

Algorithmic Optimization for Pathway Engineering and Beyond

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This talk will discuss early application of linear regression models to optimize combinatorial libraries of biosynthetic pathways and how this frames the future of AI in synthetic biology. Through a discussion of several biological systems constructed in yeast, we will show how heterologous pathway engineering lends itself to machine learning to predict desired enzyme expression levels for optimal function. We will then show how we are working to include host modifications within this framework. In the course of expanding the number of variables in algorithmic optimization workflows, we have begun to encounter limits in biological quantitation. Current methods for obtaining biological information are practically data-poor for machine learning and much of the information is aggregated by experts over the corpus of literature. Therefore, there is motivation to construct searchable databases and conduct literature mining to assemble all the information necessary to initiate and modify a design. Thus, we argue that supporting the genetic designer is a grand challenge facing those who wish to continue to find new applications for AI in synthetic biology.