Editorial

Computational Methods Enabling Next-Generation Bioprocesses

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Synthetic biology—the engineering of cells to rewire the biomolecular networks inside them—has witnessed phenomenal progress. In a little over a decade it has evolved from demonstrating proof-of-concept gene circuits in bacteria to developing a whole new class of cell factories able to produce compounds that would otherwise be prohibitively costly and/or unsustainable to obtain, e.g., squalene.

However, despite a thriving community and some notable successes, the basic task of assembling a predictable gene network from biomolecular parts is still a key challenge; it often takes many months to produce a gene circuit with the desired behavior. Mathematical models and Model-Based Systems Engineering methods offer a unique opportunity to address this issue and change fundamental procedures in Synthetic Biology.

This Special Issue on "Computational Synthetic Biology" aims to (i) review recent progress and (ii) report novel advances in the development and application of computational modeling to synthetic biology. The Special Issue consists of six papers and is available online at https://www.mdpi.com/journal/processes/special_issues/synthetic_biology

Despite over two decades worth of efforts, our ability to predict in silico the in vivo behavior of a gene circuit remains limited. One of the main reasons for this is the limited predictive ability of mathematical models for biological parts, very often due to a lack of informative experimental data. Experiments in biology tend to be time-consuming and expensive, so methods for their systematic design are very much needed. This Special Issue features two articles that attempt to tackle such a problem via Optimal Experimental Design. Bandiera and colleagues [1] show how iterative optimization of chemical stimuli leads to faster and more accurate model calibration of a building block of synthetic biology: an inducible promoter. Braniff and colleagues [2] instead use Optimal Experimental Design to extract the dependence of model parameters on the physiology of the host organism.

A necessary step after experiment design optimization is parameter identification and identifiability analysis. This is the subject of the contribution from Cinquemani [3] for the particular case of biomolecular networks. In this study, the author also proposes new reconstruction methods that leverage an increasingly common type of data in synthetic biology: population snapshots from microscopy or cytometry. Two additional contributions [4,5] tackle modelling issues. While Pasotti and colleagues focus on the derivation of mechanistic models of inducible circuits, Boeing and colleagues develop an aspect-oriented modelling framework that allows us to compose parts into circuits and study how they will interact with the host organism. The composability of parts and the use of optimization methods to automatically synthesize gene circuits robust to parametric uncertainty is the focus of Otero-Muras and Banga [6], whose contribution completes this Special Issue.

In assembling this Issue we sought to cover some of the most active areas of research in Synthetic Biology to stimulate discussion within the process engineering community. We hope these papers will ultimately serve as catalysts for cross-pollination of these fields and for their mutual benefit.

References

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