Supporting Cutting-Edge Synthetic Biology Research with Touch-Based Technology

Abstract

Our team will create a collection of software tools which address specific technical synthetic biology challenges while simultaneously advancing the way in which users interact with computing environments. The MoClo Planner application tackles the question of how human-computer interaction can enhance discovery in an emerging field such as synthetic biology, where designing complex biological systems and processing related metadata is becoming increasingly important. The MoClo Planner assists synthetic biologists in utilizing cutting-edge lab techniques for building biological systems such as Golden Gate Modular Cloning. Golden Gate Modular Cloning (MoClo) is a hierarchical modular cloning system that enables the creation of any multi-gene construct from a library of biological "parts". In this modular cloning system, "parts" are permuted and joined together in a tiered fashion to create new synthetic biology constructs, called "biobricks". The MoClo Planner abstracts and visualizes this complex process using an intuitive touch-enabled platform. Synbio Search is an online tool that links and integrates data related to over 2700 biological parts. It allows synthetic biologists to discover the most comprehensive view of freely available data concerning biological parts from a single search. SynFlo is an interactive installation that utilizes tangible interaction to help illustrate core concepts of synthetic biology in outreach programs. The playful installation allows users to explore standard synthetic biology concepts and techniques by creating useful virtual life forms from standard genetic components.

SynBio Search

SynBio Search is a web tool that provides access to a comprehensive data sheet for over 2700 biological parts. It integrates and links information from various data sources, including the MIT Registry of Standard Biological Parts, iGem Archive, Google Scholar, and PubMed. SynBio Search builds on the collected sources by providing a structured view that relates heterogeneous information, links back to original data sources, and allows users to customize and organize the display. It enables researchers to discover the most comprehensive view of freely available data about biological parts from a single online search.

Implementation

The user interface is implemented using HTML 5.0 and CSS 3.0. The back end is implemented using JavaScript, Ruby, jQuery, and JSON.

User Studies

The software development process followed a user-centered approach. A total of 37 biology and biological engineering students from Wellesley, Boston University, and MIT participated in our design and testing process. Audio and video recordings, in addition to a post-task questionnaire, were used to evaluate the usability and usefulness of the MoClo Planner and SynBio Search application, including the simplicity and intuitiveness of the design and the robustness of the back-end algorithms.

Future Work

• SynBio Search will be further developed to include user-requested databases (Clotho, SynBERC, etc) and incorporating more data fields.
• The MoClo Planner will be integrated into the Clotho application suite and incorporated in BU and MIT labs for modular cloning design.
• SynFlo will be presented as a demonstration at several upcoming conferences and will be updated to support the new Sifteo SDK.

MoClo Planner

Project Brief

The MoClo planner simplifies the complex hierarchical modular cloning design process by greatly reducing the mental workload of designing abstract synthetic constructs. The multi-touch application facilitates organized and collaborative manipulation of complex biological constructs from simple biological "parts," such as primers, ribosome binding sites, coding sequences, and terminators, to complex synthetic biology constructs called "biobricks," in the process lowering the threshold to understanding such intricate systems. Users can manually and automatically create "biobricks" in an intuitive and linear fashion, while seamlessly accessing vast amounts of metadata pertinent to each synthetic construct. The MoClo planner gives synthetic biologists access to important research material including related background information, publications, and genomic data about each "part" that would take scientists much more time and effort to compile together individually. Thus, the MoClo planner not only facilitates the design and development of increasingly complex biological systems but also increases the efficiency and level of collaboration involved in designing synthetic biology systems.

Design

The MoClo Planner is divided into three shutters for the three levels of modular cloning. In the Level 0 shutter, the users can browse the Registry of Standard Biological Parts for Level 0 parts, access a data sheet characterizing a part’s behavior, retrieve genomic sequences, and find PubMed abstracts that are related to the part. In Levels 1 and 2, users can manually or automatically construct modules from previously-selected parts, which become synthetic biology constructs called "biobricks". Modules of any level can launch the built-in primer designer, which generates primers and protocols to facilitate module assembly.

Implementation

The MoClo Planner is implemented on the Microsoft Surface device using MS SDK 2.0, Qt, and the HTML Agility Pack. Eugene, a human-and-computer-readable language, generates permutations for the backend.

Screenshots of the MoClo Planner in action. (Top) Generating L0 parts and data sheets. (Middle) Permuting L1 modules to create L2 modules. (Bottom) Manipulating fusion sites in the primer designer.