

**2017 IEEE Conference on Computational Intelligence in
Bioinformatics and Computational Biology
Preliminary Agenda**

Wednesday, August 23

10:00AM-10:30AM

Coffee and Tea Break

Room: Conference Reception Area

10:30AM-11:15AM

Tutorial: Wendy Ashlock - An introduction to CRISPR Bioinformatics

Room: The Chadwick Suite A

11:15AM-12:00PM

Tutorial: Michael Emmerich, Irina Yevseyeva - Multicriteria decision analysis and optimization for computational chemistry and drug discovery

Room: The Chadwick Suite A

12:00AM-1:00PM

Lunch Break

Room: Hotel restaurant

1:00PM-2:00PM

Plenary Talk: Keynote, Speaker: Douglas Kell

Room: The Chadwick Suite A

Elements of computational intelligence and their applications in bio(techno)logy

2:00PM-2:30PM

Coffee and Tea Break

Room: Conference Reception Area

2:30PM-4:00AM: Machine Learning in Medical Diagnosis and Prognosis I

Room: The Chadwick Suite A

Multi-objective evolution of artificial neural networks in multi-class medical diagnosis problems with class imbalance [#55]

Alex Shenfield and Shahin Rostami

A novel hybrid differential evolution strategy applied to classifier design for mortality prediction in adult critical care admissions [#41]

Alex Shenfield, Marcos Rodrigues, Hossam Nooreldeen and Jeronimo Moreno-Cuesta

Identifying Network-Biomarkers of Breast Cancer Survivability [#77]
Sheikh Jubair, Alioune Ngom and Luis Rueda

Applying brain emotional learning based fuzzy inference system for EEG signal classification between schizophrenics and control participant [#6]
Bahar Javadi Khasraghi and Saeed Setayeshi

Hybrid Feature Selection Method for Autism Spectrum Disorder SNPs [#18]
Raid Alzubi, Naeem Ramzan and Hadeel Alzoubi

4:00PM-4:30PM

Coffee and Tea Break

Room: Conference Reception Area

4:30PM-5:42AM: Digital Signal Processing for Genomics and Metagenomic Sequence Analysis

Room: The Chadwick Suite A

Marginalised Stack Denoising Autoencoders for Metagenomic Data Binning [#54]
Samaneh Kouchaki, Santosh Tirunagari, Avraam Tapinos and David L Robertson

The Identification of Replication Origin in Bacterial Genomes By Cumulated Phase Signal [#70]
Denisa Maderankova, Karel Sedlar, Helena Skutkova and Martin Vitek

De novo assembly of nucleotide sequences in a compress feature space [#60]
Avraam Tapinos and David Robertson

Binning metagenomic reads with probabilistic sequence signatures based on spaced seeds [#33]
Samuele Giroto, Matteo Comin and Cinzia Pizzi

6:30PM-7:00PM

Poster Snapshot Session

Room: The Chadwick Suite A

Reference-free compression of next-generation sequencing data in FASTQ format [#2]
Li Tan and Jifeng Sun

microRPM: a system for novel microRNA prediction [#10]
Chiang-Hsieh Yi-Fan and Wen-Chi Chang

Towards Accurate De Novo Assembly for Genomes with Repeats [#28]
Doina Bucur

Generating the Logicome from Microarray Data [#39]
Charmi Panchal and Vladimir Rogojin

Positome: A Method for Improving Protein-Protein Interaction Quality and Prediction Accuracy [#42]

Kevin Dick, Frank Dehne, Ashkan Golshani and James Green

Disease outbreak prediction by data integration and multi-task learning [#53]

Batuhan Bardak and Mehmet Tan

A multivariate Poisson log-normal mixture model for clustering transcriptome sequencing data [#57]

Anjali Silva, Paul McNicholas, Steven Rothstein and Sanjeena Subedi

An Automated Approach to Translate Bio-pathways from ODEs into Graphical Hybrid Functional Petri Nets [#67]

Imene Mecheter and Rachid Hadjidj

A Support Vector Regression Based Model for the Quantitative Prediction of Age and Body Mass Index by using Epigenetic Information from Peripheral Blood [#71]

Ferdi Sarac, Huseyin Seker and Ahmed Bouridane

Wavelet Transform Improvement of Infrared Images Using Nonlinear Contrast Processing [#80]

Osama Zahran

Towards integrating large-scale OMICS data to better understand disease pathogenesis [#85]

Mohamed Hamed

Consensus rank orderings of molecular fingerprints [#88]

Douglas Kell and Steve O'Hagan

Number of single-cell Clusters Estimation (NICE): a robust and priori knowledge independent algorithm for single-cell RNA-seq data analysis [#89]

Xin Zou, Jie Hao and Ze-Guang Han

Use of pattern recognition methods for fungal adenylation domain substrate specificity predictions [#93]

Sagar Gore and Ekaterina Shelest

A Copy Number Variation Map of the Korean Population [#94]

Jinhwa Kong, Jaemoon Shin and Jeehee Yoon

Integrative Network-based multi-OMICs Analysis of Glioblastoma Multiforme [#95]

Vasanthi Priyadarshini Gaddi and Lars Kaderali

In Silico Design and Molecular Dynamics Simulation of Glycophorin A Transmembrane Dimer, in Pure DPPC and Mixed DPPC-DMPC Phospholipid [#99]

Delara Mohammad-Aghaie and Fatemeh Razavi

Association Rule Mining of Protein Contact Maps from Protein 3D structures [#100]
Suvarna Vani Koneru and Praveen Kumar Kollu

7:00PM-9:00PM

Opening Reception/Poster Presentations

Room: The Chadwick Suite B

Thursday, August 24

8:30PM-10:00AM: General Session

Room: The Chadwick Suite A

A Comparison of Distance Metrics in Semi-supervised Hierarchical Clustering Methods [#8]
Abeer Aljohani

An Algebraic Generalization for Graph and Tensor-Based Neural Networks [#46]
Ethan Jackson, James Hughes, Mark Daley and Michael Winter

A Note On Population Size Inspired By The Extinction Of Mammoths [#12]
Daniel Ashlock and Wendy Ashlock

Evaluation of the Salmon Algorithm [#84]
John Orth, Sheridan Houghten and Lindsey Tulloch

Hybridization and Ring Optimization for Larger Sets of Embeddable Biomarkers [#26]
Daniel Ashlock and Sheridan Houghten

10:00AM-10:30AM

Coffee and Tea Break

Room: Conference Reception Area

10:30AM-12:00PM: General Session

Room: The Chadwick Suite A

Improving De novo Protein Structure Prediction using Contact Maps Information [#30]
Karina B. Santos, Gregório K. Rocha, Fábio L. Custódio, Helio J. C. Barbosa and Laurent E. Dardenne

Topological, Functional, and Structural Analyses of Protein-protein Interaction Networks of Breast Cancer Lung and Brain Metastasis [#34]

Farideh Halakou, Emel Sen Kilic, Ozlem Keskin and Attila Gursoy

Comparative Analysis on Modularization of Metabolic Network of Methanogens Based on Simulated Annealing Algorithm [#38]

Jing Chen and Lijun Ren

Optimizing Bioengineered Vascular Systems: A Genetic Algorithm Approach [#74]
Sima Mehri, Curtis Larsen, Gregory Podgorski and Nicholas Flann

Reboot Strategies in Particle Swarm Optimization and their Impact on Parameter Estimation of Biochemical Systems [#52]
Simone Spolaor, Andrea Tangherloni, Leonardo Rundo, Marco Salvatore Nobile and Paolo Cazzaniga

12:00PM-1:00PM

Lunch Break

Room: Hotel restaurant

1:00PM-2:00PM

Plenary Talk: Keynote

Room: The Chadwick Suite A, Speaker: Charlotte Dean

Improving fragment assembly protein structure prediction

2:00PM-2:30PM

Coffee and Tea Break

Room: Conference Reception Area

2:30PM-4:00PM: Multi-objective Optimization in Computational Biology and Bioinformatics

Room: The Chadwick Suite A

Modeling Protein Structural Transitions as a Multi-objective Optimization Problem [#31]
Emmanuel Sapin, Kenneth De Jong and Amarda Shehu

Using an Aggregation Tree to Arrange Energy Function Terms for Protein Structure Prediction [#27]

Gregório K. Rocha, Jaqueline S. Angelo, Karina B. Santos, Fábio L. Custódio, Laurent E. Dardenne and Helio J.C. Barbosa

Finding optimal finite biological sequences over finite alphabets: the OptiFin toolbox [#58]
Régis Garnier, Christophe Guyeux and Stéphane Chrétien

Predicting Radiation Protection and Toxicity of p53 Targeting Radioprotectors using Machine Learning [#37]

Masataka Kimura, Shin Aoki and Hayato Ohwada

CVis — towards a novel visualization tool to explore the relationship between input and output partitions in multi-objective clustering ensembles [#83]

Katti Faceli, Tiemi C. Sakata and Julia Handl

4:00PM-4:30PM

Coffee and Tea Break

Room: Conference Reception Area

4:30PM-5:42AM: General Session

Room: The Chadwick Suite A

A Novel Representation for Boolean Networks Designed to Enhance Heritability and Scalability.
[#24]

Daniel Ashlock and Gonzalo A. Ruz

Inferring bistable lac operon Boolean regulatory networks using evolutionary computation [#25]
Gonzalo A. Ruz, Daniel Ashlock, Thomas Ledger and Eric Goles

Inference of Genetic Networks from Time-series of Gene Expression Levels Using Random Forests [#11]

Shuhei Kimura, Masato Tokuhisa and Mariko Okada-Hatakeyama

Single-Objective and Multi-Objective Genetic Algorithms for Compression of Biological Networks [#78]

Tyler K. Collins, Adel Zakirov, Joseph Alexander Brown and Sheridan Houghten

6:30PM-10:00PM

Conference Dinner

Location: Manchester Museum

Drink reception from 6.30pm with food being served at 7pm

Friday, August 25

8:30AM-10:00AM: Machine Learning in Medical Diagnosis and Prognosis II

Room: The Chadwick Suite A

Deep Learning Models for Bone Suppression in Chest Radiographs [#40]

Maxim Gusarev, Ramil Kuleev, Adil Khan, Adin Ramirez Rivera and Asad Masood Khattak

Large Residual Multiple View 3D CNN for False Positive Reduction in Pulmonary Nodule Detection [#48]

Anton Dobrenkii, Ramil Kuleev, Adil Khan, Adin Ramirez Rivera and Asad Masood Khattak

A Multivariate Feature Selection Framework for High Dimensional Biomedical Data Classification [#20]

Abeer Alzubaidi and Georgina Cosma

A Multi-stage Approach to Detect Gene-gene Interactions Associated with Multiple Correlated Phenotypes [#75]

Xiangdong Zhou, Keith Chan and Danhong Zhu

Evaluation of Support Vector Machines and Random Forest Classifiers in a Real-time Fetal monitoring system based on cardiotocography data [#43]

Vinayaka Nagendra Harikishan Gude Divya Sampath, Steven Corns and Suzanna Long

10:00AM-10:30AM

Coffee and Tea Break

Room: Conference Reception Area

10:30AM-12:00PM: Computational Intelligence for Biological Feature Induction

Room: The Chadwick Suite A

Infinite String Block Matching Features for DNA Classification [#23]

Daniel Ashlock, Sierra Gillis and Wendy Ashlock

Microbial Abundance Analysis and Phylogenetic Adoption in Functional Metagenomics [#61]

Jyotsna Talreja Wassan, Haiying Wang, Huiru Zheng and Fiona Browne

Modelling Intracranial Pressure with Noninvasive Physiologic Measures [#16]

James Hughes, Ethan Jackson and Mark Daley

Structural and parametric uncertainties in full Bayesian and graphical lasso based approaches: beyond edge weights in psychological networks [#82]

Gabor Hullam, Gabriella Juhasz, Bill Deakin and Peter Antal

Finding Sub-Graphs from Contact Map Overlap Problem [#32]

Suvarna Vani Koneru, Praveen Kumar Kollu and Veda Sri Movva

12:00PM-1:00PM

Lunch Break

Room: Hotel restaurant

1:00PM-2:00PM

Plenary Talk: Keynote

Room: The Chadwick Suite A, Speaker: Julia Handl

Multi-objective optimization in bioinformatics and computational biology

2:00PM-2:30PM

Coffee and Tea Break

Room: Conference Reception Area

2:30PM-4:18PM: General Session

Room: The Chadwick Suite A

Data-Driven Longitudinal Modeling and Prediction of Symptom Dynamics in Major Depressive Disorder: Integrating Factor Graphs and Learning Methods [#68]

Arjun Athreya, Subho Sankar Banerjee, Drew Neavin, Rima Kaddurah-Daouk, A. John Rush, Mark Frye, Liewei Wang, Richard Weinshilboum, William Bobo and Ravishankar Iyer

Leveraging data mining techniques to understand drivers of obesity [#1]

Reza Salehnejad, Richard Allmendinger, Yu-Wang Chen, Manhal Ali, Azar Shahgholian, Paraskevas Yiapanis and Mohaimen Mansur

Attention Estimation System via Smart Glasses [#79]

Oscal T.-C. Chen, Pin-Chih Chen and Yi-Ting Tsai

Using Benford's Law to Detect Anomalies in Electroencephalogram: An Application to Detecting Alzheimer's Disease [#45]

Santosh Tirunagari, Simon Bull, Daniel Abasolo, Aamo Iorliam, Anthony Ts Ho and Norman Poh

A hierarchical model to predict the probability of germination of bacterial spores [#69]

Paola Lecca, Angela Re, Gary Barker and Adaocha Ihekwaba

Frequency Difference based DNA Encoding Methods in Human Splice Site Recognition [#63]

Elham Pashaei and Nizamettin Aydin

4:20PM-4:45PM

Coffee and Tea Break

Room: Conference Reception Area