An integrative genome-scale *E. coli* model and target experimentation methodology for systems and synthetic biology

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ABSTRACT

While important in their own right, integration of genome-scale host models with synthetic circuit design tools will be a boon for synthetic biology, as they will provide more accurate predictions of circuit dynamics and function. Towards this goal, we have developed the most comprehensive normalized gene expression compendium of 4,291 genes over 2,262 microarray and RNA-Seq datasets that covers knock-out, overexpression and rewiring experiments. In addition, we constructed a signal transduction database for 151 TF-effector interactions that is supplemented with a phenomics database with more than 600 growth assays. The resulting genome-scale model integrates the transcription, signal transduction and metabolic layers through a novel constraint-based framework, and exhibits high predictive performance for both growth rates and expression profiles. We have devised an iterative procedure for model refinement, which is based on targeted RNA-Seq experiments that we are conducting in our lab [1]. I will discuss how the genome-scale model can be integrated with SBROME [2][3], the first modular, automated design platform that can provide optimality guarantees in synthetic circuit design by using exact and approximation methods for rapidly traversing the solution space [4].

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