

# **Workshop Schedule**

Machine Learning in Systems Biology 15 - 16 October 2010, Edinburgh, Scotland

Friday – 15th October, 2010

08:30 Registration desk open

09:00-09:10 Welcome

#### Session 1

09:10-10:10 Invited Talk

Exploring transcription regulation through cell-to-cell variability

Nir Friedman

# 10:10-11:00 Oral presentations

Identifying proteins involved in parasitism by discovering degenerated motifs

Celine Vens, Etienne Danchin and Marie-Noelle Rosso

High throughput network analysis

Sumeet Agarwal, Gabriel Villar and Nick Jones.

11:00-11:30 Coffee break

### Session 2

11:30-12:30 Invited Talk

Computational environments for modeling biochemical networks

Ursula Kummer

# 12:30-13:20 Oral presentations

Equation Discovery for Whole-Body Metabolism Modelling

Marvin Meeng, Arno Knobbe, Arne Koopman, Jan Bert van Klinken and Sjoerd van den Berg

Parameter Estimation in an Endocytosis Model

Katerina Taškova, Peter Korošec, Jurij Šilc, Ljupčo Todorovski and Sašo Džeroski

# Poster session A

13:20-14:45 Poster presentations with catered lunch

#### Session 3

14:45-15:45 Invited Talk

Deep sequencing and systems biology: steps on the way to an individualised treatment of cancer patients Hans Lehrach

15:45-16:15 Coffee break

# **Session 4**

# 16:15-17:30 Oral presentations

Inferring Regulatory Networks from Expression Data using Tree-based Methods

Vân Anh Huynh-Thu, Alexandre Irrthum, Louis Wehenkel and Pierre Geurts

Inference in hierarchical transcriptional network motifs

Andrea Ocone and Guido Sanguinetti

On Learning Gene Regulatory Networks with Only Positive Examples

Luigi Cerulo and Michele Ceccarelli

17:30-18:00 Community meeting

19:30 Conference dinner



# **Workshop Schedule**

Machine Learning in Systems Biology 15 - 16 October 2010, Edinburgh, Scotland

# Saturday- 16th OCTOBER 2010

# Session 5

09:00- 10:00 Invited Talk

Protein-protein network inference with regularized output and input kernel methods

Florence d'Alché Buc

10:00-10:50 Oral presentations

Collaboration-based Function Prediction in Protein-Protein Interaction networks

Hossein Rahmani, Hendrik Blockeel and Andreas Bender

Prediction of DNA-Binding Proteins from Structural Features

Andrea Szabóová, Ondrej Kuzelka, Filip Zelezný and Jakub Tolar

10:50-11:20 Coffee break

#### Session 6

11:20-12:20 Invited Talk

Automatic quantification of subtle cellular phenotypes in microscopy-based high-throughput experiments Vebjorn Ljosa

12:20-13:10 Oral presentations

On the stability and interpretability of prognosis signatures in breast Cancer

Anne-Claire Haury and Jean-Philippe Vert

A fast algorithm for structured gene selection

Sofia Mosci, Silvia Villa, Alessandro Verri and Lorenzo Rosasco

# Poster session B

13:10-14:15 Poster presentations with catered lunch

## **Session 7**

14:15-15:05 Oral presentations

Automated detection of chaotic and oscillatory regimes

Daniel Silk, Paul Kirk, Christopher Barnes and Michael Stumpf *A note on Inference for reaction kinetics with monomolecular reactions* 

Manfred Opper and Andreas Ruttor

15:05-15:30 Coffee break

### Session 8

15:30-16:20 Oral presentations

Multilabel Prediction of Drug Activity

Hongyu Su, Markus Heinonen and Juho Rousu

An Integrated Generative and Discriminative Bayesian Model for Binary Classification

Keith Harris and Mark Girolami

16:20 Closing remarks