■ NIKOLAOS ANESIADIS

Image courtesy of Endang Susilawati.

Current position: Ph.D. candidate, Department of Chemical Engineering and Applied Chemistry, University of Toronto, Toronto, Canada; Advisors: Prof. W. R. Cluett and R. Mahadevan.

Education: M.A.Sc. in Chemical Engineering and Applied Chemistry, University of Toronto (2007); Advisors: Prof. W. R. Cluett and R. Mahadevan. B.A.Sc. in Chemical Engineering, Aristotle University, Thessaloniki, Greece (2005); Advisor: Prof. C. Kiparissides.

Nonscientific interests: Scandinavian cinema, volleyball, tennis.

I am interested in understanding the structure, hierarchy, and dynamics of biological systems and engineering novel genetic tools. Modeling plays a significant role in deciphering and redesigning genetic networks. Our original design of a density-dependent gene expression circuit for metabolic engineering applications was model-based. Here, we further analyze the dynamic properties of the original model construct to guide the experimental implementation of the genetic circuit. First, the analysis identifies the most sensitive parameters of the network. Then, we focus on these parameters and determine the ranges that satisfy the metabolic engineering targets. As synthetic biology moves toward more complex modular designs, mathematical modeling and analysis will become an indispensable tool to minimize the design effort. (Read Anesiadis' article; DOI: 10.1021/sb300129j)

■ PABLO CERES

Image courtesy of Robert T. Batey.

Current position: Scientist at SomaLogic, Boulder, CO.

Education: Ph.D., University of Colorado, Boulder; Advisor: Dr. Robert Batey. M.S., Oklahoma University Health Sciences Center. B.S. in Chemistry from Bethel College, Newton, KS.

Nonscientific interests: Soccer, running, biking, and spending time with my kids.

I am interested in the expanding role of RNA-based regulation of important cellular processes across biology. One of these riboregulatory elements is the riboswitch, an RNA element broadly distributed in bacteria controlling a diverse set of biosynthetic and transport genes. In this article, we demonstrate that the two domains that compose a riboswitch, the receptor and regulatory domains, are independent modules and that the regulatory domain can accommodate different biological receptor or synthetic aptamers. These chimeric riboswitches function *in vitro* and in *E. coli* with an acceptable range of genetic control. The engineering principles that we established to construct these chimeric riboswitches are easily understandable, allow for construction of genetically encodable RNA biosensors to virtually any molecule for which an aptamer can be raised through SELEX, and can be easily tuned to optimize expression levels of a target gene. Most importantly, the natural mechanism of riboswitch regulatory domains enables a simple "plug-and-play" approach with no further maturation of the chimeric riboswitch to improve interdomain communication. We envision that artificial riboswitches will be used in diverse applications including directed protein evolution, metabolic engineering, and construction of complex regulatory networks for gene expression. (Read Ceres' article; DOI: 10.1021/sb4000096)
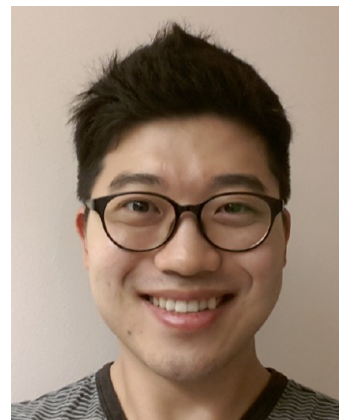
■ JIN HUH

Image courtesy of Jin Huh.

Current position: Postdoctoral fellow, KAIST Institute for the BioCentury, Korea Advanced Institute of Science and Technology; Advisor: Dr. Sun Chang Kim. Department of Biological Engineering, Massachusetts Institute of Technology; Advisor: Dr. Ron Weiss.

Education: Ph.D. in the UC Berkeley/UCSF Joint Graduate Group in Bioengineering, University of California at Berkeley and San Francisco; Advisor: Dr. J. Christopher Anderson. B.S. in

Chemical Biology, University of California at Berkeley; Advisor: Dr. Seung Wuk Lee.

Nonscientific interests: Soccer.

I am interested in cell-to-cell communication between mammalian cells. Cell-to-cell communication among engineered cells has largely depended on components of quorum sensing systems. However, the intrinsic properties of this system, such as limited choices for signaling molecules, restricted communication to a localized area, and confinement of communication in population-wide rather than between individuals may hinder further utilization for a number of applications. Instead, I am interested in a unique one-to-one communication between individual mammalian cells connected via tunneling nanotube (TNT)-like structures. Through this conduit, cellular components such as ions, nucleotides, proteins, vesicles, or even organelles are transported and are capable of acting as signals. This new mode of communication will be a critical addition to the existing toolbox for creating gene networks that encode artificial developmental programs in mammalian cells and that coordinate the action of cell-level morphogenetic processes in space and time. Moreover, this system can be implemented to develop cancer therapeutic agents with enhanced dissemination rates within the tumor microenvironment. (Read Huh's article; DOI: 10.1021/sb300107h)

■ SHRIDHAR JAYANTHI

Image courtesy of Shridhar Jayanthi.

Current position: Postdoctoral Research Associate at Rice University; Advisors: Oleg Igoshin and Jeff Tabor.

Education: Ph.D. in Electrical Engineering, University of Michigan, Ann Arbor MI (2012); Advisor: Domitilla Del Vecchio. B.S. in Computer Engineering, Instituto Tecnologico de Aeronautica, Sao Jose dos Campos-SP, Brazil (2005).

Nonscientific interests: Literature, fine arts, philosophy and the Michigan Wolverines.

My current research is on the topic of how to program bacterial populations with the goal of achieving self-organization and predictable pattern formation through synthetic programs. Since early in graduate school, I have been interested in understanding life processes from the perspective of the computation and control paradigms developed during the past 100 years. Biological systems are remarkably efficient in their use of energy and resources. If we were able to understand how they achieve this, we could design highly efficient electric, mechanical or even biological devices, and I strongly believe that true understanding of anything comes only when we are able to engineer it. (Read Jayanthi's article; DOI: 10.1021/sb300098w)
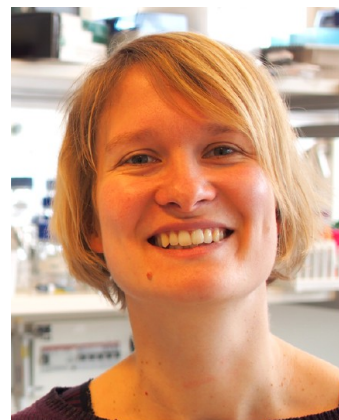
■ HENRIKE MARIE NIEDERHOLTMEYER

Image courtesy of Matthew Blackburn.

Current position: Ph.D. student, Institute of Bioengineering, École Polytechnique Fédérale de Lausanne, Switzerland; thesis advisor: Dr. Sebastian Maerkl.

Education: B.S. and M.S. in Biotechnology from University of Münster, Germany; B.S. thesis advisor: Dr. Volker Wendisc; external M.S. thesis advisor: Dr. Pamela Silver (Harvard Medical School).

Nonscientific interests: Outdoor activities like hiking, sailing, and skiing and traveling.

For my Ph.D. project I am working on *in vitro* genetic networks. To be able to assemble those networks in a way that they will produce the desired behavior, you need to know, at least roughly, the mRNA synthesis rates of all genes involved. Together with Ling Xu, a very talented summer student, who worked in our lab in 2010, we designed our first set of binary probes to measure mRNA concentrations during *in vitro* transcription and translation reactions. In continuation of her project, we further optimized the target sequence and quantitatively characterized mRNA dynamics in the PURE system. Now, I routinely use this method whenever I want to test a new promoter design or the effect of a transcription factor. (Read Niederholtmeyer's article; DOI: 10.1021/sb300104f)

■ KAYZAD SOLI NILGIRIWALA

Image courtesy of Kayzad Soli Nilgiriwala.

Current position: Postdoctoral Research Associate, Department of Mechanical Engineering, Massachusetts Institute of Technology, Cambridge; Advisor: Prof. Domitilla Del Vecchio

Education: Ph.D. in Microbiology, Mumbai University, Mumbai, India (2009); Advisor: Prof. Shree Kumar Apte, BARC, Mumbai, India.

Nonscientific interests: Swimming, badminton, table tennis, and chess.

My doctoral research involved cloning of a novel alkaline phosphatase toward studying its biochemistry and standardizing its application in bioprecipitation of heavy metals from alkaline solutions. In my present postdoctoral research I have been working on constructing a biomolecular circuit in order to study the effects of retroactivity in a two-component signal transduction system. In the paper described, it is fascinating to observe how retroactivity can dramatically affect the dynamics of a system without much effect on the steady state. It was a great learning experience for me toward actually visualizing the differences in dynamics at single-cell level. This study surely is a step forward toward realizing its value in construction of biomolecular circuits in future giving a better modeling and predictive instinct. I envision myself applying synthetic biology in the fields of extreme biology, astrobiology, and biofuel process development in future. (Read Nilgiriwala's article; DOI: 10.1021/sb300098w)
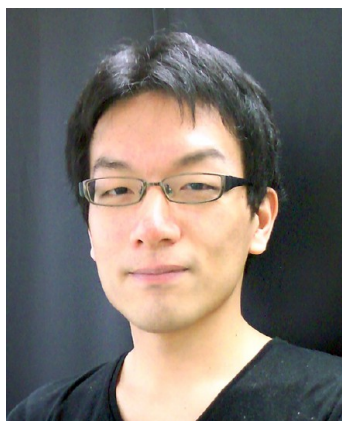
■ TAICHI UMEYAMA

Image courtesy of Taichi Umeyama.

Current position: Ph.D. candidate, Department of Computational Biology, Graduate School of Frontier Science, The University of Tokyo; Advisor: Prof. Takashi Ito.

Education: M.S. and B.S. in Biotechnology and Life Science, Tokyo University of Agriculture and Technology.

Nonscientific interests: Traveling, sports, and music.

I am generally interested in exploration and engineering of biomolecules. In this paper, we focused on the key metabolite *S*-adenosylmethionine (SAM) and developed a SAM-responsive synthetic gene circuit based on the SAM-responsive transcription factor MetJ from *Escherichia coli*, and applied it for monitoring intracellular SAM levels in *Saccharomyces cerevisiae*. Furthermore, we also demonstrated the utility of this circuit for SAM overproducer screening. These practical applications point out the utility of this circuit for various research purposes. In addition, synthetic gene circuit-mediated monitoring is not a peculiar strategy to SAM but applicable for diverse metabolites. Currently, my research focused on expanding this strategy for diverse metabolites and exploring available transcription factors. I anticipate that the ongoing explosion of genomic sequence data will provide rich sources for this strategy (Read Umeyama's article; DOI: 10.1021/sb300115n)

■ DOMITILLA DEL VECCHIO

Image courtesy of Tony Pulsone.

Current position: Associate Professor, Mechanical Engineering, MIT.

Education: Ph.D. in Control and Dynamical Systems, Caltech (2005); Advisor: Richard Murray. Laurea in Electrical Engineering, University of Rome, Tor Vergata (1999)

My research interests are in control theory and dynamical systems theory with applications in the analysis and design of biomolecular networks and in transportation systems. (Read Del Vecchio's article; DOI: 10.1021/sb300098w)