

180. Parametrizing a Genome-Scale Model of Metabolism and Expression in *E. coli* with Multi-omic Data

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The quantitative relationship between the rates of transcription, translation, and catalytic activity for any given enzyme are important constraints on models coupling metabolism with gene expression (ME). We have assembled a dataset of proteomic and transcriptomic data for *E. coli* growing in batch on four different carbon sources: glucose, fumarate, pyruvate, and acetate. We have found that the protein/mRNA ratio remains constant for most genes across the different environments. Using a recently reconstructed ME model for *E. coli*, we have developed an algorithm which uses expression from experimental data and metabolic flux computed in the model to iteratively estimate parameters constraining enzymatic activities, sampling from different starting values. The converging model parameters proved to be remarkably consistent across all four conditions, and correlate with reported enzyme efficiencies. For some reactions for which fluxomic data is available, parameters calculated using measured instead of modeled fluxes were integrated into the parameter set. Using this parameter set increases the accuracy of the ME model when predicting differential expression between different conditions.