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Modeling the Residence Time Distribution In a Batch Fermentor: Comparison of CFD Prediction with Experiment

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Abhishek Dutta[1], **Rita Lencastre Fernandes**[2], Anna-Lena Heins[3], Anna Eliasson Lantz[3], Anker D. Jensen[2], Krist V. Gernaey[2] and Ingmar Nopens[1], (1)Biomath, University of Ghent, Ghent, Belgium, (2)Department of Chemical and Biochemical Engineering, Technical University of Denmark, Kgs. Lyngby, Denmark, (3)Department of Systems Biology, Technical University of Denmark, Kgs. Lyngby, Denmark

Continuous stirred tank reactors (CSTR) are ubiquitously used as fermenters in the biotechnological production of enzymes, pharmaceuticals, metabolites, antibodies, etc. They are also used in the bioprocess industry for the production of bio-ethanol, bio-hydrogen and even in mammalian cell culture. In most cases, a scale-up of these processes is necessary to yield commercial success and viability. As with most scaling-up operations, mixing is also a crucial parameter in a biological process and is often not ideal when operating at industrial scale. Poor mixing in a CSTR may be caused by gas by-passing and back-mixing phenomena leading to the formation of dead zones where, in the case of a bioreactor, cells will experience a limited supply of nutrients and oxygen. In large-scale bioreactors gradients of e.g. substrate, oxygen and pH arise as a result of non-ideal mixing, resulting in a spatially heterogeneous extracellular environment. This fact has been suggested to be the main reason behind lower product yields, but higher cell viability, in comparison to lab scale cultivation (Enfors et al., 2001)

Understanding bioreactor hydrodynamics in general, and non-ideal mixing in particular, is a key problem to understand the inherent bioprocess. The Residence Time Distribution (RTD) is one such way to characterize the non-ideal mixing in a CSTR (Choi et al., 2004). To estimate the RTD, a glucose tracer study has been performed experimentally in a Sartorius CPlus¨ batch bioreactor, having a working capacity of 10 litres, and the results were compared using Computational Fluid Dynamics (CFD) simulations. Several cases with varying impeller speed have been considered to study the effect of mixing phenomena on the RTD. The mean and variance of the distribution are analyzed for the extent of the deviation of the reactor behavior from its ideal state. Furthermore, the sensitivity of the sliding mesh is tested by varying the position of the interface zone. This would eventually contribute to building an optimized model of the bioreactor, and will be used for integration with biological models aiming at improving performance prediction in the cases of poorly-mixed reactors.

Reference

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