The 12th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics
ACM-BCB 2021
August 1-4, 2021 (Virtual due to COVID-19)

ACM-BCB 2021 Advance Program

All sessions will become available live to all registered attendees, via the ACM-BCB 2021 Virtual Conference Platform.

Day 0 (August 1, Sunday), Workshops, Tutorials & First-Time Attendee Special Session	
Tutorials (Chairs: Jun Wan, Andy Perkins)	
9:00-11:30	***Introduction to Application Containerization Using Singularity*** William Sanders, Jason Macklin, Matthew Bradley, Richard Yanicky and Aaron McDivitt
11:30-12:20	***An Introduction to Computational Approaches for 3D Genomic Modeling*** Max Highsmith and Jianlin Cheng
12:20-1:10	***Next Generation Sequencing Data Analysis*** Nadia Lanman, Sheng Liu, Sagar Utturkar and Yucheng Zhang
1:10-2:50	***A Graphical Front-end for Rapid and Scalable Execution of Bioinformatics Workflows Using Serverless Cloud Computing*** Ling-Hong Hung, Varik Hoang, Wes Lloyd and Ka Yee Yeung
2:50-5:20	***Pytorch_EHR: A Codebase for Building Recurrent Neural Network Based Predictive Models Using Electronic Health Records*** Laila Rasmy, Ziqian Xie and Degui Zhi

Day 0 (August 1, Sunday), Workshops, Tutorials & First-Time Attendee Special Session	
Workshops (Chairs: Weihua Guan, Jason Moore, Scott Williams)	
9:00-11:00	***10th Workshop on Parallel and Cloud-based Bioinformatics and Biomedicine (ParBio)*** Giuseppe Agapito, Mario Cannataro and Wes Lloyd
9:00-9:30	*Towards Dynamic Simulation of a Whole Cell Model*

	Jae-Seung Yeom, Konstantia Georgouli, Robert Blake and Ali Navid
9:30-10:00	*CNN models for Eye State Classification using EEG with Temporal Ordering* Femi William and Feng Zhu
10:00-10:30	*Data Mining for Electroencephalogram Signal Processing and Analysis* Rossana Mancuso, Marzia Settino and Mario Cannataro
10:30-10:40	*Closing Remarks*

12:00-5:30	***Machine Learning Methods for Single-Cell Analysis (ML-SCA)*** Lana Garmire, Smita Krishnaswamy, Jie Liu and Joshua Welch
12:00-12:05	*Introduction* Lana Garmire
12:05-1:00	*Keynote: Clustering, Data Integration and Transfer Learning for Single Cell Transcriptomic Data* Kathryn Roeder
1:00-2:00	*Abstract Presentations*
2:00-2:30	Break / Poster Session
2:30-3:30	*Keynote: See Something, Seq Something: Mapping Cell Morphology to Spatial and Temporal Genomics with Computer Vision* James Zou
3:30-4:30	Abstract Presentations
4:30-5:30	*Panel Discussion: How Can Machine Learning Help Drive the New Frontier of Single Cell Research?* Rong Fan, Naftali Kaminski, David Craig, James Zou, Kathryn Roeder

1:00-4:00	***No-Boundary Thinking in Bioinformatics (NBT)*** Jason Moore, Ph.D. and Scott Williams, Ph.D.
1:00-1:15	*Introduction* Jason Moore
1:15-1:45	*Knowledge Integration* Philip Payne
1:45-2:15	*Insights from Knowledge Integration* Casey Greene

2:15-2:45	*Insights from Data Integration* Graciela Gonzalez-Hernandez
2:45-3:00	Break
3:00-3:30	*No-Boundary Thinking Education* Karl Walker
3:30-4:00	*Panel Discussion*

1:00-4:00	***High Performance Computing, Big Data Analytics and Integration for Multi-Omics Biomedical Data (HPC-BOD)*** Fahad Saeed and Serdar Bozdag
1:00-1:40	*Keynote* Mark Gerstein, Yale School of Medicine, Yale University
1:40-2:20	*Keynote* Ayman S El-Baz, J.B. Speed School of Engineering, University of Louisville
2:20-2:40	*Implementing Algorithms for Sorting by Strip Swaps* Asai Asaithambi, Chandrika Rao and Swapnoneel Roy
2:40-3:00	*SUPREME: A Cancer Subtype Prediction Methodology Integrating Multiple Biological Datatypes using Graph Convolutional Neural Networks* Ziynet Nesibe Kesimoglu and Serdar Bozdag
3:00-3:20	*GWAS analysis to compute genetic markers of progression to Alzheimer's Disease* Yashu Vashishath and Serdar Bozdag
3:20-3:40	*Search Feasibility in Distributed MS-Proteomics Big Data* Umair Mohammad and Fahad Saeed
3:40-4:00	*Real-time peptide identification from high-throughput Mass-spectrometry data* Sumesh Kumar and Fahad Saeed

9:00-11:30	***Machine Learning Models for Multi-omics Data Integration (MODI)*** Abedalrhman Alkhateeb and Luis Rueda
9:00-9:25	*Identifying Biomarkers of Nottingham Prognosis Index in Breast Cancer Survivability* Li Zhou, Maria Rueda and Abed Alkhateeb

9:25-9:50	*Histological Classification of Non-small Cell Lung Cancer with RNA-seq Data Using Machine Learning Models* Robert Eshun, Md Khurram Rabby, A.K.M. Kamrul Islam and Marwan U. Bikdash
9:50-10:15	*Prostate Biomedical Images Segmentation and Classification by Using U-NET CNN Model* Abdala Nour, Boubakeur Boufama and Sherif Saad
10:15-10:40	*Identification of gene biomarkers for breast cancer lymph nodes metastasis using a deep neural network* Ziad Omar, Ashraf Abou Tabl and Waguih Elmaraghy
10:40-11:05	*Cell Type Identification via Convolutional Neural Networks and Self-Organizing Maps on Single-Cell RNA-Seq Data* Akram Vasighizaker, Li Zhou and Luis Rueda
11:05-11:30	*General Discussion - Virtual Coffee Session*

Day 0 (August 1, Sunday), Workshops, Tutorials & First-Time Attendee Special Session	
First-Time Attendee Special Session (Chair: Anna Ritz)	
5:00-6:00	***First-Time Attendee Special Session***

Day 1 (August 2, Monday), BCB & WABI	
8:45-10:30	**BCB Session 1A: Sequence Analysis** Chair: Cuncong Zhong
8:45	*A K-mer Query Tool for Assessing Population Diversity in Pangenomes* Hang Su, Ziwei Chen, Maya Najarian, Martin Ferris, Fernando Pardo Manuel de Villena and Leonard Mcmillan
9:10	*PriSeT: Efficient De Novo Primer Discovery* Marie Hoffmann, Michael T. Monaghan and Knut Reinert
9:35	*pplacerDC: a New Scalable Phylogenetic Placement Method* Elizabeth Koning, Malachi Phillips and Tandy Warnow

10:00	*Improving the Efficiency of de-Bruijn Graph Construction Using Compact Universal Hitting Sets* Yael Ben-Ari, Dan Flomin, Yaron Orenstein, Lianrong Pu and Ron Shamir
8:45-10:30	**BCB Session 1B: Electronic Health Records** Chair: Gaurav Pandey
8:45	*COP-E-CAT: Cleaning and Organization Pipeline for EHR Computational and Analytic Tasks* Aishwarya Mandyam, Jeff Soules, Elizabeth Yoo, Krzysztof Laudanski and Barbara Engelhardt
9:10	*Supervised Multi-Specialist Topic Model with Applications on Large-Scale Electronic Health Record Data* Ziyang Song, Xavier Sumba Toral, Yixin Xu, Aihua Liu, Liming Guo, Guido Powell, Aman Verma, David Buckeridge, Ariane Marelli and Yue Li
9:35	*Concurrent Imputation and Prediction on EHR data using Bi-Directional GANs* Mehak Gupta, Thao-Ly T. Phan, H. Timothy Bunnell and Rahmatollah Beheshti
10:00	*Privacy Preserving Neural Networks for Electronic Health Records De-Identification* Tanbir Ahmed, Md Momin Al Aziz, Xiaoqian Jiang and Noman Mohammed
10:15	*DBNet: A Novel Deep Learning Framework for Mechanical Ventilation Prediction Using Electronic Health Records* Kai Zhang, Xiaoqian Jiang, Mahboubeh Madadi, Luyao Chen, Sean Savitz and Shayan Shams
8:45-10:30	**BCB Session 1C: System Biology** Chair: Leonid Chindelevitch
8:45	*Gazelle: Transcript Abundance Query Against Large-Scale RNA-Seq Experiments* Xiaofei Zhang, Ye Yu, Chan Hee Mok, Jame N. MacLeod and Jinze Liu
9:10	*MultiRBP: Multi-Task Neural Network for Protein-RNA Binding Prediction* Jonathan Karin, Hagai Michel and Yaron Orenstein
9:35	*A Spatiotemporal Model of Polarity and Spatial Gradient Establishment in Caulobacter Crescentus* Chunrui Xu and Young Cao
10:00	*Predicting Aneurysmal Degeneration of Type B Aortic Dissection with Computational Fluid Dynamics* Bradley Feiger, Erick Lorenzana, David Ranney, Muath Bishawi, Julie Doberne, Andrew Vekstein, Soraya Voigt, Chad Hughes and Amanda Randles
10:30-10:45	Break

7:30-9:00	**WABI Session 1A: Phylogenetics - Reconstruction** Chair: Nadia El-Mabrouk
7:30	*Open Remarks* Mohammed El-Kebir
7:40	*Making Sense of a Cophylogeny Output: Efficient Listing of Representative Reconciliations* Yishu Wang, Arnaud Mary, Marie-France Sagot and Blerina Sinaimeri
8:10	*The Most Parsimonious Reconciliation Problem in the Presence of Incomplete Lineage Sorting and Hybridization is NP-Hard* Matthew LeMay, Yi-Chieh Wu and Ran Libeskind-Hadas
8:40	Break
9:00-10:30	**WABI Session 1B: Pattern Matching** Chair: Alexandru Tomescu
9:00	*Efficient Privacy-Preserving Variable-Length Substring Match for Genome Sequence.* Yoshiki Nakagawa, Satsuya Ohata and Kana Shimizu
9:30	*The Maximum Duo-Preservation String Mapping Problem with Bounded Alphabet.* Nicolas Boria, Laurent Gourvès, Vangelis Paschos and Jerome Monnot
10:00	*Efficient Haplotype Block Matching in Bi-Directional PBWT.* Ardalan Naseri, William Yue, Shaojie Zhang and Degui Zhi
10:30	Break
10:45-12:00	**Plenary Session 1**
10:45	**Open Remarks by General Chairs and Program Chairs** Hongmei Jiang, Xiuzhen Huang, Jiajie Zhang, Yu Zhang, Mehmet Koyuturk, Zhongming Zhao
10:55	**Introduction** Chair: Mehmet Koyuturk
11:00	**Keynote Address: Jason Moore, Edward Rose Professor of Informatics** **Title: Accessible Artificial Intelligence for Automating Biomedical Data Science**
12:00-1:00	Break
1:00-2:00	**Featured Session on Funding**

	Chair: Jiajie Zhang and May Wang
2:10-3:25	**BCB Session 2A: Genomic Variation** Chair: Mario Cannataro
2:10	*Frontier: Finding the Boundaries of Novel Transposable Element Insertions in Genomes* Anwica Kashfeen and Leonard McMillan
2:35	*Statistical Analysis of GC-Biased Gene Conversion and Recombination Hotspots in Eukaryotic Genomes: a Phylogenetic Hidden Markov Model-Based Approach* Meijun Gao and Kevin Liu
3:00	*Novel Genomic Duplication Models through Integer Linear Programming* Jarosław Paszek, Oliver Eulenstein and Pawel Gorecki
2:10-3:50	**BCB Session 2B: Health Monitoring & Phenotyping** Chair: Yonghui Wu
2:10	*Transformer-Based Unsupervised Patient Representation Learning Based on Medical Claims for Risk Stratification and Analysis* Xianlong Zeng, Simon M. Lin and Chang Liu
2:35	*Signal Quality Detection Towards Practical Non-Touch Vital Sign Monitoring* Zongxing Xie, Bing Zhou and Fan Ye
3:00	*DeepNote-GNN: Predicting Hospital Readmission using Clinical Notes and Patient Network* Sara Nouri Golmaei and Xiao Luo
3:25	*Pheno-Mapper: An Interactive Toolbox for the Visual Exploration of Phenomics Data* Youjia Zhou, Methun Kamruzzaman, Patrick Schnable, Bala Krishnamoorthy, Ananth Kalyanaraman and Bei Wang
2:10-3:50	**BCB Session 2C: Structural Bioinformatics** Chair: Lingling An
2:10	*Modeling Protein Structures from Predicted Contacts with Modern Molecular Dynamics Potentials: Accuracy, Sensitivity, and Refinement* Russell Davidson, Mathialakan Thavappiragasam, T. Chad Effler, Jess Woods, Dwayne Elias, Jerry Parks and Ada Sedova
2:35	*Folding Soluble and Membrane Proteins via Hybridized Distance- and Contact-Based Hierarchical Structure Modeling* Rahmatullah Roche, Sutanu Bhattacharya and Debswapna Bhattacharya
3:00	*Artificial Intelligence Advances for De Novo Molecular Structure Modeling in*

	Cryo-EM and Next-Generation Molecular Biomedicine Dong Si
3:25	*Computational Modeling of SARS-CoV-2 Nsp1 binding to Human Ribosomal 40S Complex* Linkel Boateng, Anita Nag and Homayoun Valafar
3:50-4:00	Break
12:30-1:30	**WABI Session 2A: Cancer** Chair: Marco Antoniotti
12:30	*Parsimonious Clone Tree Reconciliation in Cancer.* Palash Sashittal, Simone Zaccaria and Mohammed El-Kebir
1:00	*Genome Halving and Aliquoting under the Copy Number Distance.* Ron Zeira, Geoffrey Mon and Benjamin J Raphael
1:30	Break
4:00-5:00	**SIGBIO General Meeting** Chairs: May Wang, Ananth Kalyanaraman

Day 2 (August 3, Tuesday), BCB & WABI	
8:45-10:30	**BCB Session 3A: Single Cell Omics** Chair: Zhongming Zhao
8:45	*FastCount: A Fast Gene Count Software for Single-cell RNA-seq Data* Jinpeng Liu, Xinan Liu, Ye Yu, Chi Wang and Jinze Liu
9:10	*Fast and Memory-Efficient scRNA-seq k-means Clustering with Various Distances* Daniel Baker, Nathan Dyjack, Vladimir Braverman, Stephanie Hicks and Benjamin Langmead
9:35	*TENET: Gene Network Reconstruction Using Transfer Entropy Reveals Key Regulatory Factors from Single Cell Transcriptomic Data* Junil Kim, Simon T. Jakobsen, Kedar N. Natarajan and Kyoung-Jae Won
10:00	*A Hybrid Deep Neural Network for Robust Single-Cell Genome-Wide Methylation Detection* Russell Li and Zhandong Liu
10:15	*Copy Number Variation Detection Using Single Cell Sequencing Data*

	Fatima Zare, Jacob Stark and Sheida Nabavi
8:45-10:30	**BCB Session 3B: Machine Learning & Drug Design** Chair: Ariful Azad
8:45	*SPEAR: Self-Supervised Post-Training Enhancer for Molecule Optimization* Tianfan Fu, Cao Xiao, Kexin Huang, Lucas Glass and Jimeng Sun
9:10	*A Value-Based Approach for Training of Classifiers with High-Throughput Small Molecule Screening Data* Natalia Khuri and Sarah Parsons
9:35	*Predicting Drug Resistance in M. Tuberculosis Using a Long-term Recurrent Convolutional Network* Amir Hosein Safari, Nafiseh Sedaghat, Hooman Zabeti, Alpha Forna, Leonid Chindelevitch and Maxwell Libbrecht
10:00	*LSHvec: A Vector Representation of DNA Sequences Using Locality Sensitive Hashing and FastText Word Embeddings* Lizhen Shi and Bo Chen
10:30-10:55	Break
7:40-9:00	**WABI Session 3A: Phylogenetic Networks** Chair: Manuel Lafond
7:40	*Treewidth-Based Algorithms for the Small Parsimony Problem on Networks* Celine Scornavacca and Mathias Weller
8:10	*Conflict Resolution Algorithms for Deep Coalescence Phylogenetic Networks* Marcin Wawerka, Dawid Dąbkowski, Natalia Rutecka, Agnieszka Mykowiecka and Pawel Gorecki
8:40	Break
9:00-10:30	**WABI Session 3B: Compression** Chair: Paola Bonnizoni
9:00	*Space-Efficient Representation of Genomic k-mer Count Tables.* Yoshihiro Shibuya, Djamal Belazzougui and Gregory Kucherov
9:30	*Compression of Multiple k-mer Sets by Iterative SPSS Decomposition.* Kazushi Kitaya and Tetsuo Shibuya
10:00	*Compressing and Indexing Aligned Readsets.* Travis Gagie, Garance Gourdel and Giovanni Manzini

10:30	Break
10:55-12:00	**Plenary Session 2**
10:55	**Introduction** Chair: Yu Zhang
11:00	**Keynote Address: Aidong Zhang, Fellow of ACM and IEEE** **Title: Transfer Learning and Meta Learning for Biomedical Applications**
12:00-1:00	Break
1:00-2:20	**Featured Session on Bioinformatics, Data Science, AI and COVID** Chairs: Hongmei Jiang and May Wang
2:20-2:30	Break
2:30-4:05	**BCB Session 4A: Medical Imaging** Chair: Sanjay Purushotham
2:30	*AW-Net: Automatic Muscle Structure Analysis on B-mode Ultrasound Images for Injury Prevention* Hugo Michard, Bertrand Luvison, Antonio J. Morales-Artacho, Gaël Guilhem and Quoc-Cuong Pham
2:55	*Assigning ICD-O-3 Codes to Pathology Reports using Neural Multi-Task Training with Hierarchical Regularization* Anthony Rios, Eric Durbin, Isaac Hands and Ramakanth Kavuluru
3:20	*Segmenting Thoracic Cavities with Neoplastic Lesions: A Head-to-head Benchmark with Fully Convolutional Neural Networks* Zhao Li, Rongbin Li, Kendall J. Kiser, Luca Giancardo and W. Jim Zheng
3:35	*Covid-19 Classification Using Thermal Images* Martha Rebeca Canales Fiscal, José Gerardo Tamez Peña, Victor Treviño, Luis Javier Ramírez Treviño, Rocio Ortiz Lopez, Servando Cardona Huerta, Adam Yala and Regina Barzilay
3:50	*A CNN-based Cell Tracking Method for Multi-Slice Intravital Imaging Data* Kenji Fujimoto, Tsubasa Mizugaki, Utkrisht Rajkumar, Hironori Shigeta, Shigeto Seno, Yutaka Uchida, Masaru Ishii, Vineet Bafna and Hideo Matsuda
2:30-4:15	**BCB Session 4B: Graphs & Networks** Chair: Byung-Jun Yoon
2:30	*Transfer Learning for Predicting Virus-Host Protein Interactions for Novel Virus Sequences* Jack Lanchantin, Tom Weingarten, Arshdeep Sekhon, Clint Miller and Yanjun Qi

2:55	*GNNfam: Utilizing Sparsity in Protein Family Prediction using Graph Neural Networks* Anuj Godase, Md. Khaledur Rahman and Ariful Azad
3:20	*A Multi-Resolution Graph Convolution Network for Contiguous Epitope Prediction* Lisa Oh, Bowen Dai and Chris Bailey-Kellogg
3:45	*ShareTrace: An Iterative Message Passing Algorithm for Efficient and Effective Disease Risk Assessment on an Interaction Graph* Erman Ayday, Youngjin Yoo and Anisa Halimi
4:00	*Investigating Statistical Analysis for Network Motifs* Zican Li and Wooyoung Kim
12:30-1:30	**WABI Session 4A: RNA - Structure** Chair: Elodie Laine
12:30	*Tree Diet: Reducing the Treewidth to Unlock FPT Algorithms in RNA Bioinformatics.* Bertrand Marchand, Yann Ponty and Laurent Bulteau
1:00	*BPPart: RNA-RNA Interaction Partition Function in the Absence of Entropy.* Ali Ebrahimpour Boroojeny, Sanjay Rajopadhye and Hamidreza Chitsaz

Day 3 (August 4, Wednesday), BCB & WABI	
8:45-10:05	**BCB Session 5A: COVID-19** Chair: Mohd Anwar
8:45	*Temporal Analysis of Social Determinants Associated with COVID-19 Mortality* Shayom Debopadhaya, John Erickson and Kristin Bennett
9:10	*COVID-19 Diagnosis Using Model Agnostic Meta-Learning on Limited Chest X-ray Images* Tarun Naren, Yuanda Zhu and May Dongmei Wang
9:35	*Surveillance of COVID-19 Pandemic using Social Media: A Reddit Study in North Carolina* Christopher Whitfield, Yang Liu and Mohd Anwar
9:50	*A Multi-Instance Support Vector Machine with Incomplete Data for Clinical Outcome Prediction of COVID-19* Lodewijk Brand, Lauren Zoe Baker and Hua Wang

8:45-10:30	**BCB Session 5B: Clinical Trials & Outcome Prediction** Chair: Kaiman Zeng
8:45	*Synthesized Difference in Differences* Eric Strobl and Thomas Lasko
9:10	*Match2: Hybrid Self-Organizing Map and Deep Learning Strategies for Treatment Effect Estimation* Xiao Shou, Tian Gao, Dharmashankar Subramanian and Kristin Bennett
9:35	*CytoSet: Predicting Clinical Outcomes via Set-Modeling of Cytometry Data* Haidong Yi and Natalie Stanley
10:00	*Towards an Extensible Ontology for Streaming Sensor Data for Clinical Trials* Robert Lyons, Geoff Low, Clare Bates Congdon, Melissa Ceruolo, Marissa Ballesteros, Steven Cambria and Paolo DePetrillo
10:15	*Transformer-Based Named Entity Recognition for Parsing Clinical Trial Eligibility Criteria* Shubo Tian, Arslan Erdengasileng, Xi Yang, Yi Guo, Yonghui Wu, Jinfeng Zhang, Jiang Bian and Zhe He
10:30-10:55	Break
7:40-9:00	**WABI Session 5A: RNA - Transcriptomics** Chair: Tomas Vinar
7:40	*Perplexity: Evaluating Transcript Abundance Estimation in the Absence of Ground Truth* Jason Fan, Skylar Chan and Rob Patro
8:10	*Flow Decomposition with Subpath Constraints* Lucia Williams, Alexandru I. Tomescu and Brendan Mumey
8:40	Break
9:00-10:55	**WABI Session 5B: Statistical Inference / System Biology** Chair: Mohammed El-Kebir
9:00	*An Efficient Linear Mixed Model Framework for Meta-Analytic Association Studies Across Multiple Contexts* Brandon Jew, Jiajin Li, Sriram Sankararaman and Jae Hoon Sul
9:30	*Fast Approximate Shortest Hyperpaths for Inferring Pathways in Cell Signaling Hypergraphs* Spencer Krieger and John Kececioglu

10:00	Break
10:55-12:00	**Plenary Session 3**
10:55	**Introduction** Chair: Alessandra Carbone
11:00	**Keynote Address: Mona Singh, Professor of Computer Science** **Title: Algorithms for Deciphering Disease Networks**
12:00-12:30	Break
12:30-2:00	**Featured Session on Diversity and Inclusion: Challenges and Opportunities** Chair: Xiuzhen Huang, May Wang
2:00-2:30	Break
2:30-4:15	**BCB Session 6A: Cancer** Chair: Oznur Tastan
2:30	*Cancer Molecular Subtype Classification by Graph Convolutional Networks on Multi-omics Data* Bingjun Li, Tianyu Wang and Sheida Nabavi
2:55	*Deep Neural Network Models to Automate Incident Triage in the Radiation Oncology Incident Learning System* Priyankar Bose, William C. Sleeman IV, Khajamoinuddin Syed, Michael Hagan, Jatinder Palta, Rishabh Kapoor
3:20	*Two-Stage Biologically Interpretable Neural-Network Models for Liver Cancer Prognosis Prediction using Histopathology and Transcriptomic Data* Zheng Jing, Lana Garmire, Zhucheng Zhan, Bing He, Maria Westerhoff and Eun-Young Choi
3:35	*Presence of Complete Murine Viral Genome Sequences in Patient-Derived Xenografts* Zhihao Yuan, Xuejun Fan, Jay-Jiguang Zhu, Tong-Ming Fu, Jiaqian Wu, Hua Xu, Ningyan Zhang, Zhiqiang An and W. Jim Zheng
4:00	*Extracapsular Extension Identification for Head and Neck Cancer Using Multi-scale 3D Deep Neural Network* Yibin Wang, William Duggar, Toms Thomas, Paul Roberts, Linkan Bian and Haifeng Wang
2:30-4:15	**BCB Session 6B: Ontologies & Databases** Chair: Fereydoun Hormozdiari
2:30	*KGDAL: Knowledge Graph Guided Double Attention LSTM for Rolling Mortality*

	Prediction for AKI-D Patients Lucas Jing Liu, Victor Ortiz-Soriano, Javier A. Neyra and Jin Chen
2:55	*Low Resource Recognition and Linking of Biomedical Concepts from a Large Ontology* Sunil Mohan, Rico Angell, Nicholas Monath and Andrew McCallum
3:20	*Joint Learning for Biomedical NER and Entity Normalization: Encoding Schemes, Counterfactual Examples, and Zero-Shot Evaluation* Jiho Noh and Ramakanth Kavuluru
3:45	*HYPON: Embedding Biomedical Ontology with Entity Sets* Zhuoyan Li and Sheng Wang
4:00	*BioNumQA-BERT: Answering Biomedical Questions Using Numerical Facts with a Deep Language Representation Model* Ye Wu, Hing-Fung Ting, Tak-Wah Lam and Ruibang Luo
4:15-4:30	Break
12:00-1:15	**WABI Session 6A: Metagenomics** Chair: Riccardo Vicedomini
12:00	*LRBinner: Binning Long Reads in Metagenomics Datasets* Anuradha Wickramarachchi and Yu Lin
12:30	*BISER: Fast Characterization of Segmental Duplication Structure in Multiple Genome Assemblies* Hamza Iseric, Can Alkan, Faraz Hach and Ibrahim Numanagic
1:00	Closing Remarks Chairs: Alessandra Carbone, Mohammed El-Kebir
4:30-5:00	**Recognitions and Awards Ceremony** Chairs: Hongmei Jiang, Xiuzhen Huang, Jiajie Zhang
5:00	**Closing Remarks** Chairs: May Wang, Tamer Kahveci