

■ JAUME BACARDIT



Jaume Bacardit

Current Position. Senior Lecturer in Biodata Mining, The Interdisciplinary Computing and Complex BioSystems (ICOS) research group, School of Computing Science, Newcastle University, U.K.

Education. Ph.D. in Computer Science, Ramon Llull University, Barcelona, Spain (2004); M.Eng. in Computer Engineering, Ramon Llull University, Barcelona, Spain (2000); BEng in Computer Engineering, Ramon Llull University, Barcelona, Spain (1998).

Nonscientific Interests. Anything related to science fiction and fantasy: movies, TV shows, books, comic books.

My research interests include the development of machine learning methods for large-scale problems and their application to challenging biological data. I have published papers on algorithmic advances for machine learning methods related to tackling large dimensionality spaces, large sets of records, postprocessing operators or the use of data-intensive computing technologies such as GPUs and MapReduce. The main focus of my applied research on biological data is knowledge discovery: analyzing the structure of the data mining models to discover useful knowledge, e.g. such as (panels of) biomarkers or functional networks. My methods have been applied to a variety of biological/biomedical domains and technologies: transcriptomics data from plants and humans, mass spectrometry proteomics data from dogs, mass spectrometry lipidomics data from pigs, or protein structure prediction data. (Read Bacardit's article; DOI: 10.1021/sb400161v.)

■ CLAIRE BAUDIER



Claire Baudier

Current Position. Ph.D. student, Department of Systems and Synthetic Microbiology, French National Institute for Agricultural Research (INRA), France.

Education. M.Sc. in Systems Biology, University of Amsterdam, The Netherlands (advisor: Dr. Pernette Verschure). Engineering degree, Centrale Marseille, France. Advisors (2 internships): Dr. Pablo Carbonell, Dr. Matthieu Jules.

Nonscientific Interests. I love to travel and grasp the overall atmosphere of the places I visit. When I am at home, I enjoy going to the theater as well as acting myself. I am a food lover but to compensate, I run a lot and play tennis.

Synthetic Biology is an interdisciplinary field that requires the use of informatics tools to optimize the design of biological circuits. Following this idea, this paper presents a promising computational tool for engineering metabolic circuits, called RetroPath, which reconstructs *in silico* models of chassis organisms such as *E. coli*, broadly used in the field of synthetic biology. It is a potential powerful tool to help design synthetic circuits used for biosensing, bioproduction, or even bioregulation. I am currently doing a Ph.D., which focuses on understanding how the bacteria optimize their protein production by combining both experimental and modeling approaches. This work is carried out at a fundamental level but the results are very likely to contribute to the optimal design of biological circuits. (Read Baudier's article; DOI: 10.1021/sb4001273.)

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■ TUVAL BEN-YEHEZKEL



Tuval Ben-Yehezkel

Current Position. CTO of SynVaccine and Visiting Scientist at the Weizmann Institute of Science.

Education. Ph.D. in Biotechnology, Weizmann Institute (Adviser: Prof. Ehud Shapiro).

Nonscientific Interests. Music, sports, family, and a general zest for the counter-productive.

My research interests are mainly in developing synthetic biology technologies and applying them to unsolved questions/problems in biology and health. I cofounded SynVaccine, a synthetic biology vaccine development company on the basis of some of these technologies. I currently lead innovative synthetic biology projects in industry and academia involving interdisciplinary teams of biologists, computer scientists, and engineers. (Read Ben-Yehezkel's article; DOI: 10.1021/sb400161v).

■ JONATHAN BLAKES



Paul Hathaway

Current Position. Software Engineer, Data Acquisition Group, Diamond Light Source Ltd., Harwell Campus, Didcot, Oxfordshire, U.K. Adviser: Richard Fearn.

Education. Ph.D. Computer Science, University of Nottingham, U.K. Adviser: Natalio Krasnogor; M.Sc. Biotechnology and Computation, University of Kent, Canterbury, U.K. Adviser: Gary Robinson; B.Sc. Biomedical Science, University of Kent, Canterbury, U.K.

Nonscientific Interests. Food and drink, sailing, theater.

This work is an output of my postdoc in the ICOS research group on the EU-funded project CADMAD. My scientific career has mostly focused on writing software assisting the design and analysis of biological experiments. In my current position I support the macromolecular X-ray crystallography (MX)

beamlines of the U.K.'s national synchrotron, including I23, the world's first beamline optimized for long wavelength experiments. Other research interests include algorithms (especially stringology), biological modeling and operations research. (Read Blakes' article, DOI: 10.1021/sb400161v.)

■ MICHAEL GUINN



Michael Guinn

Current Position. Research Assistant, Department of Bioengineering, University of Texas at Dallas. Adviser: Prof. Leonidas Bleris.

Education. B.S. Biochemistry, University of Texas at Dallas (2013).

Nonscientific Interests. When I am outside the lab, I enjoy reading a variety of genres, cooking, playing classical rock on the guitar, and running.

My scientific interests reside in applications of synthetic biology, microbial and mammalian systems (specifically for medical purposes), systems biology, gene therapy, and cancer biology. In this paper, we present a synthetic gene network architecture that operates as a biological decoder in human cells, converting 2 inputs to 4 outputs. As a proof-of-principle, we use small molecules to emulate the two inputs and fluorescent reporters as the corresponding four outputs. We envision future applications where the output fluorescence proteins are replaced with active biomolecules in order to interface with endogenous cellular pathways. (Read Guinn's article; DOI: 10.1021/sb4001596.)

■ LINH HUYNH



Linh Huynh

Current Position. Ph.D. Candidate, Department of Computer Science and UC Davis Genome Center, UC Davis. Adviser: Prof. Ilias Tagkopoulos.

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

Nonscientific Interests. Hiking, camping, and reading.

I am interested in the algorithmic foundations for computational synthetic biology. In particular, I work toward an integrated computer-aided design (CAD) tool for automated synthetic circuit design. An integral challenge in synthetic circuit design is the selection of optimal parts to populate a given circuit topology, so that the resulting circuit behavior best approximates the desired one. In some cases, it is also possible to reuse multipart constructs or modules that have been already built and experimentally characterized. Here, we address this problem by introducing a structured abstraction methodology and a dynamic programming-based algorithm that guarantees optimal part selection. We have evaluated the proposed methodology with a benchmark of 11 circuits and a database of experimentally constructed modules with encouraging results. We are currently working to integrate this selection strategy and a genome-scale simulator to make the proposed solutions more reliable (Read Huynh's article; DOI: 10.1021/sb400139h).

■ JONGMIN KIM



Jongmin Kim

Current Position. Postdoctoral research fellow, Wyss Institute for Biologically Inspired Engineering, Harvard University. Advisor: Peng Yin.

Education. Ph.D., Biology, California Institute of Technology, 2007. Advisor: Erik Winfree; B.S. Life Science, Pohang University of Science and Technology, 2000.

Nonscientific Interests. Reading novels, travel.

My Ph.D. work involved developing a new class of synthetic biochemical systems as a test bed for gene regulatory networks. Several interesting dynamical systems were thus obtained including bistable switches and oscillators. In recent works, we introduce control-theoretic tools to explore ways to make the operation of synthetic biochemical oscillators more robust. Also, we explore ways to adapt the synthetic transcriptional circuits to simulate arbitrary chemical reaction networks. My current research is focused on creating nucleic-acid-based regulatory tools for engineering living cells. I hope to continue developing more intricate programmable dynamical systems in synthetic biology. (Read Kim's articles; DOI: 10.1021/sb5000675; DOI: 10.1021/sb400169s.)

■ VISHWESH KULKARNI



Vishwesh Kulkarni

Current Position. Consultant at Strand Life Sciences (Bangalore, India); joining the University of Warwick as an Assistant Professor in January 2015.

Education. Ph.D. in Electrical Engineering (University of Southern California), M.Tech. (Indian Institute of Technology, Bombay), B.E. (Pune University).

Nonscientific Interests. I like experimenting with DSLR photography and practicing intermediate level linguistic skills in Mandarin and Russian.

My research interests concern (1) synthesis of programmable dynamic systems using basic biomolecular material and (2) application of system theoretic concepts in clinical genomics. In traditional engineering applications, dynamic systems such as the low-pass filters are used not only to reject noise and disturbance but also to eliminate the steady-state errors incurred in regulation and tracking. However, very few results are available today on how to synthesize these much needed systems using biomolecular material such as DNA, RNA, and enzymes. To resolve this bottleneck, we first show how linear dynamic systems that are described using ordinary differential equations can be expressed via abstract chemical reaction networks. We then extend the scope to a software platform, Visual DSD, to implement these networks using different techniques such as DNA strand displacement, the DNA Toolbox, and the genelet. We are translating these results into wet-lab constructs that have several exciting applications. (Read Kulkarni's articles DOI: 10.1021/sb5000675; DOI: 10.1021/sb400169s.)

■ PIERRE PARUTTO



Pierre Parutto

Current Position. Masters student in Bionformatics and Modeling Master, Paris VI and Intern in David Holcman's

Laboratory (Theoretical Modeling of Cellular Physiology team, Institute of Biology of the Ecole Normale Supérieure (IBENS), Paris).

Education. Computer Science, École Pour l'Informatique et les Techniques Avancées (EPITA), France (2013).

Nonscientific Interests. A fragile balance between cooking, sports, and video-games.

I am interested in combining mathematical and computer science methods in order to tackle biological problems. In this work, we present a methodology that uses metabolic models in order to extend the metabolic capability of different organisms. These new developments in the methodology allow the building of more complex metabolic circuits than the classical production circuits such as biosensing or regulatory circuits. Although the presented methodology seems simple, its realization is full of challenges: gathering inputs from different databases, using different modeling softwares and integrating everything into an easy-to-use application. This work illustrates the necessity for tight collaboration between biologists that produce and interpret data and modelers and computer scientists that propose ways to make sense and integrate these data to create applications allowing reuse of this new knowledge. (Read Parutto's article; DOI: 10.1021/sb4001273.)

■ OFIR RAZ



Ofir Raz

Current Position. Programmer and algorithms developer at the Weizmann Institute of Science. Advisor: Prof. Ehud Shapiro.

Education. B.Sc. in Computer Science and Biology at the Open University of Israel.

Nonscientific Interests. Hiking, snowboarding, and traveling.

My research is focused on computational and computer-aided design and manufacturing of DNA libraries. Biology and biotechnology research and development involves "DNA programming", which is akin to computer programming. Researchers modify and combine DNA of interest in a programmatic way to uncover its function, improve its function, or to create new functions. Whereas the composition and editing of computer programs is as easy as using a word processor, the design, construction, and editing of DNA in a programmatic fashion is still a slow, expensive, labor-intensive wet-lab process. Computer-aided design and manufacturing of DNA can enable a revolution in biology and biotechnology, in which high-throughput computer-aided and robotically executed experiments replace manual wet-lab work, resulting in accelerated progress in key areas of research and development. (Read Raz's article; DOI: 10.1021/sb400161v.)

■ 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, Poznań 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 approach is used to solve problems from other disciplines. Most of the projects I have been involved in so far 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 the field of topological analysis and interactive data visualization in the context of the biological networks (e.g., protein–protein interactions). (Read Widera's article; DOI: 10.1021/sb400161v.)

■ BOYAN YORDANOV



Boyan Yordanov

Current Position. Scientist, Biological Computation Group, Computational Science Laboratory, Microsoft Research.

Education. Ph.D. in Biomedical Engineering, Boston University. Advisor: Prof. Calin Belta. B.A. in Biochemistry and Computer Science, Clark University.

Nonscientific Interests. Digital and analog music, sci-fi books, movies.

My research is focused on enabling the programming of biological systems for robust, desirable behaviors and understanding the computation performed by living cells and organisms through the design and application of novel computational methods and tools. In our first paper (DOI: 10.1021/sb400152n), we developed procedures for the characterization of the components used for the construction of genetic devices in synthetic biology. The methods exploited recent experimental techniques together with Bayesian parameter inference and model selection and were integrated within a convenient computational tool. In our second paper (DOI: 10.1021/sb400169s), we adapted a number of strategies for the construction of nucleic acid circuits to enable the biochemical implementation of a class of control systems. This allowed us to compare these different approaches and provided a step toward the engineering of devices with potential applications in biotechnology and medicine, along with a computational tool for the design, simulation, and analysis of such biological circuits. (Read Yordanov's articles, DOI 10.1021/sb400152n and DOI 10.1021/sb400169s.)