### 12th International Conference on

## Bioinformatics and Computational Biology (BICOB 2020)

### **PROGRAM**

March 23-25, 2020

Crowne Plaza Hotel
San Francisco Airport, California USA

### Sponsored by



## International Society for Computers and Their Applications

278 Mankato Ave. #220 Winona, MN 55987 E-mail: isca@isca-hq.org; website: www.isca-hq.org

# 12<sup>th</sup> International Conference on **Bioinformatics and Computational Biology** (BICOB 2020)

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#### **Schedule at a Glance**

Monday, March 23	8:45am – 9:00am	Conference opening (Plaza I)	
	9:00am – 10:00am	Keynote (Plaza I)	
	10:30am – 12:00pm	Session 1A (Plaza II)	
	12:00-1:30pm Lunch break (on your own)		
	1:30pm – 3:00pm	Session 1B (Plaza II)	
	3:30pm – 5:00pm	Session 1C (Plaza II)	

Tuesday, March 24	9:00am – 10:00am	Keynote (Plaza I)
	10:30am – 12:00pm	Session 2A (Plaza II)
	12:00-2:00pm Conference Luncheon and Best Paper Award (Plaza III)	
	2:00pm – 3:30pm	Session 2B (Plaza II)
	4:00 – 5:30pm	Session 2C (Plaza II)

#### Monday, March 23, 2020

8:00 a.m. - 3:00 p.m. REGISTRATION - Coffee, tea, pastries -

**Location: Plaza Foyer** 

8:45 a.m. - 9:00 a.m. WELCOME - Plaza I

> Qin Ding, East Carolina University, USA Oliver Eulenstein, Iowa State University, USA

Hisham Al-Mubaid, University of Houston-Clear Lake, USA

9:00 a.m. - 10:00 a.m. **KEYNOTE SPEAKER** 

#### Dr. Ron Dror

**Department of Computer Science** and the Institute for Computational and Mathematical Engineering Stanford University

Molecular Simulation and Learning for the Design of Finely Tuned Drugs

Location: Plaza I

Session Chair: Hisham Al-Mubaid (University of Houston-Clear Lake)

10:00 a.m. - 10:30 a.m. COFFEE BREAK

**SESSION TITLE: Cancer Research** Monday March 23, 10:30 a.m. - 12:00 p.m. **SESSION 1A** 

Session Chair: Hsiu-Chuan Wei (Feng Chia University, Taiwan)

Location: Plaza II

1. Identification of Deregulated Transcription Factors Involved in Specific Bladder Cancer **Subtypes** 

Magali Champion (Universite Paris Descartes, France), Julien Chiquet (Universite Paris-Saclay, France), Pierre Neuvial (Universite de Toulouse, France), Mohamed Elati (Universite de Lille), Francois Radvanyi (PSL Research University, France), and Etienne Birmele (Universite Paris Descartes, France)

2. Ranking Variable Combinations to Characterize Breast Cancer Subtypes using the IBIF-**RF Metric** 

Isis Narvaez-Bandera and Wandaliz Torres-Garcia (University of Puerto Rico, USA)

3. In silico library design, screening and MD simulation of COX-2 inhibitors for anticancer activity

Ankita Sahu (ICMR-National Institute of Pathology, India), Dibyabhaba Pradhan (ICMR-AIIMS, India), Khalid Raza (Jamia Millia Islamia, India), Sahar Qazi (Jamia Millia Islamia, India), A K Jain (ICMR-National Institute of Pathology, India) and Saurabh Verma (ICMR-National Institute of Pathology, India)

4. Bifurcation Analysis of a Mathematical Model of Tumor Growth in MCF-7 Breast Cancer

Hsiu-Chuan Wei (Feng Chia University, Taiwan)

#### 12:00 p.m. – 1:30 p.m. LUNCH BREAK ON OWN

## SESSION TITLE: Machine Learning in Bioinformatics Monday March 23, 1:30 p.m. – 3:00 p.m. Session Chair: Roberto Rosas-Romero (Universidad de las Américas-Puebla, Mexico) Location: Plaza II

1. Classification of functional Near Infra Red Signals with Machine Learning for Prediction of Epilepsy

Roberto Rosas-Romero (Universidad de las Américas-Puebla, Mexico) and Edgar Guevara (Universidad Autónoma de San Luis Potosí, Mexico)

2. PhGC: A Machine Learning Based Workflow for Phenotype-Genotype Co-analysis on Autism

Safa Shubbar (Kent State University, USA), Chen Fu (Case Western Reserve University, USA), Anthony Wynshaw-Boris (iLambda, USA), Qiang Guan (Case Western Reserve University, USA) and Zhi Liu (Kent State University, USA)

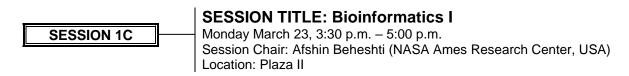
3. From Unsupervised Multi-Instance Learning to Identification of Near-Native Protein Structures

Fardina Fathmiul Alam and Amarda Shehu (George Mason University, USA)

4. Assessing Protein-Drug Resistance Due to Mutations via a Rigidity Analysis in silico Approach

Dylan Carpenter, Tess Thackray, Cecilia Kalthoff and Filip Jagodzinski (Western Washington University, USA)

#### 3:00 p.m. – 3:30 p.m. COFFEE BREAK



- 1. Virtual Experimentation Complements Real-World Experimentation
  Andrew Smith (University of California, San Francisco, USA), Glen Ropella (Tempus Dictum, Inc., USA) and C. Anthony Hunt (University of California, San Francisco, USA)
- 2. Visualizing Omics Data from Spaceflight Samples using the NASA GeneLab Platform Daniel Berrios (NASA Ames Research Center, USA), Eric Weitz (Broad Institute of MIT and Harvard, USA), Kirill Grigorev (Weill Cornell Medical College, USA), Sylvain Costes (NASA Ames Research Center, USA), Samrawit Gebre (NASA Ames Research Center, USA) and Afshin Beheshti (NASA Ames Research Center, USA)
- 3. Clique Selection and its Effect on Paraclique Enrichment: An Experimental Study Yuping Lu (Lawrence Berkeley National Laboratory, USA), Charles Phillips (University of Tennessee, USA), Elissa Chesler (The Jackson Laboratory, USA) and Michael Langston (University of Tennessee, USA)
- **4. Graphical Processing Unit Supported RNA Secondary Structure Comparison** Mutlu Mete and Abdullah Arslan (Texas A & M University Commerce, USA)

#### Tuesday, March 24, 2020

8:00 a.m. – 3:00 p.m. REGISTRATION – Coffee, tea, pastries –

**Location: Plaza Foyer** 

9:00 a.m. - 10:00 a.m. KEYNOTE SPEAKER

Dr. Rex Gantenbein

Department of Computer Science

and the College of Health Sciences

and the College of Health Sciences
University of Wyoming

How Advances in Technology are Improving Health Care

**Location: Plaza I** 

Session Chair: Gordon Lee (San Diego State University)

#### 10:00 a.m. - 10:30 a.m. COFFEE BREAK

SESSION TITLE: Genome Analysis
Tuesday March 24, 10:30 a.m. – 12:00 p.m.
Session Chair: Saeed Salem (North Dakota State University, USA)
Location: Plaza II

1. Co-expression networks uncover regulation of splicing and transcription markers of disease

Pan Zhang, Bruce R. Southey and Sandra L. Rodriguez-Zas (University of Illinois at Urbana-Champaign, USA)

- 2. Mining approximate frequent dense modules from multiple gene expression datasets San Ha Seo and Saeed Salem (North Dakota State University, USA)
- 3. Analysis of Mutation Bias in Shaping Codon Usage Bias and Its Association with Gene Expression Across Species

Zhixiu Lu, Michael Gilchrist and Scott Emrich (University of Tennessee, USA)

4. Multi-objective Optimisation of Gene Regulatory Networks: Insights from a Boolean Circadian Clock Model

Ozgur E. Akman and Jonathan E. Fieldsend (University of Exeter, United Kingdom)

## 12:00 p.m. – 2:00 p.m. CONFERENCE LUNCHEON AND AWARDS CEREMONY

Location: Plaza III

## SESSION TITLE: Neural Networks and Predictive Approaches in Bioinformatics

Tuesday March 24, 2:00 p.m. - 3:30 p.m.

Session Chair: Nicholas Leiby (Two Six Labs, USA)

Location: Plaza II

 Convolutional neural net learns promoter sequence features driving transcription strength

Nicholas Leiby (Two Six Labs, USA), Ayaan Hossain and Howard M Salis (Pennsylvania State University, USA)

2. Epileptic Focus Localization Based on iEEG Plot Images by Using Convolutional Neural Network

Xuyang Zhao (Saitama Institute of Technology, Japan), Linfeng Sui (Saitama Institute of Technology, Japan), Toshihisa Tanaka (Tokyo University of Agriculture and Technology, Japan) Jianting Cao (Saitama Institute of Technology, Japan) and Qibin Zhao (RIKEN Center for Advanced Intelligence Project, Japan)

3. Exploring Deep Neural Network Architectures: A Case Study on Improving Antimicrobial Peptide Recognition

Manpriya Dua , Daniel Barbara , and Amarda Shehu (George Mason University, USA)

**4.** ASPECT, an LDA-Based Predictive Algorithm for In Vitro Selection Puzhou Wang (Synthego Corporation, USA)

#### 3:30 p.m. – 4:00 p.m. COFFEE BREAK

SESSION TITLE: Bioinformatics II
Tuesday March 24, 4:00 p.m. – 5:30 p.m.
Session Chair: Lawrence Yu-Min Liu (National Tsing Hua University, Taiwan)
Location: Plaza II

1. Exposure Measurements on Biomimetic Lobules Using Virtual Experiments to Help Improve IVIVE

Preethi Krishnan (University of California, San Francisco, USA), Lopamudra Dutta (University of California, San Francisco, USA), Andrew Smith (University of California, San Francisco, USA), Glen Ropella (Tempus Dictum, Inc., USA), Ryan Kennedy (University of California, San Francisco, USA) and Anthony Hunt (University of California, San Francisco, USA)

2. Measurement of similarity in C. elegans healthspan using dynamic time warping on movement features

Arun Govindaswamy, Wahhaj Farooq, Yiyang Wang, Ilyas Ustun, Daniela Raicu, Jacob Furst (DePaul University, USA) and Hongkyun Kim (Rosalind Franklin University, USA)

- 3. Hepatocyte Organization Affects the Translation of Clearance from In Vitro to In Vivo Lopamudra Dutta (University of California, San Francisco, USA), Preethi Krishnan (University of California, San Francisco, USA), Andrew Smith (University of California, San Francisco, USA), Ryan Kennedy (University of California, San Francisco, USA), Glen Ropella (Tempus Dictum, Inc., USA) and C. Anthony Hunt (University of California, San Francisco, USA)
- 4. Bioinformatics analysis of hereditary disease gene set to identify key modulators of myocardial remodeling during heart regeneration in zebrafish
  Lawrence Yu-Min Liu, Zih-Yin Lai, Min-Hsuan Lin, Yu Shih and Yung-Jen Chuang (National Tsing Hua University, Taiwan)