

Dr. Evangelos Simeonidis

PUBLICATION LIST

PEER-REVIEWED JOURNAL ARTICLES

- P. Li, J.O. Dada, D. Jameson, I. Spasic, N. Swainston, K. Carroll, W. Dunn, F. Khan, H.L. Messiha, E. Simeonidis, *et al.* (2010) Systematic integration of experimental data and models in systems biology. *BMC Bioinformatics* (in press).
- P.D. Dobson, K. Smallbone, D. Jameson, E. Simeonidis, *et al.* (2010) Further developments towards a genome-scale metabolic model of yeast. *BMC Systems Biology*, **4**:145.
- E. Simeonidis, E. Murabito, K. Smallbone, H.V. Westerhoff (2010) Why does yeast ferment? A Flux Balance Analysis study. *Biochemical Society Transactions*, **38** (5), 1225-1229.
- H.V. Westerhoff, M. Verma, M. Nardelli, M. Adamczyk, K. Van Eunen, E. Simeonidis, B.M. Bakker (2010) Systems Biochemistry in practice: experimenting with modelling and understanding, with regulation and control. *Biochemical Society Transactions*, **38** (5), 1189-1196.
- K. Smallbone, E. Simeonidis, N. Swainston, P. Mendes (2010) Towards a genome-scale kinetic model of cellular metabolism. *BMC Systems Biology*, **4**:6.
- H.V. Westerhoff, C. Winder, H. Messiha, E. Simeonidis, M. Adamczyk, M. Verma, F.J. Bruggeman, W. Dunn (2009) Systems Biology: The elements and principles of Life. *FEBS Letters*, **583** (24), 3882-3890.
- E. Murabito, E. Simeonidis, K. Smallbone, J. Swinton (2009) Capturing the essence of a metabolic network: A Flux Balance Analysis approach. *Journal of Theoretical Biology*, **260** (3), 445-452.
- I. Spasić, E. Simeonidis, H.L. Messiha, N.W. Paton, D.B. Kell (2009) KiPar, a tool for systematic information retrieval regarding parameters for kinetic modelling of yeast metabolic pathways. *Bioinformatics*, **25** (11), 1404-1411.
- K. Smallbone, E. Simeonidis (2009) Flux Balance Analysis: A geometric perspective. *Journal of Theoretical Biology*, **258** (2), 311-315.
- M.J. Herrgård, N. Swainston, P. Dobson, W.B. Dunn, K.Y. Arga, M. Arvas, N. Blüthgen, S. Borger, R. Costenoble, M. Heinemann, M. Hucka, N. Le Novère, P. Li, W. Liebermeister, M.L. Mo, A.P. Oliveira, D. Petranovic, S. Pettifer, E. Simeonidis, *et al.* (2008) A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. *Nature Biotechnology*, **26**, 1155 – 1160.
- K. Smallbone, E. Simeonidis, D.S. Broomhead, D.B. Kell (2007) Something from nothing: Bridging the gap between constraint-based and kinetic modelling. *FEBS Journal*, **274** (21), 5576-5585.
- L. Dartnell, E. Simeonidis, M. Hubank, S. Tsoka, I.D.L. Tsoka, L.G. Papageorgiou (2005) Robustness of the p53 network and biological hackers. *FEBS Letters*, **579** (14), 3037-3042.
- E. Simeonidis, M.E. Lienqueo, S. Tsoka, J.M. Pinto, L.G. Papageorgiou (2005) MINLP models for the synthesis of optimal peptide tags and downstream protein processing. *Biotechnology Progress*, **21** (3), 875-884.
- E. Simeonidis, S.C.G. Rison, J.M. Thornton, I.D.L. Bogle, L.G. Papageorgiou (2003) Analysis of biochemical networks using a pathway distance metric through linear programming. *Metabolic Engineering*, **5** (3), 211-219.

PEER-REVIEWED CONFERENCE PROCEEDINGS ARTICLES

- E. Simeonidis, J.M. Pinto and L.G. Papageorgiou (2005) An MILP model for optimal design of

purification tags and synthesis of downstream processing. In *European Symposium on Computer-Aided Process Engineering-15*, L. Puigjaner and A. Espuña (eds.), pp. 1537-1542.

E. Simeonidis, L. Dartnell, I.D.L. Bogle and L.G. Papageorgiou (2005) Analysis of biochemical networks using linear programming, *7th World Congress of Chemical Engineering*, Glasgow, Scotland, UK.

E. Simeonidis, J.M. Pinto and L.G. Papageorgiou (2004) Optimal peptide tag design and synthesis of downstream protein processing. In *European Symposium on Computer-Aided Process Engineering-14*, A. Barbosa-Povoa and H. Matos (eds.), pp.289-294.

ARTICLES IN PREPARATION

E. Simeonidis, K. Smallbone, *et al.* Kinetic model of the trehalose cycle. *Methods in Enzymology* (submitted).

E. Simeonidis, L.G. Papageorgiou. A method for lattice protein folding prediction based on Mathematical Programming (in preparation).

N. Malys, E. Simeonidis, *et al.* A systems biology pipeline for biochemical networks: Application to yeast glycolysis. *Molecular Systems Biology* (in preparation).

INVITED SPEAKER

E. Simeonidis (2010) The systems biology of metabolism and computational challenges, *Austrian Centre of Industrial Biotechnology*, Vienna, Austria.

E. Simeonidis (2009) A systems biology approach to genome-scale modelling of cellular metabolism, *Interdisciplinary Bioscience Research Conference*, Manchester, UK.

E. Simeonidis (2008) MCISB and Systems Biology, *Yeast Systems Biology Network: Web Services*, Bordeaux, France.

E. Simeonidis (2007) Bridging the gap between constraint-based and kinetic modelling, *MIB Seminar Series*, Manchester, UK.

B. Papp, E. Simeonidis (2007) Flux Balance Analysis and its applications, *BioSysBio 2007*, Manchester, United Kingdom (abstract published in *BMC Systems Biology*, **1** (S1), 77).

CONFERENCE PRESENTATIONS (ORAL)

E. Simeonidis, E. Murabito, K. Smallbone, H. Westerhoff (2010) Why does yeast ferment? A Flux Balance Analysis study, *Systems Biochemistry*, York, UK.

E. Simeonidis, D. Jameson, W. Dunn, H. Westerhoff (2010) Proofing Systems Biology, *BBSRC Systems Biology Workshop*, Edinburgh, UK.

E. Simeonidis, K. Smallbone, D.S. Broomhead, D.B. Kell (2007) Bridging the gap between constraint-based and kinetic modelling, *SysBioHealth Symposium 2007*, University of Milano-Bicocca, Milan, Italy.

E. Simeonidis, J.M. Pinto, L.G. Papageorgiou (2005) An MILP model for optimal design of purification tags and synthesis of downstream processing. *ESCAPE-15*, Barcelona, Spain.

E. Simeonidis, L. Dartnell, I.D.L. Bogle, L.G. Papageorgiou (2005) Analysis of biochemical networks using linear programming, *7th World Congress of Chemical Engineering*, Glasgow, Scotland, UK.

- E. Simeonidis, J.M. Pinto, L.G. Papageorgiou (2004) Optimal peptide tag design and synthesis of downstream protein processing. *ESCAPE-14*, Lisbon, Portugal.
- E. Simeonidis, S.C.G. Rison, J.M. Thornton, I.D.L. Bogle, L.G. Papageorgiou (2002) Use of a pathway distance metric through linear programming for the analysis of metabolic networks. *Metabolic Engineering IV: Applied Systems Biology*, Il Ciocco, Italy.
- E. Simeonidis, E. Stivaktakis, M. Mitrakas (1999) Bromate ions: Formation – Control Methods – Removal techniques, *Environmental Technology for the 21st Century*, Thessaloniki, Greece.

SELECTED POSTER PRESENTATIONS

- O.J. Oshota, N. Malys, E. Simeonidis, W.B. Dunn, P. Mendes (2010) A systems biology approach to the production of red and white biotechnological products through systematic in silico studies, *Metabolic Engineering VIII*, Jeju Island, South Korea.
- K. Smallbone, P.D. Dobson, P. Pir, D. Jameson, E. Simeonidis, N. Swainston *et al.* (2010) Yeast 4.0 : A genome-scale reconstruction with improved lipid metabolism, *Systems Biochemistry*, York, UK.
- E. Simeonidis, *et al.* (2009) The Manchester Centre for Integrative Systems Biology, *FEBS-SysBio2009: The 3rd FEBS Advanced Lecture Course on Systems Biology: From Molecular Biology to Biological Function*, Alpbach, Austria.
- D. Weichart, E. Simeonidis, *et al.* (2008) Quantification of yeast metabolism: Glycolysis as a test case, *9th International Conference on Systems Biology*, Gothenburg, Sweden.
- K. Smallbone, E. Simeonidis, D.S. Broomhead, D.B. Kell (2008) Towards a genome-scale kinetic model of cellular metabolism, *9th International Conference on Systems Biology*, Gothenburg, Sweden.
- E. Simeonidis, H. Messiha, *et al.* (2008) A kinetic model of the trehalose pathway in *Saccharomyces cerevisiae*, *9th International Conference on Systems Biology*, Gothenburg, Sweden.
- D. Weichart, J. Wishart, I. Spasic, K. Carroll, H. Messiha, N. Malys, E. Simeonidis, *et al.* (2008) Quantification of yeast metabolism: Applications to glycolysis, *Genomes to Systems 2008*, Manchester, UK.
- K. Smallbone, E. Simeonidis, D.S. Broomhead, D.B. Kell (2008) Towards a full kinetic model of cellular metabolism: A linlog kinetics approach to metabolic modelling, *Genomes to Systems 2008*, Manchester, UK.
- I. Spasic, E. Simeonidis, N. Paton, D.B. Kell (2008) Systematic screening of yeast kinetic parameters for metabolic models using a text mining toolbox, *Genomes to Systems 2008*, Manchester, UK.
- E. Murabito, E. Simeonidis, F. Bruggeman (2007) Selecting among the multiple alternate optimal solutions of the Flux Balance Analysis of yeast metabolism: Use of the adaptational potential of the organism, *8th International Conference on Systems Biology*, Long Beach, California, USA.
- I. Spasic, E. Simeonidis, *et al.* (2007) Systematic screening of yeast kinetic parameters for metabolic models using a text mining toolbox, *8th International Conference on Systems Biology*, Long Beach, USA.
- K. Smallbone, E. Simeonidis, *et al.* (2007) Bridging the gap between constraint-based and kinetic modelling, *8th International Conference on Systems Biology*, Long Beach, California, USA.