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AUTOMATIC CONTROL OF FOOD AND BIOLOGICAL PROCESSES

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INTRODUCTION

Process control is one of the most important tasks of the food and biological industries. The need for high quality levels, product properties, hygiene, productivity requirements, etc., are objectives that can be obtained through better control of the process. The nature of the decisions necessary to ensure the best performance is very complex. Operators cannot involve themselves with all aspects of the process and product. After a long period of mechanization, the food and biological industries appear to be a good subject/(candidate?) for the integration of more sophisticated tasks using control science and technology. Many difficulties can be expected: complexity of raw materials and changes in their characteristics, coupling of continuous and batch processes, lack of sensors, poor knowledge of the dynamics of phenomena, hygiene requirements, and equipment constraints, etc.

From another point of view, there has been great progress in the field of control science. More and more sophisticated sensors are available every day. New, non-linear, model based strategies and adaptive control laws are being studied by teams working specifically on the control process. Computer technology applications have become available for industrial implementation. Consequently, much progress has been made in understanding the phenomena that occur during processes, specifically in control of the transient state through the dynamic behaviour of unit operations. Problems found in the food and biological industries seem to be a good area for control applications.

Despite the above, progress in industry, especially that of the food industry, is not thought about as much as it should be. An international conference is a way of establishing contact between those in research and industry, and to promote the diffusion of research results in industry. It allows demonstration of recent results and discussion on their applications. It also presents an opportunity to present open problems. This was the purpose of the ACOFOP I, II and III Symposia. The chapters of this book are written by contributors to the third one, held in Paris in 1994, and are dedicated to recent progress in the field of automation of food and biological processes. It is also an opportunity to put together a wide variety of papers covering this important subject.

The book is divided into four parts. The first part is dedicated to sensor problems. Papers present new realizations, applications and discussions on the importance of sensors for controlling the process and monitoring product quality. The second part presents results and development concerning modelling, especially dynamic modelling of food and biological processes. Some modelling applications are discussed using simulation, particularly the importance of estimation for non-measurable parameters. Progress in development of artificial intelligence tools is presented. The third, most important part of the book concerns the control process itself. It is an opportunity to bring together the presentation of many algorithms for unit operation control in such different units as dryers or fermenters. The last part is dedicated to computer aided applications in the field of control, including supervision and operator decision aided systems.

More generally, many applications at the pilot or industrial scale are presented in order to establish the feasibility of automatic control of food and biological processes. This book is, therefore, a compilation of important new results in this field.

We would like to thank all contributors to the symposium, especially those who contributed chapters on the presentation of methods, tools and results. It is also important to thank the IPA Company for the material support for organization and, last but not least, the sponsors of the symposium.

J.J. Bimbenet
E. Dumoulin
G. Trystram

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PART A

SENSORS AND MEASUREMENTS

SOFTWARE SENSORS AND ADAPTIVE CONTROL IN BIOTECHNOLOGY

D. Dochain

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Abstract

This paper presents a brief survey about recent approaches of model-based monitoring and control of bioreactors, based on material balances and which accounts for the uncertain knowledge about the process kinetics.

1 Introduction

Automatic control of industrial biotechnological processes is still developing slowly. There are two main reasons for this : the internal working and dynamics of these processes are as yet badly grasped; another essential difficulty lies in the absence, in most cases, of cheap and reliable instrumentation suited to real-time monitoring. The classical monitoring and control methods do not prove very efficient to tide over these basic difficulties. Monitoring or control algorithms will prove to be efficient if they are able to incorporate the important well-known information on the process while being able to deal with the missing informations (lack of on-line measurements, uncertainty on the dynamics. ...) in a "robust" way, i.e. such that these missing informations will not significantly deteriorate the control performance of the process. In this paper, it is shown how to incorporate the well-known knowledge about the dynamics of biochemical processes (basically, the reaction network and the material balances) in monitoring and control **algorithms** which are moreover capable of dealing with the process uncertainty (in particular on the reaction kinetics) by introducing, for instance in the control algorithms, an adaptation scheme). A key reference to this paper is the book ([1]). The paper is organized as follows. In Section 2, we shall introduce the general dynamical model for stirred tank bioreactors and illustrate it with two fermentation examples (intracellular production of biodegradable polymers (poly- β -hydroxybutyric acid (PHB)), anaerobic digestion). Section 3 is concerned with model order reduction. Section 4 will deal with the design of asymptotic observers for the process components. Finally, Section 5 will present the design of adaptive linearizing controllers for bioprocesses based on a reduced order model of the process.

2 General Dynamical Model

A biotechnological process can be defined as a set of M biochemical reactions involving N components. The dynamical model of a bioprocess in a stirred tank reactor can be

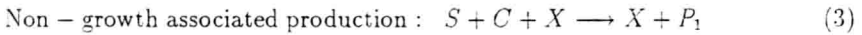
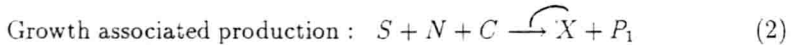
deduced from mass balance considerations and written in the following compact form :

$$\frac{d\xi}{dt} = -D\xi + Kr + F - Q \quad (1)$$

where ξ is the vector of the bioprocess component ($\dim(\xi) = N$), K is the yield coefficient matrix ($\dim(K) = N \times M$), r is the reaction rate vector ($\dim(r) = M$), F is the feed rate vector and Q the gaseous outflow rate vector ($\dim(F) = \dim(Q) = N$). The model (1) has been called the *General Dynamical Model* for stirred tank bioreactors (for further details, see [1]).

2.1 Example #1 : PHB Production Process

Let us first consider the production of poly- β -hydroxybutyric acid (PHB), which is a biodegradable polymer. The PHB can be produced in an aerobic culture of *Alcaligenes eutrophus*, and the production may follow two metabolic pathways : the first metabolic pathway for the production of PHB is growth associated (with three limiting substrates : oxygen, a source of carbon (e.g. fructose or glucose) and nitrogen (ammonia)) and characterized by a very low yield; the second metabolic pathway for the production of PHB is non-growth associated, where the biomass plays simply the role of a catalyst, and is completely inhibited by nitrogen. Therefore the production of PHB can be schematized by the following reaction network :



where S , C , N , X and P_1 represent the carbon source, the oxygen, the nitrogen, the biomass and the PHB, respectively. In the first reaction scheme, the feedback arrow means that, in a growth reaction, the biomass is an autocatalyst. The presence of X on both sides of the arrow in the second reaction scheme means that X simply plays the role of a catalyst. The dynamical equations of the PHB process can be written in the above matrix form (in which $\Delta Q_{O_2} = Q_{in} - Q_{out}$) :

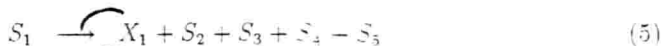
$$\frac{d}{dt} \begin{pmatrix} S \\ C \\ N \\ X \\ P_1 \end{pmatrix} = -D \begin{pmatrix} S \\ C \\ N \\ X \\ P_1 \end{pmatrix} + \begin{pmatrix} DS_{in} \\ \Delta Q_{O_2} \\ DN_{in} \\ 0 \\ 0 \end{pmatrix} - \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} + \begin{pmatrix} -k_1 & -k_2 \\ -k_3 & -k_4 \\ -k_5 & 0 \\ 1 & 0 \\ k_6 & 1 \end{pmatrix} \begin{pmatrix} r_1 \\ r_2 \end{pmatrix} \quad (4)$$

where S_{in} and N_{in} the influent carbon source and nitrogen concentrations (g/l), Q_{in} and Q_{out} the inlet and outlet gaseous oxygen flowrates (g/h), r_1 and r_2 the reaction rates of the reactions (2) and (3) (h^{-1}) respectively and k_i ($i = 1$ to 6) the yield coefficients.

2.2 Example #2 : Anaerobic Digestion

Anaerobic digestion is a biological wastewater treatment process which produces methane. Four metabolic paths can be identified in this process : two for acidogenesis and two for methanization. In the first acidogenic path (Path 1), glucose is decomposed into fatty volatile acids (acetate, propionate), hydrogen and inorganic carbon by acidogenic

bacteria. In the second acidogenic path (Path 2), OHPA (Obligate Hydrogen Producing Acetogens) decompose propionate into acetate, hydrogen and inorganic carbon. In a first methanization path (Path 3), acetate is transformed into methane and inorganic carbon by acetoclastic methanogenic bacteria, while in the second methanization path (Path 4), hydrogen combines with inorganic carbon to produce methane under the action of hydrogenophilic methanogenic bacteria. The process can then be described by the following reaction network :



where $S_1, S_2, S_3, S_4, S_5, X_1, X_2, X_3, X_4$ and P_1 are respectively glucose, propionate, acetate, hydrogen, inorganic carbon, acidogenic bacteria, OHPA (Obligate Hydrogen Producing Acetogens), acetoclastic methanogenic bacteria, hydrogenophilic methanogenic bacteria and methane. The dynamical model of the anaerobic digestion process ($N = 10, M = 4$) in a stirred tank reactor can be described within the above formalism (1) by using the following definitions :

$$\xi = \begin{pmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ X_3 \\ S_3 \\ X_4 \\ S_4 \\ S_5 \\ P_1 \end{pmatrix}, K = \begin{bmatrix} 1 & 0 & 0 & 0 \\ -k_{21} & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ k_{41} & -k_{42} & 0 & 0 \\ 0 & 0 & 1 & 0 \\ k_{61} & k_{62} & 0 & -k_{63} \\ 0 & 0 & 0 & 1 \\ k_{81} & k_{82} & 0 & -k_{84} \\ k_{91} & k_{92} & k_{93} & -k_{94} \\ 0 & 0 & k_{03} & k_{04} \end{bmatrix}, F = \begin{pmatrix} 0 \\ DS_{in} \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}, Q = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ Q_1 \\ Q_2 \\ Q_3 \end{pmatrix} \quad (9)$$

$$r = \begin{pmatrix} r_1 \\ r_2 \\ r_3 \\ r_4 \end{pmatrix} = \begin{pmatrix} \mu_1 X_1 \\ \mu_2 X_2 \\ \mu_3 X_3 \\ \mu_4 X_4 \end{pmatrix} \quad (10)$$

where $\mu_1, \mu_2, \mu_3, \mu_4$ are the specific growth rates (h^{-1}) of reactions (5), (6), (7), (8), respectively, and S_{in}, Q_1, Q_2 and Q_3 represent respectively the influent glucose concentration (g/l) and the gaseous outflow rates of H_2, CO_2 and CH_4 (g/l.h).

3 Model Order Reduction

Model simplification can be achieved by using the singular perturbation technique, which is a technique for transforming a set of $n+m$ differential equations into a set of n differential equations and a set of m algebraic equations. Consider that, for some i , the dynamics of the component ξ_i are to be neglected. The simplification is then achieved by setting ξ_i and $d\xi_i/dt$ to zero. It has been shown that the model order reduction rule is valid for low solubility products and for bioprocesses with fast and slow reactions : in the latter case,