# MLSB⁰⁹ Workshop Schedule

Machine Learning in Systems Biology
5-6 September 2009, Ljubljana, Slovenia

## Saturday – 5 SEPTEMBER 2009

08:00      Registration desk open
08:50      Opening

## Session 1: Networks and function

09:00-10:00 **Invited Talk**

*Networking Genes and Drugs: Understanding Drug Mode of Action and Gene Function from Large-scale Experimental Data*
Diego di Bernardo

10:00-10:50 **Oral presentations**

*Predicting the functions of proteins in PPI networks from global information*
Hossein Rahmani, Hendrik Blockeel and Andreas Bender

*Integrated network construction using event based text mining*
Yvan Saeys, Sofie Van Landeghem and Yves Van de Peer

10:50-11:20 **Coffee break**

## Session 2: Biomarkers and disease

11:20-12:20 **Invited Talk**

*Quantitative Microscopy: Bridge Between "Wet" Biology and Computer Science*
Yannis Kalaidzidis

12:20-13:10 **Oral presentations**

*On utility of gene set signatures in gene expression-based cancer class prediction*
Minca Mramor, Marko Toplak, Gregor Leban, Tomaž Curk, Janez Demšar and Blaž Zupan

*Evaluation method for feature rankings and their aggregations for biomarker discovery*
Ivica Slavkov, Bernard Ženko, and Sašo Džeroski

## Session 3: Posters

13:10-15:10 *Poster presentations with catered lunch and coffee*

## Session 4: Development, signalling

15:10-16:00 **Oral presentations**

*Matching models to data in modelling morphogen diffusion*
Wei Liu and Mahesan Niranjan

*Evaluation of signaling cascades based on the weights from microarray and ChIP-seq data*
Zerrin Isik, Volkan Atalay and Rengül Çetin-Atala

16:00-17:00 **Invited Talk**

*Synthetic Biology: Achievements and Prospects for the Future*
Roman Jerala

17:00      Community meeting
19:00      Guided walk through Ljubljana
20:00      Conference dinner

## Sunday– 6 SEPTEMBER 2009

### Session 5: Machine learning methodology

09:00-10:00 **Invited Talk**

*Machine Learning Methods for Protein Analyses*
William Stafford Noble

10:00-10:50 **Oral presentations**

*A comparison of AUC estimators in small-sample studies*
Antti Airola, Tapio Pahikkala, Willem Waegeman, Bernard De Baets and Tapio Salakoski

*Accuracy-rejection curves (ARCs) for comparison of classification methods with reject option*
Malik Sajjad Ahmed Nadeem, Jean-Daniel Zucker and Blaise Hanczar

10:50-11:20 **Coffee break**

### Session 6: Function prediction

11:20-12:20 **Invited Talk**

*Ontologies for Systems Biology*
Nick Juty

12:20-13:10 **Oral presentations**

*Hierarchical cost-sensitive algorithms for genome-wide gene function prediction*
Nicolo' Cesa-Bianchi and Giorgio Valentini

*Simple ensemble methods are competitive with state-of-the-art data integration methods for gene function prediction*
Matteo Re and Giorgio Valentini

### Session 7: Posters

13:10-15:10 *Poster presentations with catered lunch and coffee*

### Session 8: Phenotype prediction

15:10-16:00 **Oral presentations**

*A Subgroup Discovery Approach for Relating Chemical Structure and Phenotype Data in Chemical Genomics*
Lan Umek, Petra Kaferle, Mojca Mattiazzi, Aleš Erjavec, Črtomir Gorup, Tomaž Curk, Uroš Petrovič and Blaž Zupan

*Evaluation of methods in GA studies: yet another case for Bayesian networks*
Gábor Hullám, Peter Antal, Csaba Szalai and András Falus

16:00-17:00 **Invited Talk**
*On the Automation of Science*
Ross D. King

17:00 Discussion and closing remarks

18:00 Shuttle to Bled (for ECML/PKDD participants)