Special Issue of IEEE/ACM Trans. on Comp. Biology and Bioinformatics
on
Graph Matching Algorithms for Pattern Search in Biological Databases

Call for Papers

Graphs are a powerful data structure that can be applied to several problems in bioinformatics. For instance, 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.
Graph matching within a biological database is a very computationally-intensive problem, especially because of the size of the graphs involved. For instance, if we consider a generic protein database, while a pattern can be a small graph of ten nodes, a complete protein graph, where the pattern is to be searched, can have thousands of nodes and edges. So the number of candidate solutions for all the proteins can be huge.

In order to assess the state-of-the-art about graph matching algorithms suitable for bioinformatics graphs, using both exact and inexact approaches, we have organized the first International Contest on Graph Matching Algorithms for Pattern Search in Biological Databases, that has been hosted by the 22nd edition of the International Conference on Pattern Recognition (ICPR2014), in Stockholm, on August 24, 2014. The participating algorithms have been evaluated considering their time and space requirements, and, for the inexact ones, the accuracy of the found solutions.
The topic of the contest and of this Special Issue has been chosen so as to be attractive for both researchers working on graph-based Pattern Recognition, such as the IAPR-TC15 community, and for researchers whose interests are more related to the bioinformatics applications, with the added value of promoting the interchanges between these communities.

The proposed Special Issue of Trans. on Computational Biology and Bioinformatics will be used to provide the readers with a detailed description of the best approaches presented to the contest, and of other state-of-the-art matching algorithms, highlighting their relationships with the existing literature, the underlying theoretical foundations, and the experimental results achieved on the contest datasets and possibly on other databases. By having the papers describing the best performing matching methods gathered in a single place, the readers will be able to compare the strengths and the weak points of each of them, and thus will achieve a deeper insight on the problem and a precious reference information that will help in the choice of the algorithm or of the methodological approach to adopt to solve a specific pattern search problem in a biological database. Hence, the Special Issue has the potential to become an essential source of citations for all the future research work in this field.

The submission is open also to authors that have not participated to the ICPR 2014 Contest; in this case, the authors are warmly recommended to use in the experimental part of their papers the dataset published for the contest, that may be obtained at the address: `http://biograph2014.unisa.it`

Submission instructions
The papers must be submitted following the author instructions of the journal, that can be found at the address:
`http://www.computer.org/portal/web/tcbb/author`
In particular, authors should adhere to the guidelines for regular papers (max. 14 double-column pages).
The submission will be done using the IEEE ScholarOne portal for the TCBB journal; during the submission procedure, the authors must specify, as the Manuscript Type, "Special Issue on Graph Matching Algorithms". Submissions will be open from November 24 to December 24, 2014.

Important Dates

Manuscript submission opening:	November 24, 2014
Manuscript submission deadline:	December 24, 2014
First notification:	February 28, 2015
Revised manuscript submission:	March 20, 2015
Notification of final decision:	April 15, 2015
Tentative publication date of special issue:	July/August 2015

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