Computational Studies of Some Structured Cell Growth Models

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Keywords: Batch Fermentation Process, Cell Growth, Biomass-Substrate-Product Dynamics, Reaction Schemes, ODE Systems, Verification Methods, Numerical Simulation.

We study mathematically and computationally experimental data of batch fermentation processes. The data for the bacterial biomass, substrate and product are given together with bounds for the involved systematic errors. We first describe and motivate our modelling approach on the case study with the Henri-Michaelis-Menten (HMM) biochemical reaction of the enzyme-substrate dynamics where two fractions of enzymes (free and bound) are involved. Similarly, two phases (fractions) of the bacterial cells are considered: dividing and non-dividing cells. The HMM reaction scheme is used to describe the transitition of bacterial cells from one phase to another as well as the cell growth due to substrate uptake [1, 2]. The reaction schemes are formulated with a strong emphasis on the enzymatic competence of the cells as well as their reproduction abilities. The aim of this study is to confirm or reject the proposed reaction schemes as possible cell growth mechanisms. To this end we use verification interval methods and advanced computational tools.

References

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