MoClo Planner: Supporting Innovation in Bio-Design through Multi-touch Interaction

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Abstract

Synthetic biology is an emerging field that promises to revolutionize biotechnology through the design and construction of new biological constructs useful for medicine, agriculture, and industry. Software tools for this field are currently immature. Our research investigates how interactive tabletops and surfaces could be utilized to enhance innovation in biological design. Here, we present the MoClo Planner, a multi-touch interface, which supports the design and construction of complex biological constructs. MoClo planner was developed in close collaboration with domain scientists to simplify the design stage of a cutting-edge laboratory method.

Author Keywords

Interactive surfaces, multi-touch interaction, molecular cloning, synthetic biology.

ACM Classification Keywords

H.5.2 [Information Interfaces and Presentation]: User Interfaces.

Introduction

The emerging research field of synthetic biology offers the promise to transform biotechnology through the
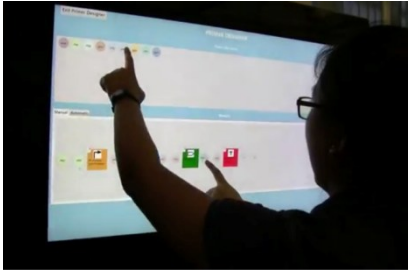
Figure 1: The Primer Designer used to actualize genetic constructs, can be accessed from Levels 0-2.

design and construction of novel biological systems useful for medicine, agriculture and industry [5].

The field applies engineering principles such as abstraction and modularity into biological research, treating genetic elements as standardized biological parts, which can be combined and swapped in a plug-and-play manner before they are inserted into host organisms. However, a limiting factor in synthetic biology research is the ability of current methods to assemble complex DNA molecules encoding multiple genetic elements [9].

Golden Gate Modular Cloning (MoClo) [9] is a novel laboratory method that allows the efficient creation of multi-gene constructs from a library of biological parts. Using this method, biological parts are permuted and joined together in a tiered fashion to create new synthetic biology constructs, which are called BioBricks. While the MoClo method reduces the number of laboratory steps required for the assembly of multi-gene constructs, it requires careful design and planning. Planning for the MoClo method includes: browsing a library over 2200 biological parts; selecting biological parts based on their function, genetic sequence, and other biological characteristics; computing possible permutations of parts in predefined arrangements; and designing primers and fusion recognition sites (a task that involves the identification and testing of short sequences of DNA marking the start and end of a particular region of DNA, which are necessary for amplifying and assembling DNA). Currently, there is no computational support for the MoClo design process. Thus, biologists use a combination of existing web-based databases and tools as well as spreadsheets in order to retrieve, store, synthesize, and organize the information required for MoClo design. This process is time consuming, error-prone, and is rarely understandable for novices in the field (e.g. student researchers).

The MoClo Planner application that we present in this paper, utilizes multi-touch interaction to simplify the design process of complex biological constructs. The application provides an interactive visualization of the MoClo process; facilitates an integrated yet flexible workflow; and utilizes direct and spatial interaction to give users more control over the design process. The application also supports co-located collaboration through multiple touch points. The goal of this research is to investigate how interactive tabletops and surfaces could be utilized to enhance innovation in biological research. Following, we describe the design, implementation, and preliminary evaluation of MoClo Planner. We begin with related work.

Related Work

Existing computational tools do not provide comprehensive support for biological design. Biologists often use a variety of existing web-based and commercial bioinformatics tools in order to retrieve, compare, and study genetic elements. Several studies indicate that current web-based bioinformatics tools show severe limitations in supporting users to gain deep insights [6]. A number of projects have been undertaken by the synthetic biology community to support data management and storage (e.g. MIT Registry of Standard Biological Parts), and facilitate the development of applications for the synthetic biology domain [Xia et al. 2011]. The Synthetic Biology Open Language [2011] and Eugene [2] are domain specific languages for synthetic biology. In addition, several research prototypes were developed to support the design of biological systems including GenoCAD [3] and Tinkercell [4]. However,
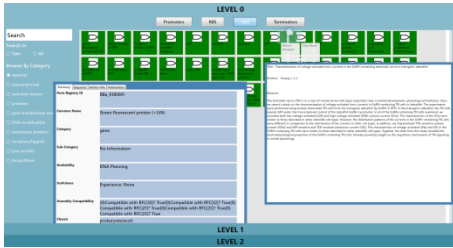
Figure 2: Level 0 design of the MoClo Planner

Figure 3: Level 1 and Level 2 of the MoClo Planner

these prototypes are limited in their functionality and compatibility with other community efforts such as the MIT Registry of Standard Biological Parts and SBOL.

Design Process and Goals

MoClo Planner is the result of a participatory design process in which we partnered with two groups of investigators and students from Boston University and MIT, who conduct research in synthetic biology. In collaboration with our design partners we defined the following design goals for MoClo Planner: 1) Lower the barriers for MoClo design, making it available for the growing community of novice synthetic biology researchers [8]; 2) Facilitate an integrated and flexible workflow; 3) Provide users with control over the design process while eliminating errors; and 4) Fostering collaborative problem solving.

MoClo Planner

The current prototype of MoClo Planner is implemented using a multi-touch vertical surface (SUR40). Our decision to use a vertical interactive surface was informed by current work practices of our users (side-by-side work on the white board or a shared screen), and by recent theories in the cognitive sciences, such as embodied cognition, that illustrates the importance of the body, external artifacts, and the environment in reasoning and learning [1].

MoClo planner organizes the design process using three "shutters"; each shutter provides a workspace corresponding to a particular level of the MoClo design process: In Level 0, the application allows users to browse a collection of biological parts (curated by the MIT Registry of Biological Parts). Upon demand (indicated by touch) the application generates a data sheet charac-

terizing the part's behavior, retrieving its genomic sequences, and displaying PubMed and iGEM abstracts related to that part drawing information in real time from the Registry of Biological Parts. Users can select parts of interest and save them by dragging them into the Level 1 shutter. Figure 2 shows the Level 0 shutter.

Parts that were saved by the users into Level 1, are automatically organized according to their biological function. In Level 1, users design transcription units (i.e. biological constructs that contain a single gene) from the basic parts selected in Level 0. The design of transcription units must satisfy several constraints that are expressed to users in the form of a template. The application enables users to automatically or manually create constraint-based permutations of the selected parts so that all possible transcription units can be considered. Users can then select those transcription units of interest and drag them to level 2. Figure 3 shows the transcription units created in Level 1 and saved to Level 2.

Finally, in Level 2 users can create multi-gene constructs that consist of series of transcription units. Again, the application enables users to automatically or manually create constraint-based permutations of selected transcription units so that all possible constructs can be considered. Figure 3 illustrates the permutations created in Level 2.

On each of the levels, users can launch the built-in primer designer, which allows users to convert abstract parts or constructs into concrete genetic elements by generating primers and protocols to facilitate construct assembly in the lab. Unlike many existing primer design applications, our primer designer provides users with
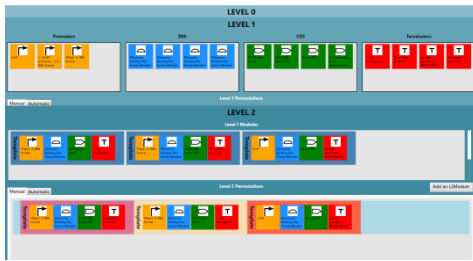
full control, allowing them to customize primer sequences and to select computational tests. Figure 1 shows a user interacting with the primer designer.

In order to facilitate an integrated and flexible workflow, the application allows users to move back and forward between levels, keeping one or multiple shutters open at any given time, and dragging elements between shutters. Leveraging this fluid interaction, users can iterate on their design, go back to select additional parts, explore information, or trace previous design decisions.

Implementation
The MoClo planner is implemented on the Microsoft Surface SUR40 device using MS SDK 2.0 and C#. Information is drawn from the MIT Registry of Biological Parts, PubMed, and the iGEM archive [8]. Eugene is used for testing and validating permutations.

Evaluation
24 undergraduate Biology and Biological Engineering student researchers from Wellesley College, Boston University, and MIT participated in our evaluation process, using MoClo Planner to conduct an inquiry-based modular cloning task in pairs.   Preliminary analysis of the quantitative and qualitative data collected indicates that users found the multi-touch interaction intuitive and the process visualization clear. Further user suggestions provide inspiration for the next iterations for our designs.

Conclusion
We presented MoClo Planner, a multi-touch interface for supporting the design of complex and useful biological constructs. We plan to iterate on the design of Mo-Clo Planner and evaluate its use and impact by deploying it in a synthetic biology research lab. Our goal is to understand how interactive tabletop and surfaces can support innovation in biological design.

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