

■ MADS T. BONDE



Mads T. Bonde

Current Position. Ph.D. candidate at the Novo Nordisk Foundation Center for Biosustainability. Advisor: Morten O.A. Sommer.

Education. B.S., M.S. Technical University of Denmark, Thesis project at Harvard Medical School with Harris H. Wang, Sriram Kosuri, and George M. Church.

Nonscientific Interests. I enjoy sailing, spending time with my wife and kids, and leading the company Labster, which I founded during my studies (www.labster.com).

I am a researcher and entrepreneur with a focus on radical innovation in biotech research and education. My research is focused on accelerated development of cell factories with novel methods utilizing DNA chips, bioinformatics, and biological circuits. In the featured article, we present the novel method MO-MAGE that enables large-scale mutagenesis of several thousand genomic targets at once. The method radically expands the scope of genome engineering projects and has the potential to greatly impact future synthetic biology and metabolic engineering projects. I have invented the laboratory simulation platform Labster with documented learning effectiveness (Bonde *et al.* (2014) *Nat. Biotechnol.*), which is now being used by thousands of students at universities globally including Massachusetts Institute of Technology, Stanford University, and Hong Kong University. (Read Bonde's article; DOI: 10.1021/sb5001565.)

■ YOICHIRO ITO



Yoichiro Ito

Current Position. Senior Postdoctoral Fellow, Technology Research Association of Highly Efficient Gene Design, Japan.

Education. Ph.D, Saitama University, Japan. Advisor: Prof. Yuzuru Husimi. Postdoctoral Fellow, Osaka University, Japan. Advisor: Prof. Tetsuya Yomo.

Nonscientific Interests. I enjoy spending time with my wife, my two sons and friends, and traveling.

My past research focused on directed evolution of proteins and promoter sequence. My current interest involves the microbial production of "Green" chemicals that utilize renewable resources and pharmaceuticals including antibodies, by combination of synthetic biology, metabolic engineering, and directed evolution. For effective production of the valuable compound of interest, control of enzyme expression level in each cascade reaction toward the target molecule is important. Thus, we created a robust and tunable expression system in yeast cells, using the synthetic biological approach. Furthermore, combination with a combinatorial screening technology can optimize the expression level of each enzyme. I believe that this article lays the groundwork for an enzyme expression platform with the potential to create a sustainable society in the near future. (Read Ito's article; DOI: 10.1021/sb500096y.)

■ ERNST OBERORTNER



Ernst Oberortner

Current Position. Postdoctoral Research Associate, Cross-disciplinary Integration of Design Automation Research (CIDAR) Group, Department of Electrical and Computer Engineering (ECE), Boston University. Advisor: Prof. Dr. Douglas Densmore.

Education. Ph.D., Vienna University of Technology. Advisors: Prof. Dr. Schahram Dustdar, Prof. Dr. Uwe Zdun. Undergraduate degree and M.Sc., Vienna University of Technology. Advisors: Prof. Dr. Schahram Dustdar.

Nonscientific Interests. Playing and watching any type of hockey; running; biking.

Synthetic Biology is a novel approach to engineer biological systems. Computer-Aided Design (CAD) tools and Languages facilitate the engineering process. Standards are inevitable to communicate the evolution of engineered synthetic biological systems. The Synthetic Biology Open Language (SBOL) community is an

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interdisciplinary group working closely together to define a standard. This paper proposes a more expressive and modular version of the SBOL standard, which covers the specification of functional and structural aspects of a synthetic biological system. (Read Oberortner's article; DOI: 10.1021/sb500176h.)

■ NICHOLAS ROEHNER



Nicolas Roehner

Current Position. Postdoctoral Research Fellow, Boston University, Douglas Densmore.

Education. Ph.D. in Bioengineering (2014), University of Utah, Chris J. Myers. B.S. in Bioengineering (2010), University of Washington, Suzie Pun.

Nonscientific Interests. I enjoy challenging myself outdoors through running, biking, and white water rafting. My hobbies include reading and playing/designing board games.

My primary research interest is in biodesign automation. In particular, I am most interested in the development of algorithms and techniques for the automated design of biological systems from abstract behavioral specifications. I am also interested in the development of standards and the reconciliation of biodesign automation tools with laboratory practice. I plan to apply my research to the design and construction of biological systems, ranging from genetic regulatory networks for sensing and computation to metabolic networks for biosynthesis and bioremediation. (Read Roehner's article; DOI: 10.1021/sb500176h.)

■ DAVEN SANASSY



Rouku Sanassy

Current Position. Ph.D. Candidate, Computing Science, Newcastle University, U.K. Advisor: Prof. Natalio Krasnogor.

Education. B.Sc. in Computer Science, University of Kent, U.K.

Nonscientific Interests. Programming, deadlifting, mixing drum, and bass records, video gaming, history, and politics.

My Ph.D. research has focused on the computational performance of stochastic simulation algorithms for biochemical systems. I have been working to address usability issues and allow these algorithms to scale with the computational demands of modern synthetic biological systems. I have shown that there is no fastest stochastic simulation algorithm for every biological model, and this paper presents an automated system to select the fastest algorithm for an arbitrary model. (Read Sanassy's article; DOI: 10.1021/sb500176h.)

■ CHRIS TAKAHASHI



Chris Takahashi

Current Position. Ph.D. candidate, University of Washington Seattle. Advisor: Eric Klavins.

Education. M.S. Control Systems, University of Michigan, Ann Arbor. B.S. Electrical Engineering, University of Washington, Seattle. B.S. Computer Engineering, University of Washington, Seattle.

Nonscientific Interests. In my spare time I enjoy amateur auto racing, apiculture, and hobby electronics.

I believe that synthetic biology is an exciting field that can greatly benefit from a multidisciplinary approach that combines biological sciences with abstractions and design philosophies inherited from engineering. In particular, I am excited about new tools and techniques that can be applied to synthetic biology. To that end, I am actively conducting research projects ranging from laboratory automation, to directed evolution, and cell strain ("chassis") engineering. Through my projects I hope to make synthetic biological experiments faster and more accessible to those who have useful insights and perspectives. In addition, I believe that more advanced and open source tools, such as the one found in my paper, should enable established synthetic biologists to explore new areas. (Read Takahashi's article; DOI: 10.1021/sb500165g.)

■ LEV TSIMRING



Lev Tsimring

Current Position. Research Scientist, BioCircuits Institute, University of California, San Diego.

Education. Ph.D. Physics, Institute of Oceanology, Moscow, Russian Academy of Sciences (1986). Advisor: Lev A. Ostrovsky. B.S. Radiophysics, Gorky State University (1980).

Nonscientific Interests. Travel, photography. In the last 10 years photography grew from a mere hobby to a rather serious endeavor marked with exhibitions, awards in photographic competitions and a published book (with another on the way) (www.levtsimring.com).

As a theoretical and computational physicist, I worked in a number of fields including nonlinear dynamics, chaos, synchronization, pattern formation, granular physics, and, in the last 10 years, biological physics and quantitative systems biology. I am interested in developing and validating quantitative dynamical models of gene regulatory networks and signaling pathways. One of the thrusts of my current research is to design *de novo* synthetic gene circuits, which can be used for dissecting, analyzing, and controlling the dynamical interactions involved in gene regulation. As an essential part of this work, we develop deterministic and stochastic models of gene circuits using novel theoretical and computational approaches. Working side-by-side with molecular biologists and bioengineers, we probe the dynamics of the circuits on a single-cell level. (Read Tsimring's article; DOI: 10.1021/sb500235p.)

■ PAWEŁ WIDERA



Paweł Widera

Current Position. Research associate, School of Computing Science, Newcastle University, U.K.

Education. Ph.D. in Computing Science, University of Nottingham. Advisor: Prof. Natalio Krasnogor. M.Sc., B.Sc. in Computing Science, Poznan University of Technology. Advisor: Prof Jacek Błażewicz.

Nonscientific Interests. Film (cinema, anime), philosophy (trans-humanism), free culture (copy left, creative commons), volleyball, board games.

I have a background in Computing Science, and I am interested in interdisciplinary research, where algorithmic approaches are used to solve problems from other disciplines. Most of the projects I have been involved insofar were related to Computational Biology. Starting from approximated algorithms for the DNA sequence assembly problem, through optimization aspects of protein structure comparison (consensus methods in protein classification, multimeasure distributed comparison), to evolutionary-based prediction of protein structure (automated design of protein energy functions and structural model refinement with genetic programming, contacts prediction with learning

classifiers). Recently, I started to explore topological analysis and interactive data visualization in the context of biological networks (e.g., protein–protein interaction networks or dependency graphs in synthetic biology models). (Read Widera's article; DOI: 10.1021/sb5001406).

■ JIFENG YUAN



Jifeng Yuan

Current Position. Postdoctoral fellow, Department of Chemical and Biomolecular Engineering, National University of Singapore; Advisor: Prof. Chi Bun Ching.

Education. Ph.D., Department of Chemical and Biomedical Engineering, Nanyang Technological University (Jan. 2008–Aug. 2012). Advisor: Prof. Chi Bun Ching. Bachelor of Engineering, School of Life Sciences and Technology, Xi'an Jiaotong University (Sept. 2003–July 2007)

Nonscientific Interests. I like to explore new countries and learn about the local cultures. I am also an amateur photographer, especially interested in landscape photography and street portraits. Besides that, I like hiking, swimming, and watching movies.

My research mainly focuses on developing new platform technologies for rapid manipulation of budding yeast for high-level production of value-added chemicals. As *S. cerevisiae* does not readily express polycistronic transcriptional units that allow multigene expressions within compact operons, there is a pressing need for a technique that enables rapid pathway assembly and easy implementation of flux balancing tools to achieve maximum productivity. In this work, we developed a new tool for rapid assembly of multiple gene pathways in a one-step fashion, which significantly simplifies the experimental procedure of pathway assembly in budding yeast. This method will be of significant interest for optimizing native pathways as well as elucidating uncharacterized heterologous pathways. Currently, I have been working on compartmentalization of metabolic pathways into different organelles to improve catalytic efficiency and avoid competing pathways. Ultimately, I hope various chemicals and therapeutics can be cost-effectively produced from renewable resources using synthetic biology approaches. (Read Yuan's article; DOI: 10.1021/sb500079f.)