ACS SyntheticBiology

In This Issue

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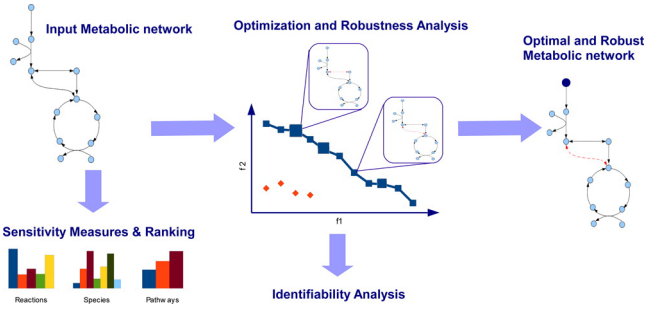
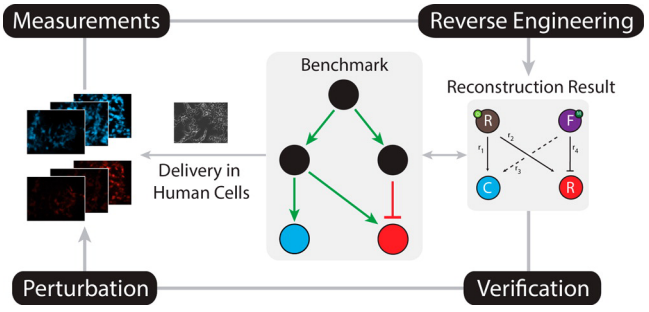
METHODOLOGIES FOR COMPARISON AND OPTIMIZATION OF PHOTOSYNTHESIS MODELS



The development of models that simulate and predict the dynamic responses of metabolic networks has posed a long-standing challenge to systems biologists. Here, Carapezza *et al.* (DOI: 10.1021/sb300102k) develop methodologies for analyzing and cross comparing models of photosynthetic carbon metabolism.

The authors use the Pareto optimality principle to compare different mathematical models of metabolism, on the basis of single- and multiobjective optimization. They investigate five important metabolic networks and discuss the complexity of biological organization of organisms and modeling system properties.

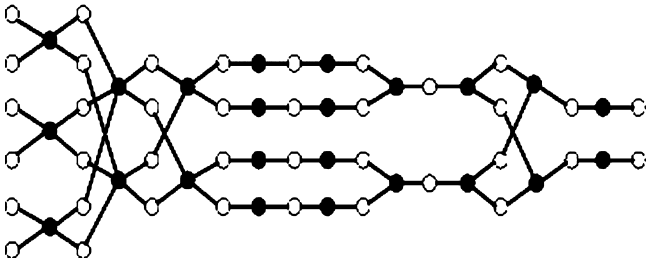
REVERSE ENGINEERING VALIDATION IN HUMAN CELLS



Life scientists and engineers have long been working toward understanding the biomolecular networks in human cells. Here, Kang *et al.* (DOI: 10.1021/sb300093y) describe an experimental platform customized for the development and verification of reverse engineering and pathway characterization algorithms in mammalian cells.

The authors use a synthetic gene network that is stably integrated in human kidney cells as a benchmark for validating reverse engineering methodologies. By performing successive perturbations to each modular component of the network and comparing protein and RNA measurements, the authors study the conditions under which the causal relationships of the integrated synthetic network can be reliably reconstructed.

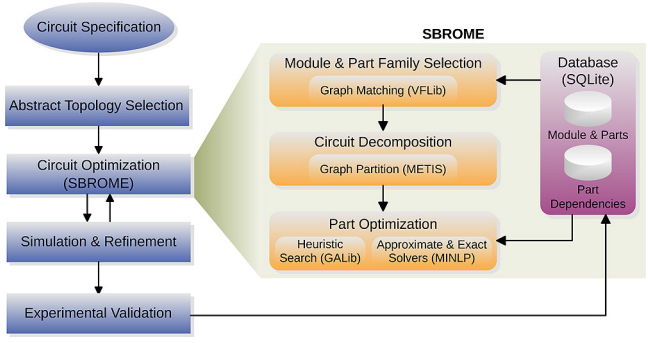
RATIONAL DESIGN OF PROTEIN CODING GENE LIBRARIES



The advent of low cost modern synthesis technologies has created an opportunity to study, in great detail, the relationship between DNA sequence and function. Here, Ryan and Papamichail (DOI: 10.1021/sb300086d) explore methods to design combinatorial synthetic libraries for protein coding genes.

The authors detail the development of algorithms to design diverse gene libraries that uniformly cover the design space of codon utilization, while minimizing the synthesis cost, in many cases by several orders of magnitude. Such methods, in conjunction with high throughput *in vitro* and *in vivo* assays, can revolutionize the functional genomics field.

SBROME: A FRAMEWORK FOR AUTOMATED BIOSYSTEMS DESIGN



With the increasing complexity of synthetic circuits, the development of a scalable framework for biodesign automation is crucial. Here, Huynh *et al.* (DOI: 10.1021/sb300095m) propose a **S**ynthetic **B**iology **R**eusable **O**ptimization **Me**thodology (SBROME) that exploits advances in computer science to adapt graph matching and optimization algorithms for synthetic biology design.

The authors develop a module and part matching database after manual curation of relevant literature and evaluate the performance of the proposed SBROME framework through the design of a three-input multiplexer and scalability analysis.

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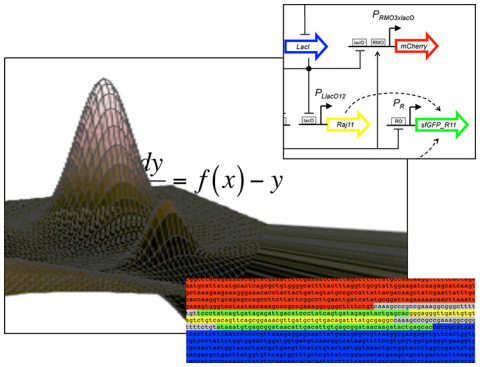
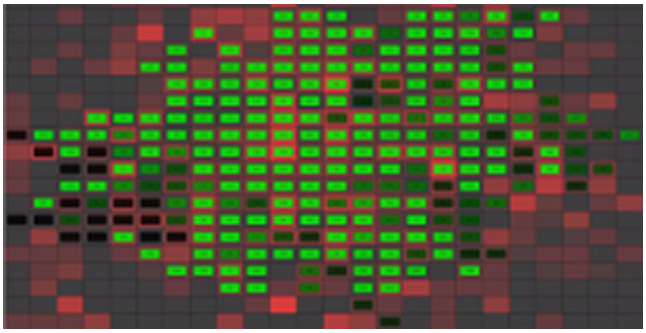
AUTOBIOCAD: FULL BIODESIGN AUTOMATION OF GENETIC CIRCUITS



Biological Design Automation (BDA) is a relatively new engineering paradigm in synthetic biology that involves the design, construction, and characterization of synthetic regulatory networks, unsupervised, by computers. Here, Rodrigo and Jaramillo (DOI: 10.1021/sb300084h) describe the development of a new tool, AutoBioCAD, that can be used to model and design genetic circuits with dynamic behavior.

AutoBioCAD designs regulatory networks from the specified behavior of the system and outputs a SBML file containing the mathematical model of that system, its simulated dynamics, and its nucleotide sequence.

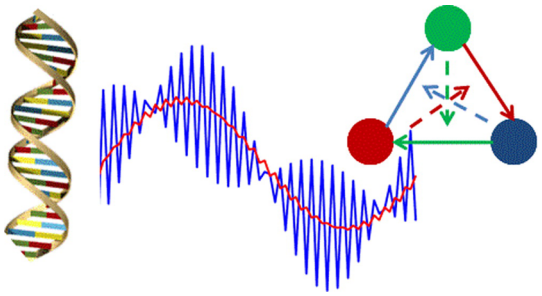
DYNAMIC MODELING WITHIN iBIOSIM



Synthetic biology is poised to address many of the pressing issues in health and society. Organisms are being engineered to produce biofuels and drugs, destroy tumors, clean up environmental waste, and perform computations, among many other tasks. As the complexity of the task increases, so does the difficulty of the engineering. Software is needed to make the design process easier for complex cellular engineering. Here, Stevens and Myers (DOI: 10.1021/sb300082b) introduce iBioSim, a tool for helping synthetic biologists design and test their circuits *in silico* before undertaking the process of implementation.

iBioSim can also work with a virtual cell population, allowing the researcher to carry out their design and test process on larger scale systems. Combined with other tools, such as plasmid editors and DNA assembly software, iBioSim can be an integral part of a software suite to make the process of cellular engineering much more tractable and efficient.

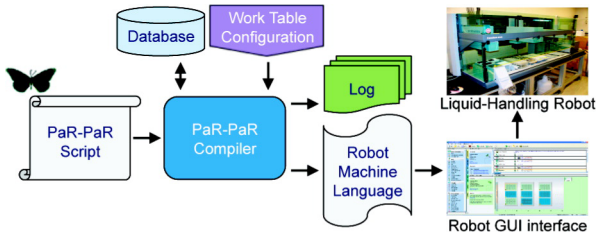
DISCRETE-TIME SIGNAL PROCESSING WITH DNA



The past several years have seen tremendous progress in the design of integrated circuits for signal processing for applications such as audio and video. Complex signal processing systems can be built using basic components like multipliers, adders, and delay units. In this paper, Jiang *et al.* (DOI: 10.1021/sb300087n) describe a methodology for implementing discrete-time signal processing operations with molecular reactions.

Using two different approaches, the authors illustrate their methodology by synthesizing a simple moving-average filter, a biquad filter, and a Fast Fourier Transform, all with potential applications in fields such as biochemical sensing and drug delivery.

PaR-PaR LABORATORY AUTOMATION PLATFORM



While well-funded research laboratories have invested in liquid-handling robots aiming to accelerate research, save time, and provide high-throughput solutions, these robots frequently remain under-utilized with very low duty cycles. To successfully integrate robotics into academic biological laboratory workflows, the efforts required to instruct and operate a robot must be much smaller than the alternative manual lab work. Linshiz *et al.* (DOI: 10.1021/sb300075t) have now developed and experimentally validates a simple high-level robot programming language for biologists.

Programming a Robot (PaR-PaR) allows researchers to use liquid-handling robots effectively and efficiently, enabling experiments previously considered impossible. The adoption of PaR-PaR as a standard cross-platform language would allow hand-written or software-generated robotic protocols to be shared across laboratories, even with different sets of robotic hardware.

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