Modeling and Dynamics of Methane Production in Bioreactors (J. Rebaza)

Bioreactors are used in processing wastewaters and slurries that typically contain high concentrations of biodegradable organic material. The pollutant concentration is reduced through the use of bacterial species that consume the organic matter, eventually producing biogas (mainly methane), in a very complex process. Identified subprocesses of degradation are hydrolysis, acidogenesis, acetogenesis and methanogenesis. First, biological (through acidogenic bacteria), chemical and physical hydrolysis is applied to carbohydrates, fats, and proteins to break them down into amino-acids, sugars and long-chain fatty acids. Then, acid-forming bacteria are used to produce volatile fatty acids, carbon dioxide and hydrogen. Acetogenic bacteria will then produce acetic acid and hydrogen. In the final step, methane bacteria will produce methane.

Several models have been proposed to study this complex process, including [1, 2, 3, 4, 5]. They all boil down to multi-dimensional dynamical systems of differential equations. Different approaches include a single bioreactor, a cascade of bioreactors, or reduction of the model to a two-stage process. Typically, all models include local stability analysis of steady states, while only very few of them introduce a numerical or graphical analysis of bifurcations. We plan to study a simplified macroscopic model of the anaerobic process mainly based on two reactions (four-dimensional system), with different types of specific growth rates of bacteria: Monod, Contoid, and Haldane models. Besides local stability analysis of the models, we aim at providing mathematical proofs of existence of bifurcations in the system, as well as locating possible heteroclinic orbits connecting two different steady states. Numerical simulations should further illustrate the main results of this study.

At a second level of research, we could include the presence of an external agent in the system that could affect the growth of one or more of the organisms [6]. The first approach is to assume that the bacteria cannot counteract the presence and growth of such external agent. The second case is when the bacteria are able to affect the growth of the external agent and its negative effect on the system itself, consequently adding one more differential equation to the system.

Prerequisites: A basic background on differential equations and linear algebra, in addition to the calculus sequence. Some programming experience is desirable but not required.

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