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Model Based *Escherichia Coli* Bacteria Fermentation

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The biological production of active compounds, ranging from small molecules, such as organic acids, vitamins or antibiotics, through to macromolecules, such as therapeutic proteins or plasmid gene therapy vectors, is of great commercial and social value [1]. *Escherichia coli* bacteria is one of representatives what is widely used industrially to produce many of highly valued bio-products, where a major advantage of this host is to successfully produce a large number of recombinant proteins used in medicine [2, 3]. The cornerstone of any such bioprocess is the cell cultivation step where a highly selected, and usually engineered, cell-line is grown under carefully controlled conditions.

Quantitative description - modeling of cellular processes is an indispensable tool in the design of fermentation processes [4]. Thus, the two most important quantitative design parameters, yield and productivity, are quantitative measures that specify how the cells convert the substrates to the product. Important aspects of efficient fermentation of microorganisms in most of cases concern the application of convenient fed-batch process, what directly influence fermentation process control and final yields. Fermentation

modeling procedure allows to calculate desirable feeding rate in every special case.

In our research we used models which state mass balance for biomass (X), substrate (S), acetate (A), vessel volume (V) and additional model for bioreactor mass flows (F). In such a way we achieved controlled and predefined biomass growth according to the process model (Fig.1). Using well defined fed-batch media which consisted from salts and glucose, in most successive runs we achieved *E. coli* cultures with biomass concentrations up to 60 g/l.

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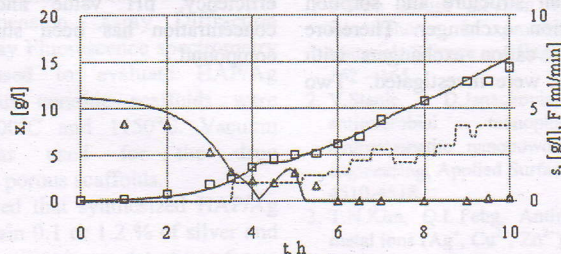


Fig.1 Fermentation process dynamics. Experimental data: biomass – squares, substrate (glucose) – triangles. Model data: biomass, substrate – solid lines, feeding rate – dashed line.

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