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## CLAUDIO ANGIONE

Annalisa Occhipinti

**Current Position.** Microsoft Research.

**Education.** Microsoft Research with Youssef Hamadi, Ph.D. research with Dr. Pietro Lio, undergraduate/graduate research with Dr. Giuseppe Nicosia.

**Nonscientific Interests.** Cycling, running, table tennis, traveling.

The increasing availability of data collected from multiple layers of biological organization ("omics") allows cellular processes to be mapped at the levels of mRNA, proteins, and metabolites. Metabolism, the set of chemical reactions that transform various compounds in living cells and organisms, is usually divided into groups of reactions named pathways. The classification of metabolic reactions into pathways, and the use of a genome-scale model of metabolism augmented with gene expression data, allows us to estimate the rate of particular groups of reactions under given growth conditions. However, since functionality and interactions cannot be measured directly at the pathway level, we propose to apply a Bayesian framework that introduces pathways as latent factors between conditions and reaction rates. We use our method on a genome-scale model of *Escherichia coli*. First, we estimate the intensity of the cross-correlations among the pathways in the model. Then, we infer pathway activation profiles over time as a bacterial response to an ensemble of growth conditions. (Read Angione's article; DOI: 10.1021/sb5003407).

## HARISH CHANDRAN

Harish Chandran

**Current Position.** Senior Software Engineer, Google Inc. Mountain View, CA.

**Education.** B.E. from Anna University in 2003 and a M.S. and Ph.D. from Duke University in 2010 and 2012, Advisor: Prof. John Reif.

**Nonscientific Interests.** Travel, history.

My interests lie in self-assembling behavior, from DNA strands self-assembling in nanoscale into complex shapes and networks, to users self-assembling on a social network around interests. We focus on the former in this paper, where we describe methods to speed up DNA based molecular circuits that perform Boolean computations in solution. We simulate these networks and analyze the potential speedups we can realize by localizing the reacting species on a substrate. (Read Chandran's article; DOI: 10.1021/acssynbio.5b00044).

## NEIL DALCHAU

Harrington Photography Ltd.

**Current Position.** Scientist, Microsoft Research, U.K.

**Education.** M.Math from University of Oxford, U.K., in 2005. Ph.D. from University of Oxford, U.K., in 2009. Advisor: Prof. Alex Webb.

**Nonscientific Interests.** I play the bass guitar in various bands, and football (soccer) in various teams. I always enjoy good food and drink.

My research is focused on developing computational approaches for the biological sciences. Computational models can not only serve as a formal representation of current knowledge, but also offer a basis for testing hypotheses, and therefore understanding. I have therefore focused on developing approaches for testing models with experimental data, but also on making it easier to construct, simulate and analyze models. During my Ph.D., I developed mathematical models of circadian signaling in plants, while in my postdoc I focused on immune system signaling. My current research is more engineering focused, with applications in synthetic biology and DNA computing. I'm now becoming increasingly interested in the intersection of biological programming and immunology, which has huge potential. (Read Dalchau's article; DOI: 10.1021/acssynbio.5b00044).

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## CHELSEA HU

Doris Yao

**Current Position.** Ph.D. student, Department of Chemical and Biomolecular Engineering, Cornell University. Advisors: Dr. Julius Lucks, Dr. Jeffery Varner.

**Education.** B.S. in Chemical and Biomolecular Engineering, UCLA.

**Nonscientific Interests.** Running, snowboarding, hiking, tennis, cooking.

I'm generally interested in designing and engineering biological circuits, and especially interested in how circuits can dynamically control gene expression. My work in the Lucks lab mainly focuses on the development of a quantitative modeling framework for sRNA circuit design. In this paper we present the first validated computational model of synthetic RNA transcriptional genetic circuitry. We show that our effective model and method of finding parameters for the model is sufficient to accurately capture the dynamics of a three-level RNA cascade. We also showed it can make simple predictions of new circuits. In the future, I hope to continue working toward the goal of improving and gaining dynamic control of biological systems with synthetic genetic circuits. (Read Hu's article; DOI: 10.1021/acssynbio.5b00077).

## LINH HUYNH

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.** Biking, camping and reading.

I am interested in computational aspects of synthetic biology. In particular, I am focusing on computational models for automated synthetic circuit design. An inherent challenge of modeling work is the trade-off between the accuracy and the computation efficiency of the model. Here, we address this challenge by introducing a hierarchical computer-aided design architecture that uses a two-step approach for biological design. Evaluation with a benchmark of 11 circuits and a library of 102 experimental designs with known characterization parameters demonstrates both the accuracy and efficiency of our new approach. We are currently working to validate our result experimentally. (Read Huynh's article; DOI: 10.1021/sb500339k).

## BENJAMIN JACK

Benjamin Jack

**Current Position.** Graduate student in the Institute for Cellular and Molecular Biology at The University of Texas at Austin. Advisor: Claus O. Wilke.

**Education.** B.S. in Biochemistry from the University of Miami.

**Nonscientific Interests.** I enjoy running, cooking, trying new foods, and graphic design.

Broadly speaking, I am interested in molecular evolution and computational methods to predict evolution in viruses and bacteria. Some viruses and bacteria have genomes that are less likely to mutate than genomes of other organisms. In viruses, understanding the factors that contribute to a more stable genome could lead to the development of live vaccines that are less likely to mutate in their hosts and revert to their pathogenic form. In bacteria such as *E. coli*, improved genetic stability could create more reliable synthetic organisms and genetic circuits. This concept motivated us to create the EFM Calculator. I am also interested in web programming and using the web as a platform to build novel, interactive ways of visualizing data and communicating scientific ideas. (Read Jack's article; DOI: 10.1021/acssynbio.5b00068).

## SEAN LEONARD

Kevin S. Dome



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**Current Position.** Graduate student in the Institute for Cellular and Molecular Biology at The University of Texas at Austin. Co-advised by Jeffrey Barrick and Nancy Moran.

**Education.** M.S., The University of Texas at San Antonio. B.S., Loyola University Maryland.

**Nonscientific Interests.** Yoga, roller-skating, crochet, and spending time with my mostly bad dog.

I think it is critical that we understand how and why synthetic biological constructs can "fail" on an evolutionary time scale. On the one hand, it is a practical consideration, relevant to companies and research laboratories spending time and money to engineer a useful function into an organism, only to have it break at the industrial scale. When we work to understand how these devices break, we also learn more about the underlying basis of genetic instability, mutation, and evolution. Unfortunately, few scientists report when their devices break or fail. This paper is important because it describes an easy-to-use web tool that any researcher can use to predict and prevent common sources of genetic instability. I hope this work will also inspire scientists to pay a little more attention when their constructs fail. By figuring out what the causes are, we can improve our design methods to engineer more stable devices from the start. (Read Leonard's article; DOI: 10.1021/acssynbio.5b00068).

## JENS NIELSEN

Jan-Olof Yxell

**Current Position.** Professor at Department of Biology and Biological Engineering, Chalmers University of Technology.

**Education.** Ph.D. in Biochemical Engineering, Technical University of Denmark. M.Sc. in Chemical Engineering, Technical University of Denmark.

**Nonscientific Interests.** Sailing, downhill skiing and history.

My research is in the field of systems and synthetic biology. My major scientific contributions are (1) development of advanced metabolic modeling approaches for industrially important microorganisms and use of this for improved design of cell factories and associated fermentation processes; (2) development of systems biology methods for detailed physiological characterization of industrially important microorganisms and use of this for metabolic engineering; and (3) implementation of a range of different metabolic engineering strategies for development of novel cell factories that can be used for production of fuels, chemicals, pharmaceuticals and food ingredients. I have published more than 500 papers and authored several textbooks that have been cited more than 16 000 times according to ISI. (Read Nielsen's article; DOI: 10.1021/acssynbio.5b00018).

## JOHN REIF

John Reif

**Current Position.** A. Hollis Edens Distinguished Professor of Computer Science, Duke University.

**Education.** M.S. and Ph.D. from Harvard University in 1975 and 1977. B.S. (*magna cum laude*) from Tufts University in 1973.

**Nonscientific Interests.** Skiing, hiking.

I developed efficient randomized and parallel algorithms for a wide variety of graph, geometric, numeric, algebraic, and logical problems. I also gave the first hardness proofs for robotic motion planning and efficient algorithms for many motion planning problems. I did applied research in parallel architectures, data compression, and optical computing. Recently, I experimentally demonstrated novel self-assembled DNA nanostructures, patterned DNA lattices, molecular computing and molecular robotic devices. I am the President of Eagle Eye, Inc., developing applications of DNA nanotechnology. An author of over 200 publications, I was awarded Fellow of Advancement of Science (AAAS), IEEE, ACM and Institute of Combinatorics. (Read Reif's article; DOI: 10.1021/acssynbio.5b00044).



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