

## Call for Participation

Graphs are a powerful data structure that can be applied to several problems in bioinformatics. A lot of biological data can be represented as graphs: molecule structures, protein secondary structures, protein interaction networks. Since all these data are stored in huge biological data banks, one of the most important challenges for bioinformatics is the development of efficient Pattern Recognition tools to retrieve relevant information. Among these, the search for patterns inside a biological database can be formulated as a graph matching problem. The aim of this contest is to assess the state-of-the-art about graph matching algorithms suitable for bioinformatics graphs, using both exact and inexact approaches. The participants will be evaluated considering the time and space requirements of the algorithms, and, for the inexact ones, the accuracy of the found solutions.

### Main Organizers

Mario Vento <mvento@unisa.it>  
Pasquale Foggia <pfoggia@unisa.it>  
Xiaoyi Jiang <xjiang@uni-muenster.de>

### Local Committee

Gennaro Percannella <pergen@unisa.it>  
Alessia Saggese <asaggese@unisa.it>  
Vincenzo Carletti <vcarletti@unisa.it>

### Important Dates

Contest registration opening: November 30, 2013  
ICPR2014 paper submission: December 20, 2013  
Submission of the executables: April 4, 2014  
Submission of the abstracts: April 24, 2014

### For more information

E-mail: [icpr2014biograph@gmail.com](mailto:icpr2014biograph@gmail.com)  
Web: <http://biograph2014.unisa.it>

### Competition task

The competition is about the application of graph matching algorithms for solving the problem of finding a pattern structure in a graph database containing molecules, protein structures and interaction networks.

The contest organizers will provide the participants with the entire original dataset needed to perform the task.

During the experimental phase of the competition, the graphs, both target and pattern, contained in the dataset will have their nodes randomly permuted.

A competitor will propose a graph matching algorithm, either exact or inexact, to find a pattern graph (subgraph) inside a target one. Since the solution can be either exact or approximate, each algorithm will be judged using three kinds of indices: accuracy, time and memory requirements.

Arrangements are being made to publish the contest results and a selection of papers describing the participant algorithms on a special issue of an international journal.

