WCSB 2010 Poster Session 1, WEDNESDAY, June 16, 14:40-16:10

1. J. Kesseli et al., Introducing correlations into mean-field Boolean network models
2. R. Schlatter et al., ON/OFF - A Boolean model of apoptosis
3. T. Merle et al., Complex update strategies for Probabilistic Boolean Networks
4. F. Fourrê et al., Coarse-graining of biochemical networks: a reduction method for noisy Boolean networks
5. T. Petrov et al., Maximal reduction of ODE semantics of rule-based models: syntax-independent setup
6. J. Seppälä et al., Comparison of four publicly available ChIP-seq alignment tools
7. P. V. Nazarov et al., Co-expression analysis of large microarray data sets using CoExpress software tool
8. M. Annala et al., Improving correlation between microarrays and transcriptome sequencing through probe set analysis
9. M. Kurki et al., TAFFEL: Independent Enrichment Analysis of gene sets
10. V. Kivinen et al., Classifier design with pathway based feature selection
11. A. Travaglione et al., Time-scale analysis from fragmented PPIN
12. K-L. Aho et al., Construction of computational data analysis pipelines using a database and workflow system
13. L. Kong et al., Identification of genes involved in the differentiation process from human embryonic stem cells to neural progenitor cells

WCSB 2010 Poster Session 2, THURSDAY, June 17, 15:00-16:30

1. S. Simmuteit et al., Hierarchical Evolving Trees together with global and local learning for large datasets in MALDI Imaging
2. M. Farhan et al., An improved clump splitting method for convex objects
3. F.-M. Schleif et al., Efficient identification and quantification of metabolites in 1-H NMR measurements by a novel data encoding approach
4. F. Vallée et al., Elementary flux mode analysis of the central metabolism of plant cells
5. K. Kruse et al., An algorithm for knockout prediction in metabolic flux redirection
6. A. Halavatyi et al., Integrated approach for the analysis of fluorescence recovery after photobleaching (FRAP) intensities in live cells
7. G. Basler et al., Thermodynamic landscapes of randomized large-scale metabolic networks
8. O-P. Smolander et al., Characterizing the activity of a gene driven by the Tet-promoter at the population and at the single cell levels
9. H. Mannerström et al., Emulation of the delayed stochastic simulation algorithm with higher order Markov chains
10. V. Pakka et al., Switches and clocks in activator gene networks
11. J. Lloyd-Price et al., Detailed model of transcription and translation at the single nucleotide level
12. A. Larjo et al., Modeling heterogeneity of yeast cell population in bioreactor
13. T. Mäki-Marttunen et al. Modeling growth in neuronal cell cultures: Network properties in different phases of growth studied using two growth simulators
14. P. Ruusuvuori et al., Image-based phenotyping of complex yeast strains