CALL FOR PAPERS

2nd International Workshop on Biological Knowledge Discovery and Data Mining (BIOKDD'10)

Held in parallel with

21st International Conference on Database and Expert Systems Applications (DEXA'10)

www.dexa.org

Bilbao, Spain

August 30-September 3, 2010

With the development of Molecular Biology during the last decades, we are witnessing an exponential growth of both the volume and the complexity of biological data. For example, the *Human Genome Project* provided the sequence of the 3 billion DNA bases that constitute the human genome. And, consequently, we are provided too with the sequences of about 100,000 proteins. Therefore, we are entering the post-genomic era: after having focused so many efforts on the accumulation of data, we have now to focus as much effort, and even more, on the analysis of these data. Analyzing this huge volume of data is a challenging task because, not only, of its complexity and its multiple and numerous correlated factors, but also, because of the continuous evolution of our understanding of the biological mechanisms. Classical approaches of biological data analysis are no longer efficient and produce only a very limited amount of information, compared to the numerous and complex biological mechanisms under study. From here comes the necessity to use computer tools and develop new *in silico* high performance approaches to support us in the analysis of biological data and, hence, to help us in our understanding of the other hand, genetic and biochemical mechanisms. *Knowledge Discovery and Data Mining* (KDD) are a response to these new trends.

Topics of BIOKDD'10 workshop include, but not limited to:

Data Preprocessing: Data Storage, Representation and Management, Data Cleaning, Feature Extraction, Feature Selection.

Data Mining: Biological Data Clustering/Biclustering, Biological Data Classification, Biological Data Regression, Association Rule Learning from Biological Data, Parallel/Cloud/Grid Computing for Biological Data Mining, Text Mining and Application to Biological Sequences, Web Mining and Application to Biological Data, Analysis of Biological Networks.

Data Postprocessing: Knowledge Filtering, Knowledge Representation and Visualization, Knowledge Combination and Integration, Error Rates and Numerical Indicators.

PAPER SUBMISSION DETAILS: Authors are invited to submit electronically original contributions in English. Submitted should exceed in **IEEE** format papers not 5 pages <www.ieee.org/web/publications/authors/transjnl/index.html>. All accepted papers will be published in the proceedings of DEXA'10 Workshops with IEEE CSP. One of the authors of an accepted paper must register to DEXA'10 conference and present the paper at BIOKDD'10 workshop. For submission paper registration and electronic see <http://confdriver.ifs.tuwien.ac.at/dexa2010/>, starting from January 2010.

IMPORTANT DATES:Submission of Full Papers: March 30, 2010Notification of Acceptance: April 20, 2010Camera-ready Copies: May 17, 2010

PROGRAM COMMITTEE:

Mourad Elloumi, UTIC, University of Tunis, Tunisia (PC Co-Chair) Jin-Kao Hao, LERIA, University of Angers, France (PC Co-Chair) Esko Ukkonen, University of Helsinki, Finland El Ghazali Talbi, University of Lille, INRIA, CNRS, France Albert Y. Zomaya, The University of Sydney, Australia Madhu Chetty, Monash University, Australia Béatrice Duval, University of Angers, France Nadia Pisanti, University of Pisa, Italy Mohammed Sohel Rahman, King's College, London, UK Sandrine Dudoit, University of California, Berkeley, USA Raffaele Giancarlo, Università degli Studi di Palermo, Italy Francesc Rosselló, University of the Balearic Islands in Mallorca, Spain Gabriel Valiente, Technical University of Catalonia, Spain Giorgio Valentini, Università degli Studi di Milano, Italy Matteo Rè, Università degli Studi di Milano, Italy Pierre Peterlongo, IRISA-INRIA, Rennes, France Alexandros Stamatakis, Technische Universität München, Germany Mohamed Elati, University of Evry Val-d'Essonne, France Michael Ng, Hong Kong Baptist University, Hong Kong Roderic Guigo, Genome Informatics Research Laboratory, Spain Alfredo Pulvirenti, University of Catania, Italy Jason H. Moore, Dartmouth Medical School, USA Dragan Bosnacki, Eindhoven University of Technology, The Netherlands Carlo Cattani, University of Salerno, Italy Giulio Pavesi, Università degli Studi di Milano, Italy Matteo Comin, University of Padova, Italy Luonan Chen, Osaka Sangyo University, Japan Chiara Epifanio, Università degli Studi di Palermo, Italy Graziano Pesole, University of Bari, Italy Elena Marchiori, Radboud Universityn, Nijmegen, The Netherlands Alioune Ngom, University of Windsor, Ontario, Canada Giulia Menconi, Istituto Nazionale di Alta Matematica, Roma, Italy Luca Bortolussi, Università di Trieste, Italy Jaume Bacardit, University of Nottingham, UK Rosalba Giugno, University of Catania, Italy Oleg Okun, The National Academy of Sciences of Belarus, Belarus Xiangchao Gan, University of Oxford, UK Florin Leon, Technical University of Iasi, Romania Mihai Horia Zaharia, Technical University of Iasi, Romania Xingming Zhao, Shanghai University, China
