

**2nd International Workshop on
Pattern Recognition in Proteomics,
Structural Biology and Bioinformatics**

PR PS BB 2013

September 9-10, 2013



in conjunction with the
17th International Conference on Image Analysis and Processing (ICIAP)

Naples, Italy

www.iciap2013-naples.org



MOTIVATIONS AND AIMS

Pattern recognition, after many years of studies and researches successfully developed in several applicative areas, has now know-how, computing strategies, technologies, methods and tools to exploit in new fields such as proteomics, structural biology and bioinformatics.

PR PS BB 2013 integrates and continues the tradition of the international conferences on image analysis and processing, one of the longest running international conferences, that started in Italy, in 1980.

Through its informal nature, the workshop is intended to become the foremost platform for exchanging ideas and giving to top researchers, practitioners and students from around the world, of the computing and biological communities, excellent opportunities to meet, interact and rise synergies.

SCOPE & CALL FOR PAPERS

The amount and complexity of bioinformatics data such as DNA and protein sequences, genetic information, biomedical text and molecular data had a sort of explosion in the past decade.

The importance of the study such amounts of data, for the analysis of structural building blocks, their comparison and their classification are instrumental to practical problems of the maximum impact, such as the design of a small molecule to bind a known protein or the scan of drugs libraries to detect a suitable inhibitor for a target molecule.

Advanced pattern recognition methods can also have a significant role in high-throughput functional genomics and system biology, where the classification of complex large scale expression profiles, and their link with motif discovery and inference of gene regulatory network, is a major research challenge in the field of Computational Biology.

However, current pattern recognition techniques to tackle these huge data are still not sufficient: the development of approaches for the improvement of the current performances is the scope of the workshop.

A list of open issues on which prospective authors are invited to submit papers is:

- Alignment and comparison of biological structures
- All-to-all comparison and research of structural motifs
- Blocks retrieval in databases
- Classification of known structures

- Computational and comparative genomics
- Docking between proteins and between protein and ligand
- Folding and prediction from amino sequences
- Morphological study for molecules interaction and comparison
- Prediction of links between protein and potential drugs
- Structural genomics and proteomics
- Pathway and network analysis
- Gene and protein expression analysis and classification
- Pattern discovery and motif detection
- High content screening and analysis

FORMAT

The workshop will feature contributed talks as well as invited presentations. Moreover, feeling that the more informal the better, open and lively discussions and exchange of ideas are solicited. Some panels are allocated to stimulate questions and discussions.

ORGANIZATION

Program Chairs

Virginio Cantoni, University of Pavia, Italy
Michele Ceccarelli, University of Sannio, Italy

Program Committee

Paola Bertolazzi, IFAC CNR Roma, Italy
Mario Cannattaro, Università della Calabria, Italy
Virginio Cantoni, University of Pavia, Italy
Alessandra Carbone, Université Pierre et Marie Curie, Paris, France
Jens Michael Carstensen, Videometer A/S, Copenhagen, Denmark
Rita Casadio, University of Bologna, Italy
Michele Ceccarelli, University of Sannio, Italy
Angelo Facchiano, Istituto di Scienze dell'Alimentazione - CNR - Avellino, Italy
Concettina Guerra, Padova University, Italy
Alamgir Hossain, Northumbria University, UK
Tom Lenaerts, Université Libre de Bruxelles, Belgium
Le Ly, Ho Chi Min International University, Vietnam
Giuseppe Maino, ENEA & Bologna University, Italy
Elena Marchiori, Radboud University, The Netherlands
Robert Murphy, Carnegie Mellon University, USA
Alfredo Petrosino, Parthenope University, Italy
Michael Schroeder, BiOTEC, TU Dresden, Germany
Roberto Tagliaferri, Università di Salerno, Italy

Workshop Organization and Scientific Secretary

Alessandra Setti, University of Pavia, Italy

IMPORTANT DATES

Paper submission: **May 15, 2013**
Notifications: **June 10, 2013**
Camera-ready due: **June 28, 2013**
Conference: **September 9-10, 2013**

PAPER SUBMISSION

Papers must be submitted to <https://cmt.research.microsoft.com/ICIAPWS2013/>.

Manuscripts should be in pdf and formatted according to Springer's Lecture Notes in Computer Science (LNCS) style. Information concerning typesetting can be obtained directly from Springer at: <http://www.springer.com/comp/lncs/authors.html>.

Papers must not exceed 8 pages and should report original work.

All submitted papers will be subject to a rigorous peer-review process. Accepted papers will appear in the workshop proceedings.

Submission implies the willingness of at least one of the authors to register and present the paper, if accepted.

WORKSHOP VENUE

The workshop takes place in one of the ICIAP2013 Conference Sites in the historical center of Naples.