun Joo Lee

12/17: 1st Afternoon Sessions

Session 6: Structure, Function, and Evolution (2)

(Session Chair: Dongqing Wei)

R	B553 "Machine Learning Approach to Assign Protein Secondary Structure Elements from Cα Trace" Mohammad Al Sallal, Wei Chen, and Kamal Al Nasr
S	B380 "A novel spatial feature for predicting lysine malonylation sites using machine learning" Yuan Liu and Changhui Yan
S	B710 "Efficient Cryo-Electron Tomogram Simulation of Macromolecular Crowding with Application to SARS-CoV-2" Sinuo Liu, Yan Ma, Xiaojuan Ban, Xiangrui Zeng, Vamsi Nallapareddy, Ajinkya Chaudhari, and Min Xu
R	B461 "GONET: A Deep Network to Annotate Proteins via Recurrent Convolution Networks" Junyi Li, Lixin Wang, Xiaoshuai Zhang, Bo Liu, and Yadong Wang
R	B780 "An two-layer predictive model of ensemble classifier chain for detecting antimicrobial peptides" Jinhao Zhang, Shuhao Li, Yijie Ding, Jijun Tang, and Fei Guo
S	B516 "Dual Graph regularized PCA based on Different Norm Constraints for Bi-clustering Analysis on Single-cell RNA-seq Data" Yu Song, Xiang-Zhen Kong, Jin-Xing Liu, Juan Wang, Sha-Sha Yuan, and Ling-Yun Dai

Session 7: Machine Learning and Modelling for Biomedicine (2)

(Session Chair: Yan Yan)

R	B462 "Bayesian Multi-scale Convolutional Neural Network for Motif Occupancy Identification" Wei Li, Qingqing Zhao, Han Zhang, Xiongwen Quan, Jing Xu, and Yanbin Yin
R	B463 "Toward high accuracy and visualization: A interpretable feature extraction method based on genetic programming and non-overlap degree" Zhuang Li, Jie He, Xiaotong Zhang, Huadong Fu, and Jingyan Qin
R	B473 "Predicting CRISPR-Cas9 Off-target with Self-supervised Neural Networks" Dong Chen, Wenjie Shu, and Shaoliang Peng
R	B488 "An End-to-end Oxford Nanopore Basecaller Using Convolution-augmented Transformer" Xuan Lv, Zhiguang Chen, yutong lu, and yuedong yang
S	B256 "Assessment of machine learning methods for classification in single cell ATAC-seq" Zhe Cui, Liran Juan, Tao Jiang, Bo Liu, Tianyi Zang, and Yadong Wang
S	B313 "Fast approximate spectral clustering via adaptive filtering of random graph signals" Tianyu Yu, Yonghua Zhao, Rongfeng Huang, Shifang Liu, and Xinyin Zhang
S	B371 "LPI-DL: A recurrent deep learning model for plant lncRNA-protein interaction and function prediction with feature optimization" Jael Sanyanda Wekesa, Yushi Luan, and Jun Meng

Session 8: AI, Machine Learning for Health Informatics (2)

(Session Chair: Hongdong Li)

R	B423 "A Domain Adaption Multi-instance Learning for Diabetic Retinopathy Grading on Retinal Images" Ruoxian Song and Peng Cao
R	B454 "Extracting biomedical relations via a multi-head attention based graph convolutional network" Erniu Wang, Fan Wang, Zhihao Yang, Lei Wang, Yin Zhang, Hongfei Lin, and Jian Wang
R	B458 "DeepComp: Which Competing Event Will Hit the Patient First?" Yingxue Li, Wenxiao Jia, Yashu Kang, Tiange Chen, Xiang Li, Xin Du, Jianzeng Dong, Changsheng Ma, Fei Wang, and Guotong Xie
R	B496 "A novel approach based on deep residual learning to predict drug's anatomical therapeutic chemical code" Haochen Zhao, Peng Ni, Cheng yan, Yaohang Li, and Jianxin Wang
S	B629 "Calibration-free Blood Pressure Assessment Using An Integrated Deep Learning Method" Chuanqi Han, Mengyin Gu, Fang Yu, Ruoran Huang, Xi Huang, and Li Cui
S	B646 "Hierarchical Attention-Based Multiple Instance Learning Network for Patient-Level Lung Cancer Diagnosis" Qingfeng Wang, Ying Zhou, Jun Huang, Zhiqin Liu, Ling Li, Weiyun Xu, and Jie-Zhi Cheng
S	B758 "An Enhanced LRMC Method for Drug Repositioning via GCN-based HIN Embedding" Haowen Sun, Xiaoqing Lyu, Bei Wang, Yifan Wang, and Zhi Tang

Session 9: Biomedical Image Analysis (2)

(Session Chair: Fa Zhang)

R	B314 "Data-Efficient Histopathology Image Analysis with Deformation Representation Learning" Jilan Xu, Junlin Hou, Yuejie Zhang, Rui Feng, Chunyang Ruan, Tao Zhang, and Weiguo Fan
R	B316 "EffiDiag: an Efficient Framework for Breast Cancer Diagnosis in Multi-Gigapixel Whole Slide Images" Shuyan Liu, Junda Ren, Zhineng Chen, Kai Hu, Fen Xiao, Xuanya Li, and Xieping Gao
R	B342 "A Network of Simultaneous Segmentation and Registration for Right Ventricle MRI" Adan Lin, Zhenzhen Li, and Xuan Yang
R	B344 "Coarse-to-fine Nasopharyngeal Carcinoma Segmentation in MRI via Multi-stage Rendering" Yang Li, Hong Peng, Tingting Dan, Yu Hu, Guihua Tao, and Hongmin Cai
S	B576 "Attention based detection for Central Serious Chorioretinopathy in fundus image" Chuan Zhou, Tian Zhang, Leiting Chen, Yang Wen, Ting Lei, and Junjing Chen
S	B343 "Reconstruction of 3D Retina from Multi-viewed Stereo Fundus Images via Dynamic Registration" Tingting Dan, Zhihao Fan, Yu Hu, Bin Zhang, Guihua Tao, and Hongmin Cai
S	B330 "Detection of Early Gastric Cancer Based on Single Shot Detector with Feature Enhancement" Dongsheng Pan, Rong Zhang, Yalei Wang, and Hui Feng

Session 10: Biomedical Signal Analysis (1)

(Session Chair: Zhu-Hong You)

R	B377 "A Sequential Graph Convolutional Network with Frequency-domain Graph Representation of EEG Signals for Epilepsy Detection" Jialin Wang, Shen Liang, DaKe He, Ye Wang, Yingpei Wu, and Yanchun Zhang
R	B404 "Channel Selection based Similarity Measurement for Motor Imagery Classification" Shiyi Chen, Yaoru Sun, Haoran Wang, and Zilong Pang
R	B480 "Designing and Application of Wearable Fatigue Detection System Based on Multimodal Physiological Signals" Xiaoxuan Qiu, Fuze Tian, Qiuxia Shi, Qinglin Zhao, and Bin Hu
R	B466 "Respiratory Sound Classification Based on BiGRU-Attention Network with XGBoost" Xuesong Zhao, Yanbo Shao, Juanyun Mai, Airu Yin, and Sihan Xu
S	B242 "ECG Pattern Discovery Algorithm Based on Local Repeatability" Yunfei Yin, Hui Cheng, and Faliang Huang
S	B489 "STCN: A Lightweight Sleep Staging Model with Multiple Channels" Yue Wu, Yui Lo, and Yujiu Yang
S	B519 "BrainSleepNet: Learning Multivariate EEG Representation for Automatic Sleep Staging" Xiyang Cai, Ziyu Jia, Minfang Tang, and Gaoxing Zheng

12/17: 2nd Afternoon Sessions

Session 11: Structure, Function, and Evolution (3)

(Session Chair: Iksoo Huh)

R	B575 "Predicting circRNA-disease associations using meta path-based representing learning on heterogenous network" Lei Deng, Jing Yang, and Hui Liu
R	B625 "Predict the Protein-protein Interaction between Virus and Host through Hybrid Deep Neural Network" Lei Deng, Jiaojiao Zhao, and Jingpu Zhang
S	B632 "A Stacked Ensemble Learning Framework with Heterogeneous Feature Combinations for Predicting ncRNA-Protein Interaction" Qiguo Dai, Zhaowei Wang, Jinmiao Song, Xiaodong Duan, Maozu Guo, and Zhen Tian
S	B713 "SeqTMPPI: Sequence-Based Transmembrane Protein Interaction Prediction" Han Wang, Jiuhong Jiang, Qiufen Chen, Chunhua Zhang, Chang Lu, and Zhiqiang Ma
S	B671 "Using a Novel Unbiased Dataset and Deep Learning Architectures to Predict Protein-Protein Interactions" Luís Silva, carlos Pereira, and Joel Arrais
S	B529 "GenFooT: Genomic Footprint of mitochondrial sequence for Taxonomy classification" Aritra Mahapatra and Jayanta Mukherjee

Session 12: Machine Learning and Modelling for Biomedicine (3)

(Session Chair: Wei Lan)

R	B492 "Tensor Robust Principal Component Analysis with Low-Rank Weight Constraints for Sample Clustering" YuYing Zhao, MaoLi Wang, Juan Wang, ShaSha Yuan, and Jinxing Liu
R	B562 "Anomaly Detection on Electroencephalography with Self-supervised Learning" Junjie Xu, Yaojia Zheng, Yifan Mao, Ruixuan Wang, and Wei-shi Zheng
R	B633 "Exploring Multi-level Mutual Information for Drug-target Interaction Prediction" Jiatao Chen, Liang Zhang, Ke Cheng, Bo Jin, Xinjiang Lu, and Chao Che
S	B525 "MetaG : a comprehensive visualization tool to explore metagenomes" Uditha Maduranga, Kalana Wijegunarathna, Sadeep Weerasinghe, Indika Perera, and Anuradha Wickramarachchi
S	B672 "MP3vec: A Reusable Machine-Constructed Feature Representation for Protein Sequences" Sanket Rajan Gupte, Dharm Skandh Jain, Ashwin Srinivasan, and Raviprasad Aduri
S	B274 "Adversarial Vulnerability of Deep Learning Models in Analyzing Next Generation Sequencing Data" Amiel Meiseles, Ishai Rosenberg, Yair Motro, Lior Rokach, and Jacob Moran-Gilad

Session 13: AI, Machine Learning for Health Informatics (3)

(Session Chair: Hongmin Cai)

R	B469 "Machine Learning to Predict ICU Admission, ICU Mortality and Survivors' Length of Stay among COVID-19 Patients: Toward Optimal Allocation of ICU Resources" Tingting Dan, Yang Li, Ziwei Zhu, Xijie Chen, Wuxiu Quan, Yu Hu, Guihua Tao, Lei Zhu, Jijin Zhu, Yuyan Jin, Longgeng Li, Chaokai Liang, Hanchun Wen, and Hongmin Cai
R	B500 "Lymph Node Metastasis Classification Based on Semi-Supervised Multi-View Network" Yiwen Luo, Jingmin Xin, Sijie Liu, Junqin Feng, Litao Ruan, Wei Cui, and Nanning Zheng
R	B555 "Modeling Multivariate Time Series via Prototype Learning: a Multi-Level Attention-based Perspective" Dengjuan Ma, Zhu Wang, Jia Xie, Zhiwen Yu, Bin Guo, and Xingshe Zhou
R	B563 "Multi-scale strategy based 3d dual-encoder brain tumor segmentation network with attention mechanism" Yazhou Zhu, Xiang Pan, Jing Zhu, and Lihua Li
R	B573 "Enhancing Tiny Tissues Segmentation via Self-Distillation" Chuan Zhou, Yuchu Chen, Minghao Fan, Yang Wen, Hang Chen, and Leiting Chen
R	B605 "Tensor-based Low-rank and Graph Regularized Representation Learning for Multi-view Clustering" Haiyan Wang, Guoqiang Han, Bin Zhang, Yu Hu, Hong Peng, Chu Han, and Hongmin Cai

Session 14: Biomedical Image Analysis (3)

(Session Chair: Pierangelo Veltri)

R	B349 "Automatic Psoriasis Lesion Segmentation from Raw Color Images using Deep Learning" Ritesh Raj, Narendra Londhe, and Rajendra Sonawane
R	B365 "DCE-MRI based Breast Intratumor Heterogeneity Analysis via Dual Attention Deep Clustering Network and its Application in Molecular Typing" Tianxu Lv, Xiang Pan, and Lihua Li
R	B210 "On the Effective Transfer Learning Strategy for Medical Image Analysis in Deep Learning" Yang Wen, Leiting Chen, Chuan Zhou, Deng Yu, Huiru Zeng, Shuo Xi, and Rui Guo
S	B337 "Attention-based Saliency Hashing for Ophthalmic Image Retrieval" Jiansheng Fang, Yanwu Xu, Xiaoqing Zhang, Yan Hu, and Jiang Liu
S	B276 "CorGAN: Context aware Recurrent Generative Adversarial Network for Medical Image Generation" Zhi Qiao, Zhen Qian, Hui Tang, Guanzhong Gong, Yong Yin, Chao Huang, and Wei Fan
S	B715 "Domain Adaptation for Heart Rate Extraction in the Neonatal Intensive Care Unit" Diogo Malafaya, Sara Domingues, and Hélder Oliveira

Session 15: Biomedical Signal Analysis (2)

(Session Chair: Sungho Won)

S	B468 "Reconstructing Temporal Dynamics of fMRI Time Series via Encoded Contextual Information" Wenjun Bai, Tomoki Tokuda, Okito Yamashita, and Junichiro Yoshimoto
R	B477 "Identifying abstinent heroin addicts on the basis of single channel's ERP and behavioral data in the gambling task" Xiaozhe Liang, Yanrong Hao, Zhihao Xu, Na Li, and Qinglin Zhao
S	B348 "A Novel Multidimensional Feature Extraction Method Based on VMD and WPD for Emotion Recognition" Min Zhang, Bin Hu, Xiangwei Zheng, and Tiantian Li
S	B579 "A Two-level Attention-based Sequence-to-Sequence Model for Accurate Inter-patient Arrhythmia Detection" Kun Jiang, Shen Liang, Lingxiao Meng, Yanchun Zhang, Peng Wang, and Wei Wang
S	B746 "Time-frequency Analysis Based on Hilbert-Huang Transform for Depression Recognition in Speech" Zhenyu Liu, Yaping Xu, ZhiJie Ding, and Qiongqiong Chen
S	B450 "Longitudinal Analysis of the Connectivity and Complexity of Complete Locked-in Syndrome Patients Electroencephalographic signal" Sophie Adama, Ujwal Chaudhary, Niels Birbaumer, and Martin Bogdan
S	B727 "Human gait model based on a machine learning and Filtering noisy signals with recursive algorithm" Diego Teran and Enrique Dominguez

12/18: Morning Sessions

Session 16: Computational Systems Biology (1)

(Session Chair: Serdar Bozdag)

S	B731 "Identification of Key Biological Pathway Routes in Cancer Cohorts" Pujan Joshi, Brent Basso, Honglin Wang, Seung-Hyun Hong, Charles Giardina, and Dong-Guk Shin
S	B707 "cTAP: A Framework for Predicting Target Genes of a Transcription Factor using a Cohort of Gene Expression Data Sets" Honglin Wang and Dong-Guk Shin
S	B540 "Deep Learning to Identify Transcription Start Sites from CAGE Data" Hansi Zheng, Xiaoman Li, and Haiyan Hu
S	B708 "BioMETA: A multiple specification parameter estimation system for stochastic biochemical models" Arfeen Khalid
S	B702 "NECo: A node embedding algorithm for multiplex heterogeneous networks" Cagatay Dursun, Jennifer R. Smith, G. Thomas Hayman, Anne E. Kwitek, and Serdar Bozdag
R	B624 "Multi-Class Metabolic Pathway Prediction by Graph Attention-Based Deep Learning Method" Zhihui Yang, Juan Liu, Zeyu Wang, Yufan Wang, and Jing Feng
R	B765 "Cooperative Driver Pathway Discovery by Hierarchical Clustering and Link Prediction" Sufang Li, Jun Wang, Maozu Guo, and Xiangliang Zhang

Session 17: Machine Learning and Modelling for Biomedicine (4)

(Session Chair: Xiujuan Lei)

R	B604 "Graph Convolution Networks Using Message Passing and Multi-Source Similarity Features for Predicting circRNA-Disease Association" Thosini Bamunu Mudiyanselage, Xiujuan Lei, Nipuna Senanayake, Yanqing Zhang, and Yi Pan
S	B472 "Predicting therapeutic outcomes in Rheumatoid Arthritis using real-world pharmacogenetic and clinical data" Fabián Hernández, Luis Fernando Niño, and Fabio Aristizábal
S	B302 "RSGSA: a robust and stable gene selection algorithm" Subrata Saha, Ahmed Soliman, and Sanguthevar Rajasekaran
S	B735 "A Predictive Model for Parkinson's Disease Reveals Candidate Gene Sets for Progression Subtype" Saya Dennis, Tanya Simuni, and Yuan Luo
R	B532 "A multi-view approach for predicting microbe-disease associations by fusing the linear and nonlinear features" Ming Liu, Wei Dai, Wei Peng, Yu Fu, and Yi Pan
R	B433 "A topological AUC-based biomarker ensemble method for the complex disease analysis" Xingyi Li, Ju Xiang, Fang-Xiang Wu, and Min Li
S	B389 "A novel synonymous processing method based on amino acid substitution matrics for the classification of G-protein-coupled receptors" Cheng Ling and Yitian Shen

Session 18: AI, Machine Learning for Health Informatics (4)

(Session Chair: Xingming Zhao)

R	B283 "Revealing Common and Rare Patterns for Peritoneal Dialysis Eligibility Decisions with Association Discovery and Disentanglement" Peiyuan Zhou, Andrew K.C. Wong, George Michalopoulos, Robert R. Quinn, Matthew J. Oliver, Yang Yang, Zahid Butt, and Helen Chen
R	B355 "Global Interpretation for Patient Similarity Learning" Mengdi Huai, Chenglin Miao, Jinduo Liu, Di Wang, Jingyuan Chou, and Aidong Zhang
S	B618 "Clinical Phrase Mining with Language Models" Kaushik Mani, Xiang Yue, Bernal Jimenez Gutierrez, Yungui Huang, Simon Lin, and Huan Sun
R	B622 "A Semi-supervised Approach for Early Identifying the Abnormal Carotid Arteries Using a Modified Variational Autoencoder" Xiaoxiang Huang, Guosheng Cui, Dan Wu, and Ye Li
R	B688 "IB-M: A Flexible Framework to Align an Interpretable Model and a Black-box Model" Mengze Li, Kun Kuang, Qiang Zhu, Xiaohong Chen, Qing Guo, and Fei Wu
R	B728 "An Ensemble Deep Learning Architecture for Multi-label Classification on TI-RADS" Xueli Duan, Shaobo Duan, Pei Jiang, Runzhi Li, Ye Zhang, Jingzhe Ma, Hongling Zhao, and Honghua Dai
S	B208 "Chest X-ray Lung Chinese Description Generation based on Semantic Labels and Hierarchical LSTM" Xin Huang, Biao Zhong, Yuanlong Cao, Yugen Yi, and Mengdan Gu

Session 19: Biomedical Image Analysis (4)

(Session Chair: Hongming Shan)

S	B441 "Automatic Extraction of Skeletal Maturity from Whole Body Pediatric Scoliosis X-rays Using Regional Proposal and Compound Scaling Convolutional Neural Networks" Audrey Ha, John Vorhies, Andrew Campion, Charles Fang, Michael Fadell II, Steve Dou, Safwan Halabi, David Larson, Emily Wang, YongJin Lee, Joanna Langner, Japsimran Kaur, and Bao Do
S	B382 "Fully automated ordering and labeling of ICA components" Mustafa Salman, Tor Wager, Eswar Damaraju, Anees Abrol, and Vince Calhoun
S	B434 "Do noises bother human and neural networks in the same way? A medical image analysis perspective" Shao-Cheng Wen, Yu-Jen Chen, Zihao Liu, Wujie Wen, Xiaowei Xu, Yiyu Shi, Tsung-Yi Ho, Meiping Huang, Haiyun Yuan, and Jian Zhuang
R	B460 "Nuclei Segmentation in Histopathology Images Using Rotation Equivariant and Multi-level Feature Aggregation Neural Network" Yiqi Chen, Xuanya Li, Kai Hu, Zhineng Chen, and Xieping Gao
R	B470 "Local Adaptive U-net for Medical Image Segmentation" Ning Liu, Liangliang Liu, and Jianxin Wang
R	B478 "Attention U-net for Interpretable Classification on Chest X-ray Image" Xuan Zhang and Ting Chen

Session 20: Biomedical Text Mining and Ontologies (1)

(Session Chair: Renchu Guan)

S	B306 "Fine-Grained Named Entity Recognition with Distant Supervision in COVID-19 Literature" Xuan Wang, Xiangchen Song, Bangzheng Li, Kang Zhou, Qi Li, and Jiawei Han
S	B686 "Predicting Early Indicators of Cognitive Decline from Verbal Utterances" Swati Padhee, Anurag Illendula, Megan Sadler, Valerie L. Shalin, Tanvi Banerjee, Krishnaprasad Thirunarayan, and William L. Romine
S	B403 "OntoSem: an Ontology Semantic Representation Methodology for Biomedical Domain" Lingling Zhao, Junjie Wang, Liang Cheng, and Chunyu Wang
R	B394 "Use of "Internal Knowledge": Biomedical Literature Search Liberated From External Resources" Tianwen Jiang, Ning Zhang, Ming Liu, Meng Jiang, Ting Liu, and Bing Qin
R	B551 "Star-BiLSTM-LAN for Document-level Mutation-Disease Relation Extraction from Biomedical Literature" Yuan Xu, Zhihao Yang, Yawen Song, Zhiheng Li, Lei Wang, Yin Zhang, Hongfei Lin, and Jian Wang
R	B440 "Hierarchical Distillation Network for Biomedical Event Extraction" Lishuang Li, Mengzuo Huang, and Beibei Zhang
S	B725 "Extracting Protein-Protein Interactions Affected by Mutations via Auxiliary Task and Domain Pre-trained Model" Yu Wang, Shaowu Zhang, Yijia Zhang, Jian Wang, and Hongfei Lin

12/18: 1st Afternoon Sessions

Session 21: Computational Systems Biology (2)

(Session Chair: Wei Peng)

R	B548 "GRRFNet: Guided Regularized Random Forest-based Gene Regulatory Network Inference Using Data Integration" Yongqing Zhang, Qingyuan Chen, Dongrui Gao, and Quan Zou
R	B733 "Identification of Cancer Development Related Pathways Based on Co-Expression Analyses" Hongyang Jiang, Zhihang Wang, Chaoyi Yin, Peishuo Sun, Ying Xu, and Huiyan Sun
R	B666 "GPPIAL: A New Global PPI Network Aligner Based on Orthologs" Yaoran Chen, Yuanyuan Zhu, Ming Zhong, Rong Peng, and Juan Liu
S	B427 "Multi-Resolutional Collaborative Heterogeneous Graph Convolutional Auto-Encoder for Drug-Target Interaction Prediction" Xu Jin, MingMing Liu, Lin Wang, WenQian He, YaLou Huang, and MaoQiang Xie
R	B264 "Locally Manifold Non-negative Matrix Factorization Based on Centroid for scRNA-seq Data Analysis" Chuan-Yuan Wang, Ying-Lian Gao, Cui-Na Jiao, Jin-Xing Liu, Chun-Hou Zheng, and Xiang-Zhen Kong
R	B759 "A robust single cell clustering method based on subspace learning and partial imputation" Ruiqing Zheng, Zhenlan Liang, Xiangmao Meng, Yu Tian, and Min Li

Session 22: Machine Learning, Modelling for Biomedicine (5)

(Session Chair: Khanh Le)

R	B722 "DRAMA: Discovering Disease-related circRNA-miRNA-mRNA Axes from Disease-RNA Information Network" Chengxin He, Lei Duan, Huiru Zheng, Jesse Li-Ling, and Longhai Li
R	B768 "Knowledge-aware Few-shot Learning Framework for Biomedical Event Trigger Identification" Shujuan Yin, Weizhong Zhao, Xingpeng Jiang, and Tingting He
R	B779 "Coronary Heart Disease Prediction Based on Combined Reinforcement Multitask Progressive Networks" Wenqi Li, DeHua Chen, and Jiajin Le
S	B409 "Meta Ordinal Regression Forest For Learning with Unsure Lung Nodules" Yiming Lei, Haiping Zhu, Junping Zhang, and Hongming Shan
S	B512 "Accurately Clustering Single-cell RNA-seq data by Capturing Structural Relations between Cells through Graph Convolutional Network" yuansong zeng, xiang zhou, jiahua rao, yutong lu, and yuedong yang
S	B549 "Generating Novel Compounds Targeting SARS-CoV-2 Main Protease Based On Imbalanced Dataset" Fan Hu, Dongqi Wang, Yishen Hu, Jiaxin Jiang, and Peng Yin
R	B255 "Mechanisms Underlying Sulfur Dioxide Pollution Induced Ventricular Arrhythmia: A Simulation Study" Shugang Zhang, Weigang Lu, Zhen Li, Shuang Wang, Mingjian Jiang, Qing Yuan, Zhiqiang Wei, and Henggui Zhang

Session 23: AI, Machine Learning for Health Informatics (5)

(Session Chair: Dougu Nam)

R	B298 "Medical Big Data Mining: Joint Symptom Name Recognition and Severity Estimation" Yang Deng, Dagang Li, Qiang Zhang, and Ying Shen
R	B332 "Towards Bootstrapping Biomedical Named Entity Recognition using Reinforcement Learning" Dongsheng Wang, Hongjie Fan, and Junfei Liu
R	B334 "Cost-Quality Adaptive Active Learning for Chinese Clinical Named Entity Recognition" Tingting Cai, Yangming Zhou, and Hong Zheng
S	B286 "Joint Cross-document Information for Named Entity Recognition with Multi-task Learning" Dongsheng Wang, Hongjie Fan, and Junfei Liu
S	B547 "Cross2Self-attentive Bidirectional Recurrent Neural Network with BERT for Biomedical Semantic Text Similarity" Zhengguang Li, Hongfei Lin, Chen Shen, Wei Zheng, Zhihao Yang, and Jian Wang
S	B505 "DLU-Net for Pancreatic Cancer Segmentation" Feng Jiang, Xiaoli Zhi, Xuehai Ding, Weiqin Tong, and Yun Bian
S	B368 "Cross-subject EEG Channel Optimization by Domain Adversarial Sparse Learning Model" Zhenhua Wu, Hong Zeng, Yue Zhao, Xiufeng Li, Jiaming Zhang, and Motonobu Hattori

Session 24: Biomedical Image Analysis (5)

(Session Chair: Jiu Liu)

R	B499 "Wheat Phenotype Extraction via Adaptive Supervoxel Segmentation" Bo Wang, Chengde Lin, and Shengwu Xiong
R	B506 "Cross-Modal Self-Attention Distillation for Prostate Cancer Segmentation" Guokai Zhang, Xiaoang Shen, Ye Luo, Jihao Luo, Zeju Wang, Weigang Wang, Binghui Zhao, and Jianwei Lu
R	B524 "Few-shot Radiology Report Generation for Rare Diseases" Xing Jia, Yun Xiong, Jiawei Zhang, Yao Zhang, and Yangyong Zhu
R	B593 "Joint Learning of Primary and Secondary Labels based on Multi-scale Representation for Alzheimer's Disease Diagnosis" Hong-Dong Li, Rui Guo, Junjian Li, Jianxin Wang, Yi Pan, and Jin Liu
S	B338 "HMOE-Net: Hybrid Multi-scale Object Equalization Network for Intracerebral Hemorrhage Segmentation in CT Images" Xizhi He, Kai Chen, Kai Hu, Zhineng Chen, Xuanya Li, and Xieping Gao
S	B373 "An Integration Convolutional Neural Network for Nuclei Instance Segmentation" Aiping Qu, Zhiming Cheng, Xiaofeng He, and Yue Li
S	B387 "Label Generation Network based on Self-selected Historical Information for Multiple Disease Classification on Chest Radiography" Yuelin Hu, Yuejie Zhang, Tao Zhang, Shang Gao, and Weiguo Fan

12/18: 2nd Afternoon Sessions

Session 25: Sequencing and High-throughput Methods (1)

(Session Chair: Guohua Wang)

R	B269 "MotiMul: A significant discriminative sequence motif discovery algorithm with multiple testing correction" Koichi Mori, Haruka Ozaki, and Tsukasa Fukunaga
R	B420 "scSNVIndel: accurate and efficient calling of SNVs and indels from single cell sequencing using integrated Bi-LSTM" Lei Cai, Yufeng Wu, and Jingyang Gao
R	B639 "DeepARC: An Attention-based Hybrid Model for Predicting Transcription Factor Binding Sites from Positional Embedded DNA Sequence" Jialong Chen and Lei Deng
R	B611 "Epistasis Detection using Heterogeneous Bio-molecular Network" Huiling Zhang, Jun Wang, Guoxian Yu, Lizhen Cui, and Maozu Guo
S	B390 "AFS-DEA: An automatic feature selection platform for differential expression analysis" Xudong Zhao, Weiqi Su, Hangyu Li, Tong Liu, Denan Kong, and Guohua Wang
S	B244 "Identification of Disease-Associated Genes Based on Differential Intron Retention" Zhenpeng Wu, Jiantao Zheng, and Hong-Dong Li
S	B475 "Variant Calling Parallelization on Processor-in-Memory Architecture" Dominique Lavenier, Remy Cimadomo, and Romaric Jodin

Session 26: Machine Learning, Modelling for Biomedicine (6)

(Session Chair: Bolin Chen)

R	B585 "MegaPath-Nano: Accurate Compositional Analysis and Drug-level Antimicrobial Resistance Detection Software for Oxford Nanopore Long-read Metagenomics" Wui Wang Lui, Amy W. S. Leung, Henry C. M. Leung, Yan Xin, Jade L. L. Teng, Patrick C. Y. Woo, Tak-Wah Lam, and Ruibang Luo
R	B331 "Drug Repositioning for SARS-CoV-2 Based on Graph Neural Network" Haifeng Liu, Hongfei Lin, Chen Shen, Liang Yang, Yuan Lin, Bo Xu, Zhihao Yang, Jian Wang, and Yuanyuan Sun
S	B615 "Drug-target Interaction Prediction Via Multiple Output Deep Learning" Qing Ye, Xiaolong Zhang, and Xiaoli Lin
S	B487 "Inferring Drug-Target Interactions Using Graph Isomorphic Network and Word Vector Matrix" Minqi Xu, Xiaolong Zhang, and Xiaoli Lin
S	B683 "A Hybrid Neural Collaborative Filtering Model for Drug Repositioning" Qianshi Yuan, Xiaomei Wei, Xiaotian Xiong, Meiyang Li, and Yaliang Zhang
S	B614 "Predicting Drugs for COVID-19/SARS-CoV-2 via Heterogeneous Graph Attention Networks" Yahui Long, Yu Zhang, Min Wu, Shaoliang Peng, Chee Keong Kwoh, Jiawei Luo, and Xiaoli Li

Session 27: AI, Machine Learning for Health Informatics (6)

(Session Chair: Khanh Le)

R	B497 "A Diversified Supervised based U-shape Colorectal Lesion Segmentor with Meaningful Feature Supplement and Multi-Level Residual Attention Mechanism" Jinjie Wang, Xiongwen Luo, Linsen Xie, and Ying Gao
S	B367 "Multi-task deep representation learning method for electronic health records" Shan Yang, Xiangwei Zheng, Xuanchi Chen, and Yi Wei
S	B216 "Multi-view Multi-label Learning with Dual-Attention Networks for Stroke Screen" Jundong Shen, Yi Zhang, Cheng Yu, and Chongjun Wang
S	B597 "A Robust Approach to Estimating Vigilance from EEG with Neural Processes" Chen-Li Yao and Bao-Liang Lu
S	B523 "What can be improved? Identifying actionable items from patient narratives" Lili Shang and Meiyun Zuo
R	B305 "PERFECTO: Prediction of Extended Response and Growth Functions for Estimating Chemotherapy Outcomes in Breast Cancer" Daria Kurz and Cristian Axenie
S	B415 "DeepCOVIDExplainer: Explainable COVID-19 Diagnosis from Chest X-ray Images" Md. Rezaul Karim, Till Döhmen, Dietrich Rebholz-Schuhmann, Michael Cochez, Oya Beyan, and Stefan Decker

Session 28: Biomedical Image Analysis (6)

(Session Chair: Minsun Song)

R	B602 "NANet: Nuclei-Aware Network for Grading of Breast Cancer in HE Stained Pathological Images" Rui Yan, Jintao Li, Xiaosong Rao, Zhilong Lv, Chunhou Zheng, Jinjin Dou, Xiaowen Wang, Fei Ren, and Fa Zhang
R	B635 "Multi-scale Generative Adversarial Network for Automatic Sublingual Vein Segmentation" Qingyue Xiong, Xinlei Li, Dawei Yang, Wei Zhang, Ye Zhang, Yajie Kong, Fufeng Li, and Wenqiang Zhang
R	B645 "Attention-Based Transformers for Instance Segmentation of Cells in Microstructures" Tim Prangemeier, Christoph Reich, and Heinz Koeppl
R	B667 "Automatic Tongue Crack Extraction For Real-Time Diagnosis" Jianqiang Peng, Xinlei Li, Dawei Yang, Wei Zhang, Ye Zhang, Yajie Kong, and Wenqiang Zhang
S	B414 "Ultrasound Image-Based Diagnosis of Cirrhosis with an End-to-End Deep Learning model" Hai Yang, Xiaohui Sun, Yang Sun, Ligang Cui, and Bingshan Li
S	B430 "Reduced Dynamics in Multivariate Regression-based Dynamic Connectivity of Depressive Disorder" Zhengwu Yang, Hanning Guo, Shanling Ji, Shan Li, Yu Fu, Man Guo, and Zhijun Yao

Session 29: Biomedical Text Mining and Ontologies (2)

(Session Chair: Xingpeng Jiang)

R	B333 "Gated iterative capsule network for adverse drug reaction detection from social media" Tongxuan Zhang, Hongfei Lin, Bo Xu, Yuqi Ren, Zhihao Yang, Jian Wang, and Xiaodong Duan
R	B595 "A Novel Method for Multiple Biomedical Events Extraction with Reinforcement Learning and Knowledge Bases" Weizhong Zhao, Yao Zhao, Xingpeng Jiang, Tingting He, Fan Liu, and Ning Li
R	B582 "An Effective Framework for Document-level Chemical-induced Disease Relation Extraction via Fine-grained Interaction between Contexts" Jinyong Zhang, Weizhong Zhao, Jincai Yang, Xingpeng Jiang, and Tingting He
R	B764 "MISSION: Multimodal-Information-Aided Similar Disease Detection Based on Disease Information Network" Wuli Xu, Lei Duan, Huiru Zheng, Jesse Li-Ling, Weipeng Jiang, Menglin Huang, and Yidan Zhang
S	B557 "Virus Named Entity Recognition Using Pre-training Model" Hanlin Mou, Tingting He, Shanshan Zheng, Haifang Wu, and Xingpeng Jiang
S	B599 "Two-perspective Biomedical Named Entity Recognition with Weakly Labeled Data Correction" Huiwei Zhou, Zhe Liu, Chengkun Lang, Yibin Xu, and Lei Du
S	B628 "A Text Mining Approach to Discovering COVID-19 Relevant Factors" Javier Sastre, Ali Vahid, Caitlin McDonagh, and Paul Walsh

12/19: Morning Sessions

Session 30: Sequencing and High-throughput Methods (2)

(Session Chair: Hyun Goo Woo)

	Invited Talk: Dr. Seung-Jong Park “Use cases of big data and deep learning for large-scale biomedical applications using supercomputers”
S	B309 "VCFC: Structural and Semantic Compression and Indexing of Genetic Variant Data" Kyle Ferriter, Frank Mueller, Amir Bahmani, and Cuiping Pan
S	B696 "A data denoising approach to optimize functional clustering of single cell RNA-sequencing data" Changlin Wan, Dongya Jia, Yue Zhao, Wennan Chang, Sha Cao, Xiao Wang, and Chi Zhang
S	B455 "Kmer2SNP: reference-free SNP calling from raw reads based on matching" Yanbo Li, Hardip Patel, and Yu Lin
S	B631 "Integration for single-cell RNA sequencing data based on the shared cell type assignment" Yin Zhang

Session 31: Machine Learning and Modelling for Biomedicine (7)

(Session Chair: Bin Liu)

R	B378 "Chemical-protein Interaction Extraction via ChemicalBERT and Attention Guided Graph Convolutional Networks in Parallel" Lei Qin, Gaocai Dong, and Jing Peng
S	B204 "LDCNN-DTI: A Novel Light Deep Convolutional Neural Network for Drug-Target Interaction Predictions" Tao Song, Shudong Wang, Zhenzhen Du, Mao Ding, Renteng Zhao, and Alfonso Rodriguez-Paton
S	B288 "Structure Enhanced Protein-Drug Interaction Prediction using Transformer and Graph Embedding" Fan Hu, Yishen Hu, Jianye Zhang, Dongqi Wang, and Peng Yin
S	B483 "On the Deep Learning-based Age Prediction of Color Fundus Images and Correlation with Ophthalmic Diseases" Yang Wen, Leiting Chen, Lifeng Qiao, Deng Yu, and Chuan Zhou
S	B642 "A Dynamic Group Equivariant Convolutional Networks for Medical Image Analysis" Yan Li, Guitao Cao, and Wenming Cao
S	B651 "Maximal Information Complemented Refinement Network for Gland Instance Segmentation" Xu Bowen, Wang Yankai, Yang Dawei, Ye Zhang, Yajie Kong, Wei Zhang, and Wenqiang Zhang

Session 32: AI, Machine Learning for Health Informatics (7)

(Session Chair: Chen Li)

R	B211 "An Efficient Weakly-Supervised Learning Method for Optic Disc Segmentation" Yang Wen, Leiting Chen, Lifeng Qiao, Chuan Zhou, Shuo Xi, Rui Guo, and Deng Yu
R	B231 "Multiview 3-D Echocardiography Image Fusion with Mutual Information Neural Estimation" Juiwen Ting, Kumaradevan Punithakumar, and Nilanjan Ray
R	B237 "Mining High-order Multimodal Brain Image Associations via Sparse Tensor Canonical Correlation Analysis" Lei Du, Jin Zhang, Fang Liu, Minjianan Zhang, Huiai Wang, Lei Guo, and Junwei Han
R	B502 "MSDAN: Multi-Scale Self-Attention Unsupervised Domain Adaptation Network for Thyroid Ultrasound Images" Xiang Ying, Yulin Zhang, Xi Wei, Mei Yu, Jialin Zhu, Jie Gao, Zhiqiang Liu, Xuewei Li, and Ruiguo Yu
S	B233 "On Automatic Detection of Central Serous Chorioretinopathy and Central Exudative Chorioretinopathy in Fundus Images" Yang Wen, Leiting Chen, Lifeng Qiao, Deng Yu, Siying Dai, Junjing Chen, and Chuan Zhou
S	B569 "Learning to Classify Skin Lesions via Self-Training and Self-Paced Learning" Sarpong Kwadwo Asare, Fei You, and Obed Tettey Nartey

Session 33: Biomedical Image Analysis (7)

(Session Chair: Antonio Martinez-Torteya)

R	B354 "Texture and signal features from hippocampal T2 maps as biomarkers for MCI to AD progression" Alejandro Trejo-Castro, Ricardo Caballero-Luna, José Garnica-López, Fernando Vega-Lara, Jose Celaya-Padilla, Jose Tamez-Pena, and Antonio Martinez-Torteya
S	B260 "Learning with Mislabels for Histopathological Identification of Microsatellite Instability in Colorectal Cancer" Jing Ke, Yiqing Shen, and Jason Wright
R	B741 "NiuEM: A nested-iterative unsupervised learning model for single-particle cryo-EM image processing" Rui Hu, Jiaming Cai, Wangjie Zheng, Yang Yang, and Hong-Bin Shen
R	B748 "LIRNet: Local Integral Regression Network for Both Strongly and Weakly Supervised Nuclei Detection" Xiao Zhou, Zhen Cheng, Miao Gu, and Fei Chang
R	B781 "Melanoma Classification in Dermoscopy Images via Ensemble Learning on Deep Neural Network" Jie Song, Jiawei Li, Shiqiang Ma, Jijun Tang, and Fei Guo
S	B464 "Boundary-aware Segmentation Network Using Multi-Task Enhancement for Ultrasound Image" Ruiguo Yu, Jiachen Hu, Mei Yu, Xi Wei, Han Jiang, Jialin Zhu, Zhiqiang Liu, Jie Gao, and Xuewei Li

Session 34: Healthcare Systems (2)

(Session Chair: Shanfeng Zhu)

R	B311 "Sparse Longitudinal Representations of Electronic Health Record Data for the Early Detection of Chronic Kidney Disease in Diabetic Patients" Jinghe Zhang, Kamran Kowsari, Mehdi Boukhechba, James Harrison, Jennifer Lobo, and Laura Barnes
S	B703 "COVID-MobileXpert: On-Device COVID-19 Patient Triage and Follow-up using Chest X-rays" Xin Li, Chengyin Li, and Dongxiao Zhu
S	B617 "Attention Mechanism with BERT for Content Annotation and Categorization of Pregnancy-Related Questions on a Community Q&A Site" Xiao Luo, Haoran Ding, Matthew Tang, Priyanka Gandhi, Zhan Zhang, and Zhe He
R	B636 "A Formative Usability Study to Improve Prescriptive Systems for Bioinformatics Big Data" Kanupriya Singh, Shangman Li, Isa Jahnke, Ashish Pandey, Zhen Lyu, Trupti Joshi, and Prasad Calyam
S	B507 "Tumor Classification Based on Approximate Symmetry Using Dual-Branch Complementary Fusion Network" Mei Yu, Minyutong Cheng, Xubin Li, Zhiqiang Liu, Jie Gao, Xuzhou Fu, Xuewei Li, and Ruiguo Yu
S	B606 "Brain MR Image Super-resolution using 3D Feature Attention Network" Lulu Wang, Jinglong Du, Huazheng Zhu, Zhongshi He, and Yuanyuan Jia

Workshop Schedule

Time	December 16	December 17	December 18	December 19
Keynote Sessions		Keynote Talk	Keynote Talk	Keynote Talk
Morning Sessions	**Workshop 1** **Workshop 3**: CMISF **Workshop 5/10**: BPBL **Workshop 6** **Workshop 7** **Workshop 8**: SEPDA **Workshop 9**: IWBNA **Workshop 12**: BHI **Workshop 13**: HPCB **Workshop 19**: DLB2H **Workshop 21**: DLBIBM **Workshop 24**: MABM **Workshop 25**: LncRNA	**Workshop 4** **Workshop 12**: BHI **Workshop 24**: MABM	**Workshop 12**: BHI **Workshop 17**: ML4BMI **Workshop 22**: AIBH	
	Lunch Break			***End of Conference***
Afternoon Sessions 1-2	**Workshop 3**: CMISF **Workshop 11**: IDASB **Workshop 16** **Workshop 21**: DLBIBM **Workshop 24**: MABM **Workshop 25**: LncRNA	**Workshop 4** **Workshop 14/15**: HiBB	**Workshop 17**: ML4BMI **Workshop 22**: AIBH	

Workshop 1: Integrating Omics Data for Cancer Therapies
Workshop 3: Computational Methods for the Immune System Function (CMISF)
Workshop 4: Data mining from genomic variants and its application to genome-wide analysis
Workshop 5: Computer-Based Processes and Algorithms for Biomedicine and Life Quality Improvement (BPBL)
Workshop 6: International Workshop on Information Technology for Chinese Medicine
Workshop 7: Biological Ontologies and Knowledge Bases
Workshop 8: International Workshop on Semantics-Powered Data Mining and Analytics (SEPDA)
Workshop 9: International Workshop on Biological Network Analysis and Integrative Graph-Based Approaches (IWBNA)
Workshop 10: BigDataNetAnalysis
Workshop 11: Integrative Data Analysis in Systems Biology (IDASB)
Workshop 12: International Workshop on Biomedical and Health Informatics (BHI)
Workshop 13: International Workshop on High Performance Computing on Bioinformatics (HPCB)
Workshop 14: International Workshop on High Performance Bioinformatics and Biomedicine (HiBB)
Workshop 15: High Performance Methods and Interdisciplinary Applications for Fighting the COVID-19 Pandemic
Workshop 16: Artificial Intelligence & Big Data vs. Pandemics
Workshop 17: Machine Learning for Biological and Medical Image Big Data (ML4BMI)
Workshop 19: International Workshop on Deep Learning in Bioinformatics, Biomedicine, and Health Informatics (DLB2H)
Workshop 21: International Workshop on Deep Learning Techniques for Bioinformatics and Biomedicine (DLBIBM)
Workshop 22: Artificial Intelligence Techniques for Biomedicine and Healthcare (AIBH)
Workshop 24: Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics (MABM)
Workshop 25: Workshop on Long Non-Coding RNAs: Mechanism, Function, and Computational Analysis (BIBM-LncRNA)

Detailed Workshop Schedule

December 16

Workshop 3

The Fourth Workshop on Computational Methods for the Immune System Function (CMISF 2020)

Workshop Chairs: Francesco Pappalardo, Giulia Russo, Marzio Pennisi

Time	Title	Presenter/Author
09:00	**Welcome message**	
09:05	**S03201** "Immunoenhancement Powered by Astragali Radix with the Tonifying Qi Effect Identified in Chinese Medicine"	Guang Zheng
09:25	**S03202**, "Emulation of dynamic multi-output simulator of risk of type-2 diabetes"	Paola Stolfi
09:45	**S03203**, "Simulating an Immune Response with a Combined Agent-Based Model of a Triple-Negative Breast Cancer Tumor and Vascular Network"	Michael Ventoso
10:00-10:30	**Coffee Break**	
10:30	**S03204**, "Classification of PBMC cell types using scRNAseq, ANN, and incremental learning"	Jiahui Zhong
10:50	**S03205**, "Automation of Gene Expression Profile Analysis in Single Cell Data"	Yihan Zhang
11:10	**S03206**, "Artificial Neural Network System for Cell Classification using Single Cell RNA Expression"	Xin Lin
11:30	**S3207**, "Single-cell mRNA profiles in PBMC"	Luning Yang
11:50	**S3208**, "Classification of Single Cell Types During Leukemia Therapy using Artificial Neural Networks"	Minjie Lyu
12:10	**S03209**, "Long-Term Molecular Dynamics Simulations Reveal Flexibility Properties of a Free and TCR-Bound pMHC-I System"	Rudolf Karch
12:30-14:00	**Lunch**	
14:00	**S03210**, "Similarity Computation based on Formal Concept Analysis for Colorectal Cancer Patients"	Ping Zhang
14:20	**S03211**, "Prediction of PBMC Cell Types Using scRNAseq Reference Profiles"	Luning Yang
14:40	**S03212**, "Uncertain Quantification of Immunological Memory to Yellow Fever Virus"	Larissa de Lima e Silva
15:00	**S03213**, "A simplified model of the Human Immune Systemresponse to the COVID-19"	Maicom Peters Xavier
15:20	**S03216**, "Tissue of origin classification from single cell mRNA expression by Artificial Neural Networks"	Bangrui ZHENG
15:40	**B587**, "Biological Rule-Based Modeling of Experimental Cell Secretion Data"	Brittany Hoard
16:00-16:20	**Coffee Break**	
16:20	**S03214**, "Evaluation of the predictive capability of PETAL tool: a retrospective study on potential tyrosine kinases drug resistance targets"	Giuseppe Sgroi
16:40	**S03215**, "Verify: a toolbox for deterministic verification of computational models"	Giuseppe Alessandro Parasiliti Palumbo
17:00	**S03217**, "Modeling, simulation and prediction of protein structures for the design of oncolytic viruses"	Valentina Di Salvatore
17:20	**Closing Remarks**	

Workshop 5/ Workshop 10

Computer-Based Processes and Algorithms for Biomedicine and Life Quality Improvement (CPBL 2020)

Workshop Chairs: Pierangelo Veltri (veltri@unicz.it)

In conj. with

10th Towards Precision Medicine: Network Based Big Data Integration and Analysis (BigDataNetAnalysis)

Workshop Chairs: Pietro H Guzzi (hguzzi@unicz.it)

Time	Title	Presenter/Author
9:00-9:05	INTRODUCTION	Pierangelo Veltri
9:05-9:20	**S05203** " Automatic Seizure Prediction based on Modified Stockwell Transform and Tensor Decomposition”	**Shasha Yuan,** Jinxing Liu, Junliang Shang, Fangzhou Xu, Lingyun Dai, and Xiangzhen Kong
9:20-9:35	**S05205** “Effects of Spatial Distributions of Biological Pacemaker Cells on the Pacemaking Ability of Cardiac Tissue”	**Yacong Li**, Kuanquan Wang, Qince Li, Yizhou Liu, and Henggui Zhang
9:35-9:50	**S05206** Modeling and simulation study on the treatment of sinus node ischemia by Chinese medicine Yiqi Tongyang	**Xiangyun Bai**, Kuanquan Wang, Qince Li, Cunjin Luo, and Henggui Zhang,
9:50-10:05	**B527 (->S05)** Extending Information Agreement by Continuity	**Alberto Casagrande,** Francesco Fabris Rossano Girometti
10:05-10:20	**B744 (->S05)** Image Based Fractal Analysis for Detection of Cancer Cells	**Jason Qin**, Lindsay Puckett, and Xin Qian
10:20-10:30	DISCUSSION	**PietroH Guzzi MODERATOR**
10:30-10:45	**S05201** Menstrual Regulation Delivered by Angelicae Sinensis Radix	**Guang Zheng**
10:45-11:00	**S05202** Multivariate Independence Set Search via Progressive Addition for Conditional Markov Acyclic Networks	**Mattia Prosperi,** Jiang Bian, and Mo Wang
11:00-11:15	**S05208** SMIT-CKD: A MOBILE APP TO IMPROVE ADHERENCE TO THERAPY IN CKD PATIENTS. A PILOT STUDY.	Antonio Vilasi, Vincenzo Panuccio, Salvatore Morante, Antonino Villa, Maria Carmela Versace, Sergio Mercuri, Maurizio Li Vigni, Giovanni Tripepi, and **Claudia Torino**
11:15-11:30	**S05209** A Framework for Patient Data Management and Analysis in Randomised Clinical Trials	**PIETRO HIRAM GUZZI**, TIZIANA LARUSSA, Rosarina Vallelunga, Ludovico Abenavoli, Giuseppe Tradigo, Francesco Luzza, and Pierangelo Veltri
11:30-11:45	**S05212** A programmable device to guide rehabilitation patients: design, testing and data collection	**Giuseppe Tradigo**, Patrizia Vizza, Pietro Hiram Guzzi, Gionata Fragomeni, Antonio Ammendolia, and Pierangelo Veltri

11:45-11:55	**S05213** Flow Analysis in VA ECMO Support: A CFD Study	**Gionata Fragomeni**, Maria Vittoria Caruso, and Michele Rossi
11:55-12:10	**S05214** Cloud-based biomedical system for remote monitoring of ALS patients	**Arrigo Palumbo**, Domenico Corchiola, Barbara Calabrese, Nicola Ielpo, Andrea Demeco, and Antonio Ammendolia
12:10-12:20	**S05210** The contribution of AI in the detection of the Diabetic Retinopathy	Ester Zumpano and **Eugenio Vocaturo**
12:20-12:30	**S05211** Machine Learning Opportunities for Automatic Tongue Diagnosis Systems	**Eugenio Vocaturo** and Ester Zumpano
12:30-12:45	**CLOSING REMARKS**	

Workshop 7

Biological ontologies and knowledge bases (BiOK 2020)

Workshop Chairs: Jiajie Peng (jiajiepeng@nwpu.edu.cn)

Time	Title	Presenter/Author
9:00-9:15	**S07201**: *SWE: a novel method with semantic-weighted edge for measuring gene functional similarity*	Zhen Tian and Haichuan Fang
9:15-9:30	**S07202**: *NCRR: A novel method for measuring disease similarity based on non-coding RNA regulation*	Ningyi Zhang and Tianyi Zang,
9:30-9:45	**S07204**: *CNN-DDI: A novel deep learning method for predicting drug-drug interactions*	Chengcheng Zhang and Tianyi Zang
9:45-10:00	**S07205**: *An Effective Hybrid Deep Learning Model for Eukaryotic Promoter Identification*	Ying Wang, Qinke Peng, Xu Mou, Tian Han, Zhao Sun, and Xiao Wang
10:00-10:15	**S07206**: *A Nonparametric Method for Detecting Differential DNA Methylation Regions*	Xifang Sun, Jiaqiang Zhu, and Shiquan Sun
10:15-10:30	**S07208**: *Multi-feature fusion and dimensional reduction based on the two-step deep ontology and the conjoint triad for the identification of cancerlectins*	Shunfang Wang, Yuan Fang, and Xu Wang
10:30-10:45	**S07209**: *Large Scale Deep Reinforcement Learning in War-games*	Hanchao Wang, Hongyao Tang, Jianye Hao, Xiaotian Hao, Yue Fu, and Yi Ma
10:45-11:00	**S07210**: *Discovering Cell Types by Integrating Single-cell RNA-sequencing and Protein Interaction Network*	Zijie Li and Xiaoke Ma
11:00-11:15	**S07211**: *Automatic Generation of Electromyogram Diagnosis Report*	QiZheng Gu, Cong Nie, Ruixiang Zou, Wei Chen, Chaojun Zheng, Dongqing Zhu, Xiaojun Mao, Zhongyu Wei
11:15-11:30	**B280**: *SeHNE: Semi-supervised Heterogeneous Network Embedding for Drug Combination*	Xiaoke Ma and Shiyin Tan
11:30-11:45	**B408**: *Medical Transdisciplinary Cluster Development for Multivariable COVID-19 Epidemiological Situation Modeling*	Maryna Popova, Oleksandr Stryzhak, Ozar Mintser, and Rina Novogrudska
	Closing Remarks	

Workshop 8

The 5th International Workshop on Semantics-Powered Data Mining and Analytics

Workshop Chairs: Zhe He, Jiang Bian, Cui Tao, Rui Zhang, Xia Hu

Time	Title	Presenter/Author
9:00 – 9:05 am	Introduction to SEPDA 2020	Zhe He
9:05 – 10:00 am	Keynote (TBA)	TBD
10:00 – 10:10 am	**Coffee Break**	
10:10 – 10:30 am	***S08201*** *A Lexical-based Formal Concept Analysis Method to Identify Missing Concepts in the NCI Thesaurus*	Fengbo Zheng and Licong Cui
10:30 – 10:50 am	***S08205*** *A Health Consumer Ontology of Fast Food Information*	Muhammad Amith, Jing Wang, Grace Xiong, Kirk Roberts, and Cui Tao
10:50 – 11:10 am	***S08207*** *NCCD – RxNorm: Linking Chinese Clinical Drugs to International Drug Vocabulary*	Yaoyun Zhang, Jing Li, and Mui Zandt
11:10 – 11:30 am	***B723*** *Generating Training Data for Concept-Mining for an 'Interface Terminology' Annotating Cardiology EHRs*	Vipina Keloth, Shuxin Zhou, Andrew Einstein, Gai Elhanan, Yan Chen, James Geller, and Yehoshua Perl
11:30 – 11:50 am	**Coffee Break**	
11:50 am – 12:10 pm	***S08202*** *A Methodology to Develop Knowledge Graphs for Indication Expansion: An Exploratory Study*	Ozge Gurbuz, Miao Sun, and Nathan Lawless
12:10 – 12:30 pm	***S08203*** *Deep Learning Identification of Asthma Inhaler Techniques in Clinical Notes*	Bhavani Singh Agnikula Kshatriya, Elham Sagheb, Chung-Il Wi, Jungwon Yoon, Hee Yun Seol, Young Juhn, and Sunghwan Sohn
12:30 – 12:50 pm	***S08206*** *KEoG: A knowledge-aware edge-oriented graph neural network for document-level relation extraction*	Tao Li, Weihua Peng, Qingcai Chen, Xiaolong Wang, and Buzhou Tang
12:50 – 13:10 pm	***S08208*** *Opioid2FHIR: A system for extracting FHIR-compatible opioid prescriptions from clinical text*	Jingqi Wang, William Mathews, Huy Pham, Hua Xu, and Yaoyun Zhang
13:10 – 13:20 pm	**Closing Remarks**	

Workshop 9

13th International Workshop on Biological Network Analysis and Integrative Graph-Based Approaches (IWBNA 2020)

Workshop Chairs: Mingon Kang, Ananda Mondal, and Young-Rae Cho

Time	Title	Presenter/Author
9:00am –10:40am	**B230** Stiffness estimate of information propagation in biological systems modelled as spring networks	Paola Lecca and Angela Re
	S09201 Evaluation of the Topological Agreement of Network Alignments	Concettina Guerra and Pietro Hiram Guzzi
	B718 Triangle-Based Tripartite Graph Clustering	Yizong Cheng, Jaswanth Yella, and Anil Jegga
	S09206 Stage-Specific Co-expression Network Analysis for Cancer Biomarker Discovery	Raihanul Tanvir and Ananda Mondal
	S09202 Prediction of LncRNA-Disease Associations Based on Network Representation Learning	Xiaorui Su, Zhuhong You, and Haicheng Yi
10:40am –10:50am	**Coffee Break**	

10:50am –12:30pm	**B775** Identification of Dementia Related Brain Functional Networks with Minimum Spanning Trees	Abdulyekeen Tunde Adebisi, Venkateswarlu Gonuguntla, Ho-Won Lee, and Kalyana C. Veluvolu
	S09208 Survey of network-based approaches of drug-target interaction prediction	Lee Soo Jung and Young-Rae Cho
	B392 An efficient method for approximating attractors in large-scale asynchronous Boolean models	Giang Trinh Van and Kunihiko Hiraishi
	S09205 A functional network study of patients with mild depression based on source location	Yun Zhang, Tao Gong, Shuting Sun, Jianxiu Li, Jing Zhu, and Xiaowei Li
	S09207 EEG-based mild depression recognition using multi-kernel convolutional and spatial-temporal feature	Yongheng Fan, Ruilan Yu, Jianxiu Li, Jing Zhu, and Xiaowei Li
	N205 Using Machine Learning to Automate Mammogram Images Analysis	Xuejiao Tang, Liuhua Zhang, Wenbin Zhang, Xin Huang, Vasileios Iosifidis, Zhen Liu, Mingli Zhang, Enza Messina, and Ji Zhang
	Closing Remarks	

Workshop 12

Biomedical and Health Informatics (BHI) Workshop

Workshop Chairs: Illhoi Yoo

Time	Title	Presenter/Author
9:00-1:00pm	Welcome	*Illhoi Yoo*
	S12202 An approach for continuous sleep quality monitoring integrated in the SmartWork system	Ioannis Konstantoulas, Otilia Kocsis, Nikos Fakotakis, and Konstantinos Moustakas,
	S12205 Finding Associations among Chronic Conditions by Bootstrap and Multiple Correspondence Analysis	Cristina Soguero-Ruiz, Natalia Alonso Arteaga, Sergio Muñoz-Romero, José Luis Rojo-Martínez, Manuel Rubio-Sánchez, Isabel Caballero López-Fajardo, and Inmaculada Mora-Jiménez,
	S12207 Examining the Effect of Deprivation on Prescribing Behaviours in Northern Ireland	Frederick Booth, Maurice Mulvenna, Raymond Bond, Kieran McGlade, and Debbie Rankin,
	B482 Supporting Diagnosis and Treatment of Scoliosis: Using Augmented Reality to Calculate 3D Spine Models in Real-Time - ARScoliosis	Saša Ćuković, Radu Emanuil Petruse, Lea Buchweitz, and Gerrit Meixner,
	B648 Storage Efficient Implementation of Standardized Electronic Health Records Data	Shelly Sachdeva, Disha Batra, and Shivani Batra,
	S12208 Competition Strategy for Healthcare Insurance Plans	Eva Lee and Jinha Lee,
	B225 Predicting Neural Deterioration in Patients with Alzheimer's Disease Using a Convolutional Neural Network	Maryam Tavakoli Hosseinabadi, Tianyi Xie, Jingyi Shi, Mirsad Hadzikadic, and Yaorong Ge,

	B240 Explanatory Analysis of a Machine Learning Model to Identify Hypertrophic Cardiomyopathy Patients from EHR Using Diagnostic Codes	Nasibeh Zanjirani Farahani, Divaakar Siva Baala Sundaram, Moein Enayati, Shivaram Poigai Arunachalam, Kalyan Pasupathy, and Adelaide Arruda-Olson,
	B253 Cortical tonic GABAergic inhibition – preliminary insights from MR Spectroscopy of subacute stroke	Ifeoma Anunoby, Vovanti Jones, Alexander Brown, and Carmen Cirstea,
	B263 A multi-modal machine learning approach towards predicting patient readmission	Somya Mohanty, Deborah Lekan, Thomas McCoy, Marjorie Jenkins, and Prashanti Manda,
	S12201 A data capture model and its associate study on the public web published COVID-19 data	Zhiwei LIANG, Pan ZHANG, Baoyan LIU, Nenggui XU, Lu TIAN, and Ying LU,
	S12204 Embracing Differential Privacy for Anonymizing Spontaneous ADE Reporting Data	Wen-Yang Lin and Zhi-Xun Shen,
	B508 Molecular Docking of Traditional Chinese Medicinal Compounds Against Dengue Virus NS3 Protease and NS3 Helicase	Jewel Mae Cadiz, Christine Joy Susana, Marla Endriga, and Enrique Jose Frio,
	B544 Gene Screening for Autism Based on Cell-type-specific Predictive Models	Yang Wang, Yiping Lin, Guoli Ji, and Jinting Guan,
	B583 iVAE: An Improved Deep Learning Structure for EEG Signal Characterization and Reconstruction	Zheng Chen, Naoaki Ono, MD Altaf-Ul-Amin, Shigehiko Kanaya, and Ming Huang,
	B590 ClinicNet: Clinical Practice Oriented Medical Representation Learning for Electronic Medical Records	Shuai Wang and Junfei Liu,

Workshop 13

The 7th International Workshop on High Performance Computing on Bioinformatics

Workshop Chairs: Che-Lun Hung, Huiru Zheng, Chuan Yi Tang, Chun-Yuan Lin

Time	Title	Presenter/Author
9:00-9:20	A Survey on Edge Computing in Bioinformatics and Health Informatics	Yin Te Tsai and Zih Yuan Lin
9:20-9:40	Classification of Cancer Types based on Gene Expression Data	Yinchao He, Ryan Bockmon, Sarah Roscoe, and Miracle Modey
	Coffee Break	
10:00-10:20	GPU-Based Texture Analysis approach for Mammograms	Che-Lun Hung and Chun-Yuan Lin
10:20-10:40	Homomorphic Computation of Local Alignment	Magsarjav Bataa, Siwoo Song, Kunsoo Park, Miran Kim, Jung Hee Cheon, and Sun Kim
10:40-11:00	Comparing phylogeny by compression to phylogeny by NJp and Bayesian Inference	John Rogers and DeAngelo Wilson
11:00-11:20	Predictive analytics on genomic data with high-performance computing	Carson K. Leung, Oluwafemi A. Sarumi, and Christine Zhang
	Closing Remarks	

Workshop 19

International Workshop on Deep Learning in Bioinformatics, Biomedicine, and Healthcare Informatics (DLB2H 2020)

Workshop Chairs: Mingon Kang and Jung Hun Oh

Time	Title	Presenter/Author
9:00am-9:10am	Welcome (chair)	Mingon Kang
9:10am-9:30am	Pan-cancer Feature Selection and Classification Reveals Important Long Non-coding RNAs	Abdullah Al Mamun, Wenrui Duan, and Ananda Mondal
9:30am-9:50am	EEG Channel Interpolation Using Deep Encoder-decoder Networks	Sari Sadiya, Tuka Alhanai, Taosheng Liu, and Mohammad Ghassemi
9:50am-10:10am	Accurate and adversarially robust classification of medical images and ECG time-series with gradient-free trained sign activation neural networks	Zhibo Yang, Yanan Yang, Yunzhe Xue, Frank Shih, Justin Ady, and Usman Roshan
10:10am-10:30am	A General Endoscopic Image Enhancement Method Based on Pre-trained Generative Adversarial Networks	Yating Li, Jingfan Fan, Danni Ai, Hong Song, Yongtian Wang, and Jian Yang
10:30am-10:50am	Detection of diabetic blindness with Deep-Learning	Anukriti Singh and Wooyoung Kim
10:50am-11:10am	Dual sentence representation model integrating prior knowledge for bio-text-mining	Zhijing Li, Yangyang Lan, Saikat Chatterjee, Pargorn Puttapirat, Xiangrong Zhang, and Chen Li
11:10am-11:30am	Protein Binding Pose Prediction via Conditional Variational Autoencoding for Plasmodium Falciparum	Tuan Tran and Chinwe Ekenna
11:30am-11:50am	Deep Learning to Discover Cancer Glycome Genes Signifying the Origins of Cancer	Abdullah Mamun, Masrur Sobhan, Raihanul Tanvir, Charles Dimitroff, and Ananda Mondal
11:50am-12:10pm	Structured Information Extraction of Pathology Reports with Attention-based Graph Convolutional Network	Jialun Wu, Kaiwen Tang, HaiChuan Zhang, Chunbao Wang, and Chen Li
	Closing Remarks	

Workshop 21

Deep Learning Techniques for Bioinformatics and Biomedicine (DLBIBM)

Workshop Chairs: Wenzhong Guo, Vincent S. Tseng, Chi-Hua Chen, Feng-Jang Hwang, Genggeng Liu, Yu-Chih Wei, Hsiao-Ting Tseng, Chia-Yu Lin

Time	Title	Presenter/Author
09:00 – 09:10	Welcome and Opening Remarks (Chair)	
09:10 – 09:30	Using nonlinear sparse Bayesian learning model to identify the correlation between multiple clinical cognitive scores and neuroimaging measurements	Jie Wu, Yibo Hu, Biyue Fan, Wei Chen, and Deyan Sun
09:30 – 09:50	The group sparse canonical correlation analysis method in the imaging genetics research	Jie Wu, Jiawei Xu, Wei Chen, and Deyan Sun

09:50 – 10:10	Improved One-Dimensional Convolutional Neural Networks for Human Motion Recognition	Shengzhi Wang, Shuo Xiao, Zhenzhen Huang, Zhiou Xu, and Wei Chen
10:20 – 10:50	**Coffee Break**	
10:50 – 11:10	Developing a Clustering Structure with Consideration of Cross-Domain Text Classification based on Deep Sparse Autoencoder	Yufan Guo, Rong Fei, Kuan Zhang, Yu Tang, and Bo Hu
11:10 – 11:30	Matching Biomedical Ontologies with Long Short-Term Memory Networks	Chao Jiang and Xingsi Xue
11:30 – 11:50	BioExpDNN: Bioinformatic Explainable Deep Neural Network	Hao Fang, Cheng Shi, and Chi-Hua Chen
11:50 - 14:00	**Lunchbreak**	
14:00 – 14:20	A Method on Face Recognition Based on Single Sample Per Person with a Contaminated Biometric Enrolment Database	Jie Li, Chenghu Tang, and Deyan Sun
14:20 – 14:40	Multi-modal Medical Image Fusion Based on GAN and the Shift-Invariant Shearlet Transform	Lei Wang, Chunhong Chang, Benli Hao, and Chunxiang Liu
14:40 – 15:00	Analysis and Detection of Lung Sounds Anomalies Based on NMA-RNN	Arslan Manzoor, Qiao Pan, Hadiqa Jalil Khan, Shahbaz Siddeeq, Hafiz Muhammd Ali Bhatti, and Mulubrhan Ayalew Wedagu
15:00 – 15:20	Improving Error Related Potential Classification by using Generative Adversarial Networks and Deep Convolutional Neural Networks	Chenguang Gao, Zhao Li, Hiroki Ora, and Yoshihiro Miyake
15:30 – 16:00	**Coffee Break**	
16:00 – 16:20	Latent Feature Representations for Human Gene Expression Data Improve Phenotypic Predictions	Yannis Pantazis, Christos Tselas, Kleanthi Lakiotaki, Vincenzo Lagani, and Ioannis Tsamardinos
16:20 – 16:40	Investigation of BERT Model on Biomedical Relation Extraction Based on Revised Fine-tuning Mechanism	Peng Su and K. Vijay-Shanker
16:40 – 17:00	A Deep Learning Knowledge Graph Approach to Drug Labelling	Javie Sastre, Faisal Zaman, Noirin Duggan, Caitlin McDonagh, and Paul Walsh
17:00 – 17:20	Multimodal Lung Disease Classification using Deep Convolutional Neural Network	Zeenat Tariq, Sayed Khushal Shah, and Yugyung Lee
	Closing Remarks	

Workshop 24

Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics

Workshop Chairs: Dr. Haiying Wang, Prof. Hui Wang, Prof. Huiru (Jane) Zheng, Mengyuan Wang

Time	Title	Presenter/Author
9:00 – 9:05	**Opening remarks**	Prof. Huiru Zheng
9:05 - 9:25	**S24206** Joint Multiclass Classification of the subjects of Alzheimer's and Parkinson's Diseases through Neuroimaging Modalities and Convolutional Neural Networks	Ahsan Bin Tufail, Yong-Kui Ma, Qiu-Na Zhang, and Lei Zhao
9:25 - 9:45	**B201** Ancestry Estimation of Skull in Chinese Population Based on Improved Convolutional Neural Network	Yang Wen, Zhou Mingquan, Lin Pengyue, Geng Guohua, Liu Xiaoning, and Li Kang
9:45 – 10:05	**B206** Deep Learning for Automatic Tracking of Tongue Surface in Real-time Ultrasound Videos, Landmarks instead of Contours	Mohammad Hamed Mozaffari Maaref, Noriko Yamane, and Won-Sook Lee

10:05 – 10:25	**B340** Depression severity prediction from facial expression based on the DRR DepressionNet network	Weitong Guo
10:25 – 10:45	**B484** Multi-detection and Segmentation of Breast Lesions Based on Mask RCNN-FPN	Hafiz Muhammad Ali Bhatti, JIYUN LI, Shahbaz Siddeeq, Abdul rehman, and Arslan Manzoor
10:45 – 11:05	**B541** Selection of CNN, Haralick and Fractal Features Based on Evolutionary Algorithms for Classification of Histological Images	David Candelero, Guilherme Roberto, Marcelo Nascimento, Guilherme Rozendo, and Leandro Neves
11:05 – 11:10	**Coffee Break**	
11:10 – 11:30	**B649** Segmentation of Oral Epithelial Dysplasias Employing Mask R-CNN and Color Normalization	Adriano Barbosa Silva, Dalí Freire Dias dos Santos, Thaína Aparecida Azevedo Tosta, Alessandro Santana Martins, Leandro Alves Neves, Bruno Augusto Nassif Travençolo, Paulo Rogério de Faria, and Marcelo Zanchetta do Nascimento
11:30 – 11:50	**B709** Comparison of Convolutional Neural Network Architectures and their Influence on Patient Classification Tasks Relating to Altered Mental Status	Kevin Gagnon, Tami Crawford, and Jihad Obeid
11:50 – 12:10	**B577** Recognition of DNA Secondary Structures as Nucleosome Barriers with Deep Learning Methods	Fedor Pavlov and Maria Poptsova
12:10 – 12:30	**B755** miTarDigger: a fusion deep-learning approach of stacked denoising autoencoders and convolutional denoising autoencoders for predicting human miRNA targets	Jianrong Yan, Yanan Li, and Min Zhu
12:30 – 12:50	**B565** Improving Molecular Property Prediction on Limited Data with Deep Multi-Label Learning	Hehuan Ma, Chaochao Yan, Yuzhi Guo, Sheng Wang, Yuhong Wang, Hongmao Sun, and Junzhou Huang
12:50 – 14:00	**Lunch**	
14:00 – 14:20	**B739** Brain Functional Connectivity Pattern Recognition for Attentiondeficit/hyperactivity Disorder Diagnosis	Harun Pirim, Miaolin Fan, and Haifeng Wang
14:20 – 14:40	**B701** A Representation Method for Cellular Lines based on SVM and Text Mining	Ivan Carrera, Ines Dutra, and Eduardo Tejera
14:40 – 15:00	**B762** Prediction of Patients Severity at Emergency Department Using NARX and Ensemble Learning	Amin Naemi, Thomas Schmidt, Marjan Mansourvar, and Uffe Kock Wiil
15:00 – 15:20	**B545** Extreme Phenotype Sampling Improves LASSO and Random Forest Marker Selection for Complex Traits	Cai John
15:20 – 15:40	**B535** Multimodal classification of Parkinson’s disease using delay differential analysis	Jonathan Weyhenmeyer, Manuel Hernandez, Claudia Lainscsek, Howard Poizner, and Terrence Sejnowski
15:40 – 15:45	**Coffee Break**	
15:45 – 16:05	**B282** Unsupervised Identification of SARS-CoV-2 Target Cell Groups via Nonlinear Dimensionality Reduction on Single-cell RNA-Seq Data	Saiteja Danda, Akram Vasighizaker, and Luis Rueda
16:05 – 16:25	**B246** Prediction of lncRNA-disease associations based on matrix factorization and neural network	Xiaocao Hu, Haoyang Wu, and Yuxin Liu
16:25 – 16:45	**B363** Network-based gene prediction for TCM symptoms	Yinyan Wang, Kuo Yang, Zixin Shu, Dengying Yan, and Xuezhong Zhou
16:45 – 17:05	**B662** TportHMM: Predicting the substrate class of transmembrane transport proteins using profile Hidden Markov Models	Shiva Shamloo, Qing Ye, and Gregory Butler

17:05 – 17:25	**B400** Alphabet reduction and distributed vector representation based method for classification of antimicrobial peptides	Shraddha Surana, Digvijay Gunjal, Divye Singh, Pooja Arora, and Jayaraman Valadi
17:25 – 17:45	**B673** A multilayer co-occurrence network reveals the systemic difference of diet-based rumen microbiome associated with methane yield phenotype	Mengyuan Wang, Haiying Wang, Huiru Zheng, Richard Dewhurst, and Rainer Roehe
	Closing Remarks	

Workshop 25

IEEE BIBM 2020 Workshop on Long Non-Coding RNAs (BIBM-LncRNA)

Workshop Chairs: Don Adjeroh, Xiaobo Zhou, Ivan Martinez, and Leonard Lipovich

Time	Title	Presenter/Author
9:00-9:10am, KST (7:00-7:10pm, NYT)	**Introduction**	
9:10-10:10 (7:10-8:10pm, NYT)	**Keynote 1: Linking RNA to Chromatin**	**John Rinn, PhD University of Colorado Boulder, USA**
10:10-10:30am, KST (8:10-8:30pm, NYT)	**S25209** Predicted Regulatory Pathways for Long Noncoding RNA-SNHG7 via miR-34a and its Targets in Alzheimer's Disease	Jian Shi, USA
10:30-10:50am, KST (8:30-8:50pm, NYT)	**S25210** Exploring neural network models for LncRNA sequence Identification	Jason Miller and Donald Adjeroh, USA
10:50-11:00am, KST (8:50-9:00pm, NYT)	Short break	
11:10-11:45am (9:00-9:45pm, NYT)	**Special Invited Speaker: Oncogenic lncRNA identification on the basis of epigenetic code**	**Kaifu Chen, PhD Harvard Medical School, USA**
11:45 – 2:00pm, KST (9:45-12:00am, NYT)	**Lunch break**	
2:00-2:20pm, KST (12:00-12:20am, NYT)	**S2520** Comparative analysis of long non-coding RNAs profiles in rice contrasting genotypes under salt stress	**Raheleh Mirdar Mansuri and Zahra-Sadat Shobbar, Iran**
2:20-2:40pm, KST (12:20-12:40am, NYT)	**S25207** mTOR inhibitor GDC-0349 improves ASO induced SAMMSON knock down resulting in enhanced antitumor efficacy in uveal melanoma	Shanna Dewaele, Boel De Paepe, Louis Delhaye, et al., Belgium
2:40-3:00pm, KST (12:40-1:00am, NYT)	**S25204** A T1D-associated lncRNA modulates the type I interferon signaling and the antiviral response in pancreatic beta cells.	Itziar Gonzalez-moro and Izortze Santin, Spain
3:00-3:20, KST (1:00-1:20am, NYT)	**S25206** Large scale interaction analysis of RNA binding proteins/ LncRNAs to identify lncRNA nuclear localization mechanisms	Yile Huang, Yulong Qiao, Yu Zhao, Jie Yuan, Jiajian Zhou, Hao Sun, and Huating Wang, China
3:20-3:40pm, KST (1:20-1:40am, NYT)	**S25211** Integrative network analysis identified master regulatory long non-coding RNAs underlying the squamous subtype of pancreatic ductal adenocarcinoma	Lina ZHU and Xin WANG, Hong Kong
3:40-4:00, KST (1:40-2:00am, NYT)	Coffee Break	
4:00-5:00pm, KST (2:00-3:00am, NYT)	**Keynote 2: Hunting for therapeutic long noncoding RNAs**	Rory Johnson, PhD University of Bern, Switzerland
5:00-5:50pm, KST (3:00-3:50am, NYT)	**Panel Session Evolving lncRNA world: Post-genomic structurefunction insights, ribosome profiling, and machine learning**	Moderator: Leonard Lipovich, PhD Mohammed Bin Rashid University of Medicine and Health Sciences, Dubai, UAE.
5:50-6:00, KST (3:50-4:00am, NYT)	**Closing Remarks**	

Workshop 1

Integrating Omics Data for Cancer Therapies

Workshop Chairs: Liang Cheng (liangcheng@hrbmu.edu.cn)

Time	Title	Presenter/Author
9:30 – 10:00am	**S01201** Machine learning-based methods and novel data models to predict adverse drug reaction	Jinxian Wang (jinxianwang@csu.edu.cn),
10:00 – 10:30am	**S01203** Gene Ontology aided Compound Protein Binding Affinity Prediction Using Bert Encoding	Lingling Zhao (zhaoll@hit.edu.cn)
10:30 – 11:30am	**S01202** Identification of gene signature associated with type 2 diabetes mellitus by integrating mutation and expression data	Zijun Zhu (youngj4ever@outlook.com)
	Closing Remarks	

Workshop 6

The 11th International Workshop on Information Technology for Chinese Medicine (ITCM 2020)

Workshop Chairs: Josiah Poon, Yong Xiao, Guozheng Li

Time	Title	Presenter/Author
11:00am-11:15am	**S06211** Syndrome Evolution and Chinese Herb Formula Regularity of TCM Heat Syndrome in Type 2 Diabetes Mellitus: Complex Network Community Discovery Algorithm and Sankey Diagram Visualization	Ying Xing
11:15am-11:30am	**S06205** Research on Medical Intelligent Consultation Based on Question Generation Technology	Zengzhen Du
11:30am-11:45am	**S06213** Analysis of diabetic comorbidities and their interrelationships in 5227 Chinese patients with type 2 diabetes	Yifei Wang
11:45am-12:00pm	**S06203** Biological Processes underlying the Reinforcing Primary Qi Delivered by Ginseng	Guang Zheng
	Closing Remarks	

Workshop 11

The 11th Integrative Data Analysis in Systems Biology (IDASB 2020)

Workshop Chairs: Profs Jane Zheng, Zhongming Zhao, Rui Jiang, Le Zhang, Dr. Ming Xiao

Time	Title	Presenter/Author
14:00 – 14:05	Opening	Prof. Jane Zheng
14:05 – 14:25	**B345** Towards a consistent evaluation of miRNA-disease association prediction models	Thi Ngan Dong and Megha Khosla
14:25 – 14:45	**B760** A multiomics discriminatory analysis approach to identify drought-related signatures in maize nodal roots	Sidharth Sen, Tyler McCubbin, …, and Trupti Joshi
14:45 – 15:05	**S11201** A Review of Artificial Intelligence Applications in Bacterial Genomics	Jianghang Xie, Le Zhang, and Ming Xiao
15:05 – 15:25	**B543** Computational identification of key pathways and differentially-expressed gene signatures in ovarian cancer stem cells	Renata Fu, Yongsheng Bai, and Qi-En Wang
15:25 – 15:45	**S11203** Immunoregulation Delivered by the Bioactive Compounds of Dioscoreae Rhizoma	Guang Zheng
15:45 – 16:05	**B737** An Auxiliary System for Calculating Effective Connectivity from Co-Activation Network Data	yaoxin nie, linlin zhu, xiaozhong fan, and zhendong niu
16:05 – 16:25	**S11202** Using bioinformatics methods to explore the connections between expression and subcellular localization of proteins and gastric cancer progression	Zhenying Tang, Ming Xiao, Senyi Deng, and Le Zhang
	Closing Remarks	

Workshop 16

Artificial Intelligence & Big Data vs Pandemics (AI&BDvsPandemics)

Workshop Chairs: Ester Zumpano, Elio Masciari, Andrea Tagarelli

Time	Title	Presenter/Author
14:30	**Workshop Introduction**	
14:40	**S16202** Consumer Demand Modeling During COVID-19 Pandemic	Shaz Hoda, Amitoj Singh, Anand Rao, Remzi Ural, and Nicholas Hodson
14:55	**S16201** Use of fuzzy sets, aggregation operators and multi agent systems to simulate COVID-19 transmission in a context of absence of barrier gestures and social distancing: application to an island region.	Sébastien REGIS, Olivier MANICOM, and Andrei DONCESCU
15:10	**S16205** Assessing the Impact of Government Interventions on the Spread of COVID-19 with Dynamic Epidemic Models: A case study of Texas	Layla Araiinejad, Jacqueline Carlton, Yuexin Li, and Jingyi Zheng
15:25	**S16206** Repositioning Molecules of Chinese Medicine to Targets of SARS-Cov-2 by Deep Learning Method	Tao Song, Yue Zhong, Mao Ding, Renteng Zhao, Qingyu Tian, Zhenzhen Du, Dayan Liu, Jiali Liu, and Yufeng Deng
15:40 – 16:00	**Coffee Break**	

16:00	**B410** An Improved SEIR Model for Reconstructing the Dynamic Transmission of COVID-19	Xiaohan Yuan, Shuyu Chen, Lu Yuwen, Shuqi An, Sha Mei, and Tianqiang Chen
16:15	**B640** Exploring Optimal Adaptive Activation Functions for Various Tasks	Haigen Hu, Aizhu Liu, Qiu Guan, Xiaoxin Li, Cheng Luo, and Qianwei Zhou
16:30	**S16203** On the use of clinical based infection data for pandemic case studies	Giuseppe Tradigo, Patrizia Vizza, Gabriel Gabriele, Maria Mazzitelli, Carlo Torti, Mattia Prosperi, Pietro Hiram Guzzi, and Pierangelo Veltri
16:45	**S16204** Experiences on Data management and indexes prediction on COVID-19 Italian case	Giuseppe Tradigo, Pietro Hiram Guzzi, Tamer Kahveci, andPierangelo Veltri,
17:00	**S16207** On the Development of a Tool for Tongue Images Analysis	Eugenio Vocaturo and Ester Zumpano
	Closing Remarks	

December 17

Workshop 24

Machine Learning and Artificial Intelligence in Bioinformatics and Medical Informatics

Workshop Chairs: Dr. Haiying Wang, Prof. Hui Wang, Prof. Huiru (Jane) Zheng, Prof. Paul Walsh

Time	Title	Presenter/Author
9:00 – 9:20	**Invited Talk: Natural Language Processing for Drug Labelling**	Prof. Paul Walsh
9:20 - 9:40	**S2409** Bayesian Network Approach to Modelling Nitrogen Utilization Efficiency of Dairy Cows	Xianjiang Chen, Huiru Zheng, Haiying Wang, and Tianhai Yan
9:40 – 10:00	**S24203** Examining the Effect of General Practitioner Practice Size on Prescribing Behaviours in Northern Ireland	Frederick Booth, Maurice Mulvenna, Raymond Bond, Kieran McGlade, Debbie Rankin, and Jonathan Wallace
10:00 – 10:20	**B24201** ERP Template Matching for EEG Single Trial Classification	Femi William, Ramazan Aygun, and Feng Zhu
10:20 – 10:40	**B24204** An Effective and Automatic Method to Aid the Diagnosis of Amyotrophic Lateral Sclerosis Using One Minute of Gait Signal	Juliana Paula Felix, Hugo Alexandre Dantas do Nascimento, Nilza Nascimento Guimarães, Eduardo Di Oliveira Pires, Gabriel da Silva Vieira, and Wanderley de Souza Alencar
10:40 – 11:00	**B24205** Graph Learning Approaches for Graph with Noise: Application to Disease Prediction in Population Graph	Lang Chen, Yangmin Huang, Bin Liao, Kun Nie, Shoubin Dong, and Jinlong Hu
11:00 – 11:05	**Coffee Break**	
11:05 – 11:25	**B24207** Feature-level Fusion for Depression Recognition Based on fNIRS Data	Shuzhen Zheng, Chang Lei, Tao Wang, Chunyun Wu, Jieqiong Sun, and Hong Peng
11:25 – 11:45	**B542** Multidimensional and multiscale Higuchi dimension for the analysis of colorectal histological images	Jaqueline Junko Tenguam, Guilherme Botazzo Rozendo, Guilherme Freire Roberto, Marcelo Zanchetta do Nascimento, Alessandro S. Martins, and Leandro Alves Neves
11:45 – 12:05	**B323** Human Arm Stabilization and Rehabilitation using Intelligent Control Techniques	william barbosa, Guilherme Temporão, and Marco Meggiolaro
12:05 – 12:25	**B362** Feature-level Fusion for Depression Recognition Based on fNIRS Data	Shuzhen Zheng, Chang Lei, Tao Wang, Chunyun Wu, Jieqiong Sun, and Hong Peng
12:25 – 12:45	**B578** RBFACO: A New Feature Selection Algorithm	Yunshuang Xiao and Shuyu Chen
	Closing Remarks	

Workshop 12

Biomedical and Health Informatics (BHI) Workshop

Workshop Chairs: Illhoi Yoo

Time	Title	Presenter/Author
10:00am-1:00pm	**B539** Phantom Tumor Tracking in Dual-Energy Fluoroscopy using a Kalman Filter	Abolfazl Meyarian, Himan Namdari, Xiaohui Yuan, John Roeske, and Mark Albert,
	B552 Weight loss, Fitness, and Health related Image Sharing using Twitter: an Observation Study	Albert Park, Chuqin Li, Jessamyn Bowling, Yaorong Ge, and Michael Dulin, *Diet,*
	B566 OptSelect: an R package for ensemble feature selection and stability assessment	Eva Lee and Karan Uppal,
	B638 Wearable spasticity estimation and validation using machine learning	Shou-Jen Wang, Jeong-Ho Park, Hyung-Soon Park, Devak Nanda, and Mark V. Albert,
	B324 A Framework for Analysis, Ontological Evaluation, and Visualization in Preparation to Predictive Analytics in Pediatric Brain Tumor Research	Alex Felmeister, Angela Waanders, Jennifer Mason, Jeff Stevens, L. Charles Bailey, Shiva Ganesan, and Ingo Helbig,
	B405 Analysis an Electronic Health Record based on Hedonic and Pragmatic Aspect of the User Experience	Danielle Alves, Valeria Cesário Times, Amadeu Campos Filho, Fred Revoredo Rabelo Ferreir, Erika Maria Alves da Silva, and Magdala Araújo Novaes,
	B716 3D Texture Feature-Based Lymph Node Automated Detection in Head and Neck Cancer Analysis	Yibin Wang, Christian Zamiela, Toms V. Thomas, William N. Duggar, P. Russell Roberts, Linkan Bian, and Haifeng Wang,
	B679 Quantification of Brain Lesions in Multiple Sclerosis Patients using Segmentation by Convolutional Neural Networks	Marcela de Oliveira, Felipe Balistieri Santinelli, Marina Piacenti-Silva, Fernando Coronetti Gomes Rocha, Fabio Augusto Barbieri, Paulo Noronha Lisboa-Filho, Jorge Manuel Santos, and Jaime dos Santos Cardoso,
	S12206 ST-MetaDiagnosis: Meta learning with Spatial Transform for rare skin disease Diagnosis	Delong Zhang, Mengqun Jin, and Peng Cao,
	B265 Sparse Regularization Tensor Robust PCA Based on t-product and Its Application in Cancer Genomic Data	Hang-Jin Yang, Yu-Ying Zhao, Jin-Xing Liu, Yu-Xia Lei, and Jun-Liang Shang,
	B267 Applying clinical guidelines to conformance checking for diagnosis and treatment: a case study of ischemic stroke	Haifeng Xu, Jianfei Pang, Xi Yang, Liqun Ma, Huajian Mao, and Dongsheng Zhao,
	B284 Prediction of patients with heart failure after myocardial infarction	Po-Yu Liang, Tun-Wen Pai, and Lee-Jyi Wang,
	B297 EEG Based Depression Recognition by Combining Functional Brain Network and Traditional Biomarkers	Shuting Sun, Huayu Chen, Xuexiao Shao, Liangliang Liu, Xiaowei Li, and Bin Hu,
	B312 A Novel Algorithm of Expansion Term Selection and Weight Assignment for Query Expansion of Chinese EMR Retrieval	Songchun Yang, Xiangwen Zheng, Fan Tong, Huajian Mao, and Dongsheng Zhao
	B664 Identifying High-Risk Breast Cancer Patients Using Microarray and Clinical Data	Azni Nasuha Ngisa and Huey Fang Ong,

	B591 TAGNet: Temporal Aware Graph Convolution Network for Clinical Information Extraction	Shuai Wang and Junfei Liu,

Workshop 4

Data mining from genomic variants and its application to genome-wide analysis 2020

Workshop Chairs: Prof. Taesung Park

Time	Title	Presenter/Author
11:30-12:30	**Session 1: Genomic Data Analysis** **(12 minutes for each talk, 3 minutes for Q and A)**	
11:30-12:30	**S04201**: Comprehensive-GWAS: a pipeline for genome-wide association studies utilizing cross-validation to assess the predictivity of genetic variations	Gabrielle Dagasso, Yan Yan, Lipu Wang, Longhai Li, Randy Kutcher, Wentao Zhang, and Lingling Jin
	B277: Genome-Wide Association Study (GWAS) on Metabolic Syndrome in Subjects with Abdominal Obesity in a Taiwanese Population.	Kuan-Hung Yeh, Tzu-Hung Hsiao, Ching-Heng Lin, and Tzu-Pin Lu
	S04204:A Kind of Epistasis Mining Method Based on K-tree and Bayesian Network	Yulong Kan, Xu Wang, Chen Yang, Xuan Yang, Liguang Wang, and Jianxiao Liu
	B689: SNPViz v2.0: A web-based tool for enhanced haplotype analysis using large scale resequencing datasets and discovery of phenotypes causative gene using allelic variations	Shuai Zeng, Maria Skrabisova, Zhen Lyu, Yen On Chan, Kristin Bilyeu, and Trupti Joshi
12:30-13:30	**Lunch**	
13:30-15:00	**Session 2: Omics Data Analysis** **(12 minutes for each talk, 3 minutes for Q and A)**	
13:30-15:00	**B612**: Investigating Genetic Signatures for Sex-Biased miRNA targeted Genes related to Intellectual Disability	Junmeng Yang, Susan Huang, Eric Li, and Yongsheng Bai
	B219: Year, Location, and Species Information In Predicting MIC Values with Beta-Lactamase Genes	Cory Kromer-Edwards, Mariana Castanheira, and Suely Oliveira
	S04209: Detection of Fetal Single Gene Mutations through Targeted Sequencing of Maternal cell-free DNA	Junghyun Namkung
	B641: ProFPred: a two-step protein function prediction model based on sequence and evolutionary information	Ruiquan Ge, Guanwen Feng, Pu Wang, and Qiguang Miao
	B668: Statistical Learning: the impact of combining feature-information structures on total genetic characterization of composite data points	Mosaab Daoud
	S04202: TensorSV: structural variation inference using alignment-based tensors and variable topology neural networks.	Timothy Becker and Dong-Guk Shin
15:00 - 15:10	**Coffee Break**	
15:10-16:40	**Session 3: Applying Statistical Method and Machine Learning to Omics Data** **(12 minutes for each talk, 3 minutes for Q and A)**	
16:40-16:40	**S04214**: Clustering analysis using Gaussian Mixture Model for SNPs	Changwoo Lee, Hyuk Kim, Eungchum Cho, Sang-Hoon Yu, Wookyum Kim, Woong Kook

	S04211: Developing weighted RFS for Type 2 Diabetes using Hierarchal Structure Component Model (HisCoM-RFS)	Catherine Apio
	Genomic Pathway Analysis of UK Biobank COVID-19	Kyulhee Han
	Prediction T2D using KARE Metabolite	Taeyoung Jung, Youngae Jung, Geum-Sook Hwang
	S04210: Penalized Generalized Estimating Equations Approach for Ordinal Response Analysis Using Longitudinal High-dimensional data.	Md Kamruzzaman and Oran Kwon
	S04208: Improving health space model using deep learning and ordinal information	Chanhee Lee and Oran Kwon
16:40-16:50	**Coffee Break**	
16:50-18:10	**Session4: Applying Statistical Method and Machine Learning to Cancer Analysis (12 minutes for each talk, 3 minutes for Q and A)**	
16:50-18:05	**S04205** Genomic landscape of somatic mutations for platinum response in high grade serous ovarian cancer	
	S04207: EV Metagenome Data Analysis of Ovarian Cancer	Nayeon Kang
	Identification of prognosis biomarker for Pancreatic Ductal Adenocarcinoma	Taewan Goo, Daechan Park, Seungyeoun Lee, Jin-Young Jang
	Novel way for pathway analysis of metabolomics data; Analysis of Hepatocellular Carcinoma from Cirrhosis	Chanwoo Park
	S04206:Analysis of Microbiome Data Identifies Biomarker Associated with Hepatocellular Carcinoma Across Countries	Boram Kim
18:05-18:10	**Closing Remarks**	

Workshop 14

11th International Workshop on High Performance Bioinformatics and Biomedicine (HiBB 2020)

Workshop Chairs: Mario Cannataro

Time	Title	Presenter/Author
14.00 - 14.20	S14201: Improving Prediction Accuracy of Microarray Cancer Data with Non-negative Matrix Factorization and Its Variant	Kalpdrum Passi, Nakul Patel, and Chakresh Jain
14.20 - 14.40	B300: MR Image Analysis to Differentiate Salivary Gland Tumors: a Preliminary Study	Chiara Losquadro, Gaetano Giunta, Luca Pallotta, Michela Gabelloni, and Emanuele Neri
14.40 - 15.00	B320:SLPal: Accelerating Long Sequence Alignment on Many-Core and Multi-Core Architectures	Xiaoming Xu, Yuandong Chan, Kai Xu, Jikai Zhang, Xiaoning Wang, Zekun Yin, and Weiguo Liu
15-00 - 15.30	**Coffee Break**	
15.30 - 15.50	B426:HRV-Spark: Computing Heart Rate Variability Measures Using Apache Spark	Xufeng Qu, Yuanyuan Wu, Jinze Liu, and Licong Cui
15.50 - 16.10	B600:J2*: A New Method for Alignment-free Sequence Similarity Measurement	Yue Jiang, Don Adjeroh, Bing-hua Jiang, and Jie Lin
16.10 - 16.30	B670:A New Framework for Spatial Modeling and Synthesis of Genome Sequence	Salman Mohamadi, Donald A. Adjeroh, Behnoush Behi, and Hamidreza Amindavar

16.30 - 17.00	**Coffee Break**
	Closing Remarks

Workshop 15

1th 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*

Time	Title	Presenter/Author
17.00 - 17.20	**S15201**: Automatic diagnosis of COVID-19 and pneumonia using FBD method	Pradeep Kumar Chaudhary and Ram Bilas Pachori
17.20 - 17.40	**B402**: Cascade SEIRD: Forecasting the Spread of COVID-19 with Dynamic Parameters Update	Yongliang Wen, Jiangnan Xu, Yunming Ye, Xutao Li, Chuyao Luo, and Tianlun Zhu
17.40 - 18.00	**B301: C**ovid-19 Signal Analysis: Effect of Lockdown and Unlockdowns on Normalized Entropy in Italy	Francesco Benedetto, Gaetano Giunta, Chiara Losquadro, and Luca Pallotta
18.00 - 18.20	**S15203:** DYVIC: DYnamic VIrus Control in Peru	Juan Antonio Lossio-Ventura, Hugo Alatrista-Salas, Eleni Linos, Miguel Nunez-del-Prado, and Alvaro Talavera
15-00 - 15.30	**Coffee Break**	
	Closing Remarks	

December 18

Workshop 17

Machine Learning for Biological and Medical Image Big Data

Workshop Chairs: Fa Zhang, zhangfa@ict.ac.cn, Xuefeng Cui, xfcui@email.sdu.edu.cn

Time	Title	Presenter/Author
9:00	**B308**: An Adaptive Segmentation Technique to Detect Brain Tumors Using 2D Unet	Mohammed Aledhari and Rehma Razzak
9:20	**S17208**: An Unsupervised and Iterative Model for Single-Particle Cryo-EM Image Denoising Based on Siamese Neural Network	Wangjie Zheng and Yang Yang
9:40	**S17206**: Chromosome Cluster Identification Framework Based on Geometric Features and Machine Learning Algorithms	Chengchuang Lin, Aihua Yin, Qinglan Wu, Hanbiao Chen, Li Guo, Gansen Zhao, Xiaomao Fan, Haoyu Luo, and Hua Tang
10:00	**B616**: ChromSeg: Two-Stage Framework for Overlapping Chromosome Segmentation and Reconstruction	Xu Cao, Fangzhou Lan, Chi-Man Liu, Tak-Wah Lam, and Ruibang Luo
10:20	**S17204**: Exploration of the Possibility of Early Diagnosis for Digestive Diseases Using Deep Learning Techniques	Rory Liao, Kevin Qi, Daniel Che, and Tingying Helen Zeng
10:40	**B254**: Image-based early predictions of functional properties in cell manufacturing	Hong Seo Lim, Madeline Smerchansky, Jingxuan Zhou, Paramita Chatterjee, Angela Jimenez, Xingyu Yang, Krishnendu Roy, and Peng Qiu
	Coffee Break	
14:00	**S17207**: LR-Net: A Multi-task Model Using Relationship-based Contour Information to Enhance the Semantic Segmentation of Cancer Regions	Baorong Shi, Hong Zhang, Rui Yan, Wang Jing, Jinfeng Zang, and Fa Zhang
14:20	**B714**: Modality-Classification of Microscopy Images Using Shallow Variants of Deep Networks	Juan Trelles Trabucco, Pengyuan Li, Cecilia Arighi, Hagit Shatkay, and G. Elisabeta Marai
14:40	**S17203**: Mut-Detecter : An EGPR activating mutation type classification method with a deep convolutional neural network	Yaojun Wang, Xinyu Hua, Yu Wang, Chunming Zhang, Dongbo Bu, Shiwei Sun, and Xingce Wang
15:00	**S17202**: Stature estimation using measurements of the skull in Chinese populations	Yang Wen, Zhou Mingquan, Lin Pengyue, Geng Guohua, Liu Xiaoning, and Li Kang
15:20	**S17210**: Tripfly: Predicting Gene-gene Interaction of Drosophila Eye Development Using Triplet Loss	Zhenhuan Liu, Jiafeng Chen, and Yang Yang
	Closing Remarks	

Workshop 22

Artificial Intelligence Techniques for BioMedicine and HealthCare

Workshop Chairs: Ester Zumpano, Pierangelo Veltri, Luciano Caroprese

Time	Title	Presenter/Author
9:00	**Workshop Introduction**	

9:10	**S22211** Current Trends And Practices In Smart Health Monitoring And Clinical Decision Support	Deborah Falcone, Carmela Comito, and Agostino Forestiero
9:25	**S22206** Mining Potentially Unreported Effects from Twitter Posts through Relational Similarity: A Case for Opioids	Keyuan Jiang, Liyuan Huang, Tingyu Chen, Gelareh Karbaschi, Dingkai Zhang, and Gordon Bernard
9:40	**S22203** Cross-Modality Medical Image Retrieval with Deep Features	Ashery Mbilinyi and Heiko Schuldt
9:55	**S22204** Sequence-level Supervised Deep Neural Networks for Mitosis Event Detection in Time-Lapse Microscopy Images	Siteng Chen, Ao Li, and Janet Roveda
10:05-10:20	**Coffee Break**	
10:20	**S22205** Predicting eye movement and fixation patterns on scenic images using Machine Learning for Children with Autism Spectrum	Raymond Anden and Erik Linstead
10:35	**S22202** A Convolutional Gated Recurrent Neural Network for Seizure Onset Localization	Hisham Daoud and Magdy Bayoumi
10:50	**S22207** Lower-Gait Tracking Mobile Application: A Case Study of Lower body Motion Capture Comparison Between Vicon T40 System and Apple Augmented Reality	TRUONG TRAN, Chang-kwon Kang, and Shannon Mathis
11:00 – 11:15	**Coffee Break**	
11:15	**S22208** Neural network based prediction of knee contact forces for different gait speeds	Georgios Giarmatzis, Evangelia I. Zacharaki, and Konstantinos Moustakas
11:30	**S22209** Challenges in predicting glioma survival time in multi-modal deep networks	Abdulrhman Aljouie, Yunzhe Xue, Meiyan Xie, and Usman Roshan
11:45	**S22210** SeqMed: Recommending Medication Combination with Sequence Generative Adversarial Nets	Shuai Wang
12:00	**S22201** Accelerometer based classification of elbow flexion and extension exercises	Gamze Uslu, Sebnem Baydere, Ata Tekin, and Feryal Subaşı
12:15 – 12:30	**Coffee Break**	
12:30	**S22213** Vessel lumen segmentation in carotid artery ultrasounds with the U-Net convolutional neural network	Meiyan Xie, Yunzhu Li, Yunzhe Xue, Lauren Huntress, William Beckerman, Saum Rahimi, Justin Ady, and Usman Roshan
12:45	**S22214** Weakly Supervised Instance Segmentation of SEM Image via Synthetic Data	Yunfeng Wang, Xiaoqin Tang, Jingchuan Fan, and GuoQiang Xiao
13:00	**B538** Personalized Cardiovascular Disease Risk Mitigation via Longitudinal Inverse Classification	Michael Lash and Nick Street
13:15 - 14:30	Break	
14:30	**B229** Feature selection algorithms for predicting preeclampsia: A comparative approach	Jose Francisco Carreño Martínez and Peng Qiu
14:45	**B232** The Challenge of Metrics in Automated Dietary Monitoring as Analysis Transitions from Small Data to Big Data	Surya Sharma and Adam Hoover
15:00	**B374** Pneumonia outcome prediction using structured and unstructured data from EHR	Cherubin Mugisha and Incheon Paik
15:15	**B376** SE-ECGNet: A Multi-scale Deep Residual Network with Squeeze-and-Excitation Module for ECG Signal Classification	Haozhen Zhang, Wei Zhao, and Shuang Liu
15:30 – 15:45	**Coffee Break**	
15:45	**B388** Anxiety Detection with Nonlinear Group Correlation Fusion of Electroencephalogram and Eye Movement	Zhihua Guo, Enli Fu, Jing Pan, Xiaowei Zhang, and Bin Hu
16:00	**B202** Prediction of anticancer peptides with dictionary learning method	Ruiquan Ge, Xiaomao Fan, and Pu Wang
16:15	**B564** FOIT: Fast Online Instance Transfer for Improved EEG Emotion Recognition	Jinpeng Li, Hao Chen, and Ting Cai

	Closing Remarks	

Workshop 12

Biomedical and Health Informatics (BHI) Workshop

Workshop Chairs: Illhoi Yoo

Time	Title	Presenter/Author
10:00am-1:00pm	**B684F**: *Statistical Chest Shape Modeling: Application to the Evaluation of Pectus Excavatum Treatment Outcomes*	Nahom Kidane, Mohammad Obeid, Rick McKenzie, Robert Kelly, and Robert Obermeyer
	B685S: *NoSQL distributed database for DICOM objects*	Ana Almeida, Francisco Oliveira, Rui Lebre, and Carlos Costa
	B692S: *Learning Room Structure and Activity Patterns Using RF Sensing for In-Home Monitoring of Older Adults*	Maira Moran, Marcelo Faria, Gilson Giraldi, Luciana Bastos, Bruno Inacio, and Aura Conci
	B694F: DYVIC: DYnamic VIrus Control in Peru	Nuerzati Resuli, Marjorie Skubic, and Scott Kovaleski
	B705S: *Analysis of SARS-CoV-2 sequences reveals transmission path and emergence of SD 614G mutation*	Mingjia Li, Nishita Prasad, Dwight Hall, and Huanmei Wu
	B717S: *A Comparison of Pre-trained Vision-and-Language Models for Multimodal Representation Learning across Medical Images and Reports*	Yikuan Li, Hanyin Wang, and Yuan Luo
	B761F: *Can MED-RT Summarization Support Missing Adverse Drug Reactions Discovery?*	Ling Zheng and Joan Kapusnik-Uner
	B347F: *Emotion Classification Based on Brain Functional Connectivity Network*	Xiaofang Sun, Bin Hu, Xiangwei Zheng, Cun Ji, and Yongqiang Yin
	B375F: *Automatic Classification of Antepartum Cardiotocography Using Fuzzy Clustering and Adaptive Neuro-Fuzzy Inference System*	Yue Fei, Xiaoqian Huang, Qinqun Chen, Jiamin Chen, Li Li, Jiaming Hong, Zhifeng Hao, and Hang Wei
	B424F: *A robust fuzzy clustering algorithm using spatial information combined with local membership filtering for brain MR images*	Lanting Li and Peng Cao
	B444F: *Learnable Bag Similarity Based Deep Multi-Instance Network for Breast Cancer Diagnosis*	Rui Cheng, Liming Yuan, Haixia Xu, Zhenliang Li, and Xianbin Wen
	B447F: *Stroke screening data modeling based on openEHR and NINDS Stroke CDE*	Yu Yang, Haifeng Xu, Bin Qi, Xiaodong Niu, Mei Li, and Dongsheng Zhao
	B479F: *CSABlock-based Cascade RCNN for Breast Mass Detection in Mammogram*	He Xiao, Qingfeng Wang, Zhiqin Liu, Jun Huang, Yuwei Zhou, Ying Zhou, and Weiyun Xu
	B778S: *Academic journal recommendation for human neuroimaging studies via brain activation-based filtering*	Junsol Kim
	B608F: *SEAUNet: Domain Adaptation for Biomedical Image Segmentation*	Hang Chen, Leiting Chen, Yuchu Chen, Minghao Fan, and Chuan Zhou
	Closing Remarks	

Posters

Time	December 19
Keynote Sessions	Keynote Talk
Morning Sessions	P201 “Additional Value of Augmenting Current Subscales in Braden Scale with Advanced Machine Learning Technique for Pressure Injury Risk Assessment”. Kathan Vyas, Ali Samadani, Mladen Milosevic, Sarah Ostadabbas, and Saman Parvaneh P202 “A New Data Visualization and Digitization Method for Building Electronic Health Record”. Nan Liu, Chuan Wang, Xinyu Miao, Hua Bai, Yunan Wang, Limin Yang, Yiming Lei, Wei Zhang, and Hong Wang P203 “Stable and Accurate Feature Selection from Microarray Data with Ensembled Fast Correlation Based Filter”. Aiguo Wang, Huancheng Liu, Jinjun Liu, Huitong Ding, Jing Yang, and Guilin Chen P208 “Analysis of TCM prescription rule of stroke based on FP-growth algorithm”. Wang Yan, Qi Hao, and Huang zhengzheng P209 “The Likelihood Prediction of Phylogenetic Trees based on Artificial Neural Network: a new perspective and preliminary attempt”. MingYan Li and Cheng Ling P210 “Human ability enhancement for reading mammographic masses by a deep learning technique”. Noriyasu Homma, Kyohei Noro, Xiaoyong Zhang, Yutaro Kon, Kei Ichiji, Ivo Bukovsky, Akiko Sato, and Naoko Sato P211 “A hierarchical knowledge-aware neural network for protein-protein interaction article classification”. Hao Wei, Ai Zhou, Yijia Zhang, Fei Chen, Wen Qu, and Mingyu Lu P212 “Sleep Stages Discrimination by Head Motion”. Motoki Yoshihi, Shima Okama, Tianyi Wang, and Masaaki Makikawa P213 “Sleep Stage Estimation Using ECG”. Hirotaka Matsumoto, Shima Okada, Tianyi Wang, and Masaaki Makikawa P214 “Towards BacterioPhage Genetic Edition: Deep Learning Prediction of Phage-Bacterium Interactions”. Shabnam Ataee, Óscar Rodríguez, Xavier Brochet, and Carlos Andrés Pena P215 “Computational Prediction of Functional Effects for Cancer Related Genetic Sequence Variants”. Bofei Wang, Jonathon Mohl, and Ming-Ying Leung P216 “A Hybrid Approach for Cancer Biomarker Extraction”. Xiangyu Gao, Jinhe Shi, Wenjin Chen, Nancy Sazo, Huiqi Chu, Evita Sadimin, David Foran, and Yi Chen P217 “Web-QuateXelero: Web-based efficient network motif detection tool”. Marko Lakic, Bazen Nega, and Wooyoung Kim P218 “The effect of blurring on lung cancer subtype classification accuracy of convolutional neural networks”. Tejal Nair, Ali Foroughi pour, and Jeffrey Chuang P219 “Quality Assessment of Inpatient Medical Claim Data”. Prachiti Aras, Lou Chitkushev, Guanglan Zhang, Mary Lucas, Reza Rawassizadeh, and Irena Vodenska P220 “A Model for Predicting the Amount of Urine in the Bladder Based on App-generated Tracking Data”. Pascal Fechner, Jannik Lockl, Nicolas Ruhland, Tristan Zürl, and Till Zwede P221 “Pediatric Patient Traumatic Brain Injury Prediction”. Franklin Fuchs, Omar Kamal, Hanao Li, Mihye Ahn, and So Young Ryu P222 “Uncovering Machine Learning-Ready Data from Public Clinical Trial Resources: A case-study on normalization across Aggregate Content of ClinicalTrials.gov”. Emmette Hutchison, Youyi Zhang, Sreenath Nampally, Jim Weatherall, Faisal Khan, and Shameer Khader P223 “Genome-wide association study identified genetic variants associated with severity of COPD in Korean participants”. Geumkyung Nah, Ji-Won Kim, Eun-A Choi, Jeom Kyu Lee, Woo Jin Kim, Kwang Ha Yoo, and Dankyu Yoon P224 “A Search and Filter Strategy for Identifying Differentially Co-Expressed Analyte Modules” Jamie Lea and Sharlee Climer P225 “Recognition of hyperparathyroidism based on transfer learning”. Jiabo Chen, Qing Guo, Zixun Jiang, Huaqing Wang, Mingan Yu, and Ying Wei P226 “Colorectal Cancer Image Segmentation and Classification with Deep Neural Network Based on Information Theory”. Hwa-Rang Kim, Kwang-Ju Kim, Kil-Taek Lim, and Doo-Hyun Choi P227 “Detection of Mammalian Coding Sequences Using a Hybrid Approach of Chaos Game Representation and Machine Learning”. Mohamed Emam, Amna Ali, Eman Abdelrazik, Mustafa Elattar, and Mohamed El-Hadidi P228 “Constructing a Relevance-oriented Dataset for Training Transformer Rankers for Medical Search”. Zhi Zheng and Ben He P229 “A Review of Telemedicine in time of COVID-19”. hidong Wu, Guanglan Zhang, and Lou Chitkushev P230 “Deep Learning to Discover Genomic Signatures for Racial Disparity in Lung Cancer”. Masrur Sobhan, Abdullah Mamun, Raihanul Tanvir, Mario Alfonso, Pablo Valle, and Ananda Mondal
	End of Conference