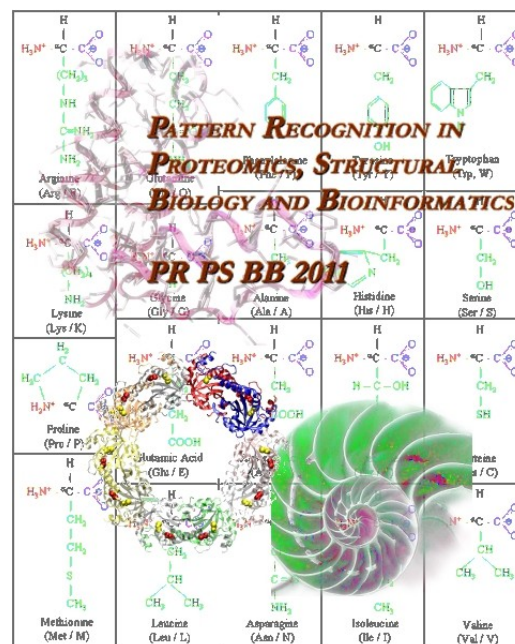# 1st International Workshop on Pattern Recognition in Proteomics, Structural Biology and Bioinformatics

PR PS BB 2011

September 13, 2011
Ravenna, Italy

http://avires.dimi.uniud.it/iciap2011/

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 2011 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. As of Tuesday Feb 15, 2011 at 4 PM PST there are 71264 experimentally determined 3D structures of protein deposited in the Protein Data Bank (with an increment of about 700 new molecules for month).

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
- Etc.

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, Pavia University
Giuseppe Maino, ENEA & Bologna University

Program Committee

Paola Bertolazzi, IFAC CNR Roma
Mario Cannattaro, Università della Calabria
Virginio Cantoni, Pavia University
Michele Ceccarelli, Sannio University
Concettina Guerra, Padova University
Giuseppe Maino, ENEA & Bologna University
Alfredo Petrosino, Parthenope University

IMPORTANT DATES

Paper submission: May 29, 2011
Notifications: June 19, 2011
Camera-ready due: July 2, 2011
Conference: September 13, 2011

PAPER SUBMISSION

Papers must be submitted electronically to alessandra.setti@unipv.it. 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 10 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 at the Casa Matha building.. Casa Matha is the oldest establishment of university education in Ravenna and is located in the center of the town near Piazza del Popolo.

Images of Casa Matha, Ravenna, workshop venue