

## ■ CLAUDIO ANGIONE



Image courtesy of Andrea Sigona.

**Current position:** Ph.D. Student, Computer Laboratory, University of Cambridge, UK. Advisor: Dr. Pietro Lió.

**Education:** B.Sc. in Applied Mathematics, M.Sc. in Mathematics, University of Catania, Italy. Advisor: Prof. Giuseppe Nicosia.

**Nonscientific interests:** Cycling, running, table tennis, traveling, trekking on Mount Etna (when it does not erupt).

My current research interests include synthetic biology, multiobjective optimization in bacterial metabolic networks, and computation with molecular machines. In this work, we perform a comprehensive analysis of the main pathways involved in the metabolism of an organism, modeled using flux balance analysis or differential equations. This includes concurrent optimization of many fluxes or metabolite concentrations, sensitivity, robustness and identifiability analyses. I am looking forward to combining the approach described in our paper with formal methods in order to address emerging questions in this hybrid research field: Does a bacterium have computational capability? What is the computational complexity of its routines? (Read Angione's article; DOI: 10.1021/sb300102k).

## ■ CHANGHAO BI



Image courtesy of Changhao Bi.

**Current position:** Postdoctoral Researcher, The Joint BioEnergy Institute (JBEI), Lawrence Berkeley National Laboratory. Advisor: Dr. Nathan J. Hillson.

**Education:** Ph.D. Microbiology. University of Florida, Advisor: Dr. James F. Preston. M.S. and B.S. in Molecular and Biochemistry, Nankai University, China. Advisor: Qimin Chen

**Nonscientific interests:** Music, reading, comics, video games.

My research is focused on developing a broad-host synthetic biology toolbox to engineer atypical bacteria for various applications and researches. Most engineering activities reported are mainly focused on model microbial hosts, such as *E. coli* and yeast. However, some challenges for these model organisms as biocatalysts were not addressed due to the limitation of the hosts themselves. One solution is engineering atypical organisms with desired phenotypes. Bacteria can be selected with desired features from environmental samples. To simplify and streamline the process to identify functional expression systems for engineering any given bacterial strains, a synthetic toolbox for broad-host engineering composed of genetic elements, such as plasmid origins of replication, promoters, RBSs, and terminators, is to be established. Read Bi's article; DOI: 10.1021/sb300075t).

## ■ LINH HUYNH



Image courtesy of Linh Huynh.

**Current position:** Ph.D. Candidate, Department of Computer Science and UC Davis Genome Center, UC Davis. Advisor: Prof. Ilias Tagkopoulos.

**Education:** B.S. in Computer Science, Ho Chi Minh City University of Technology, Vietnam.

**Nonscientific interests:** Hiking, camping and reading.

As a Ph.D. student, I am working toward setting the algorithmic foundations for computational synthetic biology. In particular, I work toward a scalable computer-aided design (CAD) and optimization tool for automated synthetic circuit design. In this paper, we introduce a novel methodology based on a step-by-step refinement process that aims to increase performance while systematically investigating the design solution space to find the optimal solution. Our tool, SBROME, has been applied successfully for the design of a 2-bit multiplexer *in silico* that utilizes pre-existing logic gates and characterized biological parts. We are currently working to improve an online service and graphical interface for this freely available tool, to make it more user-friendly and useful to synthetic biologists. (Read Huynh's article; DOI: 10.1021/sb300095m).

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## ■ HUA JIANG



Image courtesy of Hua Jiang.

**Current Position:** R&D engineer, Synopsys Inc., Mountain View, CA

**Education:** Ph.D. in Electrical Engineering at the University of Minnesota, Minneapolis. Ph.D. advisor: Dr. Keshab Parhi and Dr. Marc Riedel. M.E. in Electrical Engineering at Shanghai Jiao Tong University, China. B.E. in Electrical Engineering at the University of Electronics Science and Technology of China.

**Nonscientific interests:** In my spare time, I play outfield in softball. I am also holding an Amateur Extra Class license for amateur radio activities.

My Ph.D. work focused on analysis and design of signal processing systems with molecular reactions. Just as electronic systems implement computation in terms of voltage (energy per unit charge), molecular systems compute in terms of chemical concentrations (molecules per unit volume). We have developed strategies for implementing signal processing with molecular reactions including operations such as filtering. We have demonstrated robust designs for Finite-Impulse Response (FIR), Infinite-Impulse Response (IIR) filters, and Fast Fourier Transforms (FFTs). The impetus for this research is not computation per se. Molecular computation will not compete with conventional computers made of silicon integrated circuits for tasks such as number crunching. Rather, the goal is to create “embedded controllers”, viruses and bacteria that are engineered to perform useful molecular computation in situ where it is needed, for instance, for drug delivery and biochemical sensing. (Read Jiang’s article; DOI: 10.1021/sb300087n).

## ■ TAEK KANG

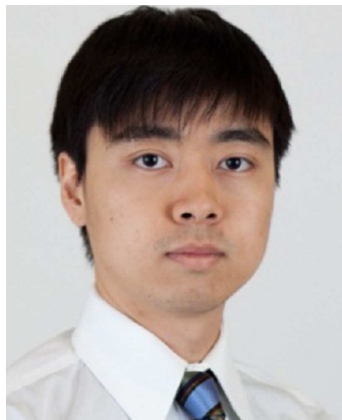


Image courtesy of Doyen Rainey.

**Current Position:** Research Assistant, Department of Bioengineering, University of Texas at Dallas. Advisor: Dr. Leonidas Bleris.

**Education:** B.S. Chemical and Biomolecular Engineering, Johns Hopkins University (2009).

**Nonscientific interests:** Reading, watching and playing soccer.

I am interested in all aspects of mammalian synthetic biology. In this paper, we show that synthetic gene circuits integrated in human kidney cells can be used as a platform for testing and refining reverse engineering methodologies. Specifically, using a benchmark circuit that combines transcriptional and post-transcriptional regulation, we show that we can reliably reconstruct causal relationships by perturbing selected components of the network. In the future, I would like to contribute toward expanding the application of transgenic cells by exploring ways to efficiently control epigenetic modifications. (Read Kang’s article; DOI: 10.1021/sb300093y).

## ■ GREGORY LINSHIZ



Image courtesy of Gregory Linshiz.

**Current position:** Postdoctoral fellow, Synthetic Biology Group Joint Bioenergy Institute (JBEI) - Lawrence Berkeley National Laboratory. Advisor: Dr. Nathan Hillson.

**Education:** Ph.D. Computer Science and Biological Chemistry, Weizmann institute of Science, Israel. Advisor: Prof. Ehud Shapiro. M.Sc Structure Biology, Weizmann institute of Science, Israel. Advisor: Prof. Mark Safro. B.Sc. Computer Science and Life Science, Bar-Ilan University, Israel.

**Nonscientific interests:** I like to travel and meet with interesting people, come back home and spend time with my family. At the short time left out of my lab I like to hang out with friends, throw parties, cook and eat tasty food. I also try to make time for gardening, handcrafts, cycling and hiking.

My scientific interests lie in the fields of synthetic biology, laboratory automation, microfluidics, nanotechnology and bioenergy. My cross-disciplinary expertise with formal computer and life science education and extensive hands-on biological laboratory experience enables me to integrate diverse approaches and combine ideas from biology, computer science, and engineering to find creative solutions. Development of biology-friendly automated platforms is a crucial step toward laboratory automation and modernization of life sciences. We have developed the biology-friendly high-level language PaR-PaR (Program a Robot). Its syntax and compiler are based on computer science principles and deep understanding of biological needs. Our language allows researchers to use automated platforms, enabling a plethora of new experiments not considered previously. This is a good example of how biology-friendly computational tools can give a real boost to research and open new scientific horizons. Our goal is to make PaR-PaR the standard for description and

automation of laboratory protocols. (Read Linshiz's article; DOI: 10.1021/sb300075t).

### ■ DIMITRIS PAPAMICHAIL



Image courtesy of Dimitris Papamichail.

**Current Position:** Assistant Professor, Department of Computer Science, University of Miami.

**Education:** Ph.D. in Computer Science, Stony Brook University, USA (2007). Advisor: Prof. Steven Skiena; M.S. in Computer Science, University of Arizona, USA (1998); B.E. in Computer Engineering and Informatics, University of Patras, Greece (1996).

**Nonscientific interests:** Classical guitar, table tennis, cycling.

My research focuses on applied algorithms, with a primary interest on problems arising in computational synthetic biology. I have worked on the design of DNA coding sequences, which when synthesized exhibit novel properties. My lab has developed algorithms to optimize the design of genomic sequences according to criteria that alter translation rates, while introducing and/or avoiding specific patterns and signals. I have also worked on problems related to classification of genomic sequences, analysis of populations and estimation of their diversity, as well as sequence alignment and primer design. This paper describes a methodology to design diverse protein coding gene libraries in a cost-effective manner, utilizing large-scale oligonucleotide synthesis and multiplex assembly. (Read Papamichail's article; DOI: 10.1021/sb300086d).

### ■ SEAN POUST



Image courtesy of John Cunha.

**Current position:** Ph.D. Candidate, Department of Chemical Engineering, University of California, Berkeley. Advisor: Dr. Jay Keasling.

**Education:** M.S. Environmental Engineering, University of Illinois (2010) Advisor: Julie Zilles; B.S. Chemical Engineering, University of Illinois (2007).

**Nonscientific interests:** Camping, hiking, biking, cooking, adventures in the Bay Area.

My graduate work focuses on engineering polyketide synthases to produce new chemicals. These enzymes function as assembly lines, but when we try to mix and match assembly lines to form chimeric proteins that should make new products, we usually produce non-functional proteins. My interest in developing the robotic platform in this paper arose from my need to make and test more chimeric proteins. My hope is that scientists will be able to forget about the mechanical task of doing cloning using technologies such as PaR-PaR and j5. The focus can then be the interesting scientific issues, like testing hypotheses about how to make functional chimeric proteins. I also hope that scientists will be enabled by the throughput one can achieve with easily programmable robotics not only to do experiments faster and more accurately but also to do new experiments that would have seemed impossible manually. (Read Poust's article; DOI: 10.1021/sb300075t).

### ■ GUILLERMO RODRIGO

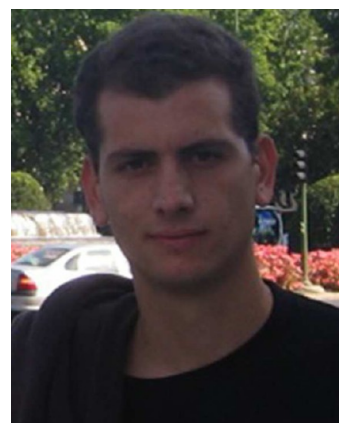


Image courtesy of Guillermo Rodrigo.

**Current position:** Postdoctoral fellow (EMBO long-term), Institute of Systems and Synthetic Biology, CNRS–UEVE–Genopole, France. Advisor: Prof. Alfonso Jaramillo.

**Education:** Ph.D. Biotechnology, Universidad Politécnic de Valencia, Spain (2011). M.Sc. in Applied Mathematics, Universidad Politécnic de Valencia, Spain (2008). B.Eng. Industrial Engineering, Universidad Politécnic de Valencia, Spain, and École Polytechnique, France (2006).

**Nonscientific interests:** Sports, chess, traveling.

My research in systems and synthetic biology has been focused on the model-based design of biological regulatory systems using computational techniques. I have worked in the *de novo* design of transcription, RNA-based, and metabolic networks with specified behavior using *in silico* evolutionary procedures. In addition, I have been interested in the reconstruction of regulatory models, both deterministic and stochastic, at the molecular level, as well as the development of effective genome-scale ones. (Read Rodrigo's article; DOI: 10.1021/sb300084h).

**■ JASON STEVENS**

Image courtesy of Jason Stevens.

**Current position:** Graduate student in the University of Washington Bioengineering Department. Advisor: Dr. James Carothers.

**Education:** B.S. in Mathematics from the University of Kansas.

**Nonscientific interests:** I enjoy rock climbing, cycling, walking/hiking, electronic music, dancing, vegan cooking, and exploring Seattle.

My general interests are in increasing the predictability and complexity of synthetic biological systems via the interplay of modeling, computation, and experiment. This work was an effort to expand the iBioSim modeling software to multicellular systems, thereby creating an easy-to-use design and analysis platform for synthetic multicellular behaviors *in silico*. The software allows for dynamic population models, includes a dynamic implementation of the SSA Composition and Rejection method for simulation, supports time-lapse visualization, and integrates SBML and SBOL. Currently, I am developing a model-guided strategy for designing and implementing RNA-based dynamic control systems for predictable metabolic pathway engineering in *E. coli*. (Read Stevens' article; DOI: 10.1021/sb300082b).

**■ ATHANASIOS TSOUKALAS**

Image courtesy of Athanasios Tsoukalas.

**Current position:** Postdoctoral research associate, Department of Computer Science and UC Davis Genome Center, University of California, Davis, USA.

**Education:** Ph.D. in Electrical and Computer Engineering, University of Patras, Greece, (2012). Advisor: Dr. Anthony Tzes. Diploma in Electrical and Computer Engineering (with a concentration in microelectronics), University of Patras, Greece.

**Nonscientific interests:** Video game design, art, painting, 3D modeling and visualization, AI modeling, swimming

My current work focuses on computer-aided design automation in synthetic biology, and I am interested in exploring how to merge traditional electrical engineering approaches to synthetic circuit design. With a Ph.D. in robotics, modeling, and control, I look forward to applying automation solutions to this nascent field. This is a very exciting time for people like myself who want to explore the interface between engineering and life sciences. (Read Tsoukalas' article; DOI: 10.1021/sb300095m).