



ACM Journal on Emerging Technologies in Computing

Special Issue on BioFoundries and Cloud Laboratories

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Synthetic biology ushered in the appearance of engineering approaches applied to the design of novel biological systems. These approaches include abstraction, automation, and compositional design of living systems using engineered DNA building blocks. These forward-engineered, complex systems allow for advances in medicine, materials, and energy. Many of these systems also include biological sensors that replicate traditional computational paradigms as well as living memory elements that can sense and record their environment.

Synthetic biology in particular advocates a “design-build-test” cycle and the democratization of engineering biology. A natural manifestation of this approach is to provide remote “biofoundry” services that allow for the experimental execution of the “build and test” portions of the cycle. Not only do these services allow practitioners to emerge that do not have access to experimental facilities, but they also allow for standardized, reproducible, high-throughput workflows. Ultimately these facilities will help to drive innovation while preventing costly errors due to manual approaches and underspecified protocols.

Cloud labs are a natural extension of the biofoundry model with improved remote access via well-defined APIs to allow computational tools to interact directly with the experimental equipment and personnel. Ideally, this interaction includes controlling the process as well as viewing and manipulating the data being generated. Cloud labs will allow for experimental capabilities to be exposed as “services”. Those services can then be scheduled across jobs, locations, and personnel. A robust cloud lab infrastructure if properly developed could usher in a new era of engineered biology as the user base expands exponentially and machine learning and AI approaches refine protocols to be faster, more efficient, and more portable.

Despite all the potential benefits of cloud labs and biofoundries, they are not without their challenges. These include how to efficiently expose services to the user, comprehensive standardized data exchange, and hardware/software scheduling. In addition, data privacy and security must be maintained at all times. Biosafety protections from both accidental and malicious usage must also be guarded against.

The goal of the special issue is to begin the process of outlining the requirements, technologies, approaches, software, hardware, and expertise required to create a biofoundry or cloud laboratory. A particular focus is on approaches that borrow techniques from computer science and engineering. The scope of this Special Issue of ACM JETC should be on the computational as opposed to the experimental aspects of the process.

Topics

1. Protocol Formalization
 - How to electronically capture experimental protocols unambiguously and formally
 - Programming languages and environments for protocol specification and test
 - Online repositories, databases, and data structures for protocols
 - Protocol verification and simulation algorithms and software

2. Data Exchange Mechanisms

- Standards for data capture and exchange
- APIs and associated workflows to enable robust data exchange
- Privacy and security of data exchange associated with cloud labs and Biofoundries
- Data conversion and analysis methods to support multiple workflows, equipment, and protocols.

3. Scheduling and Automation

- Scheduling algorithms for biofoundry operations
- High-throughput automation approaches for liquid handling robotic and microfluidic integration
- Bio-Safety best practice and screening approaches

4. Rapid Optimization of Genetic Designs

- Hardware and software tools for designing and fabricating genetic constructs at large-scales
- Computational approaches for high-throughput, automated experimental data screening, and analytics of bio-materials and market-value products
- AI algorithms for accurate sampling of design parameter landscapes, and predicting dynamic properties of genetic systems
- Computational tools for multi-scale integration of single cell-omics (transcriptomics, proteomics, and metabolomics) data of cellular systems

5. Biofoundries as “Data-Centers of the Future”

- Compilers, formal semantics for translating programming languages to DNA based computation
- Coding theory, encoding, decoding schemes for DNA storage
- Network theory and mathematical models for multi-cellular communication paradigms and topologies
- Applications of DNA origami for DNA computing applications

Important Dates

- Submission deadline: November 1, 2021
- First round review decisions: January 15, 2022
- Deadline for revision submissions: February 15, 2022
- Second round review decisions: April 1, 2022
- Deadline for revision submissions: May 1, 2022
- Notification of Acceptance: June 1, 2022
- Publication date: TBD

Submission Information

All original manuscripts or revisions to the ACM JETC must be submitted electronically online at mc.manuscriptcentral.com/jetc. The author guideline for ACM JETC can be found at dl.acm.org/journal/jetc/author-guidelines. Select the paper type "SI: BioFoundries" upon submission to ensure that the article is considered for this special issue. The authors must also mention the same in their submission cover letter.

Submitted articles must not have been previously published or currently submitted for publication elsewhere. For previously published conference papers, it is required that submissions to the special issue have at least 30% new content. Submissions that do not meet this requirement will be summarily rejected.

For questions and further information, please contact **Douglas Densmore** at dougd@bu.edu