



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

The EDGE, enhanced definition of genomic entities for systems biomedicine in oncology

Aims and scope

Current biomedical research is facing the systems challenge involving the use of dedicated mathematical, bioinformatics and biostatistical tools. The key issues of integrating data collected across multiple sources, the dynamics of disease processes, risk factors and biomarkers related to diagnosis, prognosis and response to treatments, as well as their modulation by genetic, epigenetic, lifestyle determinants, and environmental influences was a major challenge. Recent initiatives in system biomedicine as those of the EU CASyM, pointed out the issues of the paradigm shift towards integrative (cross-disciplinary Systems Medicine). Systems Medicine consortia should implement "collective" rather than individualistic ways of working. There is an unmet need for understanding the biological complexity of cancer. An interdisciplinary approach is needed for reaching successful, long-term goals. Involvement and education of the general public must be stressed. To face these issues data integration is considered the top priority for supporting the evidence on new genomic entities for improving diseases knowledge and supporting better prevention, diagnosis and therapy. The aim of this special session is to continue the challenge faced during the previous CIBB 2014 in Cambridge UK to bring together biomedical researchers interested in major diseases genomics with those facing the development of computational biostatistics methods to address the applied and methodological challenges posed by the Systems Biomedicine research paradigm. Relevant topics within this context include the development and application of methods for the analysis of NGS data, disease dynamics and omic information, diagnosis and prognostic tools based on complex biomarkers as well as experimental design and data analysis approaches for pharmacogenomics and response to polytherapies.

Organisers

Prof. **Elia Mario Biganzoli** (Università degli Studi di Milano)

Prof. Maria Clelia Di Serio

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

Prof. **Elia Mario Biganzoli** (Università degli Studi di Milano)

Elia Mario Biganzoli. Professor in Medical Statistics of the University of Milan and Senior Biostatistician, Unit of Medical Statistics, Biometry and Bioinformatics, Fondazione IRCCS Istituto Nazionale dei Tumori, Task Force Leader Evaluation & Benchmarking, BIOPATTERN Network of Excellence FP6 project: "Computational Intelligence for Biopattern Analysis in Support of eHealthcare". Cofounder of the IEEE Neural Network Society Special Interest Group Biopattern. He was responsible and participated to national and international projects with Associazione Italiana per la Ricerca sul Cancro, National Research Council-Polish Academy of Sciences, Italian Ministry of Health, Italian Ministry of the University and Research, European Commission. His main research fields concern statistical methods for survival analysis and biological assay development. He participated in the planning of diagnostic and prognostic studies in cancer, cardiovascular diseases, rheumatology, hematology and the analysis of their results with special interest on molecular biomarkers and bioprofiles. He developed statistical approaches for the extension of generalized linear models with artificial neural networks and splines for the flexible analysis of censored survival data.

Prof. **Maria Clelia Di Serio** (Università Vita-Salute San Raffaele, Milano)

Professore di Statistica presso la Facoltà di Psicologia dell'Università Vita-Salute S. Raffaele di Milano. Già docente nella Facoltà di Medicina dello stesso Ateneo, dal 2005 vi dirige il Centro universitario di statistica per le scienze biomediche. Consegue il dottorato di ricerca nel 1996, dopo due anni di formazione all'estero nel programma di PhD in Statistica Matematica della Università della Carolina del Nord (UNC, Chapel Hill, USA). Ha al suo attivo vari progetti internazionali di ricerca accademica: prima (1995-1996) a Copenhagen, Danimarca, poi (2001-2002) in Germania (Technical University, Monaco di Baviera). Dal 1996 al 2000 ha trascorso periodi

negli Stati Uniti quali visiting researcher and postdoc: DukeUniversity, UCLA, Case Western University, e la Johns Hopkins.