

# MLSB09

## Third International Workshop on Machine Learning in Systems Biology

5-6 September 2009, Ljubljana, Slovenia

<http://mlsb09.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 5-6 September 2009 at the Jozef Stefan Institute, Ljubljana, Slovenia. It will immediately precede ECML PKDD 2009, taking place 7-11 September 2009 in Bled, Slovenia (Bled is 30 miles from Ljubljana, transport will be organized).

**Submission deadline:** Submit extended abstracts for oral presentations by **1 June 2009**.

Other key dates: 25 June: notification for oral presentations

03 August: deadline for submission of abstracts for poster presentations

10 August: notification for posters & camera ready versions due

5-6 September: workshop

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

Methods	Applications
Machine learning algorithms	Sequence annotation
Bayesian methods	Gene expression and post-transcriptional regulation
Data integration/fusion	Inference of gene regulation networks
Feature/subspace selection	Gene prediction and whole genome association studies
Clustering	Metabolic pathway modeling
Biclustering/association rules	Signaling networks
Kernel methods	Systems biology approaches to biomarker identification
Probabilistic inference	Rational drug design methods
Structured output prediction	Metabolic reconstruction
Systems identification	Protein function and structure prediction
Graph inference, completion, smoothing	Protein-protein interaction networks
Semi-supervised learning	Synthetic biology

**The history and future of MLSB:** Inspired by the workshop on Probabilistic Modeling and Machine Learning in Structural and Systems Biology organized in Finland in 2006, the first MLSB workshop was organized in Evry in September 2007. Following its success, the second MLSB workshop was organized in Brussels in September 2008.

Both workshops were attended by about 80 researchers (each) interested in applying machine learning to systems biology, who gathered and exchanged experiences and research ideas in a very fruitful two-day single session event. The scientific program was based on invited talks given by internationally renowned speakers, oral presentations of peer-reviewed original works, as well as poster sessions. Revised versions of (selected) papers are (being) published in BMC Proceedings.

The unanimous opinion of the attendees and organizers was that MLSB should become a recurrent annual event, keeping the same single session format. It should also alternate between co-location with Machine Learning and Systems Biology events: MLSB 2010 should thus be co-located with ICSB to take place in Edinburgh in October 2010.

**Submissions instructions:** For an oral presentation, please submit an extended abstract of maximum eight pages, formatted according to the Springer Lecture Notes in Computer Science style. Extended abstracts should be submitted online by **1 June 2009** via the EasyChair submission system at <http://www.easychair.org/conferences/?conf=mlsb09/>. The accepted submissions will be collected in the proceedings of the workshop. Selected papers will be published after the workshop in a special issue of an International Journal of Bioinformatics or Systems Biology.

## MLSB09 Program chairs

*Sašo Džeroski*, Jozef Stefan Institute, Ljubljana, Slovenia

*Pierre Geurts*, GIGA-Research, University of Liège, Belgium

*Juho Rousu*, Department of Computer Science, University of Helsinki, Finland

## MLSB09 Local organization

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