

Dr. Evangelos Simeonidis

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RESEARCH EXPERIENCE

2006 - present *Mathematical modeller (Post-doc)*

Manchester Centre for Integrative Systems Biology, University of Manchester, UK

I work as an Experimental Officer for the Manchester Centre for Integrative Systems Biology (MCISB) at the University of Manchester. My research focuses on the development of mathematical models for the analysis of biological systems. I am officially affiliated with the School of Chemical Engineering and Analytical Science (CEAS). I work with Professors Hans Westerhoff (Director of MCISB and Professor of Systems Biology), Pedro Mendes (Chair of Computational Biology) and Douglas Kell (Chair in Bioanalytical Science and currently BBSRC Chief Executive). My responsibilities include:

- producing quantitative mathematical models of complex biological systems, ultimately leading to whole-cell models. The research mainly focuses on the metabolism of baker's yeast;
- building kinetic, ODE-based models to describe metabolic pathways;
- using constraint-based and control theory approaches (e.g. Flux Balance Analysis (FBA), Metabolic Control Analysis (MCA) or Elementary Mode Analysis) for larger models, up to genome scale;
- utilising data standards for systems biology models (e.g. SBML, ontologies, etc.) and integrating them with other -omics data standards;
- developing methods for the visualisation of complex biological networks;
- contributing towards the development of new research areas and attracting new funding;
- teaching for the Doctoral Training Centre for Systems Biology, attached to the MCISB

2005 *Research Assistant*

University College London, London, United Kingdom

During this six-month post-doc, I had the chance to complete and extend my work on the research areas and issues which were left open after the completion of my PhD. I worked on the application of mathematical programming to protein folding, and the design of purification tags for protein purification.

EDUCATION

2000 - 2005

PhD in Chemical Engineering,
University College London, UK

May 2005

Research Project: Optimisation of Biochemical Systems

The goal of my PhD was the application of mathematical programming and optimisation methodologies to problems of biological and biochemical nature. My work was performed on the interface of Systems Biology, Metabolic Engineering, Optimisation and Process Systems Engineering. The main research areas that I examined were: Systems Biology, Metabolic Pathways, Protein Folding, p53 Apoptotic Control Network and Synthesis of Peptide Purification Tags for Downstream Protein Processing.

- 1999 - 2000** *MSc in Process Systems Engineering* *September 2000*
 Imperial College, London, UK (Centre for Process Systems Engineering)
Research Project: A re-configurable supply chain simulation system
 Utilising object-oriented technology (C++), I developed a library of flexible, connectable supply chain objects for the modelling of multi-echelon inventory management systems.
- 1993 - 1999** *Diploma in Chemical Engineering* *July 1999*
 Aristotle University of Thessaloniki, Greece
Research Project: Spectrophotometric determination of bromate ions using phenothiazines
 I developed a method for determining the concentration of bromate ions (suspected to be tumourigenic) in drinking water. This was a nine-month experimental project that required daily operation of a spectrophotometer.
- 1987 - 1993** *Secondary Education*
Anatolia, American College of Thessaloniki, Greece

RESEARCH FUNDING

- Grants** Attracting new funding is part of my responsibilities in MCISB. I am currently participating and contributing as named researcher in a number of MCISB grant applications to national (e.g. the Biotechnology and Biological Sciences Research Council – <http://www.bbsrc.ac.uk>) and international (e.g. European Union FP7 grants) bodies. Many of these applications are pending. I was also a named researcher on MOSES, a project funded under the SysMO initiative (<http://www.sysmo.net>), a joint research activity of ERASysBio (<http://www.erasysbio.net/>). In addition, I am participating in grant applications outside the MCISB; examples of pending proposals include:
- Multiscale analysis of complex networks in systems biology. *Funding body:* COST (<http://www.cost.esf.org/>); €400,000
 - Epigenetics and innovative applications. *Funding body:* Thalis, Greek Ministry of Education; €510,000
 - From reconstruction to model: Collaborative tool development to automate network reconstructions and improve their predictive power in Systems Biology. *Funding body:* US Partnership Awards, BBSRC; £50,000
- Industrial partners** I am the main contact person for MCISB for a planned collaboration with UCB, a pharmaceutical company. The proposed research is now in the last stages of being finalised. The proposed collaboration is planned to last for a minimum of 3 years at a cost of in excess of £1,000,000.
- Personal awards** Centre for Process Systems Engineering (Imperial) Scholarship (2000; £36,000)
 EPSRC Scholarship (2001; £12,000)
 Several small travel grants from the UCL Graduate School (2001-2005)
 Marie Curie Fellowship (2004; travel grant)
 Four International Travel Grants, Royal Academy of Engineering (2005, 2007, 2008, 2009)

PUBLICATIONS

PEER REVIEWED PUBLICATIONS

- K. Smallbone, E. Simeonidis, N. Swainston and 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 and J. Swinston (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, *et al.* (2009) KiPar, a tool for systematic information retrieval regarding parameters for kinetic modelling of yeast metabolic pathways. *Bioinformatics*, **25** (11), 1404-1411.
- K. Smallbone and 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 and D.B. Kell (2007) Something from nothing: Bridging the gap between constraint-based and kinetic modelling. *FEBS Journal*, **274** (21), 5576-5585.
- 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.
- L. Dartnell, E. Simeonidis, *et al.* (2005) Robustness of the p53 network and biological hackers. *FEBS Letters*, **579** (14), 3037-3042.
- E. Simeonidis, M.E. Lienqueo, *et al.* (2005) MINLP models for the synthesis of optimal peptide tags and downstream protein processing. *Biotechnology Progress*, **21** (3), 875-884.
- 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.
- E. Simeonidis, S.C.G. Rison, *et al.* (2003) Analysis of biochemical networks using a pathway distance metric through linear programming. *Metabolic Engineering*, **5** (3), 211-219.

IN PREPARATION

- E. Simeonidis, E. Murabito, K. Smallbone, H.V. Westerhoff. Why does yeast ferment? A Flux Balance Analysis study. *Biochemical Society Transactions* (submitted).
- P. Dobson, K. Smallbone, K. Lanthaler, D. Jameson, E. Simeonidis, N. Swainston, W.B. Dunn, D. Hull, C. Lu, M.L. Mo, O. Oshota, P. Pir, N. Stanford, A. Villeger, D. Weichart, R.D. King, S.G. Oliver and P. Mendes. Yeast 4.0: A consensus network reconstruction of lipid metabolism. *BMC Systems Biology* (submitted).
- E. Simeonidis, K. Smallbone, *et al.* Kinetic model of the trehalose cycle. *Methods in Enzymology* (in preparation).
- E. Simeonidis and L.G. Papageorgiou. A method for lattice protein folding prediction based on Mathematical Programming (in preparation).
- P. Li, J.O. Dada, D. Jameson, I. Spasic, N. Swainston, E. Simeonidis, *et al.* Systematic integration of experimental data and models in systems biology. *Bioinformatics* (submitted).
- N. Malys, E. Simeonidis, *et al.* A systems biology pipeline for biochemical networks: Application to yeast glycolysis. *Molecular Systems Biology* (in preparation).

SELECTED ORAL PRESENTATIONS AND POSTERS

INTERNATIONAL CONFERENCE PRESENTATIONS

- 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 and H. Westerhoff (2010) Proofing Systems Biology, *BBSRC Systems Biology Workshop*, Edinburgh, 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. 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. 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.
- E. Simeonidis, B. Papp (2007) Flux Balance Analysis and its applications. *BioSysBio 2007: Systems Biology, Bioinformatics, Synthetic Biology*, Manchester, UK.
- E. Simeonidis, L. Dartnell, *et al.* (2005) Analysis of biochemical networks using linear programming. *7th World Congress of Chemical Engineering*, Glasgow, Scotland, UK.
- E. Simeonidis, S.C.G. Rison, *et al.* (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.
- S.C.G. Rison, E. Simeonidis, *et al.* (2001) A rapid algorithm for generating minimal pathway distances. *9th International Conference on Intelligent Systems for Molecular Biology*, Copenhagen, Denmark.
- E. Simeonidis, E. Stivaktakis and M. Mitrakas (1999) Bromate ions: Formation – Control Methods – Removal techniques, *Environmental Technology for the 21st Century*, Thessaloniki, Greece.

INVITED SPEAKER

- 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: Systems Biology – Bioinformatics – Synthetic Biology*, Manchester, United Kingdom (abstract published in *BMC Systems Biology*, **1** (S1), 77).

SUPERVISION/MENTORING

- International mentoring** I have volunteered my services as a mentor for the ‘International Mentoring’ programme between the Biochemical Society and the University of Ibadan, Nigeria. The pilot project will develop a toolkit for building and maintaining mentoring relationships by email which can then be shared with other learned societies. My aim is to enhance the educational experience of students and early-career scientists by sharing scientific knowledge, providing a source of motivation and inspiration and offering advice.
- 2007 - present** Supervision of PhD students (University of Manchester):
- Ettore Murabito, “Understanding cancer metabolism using differential metabolic control analysis”, 2007-present.
 - Natalie Stanford, “Building a genome-scale kinetic model of yeast metabolism”, 2008-present.
 - Olusegun Oshota, “Identifying red and white biotechnological products through a systematic *in silico* gene deletion study”, 2008-present.
- 2007 - 2009** Supervision of research of a number of postgraduate students from the MCISB Doctoral Training Centre (DTC) for their rotation research projects (University of Manchester).
- 2004 - 2005** Supervision of the research of two postgraduate (MSc) students (University College London).
- 2001 - 2004** Supervision of postgraduate students, and Teaching Assistant in the Process Engineering MSc course at the Chemical Engineering Department (University College London).

TEACHING EXPERIENCE

- 2009** Course coordinator of Data Analysis Unit for MRes in Translational Medicine (University of Manchester).
- 2006, 2007, 2009** Preparation and teaching of the Mathematics refresh course for the MCISB DTC (University of Manchester).
- 2007, 2008** Preparation and presentation of the Modelling and Flux Balance Analysis workshop for the MCISB DTC (University of Manchester).
- 2007** Preparation and teaching of the postgraduate course on Metabolic Engineering for the School of Chemical Engineering and Analytical Science (University of Manchester, Spring semester)
- 2000 - 2004** Teaching the use of GAMS software (General Algebraic Modelling System) to Chemical Engineering students (University College London).

OTHER ACTIVITIES

- Metabolic reconstructions** *Saccharomyces cerevisiae* reconstruction: I participate in a collaboration of leading groups in the field for the reconstruction of the metabolic network of yeast, which produced a consensus model of yeast metabolism. I played an integral role both in organising the meetings and helping with the annotation of reactions, metabolites and enzymes. Our efforts resulted in a group-wide publication in Nature Biotechnology (Herrgard et al., 2008. A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. *Nature Biotechnology*, 26:1155).
- Homo sapiens* reconstruction: This is an ongoing effort from experts on metabolism and human physiology to build a reconstruction for human metabolism based on community consensus. A number of reconstructions of the human metabolic network based on genomic and literature data have been published in the past, but with significant differences. The aim of the research groups working together on this project is to merge these reconstructions. On 3 occasions (Manchester and Gothenburg 2008, Reykjavik 2009), we concentrated on accumulating, reviewing and curating the biochemistry, genetics and genomics of human metabolism.

- Project manager** I recently served as interim Project Manager for MCISB, responsible for operation and coordination within the centre and for the progress of the project. I was also the contact point for the Centre, which provides a hub for activities in the UK and worldwide in the field of systems biology.
- BMNet** I am the founder and organiser of the BioModelling Network (BMNet); a network of researchers of Biological Modelling in MIB and in the University of Manchester. The network provides a platform for its members to collaborate, and further explore the field of biological modelling. Equally, we organise lectures and events related to common interests. More details can be found at BMNet's official website (<http://www.mcisb.org/bmnet>).
- Refereeing** BioSystems (2008)
FEBS Journal (2007)
European Symposium for Computer Aided Process Engineering (2005)
International Conference on Computer Aided Metabolic Engineering (2005)
European Symposium for Computer Aided Process Engineering (2004)
- Service** I have organised a series of research-related workshops, lectures, seminars and meetings, as part of the MCISB's and BMNet's mission to disseminate Systems Biology. I am furthermore a member of the scientific and organising committee of the annual Manchester Interdisciplinary Bioscience conference.

GENERAL

- Nationality** Greek
- DOB** 27/04/1975
- Languages** English (fluent), French (intermediate), German (basic), Dutch (learning), Greek (native)
- Professional memberships** Member of the International Society for Systems Biology
Member of the Biochemical Society
Affiliate member of the Institution of Chemical Engineers (IChemE)
Member of the Yeast Systems Biology Network (YSBN)
Member of the Technical Chamber of Greece (TEE-TCG)
- Computer skills** Excellent knowledge of modelling tools, optimisation computer packages and Systems Biology software tools (*e.g.* GAMS, MATLAB, COPASI, and others)
Frequent user of Systems Biology Markup Language (SBML) and other systems biology standards
Good programming skills and fair knowledge of programming languages such as C++, Perl, FORTRAN
Extremely familiar with both UNIX and Windows and most popular commercial programs and packages for the two operating systems
Fair grasp of Mathematica
- Hobbies & interests** I have a great interest in basketball; I am a player, certified referee and coach. I was treasurer and coach of the UCL Union Men Basketball Club for the 4 years I played for them, awarded Full Colours for services in '02, '03 and '04. I currently play for the Tropics in the Manchester Area Basketball League (MABL). I enjoy a variety of outdoors activities such as skiing, hiking, rafting, etc. My interests also include reading, cinema, and dancing.