CALL FOR PAPERS – Special Session on Large-Scale and HPC data analysis in bioinformatics: intelligent methods for computational, systems and synthetic biology.

CIBB 2014

11th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics

Computer Laboratory, University of Cambridge, Cambridge, United Kingdom

June 26-28 2014

http://www.cussb.unisr.it/cibb2014/

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Aims and scope

Biomedical research is currently facing the Big Data wave created by the huge amount of experiments performed every days in omics sciences. This new situation demands appropriate IT-infrastructures and scalable software to analyse data within an acceptable timespan. Massive parallel clusters, distributed technologies, on-Chip solutions such as GPGPU and Xeon Phi must be exploited with adequate algorithmic solutions to reach their full potential.

The aim of this special session is to bring together researchers interested in cutting-edge methods to address the challenges posed by the huge amount of data produced in omics science. The idea is to present the latest advancements concerning High Performance Computing solutions required to treat multi-omics data and the related Big Data paradigms that are needed to manage the Large-Scale challenges of nowadays computational biology.

Relevant topics within this context include all the field of Next-Generation Sequencing data analysis and interpretation, Genomics patterns identification and mining, Transcriptomics and Proteomics data integration, Systems Biology models simulation and optimization, Structural Biology and Molecular Dynamics, Synthetic Biology circuits design and simulation.

Organisers
Dr. Andrea Bracciali (Dept. of Computing Science and Mathematics, University of Stirling, UK)
Dr. Ivan Merelli (Institute for Biomedical Technologies – Italian National Research Council, Italy)

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 5, 2014
Notification of Acceptance: May 10, 2014
Final papers due: May 30, 2014 (*)
Conference: June 26-28, 2014

 (*) for the inclusion in the CIBB14 conference proceeding

About the organisers

Dr. **Andrea Bracciali** is currently a SICSA lecturer at the Department of Computing Science and Mathematics of the University of Stirling (from August 2010). Before that, he worked as a postdoctoral researcher at CNR, Italy (2009-2010) in the Applied Formal Methods group, and at the Computer Science Department of the University of Pisa (2003-2008), where he received his Ph.D. (2003) in Computer Science. His main research interests are centred in the formal description of interaction in computing with application for Systems Biology and Crowd Dynamics. His main research interests regard the formal description of interaction in computational systems and theories and tools for reasoning about such descriptions. This stream of research spawns form Theoretical Computer Science, Concurrency Theory and, more recently, Systems Biology.

Web: http://www.cs.stir.ac.uk/~abb/

Dr. **Ivan Merelli** is currently research fellow at the Institute for Biomedical Technologies (ITB) of the National Research Council (CNR) in the Bioinformatics Division. He received his Master of Science in Biomedical Engineering from the Politecnico di Milano, with a thesis about molecular surface

modelling and analysis. In February 2009 he received a PhD in Computer Science from the university of Milano - Bicocca with a research project about surface matching for macromolecular docking and functional annotation. His research activities concern the development of software for sequence based genomics and for structural proteomics research, with particular interest in protein-protein interactions. He works actively on the implementation of high performance bioinformatics software using cluster infrastructures and grid distributed platforms. He has been involved in the development of databases and computational solutions for projects of Integrative System Biology, gene expression analyses and drug discovery.

Web: http://www.itb.cnr.it/web/bioinformatics/staff