Yield and kinetic parameters estimation and model reduction in a recombinant *E. coli* fermentation

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Abstract
A genetic algorithm was used to estimate both yield and kinetic coefficients of an unstructured model representing a high-cell density fermentation of *E. coli*. The model is composed of mass balance equations with 3 states: Biomass, Glucose, and Acetate. Kinetic equations are based on the 3 main metabolic pathways of the microorganism: glucose oxidation, fermentation of glucose and acetate oxidation. Genetic Algorithms were used to minimize the normalized quadratic differences between simulated and real values of the state variables, by manipulating both yield and kinetic coefficients. Data from real fed-batch fermentation runs were analyzed with this optimization routine, the new parameter set obtained allowing a much better description of the process behaviour when compared to simulations conducted with non-optimized parameters (obtained from literature).

After parameter estimation, a sensitivity function analysis was applied to evaluate the influence of the various parameters on the state variables biomass, acetate, and glucose. Thus, essential parameters were selected and the model was re-written in a more simplified form that could also describe accurately experimental data.

Keywords: Genetic Algorithms, *E. coli*; fed-batch fermentation; sensitivity function; model reduction.