ICCABS 2021

11th International Conference on Computational Advances in Bio and medical Sciences (ICCABS)

December 16-18, 2021,
Virtual Conference (Due to COVID'19)
http://www.iccabs.org

National Science Foundation
WHERE DISCOVERIES BEGIN

UCONN
UNIVERSITY OF CONNECTICUT

ICCABS 2021 Program

Videoconferencing access link for main conference: https://snp.engr.uconn.edu/b/iccabs2021
Access link for CANGS workshop: https://snp.engr.uconn.edu/b/cangs2021
Access link for CAME workshop: https://snp.engr.uconn.edu/b/came2021
Access link for CASCODA workshop: https://snp.engr.uconn.edu/b/cascoda2021
Access link for ASI workshop: https://snp.engr.uconn.edu/b/asi2021

Access link for breaks: https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

Note: All links require an access code sent to participants by email; contact zigeng.wang@uconn.edu (for main conference) or ion@engr.uconn.edu if you have not received the access code.

Thursday, Dec. 16, 2021 (EST)

8:50am - 9:00am	**Opening Remarks**	https://snp.engr.uconn.edu/b/iccabs2021

9:00am - 10:00am	**Keynote Talk** **Chair:** *Sanguthevar Rajasekaran*	https://snp.engr.uconn.edu/b/iccabs2021

Jan Korbel - European Molecular Biology Laboratory
Title: Multi-platform genomic sequencing reveals patterns of recurrent mutation associated with human diseases

10:00am - 10:30am	**Break**	https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

10:30am - 12:10pm	**Parallel Sessions**

ICCABS Session 1
Chair: *João Lourenço Coelho da Silva*
https://snp.engr.uconn.edu/b/iccabs2021

CANGS Session 1
Chair: *Alex Zelikovsky*
https://snp.engr.uconn.edu/b/cangs2021

- André Louzada Colodette, Fabiano Novaes Barcellos Filho, Gustavo Carreiro Pinasco, Sheila Cristina de Souza Cruz and Sérgio Nery Simões. Selection of Characteristics For Identification of Risk Factors Associated with Infant Mortality
- Alexandre Babilone Fonseca, David Correa Martins-Jr, Zofia Wicik, Marek Postula and Sérgio Nery Simões. Addressing classification on highly imbalanced clinical datasets

- Pasaniuc. Methods to quantify polygenic risk score accuracy for a single target individual
- Tan, Zhao, Zhao, Burns, Tian. A novel network method MMVC for analysis of WGS data unveils high-resolution linkages in poliovirus clusters: application to polio eradication
- Tithi, Aylward, Jensen, Zhang. Recovering Draft Genomes of Novel Phages in Metagenomic Data
- Yu, Sankoff. Syntenic dimensions of evolutionary divergence
- Chen, Shaw, Bu, Jiang. FINER: enhancing the prediction of tissue-specific functions of isoforms by refining isoform interaction networks

12:10pm - 1:00pm	**Break**	https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

1:00pm - 2:00pm	**Keynote Talk** **Chair:** *Ion Mandoiu*	https://snp.engr.uconn.edu/b/iccabs2021

Pavel Skums - Georgia State University
Title: Phylodynamic analysis of tumors using single cell sequencing data

2:00pm - 2:30pm	**Break**	https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

2:30pm - 3:50pm	Parallel Sessions

ICCABS Session 2
Chair: *Manish Bhattarai*
https://snp.engr.uconn.edu/b/iccabs2021

- Dan Gusfield and Hannah Brown. Unified SAT-Solving for Hard Problems of Phylogenetic Network Construction
- Kazi Lutful Kabir, Manish Bhattarai, Boian Alexandrov and Amarda Shehu. Single Model Quality Estimation of Protein Structures via Non-negative Tensor Factorization
- Audrey Mitchell, Marco Ruiz, Soua Yang, Chen Wang and Jaime Davila. Excerno: Filtering mutations caused by the clinical archival process in sequencing data

CANGS Session 2
Chair: *Ion Mandoiu*
https://snp.engr.uconn.edu/b/cangs2021

- Ayyala, Mangul. Rigorous Benchmarking of HLA Callers for RNA Sequencing Data
- Icer, Mangul. Robustness and reproducibility of computational genomic tools
- Li, Chen, George, Karuturi, Liu. Adaptive sentinel testing in workplace for COVID19 pandemic
- Liu, Heber. Mapping the Landscape of RNA-seq Bioinformatics Tools

3:50pm - 4:20pm	Break	https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

4:20pm - 6:00pm **Parallel Sessions**

ICCABS Session 3
Chair: *Jaime Davila*
https://snp.engr.uconn.edu/b/iccabs2021

- Taseef Rahman, Yuanqi Du and Amarda Shehu. Graph Representation Learning for Protein Conformation Sampling
- Pramesh Shakya, Ardalan Naseri, Degui Zhi and Shaojie Zhang. mcPBWT: Space-efficient Multi-column PBWT Scanning Algorithm for Composite Haplotype Matching
- An-Chi Shau, Nai-Shuan Hwang and Shu-Yu Chang. MELEPS: Multiple Expert Linear Epitope Prediction System
- João Silva, Miguel Nobre Menezes, Tiago Rodrigues, Beatriz Silva, Fausto J. Pinto and Arlindo L. Oliveira. Encoder-Decoder Architectures for Clinically Relevant Coronary Artery Segmentation

CAME Session 1
Chair: *Pavel Skums*
https://snp.engr.uconn.edu/b/came2021

- Novikov, Knyazev, Zelikovsky. Scalable Reconstruction of SARS-CoV-2 Phylogeny with Recurrent Mutations
- Zaman, Sledzieski, Berger, Wu, Bansal. Phylogenetic reconciliation reveals extensive ancestral recombination in Sarbecoviruses and the SARS-CoV-2 lineage
- Tariq, Chowell-Puente. Multi-scale models to infer transmission dynamics and short term-forecast the COVID-19 pandemic in four Latin American countries
- Ali, Bello, Tayebi, Patterson. Classifying SARS-CoV-2 Spike Sequences by Geographic Location Using Deep Learning
- Mohebbi, Skums. Inference of the fitness landscape and epistatic interaction network of SARS-CoV-2

Friday, Dec. 17, 2021 (EST)

9:00am - 10:20am	**Parallel Sessions**

ASI Session 1
Chair: *Ion Mandoiu*
https://snp.engr.uconn.edu/b/asi2021

- Ebrahimi-Nik, Moussa, et al., Reversion analysis reveals the in vivo immunogenicity of a poorly MHC I-binding cancer neoepitope
- Sahoo, Zelikovsky, Mandoiu, Ionov, Srivastava. CiPAS based therapeutic vaccine against tumors with p53 gene mutations.
- Nevin, Moussa, Corwin, Mandoiu, Srivastava. Sympathetic nervous tone limits the development of myeloid-derived suppressor cells
- Geyer, Moussa, Mandoiu, Srivastava, Nevin. Sympathetic nervous system signaling regulates natural killer cell maturation

CAME Session 2
Chair: Alex Zelikovsky
https://snp.engr.uconn.edu/b/came2021

- Bunimovich, Ram. Cross-immunoreactivity and Local Immunodeficiency
- Campo, Mosa, Khudyakov. Entropy-based distance for categorical data: Application to the clustering of protein sequences
- Tayebi, Patterson, Skums. Machine Learning and Deep Learning to Predict Crossmmunoreactivity of Viral Epitopes
- Ali, Chourasia, Ciccolella, Della Vedova, Bonizzoni, Patterson. An Efficient and Alignment-Free Embedding Approach for High-Throughput Viral Sequencing Data

10:20am - 10:50am	**Break**	https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

10:50am - 12:10pm	Parallel Sessions

ASI Session 2
Chair: *Marmar Moussa*
https://snp.engr.uconn.edu/b/asi2021

CAME Session 3
Chair: *Mukul Bansal*
https://snp.engr.uconn.edu/b/came2021

- Al Seesi, Sherafat, Shcheglova, et al. GeNeo: Bioinformatics Toolbox for Genomics Guided Neoepitope prediction
- George. An unbiased approach to defining bona fide cancer neoepitopes that elicit immune-mediated cancer rejection
- Sherafat, Srivastava, Mandoiu. Towards accurate prediction of tumor rejection-mediating neoepitopes using machine learning
- Huang, Mangul. Assessing the completeness of immunogenetics databases across diverse populations

- Yooseph. Bacterial Associations in the Human Microbiome
- Snir. Genome Dynamics under the Jump Model
- Schwartz. Multi-modal data integration for reconstructing and predicting cancer progression processes
- Piontkivska, Plonski, Nitirahardjo, Wales-McGrath, Luczywo, Hutchison. RNA editing and viral evolution: changes to monitor

12:10pm - 1:00pm	Break	https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

1:00pm - 2:00pm	Keynote Talk **Chair:** *Mukul Bansal*	https://snp.engr.uconn.edu/b/iccabs2021

Sharma Thankachan - University of Central Florida
Title: A Brief History of Genomic Data Indexing in Compressed Space

2:00pm - 2:30pm	Break	https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

2:30pm - 3:30pm	CAME Workshop

CAME Session 4
Chair: *Pavel Skums*
https://snp.engr.uconn.edu/b/came2021

- Fiona Senchyna, Singh. Local-to-global topological analysis of viral infection-spread using temporal molecular networks
- Longmire, Khudyakov. Artefacts affecting viral transmission detection using amplicon deep sequencing
- Skums, Mohebbi, Tsyvina, Icer. SOPHIE: viral outbreak investigation and transmission history reconstruction in a joint phylogenetic and network theory framework

3:30pm - 4:00pm	Break	https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

4:00pm - 6:00pm	CASCODA Workshop

CASCODA Session 1
Chair: *Alex Zelikovsky*
https://snp.engr.uconn.edu/b/cascoda2021

- Blum, Stegle. Computational tools to dissect single-cell readouts across time and space
- Moravec, Gavryushkin. Cancer phylogenetics using single-cell multiomics data
- Pinello. SIMBA: SIngle-cell eMBedding Along with features
- Wang, Li, Nabavi. Single-cell RNA sequencing data clustering using graph convolutional networks
- Ghosn. SuPERR-seq: new approach for multi-OMICs single-cell data integration reveals greater heterogeneity in the human immune system
- Natarajan. Single-cell gene regulatory networks in health and disease

Saturday, Dec. 18, 2021 (EST)

9:00am - 10:00am	**CASCODA Workshop**

CASCODA Session 2
Chair: *Murray Patterson*
https://snp.engr.uconn.edu/b/cascoda2021

- Zhou, Patterson. Towards a complete workflow for inferring tumor phylogeny from raw single-cell sequencing reads
- Szczurek. CONET: Copy number event tree model of evolutionary tumor history for single-cell data
- Germain, Robinson. Doublet identification in single-cell sequencing with scDblFinder

10:00am - 10:30am	**Break**	https://gather.town/app/6l93Dw2qk8gZViEX/ICCABS

10:30am - 12:00pm	**CASCODA/ASI/ICCABS**

Joint CASCODA/ASI/ICCABS Session
Chair: *Marmar Moussa*
https://snp.engr.uconn.edu/b/cascoda2021

- Bonizzoni, Pirola, Rizzi, Zaccagnino, Zizza. Detecting gene-fusion from PacBio HIFI by Lyn2vec: a machine learning approach
- Kızılkale, Rashidi Mehrabadi, Ergun, Buluc, Sahinalp, Malikic. Provably Fast Intratumor . Heterogeneity Inference from Single-Cell Sequencing Data
- Jordan Force, Ion Mandoiu. Immuno-peptide identification from tandem mass-spectrometry data
- Abdurrahman Abul-Basher and Steven Hallam. Relabeling metabolic pathway data with groups to improve prediction outcomes