



CIBB 2015: 12th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics,

CNR Research Area, Naples, Italy, 10-12 September 2015

<http://bioinfo.na.iac.cnr.it/cibb2015/>

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CALL FOR PAPERS – Special Session on

New knowledge from old data: power of data analysis and integration methods

Aims and scope

Mammalian system constitutes over 200 cell types each specialized to perform a distinct function and yet all cell types share the same DNA sequence. The epigenetic marks on DNA and histone tails together with transcription factors are responsible for the interpretation of the DNA sequence in each cellular context to produce a cell type specific transcription signature and disruptions to these processes lead to disease. Advances in sequencing techniques have accelerated characterization of epigenetic and transcription landscape across many normal and malignant cell types. The challenge now is to integrate these data to understand transcriptional control at a systems level.

This session will focus on data analysis and data integration methods developed using data from but not limited to large consortia projects such as ENCODE, roadmap to epigenomics or FANTOM to get new biological insights.

Organisers

Dr. Anagha Joshi (Roslin institute, University of Edinburgh)

Prof. Tom Michoel (Roslin institute, University of Edinburgh)

Submissions

Conference papers must be prepared following the guidelines illustrated on the CIBB website, which include the requirement of being between 4 and 6 pages in length and having five sections:

1. Scientific background
2. Material and methods
3. Results
4. Conclusion
5. References (no more than 10)

These papers should be submitted in PDF format on the Easy Chair conference system (it is necessary to select this special session in the submission system).

A second submission after the conference, in an extended version, is required to be considered for publication in the Springer's Lecture Notes in Bioinformatics (LNBI) series (<http://www.springer.com/computer/lncs?SGWID=0-164-6-73658-0>). Moreover, as it has been the case in previous CIBB conferences, we are planning to publish the best papers of CIBB 2014 in an extended form in a special issue of an international scientific journal, including special session papers.

Important dates

Paper submission deadline : May 30, 2015
Abstract submission deadline: May 30, 2015
Notification of Acceptance: June 19, 2014
Final papers due: July 20, 2015 (*)
Conference: September 10-12, 2015

(*) for the inclusion in the CIBB15 conference proceeding

About the organisers

Dr. **Anagha Joshi** leads a bioinformatics group within the division of Developmental biology at the Roslin institute, University of Edinburgh. She was awarded Chancellor's fellowship to start a research group at the Roslin institute, University of Edinburgh in 2012. The research in her group includes the development of innovative mathematical and computational approaches for integrating large-scale data, building predictive models and learning new biology, using blood as a model system. Her expertise in next generation sequencing data analysis (RNA and ChIP sequencing) has led to many collaborative projects including FANTOM5 consortium resulting into over 30 peer reviewed publications. During her PhD at VIB and Ghent University, she developed algorithms for building transcriptional regulatory networks using gene expression and high-throughput interaction data in diverse systems, from yeast, to plants, to human cancers. For her post-doctoral training, she joined Professor Gottgens's group at the University of Cambridge to study regulatory mechanisms controlling the blood developmental system.

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Prof. **Tom Michoel** leads a computational group within the Genetics and genomics division of the Roslin institute, University of Edinburgh. The aim of his research team is develop the theory, algorithms and software necessary to reverse-engineer gene regulatory network models from transcriptome sequencing and other 'omics' data, and to learn from these models the molecular control mechanisms that can influence cells or whole organisms to achieve a desired phenotypic goal. Before moving to the University of Edinburgh, he was a group leader at Freiburg Institute for Advanced Studies, University of Freiburg, Germany.

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