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RESEARCH UNIVERSITY

International Journal
of
Innovative Computing

Journal Homepage: http://se.fsksm.utm.my/ijic/index.php/ijic

Characterization of Biological Parts for Modular Genetic Devices: A Comparative Analysis

Jalilah Arijah Mohd Kamarudin[a], Nur Izzati Mohd Noh[a] and Afnizanfaizal Abdullah[a*]
[a]Synthetic Biology Research Group, Health and Wellness Research Alliance,
Universiti Teknologi Malaysia, 81310 UTM, Johor, Malaysia
[*]afnizanfaizal@utm.my

Mohd Adham Isa[b]
[b]Software Engineering Research Group, Faculty of Computing,
Universiti Teknologi Malaysia, 81310 UTM, Johor, Malaysia

***Abstract*— Synthetic biology is a new field that attempting to catalyze new approaches in biotechnology, medicine and other scientific research for engineer biological systems. The area focuses on designing modular and robust genetic devices to facilitate their reuse and reliability in different context. Biological parts are characterized according to their suitable joining to create genetic devices. These biological parts and devices are represented in form of electronic gates. In this paper, we reviewed existing method in designing biological parts and genetic devices in order to build complex system biology. We also highlighted a research to help researchers for expecting forthcoming trends in this area.**

Keywords — Synthetic Biology, Abstraction Hierarchy, Characterization, Genetic Circuit, Electronic Gates

I. INTRODUCTION

Synthetic biology is a new field of study that merges biotechnology, medicine, engineering and scientific research to catalyze new approaches for engineering biological systems [1-6]. In other words, synthetic biology is established to design and construct the novel DNA, protein and cells that produce high-value applications.

Ideally, synthetic biology applies the engineering principle namely hierarchical design, modular reusable parts and standard interfaces to construct biological systems [7]. The elements that include in hierarchical design are genetic information, biological parts, genetic devices and synthetic biology systems [8]. A biological part is a discrete and genetically encoded sequence that exhibits a fundamental biological function, such as a promoter, ribosomal binding sites and coding sequence. Meanwhile, genetic device is an assembly of one or more biological parts that executes a biological function, typically in a form of logical, information-processing circuitries such as genetic switches, logic gates and oscillations [9]. The system that formed by the synthetic biology approach is used to represent as a genetically encoded models to execute a useful user-defined function, which synthesizing a molecule of interest, detecting and processing complex environmental inputs [9].

Synthetic biology sparks new methods and technologies that indicate improvement of design process and functional capabilities of synthetic genetic programs [9]. In order to create biological parts and functional integrations of parts into devices and systems, new tools for DNA synthesis and assembly are proposed [9]. However, there are some limitations in synthetic biology that has been faced by synthetic biologists. One of the limitations is the lack of well-characterized parts for preferred functions. In specific, this is driven by the issues that the engineering methods are highly dependable to the characterization of biological parts that capable in synthesizing genetic functions [9].

As a matter of fact, characterizing biological parts for desired cellular functions is a major challenge in synthetic biology. This is due to the fact that identifying the biological parts is usually hindered by the design of modular and robust genetic devices. The design of these genetic devices is used to synthesize complex biological processes. In this paper, a comparative analysis of computational approaches for characterizing biological parts for modular and robust genetic device design is presented.

TABLE 1: SUMMARY OF ADVANTAGES AND DISADVANTAGES OF BIOLOGICAL PARTS CHARACTERIZATION APPROACHES.

Approach	Related Works	Features	Advantages	Disadvantages
Abstraction Hierarchy	[7]	A molecular element categorized as biological parts able to be used to build biological devices which assembled the parts together to execute desired function and also capable to further combined into systems.	Able to engineer complex system.	Ignoring the unnecessary details. Focus only on high level issues.
Standardization	[10]	Genetically encoded object that perform biological function in order to construct specific design and well-performance into digital catalog.	Standard format to explain parts, construct design and assist - exchange. Parts are able to be translated into computational language. Continuously used in simple circuit design.	Characterized parts unable to function well in different environment context from their origin. Too conservative for development of complex circuit.
Characterization	[14]	Characterizing possible parts and sub-module systematically in different context in order to construct functional devices in related context.	Able to predict behaviour of constructed circuit. Characterized parts able to function well even in different environmental context. Possibly for larger circuit. Less time consuming.	Lack of experimental approaches and new technologies.

II. APPROACH

A. Biological Parts Characterization Approach

In order to predict behavior of the system, several methods or concepts may be used in allowing the design of systems. However, the construction of genetic devices or systems has been limited by the lack of biological parts that may implement the desired functions [9]. In this review, there are three approaches for biological parts characterization are described. The two commonly approaches are abstraction hierarchy and parts standardization and the recent approach is characterization.

B. Abstraction Hierarchy

Abstraction hierarchy is defined as integrating detailed information about individual components into simplified representations of their behavior. Generally, the abstraction hierarchy includes DNA, biological part, genetic device and biological system [8] as illustrates in Figure 1. To design sub-system, these abstract parts may be used of which genetic parts are combined to construct genetic devices that encapsulate certain biological functions [7].

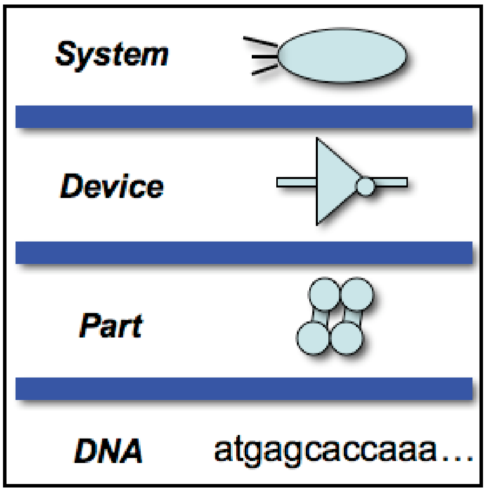


Fig. 1 Abstraction hierarchy in synthetic biology [15]

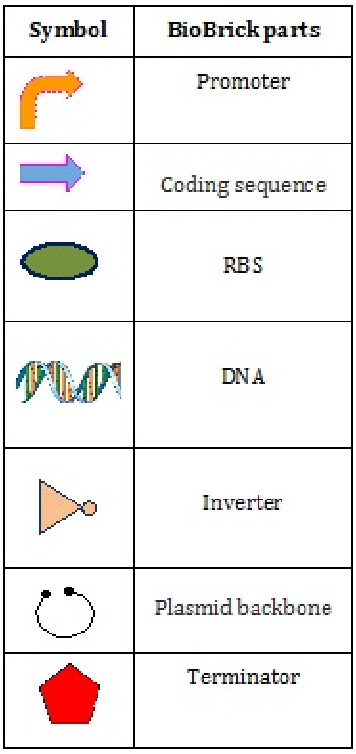
This hierarchical design helps researchers to design complex systems, by disregarding few implementation details and allow them to focus on the high level design issues [8]. This limitation significantly destabilizes the strength of abstraction hierarchy and modular design architectures in synthetic biology.

C. Standardization

Most of synthetic biologists depend on a catalog of short gene sequences called biological parts. These biological parts are mostly retrieved from nature organisms because they are matched to be standard in developing new cells. The production of the biological parts inhibited sets of sequences that fit to certain requirements [10]. Attempting to refine and standardize natural biological parts is an important step for producing new cells. The standard biological parts are defined as genetically encoded sequences that execute a specific biological function and have been engineered to assemble stipulated design or performance needs [10].

The standardization of biological parts is directly encoded through DNA or molecule that primary structure is originated from the existing DNA samples. BioBrick assembly standard is an example of standard supporting the process which two or more parts are connected with genetic devices. BioBrick assembly standard is used to facilitate physical composition of standard biological parts. Figure 2 shows the examples of Biobrick parts and their corresponding standards or symbols.

In order to depict biological parts, construct design and assist their exchange, this BioBrick assembly standard gives a standard format to translate the standard biological parts into computational language [12].



Symbol	BioBrick parts
	Promoter
	Coding sequence
	RBS
	DNA
	Inverter
	Plasmid backbone
	Terminator

Fig. 2 Genetic parts in standardized BioBrick Parts List [16]

However, these well-characterized parts unable to function when they are required to adapt into different environment context from their origin, especially when they moved into new circuits and gather with other parts that naturally incapable to be functioning well. Due to this difficulty, the standard parts failed to contributes in development of complex circuit [13].

D. Characterization

Another approach to resolve the issues on lack of predictability of biological parts is by systematic part characterization. This approach commonly symbolizes a set of potential diverse biological parts and chooses the suitable ones to accommodate the genetic circuit. Furthermore, this characterization process is used to provide a reliable option of components to fabricate functional devices for related functions [14]. In additional, the description of specific quantitative genetic devices can be utilized in reproducing biological parts or new devices. This is required to facilitate the specification for establishing next generation parts and devices, especially in improving new sequence composition and abstraction [10].

III. CONCLUSION

This paper presented a comparative analysis of computational methods for characterizing biological parts for modular and robust genetic devices design. The analysis showed that the abstraction method facilitates researchers to design complex systems by allowing them to focus on the higher level of developmental procedures. At the same time, the construction of genetic devices and systems through standardization method only depends on catalog of synthetic parts. The results suggested that characterization method is most effective method to design multi-function parts and devices. In the future, we planned to propose a new method based on the characterization method. The method is used to facilitate the robust and modular design of genetic devices.

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