ACS Synthetic Biology

Editorial

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IWBDA 2015

The International Workshop on Bio-Design Automation (IWBDA) brings together researchers from the synthetic biology, systems biology, and design automation communities. One of the key challenges of synthetic biology is the sheer complexity of engineering biological systems, with regards to both the nature of biological organisms and the profusion of components, protocols, and methods with which these organisms are engineered. The motivating goal of IWBDA is to address these challenges by fostering cross-disciplinary discussion and collaboration between researchers with backgrounds in biology, computation, and other relevant disciplines.

The seventh IWBDA, organized by the nonprofit Bio-Design Automation Consortium (BDAC), was held at the University of Washington in Seattle, Washington on August 19th through 21st, 2015. This special ACS Synthetic Biology issue includes eight papers associated with the work presented at IWBDA, spanning a wide range of different topics and focus areas.

Two of these paper focus on the modeling and optimization of particular biological processes. Woods *et al.* (DOI: 10.1021/acssynbio.5b00179) use a sampling method to explore both the topological and parametric space of biological oscillators, finding both limits on the stability that can be achieved through genetic tuning and some classes of oscillator networks that are predicted to be surprisingly stable. On the metabolic side, Mellor *et al.* (DOI: 10.1021/acssynbio.5b00294) use a machine-learning approach to predict the behavior of enzymatic reactions, which they then show can be used both for pathway design and to predict key reaction parameters.

Three other papers focus on the construction and editing of sequences at large scales. Wilson *et al.* (DOI: 10.1021/acssynbio.5b00194) demonstrate how their new Genome Specification Language can systematize the natural language notations already used by biologists into a formal machine-interpretable language for specifying large-scale DNA sequence designs at multiple levels of abstraction. For large editing of sequences, Quintin *et al.* (DOI: 10.1021/acssynbio.5b00219) present a tool for accelerating MAGE genome editing through automation of oligo design, and for combinatorial design, Roehner *et al.* (DOI: 10.1021/acssynbio.5b00232) use factorial experiment design methods to explore combinatorial design spaces through principled selection of particular designs to test.

Finally, the remaining three papers focus on the challenges of integration and exchange of information about genetic designs across different organizations and tools. Roehner *et al.* (DOI: 10.1021/acssynbio.5b00215) introduce readers to the recently released Synthetic Biology Open Language (SBOL) 2.0 standard for data exchange and illustrate how it can be used to exchange both structural and functional information about biological designs. The other two papers connect to this core by leveraging the new representational power of SBOL 2.0: Wipat *et al.* (DOI: 10.1021/acssynbio.5b00210) present a new form of repository for biological designs, building off of SBOL 2.0 to introduce capabilities not present in prior repositories, and Nguyen *et al.* (DOI: 10.1021/acssynbio.5b00212) present a principled method for integrating sequence information and biological models with a converter between SBOL and the widely used modeling framework Systems Biology Markup Language (SBML).

As the discipline of synthetic biology matures and the goals of its practitioners increase in complexity, design tools are playing an increasingly important role. Together, these papers represent three important aspects of these challenges: deeper models of key processes, large-scale sequence engineering, and integration of tools, information, and processes from across the highly heterogeneous world of synthetic biology.

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Notes

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