

# 11<sup>th</sup> INTERNATIONAL MEETING ON COMPUTATIONAL INTELLIGENCE METHODS FOR BIOINFORMATICS AND BIostatISTICS

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

26-28 June 2014, The Computer Laboratory, University of Cambridge, UK

## General Chairs

Clelia Di Serio, Vita-Salute San Raffaele University, Italy  
Pietro Liò, University of Cambridge, UK  
Sylvia Richardson, University of Cambridge, UK  
Roberto Tagliaferri, University of Salerno, Italy

## Biostatistics Technical Chair

Ernst Wit, University of Groningen, The Netherlands

## Bioinformatics Technical Chair

Claudia Angelini IAC-CNR, Italy)

## Publicity Chair

Francesco Masulli, University of Genoa, Italy and Temple University, PA, USA

## Local Organizing Committee Chairs

Mohammad Moni, University of Cambridge, UK  
Alessandro Nonis, Vita-Salute San Raffaele University, Italy

## Special Session and Tutorial Chairs

Pedro Ballester, EBI, Cambridge, UK  
Yoli Shavit, University of Cambridge, UK

## Publication Chair

Riccardo Rizzo, ICAR-CNR, Italy

## Finance Chair

Elia Biganzoli, University of Milan, Italy

## Steering Committee

Pierre Baldi, University of California, Irvine, CA, USA  
Elia Biganzoli, University of Milan, Italy  
Alexandru Floares, Oncological Institute Cluj-Napoca, Romania  
Jon Garibaldi, University of Nottingham, UK  
Nikola Kasabov, Auckland University of Technology, New Zealand  
Francesco Masulli, University of Genova, Italy and Temple University, PA, USA  
Leif Peterson, TMHRI, Houston, Texas, USA  
Roberto Tagliaferri, University of Salerno, Italy

Molecular Biology is an exciting experimental field that is producing an explosion of new data. In recent years, a number of developments have enabled Bioinformatics and Biostatistics methodologies to keep pace. CIBB is a meeting with a 10-year history of convening bioinformaticians and biostatisticians to discuss cutting edge methodologies and accelerate life science discovery. Following his traditions and roots, this year's forum will discuss problems concerning computational techniques in bioinformatics, systems biology, medical informatics and biostatistics. The location is the Computer Laboratory, which is the department of Computer Science of the University of Cambridge.

## Topics of interest include but are not limited to:

Next Generation Sequencing Bioinformatics, Multi omics integration; Methods for the integration of clinical and genetic data; Algorithms for alternative splicing analysis; Methods for the functional classification of genes; Methods for the unsupervised analysis, validation and visualization of structures discovered in bio-molecular data; Prediction of protein structures; Mass spectrometry data analysis in proteomics; Methods for comparative genomics; Algorithms for molecular evolution and phylogenetic analysis; Mathematical modelling and simulation of biological systems; Systems and synthetic biology; Heterogeneous data integration and data fusion for diagnostics; Bio-molecular databases and data mining; Algorithms for pharmacogenetics; Bio-medical text mining and imaging; Modeling and evaluation methods for diagnosis and prognosis; Software tools for bioinformatics.

The scientific program will include, besides some plenary talks, contributed papers that will be presented in plenary oral and poster sessions. Accepted papers will be published in the conference proceedings. A selection of papers presented at CIBB 2014 will be published in a post conference volume printed by an international publisher. Moreover, we are planning to publish the best papers in extended form in a special issue of BMC Bioinformatics.

## Important Dates (new deadlines):

Tutorial and Special Session Proposal:	5 - March - 2014
Paper submission deadline:	5 - April - 2014
Notification of acceptance:	10 - May - 2014
Final paper due:	30 - May - 2014
Conference:	26-28 - June - 2014