MLSB10

The Fourth International Workshop on Machine Learning in Systems Biology

15-16 October 2010, Edinburgh, Scotland

http://mlsb10.ijs.si/

Motivation

Molecular biology and all the biomedical sciences are undergoing a true revolution as a result of the emergence and growing impact of a series of new disciplines/tools sharing the "-omics" suffix in their name. These include in particular genomics, transcriptomics, proteomics and metabolomics, devoted respectively to the examination of the entire systems of genes, transcripts, proteins and metabolites present in a given cell or tissue type.

The availability of these new, highly effective tools for biological exploration is dramatically changing the way one performs research in at least two respects. First, the amount of available experimental data is not a limiting factor any more; on the contrary, there is a plethora of it. Given the research question, the challenge has shifted towards identifying the relevant pieces of information and making sense out of it (a "data mining" issue). Second, rather than focus on components in isolation, we can now try to understand how biological systems behave as a result of the integration and interaction between the individual components that one can now monitor simultaneously (so called "systems biology").

Taking advantage of this wealth of "genomic" information has become a conditio sine qua non for whoever ambitions to remain competitive in molecular biology and in the biomedical sciences in general. Machine learning naturally appears as one of the main drivers of progress in this context, where most of the targets of interest deal with complex structured objects: sequences, 2D and 3D structures or interaction networks. At the same time bioinformatics and systems biology have already induced significant new developments of general interest in machine learning, for example in the context of learning with structured data, graph inference, semi-supervised learning, system identification, and novel combinations of optimization and learning algorithms.

Objective

The aim of this workshop is to contribute to the cross-fertilization between the research in machine learning methods and their applications to systems biology (i.e., complex biological and medical questions) by bringing together method developers and experimentalists. We encourage submissions bringing forward methods for discovering complex structures (e.g. interaction networks, molecule structures) and methods supporting genome-wide data analysis.

Location and co-location

The workshop will take place 15-16 October 2010 at the Edinburgh International Conference Centre and the Informatics Forum of the University of Edinburgh. It will be part of the wokshop program of ICSB 2010, The 11th International Conference on Systems Biology (11-14 OCT 2010, http://www.icsb2010.org.uk/).

Submission instructions

We invite you to submit an extended abstracts of up to 4 pages describing new or recently published (2010) results, formatted according to the Springer Lecture Notes in Computer Science style. Each extended abstract must be submitted online via the Easychair submission system: http://www.easychair.org/conferences/?conf=mlsb10

The extended abstracts will be reviewed by the scientific programme committee. They will be selected for oral or poster presentation according to their originality and relevance to the workshop topics. Electronic versions of the extended abstracts will be accessible to the participants prior to the conference, distributed in hardcopy form to participants at the conference, and will be made publicly available on the conference web site after the conference. However, the book of abstracts will not be published and the extended abstracts will not constitute a formal publication.

We expect that authors of selected contributions will be invited to submit full papers to special issues of high-ranking Machine Learning/Systems Biology journals.

Key Dates

15 May: Submission site open
25 June: deadline for submission of extended abstracts
25 July: notification of acceptance
15-16 October: workshop

Topics

A non-exhaustive list of topics suitable for this workshop is given below:

Methods

Machine learning algorithms
Bayesian methods
Data integration/fusion
Feature/subspace selection
Clustering
Biclustering/association rules
Kernel methods
Probabilistic inference
Structured output prediction
Systems identification
Graph inference, completion, smoothing
Semi-supervised learning

Applications

Sequence annotation
Gene expression and post-transcriptional regulation
Inference of gene regulation networks
Gene prediction and whole genome association studies
Metabolic pathway modeling
Signaling networks
Systems biology approaches to biomarker identification
Rational drug design methods
Metabolic reconstruction
Protein function and structure prediction
Protein-protein interaction networks
Synthetic biology

MLSB10 program chairs

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Simon Rogers, University of Glasgow, UK
Guido Sanguinetti, University of Sheffield/University of Edinburgh, UK

Scientific program committee

Florence d'Alché-Buc, University of Evry, France
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Local organization

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