

IWBDA 2013

The International Workshop on Bio-Design Automation (IWBDA), organized by the Bio-Design Automation Consortium (BDAC), encompasses research in synthetic biology, systems biology, computer science, and design automation. The focus is on concepts, methodologies, and software tools to enable the computational analysis and experimental characterization of biological systems, especially for synthesis of novel biological functions. This special ACS *Synthetic Biology* issue includes 11 papers based on work introduced during IWBDA at Imperial College London on July 12th and 13th of 2013. The topics covered range from computer-aided-design (CAD) tools for part selection and DNA assembly, to novel CAD algorithms, to nucleic acid circuit design and novel circuit components.

The first set of papers deals with part selection and DNA assembly optimization, ongoing challenges faced by biocircuits designers attempting to leverage the growing repositories of standard biological parts. Blakes, Raz *et al.* introduce a new algorithm for maximizing DNA reuse in synthetic DNA library assembly that beats the runtime of the previous best approach by orders of magnitude. Roehner and Myers apply the directed acyclic graph (DAG) based mapping techniques originally used to select parts for digital electronic circuit designs to genetic circuit design. Huynh and Tagkopoulos extend a dynamic programming (DP) based topology mapping technique from electronic circuits to optimize biological part and module selection. At the laboratory level, Linshiz *et al.* describe the addition of new DNA assembly automation units to the PR-PR system to support a robotic liquid handler, a microfluidic device, and manual steps.

The second set of papers includes several new CAD tools. RetroPath (Carbonell *et al.*) introduces a new type of CAD tool capable of enumerating metabolic circuits that match a desired specification within a metabolic search space. Other new tools include R2oDNA Designer (Casini *et al.*) for generating orthogonal sets of DNA sequences (e.g., for multiway DNA assembly), and a computational method for automated characterization of genetic components (Yordanov, Dalchau *et al.*).

The third set of papers captures the growing interest in the use of feedback in both the production and the operation of nucleic acid circuits. Franco *et al.* demonstrate a framework for applying negative autoregulation to balance supply and demand of synthetic gene products composed of multiple parts ("genelets"). Yordanov, Kim *et al.* address the computational design of nucleic acid feedback control circuits (for example, DNA strand displacement circuits) with application to the design of a Proportional Integral (PI) controller. Kulkarni *et al.* improve the load capacity of nucleic acid based system using partially open feedback control.

Finally, Guinn and Bleris present a mammalian implementation of a 2-input decoder, an important digital building block, based on transcription factors and a synthetic microRNA. In conclusion, the papers in this issue demonstrate remarkable progress in the field, improving upon classic approaches while

introducing new CAD tools and design methodologies for the next generation of synthetic biocircuits.

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Special Issue: IWBDA 2013

Received: July 31, 2014

Published: August 15, 2014