

CIBCB 2018 Schedule

Wednesday May 30: Tutorials

- 8:00 Continental Breakfast
8:30 Registration
9:30-11:30 Representation in Bioinformatic Applications of Evolutionary Computation.
Presenter: *Daniel Ashlock* Location: Orly Room
10:30 Coffee Break (during the tutorial)
11:30-1:00 Lunch, on your own
1:00-2:40 An Introduction to CRISPR for Bioinformaticists.
Presenter: *Wendy Ashlock* Location: Orly Room
2:40-3:00 Coffee Break
3:00-5:00 Feature Selection Methods for Efficient Classification of Gene Expression Data
Presenter: *B. Chandra* Location: Orly Room
5:00 Conference Reception.
Location: Lambert CD

Abstract Session I

5:00 Friday June 1

EEG Emotion Detection Review

Mohamed Ahmed Abdullah and Lars Rune Christensen

Multiple Omics Data Integration to Identify Long Noncoding RNA Responsible for Breast Cancer Related Mortality

Tapasree Roy Sarkar, Arnab Kumar Maity, Yabo Niu and Bani K Mallick

Single Nucleotide Polymorphisms: Identification and Association with Breast Cancer using Biocomputing Approach

Neelofar Sohi and Amardeep Singh

Feature extraction and prediction of acidosis from cardiocography data based on antepartum pH data

Vinayaka Nagendra Harikishan Gude Divya Sampath and Steven Corns

A novel computational approach to simulate intracellular complex network in type 1 diabetes progression

Zhenzhen Shi and Majid Jaber-Douraki

Abstract Session II

11:00 Saturday June 2

The Ethical Status of an AI

James A. Foster and Donald Wunsch

A Future Direction for the Disease Gene Association Problem

Tyler Collins and Sheridan Houghten

On Christian Bök's *The Xenotext*: Computation and Biology in Poetry

Joseph Alexander Brown

Deep learning based machine learning technique for reconstructing heterogeneous drug target interaction networks

Hetal Rajpura and Alioune Ngom

Gene Expression Analysis using Adaptive Resonance Theory

Niklas Melton and Donald Wunsch

Thursday May 31

- 8:00** Continental Breakfast Location: Orly Room
8:30 Registration and Welcome to CIBCB
9:00-10:00 Neuromorphic Engineering and Computing at a Crossroads
Shantanu Chakrabartty
10:00-10:30 Coffee
- 10:30-12:00** Session: **Understanding biological systems** Location: Orly Room
10:30-10:55 An Improved Feature Selection Technique for Gene Expression Data
B. Chandra
- 11:00-11:25 Ensemble Validation Paradigm for Intelligent Data Analysis in Autism Spectrum Disorders Thy
Nguyen, Kerri Nowell, Kimberly E. Bodner and Tayo Obafemi-Ajayi
11:30-11:55 CCA based multi-view feature selection for multi-omics data integration
Yasser El-Manzalawy
- 12:00-1:30** Box Lunch in the foyer
- 1:30-3:30** Session: **Gene Expression** Location: Orly Room
1:30-1:55 Deep Learning Pipeline to Classify Different Stages of Alzheimer's Disease From fMRI Data
2:00-2:25 *Yosra Kazemi and Sheridan Houghten*
Analysis of Grapevine Gene Expression Data using Node-Based Resilience Clustering Jeffrey Dale,
John Matta, Susanne Howard, Gunes Ercal, Wenping Qiu and Tayo Obafemi-Ajayi
2:30-2:55 Application of Ensemble Learning to the Differential Gene Expression in Left-Right Breast Tumors
Casey Cole, Kenneth Nesbitt and Homayoun Valafar
- Coffee
- 3:00-3:30**
- 3:30-5:30** Session: **Sequence Analysis** Location: Orly Room
3:30-3:55 Computational Analysis of Plasmodium falciparum RNA-Seq data reveals Protein Interac-tions
that might be implicated in the Invasion of the Red Blood Cells
Jumoke Soyemi, Itunuluwa Isewon, Olubanke Ogunlana, Solomon Rotimi, Jelili Oyelade and
Ezekiel Adebisi
4:00-4:25 RNA Secondary Structure Graphical Rendering Library
Abdullah N. Arslan and Keith A. Monschke
4:30-4:55 Edit Metric Decoding: Return of the Side Effect Machines
Sheridan Houghten, Tyler K. Collins, James Alexander Hughes and Joseph Alexander Brown
5:00-5:25 Tandem mass intensity estimation for de novo peptide sequencing
Hatem Loukil
5:30-5:55 Chemical Structure Recognition and Prediction: A Machine Learning Technique Fakheredine
Keyrouz, Lara Tauk and Elias Feghali
- 6:30-8:30** Conference Banquet Location: Lambert CD

Friday June 1

- 8:00** Continental Breakfast Location: Orly Room
8:30 Registration
- 9:00-10:00** Clustering is much stranger than you thought. Daniel Ashlock
- 10:00-10:30** Coffee break
- 10:30-12:00** Session: **Models of Biological Systems** Location: Orly Room
10:30-10:55 High-Performance and Distributed Computing in a Probabilistic Finite Element Comparison Study of the Human Lower Leg Model with Total Knee Replacement
Corneliu Arsene
- 11:00-11:25 On the Generalizability of Linear and Non-Linear Region of Interest-Based Multivariate Regression Models for fMRI Data
Ethan Jackson, James Hughes and Mark Daley
- 11:30-11:55 Pavlov Principle and Brain Reverse Engineering
Witali Dunin-Barkowski and Ksenia Solovyeva
- 12:00-1:30** Box Lunch in the foyer
1:30-3:00 Bioinformatics and Bioengineering Technical Committee Meeting and Coffee Break
All are welcome! Location: Orly Room
- 3:00-5:00** Session: **Data Analysis** Location: Orly Room
- 3:00-3:25 Hierarchical Clustering and Tree Stability
Amanda Saunders, Daniel Ashlock and Sheridan Houghten
- 3:30-3:55 Parameter Selection for Modeling of Epidemic Networks
Michael Dube, Sheridan Houghten and Daniel Ashlock
- 4:00-4:25 Analysis of Symbolic Models of Biometric Data and their use for User and Task Identification
James Hughes, Joseph Brown, Adil Khan, Asad Khattak and Mark Daley
- 4:25-5:00 Data Driven Point Packing for Fast Clustering
Matthew Stoodley, Daniel Ashlock and Steffen Graether
- 5:00-6:00** Abstract Session I (See the Wednesday Schedule) Location: Orly Room

Saturday June 2

- 8:00** Continental Breakfast
- 9:00-11:00** Session: **Learning and Data Mining** Location: Orly Room
- 9:00-9:25 Improving Medical Search Tasks Using Learning to Rank
Mohammad Alsulmi and Benjamin Carterette
- 9:30-9:55 Cross-validation and cross-study validation of kidney cancer with machine learning and whole exome sequences from the National Cancer Institute
Abdulrhman Aljouie, Usman Roshan and Nihir Patel
- 10:00-10:25 Drug target interaction predictions using PU-Learning under different experimental setting for four formulations namely known drug target pair prediction, drug prediction, target prediction and unknown drug target pair prediction
Hetal Rajpura and Alioune Ngom
- 10:30-11:45** Abstract Session II (See the Wednesday Schedule) Location: Orly Room
- 11:45-12:00** **Wrap up of CIBCB 2018**
- 12:00** Goodbye snack

Thursday Plenary Talk

Neuromorphic Engineering and Computing at a Crossroads

Speaker:

Professor Shantanu Chakrabartty,
Department of Electrical and Systems Engineering,
Division of Biological and Biomedical Sciences (Neurosciences),
Washington University in St. Louis

Abstract:

In neurobiology, a single neuron has evolved to encode information as a sequence of spike signals, dissipating as little energy as possible within its physical constraints. In spite of the energy and physical limitations, networks of spiking neurons observed in biology are remarkably accurate and are able to process, identify and learn complex stimuli with very high resolution and fidelity. The biological basis for such energy-efficient and robust representation lies in the nature of the spatiotemporal network dynamics, in the physics of noise-exploitation and through the use of neural oscillations. On the other hand, most synthetic and large-scale neuromorphic systems ignore these network dynamics, focusing instead on a single neuron and building the network bottom-up. From this approach, it is not evident how the shape, the nature and the dynamics of each individual spike is related to the overall system objective and how a population of neurons when coupled together can self-optimize itself to produce an emergent spiking or population response, for instance spectral noise-shaping or synchrony. Other well established synthetic neural network formulations (for example deep neural networks and support vector machines) follow a top-down synthesis approach starting with a system objective function and then reducing the problem to a model of a neuron that inherently does not exhibit any spiking or complex dynamics. This talk will provide an overarching view of the discipline of neuromorphic engineering and discuss new perspectives on how to combine machine learning principles with biologically relevant neural dynamics.

Speaker Biography:

Shantanu Chakrabartty is a professor in the school of applied sciences and engineering at Washington University in St. Louis. He also holds an appointment in the neurosciences division of biology and biological sciences at Washington University. Dr. Chakrabartty received his B.Tech degree from Indian Institute of Technology, Delhi in 1996, M.S and Ph.D in Electrical Engineering from Johns Hopkins University, Baltimore, MD in 2002 and 2004 respectively. From 2004-2015, he was with the department of electrical and computer engineering at Michigan State University (MSU). From 1996-1999 he was with Qualcomm Incorporated, San Diego and during 2002 he was a visiting researcher at The University of Tokyo. Dr. Chakrabartty's work covers different aspects of analog computing, and in particular neuromorphic, machine learning and self-powered systems. Dr. Chakrabartty was a Catalyst foundation fellow from 1999-2004 and is a recipient of National Science Foundation's CAREER award, University Teacher-Scholar Award from MSU, the 2012 Technology of the Year Award from MSU Technologies and several best paper awards. Dr. Chakrabartty is a senior member of the IEEE with over 170 journal and conference publications along with ten issued and pending US patents. He is currently serving as the associate editor for IEEE Transactions of Biomedical Circuits and Systems and a review editor for Frontiers of Neuromorphic Engineering journal.

Friday Plenary Talk

Clustering is much stranger than you thought.

Speaker:

Daniel Ashlock
University of Guelph
Department of Mathematics and Statistics

Abstract:

This talk will introduce some problems with clustering algorithms, suggest some solutions, and discuss a new class of clustering algorithms called *associator based* clustering.

Speaker Biography:

Dr. Ashlock is a past head of the bioinformatics and bioengineering technical committee. He serves as an editor on the IEEE/ACM Transactions on computational biology and bioinformatics, the IEEE Transactions on Evolutionary Computation, the IEEE Transactions on Games, Biosystems, and Game and Puzzle Design. Dr. Ashlock is an abstract mathematician who has wandered into computational intelligence. His primary work is on representation for evolutionary computation. He is currently the chair of the Games Technical Committee and a member of the Bioinformatics and Bioengineering Technical Committee. Dr. Ashlock has 275 peer-reviewed scientific publications and holds the Bioinformatics Chair of the Mathematics and Statistics Department at Guelph.