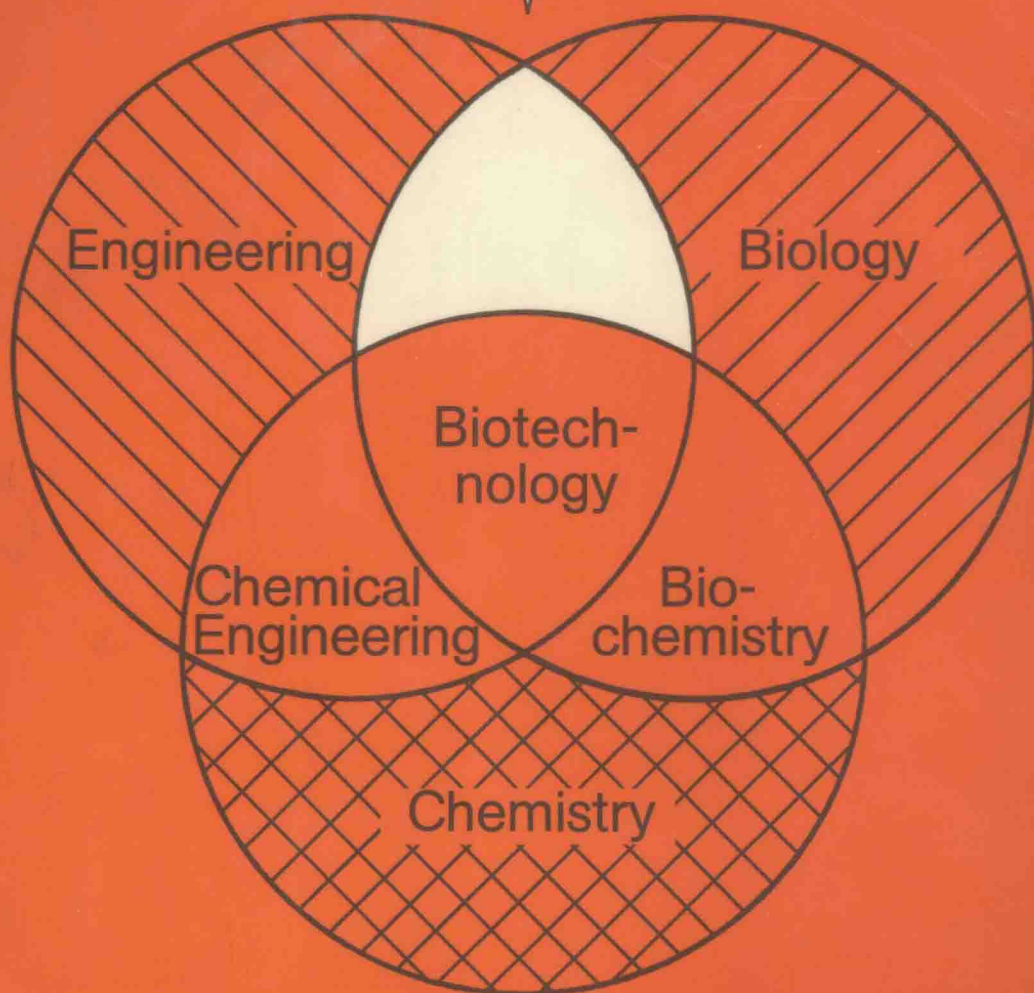


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Biochemical Engineering



Gustav Fischer

Biochemical Engineering

A Challenge for Interdisciplinary Cooperation

Edited by

H. Chmiel, W.P. Hammes and J.E. Bailey

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Preface

In 1986, the Minister for Research and Technology of the Federal Republic of Germany and the Minister of State of Baden-Württemberg agreed to establish and financially support a research center in Stuttgart concentrating on biochemical engineering. The motivation for this joint venture is to complement biotechnological activities in industry as well as at universities and other research institutes of Baden-Württemberg by research activities concentrating on biochemical engineering and applied biosciences. Cooperation among different biochemical disciplines and a transfer of know-how to industry from fundamental university research will be facilitated via applied research undertaken by the Fraunhofer-Gesellschaft.

An international congress, attended by over 500 delegates representing industry and universities from more than 15 countries, was held in Stuttgart in September 1986, to mark the start of this new activity. The overall themes of the congress were the opportunities and the challenges of the future, to integrate advances in biology, chemistry, and process engineering to promote the industrial practice of biotechnology. Some new products and new processes will not be commercially viable unless engineers and scientists can cooperate to combine synergistically the complete spectrum of genetic, chemical, and process methods for optimizing the product and the bioprocess.

In this volume, which contains most of the papers presented at the congress, new developments and future problems in biochemical engineering and in the related biological sciences are highlighted. These papers address the following main themes in biochemical engineering:

- Bioprocess technology with special attention to scale-up
- The application of bioprocesses for the production of foodstuffs, fine chemicals, and pharmaceuticals
- Optimization of existing types of bioreactors and development of a new generation of bioreactors
- Downstream processing, including product separation, concentration and purification

Hopefully this volume will aid the international biochemical engineering community to identify new opportunities for cooperation and for future contributions to the emerging biotechnology industry.

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H. Chmiel, W.P. Hammes, J.E. Bailey

Stuttgart, December 1987

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Growth and Product Formation Kinetics in Recombinant Microbes

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The central theme of this presentation is the set of exciting opportunities which exist for cooperation between biochemical engineers and molecular biologists to optimize organisms and processes for production of valuable compounds using genetically engineered cells. The examples which follow, which will illustrate productive interactions between information and methods from the biological and engineering sciences, focus on the cell as a complex chemical reactor. Understanding of the response of the cell to different types of genetic and environmental manipulations is central to bioreactor optimization and to placing bioreactor scale-up on a more reliable and systematic basis.

Considering the rate of synthesis of a single protein product expressed from a cloned gene, the prototype example through most of this presentation, it is apparent that the synthesis rate is given by the integral of product of the density of cells in the culture, the rate at which plasmid-containing cells synthesize the product protein as a function of the number of plasmid copies in the cell, and the distribution of plasmid content within individual cells in the population. In the following examples we will examine how engineering methods can be used to analyze and describe in quantitative terms the plasmid replication and segregation properties in a recombinant population, the rates of product synthesis, and the growth characteristics of plasmid-harboring cells.

Genetically Structured Models: Plasmid Replication

As an example of one type of analysis at the level of molecular interactions, we shall first consider plasmid replication kinetics. Like the kinetics of synthesis of many biological macromolecules, it is the frequency of initiation of synthesis which dictates the synthesis rates. As a particular example, we shall examine the replication of plasmid λ dv and a detailed mathematical model that has been formulated to describe this system (1-3). This system serves as a prototype for a class of kinetic models which seek to describe the detailed interactions between regulatory molecules in the cell and the key processes which determine synthesis rates of classes of molecules of central interest. λ dv is a deletion derivative of phage λ which replicates autonomously in *Escherichia coli*. There is a wealth of information on the control of replication initiation in λ dv which is based upon the work of Matsubara, Ptashne, and others.

Examining the origin of replication of plasmid λ dv, we see that replication depends upon interaction of a number of proteins with different domains of the DNA. A critical regulating factor in replication initiation of this plasmid is the frequency of transcription which begins at the promoter P_R which is upstream of the binding site for initiator proteins at the *ori* site in the origin of replication. Transcription activity at P_R is regulated at binding of the *cro* gene product, here designated R, at three different binding sites, two of which overlap and hence, when bound with R, inactivate the promoter P_R .

Based upon this mechanistic picture of the control system which has been provided by extensive molecular biology research, we can formulate material balances on the key components and complexes, applying the tools of thermodynamic and kinetic calculations and material balances from chemical engineering in a straightforward way. For example, calculation of the transcription efficiency at the promoter P_R can be accomplished by assuming equilibrium binding of the repressor R at the three binding sites designated O_{R1} , O_{R2} , O_{R3} . In addition to delineating this mechanism, our colleagues in molecular biology have also measured the binding constant for repressor association with each of these different binding domains, providing the needed parameters to calculate this transcription efficiency. Similarly, information from the molecular biology literature provides values of the other parameters which enter into the set of differential equations required to describe the replication of plasmid λ dv during life cycle of single *E. coli* cell. All but one of the model parameters is so available, and this final parameter may be adjusted in order to make the calculated number of plasmids per cell agree with the observed value for the wild-type plasmid.

Calculations with the model converge to a repetitive, cyclic state after a few cell cycles. In this cyclic state, the concentrations of all species at the end and the beginning of the cell cycle are equal. After adjusting the single model parameter to obtain the correct number of plasmids, it is important to note that the corresponding calculated value of repressor content of the cell is very close to the experimentally measured value, suggesting that the model has the correct structure for consistent description of this replication apparatus.

Of course, simpler models could be used to calculate the time progression of plasmid content for this plasmid. However, the model formulated at the molecular level serves a different function. It can be used to relate fine scale genetic changes to the corresponding cellular properties. To illustrate for the plasmid λ dv, we note that a number of replication mutants of this plasmid have been isolated and the locus of several mutations in the repressor binding sites have been determined at the level of nucleotide sequence. Knowing the precise location of each location, we can, with a model formulated in molecular level detail, identify a corresponding specific model parameter with each mutation so that the effect of each mutation, in terms of the model, is to alter one or a very small number of clearly identified model parameters. Based upon this correspondence, simulations show consistently good agreement between calculated plasmid and repressor levels and the experimental values for these quantities for all mutants (2). This example illustrates an important theme of genetically structured models. These models provide the potential for a quantitative mapping from nucleotide sequence of key regulatory and functional regions to the eventual outcome in terms of cellular properties, in this case plasmid content of the cells. Using such models, biochemical engineers can cooperate with molecular biologists to probe and to alter in a systematic fashion the control systems used in recombinant cells to obtain the desired cellular levels of plasmid content and cloned gene expression.

Rapid Analysis of Plasmid Propagation Using Flow Cytometry

The plasmid content of a recombinant culture is determined not only by the replication characteristics of the plasmid in the host cell but also by the segregation properties of the plasmid. Unlike chromosomes which are almost always faithfully partitioned between dividing and offspring cells, plasmids often segregate in a less precise fashion upon cell division. The result is a population of cells which is heterogeneous with respect to plasmid content and which may contain a significant fraction of cells without any plasmids at all. The simplest model for growth of an unstable recombinant population, developed and studied by many different research groups over the past several years, divides the culture into two populations, one plasmid-free cells and the other plasmid-containing cells (e.g. 4,5). The central parameters which determine the dynamics and the eventual time-invariant properties of this model are the ratio of specific growth rates of plasmid-free to plasmid-containing cells and the probability that plasmid-free cells are formed upon cell division. The fraction of cells which contain plasmid after 25 generations have been evaluated in terms of these two parameters by Imanaka and Aiba (4).

Their results show clearly that, in the absence of selection which means that plasmid-free cells grow more rapidly than plasmid-containing cells, the fraction of plasmid-containing cells in the culture after 25 generations can be much less than 0.1 for even very small asymmetric partitioning probabilities. The choice of 25 generations for this calculation is based upon an approximate estimate of the number of generations involved between a stock culture and a production fermentor.

In order to understand and to minimize problems of plasmid loss during production using recombinant cells, it is important to determine the effects which different plasmid constructions, different hosts, and different growth conditions have on plasmid segregational stability. The traditional method of determining the fraction of plasmid-containing cells in the culture involves plating a sample of cells simultaneously on selective and nonselective solid media, growing up several such plates, counting colonies, and evaluating the results. This process takes in excess of one day for recombinant *Saccharomyces cerevisiae* cells, and a more rapid and more statistically rich measurement approach is necessary.

An alternative strategy for measuring plasmid replication and segregation characteristics has been developed in this laboratory based upon specific labeling of plasmid-containing cells and analysis of this labeling using flow cytometry (6 - 8). To summarize, a marker is placed in the plasmid which consists of a *lac Z* fragment, expression of which results in *E. coli* β -galactosidase activity in yeast. Expression of this gene in *S. cerevisiae* is regulated by an inducible *GAL10/CYC1* promoter, and a host strain containing the *reg1* mutation is used in order to eliminate catabolite repression of the *GAL* promoter. In order to label plasmid-containing cells, a sample from the growing recombinant population is induced to express β -galactosidase by addition of galactose and, after about one generation of growth in induction medium, the cells are chilled and permeabilized. Then, a fluorogenic substrate and trapping reagent are added. The substrate is hydrolyzed by β -galactosidase, and the product of this enzyme-catalyzed reaction subsequently undergoes reaction with a trapping reagent to form a precipitate in the cell which can be detected in the microscope and in the flow cytometer. Examining a population of *S. cerevisiae* D603 containing the plasmid pLGSD5 shows very heterogeneous labeling of the cells, indicating significant cell-to-cell heterogeneity with