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TALIMAN AFROZ

Rashed Khan

Current Position. Postdoctoral Associate, Department of Biomedical Engineering, Duke University. Advisor: Dr. Lingchong You.

Education. Ph.D. Chemical Engineering, North Carolina State University (2015). Advisor: Dr. Chase L. Beisel; M.Sc. Chemical Engineering, North Carolina State University; B.Sc. Chemical Engineering, Bangladesh University of Engineering & Technology.

Nonscientific Interests. Reading books, yoga, traveling.

My Ph.D. work focused on understanding the diverse single-cell responses of *Escherichia coli* to various sugars and how the cells can be engineered to yield desirable responses. In this work, we engineered the L-arabinose and D-xylose utilization pathways to convert the natural bimodal, sharp response into a unimodal, titratable response suitable for inducible control. Importantly, we found that there is no perfect set of modifications; instead each modification came with a trade-off. For nonmodel microorganisms with limited genetic tools, the findings for this paper can potentially be used as a guide to exploit natural sugar utilization pathways as titratable systems. Currently, I am working with synthetic gene circuits to understand how cells become tolerant to traditional antibiotics. (Read Afroz's article; DOI: 10.1021/sb400162z).

ZHEN CHEN

Zhen Chen

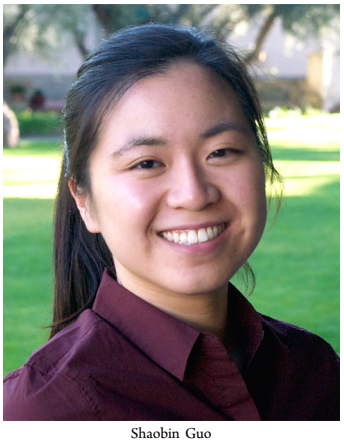
Current Position. Assistant Professor, Department of Chemical Engineering, Tsinghua University, China.

Education. Ph.D. in Biochemical Engineering, Hamburg University of Technology, Germany (2012). Advisor: An-Ping Zeng; M.S. and B.S. in Chemical Engineering, Tsinghua University, China.

Nonscientific Interests. Swimming, travel, music.

My research interest is focused on integrating systems and synthetic biology tools to develop industrial hosts for the production of valuable products. In particular, we are developing new tools for structure-based protein and pathway design to expand the available biological parts for engineering metabolic and regulatory systems of cells toward desired phenotype. This paper represents a significant step toward the design of non-natural allosteric proteins that can be used as a molecular biosensor or regulatory element for dynamic control of cellular metabolism. (Read Chen's article; DOI: 10.1021/sb400133g).

VICTORIA HSIAO



Shaobin Guo

Current Position. Ph.D. candidate, Bioengineering, California Institute of Technology. Advisor: Prof. Richard M. Murray.

Education. B.S. in Engineering with a concentration in Bioengineering, Franklin W. Olin College of Engineering (2010).

Nonscientific Interests. Volleyball, traveling, food, situational comedies and murder mysteries.

One of my primary research interests is the transition between single-function synthetic gene circuits to higher-order networks. I am interested in investigating ways in which circuit inputs and outputs can be modularized and regulated. In this particular project, my collaborators and I have utilized synthetic protein scaffolds to create a biomolecular concentration tracker that tightly regulates the ratio between the input and output proteins via a negative feedback loop. Not only were we able to show good agreement between our mathematical model and *in vivo* population data, but we also were excited to be able to quantify this tracking behavior in single cells. Looking ahead, I hope to engineer additional ways to bring together existing circuits for the development of more complex bacterial devices. (Read Hsiao's article; DOI: 10.1021/sb500024b).

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JEAN-BAPTISTE LUGAGNE

Jean-Baptiste Lugagne

Current Position. Ph.D. candidate, National Institute for Research in Computer Science and Automation (INRIA), Paris-Rocquencourt, under the supervision of Dr. Gregory Batt and Dr. Pascal Hersen.

Education. Undergraduate student at Grenoble INP Phelma Engineering School, Grenoble. Eight-month Internship at Imperial College, London, under the supervision of Dr. G. B. Stan and Dr. Diego A. Oyarzún.

Nonscientific Interests. Climbing, homebrewing, cooking.

My current research focuses on real-time and long-term control of gene expression in bacteria at the single-cell level. Microfluidics, synthetic biology and new imaging and processing methods now make it possible to precisely control the concentration of a protein of interest *in vivo* by fine-tuning the cell's environment. A number of techniques have been successfully used to drive the concentration of a protein through complex, time-varying profiles and study the dynamics of synthetic or natural gene circuits. Because the vast majority of synthetic or natural genetic circuits are part of the more complex family of multistable systems, my goal is to prove that those systems also can be tightly controlled, even with little prior knowledge of their behavior. The ability to easily control such systems makes it possible to obtain single-cell, high-resolution, user-driven data for a majority of genetic networks. (Read Lugagne's article; DOI: 10.1021/sb400126a).

DIEGO OYARZÚN

Diego Oyarzún

Current Position. Research Fellow in Biomathematics, Department of Mathematics, Imperial College London. Previously: Postdoctoral Researcher (2011−2013), Department of Bioengineering (Centre for Synthetic Biology and Innovation), Imperial College London; Marie Curie Fellow (2010), INRIA Sophia Antipolis, France.

Education. Ph.D. Engineering (2010), National University of Ireland, Maynooth; M.Sc. (2005) and B.Sc. (2003) in Electronic Engineering, Universidad Técnica Federico Santa María, Chile.

Nonscientific Interests. Traveling and street photography.

In my research I study how cells use their biochemical machinery to self-regulate and survive environmental changes. Combining mathematical analysis and control theory, I develop new theories to understand the function of natural regulatory networks as well as to design synthetic gene circuits for biotechnology. In our paper here, we present the first quantitative characterization of metabolic noise caused by stochastic fluctuations in enzyme expression; we predict conditions under which transcriptional regulation amplifies or attenuates noise in metabolic products. The paper lays out a first step toward a theory to pinpoint the sources of metabolic variability and to control or exploit variability in metabolic engineering. (Read Oyarzún's article; DOI: 10.1021/sb400126a).

DEBOSMITA SARDAR

Debosmita Sardar

Current Position. Graduate Student, Department of Medicinal Chemistry, University of Utah, USA. Advisor: Dr. Eric W. Schmidt.

Education. Masters in Biotechnology, Vellore Institute of Technology, India.

Nonscientific Interests. Cooking and writing.

My research is focused on the biosynthesis of a class of peptide natural products called cyanobactins. They are ribosomally synthesized and posttranslationally modified peptides (RiPPs), which include interesting modifications such as heterocyclization and N−C macrocyclization. The enzymes responsible for the generation of these modifications are highly promiscuous, and the current work explores the basis of this promiscuity. Understanding the rules that drive the activity of these enzymes to accept a wide range of substrates allowed us to define a simple toolkit to exploit these enzymes for the generation of tailored peptides both *in vitro* and through heterologous expression in *E. coli*. This in turn carries potential for the enzymatic synthesis of biologically active peptide motifs. (Read Sardar's article; DOI: 10.1021/sb500019b).

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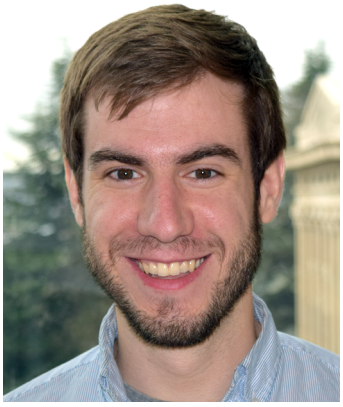
JASON STEVENS



Jason Stevens

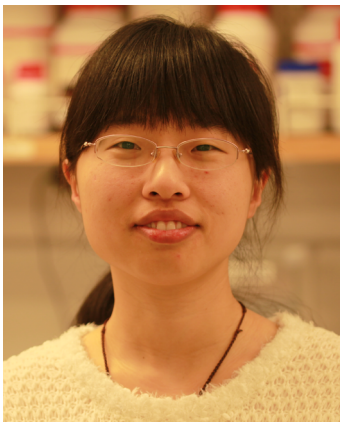
Current Position. Graduate Student in the University of Washington Department of Bioengineering, Advisor: James Carothers.

Education. B.S. in Mathematics from University of Kansas (2011).

Nonscientific Interests. I produce house and techno music. I also enjoy dancing, cooking, reading fiction, long strolls, hiking, and exploring the arts/music/cultural offerings around Seattle with friends.

I'm interested in using RNA devices for programming functions in engineered metabolic pathways, as well as in creating computational methods to explore functional design space and increase the complexity and tractability of RNA-based genetic control systems. In this work, we investigated the potential for dynamic RNA-based genetic control systems to increase production yields of an engineered paminostyrene (p-AS) pathway in *E. coli*. We did this by developing mathematical models of 729 distinct control systems then performing simulations using thousands of sampled parameters for each control system. We were thereby able to analyze a large portion of control system design space to understand relationships between control system architecture and pathway yields. Moreover, we investigated the performance of different genetic mechanisms for implementing control functions. In the future, I hope to both validate this computational strategy experimentally and develop software to enable others to easily utilize this strategy. (Read Stevens' article; DOI: 10.1021/sb400201u).

DI LIU



Fengbo Zhou

Current Position. Ph.D. candidate, Department of Energy, Environmental and Chemical Engineering, Washington University in St. Louis. Advisor: Dr. Fuzhong Zhang.

Education. B.S. in Materials Chemistry, University of Science and Technology of China.

Nonscientific Interests. I love music and enjoy playing the piano. I also enjoy travelling, hiking, and reading novels.

I'm amazed by the complex regulation networks that cells have evolved to dynamically control gene expression for optimal fitness. Inspired by this, I'm interested in developing engineered circuits to regulate metabolic pathways to improve the production of valuable compounds. In this work, we developed a malonyl-CoA-based negative feedback circuit in *Escherichia coli* to regulate the fatty acid pathway. We demonstrated this circuit was able to improve cell growth and fatty acid production. This system can be readily extended to improve the production of other malonyl-CoA-derived compounds. I'm currently working on studying the metabolic dynamics to further understand the interaction between synthetic regulation and metabolic dynamics, and I look forward to employing dynamic regulation to improve the production of a variety of chemicals. (Read Liu's article; DOI: 10.1021/sb400158w).

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