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**THIRD CALL FOR PAPERS**  
**PAPER SUBMISSION: 12<sup>th</sup> June 2016 (EXTENDED)**

**CIBB 2016**

**13<sup>th</sup> International Meeting on Computational Intelligence methods for  
Bioinformatics and Biostatistics**

**University of Stirling, Stirling, Scotland UK**  
**September 1-3 2016**

<http://www.cs.stir.ac.uk/events/cibb2016/>  
[cibb2016@gmail.com](mailto:cibb2016@gmail.com)

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**In evidence** (please see below and the web for details):

- Due to numerous request paper submission has been extended:

**Paper submission deadline: 12<sup>th</sup> June 2016 (EXTENDED)**

- the very interesting list of **invited speakers** is growing !
- five **special sessions** are running
- please, connect to the conference via **@CIBB2016** on twitter

**Keynote Speakers** (to be completed)

**Prof. Mark Beaumont**  
School of Biological Sciences, Bristol University  
[Evolutionary Biology](#)

**Prof. Natalio Krasnogor**  
School of Computing Science, Newcastle University  
[Computing Science and Synthetic Biology](#)

**Prof. Bud Mishra**  
Courant Institute of Mathematical Sciences and NYU School of Medicine,  
New York University NYU,  
and Mt Sinai School of Medicine  
[Computer Science, Cell Biology and Genetics](#)

**Dr. Guido Sanguinetti**  
School of Informatics, University of Edinburgh  
[System design of stochastic models](#)

## Special Sessions

[Engineering Bio-interfaces and Rudimentary Cells as a way to develop Synthetic Biology](#)

Contacts: Maria Raposo, [mfr@fet.unl.pt](mailto:mfr@fet.unl.pt)

[Biocuration and integration of biomedical databases](#)

Contacts: Riccardo Rizzo, [ricrizzo@pa.icar.cnr.it](mailto:ricrizzo@pa.icar.cnr.it)

[Modeling and simulation methods for Systems Biology and Systems Medicine](#)

Contacts: Paolo Cazzaniga, [paolo.cazzaniga@unibg.it](mailto:paolo.cazzaniga@unibg.it)

[High-Performance Computing and Deep learning methods for Genomic Data Analysis](#)

Contacts: Fabio Tordini, [tordini@di.unito.it](mailto:tordini@di.unito.it)

[Statistical inference in mechanistic models of biological system](#)

Contacts: Dirk Husmeier, [Dirk.Husmeier@glasgow.ac.uk](mailto:Dirk.Husmeier@glasgow.ac.uk)

## Scope

The main goal of this 13th edition of the CIBB international conference is to provide a multi-disciplinary forum open to researchers interested in the application of computational intelligence, in a broad sense, to open problems in bioinformatics, biostatistics, systems and synthetic biology and medical informatics. Cutting edge methodologies capable of accelerating life science discoveries will be discussed. Following its tradition and roots, this year's meeting will bring together researchers from the international scientific community interested in advancements and future perspectives in bioinformatics and biostatistics. Also, looking at current trends and future opportunities at the edge of computer and life sciences, the application of computational intelligence to system and synthetic biology, and the consequent impact on innovative medicine will be of great for the conference. Theoretical and experimental biologists are also invited to participate in order to present novel challenges and foster multidisciplinary collaboration.

The scientific program of CIBB 2016 will include Keynote Speakers, tutorials and special sessions. Contributed papers will be presented in plenary oral sessions, special sessions, or poster sessions.

Topics of interest include, but are not restricted to:

- Next generation sequencing bioalgorithms
- Multi-omics data analysis
- High dimensional statistical analysis of omics data
- Algorithms for alternative splicing analysis
- Algorithms for molecular evolution and phylogenetic analysis
- Methods for the visualization of high dimensional complex omic data
- Software tools for bioinformatics
  
- Methods for comparative genomics
- Methods for functional classification of genes
- Methods for unsupervised analysis, validation and visualization of structures discovered in bio-molecular data

- Health-Informatics and Medical Informatics.
- Methods for the integration of clinical and genetic data
- Heterogeneous data integration and data fusion for diagnostics
- Algorithms for pharmacogenomics
- Biomedical text mining and imaging
- Methods for diagnosis and prognosis within personalized medicine
- Statistical methods for the analysis of clinical data
  
- Prediction of secondary and tertiary protein structures
- Mass spectrometry data analysis in proteomics
- Algorithms for molecular evolution and phylogenetic analysis
- Bio-molecular databases and data mining
  
- Mathematical modeling and automated reasoning on biological and synthetic systems
- Computational simulation of biological systems
- Methods and advances in systems biology
- Spatio-temporal analysis of synthetic and biological systems
- Network systems biology
- Models for cell populations and tissues
- Methods for the engineering of synthetic components
- Modelling and engineering of interacting synthetic and biological systems
  
- Software tools for bioinformatics, biostatistics, systems and synthetic biology

## Publication

Accepted papers will be presented at the conference (at least one author is expected to register), and will be published on proceedings for conference distribution. Extended and revised versions of the papers presented at CIBB 2016 will be invited for a post-conference monograph. This is traditionally published in the Springer series of Lecture Notes in Bioinformatics (LNBI), (arrangements undergoing). Continuing the tradition of CIBB, we are planning to publish best papers in one (or more, as appropriate) special issue of an international scientific journal (such as BMC Bioinformatics, in the latest editions).

## Paper Submission

Papers must be prepared following the guidelines illustrated on the CIBB web site and should be long between 4 and 6 pages.

Papers should be submitted in PDF format on the Easy Chair conference system (link available on the web site).

## Important Dates

Paper submission deadline:	<del>29<sup>th</sup> May 2016</del>	<b>12<sup>th</sup> June 2016 (EXTENDED)</b>
Notification of acceptance:	<del>22<sup>nd</sup> June 2016</del>	3 <sup>rd</sup> July 2016
Final paper due:	<del>8<sup>th</sup> July 2016</del>	24 <sup>th</sup> July 2016
Conference:	<del>1<sup>st</sup> -3<sup>rd</sup></del>	September 2016

## **General Chairs**

Andrea Bracciali, University of Stirling, UK  
David Gilbert, Brunel University London, UK  
Gilbert MacKenzie, UL, ENSAI and Keele, UK

## **Biostatistics Technical Chair**

Marco Bonetti, Università Bocconi, Italy

## **Bioinformatics Technical Chair**

Ivan Merelli, ITB-CNR, Italy

## **Local Organizing Committee Chairs**

Leslie Smith, University of Stirling, UK  
Giulio Caravagna, Edinburgh University, UK

## **Publicity Chair**

Francesco Masulli, University of Genoa, Italy

## **Special Session and Tutorial Chair**

Claudia Angelini, IAC-CNR, Italy

## **Publication Chair**

Riccardo Rizzo, ICAR-CNR, Italy

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