

Title: Biophysical Models of Translation, Translational Coupling, and Small RNA Regulation to Predict and Control Protein Expression

Abstract: The Salis Lab develops biophysical models of gene expression and regulation to predict protein expression levels from DNA sequence. We combine kinetics, statistical thermodynamics, and optimization to calculate binding energies between ribosome, mRNA, and regulatory RNAs in bacteria, enabling the prediction of translation initiation rates, the effects of small RNA regulation, and the coordination of protein expression via translational coupling in multi-cistronic operons. We experimentally evaluate model predictions on synthetic and natural sequences, using reporter proteins, flow cytometry, and qRT-PCR to quantify mRNA and protein expression levels. User-friendly web interfaces to these biophysical models are available at <http://salis.psu.edu/software>.

Thank you,
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