



INSTITUTE FOR CELLULAR ENGINEERING

Using Flux Balance Analysis to Model Substrate-Specific and Wild-Type *E. coli* Fermentations

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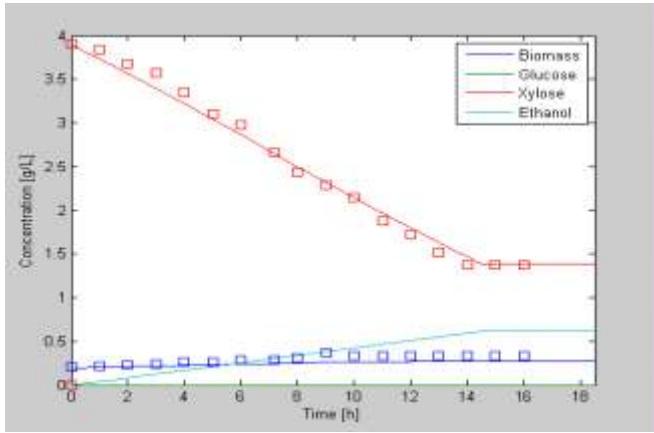


Figure 1. Pictured is data collected during an anaerobic run at 37oC and pH 7. The lines represent the models respective predictions according to the lab's determined parameters.

Dynamic Flux Balance Analysis (DFBA) is a constraint based approach to modeling cell metabolism. It derives a feasible set of steady-state fluxes that optimize a stated objective while adhering to a set of constraints derived principally from mass balances. By fitting DFBA models to experimental data, unknown parameters, such as the maximum uptake rates and uptake saturation constants for different substrates, may be determined

My project's goal is to aid in using DFBA to model the cell metabolism of *E. coli*. My focus is on developing parameters for *E. coli*'s consumption of xylose so that this process may be better predicted in subsequent runs. Understanding *E. coli*'s consumption of xylose is of particular importance because xylose is a major component of lignocellulosic biomass and it must be converted for the viable production of bioproducts from this abundant material.

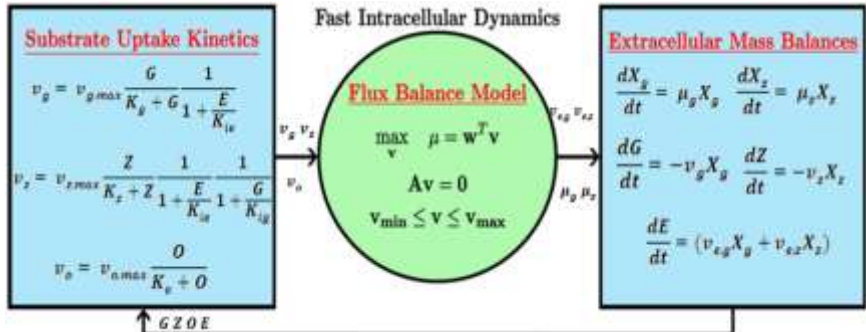


Figure 2. A summary of the mathematics behind Dynamic Flux Balance Analysis.