BRC Science Highlight
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Towards a Fully Automated Algorithm-Driven Platform for Biosystems Design

Background/objective

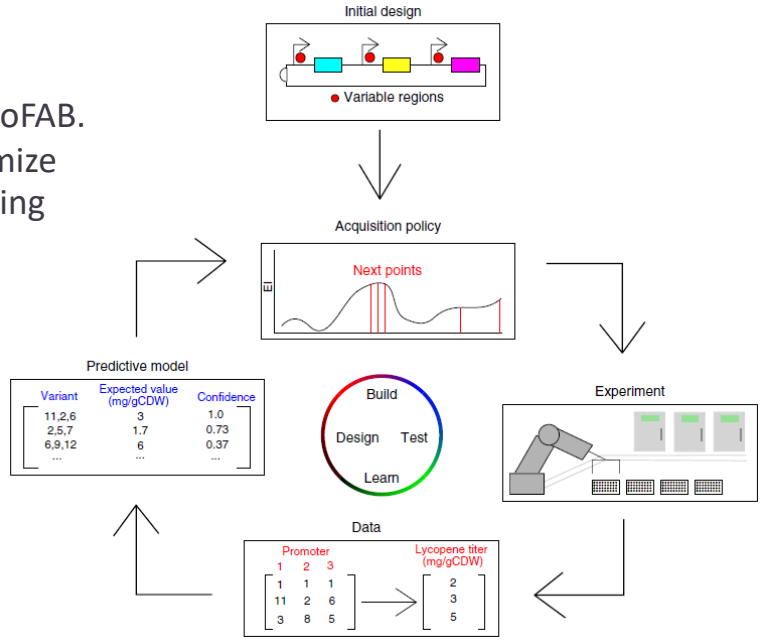
Biological systems are increasingly being explored for biotechnology applications. However, due to their complexity, successful engineering requires many rounds of the design, build, test, learn (DBTL) cycle. Automated biofoundries, such as the Illinois Biological Foundry for Advanced Biomanufacturing (iBioFAB) have expedited the DBT portion of the cycle, but integrating an automated learn step into the cycle has remained a largely unrealized challenge. Here, researchers present BioAutomata, the first demonstration of a fully automated DBTL system for biosystems design.

Approach

- A Bayesian optimization algorithm was developed and tested on random Gaussian mixture models before integrating it with the iBioFAB.
- As a proof of concept, the automated process was applied to optimize the lycopene biosynthetic pathway in *E. coli* BL21(DE3) by fine-tuning flux through each step in the multi-step pathway.

Results

- The Bayesian model was able to find the maximum for all functions with less than 20% error.
- An optimization between the experimental cost (total number of experiments) and time (number of DBTL cycles) was performed and 46 samples per run was found to be the optimum number.
- Maximum lycopene titer after three rounds of BioAutomata was 1.77 times that of the maximum obtained via random sampling.



After setting initial parameters, the workflow of BioAutomata selects and runs experiments, generates data, and updates the predictive model to optimize the system toward a predetermined outcome.

Significance

These results are the first demonstration of a fully automated DBTL cycle. Beyond pathway optimization, BioAutomata can be used for other black-box optimization problems such as protein engineering, genome engineering, or buffer and media optimizations.

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