

Computational Design of Biological Systems

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Synthetic biologists' aim of designing predictable and novel genetic circuits becomes ever more challenging as the size and complexity of the designs increase. One way to facilitate this process is to use the huge amount of biological data that already exist. However, biological data are often spread in many databases, and are available in different formats and semantics. New computational methods are required to integrate data and to make it available for further mining. Moreover, once integrated, these data can be used to derive designs and mathematical models of biological parts. Computational modelling and simulation will become essential for large-scale synthetic biology. Using model-driven design approaches, biological systems under design can be simulated *in silico* prior to implementation *in vivo*. Whilst there are many tools, that demonstrating the usefulness of model-driven design paradigms, these tools often lack access to modular models of biological parts. Here, we show how data integration and mining can be facilitated using Semantic Web technologies. We use an ontology to represent a wealth of biological information for synthetic biology, and to automate the identification of biological parts relevant to the design of biological systems. We then present an approach to represent modular, reusable and composable models of biological parts. These models, termed standard virtual parts, are created mining biological data and are available from the Virtual Parts Repository. The repository provides data in standard formats, such as the Synthetic Biology Open Language, a standard exchange format for synthetic biology designs. These resources provide computational access to data in standard formats allowing the construction of automated workflows, and facilitate large-scale engineering of biological systems.