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Bioalgorithms for rational design of biological systems

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In synthetic biology and systems biology, a bottom-up approach is a powerful strategy to understand complex, modular, hierarchical systems of biochemical networks.

To analyze or design biochemical networks where the biological parts or molecular modules interact with each other, it is critically important to understand a variety of the network-function relationships (NFR), the mechanism of how the biological parts are assembled to form building blocks or subnetwork modules with particular functions. To make clear NFRs, a new term "bioalgorithm" is defined as the step-by-step molecular process of how molecular modules and subnetwork modules are combined to generate their particular functions. The bioalgorithms would provide the mechanism of how we analyze the structures of large-scale biochemical networks and the instruction of how we create robust biological circuits that carry out a target function.

We develop a database of bioalgorithms that potentially can cover the whole cells at the molecular interaction level. This database provides the sound bases for an understanding of how elementary networks are assembled to create biological functions and for rational design of biochemical networks for engineering purpose. Extensive study of bioalgorithms would lead to an exploration of biological design principles underlying molecular architectures. The proposed database takes an advantage in simulation function of mathematical models, facilitating an understanding of each bioalgorithm.