

**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-4:00PM: 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

*Attention Estimation System via Smart Glasses [#79]*  
Oscal T.-C. Chen, Pin-Chih Chen and Yi-Ting Tsai

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

*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-6:00PM: 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

*Using Benford's Law to Detect Anomalies in Electroencephalogram: An Application to Detecting Alzheimer's Disease [#45]*  
Santosh Tirunagari, Daniel Abasolo, Aamo Iorliam, Anthony Ts Ho and Norman Poh

**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

*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

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

Imene Mecheter, Rachid Hadjidj, and Sebti Fougou

*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, Jeehee Yoon and Keonbae Lee

*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**

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

Room: The Chadwick Suite A

*Generating the Logicome from Microarray Data [#39]*

Charmi Panchal and Vladimir Rogojin

*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-5:42PM: General Session**

Room: The Chadwick Suite A

*Inferring bistable lac operon Boolean regulatory networks using evolutionary computation [#25]*

Gonzalo A. Ruz, Daniel Ashlock, Thomas Ledger and Eric Goles

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

Daniel Ashlock and Gonzalo A. Ruz

*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 cardiocography 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-4:00PM: 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

*A hierarchical model to predict the probability of germination of bacterial spores [#69]*  
Paola Lecca, Angela Re, Gary Barker and Adaoha Ihekweba

*Statistical Report on the 2017 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology*  
Wendy Ashlock

*An Invitation to the 2018 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology*  
Steven Corns

**4:00PM-4:30PM**

**Coffee and Tea Break**

Room: Conference Reception Area