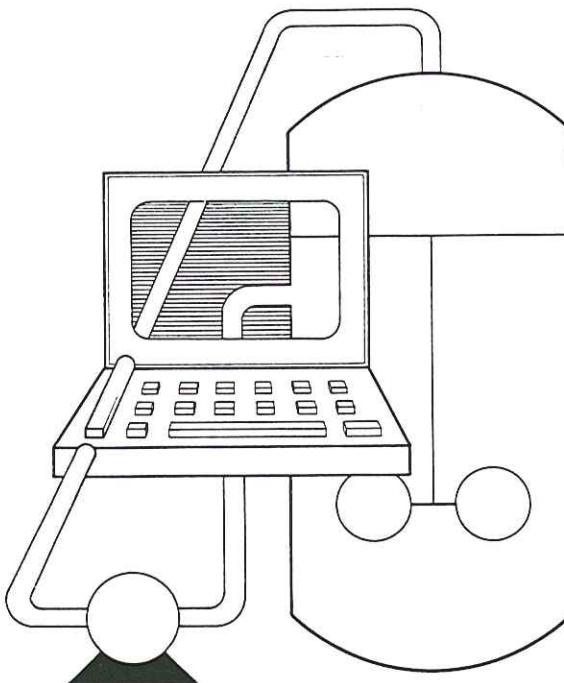


Process Measurement and Control, 1

On-line Estimation and Adaptive Control of Bioreactors

G. Bastin and D. Dochain



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PREFACE

The development of modern control science in biotechnology has been hampered by two important obstacles.

First, since bioprocesses involve living organisms, their dynamics are often poorly understood, strongly nonlinear and non-stationary. The reproducibility of experiments is uncertain. The model parameters do not remain constant over long periods, due to metabolic variations and physiological modifications.

Another essential difficulty lies in the absence, in most cases, of cheap and reliable instrumentation suited to real time monitoring. To date, the market offers very few sensors capable of providing reliable, direct, on-line measurements of the biological variables (such as biomass or metabolite concentration) required to implement high performance control strategies.

The aim of this book is to present an integrated theoretical framework which overcomes both of these difficulties. The notion of *minimal modelling* will be central throughout the book. We shall show how efficient monitoring and control algorithms can be designed, in a systematic and rigorous way, from a minimal knowledge of the process kinetics. In particular, a great part of the text will be devoted to the design of *software sensors* for the on-line monitoring of biological variables and reaction kinetics, which are capable of coping with the lack of instrumental sensors just mentioned.

One of our objectives is also to acquaint the reader with the application of mathematical modelling techniques and dynamical systems analysis in the solution of engineering problems in bioreactors. The methodology is abundantly illuminated and illustrated by a variety of practical examples drawn

from the experience we have gained in collaboration with our colleagues of the bioengineering laboratories within the Biotechnology Action Programme of the Commission of the European Communities, and also of the Research Institute of Biotechnology in Montreal, Canada.

The book is the result of an intensive joint research effort by the authors during the last decade. (The authors' names therefore appear in a purely alphabetical order.) It is intended as a graduate level text for students of bioengineering as well as a reference text for scientists and engineers involved in the design and optimisation of bioprocesses.

In the first chapter the mathematical framework necessary for the analysis of bioreactor dynamics is established. In particular, it is shown how a general dynamical model of a biotechnological process may be derived from the reaction network. The main mathematical properties of this general dynamical model are also analysed.

A review of the estimation and control problems that we address in the remaining chapters is given in Chapter 2.

In Chapter 3 the design of state observers and on-line kinetic estimators is examined in great detail under the assumption that the yield coefficients of the process are known. The same issues are discussed in Chapter 4, but on the basis of the yield coefficients being unknown.

Finally, Chapter 5 deals with adaptive control of bioreactors by combining feedback linearization techniques with the observers and estimators presented in the previous chapters.

The writing of this book would not have been possible without the support of the Biotechnology Action Programme of the European Communities which is gratefully acknowledged. In particular, we would like to thank Dr Economidis for his constant interest in our work. We are also indebted to G. Corrieu, C. Beal, P. Louvet and E. Spinnler from the Institut National de Recherche Agronomique (France), C. Sola and M. Poch from the Universitat Autonoma de Barcelona (Spain), A. Cheruy, M.P. Bernier, J.F. Beteau, R. Montellano and C. Vialas from the Institut National Polytechnique de Grenoble (France), J.C.

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Our interest in the application of systems analysis to biological processes goes back to the late seventies. We are particularly indebted to M. Installé, who introduced us to the subject, and to our colleagues of the Unit of Bioengineering in Louvain-la-Neuve : H. Naveau, E.J. Nyns, D. Poncelet and P. Renard.

During the writing of this book we also had the pleasure of interacting with many people, who helped us to penetrate the mysteries of biology and of adaptive systems and gave us useful hints, insights, advice and criticism. We would particularly like to thank M.Y. Andersen, G. André, J.P. Axelsson, J.P. Babary, B. Bitmead, G. Campion, G. Chamlothoris, C. Chavarie, L. Chen, B. Coupal, B. Dahou, S. Dasgupta, P. De Larminat, M. Dewan, L. Dugard, Y. Goma, R. Gorez, A.M. Guillaume, M. Haest, L. Joassin, S.B. Jorgensen, J. Levine, I. Mareels, A.J. Morris, P. Peringer, Y. Pomerleau, L. Praly, Y. Prigent, Y. Sevely, E. Sinivitu, V. Wertz.

Part of the book has been written during the stays of D. Dochain at the Ecole Polytechnique de Montréal (Canada) in 1987-88 and at the LAAS (Laboratoire d'Automatique et d'Analyse des Systèmes) of the CNRS in Toulouse (France) during the spring of 1989 : these institutions are gratefully acknowledged.

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*Louvain-la-Neuve, 1 January 1990
Georges Bastin and Denis Dochain*

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CHAPTER 1

DYNAMICAL MODELS OF BIOREACTORS

1.0. Introduction

Basically, a bioreactor is a tank in which several biological reactions occur simultaneously in a liquid medium. A standard schematic diagram of a completely mixed continuous stirred tank (CST) bioreactor is shown in Fig.1.1. The biological reactions which are involved in the process may be roughly classified into two categories : microbial growth reactions (often referred to as microbiological reactions) and enzyme catalysed reactions (also termed biochemical reactions or biotransformations).

The growth of the microorganisms (bacteria, yeasts, etc.) proceeds by consumption of appropriate nutrients or *substrates* (involving carbon, nitrogen, oxygen, etc.) provided the environmental conditions (temperature, pH, etc.) are favourable. The mass of living microorganisms or living cells is called the *biomass*.

Associated with cell growth, but often proceeding at a different rate, are the enzyme catalysed reactions in which some reactants are transformed into products (sometimes called metabolites) through the catalytic action of intracellular or extracellular enzymes.

Once a bioreactor has been designed, one of the main challenges of the bioengineer is the implementation of efficient strategies for on-line monitoring and control of the process. Our main concern in this book will be to present (and to illustrate with practical applications) a general methodology, based on mathematical modelling and dynamical systems analysis, for the solution of such engineering problems.

In this first chapter we introduce mathematical models of the dynamics of bioreactors. The objective is not to provide a comprehensive overview of the modelling problem of biotechnological processes. The goal is rather to establish a firm background for the design and the analysis of estimation and control algorithms which will be discussed in subsequent chapters.

Outline of the chapter

In the first three sections we follow the conventional route for the description of dynamical models of stirred tank bioreactors. The basic model of the growth of a single microorganism population on a single substrate is presented in Section 1.1. This model is shown to be valid for different operating modes : batch, fed-batch, continuous operations. The way in which the basic model may be extended for complex cultures is outlined in Section 1.2, using the example of product synthesis and that of oxygen consumption in aerobic fermentations. The most commonly used kinetic models of the specific growth rate, which is a key parameter for bioreactor description, are reviewed in Section 1.3.

From Section 1.4 we move to a more general viewpoint. Our aim is to establish a global and rigorous theoretical framework for the analysis of bioreactor dynamics. The concept of "reaction scheme" of a biotechnological process is introduced and illustrated with four practical examples : yeast fermentation, anaerobic digestion, production of PHB acid, and lactic fermentation. Then, in Section 1.5, it is shown that, once the reaction scheme of a biotechnological process is given, the derivation of a general state space model for the process

is made fully automatic. Several practical examples are described in Section 1.6.

Sections 1.7 to 1.9 are devoted to the mathematical properties of the general state space model introduced in Section 1.5.

A basic algebraic structural property which will be critical for both estimation and control design is presented in Section 1.7.

The general state-space model can be fairly complex and may involve a large number of differential equations. But there are many practical applications where a simplified model is sufficient from an engineering viewpoint. Model reduction can be achieved via the technique of singular perturbations : this leads to a general rule for the reduction of bioreactor models presented in Section 1.8.

The stability of the general state-space model of bioreactors is analyzed in Section 1.9. Two issues are discussed : global bounded-input bounded-state stability and local stability of equilibrium points.

Finally, the extension of the state space model to more general situations than the stirred tank bioreactors (such as fixed bed reactors and recycle reactors) is considered in Section 1.10.

1.1. The Basic Dynamics of Microbial Growth in Stirred Tank Reactors

In stirred tank reactors, the process is assumed to be in a completely mixed condition : this implies that the composition of the medium is homogeneous in the reactor.

The dynamical behaviour of the growth of one population of microorganisms on a single limiting substrate in a stirred tank reactor (Fig.1.1) is most often expressed by equations (1.1), which are obtained from straightforward mass balances.

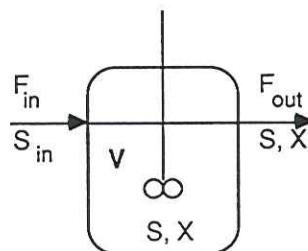


Fig.1.1. Stirred tank bioreactor

The net accumulation of biomass in the reactor

$$\frac{d(VX)}{dt} = \mu VX - F_{out}X \quad (1.1.a)$$

The net accumulation of substrate in the reactor

$$\frac{d(VS)}{dt} = -k_1\mu VX + F_{in}S_{in} - F_{out}S \quad (1.1.b)$$

The variation of volume

$$\frac{dV}{dt} = F_{in} - F_{out} \quad (1.1.c)$$

with X being the concentration of the microorganism population (the biomass) in the reactor and in the effluent, S the substrate concentration in the reactor and in the effluent, S_{in} the substrate concentration in the influent, F_{in} the

influent flow rate, F_{out} the effluent flow rate, μ the specific microbial growth rate, k_1 the yield coefficient of the substrate consumption by the biomass, and V the volume of the culture medium.

In these equations the only modelling assumption is that the biomass growth term (μX) and the substrate consumption term ($k_1\mu X$) are proportional to the biomass concentration X . This assumption has been validated many times and has become commonly accepted since Monod introduced it in 1942.

Two additional terms are sometimes included in equations (1.1.a-b).

- A decay term ($-k_d V X$) in the biomass growth equation (1.1.a) to account for the natural death of microorganisms.
- A maintenance term ($-k_m V X$) in the substrate consumption equation (1.1.b) to account for that part of the substrate used for biomass survival.

With these terms, equations (1.1.a-b) may be rewritten as :

$$\frac{d(VX)}{dt} = (\mu - k_d)VX - F_{out}X \quad (1.2.a)$$

$$\frac{d(VS)}{dt} = -(k_1\mu + k_m)VX + F_{in}S_{in} - F_{out}S \quad (1.2.b)$$

However the coefficients k_d and k_m are considered to be negligible in many industrial fermentations. Therefore, except where otherwise specified (see for instance Section 1.4.3), they will frequently be omitted in this book.

On the other hand, by defining the *dilution rate* :

$$D = \frac{F_{in}}{V}$$

a useful alternative formulation of equations (1.1.a-c) is obtained as follows :

$$\frac{dX}{dt} = (\mu - D) X \quad (1.3.a)$$

$$\frac{dS}{dt} = -k_1 \mu X + D(S_{in} - S) \quad (1.3.b)$$

$$\frac{dV}{dt} = DV - F_{out} \quad (1.3.c)$$

We now describe three particular cases of this model corresponding to the most frequently encountered operating conditions : batch, fed-batch and continuous operations.

a) The batch reactor

A batch reactor is a reactor with neither inflow nor outflow :

$$F_{in} = F_{out} = 0 \quad (1.4)$$

The tank is initially filled with a large amount of substrate and a small amount of biomass (the inoculum). No substrate is introduced during the fermentation, which is stopped when enough substrate has been consumed. The total amount of biomass produced (and possibly of by-products) is then harvested. Clearly the culture volume is constant and the dynamical model is given by (1.3.a-b) with $D = 0$.

b) The fed-batch reactor

A fed-batch reactor is a reactor with no outflow :

$$F_{out} = 0 \quad (1.5)$$

The tank initially contains a small amount of both substrate and biomass and is progressively filled with the influent substrate. The model is then given by (1.3.a,b,c) with $F_{out} = 0$

c) The continuous stirred tank reactor (CSTR)

In the continuous cultivation of microorganisms, the reactor is continuously fed with the substrate influent. The rate of outflow is equal to the rate of inflow and the volume of culture remains constant :

$$F_{in} = F_{out} = F \quad (1.6)$$

$$\frac{dV}{dt} = 0 \quad (1.7)$$

The model is therefore given by (1.3.a-b) with :

$$D = \frac{F}{V} \quad (1.8)$$

1.2. Extensions to the Basic Dynamics

The situation encountered in many fermentation applications is much more complex than the one described by the basic dynamical model of Section 1.1. : several biochemical and microbial growth reactions can coexist in the bioreactor, each of them possibly involving several limiting substrates and several reaction products or metabolites. In these cases, other dynamical equations need to be introduced in order to make the dynamical description of the process more complete. Later in this chapter we shall present a general theoretical framework designed to describe the complexity of the entire process for a wide range of potential applications. In this section we limit ourselves to the introduction of the issue with two specific situations :

- the formation of an extracellular synthesis product
- the dynamics of dissolved oxygen in aerobic fermentations.

Formation of a synthesis product

The growth of microorganisms in bioreactors is often accompanied by the formation of products which are either soluble in the culture or which are given off in gaseous form. The mass balance relative to the product in the bioreactor is given by :

$$\frac{dP}{dt} = \nu X - DP - Q \quad (1.9)$$

with P being the synthesis product concentration (in the liquid phase), Q the rate of mass outflow of the product from the reactor in gaseous form, and ν the specific production rate.

The term νX in (1.9) represents the rate of product formation : it expresses the fact that the production is, in some way, "catalysed" by the biomass X.

In some instances (e.g. methane CH₄), the liquid concentration is negligible (P=0). The gaseous outflow rate is then usually considered as being equal to the production rate and is written as follows :

$$Q = \nu X \quad (1.10)$$

An important special case arises when the product formation is "growth-associated", i.e. the specific production rate is assumed to be proportional to the specific growth rate :

$$\nu = k_2 \mu \quad (1.11)$$

with k_2 a yield coefficient.

However, the specific production rate may also be completely or partially independent of the specific growth rate. A classical example is the lactic fermentation for which Luedeking and Piret (1959) have proposed the following expression :

$$\nu = k_2 \mu + \rho \quad (1.12)$$

where ρ is the non-growth associated specific production rate.

Dissolved oxygen dynamics in aerobic fermentations

Aerobic fermentations are processes in which the microorganisms need oxygen in order to develop properly. Typical examples are yeast growth processes and activated sludge processes. In such cases dissolved oxygen in the culture medium can be considered as an additional substrate.

The dissolved oxygen (DO) mass balance in the bioreactor is described as follows :

$$\frac{dC}{dt} = OTR - OUR - DC \quad (1.13)$$

where C is the DO concentration in the reactor, OTR is the oxygen transfer rate and OUR is the oxygen uptake rate.

The oxygen uptake rate OUR obviously depends on the growth of the biomass. This is often expressed as follows :

$$OUR = k_3 \mu X \quad (1.14)$$

with k_3 being a yield coefficient. A term proportional to the biomass concentration ($k_r X$) is sometimes included in equation (1.14) to account for the endogenous respiration.

By using a line of reasoning based on Henry's law to model the liquid-gas transfer dynamics, the oxygen transfer rate, OTR, is expressed as follows :

$$\text{OTR} = k_L a (C_S - C) \quad (1.15)$$

where $k_L a$ is the mass transfer coefficient and C_S is the oxygen saturation concentration.

However expression (1.15) is often useless because the coefficients C_S and $k_L a$ may be unknown and may vary greatly with time : it is well known that the oxygen saturation concentration C_S depends on variables such as the oxygen partial pressure in the surrounding atmosphere, temperature, salinity and concentration of surfactants in the liquid, and that factors such as the type and geometry of the aerator or the air flow rate determine the value of $k_L a$.

Fortunately, in most industrial applications, the input and output gaseous oxygen flow rates are measured on-line. Hence, if the liquid-gas transfer dynamics are negligible (as is often assumed), the OTR can simply be expressed from the gaseous oxygen balance :

$$\text{OTR} = Q_1 - Q_2 \quad (1.16)$$

where Q_1 and Q_2 are respectively the input and output oxygen flow rates (per volume unit).

1.3. Models of the Specific Growth Rate

It can clearly be seen from equations (1.3.a-b), (1.11) and (1.14) that the specific growth rate μ is a key parameter for the description of biomass growth, substrate consumption and product formation. Biochemical experiments carried out over more than half a century on pure cultures as well as on open cultures (with non-sterile substrates) have clearly indicated that the parameter

μ varies with time and is influenced by many physico-chemical and biological environmental factors among which the most important ones are : substrate concentration, biomass concentration, product concentration, pH, temperature, dissolved oxygen concentration, light intensity and various inhibitors of microbial growth.

The specific growth rate is then commonly expressed by the multiplication of individual terms, each of them referring to one of the influencing factors :

$$\mu(t) = \mu(S) \mu(X) \mu(P) \mu(\text{pH}) \mu(T) \mu(C) \mu(L) \mu(I) \dots \quad (1.17)$$

where X , S , P , C have been defined above while T , L , and I refer to temperature, light intensity and inhibitor concentration respectively.

We shall present, in the following paragraphs, some of the most commonly used kinetic models for the different terms of equation (1.17). A list including more than fifty different growth rate structures may be found in Appendix 1.

Influence of the substrate concentration S

The most widespread analytical specific growth rate model is certainly the "Michaelis-Menten law", also often called the "Monod law", which expresses the dependence of μ on the substrate concentration S as follows (Fig.1.2) :

$$\mu(S) = \frac{\mu^* S}{K_M + S} \quad (1.18)$$

where μ^* is the maximum growth rate and K_M is the "Michaelis-Menten" constant.

In fact, this expression was initially proposed by Michaelis and Menten in 1913 and physically justified by Briggs and Haldane later, in 1925, to express the reaction rate of enzyme-catalysed reactions with a single substrate. It was

extended by Monod in 1942 to the case of microorganism growth, but without any specific physical justification.

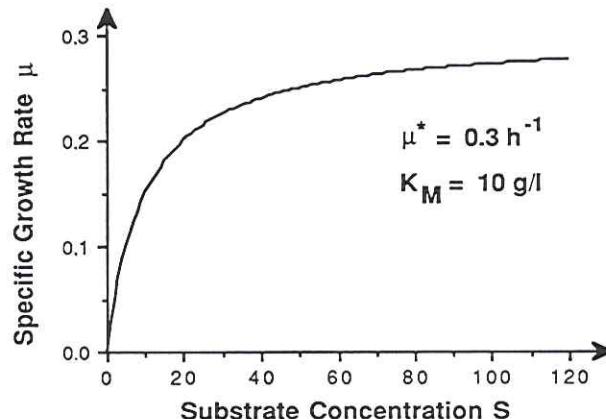


Fig.1.2. The Monod law

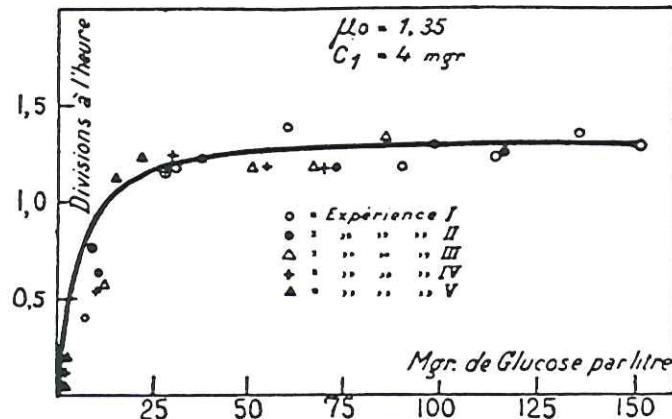


Fig.1.3. Fitting of the Monod law to experimental data (reprinted by permission from J. Monod (1942). *Recherches sur la Croissance des Cultures Bactériennes*. Hermann, Paris).

Expression (1.19) was adopted by Monod because it fits experimental data well (see, for instance, Fig.1.3). But, as Monod himself recognized, "toute courbe d'allure sigmoïde pourrait être ajustée aux données expérimentales" (any sigmoidal curve could be fitted to the experimental data). Besides, another expression was suggested by Tessier in the same year of 1942 :

$$\mu(S) = \mu^* \left[1 - \exp \left(- \frac{S}{K_M} \right) \right] \quad (1.19)$$

Clearly this equation could fit the Monod data equally well. Many different (and more or less esoteric) formulas have been proposed since then and these are partially listed in Appendix 1.

A drawback of the Monod or Teissier laws is that they do not allow any account to be taken of possible substrate inhibitory effects at high concentrations (overloading).

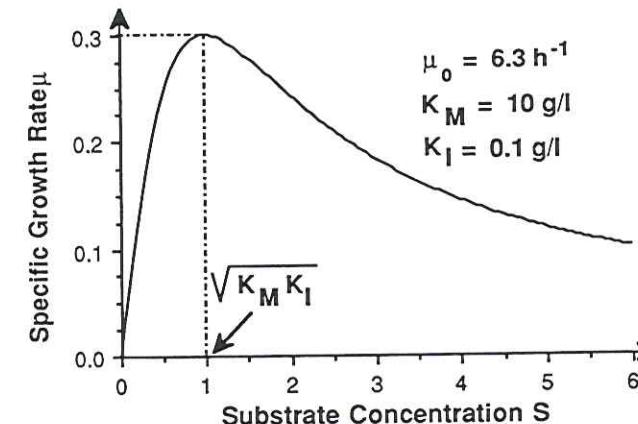


Fig.1.4. The Haldane law

Andrews suggested that substrate inhibition be treated by the "Haldane law" which was initially derived by Haldane to describe inhibition in enzyme-substrate reactions (Fig.1.4) :

$$\mu(S) = \frac{\mu_0 S}{K_M + S + S^2/K_I} \quad (1.20.a)$$

where K_I is the "inhibition parameter" and :

$$\mu_0 = \mu^* \left(1 + \sqrt{\frac{K_M}{K_I}} \right) \quad (1.20.b)$$

If the substrate inhibition is neglected, the Haldane law reduces to the Monod law .

Influence of the biomass concentration X

The biomass growth is often presumed to be slowed down at high biomass concentration (and this has been experimentally observed in particular instances). A simple model that accommodates for this situation assumes that the specific growth rate decreases linearly with the biomass concentration :

$$\mu(X) = \mu^*(1 - aX) \quad (1.21)$$

where μ^* is the maximum growth rate and a the inhibition constant. It is often called the "logistic model" and was proposed by Verhulst in 1838. Another model which is a function of both S and X is the following :

$$\mu(S, X) = \frac{\mu^* S}{K_C X + S} \quad (1.22)$$

with K_C constant.

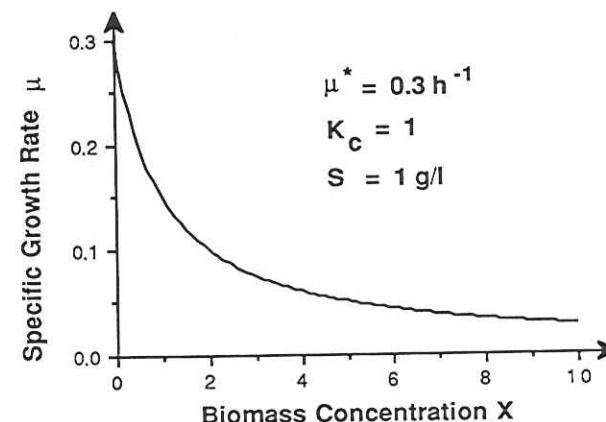


Fig.1.5. The Contois model

This model was proposed by Contois in 1959, and is illustrated in Fig.1.5, which shows the inhibition dependence of μ with respect to X (for constant S).

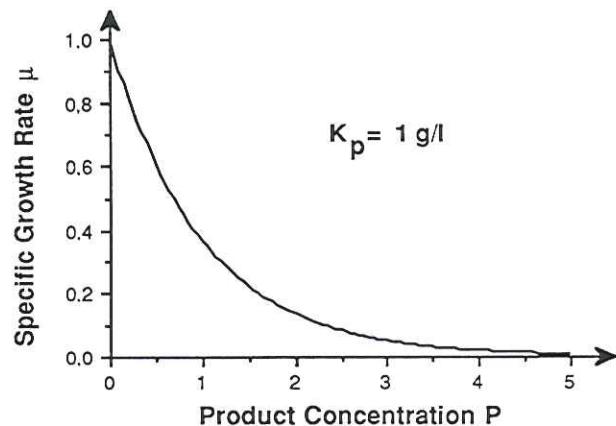
Influence of the synthesis product concentration P

It is a well known fact that, in particular fermentations, the synthesis product can also inhibit the biomass growth. Typical examples are alcoholic or ethanolic fermentations on glucose for which the following models have been suggested (Fig.1.6) :

$$\mu(P) = \frac{K_p}{K_p + P} \quad (1.23)$$

$$\mu(P) = \exp(-K_p P) \quad (1.24)$$

with K_p constant.

Fig.1.6. $\mu(P) = \exp(-K_p/P)$ **Influence of pH and temperature**

As we have indicated in the introduction, the biomass growth can actually take place only if pH and temperature lie within (usually small) ranges of admissible values.

In anaerobic digestion, for instance, the process is known to operate correctly only for nearly neutral pH (= 7). For this process, Rozzi proposes treating the influence of pH by a parabolic law derived from experimental data (Fig.1.7) :

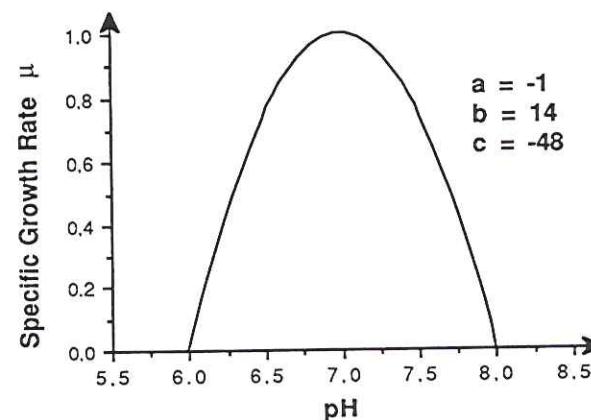
$$\mu(\text{pH}) = a \text{ pH}^2 + b \text{ pH} + c \quad (1.26)$$

with a, b, c constants.

In a similar case, Jackson and Edwards suggest using the Haldane function (1.21) in terms of hydrogen ion concentration :

$$\mu(H^+) = \frac{H^+}{K_M + H^+ + K_l(H^+)^2} \quad (1.27)$$

with H^+ representing the hydrogen ion concentration.

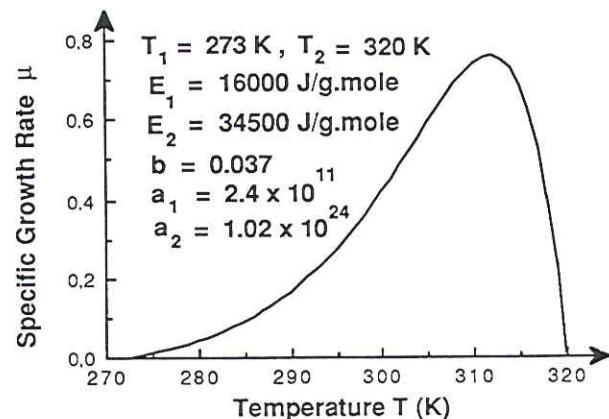
Fig.1.7. $\mu(\text{pH})$

On the other hand, the influence of temperature is most often modelled by an Arrhenius-type law, as has been done, for instance, by Topiwala and Sinclair :

$$\begin{aligned} \mu(T) &= a_1 \exp(-E_1/RT) - a_2 \exp(-E_2/RT) - b && \text{if } T_1 \leq T \leq T_2 \\ &= 0 && \text{if } T < T_1 \text{ or } T > T_2 \end{aligned} \quad (1.28)$$

with E_1, E_2 : activation energies
 R : gas constant
 a_1, a_2, b : constants

This expression shows that the specific growth rate increases continuously with temperature up to a maximum value T_2 (at which the cells die) (see Fig.1.8).

Fig.1.8. $\mu(T)$

1.4. The Reaction Scheme of a Biotechnological Process

So far in this chapter the standard intuitive way of presenting the modelling of biotechnological processes has been followed. Our aim, however, is to propose a more global and rigorous theoretical framework for the analysis of bioreactor dynamics. In the next section we shall present a general class of state space models which can describe a wide class of complex biotechnological processes in stirred tank bioreactors. It will be shown that the elaboration of these models can be made fully systematic provided a process description in terms of *reaction schemes* is available. These reaction schemes, which are presented in this section, are analogous (but not equivalent) to those commonly used in classical chemical engineering.

The section is organised as follows. An abstract definition of the notion of reaction scheme is given in Section 1.4.1. This allows a precise definition of the concept of *biotechnological process* in the sense used in this book

(Section 1.4.2). The definition is then illustrated and explained with a number of concrete situations and applications in Section 1.4.3.

1.4.1. The notion of reaction scheme

Scheme of simple reactions

A simple irreversible reaction involving two reactants and yielding a reaction product is commonly represented by a scheme of the following form :



where ξ_1 and ξ_2 are the two *reactants* which are irreversibly combined to give the *reaction product* ξ_3 . φ is the reaction rate, i.e. the rate of consumption of the reactants, which is equal to the rate of formation of the product.

Generally, the number of reaction components (reactants and/or products) is arbitrary and the scheme is written :



Catalysed reactions

A *catalysed* reaction is a reaction in which a component (termed a *catalyst*) appears on both sides of the scheme : this means that the catalyst is assumed to be consumed and produced simultaneously at the same rate by the reaction (in such a way that the balance of this component is continuously in equilibrium).

Autocatalysed reactions

In an *autocatalysed* reaction, one product is a catalyst of its own production. In that case, the scheme is as follows :



The *feedback arrow* indicates the presence of an *autocatalyst* ξ_2 . It is a *pseudoreactant* which is not consumed by the reaction, but which can be accumulated in the reactor.

1.4.2. Definition of a biotechnological process

A biotechnological process is a set of M reactions involving N components (i.e. reactants and reaction products). The various applications addressed later in this section will show that this definition is efficient and allows a very wide class of practical situations to be covered. However, the following comments are important for a correct understanding of this definition and to avoid any confusion regarding the notion of reaction scheme and the definition of biotechnological processes as they are used in this book.

- 1) The reaction scheme does *not* represent a stoichiometric relationship between the components, in contrast to the common practice in chemical kinetics. It simply represents a *qualitative* relation. This allows us to include chemical, biochemical and microbial growth processes in a unified approach.
- 2) The components ξ_j of the reaction scheme are basically of four kinds :
 - populations of microorganisms
 - enzymes
 - external substrates (i.e. substrates which are introduced into the reactor from outside)

- products/internal substrates (i.e. components which are produced by one reaction and can possibly be the substrate of another reaction).

However, other chemical components can be included in the reaction scheme if they are useful from an engineering viewpoint (for instance, components used for controlling the pH of a reaction).

- 3) The reaction scheme of a biotechnological process is a tool for deriving an operational dynamical model of the process and for solving engineering problems. It is *never* an exhaustive description of the process. For instance, substrates which are not limiting are most often omitted from the scheme. Similarly, by-products of a reaction which are not substrates in other reactions and are of no interest to the user may also be omitted. Consequently, the reaction scheme may be inconsistent with the law of conservation of mass without causing any damage from an engineering viewpoint.

We shall now illustrate the concept of a reaction scheme of a biotechnological process using several typical examples.

1.4.3. Illustration

Microbial growth, death and maintenance

We consider a biotechnological process involving simultaneous growth, death and maintenance of microorganisms on a single limiting substrate (as described by the model (1.2)). The process is represented by the following set of M = 3 reactions involving N = 3 components :



The three components are the living biomass X, the dead biomass X_d and the limiting substrate S.

Notice that the three kinds of reactions mentioned above are present in the scheme : simple reaction, catalysis, and autocatalysis.

The first reaction (1.32.a) represents the growth of the microorganism population (growth rate ϕ_g) : it is obvious that this reaction is autocatalysed since the biomass X is a catalyst of its own production (there is no biomass growth without initial biomass) but is not consumed by the growth reaction.

The second reaction (1.32.b) represents the death of microorganisms (decay rate ϕ_d) : it is a simple irreversible reaction.

The third reaction (1.32.c) represents the maintenance of the microorganisms (maintenance rate ϕ_m) : it is a catalysed reaction (catalyst X) since the biomass is neither consumed nor produced by the reaction, but simply *Maintained*.

It is however important to note that in many practical applications, the death and maintenance phenomena may be neglected in the analysis, so that the process reduces to the simple autocatalytic reaction :



This reaction will very often serve as a basic example throughout the book to illustrate the theory, under the name of *simple microbial growth process* or *single biomass/single substrate process*.

Enzymatic Catalysis

Production by enzymatic catalysis is certainly one of the most common biotechnological processes. The reaction scheme is as follows :



with S representing the substrate, P the product and E the enzyme. It may occur that the enzyme cannot be isolated from the microorganism with which it is associated and that the enzymatic catalysis is possible only in the presence of biomass growing on the same substrate. In that case, the reaction scheme is as follows:



It is then realistic to assume that the enzyme concentration is proportional to the biomass concentration in such a way that the biomass itself can be considered as the catalyst :



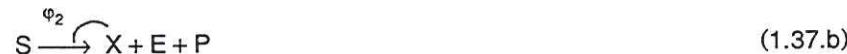
In the sequel we shall usually characterise the enzyme catalysed (or non-growth associated) production of a synthesis product P by a reaction scheme of the type (1.36.b).

Yeast growth

Yeast (*Saccharomyces cerevisiae*) growth is usually characterised by three metabolic reactions :

- respiratory growth on glucose
- fermentative growth on glucose
- respiratory growth on ethanol

It can be represented by the following set of $M = 3$ reactions involving $N = 5$ components :



with X : yeast concentration

S : glucose concentration

C : dissolved oxygen concentration

E : ethanol concentration

P : dissolved carbon dioxide concentration

φ_1 : glucose respiration reaction rate

φ_2 : glucose fermentation reaction rate

φ_3 : ethanol respiration reaction rate

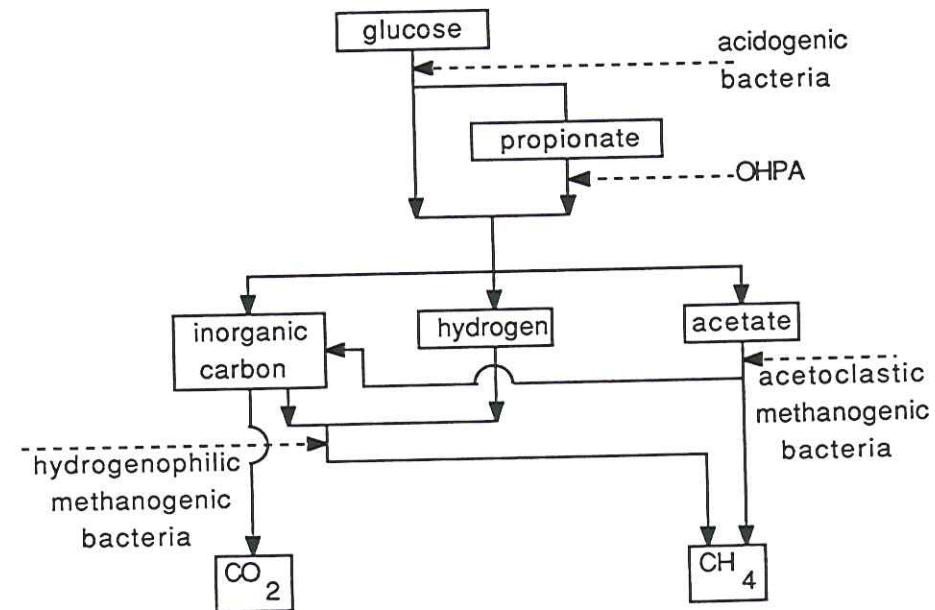


Fig.1.9. Reaction scheme of anaerobic digestion

Anaerobic digestion

Anaerobic digestion is a process for the biological treatment of organic wastes with production of methane gas. Four metabolic paths can be identified in this process : two for acidogenesis and two for methanization (Fig.1.9). 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 following reaction scheme follows from Fig.1.9 ($M = 4$ reactions, $N = 10$ components) :



with X_1 : acidogenic bacteria concentration

X_2 : acetoclastic methanogenic bacteria concentration

X_3 : OHPA concentration

X_4 : hydrogenophilic methanogenic bacteria concentration

S_1 : glucose concentration

S_2 : acetate concentration

S_3 : propionate concentration

S_4 : hydrogen concentration

S_5 : inorganic carbon concentration

P_1 : methane concentration

φ_1 : 1st acidogenesis reaction rate

φ_2 : 1st methanization reaction rate

φ_3 : 2nd acidogenesis reaction rate

φ_4 : 2nd methanization reaction rate

Intracellular production of PHB acid

The process under consideration is an aerobic culture of *Alcaligenes eutrophus* with intracellular production of poly-β-hydroxybutyric (PHB) acid.

The main features of this process are as follows :

- 1) Two limiting substrates are needed for the microbial growth : fructose as carbon substrate and ammonia as nitrogen substrate.
- 2) The intracellular production of the PHB acid, by fructose degradation, can take two different paths :
 - the first being associated with the growth but with a very small yield;
 - the second being enzyme catalysed and completely inhibited by nitrogen.
- 3) Both microbial growth and product formation yield gaseous carbon dioxide. The respiratory quotient is close to unity.

According to these features 1) to 3), the process is described by the following reaction scheme ($M = 2, N = 5$) :



with X : biomass concentration

S_1 : fructose concentration

S_2 : ammonia concentration

P_1 : PHB acid concentration

P_2 : dissolved carbon dioxide concentration

C : dissolved oxygen concentration

φ_1 : growth associated product formation rate

φ_2 : enzyme-catalysed product formation rate

Lactic fermentation

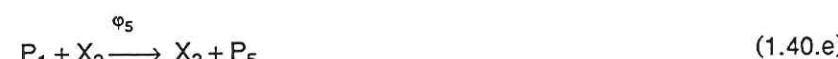
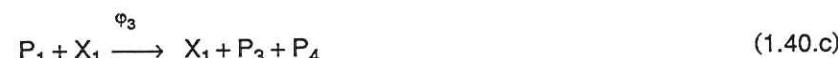
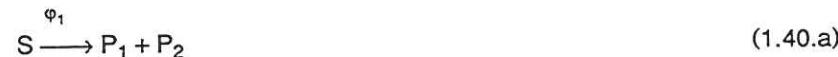
We consider the coculture of two thermophilic bacteria : *Lactobacillus bulgaricus* and *Streptococcus thermophilus* used for producing starters for the manufacture of yoghurt.

In this anaerobic mixed culture, the influent substrate, in this case lactose, is hydrolyzed into galactose and glucose which is in turn the unique limiting substrate of four different biochemical reactions :

- growth of *Lactobacillus bulgaricus* with production of CO_2
- production of D-lactate and CO_2 catalysed by *Lactobacillus bulgaricus*
- growth of *Streptococcus thermophilus*
- production of L-lactate catalysed by *Streptococcus thermophilus*.

Hence, the process is represented by the following reaction scheme ($M = 5$,

N = 8) :



with S : lactose concentration

 X_1 : *Streptococcus thermophilus* concentration X_2 : *Lactobacillus bulgaricus* concentration P_1 : glucose concentration P_2 : galactose concentration P_3 : dissolved carbon dioxide concentration P_4 : L-lactate concentration P_5 : D-lactate concentration φ_1 : lactose hydrolysis reaction rate φ_2 : *S. thermophilus* growth reaction rate φ_3 : L-lactate formation reaction rate φ_4 : *L. bulgaricus* growth reaction rate φ_5 : D-lactate formation reaction rate

1.5 General Dynamical Model of Bioreactors

In this section we shall present a general state space model for the description of biotechnological processes in stirred tank bioreactors. To simplify the presentation, the same notation ξ_i will be used to denote a component or its concentration (unit mass/unit volume) in the liquid phase of the reactor.

1.5.1. Dynamics of the process components

Once the reaction scheme of a biotechnological process is given, the derivation of a dynamical model is made fully systematic by applying the following rules :

R1) The reaction scheme of the process involves N components ξ_i ($i = 1, \dots, N$) and M reactions ($j=1, \dots, M$). The reaction rates are denoted φ_j ($j=1, \dots, M$)

R2) The dynamics of the concentration of each component ξ_i are written as follows :

$$\frac{d\xi_i}{dt} = \sum_{j-i} (\pm) k_{ij} \varphi_j - D\xi_i - Q_i + F_i \quad (1.41)$$

R3) the notation $j-i$ means that the summation is taken on the reactions with index j which involve the component with index i.

R4) k_{ij} are strictly positive constant yield coefficients, without dimension (i.e. units of mass / mass). They have a "-" sign when ξ_i is a reactant (i.e. when it appears on the left hand side of the reaction scheme) and a "+" sign when ξ_i is a product of the reaction (i.e. it appears on the right hand side).

R5) Q_i is the rate of mass outflow of the component ξ_i from the reactor in gaseous form.

R6) F_i is the mass feed rate in the reactor of the component ξ_i if it is an external substrate. Otherwise $F_i = 0$.

1.5.2. State space model

We introduce the following matrix notations :

$$\xi^T = [\xi_1, \xi_2, \dots, \xi_N] \quad (1.42.a)$$

$$\phi^T = [\phi_1, \phi_2, \dots, \phi_M] \quad (1.42.b)$$

$$Q^T = [Q_1, \dots, Q_N] \quad (1.42.c)$$

$$F^T = [F_1, \dots, F_N] \quad (1.42.d)$$

$$K = [K_{ij}] : N \times M \text{ matrix with } K_{ij} = (\pm) k_{ij} \text{ if } j \sim i \\ K_{ij} = 0 \text{ otherwise} \quad (1.42.e)$$

Then, from (1.41), the dynamics of biotechnological processes can thus be represented by the following general nonlinear state space model, written in matrix form :

General Dynamical Model

$$\frac{d\xi}{dt} = K\phi(\xi, t) - D\xi - Q(\xi) + F \quad (1.43)$$

In this expression we have introduced the notations $\phi(\xi, t)$ and $Q(\xi)$ to emphasize that ϕ and Q (and also F in some instances) may be time varying and may depend on the process state ξ . The issue of modelling ϕ , Q and F as functions of ξ will be addressed later.

The state space model (1.43) is in fact the backbone of this book because it will serve as the basic ingredient for the derivation of all the estimation and control algorithms proposed throughout the subsequent chapters. It should be stressed for the reader that, in our view, the model (1.43) is not a mathematical oddity but has a definite physical meaning :

- the first term $K\phi(\xi, t)$ describes the kinetics of the biochemical and microbiological reactions which are involved in the process;
- the remaining terms $-D\xi - Q(\xi) + F$ describe the transport dynamics of the components through the bioreactor.

The state space model (1.43) is thus mainly a way to express, in a single compact mathematical form, the two physical phenomena (namely kinetics and transport dynamics) which are in intimate interaction in a bioreactor.

Example : Microbial growth, death and maintenance (continued)

The process involves $N = 3$ components and $M = 3$ reactions and is described by the reaction scheme (1.32). The following change of notation is introduced:

$$\xi_1 = X \quad \xi_2 = S \quad \xi_3 = X_d \quad (1.44.a)$$

$$\phi_1 = \phi_g \quad \phi_2 = \phi_d \quad \phi_3 = \phi_m \quad (1.44.b)$$

Then, applying the rules R1 to R6 to the scheme (1.32), the dynamical model is easily written as follows :

$$\frac{d\xi_1}{dt} = k_{11}\varphi_1 - k_{12}\varphi_2 - D\xi_1 \quad (1.45.a)$$

$$\frac{d\xi_2}{dt} = -k_{21}\varphi_1 - k_{23}\varphi_3 - D\xi_2 + F_2 \quad (1.45.b)$$

$$\frac{d\xi_3}{dt} = k_{32}\varphi_2 - D\xi_3 \quad (1.45.c)$$

or, in matrix form

$$\frac{d}{dt} \begin{bmatrix} \xi_1 \\ \xi_2 \\ \xi_3 \end{bmatrix} = \begin{bmatrix} k_{11} & -k_{12} & 0 \\ -k_{21} & 0 & -k_{23} \\ 0 & k_{32} & 0 \end{bmatrix} \begin{bmatrix} \varphi_1 \\ \varphi_2 \\ \varphi_3 \end{bmatrix} - D \begin{bmatrix} \xi_1 \\ \xi_2 \\ \xi_3 \end{bmatrix} + \begin{bmatrix} 0 \\ F_2 \\ 0 \end{bmatrix} \quad (1.46)$$

It is easy to check that the first two equations of the state space model (1.46) exactly coincide with the "classical" model (1.2), provided the following change of notation is considered (in addition to (1.44)) :

$$k_{11}=1 \quad k_{12}=1 \quad k_{21}=k_1 \quad k_{23}=1 \quad k_{32}=1$$

$$\varphi_1=\varphi_g=\mu X \quad \varphi_2=\varphi_d=k_d X \quad \varphi_3=\varphi_m=k_m X$$

It should also be noted that this example clearly shows that the reaction rates φ_1 , φ_2 and φ_3 depend on the process state.

1.5.3. Modelling the reaction rates

The reaction rate $\varphi(\xi,t)$ is most often a very complex function of the operating conditions and of the state of the process. The analytical modelling of this function is often cumbersome and is the subject of continuing, intensive investigation (and sometimes of controversy). For instance, in the case where φ is proportional to the specific growth rate μ , there are several dozens of possible models, as shown in Section 1.3 and in Appendix 1.

In this book, we adopt a unifying (but not simplifying) stance for modelling φ based on the following fact : *the reaction can take place only if all the reactants are present in the reactor*. In other words, the reaction rate is necessarily zero whenever the concentration of one of the reactants is zero. This is represented as follows :

$$\varphi_j(\xi,t) \stackrel{\Delta}{=} \alpha_j(\xi,t) \left(\prod_{n-j} \xi_n \right) \quad (1.47.a)$$

$$0 \leq \alpha_j(\xi,t) \leq \alpha_{\max} \quad (1.47.b)$$

The notation $n-j$ means that the multiplication \prod is taken over the components with index n which are reactants in the reaction j (*including the autocatalysts*) which are considered as reactants when writing (1.47.a)).

$\alpha_j(\xi,t)$ is called the *specific reaction rate* since it is the reaction rate per unit of each reactant. It must be a bounded function for evident reasons of mathematical consistency.

Define the vector α and the matrix $G(\xi)$:

$$\alpha^T = [\alpha_1, \dots, \alpha_M] \quad (1.48.a)$$

$$G(\xi) = \text{diag} \left\{ \prod_{n-j} \xi_n \right\}_{j=1, \dots, M} \quad (1.48.b)$$

The notation "diag" is used to denote a diagonal matrix, i.e. :

$$\text{diag}_{j=1,\dots,M} \left\{ \prod_{n=j}^M \xi_n \right\} = \begin{bmatrix} \prod_{n=1}^M \xi_n & 0 & \dots & 0 \\ 0 & \prod_{n=2}^M \xi_n & \dots & 0 \\ 0 & 0 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & \prod_{n=M}^M \xi_n \end{bmatrix}$$

The state-space model (1.43) is then rewritten :

$$\frac{d\xi}{dt} = KG(\xi)\alpha - D\xi + F - Q(\xi) \quad (1.49)$$

An important special case occurs when the specific reaction rates α are independent of the state ξ and depend only on the temperature (e.g. according to the Arrhenius law) :

$$\alpha(\xi, t) = \alpha(T(t)) \quad (1.50)$$

In particular, when the temperature is regulated at a constant value, a multilinear state space model with constant parameters is obtained. In terms of chemical kinetic theory such a model corresponds to the assumption that all the reactions are governed by the *law of mass action* with a unit partial order with respect to each reactant.

The specific growth rate

In the particular case where the reaction rate $\phi(\xi)$ is actually a *microbial growth rate*, an alternative representation, which has already been evoked several times, is commonly used in bioengineering studies.

Let us suppose that $\phi_j(\xi)$ denotes the growth rate of a particular biomass population X_i . It is clear, from our preceding discussion, that the concentration X_i necessarily appears as a factor in the multiplication term of (1.47.a). Hence the reaction rate $\phi_j(\xi)$ can equivalently be represented as follows :

$$\phi_j(\xi) \stackrel{\Delta}{=} \mu_j(\xi)X_i \quad (1.51)$$

where $\mu_j(\xi)$ is termed *the specific growth rate*, since it is the growth rate per unit of biomass.

Remark that the notation has been implicitly used many times in Sections 1.1 to 1.3, and explicitly in the example of Section 1.5.2 (namely $\phi_g = \mu X$).

The definitions of specific reaction rate and specific growth rate are now further illustrated by an example.

Example : Basic dynamics of microbial growth

Consider the simple microbial growth process (1.33) :



for which the following dynamical model is derived from the rules R1-R6 :

$$\frac{d}{dt} \begin{bmatrix} S \\ X \end{bmatrix} = \begin{bmatrix} -k_1 \\ k_2 \end{bmatrix} \phi - D \begin{bmatrix} S \\ X \end{bmatrix} + \begin{bmatrix} F \\ 0 \end{bmatrix} \quad (1.52)$$

The growth rate ϕ can be represented either as :

$$\phi(S, X) = \alpha(S, X) SX \quad (1.53)$$

or as :

$$\varphi(S, X) = \mu(S, X) X \quad (1.54)$$

Notice that, with the latter expression, the model (1.52) coincides with the "classical" representation (1.3.a-b), for $k_2 = 1$ and $F = DS_{in}$.

Suppose that the specific growth rate $\mu(S, X)$ is described by the "Contois law" (1.22) :

$$\mu(S, X) = \frac{\mu^* S}{K_c X + S}$$

This implies that the reaction rate $\varphi(X, S)$ is written :

$$\varphi(X, S) = \mu(X, S) X = \frac{\mu^* S X}{K_c X + S} \quad (1.55)$$

which in turn implies that the specific reaction rate $\alpha(X, S)$ is defined as :

$$\alpha(X, S) = \frac{\mu^*}{K_c X + S} \quad (1.56)$$

The example shows the consistency between the two alternative representations (1.53) and (1.54) when the Contois law is used.

1.5.4. Modelling the gaseous outflow rates

In equation (1.41), Q_i represents the rate of mass removal in gaseous form for those components ξ_i which are soluble in the liquid phase and gasifiable at atmospheric pressure. According to common industrial practice, we suppose that these compounds are freely given off from the reactor. As long as the concentration is lower than the saturation level, if we neglect the liquid-gas transfer dynamics, it is natural to assume that the outflow rate in the gaseous phase is simply proportional to the concentration in the liquid phase :

$$Q_i = \beta_i \xi_i \quad 0 \leq \beta_i \quad 0 \leq \xi_i \leq \xi_{is} \quad (1.57)$$

where β_i is the *specific liquid-gas transfer rate* and ξ_{is} is the saturation concentration.

Obviously, $\beta_i = 0$ if the component ξ_i is not gasifiable (as for biomass or enzymes, for instance).

Defining the matrix B :

$$B = \text{diag}\{\beta_i\} \quad i = 1, \dots, N \quad (1.58)$$

the general dynamical model (1.43) is rewritten :

$$\frac{d\xi}{dt} = K\varphi(\xi) - D\xi + F - B\xi \quad (1.59)$$

If $\xi_i > \xi_{is}$, it is clear that the mass balance expressed by equation (1.59) is no longer valid. This point will be revisited in Section 1.8.2.

1.5.5. Modelling the feed rates

In equation (1.41), F_i represents the feed rate (per unit of volume) of those components ξ_i which are external substrates introduced in the reactor from the outside. The way the reactor is fed and the nature of the substrate (liquid or gaseous) lead to various methods of modelling the feed rates.

Liquid substrates

There are essentially two ways of introducing a liquid substrate into the reactor: either diluted in the influent stream (Fig.1.10.b) or independently of the influent stream (Fig.1.10.a).

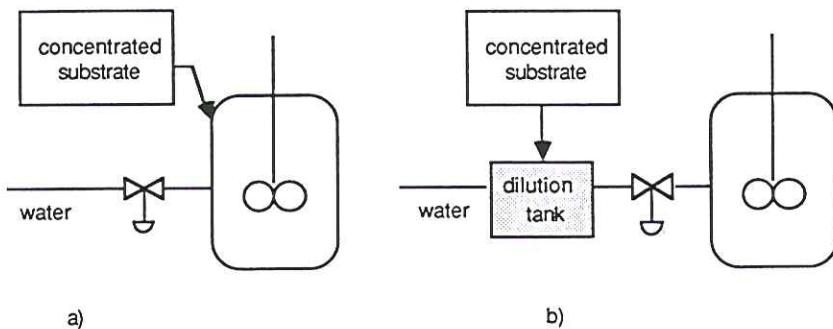


Fig.1.10. Influent liquid substrates

In the latter case (Fig.1.10.a), there is no need for specific further modelling of the substrate feed rate F_i . However, in the former case, when the substrate is diluted in the water stream, the feed rate is proportional to the substrate concentration in the influent. The proportionality coefficient is precisely the dilution rate D (see for instance model (1.3)). In that case, each nonzero feed rate F_i is written:

$$F_i = DS_{in,i} \quad (1.60)$$

where $S_{in,i}$ denotes the influent substrate concentration.

When all the external substrates are in liquid form, we can define the vector :

$$S_{in} = [S_{in,1}, S_{in,2}, \dots, S_{in,N}]^T \quad (1.61)$$

where, obviously, $S_{in,i} = 0$ when ξ_i is not an external substrate; then :

$$F = DS_{in} \quad (1.62)$$

and the general dynamical model (1.43) is rewritten :

$$\frac{d\xi}{dt} = K\varphi(\xi) - D\xi + DS_{in} - Q(\xi) \quad (1.63)$$

Gaseous substrates

It may occur that substrates are introduced into the bioreactor in gaseous form. The archetype is the class of aerobic processes where the reactor is fed with gaseous oxygen by aeration of the culture medium. Let us suppose that ξ_n denotes such a gaseous substrate. Then, as we have seen in Section 1.2 (e.g. expression (1.15)), the corresponding feed rate is written :

$$F_n = k_L a(F_g) (\xi_{ns} - \xi_n)$$

where $k_L a(F_g)$ is a time-varying transfer coefficient depending on the "aeration" feed rate F_g (and also on other factors such as, for instance, the geometry of the aerator) and ξ_{ns} is the saturation concentration.

It is worth noting that in this particular case the feed rate F_n is itself a function of the process state ξ_n .

1.5.6. Scaling of the yield coefficients

The rates of consumption of reactants and the rates of production of products are expressed in the model (1.41) by terms of the form $(\pm)k_{ij}\varphi_j$ whose common dimension is unit of mass per unit of time.

In each reaction, let us choose, one component ξ_n which is called the *nominal* component of the reaction. It can easily be seen that the fraction k_{ij}/k_{in} represents the yield of consumption or production of the component ξ_i per *unit* of consumption or production of the nominal component ξ_n . It is then obvious that the coefficient k_{nj} can be arbitrarily fixed to 1 without any loss of generality in the general dynamical model (1.43). This method of scaling the yield coefficients will be used repeatedly throughout the book and, in particular, in the examples of models presented in the next section.

1.6. Examples of State Space Models

In this section the state space models (1.43) and (1.49) are established for the examples of Section 1.4.3.

1.6.1. Yeast growth

The external influent substrates are glucose and oxygen. The application of rules R1-R6 to the scheme (1.37) leads to the following definitions :

$$\xi^T = [X, S, E, C, P] \quad (1.64.a)$$

$$F^T = [0 \ F_1 = DS_{in} \ 0 \ Q_{in} \ 0] \quad (1.64.b)$$

$$Q^T = [0 \ 0 \ 0 \ 0 \ Q_1] \quad (1.64.c)$$

$$K^T = \begin{bmatrix} 1 & -k_1 & 0 & -k_5 & k_7 \\ 1 & -k_2 & k_4 & 0 & k_8 \\ 1 & 0 & -k_3 & -k_6 & k_9 \end{bmatrix} \quad (1.64.d)$$

$$\varphi^T = [\varphi_1 \ \varphi_2 \ \varphi_3] \quad (1.64.e)$$

$$\alpha^T = [\alpha_1 \ \alpha_2 \ \alpha_3] \quad (1.64.f)$$

$$G(\xi) = \begin{bmatrix} SCX & 0 & 0 \\ 0 & SX & 0 \\ 0 & 0 & ECX \end{bmatrix} \quad (1.64.g)$$

with Q_{in} : oxygen feed rate

Q_1 : output carbon dioxide flow rate

S_{in} : influent glucose concentration

k_i ($i = 1$ to 9) : yield coefficients

α_i ($i = 1$ to 3) : specific reaction rates

Note the scaling of the yield coefficients in the matrix K (1.64.d).

1.6.2. Anaerobic digestion

The following model is associated with the reaction scheme (1.38) :

$$\xi^T = [X_1 \ S_1 \ X_2 \ S_2 \ X_3 \ S_3 \ X_4 \ S_4 \ S_5 \ P_1] \quad (1.65.a)$$

$$Q^T = [0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ Q_3 \ Q_2 \ Q_1] \quad (1.65.b)$$

$$F^T = [0 \ F_1 = DS_{in} \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0] \quad (1.65.c)$$

$$K^T = \begin{bmatrix} 1 & -k_{21} & 0 & k_{41} & 0 & k_{61} & 0 & k_{81} & k_{91} & 0 \\ 0 & 0 & 1 & -k_{42} & 0 & 0 & 0 & 0 & k_{92} & k_{02} \\ 0 & 0 & 0 & k_{43} & 1 & -k_{63} & 0 & k_{83} & k_{93} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & -k_{84} & -k_{94} & k_{04} \end{bmatrix} \quad (1.65.d)$$

$$\varphi^T = [\varphi_1 \ \varphi_2 \ \varphi_3 \ \varphi_4] \quad (1.65.e)$$

$$\alpha^T = [\alpha_1 \ \alpha_2 \ \alpha_3 \ \alpha_4] \quad (1.65.f)$$

$$G(\xi) = \begin{bmatrix} S_1 X_1 & 0 & 0 & 0 \\ 0 & S_2 X_2 & 0 & 0 \\ 0 & 0 & S_3 X_3 & 0 \\ 0 & 0 & 0 & S_4 S_5 X_4 \end{bmatrix} \quad (1.65.g)$$

with Q_1 : methane gas flow rate

Q_2 : gaseous CO_2 flow rate

Q_3 : gaseous hydrogen flow rate

S_{in} : influent glucose concentration

k_{ij} ($i=0$ to 9, $j=1$ to 4) : yield coefficients

α_j ($j=1$ to 4) : specific growth rate of X_j

$$\xi^T = [S \ X_1 \ X_2 \ P_1 \ P_2 \ P_3 \ P_4 \ P_5] \quad (1.67.a)$$

$$Q^T = [0 \ 0 \ 0 \ 0 \ 0 \ Q_1 \ 0 \ 0] \quad (1.67.b)$$

1.6.3. Intracellular production of PHB acid

The following model is associated with the reaction scheme (1.39) :

$$\xi^T = [X \ S_1 \ S_2 \ P_1 \ C \ P_2] \quad (1.66.a)$$

$$Q^T = [0 \ 0 \ 0 \ 0 \ 0 \ Q_1] \quad (1.66.b)$$

$$F^T = [0 \ DS_{1,in} \ DS_{2,in} \ 0 \ Q_{in} \ 0] \quad (1.66.c)$$

$$K^T = \begin{bmatrix} 1 & -k_1 & -k_2 & k_3 & -k_4 & k_7 \\ 0 & -k_5 & 0 & 1 & -k_6 & k_8 \end{bmatrix} \quad (1.66.d)$$

$$\phi^T = [\varphi_1 \ \varphi_2] \quad (1.66.e)$$

$$\alpha^T = [\alpha_1 \ \alpha_2] \quad (1.66.f)$$

$$G(\xi) = \begin{bmatrix} S_1 S_2 C X & 0 \\ 0 & S_1 C X \end{bmatrix} \quad (1.66.g)$$

Q_1 : output gaseous carbon dioxide flow rate

Q_{in} : oxygen feed rate

$S_{1,in}$: influent fructose concentration

$S_{2,in}$: influent ammonia concentration

k_j ($j=1$ to 6) : yield coefficients

α_i ($i=1$ to 2) : specific reaction rates

1.6.4. Lactic fermentation

The following model is associated with the reaction scheme (1.40) :

$$F^T = [F_1 = DS_{in} \ 0 \ 0 \ 0 \ 0 \ 0 \ 0] \quad (1.67.c)$$

$$K^T = \begin{bmatrix} -k_1 & 0 & 0 & 1 & k_6 & 0 & 0 & 0 \\ 0 & 1 & 0 & -k_2 & 0 & k_7 & 0 & 0 \\ 0 & 0 & 0 & -k_3 & 0 & k_8 & k_9 & 0 \\ 0 & 0 & 1 & -k_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -k_5 & 0 & 0 & 0 & k_{10} \end{bmatrix} \quad (1.67.d)$$

$$\phi^T = [\varphi_1 \ \varphi_2 \ \varphi_3 \ \varphi_4 \ \varphi_5] \quad (1.67.e)$$

$$\alpha^T = [\alpha_1 \ \alpha_2 \ \alpha_3 \ \alpha_4 \ \alpha_5] \quad (1.67.f)$$

$$G(\xi) = \begin{bmatrix} S & 0 & 0 & 0 & 0 \\ 0 & P_1 X_1 & 0 & 0 & 0 \\ 0 & 0 & P_1 X_1 & 0 & 0 \\ 0 & 0 & 0 & P_2 X_2 & 0 \\ 0 & 0 & 0 & 0 & P_2 X_2 \end{bmatrix} \quad (1.67.g)$$

with Q_1 : gaseous CO_2 flow rate

S_{in} : influent lactose concentration

k_j ($j=1$ to 10) : yield coefficients

α_i ($i=1$ to 5) : specific reaction rates

1.7. A Basic Structural Property of the General Dynamical Model

We consider the general dynamical model (1.43) :

$$\frac{d\xi}{dt} = K\phi(\xi, t) - D\xi - Q(\xi) + F \quad (1.43)$$

with $\dim(\xi) = \dim(F) = \dim(Q) = N$, $\dim(\phi) = M$ and $\dim(K) = NxM$.

We define :

$p = \text{rank}(K)$;

K_a a (pxM) full rank arbitrary submatrix of K ;

K_b the remaining submatrix of K ;

(ξ_a, ξ_b) , (Q_a, Q_b) and (F_a, F_b) the partitions of ξ , Q and F induced by (K_a, K_b) .

The general dynamical model (1.43) is rewritten :

$$\frac{d\xi_a}{dt} = K_a \varphi(\xi_a, \xi_b) - D\xi_a - Q_a + F_a \quad (1.68)$$

$$\frac{d\xi_b}{dt} = K_b \varphi(\xi_a, \xi_b) - D\xi_b - Q_b + F_b \quad (1.69)$$

We then have the following property :

There exists a state transformation :

$$Z = A_0 \xi_a + \xi_b \quad (1.70)$$

where A_0 , of dimension $(N-p)xp$, is the unique solution of the matrix equation :

$$A_0 K_a + K_b = 0 \quad (1.71)$$

such that the state-space model is equivalent to :

$$\frac{d\xi_a}{dt} = K_a \varphi(\xi_a, \xi_b) - D\xi_a - Q_a + F_a \quad (1.72)$$

$$\frac{dZ}{dt} = -DZ + A_0(F_a - Q_a) + (F_b - Q_b) \quad (1.73)$$

When $(F_a - Q_a)$ is identically zero, the partition (ξ_a, ξ_b) is said to be *nice* (because the dynamics of Z are independent of both K and φ).

Example : Intracellular production of PHB acid

$$\begin{aligned} \xi_a &= \begin{bmatrix} X \\ S_1 \end{bmatrix} & \xi_b &= \begin{bmatrix} S_2 \\ P_1 \\ C \\ P_2 \end{bmatrix} \end{aligned}$$

Consider the state space model (1.66) for the intracellular production of PHB. If we choose the partition :

$$\begin{aligned} \xi_a &= \begin{bmatrix} X \\ S_1 \end{bmatrix} & \xi_b &= \begin{bmatrix} S_2 \\ P_1 \\ C \\ P_2 \end{bmatrix} \end{aligned}$$

we have from (1.56.d) :

$$\begin{aligned} K_a &= \begin{bmatrix} 1 & 0 \\ -k_1 & -k_5 \end{bmatrix} & K_b &= \begin{bmatrix} -k_2 & 0 \\ k_3 & 1 \\ -k_4 & -k_6 \\ k_7 & k_8 \end{bmatrix} \end{aligned}$$

Clearly the matrix K_a is full rank and the partition is admissible. Hence, from (1.71) :

$$A_0 = \frac{1}{k_5} \begin{bmatrix} k_2 k_5 & 0 \\ -k_3 k_5 + k_1 & 1 \\ +k_4 k_5 - k_1 k_6 & -k_6 \\ -k_5 k_7 + k_1 k_8 & k_8 \end{bmatrix}$$

i.e. the auxiliary state transformation (1.70) is as follows :

$$\begin{bmatrix} Z_1 \\ Z_2 \\ Z_3 \\ Z_4 \end{bmatrix} = \begin{bmatrix} k_2 X + S_2 \\ (k_3 + k_1/k_5) X + S_1/k_5 + P_1 \\ -(k_4 + k_1 k_6/k_5) X - k_6 S_1/k_5 + C \\ -(k_7 - k_1 k_8/k_5) X + k_8 S_1/k_5 + P_2 \end{bmatrix}$$

This is not, however, a *nice* partition since $F_a = [0 \ DS_{in}]^T$ is not identically zero. We shall obtain a nice partition, in this example, by considering the following partition (it is easy to check that it is also the only nice partition) :

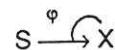
$$\xi_a = \begin{bmatrix} X \\ P_1 \end{bmatrix} \quad \xi_b = \begin{bmatrix} S_1 \\ S_2 \\ C \\ P_2 \end{bmatrix}$$

1.8. Reduction of the General Dynamical Model

The examples of biotechnological processes in Section 1.6 have shown that a bioreactor dynamical model may be fairly complex in some instances and involve a large number of differential equations. But there are many practical applications where a simplified reduced order model is sufficient from an engineering viewpoint. 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. This technique is suitable when neglecting the dynamics of substrates and of products with low solubility in the liquid phase. The method will be illustrated with two specific examples before stating the general rule for order reduction.

1.8.1. Singular perturbation technique for substrates

We return to the simple microbial growth process (1.33) :



The dynamics corresponding to this scheme are represented by the model (1.1.a-b) rewritten as follows :

$$\frac{dX_T}{dt} = \mu X_T - DX_T \quad (1.74.a)$$

$$\varepsilon \frac{dS}{dt} = -k_1 \mu X_T - \varepsilon DS + F_r \quad (1.74.b)$$

where X_T is the *total* amount of biomass in the reactor (i.e. not the concentration), S is the substrate concentration, $\varepsilon = V$ is the reactor volume, and F_r is the substrate feed rate.

Notice that equations (1.74.a-b) are *true* mass balance equations, expressed in terms of total quantities and not in terms of concentrations.

Clearly, for any $\varepsilon > 0$, the system (1.74) consists of two differential equations. However, if $\varepsilon = 0$, the system consists of one differential equation and one algebraic equation, because (1.74.b) reduces to :

$$k_1 \mu X_T = F_r \quad (1.75)$$

Consequently, the first differential equation (1.74.a) may be rewritten :

$$\frac{dX_T}{dt} = -DX_T + \frac{1}{k_1} F_r \quad (1.76)$$

Setting $\varepsilon = 0$ in (1.74.b) is called a *singular perturbation*. The objective is to examine the simplified model (1.76) in order to draw conclusions about the original system with $\varepsilon \neq 0$. It must be well understood that we are not assuming that the volume of the reactor is zero. We actually assume that the volume V is small enough to neglect $\varepsilon(dS/dt)$ and εdS in (1.74.b). This means that it is legitimate to consider the simplified model with the actual nonzero value of V and hence rewrite it in the standard form (see Section 1.5.3) :

$$\frac{dX}{dt} = \alpha(X, S)XS - DX \quad (1.77.a)$$

$$k_1\alpha(X, S)XS = DS_{in} \quad (1.77.b)$$

with $X = X_T/V$ and $\phi = \alpha(X, S)XS = \mu(X, S)X$

1.8.2. Singular perturbation technique for products

Let us consider a biochemical reaction described by the following reaction scheme :



where P is a volatile product which can be given off in gaseous form and has low solubility in the liquid phase. According to the rules of Section 1.5.1, the dynamical model is as follows :

$$\frac{dS}{dt} = -\phi - DS + F \quad (1.78.a)$$

$$\frac{dP}{dt} = k\phi - DP - Q \quad (1.78.b)$$

The consistency of this model requires that the product concentration P be lower than a *saturation concentration* representative of the product solubility, which is expressed as :

$$P = \Pi P_{sat} \quad 0 \leq \Pi(t) \leq 1$$

where P_{sat} is the saturation concentration which is constant in a stable physico-chemical environment. The model (1.78) is rewritten in the standard singular perturbation form, with $\varepsilon = P_{sat}$:

$$\frac{dS}{dt} = -\phi - DS + F \quad (1.79.a)$$

$$\varepsilon \frac{d\Pi}{dt} = k\phi - \varepsilon D\Pi - Q \quad (1.79.b)$$

If the solubility is very low, we obtain a reduced order model by setting $\varepsilon = 0$ and replacing the differential equation (1.79.b) by the algebraic one :

$$Q = k\phi \quad (1.80)$$

1.8.3. A general rule for order reduction

The above examples show that the rule for model simplification is actually very simple and that an explicit singular perturbation analysis is not really needed. Consider that, for some i , the dynamics of the component ξ_i are to be neglected. The dynamics of ξ_i are described by equation (1.41) :

$$\frac{d\xi_i}{dt} = \sum_{j-i} (\pm) k_{ij}\phi_j - D\xi_i - Q_i + F_i \quad (1.41)$$

The simplification is then achieved by setting ξ_i and $d\xi_i/dt$ to zero i.e. by replacing the differential equation (1.39) by the following algebraic equation :

$$\sum_{j-i} (\pm) k_{ij}\phi_j = Q_i - F_i \quad (1.81)$$

1.8.4. Example : The anaerobic digestion process

We shall now show how these rules for order reduction can be applied to derive a simplified model of the anaerobic digestion process. The third reaction (decomposition of propionate by the OHPA) and the fourth reaction (decomposition of hydrogen) are supposed to be characterised by fast dynamics. This is expressed by setting S_3 , dS_3/dt , and S_4 , dS_4/dt to zero in the dynamical model (1.65). We derive the following algebraic equations :

$$\varphi_3 = \frac{k_{61}}{k_{63}} \varphi_1 \quad (1.82)$$

$$\varphi_4 = \frac{k_{81}}{k_{84}} \varphi_1 + \frac{k_{83}}{k_{84}} \varphi_3 = \frac{k_{63}k_{81} + k_{61}k_{83}}{k_{63}k_{84}} \varphi_1 \quad (1.83)$$

Moreover, it is well known that the solubility of methane is extremely low. Therefore we write :

$$Q_1 = k_{02}\varphi_2 + k_{04} \frac{k_{63}k_{81} + k_{61}k_{83}}{k_{63}k_{84}} \varphi_1 \quad (1.84)$$

By using the above approximations (1.82), (1.83), (1.84), we finally obtain the classical two-step (acidogenesis-methanisation) dynamical representation of anaerobic digestion processes :

$$\frac{dX_1}{dt} = \varphi_1 - DX_1 \quad (1.85.a)$$

$$\frac{dS_1}{dt} = -k_1\varphi_1 - DS_1 + DS_{in} \quad (1.85.b)$$

$$\frac{dX_2}{dt} = \varphi_2 - DX_2 \quad (1.85.c)$$

$$\frac{dS_2}{dt} = k_3\varphi_1 - k_2\varphi_2 - DS_2 \quad (1.85.d)$$

$$\frac{dP_2}{dt} = k_4\varphi_1 + k_5\varphi_2 - DP_2 - Q_2 \quad (1.85.e)$$

$$Q_1 = k_6\varphi_2 + k_7\varphi_1 \quad (1.85.f)$$

with :

$$k_1 = k_{11}, \quad k_2 = k_{42}, \quad k_3 = k_{41} + \frac{k_{61}k_{43}}{k_{63}}$$

$$k_4 = k_{91} + \frac{k_{61}k_{93}}{k_{63}} - k_{94} \left(\frac{k_{63}k_{81} + k_{61}k_{83}}{k_{63}k_{84}} \right)$$

$$k_5 = k_{92}, \quad k_6 = k_{02}, \quad k_7 = k_{04} \frac{k_{63}k_{81} + k_{61}k_{83}}{k_{63}k_{84}}$$

$$P_2 = S_5$$

This model corresponds to the following simplified reaction scheme (compare with scheme (1.38)) :



Comment

In some instances (e.g. when the influent substrate is not composed mainly of glucose) the presence, formation and decomposition of hydrogen are negligible. The formation of methane is then assumed to result almost exclusively from the decomposition of acetate (i.e. $k_4 = k_7 = 0$), and the reaction scheme simplifies as follows :



while equation (1.85.f) reduces to :

$$Q_1 = k_6 \varphi_2 \quad (1.88)$$

1.9. Stability Analysis

In this section, we analyse the stability of the state space dynamical model. In Section 1.9.1, we shall prove the global Bounded Input Bounded State (BIBS) stability of the system (in accordance with the physical reality). In Section 1.9.2, we introduce the concept of equilibrium state and we show that bioprocesses generically possess several equilibrium states whose stability is analysed in Section 1.9.3.

1.9.1. Bounded Input Bounded State stability

The BIBS stability will be analysed under the following assumptions :

A1. The dilution rate is bounded below as follows :

$$0 < D_{\min} \leq D(t) \quad \forall t \quad (1.89)$$

A2. The feed rates are bounded as follows :

$$0 \leq F_i(t) \leq F_{\max} \quad \forall i, \forall t \quad (1.90)$$

A3. Each reaction involves at least one reactant which is *neither* a catalyst *nor* an autocatalyst.

We have the following stability theorem.

Theorem 1.1 : Under Assumptions A1 to A3, the state variables of the general dynamical model (1.59) are positive and bounded for all t .

Proof : The proof of the theorem will be divided into two parts. We shall first show that the state variables are positive, and then that they have upper bounds.

1) *the state variables are positive : $\xi_i(t) \geq 0 \quad \forall i, \forall t$*

Suppose that $\xi_i(t) = 0$ for some i . Then, from (1.47) and (1.59), the dynamical equation reduces to :

$$\frac{d\xi_i}{dt} = \sum_j (+) k_j \varphi_j + F_i \geq 0 \quad (1.91)$$

where the summation is taken only over those reactions with index j which involve ξ_i as a product but neither as a substrate nor as an autocatalyst. Hence, the right hand side of (1.91) is necessarily nonnegative and, since $\xi_i(0) \geq 0$, $\xi_i(t) \geq 0$ for all t .

2) *The state variables are upper bounded.*

Let us select one reactant of the process which is, at least in one reaction, neither a catalyst nor an autocatalyst. This reactant (which necessarily exists by Assumption A3) is denoted ξ_n ($n \in [1, N]$).

We define two sets of indices :

$$J = (m_1, m_2, \dots, m_p) \quad I = (n_1, n_2, \dots, n_q) \quad (1.92)$$

m_i ($i=1, \dots, p$) are the indices of the reactions which involve ξ_n as a reactant (i.e. *not* as a product).

n_j ($j=1, \dots, q$) are the indices of the components (excluding ξ_n) involved in the reactions with an index $m_j \in J$.

We define the auxiliary variable :

$$z_n = a_n \xi_n + \sum_{i \in I} \xi_i \quad (1.93)$$

with

$$a_n = \max_{j \in J} \frac{\sum_{i \in I} \bar{k}_{ij}}{-\bar{k}_{nj}} \geq 0 \quad (1.94)$$

where \bar{k}_{ij} denotes entry (i,j) of the matrix K .

The dynamics of z_n can then easily shown to be :

$$\frac{dz_n}{dt} = \sum_{j \in J} [a_n \bar{k}_{nj} + \sum_{i \in I} \bar{k}_{ij}] \varphi_j - Dz_n - a_n \beta_n \xi_n - \sum_{i \in I} \beta_i \xi_i + a_n F_n + \sum_{i \in I} F_i \quad (1.95)$$

From Assumption A2 and the definition of a_n it follows that :

$$\frac{dz_n}{dt} \leq -Dz_n + (a_n + q) F_{\max} \quad (1.96)$$

At this point, there are two possibilities depending on the initial value of z_n .

a) $z_n(0) > \frac{(a_n + q) F_{\max}}{D_{\min}}$

It is clear from Assumption A1 and (1.96) that the time derivative of $z_n(0)$ is negative and hence that $z_n(t) \leq z_n(0)$ for all t .

b) $z_n(0) \leq \frac{(a_n + q) F_{\max}}{D_{\min}}$

It then follows from (1.96) that $z_n(t)$ is bounded as follows for all t :

$$z_n(t) \leq \frac{(a_n + q) F_{\max}}{D_{\min}} \quad (1.97)$$

The boundedness of $z_n(t)$ obviously implies that of $\xi_i(t)$, $i \in I$, and of $\xi_n(t)$.

The theorem follows by repeating the same argumentation for all the reactants.
Q.E.D.

An explicit expression for the upper bound on the state variables can be formulated by introducing the following assumption on the initial conditions :

A4. The initial values of the state variables $\xi_i(t)$ have upper bounds as follows :

$$a_n \xi_n(0) + \sum_{i \in I} \xi_i(0) \leq \frac{(a_n + q) F_{\max}}{D_{\min}} \quad (1.98)$$

for all n and $i \in I$ as defined in Theorem 1.1.

Corollary 1.2 : Under Assumptions A1 to A4, the state variables $\xi_i(t)$ of the general dynamical model (1.59) are non-negative and bounded as follows for all t :

$$0 \leq \xi_i(t) \leq \max \left\{ 1, \frac{1}{a_n} \right\} (a_n + q) \frac{F_{\max}}{D_{\min}} \quad (1.99)$$

Proof : Straightforward from (1.97).

Comment

Assumption A1 is rather restrictive, since it requires a *strictly positive* lower bound D_{\min} on the dilution rate $D(t)$. It can easily be relaxed in cases where all the external substrates are in the liquid phase (with the exception of any gaseous external reactant such as oxygen, see Section 1.5.5). In that case, the vector F of feed rates is written (see (1.61) (1.62)) :

$$F = DS_{in} = D [S_{in,1}, S_{in,2}, \dots, S_{in,N}]^T \quad (1.100)$$

Assumptions A1, A2 and A4 are replaced by the following ones :

$$A1'. D(t) \geq 0 \quad \forall t \quad (1.101)$$

$$A2'. 0 \leq S_{in,i}(t) \leq S_{max} \quad \forall i, \forall t \quad (1.102)$$

$$A4'. a_n \xi_n(0) + \sum_{i \in I} \xi_i(0) \leq (a_n + q) S_{max} \quad (1.103)$$

and Corollary 1.2 is reformulated as follows :

Corollary 1.3 : Under Assumptions A1', A2', A3 and A4', the state variables $\xi_i(t)$ of the general dynamical model (1.59) are positive and bounded as follows for all t :

$$0 \leq \xi_i(t) \leq \max \left\{ 1, \frac{1}{a_n} \right\} (a_n + q) S_{max} \quad (1.104)$$

Proof : Straightforward from Theorem 1.1 and Corollary 1.2 by noting that equations (1.96) and (1.97) become :

$$\frac{dz_n}{dt} \leq D(-z_n + (a_n + q)S_{max}) \quad (1.105)$$

$$z_n \leq (a_n + q)S_{max} \quad (1.106)$$

Q.E.D.

A simple example

Consider an autocatalytic reaction with one substrate and one product :



The dynamics are as follows :

$$\frac{d}{dt} \begin{bmatrix} S \\ X \\ P \end{bmatrix} = \begin{bmatrix} -k_1 \phi \\ 1 \\ k_2 \end{bmatrix} + D \begin{bmatrix} S \\ X \\ P \end{bmatrix} + \begin{bmatrix} DS_{in} \\ 0 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ Q_1 \end{bmatrix} \quad (1.108)$$

If we directly apply the result of the above Corollary 1.2 by setting :

$$\xi_n = S \quad (1.109)$$

$$a_n = \frac{1 + k_2}{k_1} \quad (1.110)$$

and if the initial values of S , X and P are bounded according to Assumption A4' :

$$\left(\frac{k_1}{1 + k_2} \right) S(0) + X(0) + P(0) \leq \left(\frac{k_1}{1 + k_2} \right) S_{max} \quad (1.111)$$

it follows that the concentrations of the substrate S , the biomass X and the product P are bounded as follows, for all t :

$$0 \leq S(t) \leq S_{max} \quad \forall t \quad (1.112.a)$$

$$0 \leq X(t) \leq \frac{1 + k_2}{k_1} S_{max} \quad \forall t \quad (1.112.b)$$

$$0 \leq P(t) \leq \frac{1 + k_2}{k_1} S_{max} \quad \forall t \quad (1.112.c)$$

where S_{\max} is the maximum substrate concentration in the influent ($0 \leq S_{in}(t) \leq S_{\max}, \forall t$).

Expressions (1.112.a-c) strengthen the plausibility of the dynamical model since they guarantee that the different concentrations remain positive, that the substrate concentration S remains lower than the higher influent substrate concentration S_{\max} and that the concentrations of the two "products" X and P are upper bounded proportionally to the (maximum) influent substrate concentration, the proportionality factor being determined by the yield coefficients.

However, the general formulation of Theorem 1.1 and Corollaries 1.2 and 1.3 often leads in practice to rather conservative upper bounds. By taking advantage of the structure of the reaction scheme in specific applications, less conservative bounds may be written down. In fact, this is easily achieved in the above example by defining two auxiliary variables (instead of one in Theorem 1.1) :

$$Z_1 = \frac{1}{k_1} S + X \quad (1.113.a)$$

$$Z_2 = \frac{k_2}{k_1} S + P \quad (1.113.b)$$

These are immediately derived from the basic structural property (Section 1.7) by considering :

$$\xi_a = S \quad \xi_b = [X \ P]^T \quad (1.114)$$

The dynamics of Z_1 and Z_2 are clearly governed by the following equations :

$$\frac{dZ_1}{dt} = -DZ_1 + \frac{1}{k_1} DS_{in} \quad (1.115.a)$$

$$\frac{dZ_2}{dt} = -DZ_2 + \frac{k_2}{k_1} DS_{in} - Q \quad (1.115.b)$$

From Assumption A2', the time derivatives of Z_1 and Z_2 are bounded as follows :

$$\frac{dZ_1}{dt} \leq -DZ_1 + \frac{1}{k_1} DS_{\max} \quad (1.116.a)$$

$$\frac{dZ_2}{dt} \leq -DZ_2 + \frac{k_2}{k_1} DS_{\max} \quad (1.116.b)$$

It follows immediately that if, at the initial time, S , X and P satisfy the inequalities :

$$S(0) + k_1 X(0) \leq S_{\max} \quad (1.117.a)$$

$$S(0) + \frac{k_1}{k_2} P(0) \leq S_{\max} \quad (1.117.b)$$

then they have the following upper bounds :

$$S(t) \leq S_{\max} \quad \forall t \quad (1.118.a)$$

$$X(t) \leq \frac{1}{k_1} S_{\max} \quad \forall t \quad (1.118.b)$$

$$P(t) \leq \frac{k_2}{k_1} S_{\max} \quad \forall t \quad (1.118.c)$$

These upper bounds are clearly less conservative than those given directly by (1.112). They are also more realistic in the sense that they are closer to the mass balances of the biochemical reaction : it is obvious, for instance, that, according to (1.118.b), the maximum quantity of biomass that can be synthesised is given by the maximum available amount of substrate divided by the yield coefficient k_1 from S to X .

1.9.2. Equilibrium states

An equilibrium state is, by definition, a *constant* state, denoted ξ , which satisfies the equation of the general dynamical model (1.43), i.e. the following nonlinear multivariable algebraic equation :

$$\frac{d\xi}{dt} = 0 \Rightarrow K\phi(\xi) - \bar{D}\xi + \bar{F} - Q(\xi) = 0 \quad (1.119)$$

for given constant values \bar{D} and \bar{F} of the dilution rate D and the vector of feed rates F .

The problem of calculating the equilibrium state ξ of a bioreactor model is that of solving equation (1.119). The latter has no general analytical solution and can be solved only in specific applications.

Furthermore, it is a characteristic of biotechnological processes that they exhibit multiple equilibrium states (i.e. several different solutions to (1.119)), as a consequence of the autocatalytic action of microorganisms. This issue, which will be extensively discussed in the following paragraphs, is introduced via a simple example.

Example

We begin with the example of a simple irreversible reaction of the form :



with one reactant S and two products P_1 and P_2 . This is, for instance, a plausible model of the hydrolysis of lactose into glucose and galactose, which is the first step (1.40.a) of lactic fermentation.

We suppose that the reaction rate ϕ is modelled by equation (1.47), i.e. :

$$\phi = \alpha S \quad \alpha = \text{constant} \quad (1.121)$$

which corresponds to first order kinetics. The dynamical model (1.63) may therefore be written :

$$\frac{dS}{dt} = -\alpha S + DS_{in} - DS \quad (1.122.a)$$

$$\frac{dP_1}{dt} = k_1 \alpha S - DP_1 \quad (1.122.b)$$

$$\frac{dP_2}{dt} = k_2 \alpha S - DP_2 \quad (1.122.c)$$

The equilibrium state $(\bar{S}, \bar{P}_1, \bar{P}_2)$ is the solution of the following algebraic equations :

$$-\alpha \bar{S} + \bar{D}\bar{S}_{in} - \bar{D}\bar{S} = 0 \quad (1.123.a)$$

$$k_1 \alpha \bar{S} - D\bar{P}_1 = 0 \quad (1.123.b)$$

$$k_2 \alpha \bar{S} - D\bar{P}_2 = 0 \quad (1.123.c)$$

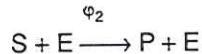
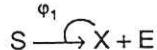
This equilibrium state is unique and given by :

$$\bar{S} = \frac{\bar{D}\bar{S}_{in}}{\alpha + \bar{D}} \quad \bar{P}_1 = \frac{k_1 \alpha \bar{S}_{in}}{\alpha + \bar{D}} \quad \bar{P}_2 = \frac{k_2 \alpha \bar{S}_{in}}{\alpha + \bar{D}} \quad (1.124)$$

Multiple equilibrium states

We shall now explain why biotechnological processes, as a class, possess multiple equilibrium states. The issue is first discussed on the basis of an

example. Consider the reaction scheme (1.35.a-b) of a microbial growth process with associated enzymatic production :



Applying the rules of Section 1.5.1 and the feed rate modelling (1.62), the general state space model is written :

$$\frac{d}{dt} \begin{bmatrix} X \\ S \\ E \\ P \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ -k_1 & -k_2 \\ k_3 & 0 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} \varphi_1 \\ \varphi_2 \end{bmatrix} - D \begin{bmatrix} X \\ S \\ E \\ P \end{bmatrix} + \begin{bmatrix} 0 \\ DS_{in} \\ 0 \\ 0 \end{bmatrix} \quad (1.125)$$

According to Section 1.5.3, we assume in addition that the reaction rates φ_1 and φ_2 are modelled as follows :

$$\varphi_1 = \mu(X, S)X \quad 0 \leq \mu(X, S) \leq \mu^* \quad (1.126.a)$$

$$\varphi_2 = \alpha(E, S)ES \quad (1.126.b)$$

where $\mu(X, S)$ is the specific growth rate and $\alpha(E, S)$ is the specific enzymatic production rate.

An equilibrium state is defined as a set of constant states $(\bar{X}, \bar{S}, \bar{E}, \bar{P})$ which satisfy $d(X, S, E, P)/dt = 0$ for given constant values \bar{D} and \bar{S}_{in} . From the model (1.125)-(1.126), it follows readily that there are necessarily two different sets of equilibrium states :

a) Wash-out equilibrium states :

$$\bar{X} = 0 \quad \bar{E} = 0 \quad \bar{P} = 0 \quad \bar{S} = \bar{S}_{in} \quad (1.127)$$

b) Operational equilibrium states

$$k_3 \bar{X} = \bar{E} \quad (1.128.a)$$

$$\mu(\bar{X}, \bar{S}) = \bar{D} \quad (1.128.b)$$

$$k_1 \bar{X} + k_2 \bar{P} = \bar{D} (\bar{S}_{in} - \bar{S}) \quad (1.128.c)$$

$$\alpha(\bar{S}, \bar{E}) \bar{E} \bar{S} = \bar{D} \bar{P} \quad (1.128.d)$$

The wash-out equilibrium states (1.127) are so called because they correspond to a wash-out of the biomass from the reactor. They can occur for any value of \bar{D} and \bar{S}_{in} . They are also the only possible equilibrium states when $\bar{D} > \mu^*$. It is obvious that wash-out equilibrium states are undesirable and must be avoided as far as possible in industrial applications.

On the other hand, the operational equilibrium states implicitly defined by (1.128) are those of practical interest. Their characterization obviously requires the specification of analytical models for the specific rates $\mu(\bar{X}, \bar{S})$ and $\alpha(\bar{E}, \bar{S})$. In general, however, the explicit calculation of the operational equilibrium states is impossible because the set of nonlinear algebraic equations (1.128) has no explicit analytical solution and can only be solved numerically. An analytical solution of (1.128) can nevertheless be calculated using simple models for $\mu(\bar{X}, \bar{S})$ and $\alpha(\bar{E}, \bar{S})$. This is shown in the next paragraph.

Example of calculation of the operational equilibrium states

We assume that the specific growth rate $\mu(\bar{X}, \bar{S})$ obeys the Contois law (1.22) :

$$\mu(\bar{X}, \bar{S}) = \frac{\mu^* \bar{S}}{K_c \bar{X} + \bar{S}} \quad (1.129)$$

while the specific production rate $\alpha(\bar{E}, \bar{S})$ is constant.

The system (1.128.a-d) is rewritten as follows :

$$k_3 \bar{X} = \bar{E} \quad (1.130.a)$$

$$\bar{D} K_c \bar{X} = (\mu^* - \bar{D}) \bar{S} \quad (1.130.b)$$

$$k_1 \bar{X} + k_2 \bar{P} = \bar{D} \bar{S}_{in} - \bar{D} \bar{S} \quad (1.130.c)$$

$$\alpha \bar{E} \bar{S} = \bar{D} \bar{P} \quad (1.130.d)$$

Equation (1.130.b) is obtained by substituting (1.129) into (1.128.b).

We notice that (1.130.b) and (1.130.c) make sense only if

$$\bar{D} < \mu^* \quad \bar{S} < \bar{S}_{in} \quad (1.131)$$

This means that, as pointed out above, the operational equilibrium states exist only if these inequalities are satisfied. Otherwise, only the wash-out equilibrium states are possible.

Substituting (1.130.b) into (1.130.a) gives :

$$\bar{E} = k_3 \bar{X} = \frac{k_3(\mu^* - \bar{D})}{\bar{D} K_c} \bar{S} \quad (1.132)$$

which implies that the equilibrium values $\bar{E}, \bar{X}, \bar{S}$ are proportional to one another. Substituting (1.132) into (1.130.d) gives :

$$\bar{P} = \frac{\alpha k_3(\mu^* - \bar{D})}{\bar{D}^2 K_c} \bar{S}^2 \quad (1.133)$$

which means that the product equilibrium concentration \bar{P} is proportional to the square of the substrate concentration \bar{S} .

Finally, substituting (1.133) into (1.30.c) leads to the following second degree equation :

$$\alpha k_2 k_3 A \bar{S}^2 + \bar{D}(\bar{D} + K_1 A) \bar{S} - \bar{D}^2 \bar{S}_{in} = 0 \quad (1.134)$$

$$\text{with } A = \frac{\mu^* - \bar{D}}{\bar{D} K_c}$$

the solutions of which are written :

$$\bar{S} = \frac{-\bar{D}(\bar{D} + k_1 A) \pm \sqrt{(\bar{D}^2 + \bar{D} k_1 A)^2 + 4 \alpha k_2 k_3 A \bar{D}^2 \bar{S}_{in}}}{2 \alpha k_2 k_3 A} \quad (1.135)$$

It appears immediately that only one of these solutions is positive, and hence physically plausible (the one which corresponds to the "+" sign). Then the equilibrium state is therefore fully analytically characterised by equations (1.132), (1.133) and (1.135).

This simple example clearly shows that the explicit calculation of equilibrium states may rapidly become very involved when the process is a combination of several biological reactions and when plausible analytical models are adopted for the reaction rates.

Generic nature of the multiplicity of the equilibrium states

With (1.127)-(1.128), we have emphasised the existence of multiple equilibrium states in a particular example. It is, however, obvious from that example that it is a generic situation which occurs in every case where the biotechnological process is a combination of autocatalysed microbial growth reactions and enzyme catalysed productions.

In particular, if the process dynamics are described by the model (1.59) :

$$\frac{d\xi}{dt} = K\phi(\xi) - D\xi + F - B\xi$$

it can easily be shown that the wash-out equilibrium states are characterised as follows :

- concentrations of biomass and products/internal substrates : $\bar{\xi}_i = 0$

$$\text{- concentrations of external substrates : } \bar{\xi}_i = \frac{\bar{F}_i}{\bar{D} + \beta_i}$$

1.9.3. Stability of equilibrium states

It is a basic feature of nonlinear systems in general, and consequently of bioreactor models in particular, that the equilibrium states can be stable or unstable depending on the operating point; that is, on the values of \bar{D} and \bar{F} . It is beyond the scope of this book to give a mathematical presentation of the concept of stability, the intuitive meaning being sufficient for our purpose. We shall limit ourselves to exposing the technique of stability analysis by linearization (Lyapunov's first method, see Appendix 2) and to giving an example of its application.

Stability analysis

Consider a biotechnological process described by the model (1.59) :

$$\frac{d\xi}{dt} = K\phi(\xi) - D\xi + F - B\xi \stackrel{\Delta}{=} g(\xi, F, D) \quad (1.136)$$

where the function g is introduced for convenience. Suppose that we are concerned with checking whether some equilibrium state $(\bar{\xi}, \bar{D}, \bar{F})$ is stable or not. Then, the linearized approximation of the model (1.136) around the

equilibrium state (which is also called the "linearized tangent model") is defined as follows :

$$\frac{d}{dt}(\xi - \bar{\xi}) = \left(\frac{\partial g}{\partial \xi} \right)(\xi - \bar{\xi}) + \left(\frac{\partial g}{\partial D} \right)(D - \bar{D}) + \left(\frac{\partial g}{\partial F} \right)(F - \bar{F}) \quad (1.137)$$

where the partial derivatives are evaluated at the equilibrium state. An explicit calculation of the "linearized tangent model" of (1.136) readily yields :

$$\frac{d}{dt}(\xi - \bar{\xi}) = A(\bar{\xi}, \bar{D}, \bar{F})(\xi - \bar{\xi}) - (D - \bar{D})\xi + (F - \bar{F}) \quad (1.138.a)$$

with :

$$A(\bar{\xi}, \bar{D}, \bar{F}) \stackrel{\Delta}{=} \left\{ K \left[\frac{\partial \phi}{\partial \xi} \right]_{\xi=\bar{\xi}} - \bar{D} I_N - B \right\} \quad (1.138.b)$$

Lyapunov's first method utilizes the eigenvalues of the matrix $A(\bar{\xi}, \bar{D}, \bar{F})$ to check on the stability of the equilibrium state. If the real parts of all the eigenvalues are negative, the equilibrium state is stable. If any of the real parts of the eigenvalues are positive, the equilibrium state is unstable. No conclusion may be drawn in the case of all eigenvalues having zero real parts.

Example : substrate inhibition

We consider the case of a simple microbial growth process (1.33) :



for which the dynamical model is as follows :

$$\frac{dX}{dt} = \mu X - DX \quad (1.139.a)$$

$$\frac{dS}{dt} = -k_1 \mu X - DS + DS_{in} \quad (1.139.b)$$

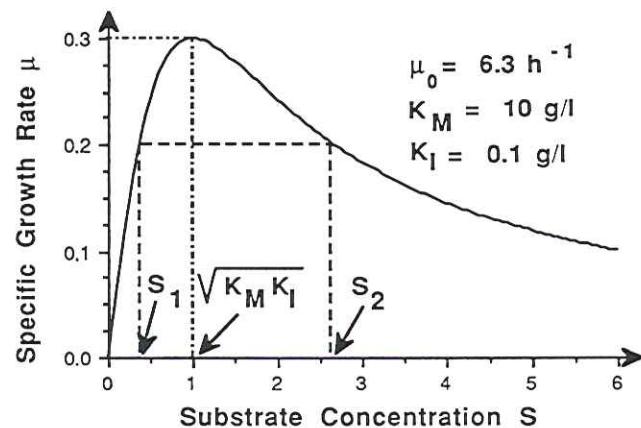


Fig.1.11. Stable and unstable equilibrium states with the Haldane law

We assume that substrate inhibition occurs at high substrate concentrations and is expressed by the Haldane law (1.20) :

$$\mu(\bar{S}) = \frac{\mu_0 S}{K_M + \bar{S} + \bar{S}^2/K_I} \quad (1.140)$$

which is graphically represented in Fig 1.11.

From this figure and the model (1.139), we conclude that, apart from the wash-out equilibrium state, two operational equilibrium states may exist, which are denoted :

$$\left(\bar{S}_1, \bar{X}_1 = \frac{\bar{S}_{in} - \bar{S}_1}{k_1} \right) \quad \left(\bar{S}_2, \bar{X}_2 = \frac{\bar{S}_{in} - \bar{S}_2}{k_1} \right) \quad (1.141)$$

and which fulfil the following conditions :

$$0 \leq \bar{S}_1 \leq \sqrt{K_M K_I} \leq \bar{S}_2 \quad (1.142.a)$$

$$\mu(\bar{S}_1) = \mu(\bar{S}_2) = \bar{D} \quad (1.142.b)$$

(\bar{S}_1, \bar{X}_1) exists for all $\bar{D} \leq \mu^*$ while (\bar{S}_2, \bar{X}_2) exists only when $\mu(\bar{S}_{in}) \leq \bar{D} \leq \mu^*$ (since \bar{S}_2 cannot be physically greater than \bar{S}_{in} , see (1.118)).

In this particular example, the coefficient matrix of the linearized tangent model is written :

$$A(\bar{X}, \bar{S}, \bar{D}) = \begin{bmatrix} 0 & \Omega \\ -k_1 \mu(\bar{S}) & -k_1 \Omega - \bar{D} \end{bmatrix} \quad (1.143)$$

with :

$$\Omega = \frac{\mu_0 \bar{X} \left(K_M - \frac{\bar{S}^2}{K_I} \right)}{\left(K_M + \bar{S} + \frac{\bar{S}^2}{K_I} \right)^2} \quad (1.144)$$

The eigenvalues of this matrix are $(-\kappa\Omega)$ and $(-\bar{D})$. It is obvious that the equilibrium state is stable if and only if :

$$\Omega > 0 \quad \text{or} \quad \bar{S} < \sqrt{K_M K_I} \quad (1.145)$$

Thus, it is clear that the equilibrium state (\bar{S}_1, \bar{X}_1) is stable while (\bar{S}_2, \bar{X}_2) is unstable.

In fact, it is a general property of biological reactions which involve substrate inhibition that they exhibit unstable equilibrium states.

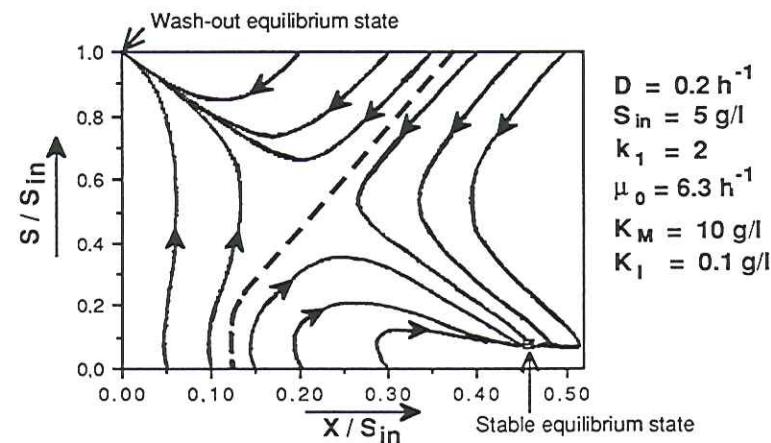


Fig.1.12. Phase plane representation

An important point in the above example is obviously the determination of the set of initial conditions $(X(0), S(0))$ for which the steady-states \bar{X}_1, \bar{S}_1 are stable over a broad range. Such an investigation can be carried out by using phase plane analysis. A typical phase-plane representation is shown in Fig.1.12. The steady-state \bar{X}_1, \bar{S}_1 is asymptotically stable with respect to the initial conditions below the separatrix, while the initial conditions above the separatrix irreversibly lead to a wash-out steady-state.

Therefore, when substrate inhibition takes place in a bioreactor, we discover not only that the process can exhibit unstable behaviour but also that it can lead to wash-out steady-states, in which the microbial life disappears completely and the reactor comes to a definite stop. Therefore, in such a situation, it is clear that industrial fermentations in the continuous operation mode absolutely require feedback control in order to stabilise the process : this issue will be addressed in Chapter 5.

1.10. Extending the General Dynamical Model

So far, in this chapter, we have focused on the derivation and the analysis of the general dynamical model (1.43) for biotechnological processes which take place in a single, perfectly mixed bioreactor :

$$\frac{d\xi}{dt} = K\phi(\xi) - D\xi + F - Q(\xi) \quad (1.146)$$

This model may easily be extended to deal with complex processes consisting of several interconnected tanks, possibly with special constructional features which allow, for instance, for biomass recycling or biomass accumulation. The extension is simply obtained by considering an appropriate *matrix* dilution rate:

$$D = [D_{ij}] \quad (1.147)$$

in equation (1.146) instead of the single scalar dilution rate adopted so far. This issue is illustrated with two examples (Sections 1.10.1 and 1.10.2). Furthermore, distributed parameter extensions of the general dynamical model can also be derived, if necessary, as is shown in Section 1.10.3 for fixed bed reactors.

1.10.1 Recycle bioreactor

In some fermentation processes (e.g. activated sludge processes), part of the effluent biomass is recycled to the bioreactor. The bioreactor effluent is fed to a clarifier (settler) which is used to separate substrate and biomass (Fig. 1.13).

Part of the settled biomass is then fed back to the bioreactor, while the surplus biomass is removed from the process. We suppose that the process is a "single substrate - single biomass" fermentation (1.33) and that the clarifier is

such that the whole biomass is settled (none is left in the supernatant of the settler). The dynamics of the process are written :

$$\frac{d}{dt} \begin{bmatrix} X \\ S \\ X_R \end{bmatrix} = \begin{bmatrix} 1 \\ -k_1 \\ 0 \end{bmatrix} \mu X - \begin{bmatrix} D_b & 0 & -D_1 \\ 0 & D_b & 0 \\ -D_2 & 0 & D_s \end{bmatrix} \begin{bmatrix} X \\ S \\ X_R \end{bmatrix} + \begin{bmatrix} 0 \\ D_{in}S_{in} \\ 0 \end{bmatrix} \quad (1.148)$$

where X is the biomass in the bioreactor, S is the substrate in the bioreactor and X_R is the recycled biomass.

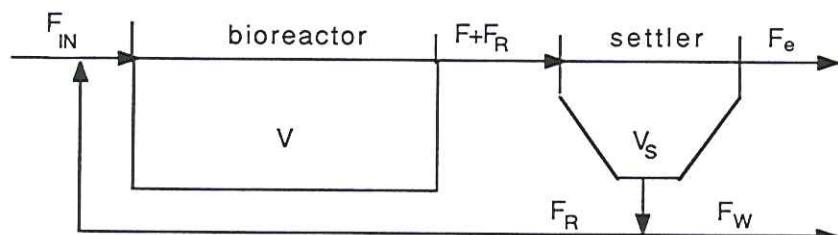


Fig.1.13. Schematic view of a recycle bioreactor

It appears clearly that this model exactly fits the form of equation (1.146) but with a matrix dilution rate. The entries of this matrix are defined as follows :

$$D_b = \frac{F_{IN} + F_R}{V} \quad \text{bioreactor dilution rate} \quad (1.149.a)$$

$$D_s = \frac{F_R + F_W}{V_s} \quad \text{settler dilution rate} \quad (1.149.b)$$

$$D_1 = \frac{F_R}{V} \quad (1.149.c)$$

$$D_2 = \frac{F_{IN} + F_R}{V_s} \quad (1.149.d)$$

$$D_{IN} = \frac{F_{IN}}{V} \quad (1.149.e)$$

with the notations of Fig.1.13, i.e. F_{IN} is the influent flow rate, F_R the recycle flow rate, F_W the waste flow rate, V the bioreactor volume, and V_s the settler volume.

It should be noted also that, in this extended model, the matrix K may contain rows of zeros corresponding to tanks in which no reaction occurs (as in the clarifier of the example).

1.10.2. Two-stage anaerobic digestion process with biomass accumulation

Several times in this chapter (Sections 1.4.3, 1.6.2, 1.8.4) we have described and discussed in detail the general dynamical model of the anaerobic digestion process in a single bioreactor in which all the reactions involved take place simultaneously. It is, however, common practice to implement the process in a "two-stage" bioreactor as depicted in Fig.1.14. Assuming that the reduced order scheme (1.87) holds, the idea is to devote the first tank to the first reaction (acidification) and the second tank to the second reaction (methanization). This means that the reaction scheme (1.87) has to be modified as follows. In the first tank, we have :



where S_1 is the organic substrate, X_1 the acidogenic biomass, S_{21} the acetate in the first tank and P_{21} the inorganic carbon in the first tank.

Moreover, in the second tank, we have :



where S_{22} is acetate in the second tank, X_2 is the methanogenic biomass, P_1 is the methane and P_{22} the inorganic carbon in the second tank.

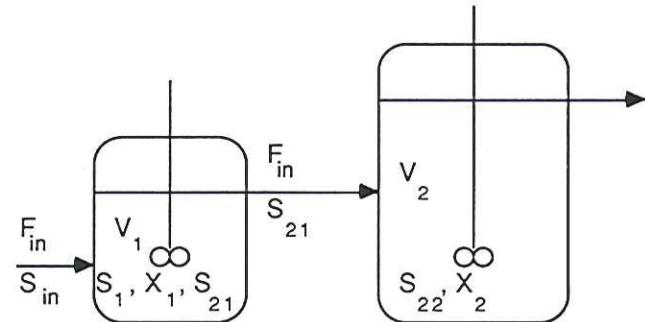


Fig.1.14. Two-stage anaerobic digestion reactor

The reaction scheme (1.150)-(1.151) excludes transfer of acidogenic biomass between the two tanks, which is supposed to be achieved by an appropriate filtration device. We also note that, as shown in Fig.1.14, the volume V_2 of the second reactor is larger than that of the first tank V_1 , because methanization is the limiting step of the process. Then, applying the rules of Section 1.5.1, we obtain the following dynamical model (compare with (1.85)) :

$$\frac{dX_1}{dt} = \varphi_1 - D_1 X_1 \quad (1.152.a)$$

$$\frac{dS_1}{dt} = -k_1 \varphi_1 - D_1 S_1 + D_1 S_{in} \quad (1.152.b)$$

$$\frac{dS_{21}}{dt} = k_3 \varphi_1 - D_1 S_{21} \quad (1.152.c)$$

$$\frac{dX_2}{dt} = \varphi_2 - D_2 X_2 \quad (1.152.d)$$

$$\frac{dS_{22}}{dt} = -k_2 \varphi_2 - D_2 S_{22} + D_2 S_{21} \quad (1.152.e)$$

(The dynamics of P_1 , P_{21} , P_{22} are omitted for simplicity).

The model is written in matrix form :

$$\frac{d}{dt} \begin{bmatrix} X_1 \\ S_1 \\ S_{21} \\ X_2 \\ S_{22} \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ -k_1 & 0 \\ k_3 & 0 \\ 0 & 1 \\ 0 & -k_2 \end{bmatrix} \begin{bmatrix} \varphi_1 \\ \varphi_2 \end{bmatrix} - \begin{bmatrix} D_1 & 0 & 0 & 0 & 0 \\ 0 & D_1 & 0 & 0 & 0 \\ 0 & 0 & D_1 & 0 & 0 \\ 0 & 0 & 0 & D_2 & 0 \\ 0 & 0 & -D_2 & 0 & D_2 \end{bmatrix} \begin{bmatrix} X_1 \\ S_1 \\ S_{21} \\ X_2 \\ S_{22} \end{bmatrix} + \begin{bmatrix} 0 \\ D_1 S_{in} \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad (1.153)$$

In this model, $D_1 = F_{in}/V_1$, $D_2 = F_{in}/V_2$, and the yield coefficients k_1 , k_2 , k_3 have exactly the same meaning as in (1.85).

Again, we see that equation (1.153) has exactly the same format as (1.146) but with a *generalised* dilution rate matrix.

1.10.3. A distributed parameter model for a fixed bed bioreactor

A fixed bed bioreactor is a reactor where the biomass is immobilised on fixed carriers such as polymers, porous glass or ceramics.

We consider a horizontal bioreactor operating under plug flow conditions (rather than complete mixing conditions) as shown in Fig.1.15.

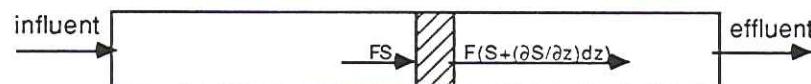


Fig.1.15. plug-flow reactor

We suppose that a "single biomass/single substrate" reaction (1.33) takes place in the reactor :



with a reaction rate $\varphi = \mu X$.

The length of the bioreactor is equal to L . Consider a section of the reactor with length "dz" located at a distance z from the bioreactor input (shaded area in Fig 1.15). The constant reactor cross-section is denoted A . The volume of the section is thus Adz .

The mass balance for the substrate concentration S around this section is written as follows :

$$\frac{\partial}{\partial t}[SAdz] = FS - F\left(S + \frac{\partial S}{\partial z}dz\right) - k_1\mu XAdz \quad (1.154)$$

time variation of the amount of substrate in the section dz	influent substrate into the section dz	effluent substrate out of the section dz	amount of substrate consumed by the biomass in the section dz
--	---	---	---

Equation (1.154) is rewritten :

$$\frac{\partial S}{\partial t} = -\frac{F}{A} \frac{\partial S}{\partial z} - k_1\mu X \quad (1.155)$$

while the mass balance of the biomass leads to :

$$\frac{\partial X}{\partial t} = \mu X \quad (1.156)$$

where the hydraulic term has disappeared since the biomass is immobilised.

Equations (1.155) - (1.156) constitute the distributed parameter equivalent of the dynamical model (1.52).

For completeness, we must define the limit conditions :

$$S(t, z=0) = S_{in}(t) \quad X(0, z) = X_0(z) \quad S(0, 0 < z \leq L) = S_0(z) \quad (1.157)$$

where $S_{in}(t)$ is the influent substrate concentration, and $X_0(z)$ and $S_0(z)$ the initial immobilised biomass and substrate concentrations.

1.11. References and Bibliography

The following are two excellent basic textbooks on bioprocesses :

- Bailey J.E. and D.F. Ollis (1986). *Biochemical Engineering Fundamentals*. Mac-Graw Hill Kogakusha, Tokyo, 2nd edition.
- Moser A. (1988). *Bioprocess Technology. Kinetics and Reactors*. Springer Verlag, New York.

Section 1.3

Many papers are concerned with the kinetics of fermentation processes. The following book chapter gives a survey of specific growth rate models :

Frederickson A.G. and H.M. Tsuchiya (1977). Microbial kinetics and dynamics, in L. Lapidus and N.R. Amudson (Eds.), *Chemical Reactor Theory*, Prentice-Hall, Englewood Cliffs, NJ.

A large number of specific growth rate expressions are presented in Appendix 1. The references of those presented in section 1.3 are listed below :

Andrews J.F. (1968). A mathematical model for the continuous culture of microorganisms utilizing inhibiting substrates. *Biotechnol. Bioeng.*, **10**, 707-723.

Briggs G.E. and J.B.S. Haldane (1925). *Biochem. J.*, **242**, 3973.

Contois D. (1959). Kinetics of bacterial growth relationship between population density and specific growth rate of continuous cultures. *J. Gen. Microbiol.*, **21**, 40-50.

Haldane J.B.S (1930). *Enzymes*, Longmans, London.

Jackson J.V. and V.H. Edwards (1975). Kinetics of substrate inhibition of exponential yeast growth. *Biotechnol. Bioeng.*, **17**, 943-964.

Michaelis L. and M.L. Menten (1913). Die kinetic der Invertinwirkung. *Biochemische Zeitschrift*, **49**, 334-369.

Monod J. (1942). *Recherches sur la Croissance des Cultures Bactériennes*. Hermann, Paris.

Rozzi A. (1984). Modelling and control of anaerobic digestion processes. *Trans. Inst. Meas. Control.*, **6**, n°3, 153-159.

Tessier G. (1942). Croissance des populations bactériennes et quantités d'aliments disponibles. *Rev. Sci.*, Paris, 80-209.

Topiwala H. and C.G. Sinclair (1971). Temperature relationship in continuous culture. *Biotechnol. Bioeng.*, **13**, 795-813.

Verhulst R. (1838). Notice sur la loi que la population suit dans son accroissement. *Corr. Math. et Phys.*, A. Quetelet (Ed.), **t. X**, 113.

The specific growth rate models including product inhibition are drawn from :

Aiba S., M. Shoda and M. Nagatani (1968). Kinetics of product inhibition in alcohol fermentation. *Biotechnol. Bioeng.*, **10**, 845-864.

Section 1.4

The process examples presented in this section are adapted from the following references :

Yeast growth:

Sonneitner B. and O. Käppeli (1986). Growth of *Saccharomyces cerevisiae* is controlled by its limited respiratory capacity : formulation and verification of a hypothesis. *Biotechnol. Bioeng.*, **28**, 927-937.

Anaerobic digestion :

Mosey F.E. (1983). Mathematical modelling of the anaerobic digestion process: regulatory mechanisms for the formation of short-chain volatile acids from glucose. *Water Sci. Technol.*, **15**, 209-232.

Sinéchal X., M. Installé and E.J. Nyns (1979). Differentiation between acetate and higher volatile acids in the modeling of the anaerobic biomethanization process. *Biotechnol. Lett.*, **1**, 309-314.

Lactic fermentation:

Spinnler H.E., C. Bouillanne, M.S. Desmazeaud and G. Corrieu (1987). Measurement of the partial pressure of dissolved CO₂ for estimating the concentration of *St. thermophilus* in coculture with *Lb. bulgaricus*. *Appl. Microbiol. Biotechnol.*, **25**, 464-470.

Section 1.5

Reaction networks and some of their algebraic properties have been studied by :

Feinberg M. and F.J.M. Horn (1974). Dynamics of open chemical systems and the algebraic structure of the underlying reaction network. *Chem. Eng. Sci.*, **29**, 775-787.

The modelling of the gaseous outflow rates is studied in particular in :

Bellgard K.H., W. Kuhlman and H.D. Meyer (1983). Deterministic growth model of *Saccharomyces cerevisiae*. Parameter identification and simulation; In A. Halme (Ed.), *Modelling and Control of Biotechnical Processes*, Pergamon, Oxford, 67-74.

Section 1.7

In this section and throughout the book we refer, when needed, to properties of matrices and linear algebra. The following book constitutes a good introduction and summary on the subject :

Strang G. (1980). *Linear Algebra and its Applications*. Academic Press, Orlando.

Section 1.8

Singular perturbation techniques have been used for reducing the general dynamical model. The theory of singular perturbation is treated in :

Kokotovic P., H.K. Khalil, J. O'Reilly (1986). *Singular Perturbation Methods in Control : Analysis and Design*. Academic Press, London.

Section 1.9

The concepts and notions of stability theory of linear and nonlinear systems are described e.g. in :

Vidyasagar M. (1978). *Nonlinear Systems Analysis*. Prentice-Hall, Englewood Cliffs, NJ.

Willems J.L. (1970). *Stability Theory of Dynamical Systems*. Nelson, London.

Equilibrium states of bioreactors have been widely studied, especially the appearance of possible unstable equilibrium states, e.g. in :

Agrawal P., C. Lee, H.C. Lim and D. Ramkrishna (1982). Theoretical investigations of dynamic behavior of isothermal continuous stirred tank biological reactors. *Chem. Eng. Sci.*, **37**, n°3, 453-462.

Agrawal P. and H.C. Lim (1984). Analysis of various control schemes for continuous bioreactors. *Adv. Biochem. Eng.*, **30**, 61-90.

Antunes S. and M. Installe (1981). The use of phase-plane analysis in the modelling and the control of a biomethanization process. *Proc. 8th IFAC World Congress*, **22**, 165-170.

DiBiasio D., H.C. Lim, W.A. Weigand and G.T. Tsao (1978). Phase-plane analysis of feedback control of unstable steady-states in a biological reactor. *AIChE J.*, **24**, n°4, 686-693.

Van den Heuvel J.C. and R.J. Zoetmeyer (1982). Stability of the methane reactor : a simple model including substrate inhibition and cell recycle. *Process Biochem.*, May-June, 14-19.

Section 1.10

Biotechnological processes in fixed bed and fluidised bed reactors are presented e.g. in :

Poncelet D., R. Binot, H. Naveau and E.J. Nyns (1985). Biotechnologie des lits fluidisés en réacteurs cylindriques et tronconiques. *Trib. Cébédeau*, 38 (494), 3-12; 38 (497), 33-48.

Schugerl K. (1989). Biofluidization : application of the fluidization technique in biotechnology. *Can. J. Chem. Eng.*, 67, 178-184.

Wang D.I.C., C.L. Cooney, A.L. Demain, P. Dunhill, A.E. Humphrey and M.D. Lilly (1979). *Fermentation and Enzyme Technology*. John Wiley & Sons, New York.

Wiseman A. (1978). *Topics in Enzyme and Fermentation Biotechnology*. John Wiley & Sons, New York.

CHAPTER 2

KINETIC MODELLING, ESTIMATION AND CONTROL IN BIOREACTORS : AN OVERVIEW

2.0. Introduction

When a bioengineer is faced with the problem of developing a mathematical model for a bioreactor (with a view to performance assessment or control design), his first task is to establish the reaction scheme for the process. Numerous examples of this have been given in Chapter 1. He can then easily write down the General Dynamical Model (1.43) associated with the scheme by using the rules of Section 1.5.2. This is simply a set of ordinary differential equations of the following form :

$$\frac{d\xi}{dt} = K\varphi(\xi) - D\xi + F - Q \quad (1.43) = (2.1)$$

where ξ is the state vector (i.e. the set of component concentrations), K a yield coefficient matrix, $\varphi(\xi)$ the vector of reaction kinetics (also called reaction rates), D the dilution rate, F a set of feed rates and Q a set of gaseous outflow rates.

Once equation (2.1) is written, however, the model construction is far from being completed. Actually, the most difficult task remains to be performed, namely the task of modelling the reaction kinetics $\varphi(\xi)$ which is discussed in

Section 2.1. On the grounds of that discussion, the concept of *minimal modelling* of the kinetics is introduced and illustrated with simple examples in Section 2.2.

A review of the monitoring and control problems which are addressed in the remaining chapters of the book, is then presented in Sections 2.3 and 2.4.

2.1. Difficulties in Modelling the Reaction Kinetics

In Section 1.4.4, the reaction rates $\varphi_j(\xi)$ ($j = 1, \dots, M$) were represented by :

$$\varphi_j(\xi) \stackrel{\Delta}{=} \alpha_j(\xi) \left(\prod_{n-j} \xi_n \right) \quad (1.47) = (2.2)$$

The significance of this equation is as follows : the reaction rate φ_j is proportional to the concentrations of the reactants ξ_n (including the auto-catalysts) involved in the reaction *and* to another function $\alpha_j(\xi)$, termed the *specific reaction rate*. The usual approach in bioreactor modelling consists in adopting a particular analytical structure for each specific reaction rate $\alpha_j(\xi)$ and in calibrating its internal coefficients on the basis of experimental data.

However, this modelling exercise is often very hazardous because it comes up against three major difficulties :

- 1) First of all, one has to select, for each particular fermentation, the biological and physico-chemical factors which are supposed to influence the kinetics and must therefore be incorporated in the model.
- 2) Second, once this selection has been made, one has to choose an appropriate analytical description for each $\alpha_j(\xi)$, for instance among the (long) list of Appendix 1; this critical choice is the subject of continuing controversy in the literature (which is probably why the list of Appendix 1 is so long); most often these analytical expressions take the form of rational

functions (i.e. polynomial ratios) of both the state variables and a set of constant *kinetic coefficients*.

- 3) Finally, once a specific structure has been chosen one faces intricate *parameter identifiability* difficulties when trying to calibrate the kinetic coefficients from experimental data; the difficulties arise mainly from a lack of experimental reproducibility and a lack of statistical significance of the data; this issue will be discussed further on in this section.

A typical example of kinetic modelling has been given in Section 1.4 for a simple microbial growth process governed by the Contois law. The reaction rate was written :

$$\varphi(X, S) = \alpha(X, S) XS = \mu(X, S) X \quad (2.3)$$

$$\text{with } \alpha(X, S) \stackrel{\Delta}{=} \frac{\mu^*}{K_c X + S} \quad (2.4)$$

In that example, there are two kinetic coefficients : μ^* and K_c . It can also be seen that $\alpha(X, S)$ effectively has the form of a rational function. Another example follows.

Example of kinetic modelling

Consider a culture of *L. Bulgaricus* in a lactic fermentation process, described by the reaction scheme (1.40.d)-(1.40.e), which is written as follows :



with glucose S, biomass X and lactic acid P. Note that it is the standard scheme (1.36) of microbial growth with associated enzyme catalysed production. It can easily be shown that the dynamical model can be written :

$$\frac{d}{dt} \begin{bmatrix} S \\ X \\ P \end{bmatrix} = \begin{bmatrix} -1 & -1 \\ k_1 & 0 \\ 0 & k_2 \end{bmatrix} \begin{bmatrix} \varphi_g \\ \varphi_c \end{bmatrix} - D \begin{bmatrix} S \\ X \\ P \end{bmatrix} + \begin{bmatrix} DS_{in} \\ 0 \\ 0 \end{bmatrix} \quad (2.6)$$

We first suppose that the enzymatic catalysis is governed by the conventional Michaelis-Menten law. The reaction rate φ_c is therefore as follows :

$$\varphi_c(X, S) = \frac{\mu_1^* X S}{K_1 + S} \quad (2.7)$$

On the other hand, it is well known that the bacterial growth is inhibited by lactic acid. Hence, according to Section 1.3, it is a reasonable assumption to represent the specific growth rate by the combination of a Monod law (1.18) and a product inhibition function of the form (1.23), as follows :

$$\mu(S, P) = \frac{\mu_2^* S}{K_2 + S} \frac{K_p}{K_p + P} \quad (2.8)$$

which implies that the growth kinetics are as follows :

$$\varphi_g(S, X, P) = \frac{\mu_2^* K_p S X}{(K_2 + S)(K_p + P)} \quad (2.9)$$

The full model contains five kinetic coefficients :

$$\mu_1^*, \mu_2^*, K_1, K_2, K_p \quad (2.10)$$

while the specific reaction rates are the following rational functions :

$$\alpha_g(S, P) = \frac{\mu_2^* K_p}{(K_2 + S)(K_p + P)} \quad \alpha_c(S) = \frac{\mu_1^*}{K_1 + S} \quad (2.11)$$

Thus, with the definitions (2.11), we have adopted one plausible kinetic model for this fermentation process. The reader should, however, easily realize that many other models, just as plausible as (2.11), could have been chosen from the list of Appendix 1. In fact, the choice is a priori virtually unlimited. It should, however, be obvious that identification techniques could help to discriminate between the models.

On the identifiability of kinetic constants

Clearly, kinetic modelling (with a view to performance assessment in particular applications) makes sense only if the kinetic coefficients have a well specified numerical value. Since these values are generally not known a priori, they need to be estimated (identified) from process measurements. Unfortunately, numerous studies (see references) devoted to parameter estimation in biological models have shown that, in practice, the identifiability of the kinetic coefficients is far from being guaranteed and may even be an insuperable difficulty in most applications. A detailed discussion of this question is beyond the scope of this book.

The reader will, however, be convinced of the relevance of the issue simply by considering Table 2.1 and Fig.2.1 taken from Holmberg (1983). Table 2.1 summarizes the identification results of the kinetic coefficients μ^* and K_m of a Monod law from batch cultivation data of *B. Thuringiensis*. In each experiment, the environmental conditions were identical except for the initial substrate concentration (S_0 in the Table). It is clear that the different identification runs produce a wide dispersion of the numerical values of the two parameters. Furthermore, the confidence intervals are so large that, in some instances, the coefficients could just as well be negative. Fig 2.1 illustrates the point in a complementary way by showing that very different sets of kinetic coefficients can actually provide quite similar simulation results which fit the data equally well.

Cultivation	Initial substrate S_0 (g/l)	Estimates Kinetic Coeff. μ^* (h ⁻¹) K_M (g/l)	
1	11.6	1.0 ± 2.0	6.8 ± 22.3
2	7.0	1.1 ± 0.8	1.8 ± 2.2
3	18.2	0.7 ± 0.2	$12.9 \pm$
4	25.0	0.3 ± 0.2	7.0 ± 11.9

Table 2.1. Identification results of the kinetic coefficients μ and K_M (Reprinted by permission from A. Holmberg (1983). On the accuracy of estimating the parameters of models containing Michaelis-Menten type nonlinearities. In G.C. Vansteenkiste and P.C. Young (Eds.), Modelling and Data Analysis in Biotechnology and Medical Engineering, North-Holland, Amsterdam, p.202)

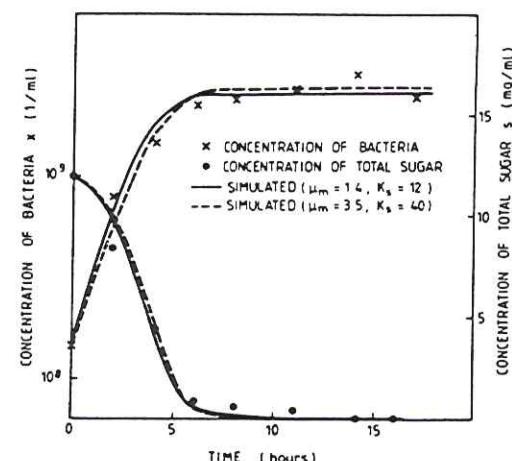


Fig.2.1. Simulation with two different sets of kinetic coefficients (Reprinted by permission from A. Holmberg (1983). On the accuracy of estimating the parameters of models containing Michaelis-Menten type nonlinearities. In G.C. Vansteenkiste and P.C. Young (Eds.), Modelling and Data Analysis in Biotechnology and Medical Engineering, North-Holland, Amsterdam, p.202)

2.2. Minimal Modelling of Reaction Kinetics

On the grounds of the previous discussion, there is a clear incentive, at least from an engineering viewpoint, to try to avoid kinetic modelling. This will be the main challenge of this book :

To design monitoring and control algorithms for bioprocesses with a minimal modelling of the kinetics.

This notion of *minimal modelling* is formalised as follows. We shall represent the reaction rates $\phi_j(\xi)$ ($j = 1, \dots, M$) by :

$$\phi_j(\xi) = h_j(\xi)p_j(\xi) \quad (2.12)$$

where $h_j(\xi)$ is a *known* function of the state ξ while $p_j(\xi)$ is an *unknown* function. More generally, the vector $\phi(\xi)$ of reaction rates will be written as :

$$\phi(\xi) = H(\xi)p(\xi) \quad (2.13)$$

with $H(\xi)$ an $M \times r$ known matrix and $p(\xi)$ a vector of unknown functions of ξ , with $\dim p(\xi) = r$.

The idea is to insert into $H(\xi)$ only the (possibly very limited) prior knowledge which is available regarding the kinetics and then to consider p as a completely unknown time varying parameter.

The form of equation (2.13) is very flexible and allows us to account for various kinds of uncertainty and to cover a wide spectrum of practical situations.

A first situation occurs when there is no prior knowledge at all concerning the kinetics. Minimal modelling then reduces to *no modelling*, i.e. the reaction kinetics are the unknowns of the model :

$$p(\xi) = \phi(\xi) \quad H(\xi) = I_M \quad (2.14)$$

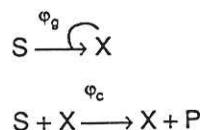
Another possibility is to consider that the unknown parameters are the specific reaction rates $\alpha(\xi)$ introduced in Section 1.5.3. In that case, we have :

$$\rho(\xi) = \alpha(\xi) \quad H(\xi) = G(\xi) \quad (2.15)$$

But many other (more or less complicated) variants are obviously possible. This is illustrated by some examples.

Examples of minimal modelling

Consider again the reaction scheme (2.5) of an enzyme catalysed production process :



If there is no prior knowledge of the kinetics, we simply define the unknown parameters as follows :

$$\rho_1(\xi) = \varphi_g(S, X, P) \quad \rho_2(\xi) = \varphi_c(S, X, P) \quad (2.16)$$

If the specific reaction rates are the unknown parameters, we have :

$$\rho_1(\xi) = \alpha_g(S, P) \quad \rho_2(\xi) = \alpha_c(S, X) \quad (2.17)$$

while the corresponding matrix $H(\xi)$ is written :

$$H(\xi) = \begin{bmatrix} SX & 0 \\ 0 & SX \end{bmatrix} \quad (2.19)$$

so that we have (compare with (2.7), (2.9)) :

$$\begin{bmatrix} \varphi_g(S, X, P) \\ \varphi_c(S, X) \end{bmatrix} = \begin{bmatrix} SX & 0 \\ 0 & SX \end{bmatrix} \begin{bmatrix} \rho_1 \\ \rho_2 \end{bmatrix} \quad (2.20)$$

If we wish the specific growth rate $\mu(S, P)$ (see (2.8)) to be treated as an unknown parameter of the model, we may define :

$$\rho_1(\xi) = \mu(S, P) \quad \rho_2(\xi) = \alpha_c(S, X) \quad (2.21)$$

The corresponding $H(\xi)$ is then :

$$H(\xi) = \begin{bmatrix} X & 0 \\ 0 & SX \end{bmatrix} \quad (2.22)$$

We may also suppose that, in the specific growth rate model (2.8), the kinetic coefficients μ_2^* and K_2 are known, while the product inhibition function is unknown, and that the specific production of the enzymatic reaction has to be treated as an unknown parameter. Hence we have (compare again with (2.7), (2.9)) :

$$\begin{bmatrix} \varphi_g(S, X, P) \\ \varphi_c(S, X) \end{bmatrix} = \begin{bmatrix} \frac{\mu_2^* SX}{K_2 + S} & 0 \\ 0 & X \end{bmatrix} \begin{bmatrix} \rho_1(P) \\ \rho_2(S) \end{bmatrix} \quad (2.23)$$

2.3. Software Sensors for Bioreactors

Besides the problems inherent to kinetic modelling, another essential difficulty lies in the absence, in most applications, of cheap and reliable sensors capable of providing direct real-time measurements of the state variables required to implement advanced monitoring and control methods on bioreactors. The main variables (such as biomass, substrate or metabolite concentrations) generally need to be determined through laboratory analyses. The cost and duration of these analyses limit the frequency of the sampling. In

addition, even when on-line sensors exist for biomass or metabolites, they are often not robust enough for routine industrial applications.

The design of *Software Sensors* to cope with the lack of instrumental sensors in bioreactors is one of the main concerns of this book. A software sensor is an algorithm for the on-line estimation of the state variables and the parameters which are not measurable in real time, on the basis of related measurements which are more easily accessible. The General Dynamical Model of the process (2.1) is the main ingredient for the design of a software sensor.

In control science terminology, a software sensor for the estimation of state variables is called a *state observer* (or simply an *observer*) while for the estimation of internal model parameters, it is called a *parameter estimator*. We shall adopt this terminology in the sequel. The design of software sensors, i.e. of state and parameter estimation algorithms, will be extensively studied in Chapters 3 and 4.

PRIOR KNOWLEDGE		
	Reaction Kinetics (vector $\varphi(\xi)$)	Yield Coefficients (matrix K)
Chapter 3 - Section 3.2	Known	Known
Chapter 3 - Section 3.3	Unknown	Known
Chapter 4 - Section 4.3	Unknown	Unknown

Table 2.2. Assumptions for the design of state observers

Different state observers will be presented, depending on the prior knowledge available concerning the reaction kinetics and the yield coefficients. The presentation is organised according to Table 2.2.

With the definition (2.13), the general dynamical model (1.43) is rewritten :

$$\frac{d\xi}{dt} = KH(\xi)\rho(\xi) - D\xi + F - Q \quad (2.24)$$

As we have mentioned previously, the parameters $\rho(\xi)$ will be considered throughout the book (except in Sections 3.1 and 3.2), as completely unknown time varying parameters. They are therefore of primary concern in the design of parameter estimators. But, in some instances, the yield coefficients (matrix K) are also badly known and/or time varying, and therefore also concerned. An overview of the presentation of the parameter estimators is given in Table 2.3.

Chapter 3 - Section 3.4	Estimation of ρ with known K
Chapter 4 - Section 4.1	Estimation of $\rho = \alpha$ independently of K
Chapter 4 - Section 4.2	Joint estimation of $\rho = \alpha$ and K
Chapter 4 - Section 4.4	Estimation of K independently of $\varphi = Hp$

Table 2.3. Overview of the presentation of parameter estimators

The advantages of considering $\rho(\xi)$ as unknown time varying parameters to be estimated on-line are threefold :

- 1) First of all, it allows avoidance of the difficult choice of a particular analytical expression for the process kinetics of the application under study.
- 2) Secondly, it allows avoidance of the identifiability difficulties (mentioned and illustrated in Section 2.1) arising when trying to calibrate the coefficients of the chosen analytical expression from input-output data.
- 3) Finally, it allows a search for possible correlations between the estimated reaction rates and the different physico-chemical and biochemical factors which are assumed to influence them. This latter point will be illustrated in Chapter 4 (Section 4.1.3).

2.4. Adaptive Control of Bioreactors

In industry, the control of bioreactors is most often limited to the regulation of pH and temperature. There is, however, no doubt that computer control of the biochemical state variables (such as substrate or product concentrations) can help to increase the process performance significantly. This issue will be treated in Chapter 5, where we shall present several methods for the design of adaptive linearizing controllers.

The purpose of computer control is to keep some process state variable close to a prespecified value (called a *set point*), in spite of disturbances and variations in the process kinetics, by acting on the feed rate of an external substrate. The task of the controller is to determine, at each instant, the best control action (i.e. the best substrate feed rate), on the basis of the data collected on line by the sensors *and* of the estimates provided by the *state observers* (which then more particularly deserve the name of software sensors).

	Adaptive Control
Chapter 5 - Section 5.2	independently of the kinetics, with known or unknown yield coefficients
Chapter 5 - Sections 5.3, 5.4	with unknown kinetics and known yield coefficients
Chapter 5- Section 5.5	with unknown kinetics and unknown yield coefficients.

Table 2.4. Assumptions for adaptive control design

The control algorithms will be obtained by appropriate algebraic manipulations of the General Dynamical Model (2.1). But, since the kinetics are not fully known (recall that our viewpoint is a minimal modelling of the kinetics), they are replaced in the control algorithm by on-line estimates provided by one of the various *parameter estimators* listed in Table 2.3. A control algorithm which incorporates a parameter estimator is called an *adaptive controller* because it has the potential to adapt itself to variations in the kinetics. Different adaptive controllers will be presented depending on the prior knowledge available concerning the reaction kinetics and the yield coefficients. The presentation is organised according to Table 2.4.

2.5. Conclusions and Perspectives

An overview of the monitoring and control problems, which are addressed in the subsequent chapters of this book, has been presented. The software sensors and the adaptive control algorithms will be designed on the assumption of a poor knowledge and a minimal modelling of the kinetics. This is justified by the difficulties that usually appear when trying to identify analytical models of the kinetics of bioprocesses, as has been discussed in Section 2.1.

We would also like to stress the point that, in the rest of the book, we shall be concerned only with *stirred tank* bioreactors (either in batch, fed-batch or continuous operating modes). The extension of the estimation and control algorithms to more general biotechnological systems (such as those mentioned in Section 1.10 : biomass recycling, biomass accumulation, fixed and fluidised beds, distributed models) is far from straightforward and has received little attention in the literature. Some relevant references are listed in the next section.

2.6. References and Bibliography

The following paper is a survey on various aspects (instrumentation, estimation, control) of computer applications to fermentation processes :

Wang N.S. and G.N. Stephanopoulos (1984). Computer applications to fermentation processes. *CRC Critical Reviews in Biotechnology*, 2, 1-103.

Section 2.1

The problem of choosing one particular analytical structure for the specific growth rate is discussed in e.g. :

Spiert J. (1982). Modelling the growth of microorganisms : a critical appraisal. In S. Rinaldi (Ed.), *Environmental Systems Analysis and Management*, North-Holland, Amsterdam, 451-465.

The practical identifiability of the specific growth rate models is discussed e.g. in :

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Section 2.3

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Section 2.4

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- Beck M.C. (1986). Identification, estimation and control of biological wastewater treatment processes. *Proc. IEE, Part D*, 133, 254-264.
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- Hämäläinen R.P., A. Halme and A. Gyllenberg (1975). A control model for activated sludge wastewater treatment process. *Proc. 6th IFAC World Congress*. Boston, the Instrument Society of America, Paper 61:6.
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 Marsili-Libelli S. (1980). Reduced-order modelling of the activated sludge process. *Ecological Modelling*, 9, 15-32.
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Section 2.5

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CHAPTER 3

STATE AND PARAMETER ESTIMATION WITH KNOWN YIELD COEFFICIENTS

3.0. Introduction

This chapter deals with state estimation and parameter estimation in bioreactors when the yield coefficients are known.

In Sections 3.1, 3.2 and 3.3 we address the *state estimation problem*, that is the problem of reconstructing the time evolution of the non measured state variables from the measured ones. An algorithm designed for that purpose is called an *observer*.

In Section 3.1 the concept of observability is discussed in relation to the structure of the general dynamical model of biotechnological processes. We introduce a distinction between *exponential observers* (for which it is possible arbitrarily to fix the speed of convergence of the estimated variables towards their true values) and *asymptotic observers* (for which the speed of convergence is exclusively determined by the experimental conditions). Examples of lack of exponential observability are also given.

Section 3.2 is dedicated to the design of *exponential observers* for biotechnological processes, under the (hypothetical) assumption of full model

knowledge : we assume in particular a knowledge of the mathematical structure of the kinetic functions $\varphi(\xi)$ and of their parameters. The design procedure for extended Luenberger and Kalman observers is presented and illustrated with practical examples.

In Section 3.3 we show how specific dedicated *asymptotic observers* can be designed in the (realistic) situation of partial model knowledge, namely when the mathematical structure of the kinetics $\varphi(\xi)$ is unknown.

Two real life applications of asymptotic observers are presented : the first one concerns biomass estimation in an anaerobic digestion process from acetic acid and methane measurements; the second one refers to biomass and product estimation in a PHB acid production process from oxygen measurements. Some practical implementation aspects are also briefly discussed.

Section 3.4 deals with the on-line estimation of the reaction kinetics $\varphi(\xi)$ in bioreactors. Two different parameter estimators are proposed : the first one is called an observer-based estimator because it is based on a variant of the observers described before; the second one is based on the reformulation of the process model in a linear regression form. An example of convergence analysis is given. A case study devoted to the on-line estimation of microbial specific growth rates is then carried out in depth. The use of extended Kalman filtering for on-line estimation of the kinetics is also presented and compared with the previous algorithms. Three experimental applications are described : estimation of the specific growth rate in a fed-batch ethanolic fermentation process, estimation of the specific reaction rates in a continuous anaerobic digestion process, estimation of the reaction rates in a lactic fermentation process.

3.1. On State Observation in Bioreactors

We consider a biotechnological process described by the general state space model (1.43) introduced in Chapter 1, that is :

$$\frac{d\xi}{dt} = K\varphi(\xi) - D\xi - Q + F \quad (1.43) = (3.1)$$

We suppose that we have a full knowledge of this model (see Chapter 2) : the structure of the reaction kinetics $\varphi(\xi)$ is completely known; also the numerical values of all the coefficients involved in the model (i.e. yield coefficients and kinetic coefficients) are given.

In addition, we assume that the dilution rate D , the feed rates F and the gaseous outflow rates Q are known on-line, and that a subset of the state variables is measured on-line. The vector of these measurements is denoted ξ_1 and is related to the state of the system as follows :

$$\xi_1 = L\xi$$

where the qxN matrix L is an elementary matrix which selects the measured components of ξ . On the other hand, the vector of unmeasured states is denoted ξ_2 , so that (ξ_1, ξ_2) constitutes a partition of ξ .

A *state observer* is an algorithm designed to reconstruct the non measured state variables from the measured ones.

A general class of state observers for nonlinear systems of the form (3.1) is as follows :

General state observer

$$\frac{d\hat{\xi}}{dt} = K\varphi(\hat{\xi}) - D\hat{\xi} - Q + \Omega(\hat{\xi})[\xi_1 - \hat{\xi}_1] \quad (3.2)$$

where $\hat{\xi}$ denotes the on-line estimate of ξ , $\Omega(\hat{\xi})$ is an $N \times q$ gain matrix depending on $\hat{\xi}$, and $\hat{\xi}_1 = L\hat{\xi}$.

The observer equation (3.2) can be interpreted as a copy of the model (3.1) with an additional driving term which is proportional to the observation error of the measured part of the state ($\xi_1 - \hat{\xi}_1$), and which disappears in the case of perfect estimation.

In practice, the on-line reconstruction (observation) of the missing states is obtained simply by integrating equation (3.2) on the supervising computer. We note that the estimated state vector $\hat{\xi}$ includes all the state variables, even those which are measured.

The state observer design problem reduces to that of a reasonable choice of the gain matrix $\Omega(\hat{\xi})$.

To solve this problem, we introduce the observation error :

$$e = \xi - \hat{\xi} \quad (3.3)$$

the dynamics of which are easily shown to be governed by the following differential equation (obtained by subtracting (3.2) from (3.1)) :

$$\frac{de}{dt} = K[\varphi(\hat{\xi} + e) - \varphi(\hat{\xi})] - De - \Omega(\hat{\xi})Le \quad (3.4)$$

A zero observation error $e = 0$ is clearly an equilibrium point of the error model (3.4). Hence, it makes sense to consider the linearized tangent approximation

of (3.4) around $e = 0$ (see Section 1.10.3 for a definition of the linearized tangent approximation of a nonlinear model). It is written as follows :

$$\frac{de}{dt} = [A(\hat{\xi}) - \Omega(\hat{\xi})L]e \quad (3.5.a)$$

with :

$$A(\hat{\xi}) \stackrel{\Delta}{=} K \left[\frac{\partial \varphi(\xi)}{\partial \xi} \right]_{\xi=\hat{\xi}} - DL_N \quad (3.5.b)$$

Thus, the design problem can be stated as the problem of choosing $\Omega(\hat{\xi})$ in such a way that the linear time-varying model (3.5) has desirable properties.

Exponential observability

The particular form (3.5.a) of the observation error dynamics indicates that we can hope to assign an arbitrarily fast (exponential) rate of convergence of the observation $\hat{\xi}(t)$ to its true value $\xi(t)$ if we can freely fix the eigenvalues of the matrix $[A(\hat{\xi}) - \Omega(\hat{\xi})L]$ by an appropriate choice of the matrix $\Omega(\hat{\xi})$.

When such a possibility exists, the system (3.1) is said to be exponentially observable and the observation scheme (3.2) is called an *exponential observer*.

A simple test to check whether a given system is exponentially observable or not is expressed by the following property.

Property 3.1. A necessary condition for the process (3.1) to be exponentially observable is that the following rank condition holds :

Exponential observability condition

$$\text{rank}(\mathbf{O}) \stackrel{\Delta}{=} \text{rank} \begin{bmatrix} L \\ LA(\xi) \\ LA(\xi)^2 \\ \vdots \\ LA(\xi)^{N-1} \end{bmatrix} = N \quad A(\xi) \stackrel{\Delta}{=} K \left[\frac{\partial \phi(\xi)}{\partial \xi} \right] - D I_N \quad (3.6)$$

along the process trajectories. The matrix \mathbf{O} is called the *observability matrix*.

It is important to note that condition (3.6) is only a necessary (but not a sufficient) exponential observability condition. Its main interest is to provide an easy way to detect those processes which are generically *not* exponentially observable. This is illustrated by two simple examples.

Example 1

Consider the simple microbial growth process (1.33) :



the dynamics of which are written :

$$\frac{d}{dt} \begin{bmatrix} S \\ X \end{bmatrix} = \begin{bmatrix} -k_1 \end{bmatrix} \phi - D \begin{bmatrix} S \\ X \end{bmatrix} + \begin{bmatrix} DS_{in} \\ 0 \end{bmatrix}$$

It is easy to see that the matrix $A(\xi)$ can be written as follows :

$$A(\xi) = \begin{bmatrix} -k_1 \phi_S - D & -k_1 \phi_X \\ \phi_S & \phi_X - D \end{bmatrix}$$

$$\text{with } \phi_X = \frac{\partial \phi}{\partial X} \text{ and } \phi_S = \frac{\partial \phi}{\partial S}$$

Assume now that the substrate concentration S is measured on-line. Thus, using the notations introduced before, we have :

$$\xi = [\xi_1, \xi_2]^T \quad \xi_1 = S \quad \xi_2 = X \quad L = [1 \ 0]$$

The observability matrix \mathbf{O} of property 3.1 is then equal to:

$$\mathbf{O} = \begin{bmatrix} L \\ LA \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ -k_1 \phi_S - D & -k_1 \phi_X \end{bmatrix}$$

The observability condition (3.6) is fulfilled if $\text{rank}(\mathbf{O}) = 2$, i.e. if $\phi_X \neq 0$. If $\phi = \mu X$ (see 1.51), we must have :

$$\phi_X = \mu + \frac{\partial \mu}{\partial X} X \neq 0$$

In the particular (but widely used) case when the specific growth rate μ is only a function of the substrate concentration S , $\partial \mu / \partial X = 0$, we can expect the biomass concentration X to be exponentially observed from S by using an observation scheme such as (3.2) whenever $\mu(S) \neq 0$.

Example 2

Consider now a process similar to the previous one but with an additional synthesis product P :



(3.7)

for which the dynamics are written :

$$\frac{d}{dt} \begin{bmatrix} S \\ X \\ P \end{bmatrix} = \begin{bmatrix} -k_1 \\ 1 \\ k_2 \end{bmatrix} \varphi - D \begin{bmatrix} S \\ X \\ P \end{bmatrix} + \begin{bmatrix} DS_{in} \\ 0 \\ 0 \end{bmatrix} \quad (3.8)$$

The matrix $A(\xi)$ is as follows :

$$A(\xi) = \begin{bmatrix} -k_1\varphi_S - D & -k_1\varphi_X & -k_1\varphi_P \\ \varphi_S & \varphi_X - D & \varphi_P \\ k_2\varphi_S & k_2\varphi_X & k_2\varphi_P - D \end{bmatrix}$$

Suppose that the product concentration P is the only component available for on-line measurement. The matrix L is equal to :

$$L = [0 \ 0 \ 1]$$

The observability matrix O is obtained after some calculation :

$$O = \begin{bmatrix} 0 & 0 & 1 \\ k_2\varphi_S & k_2\varphi_X & k_2\varphi_P - D \\ k_2\varphi_S\bar{\varphi} & k_2\varphi_X\bar{\varphi} & k_2\varphi_P\bar{\varphi} + D^2 \end{bmatrix}$$

$$\text{with } \bar{\varphi} = \varphi_X - k_1\varphi_S + k_2\varphi_P - 2D$$

It is straightforward to check that the determinant of O is equal to zero whatever the values of φ_S , φ_X and φ_P . Therefore, we know from the observability test (3.6) that the process components S and X cannot be reconstructed at an arbitrary exponential rate from measurements of P by using the observation scheme (3.2).

As a matter of fact, the above calculations can be repeated with S or X as the only measured variable : they lead to the same result, i.e. the determinant of O is equal to zero.

We can then draw the following important conclusion : the above process (3.7) is not exponentially observable if *only one component is measured*; its state cannot be exponentially reconstructed, at an arbitrarily fast rate, with an observation scheme of the form (3.2). This result is *generic* since it is independent of the values of φ_S , φ_X and φ_P , and therefore of the structure of the reaction rate φ .

Asymptotic observers

When the system (3.1) is not exponentially observable (i.e. when the eigenvalues of $A(\hat{\xi}) - \Omega(\hat{\xi})L$ cannot be freely assigned) but when the error system (3.5.a) nevertheless has an asymptotically stable equilibrium point at $e = 0$, the process can still be observed, but its dynamics will be partially determined by the experimental conditions through $A(\hat{\xi})$. Observers of this kind are called *asymptotic observers* (since one cannot freely assign their dynamics).

Other forms of asymptotic observers can be derived from equivalent state space models, obtained through suitable state transformations such as that introduced in Section 1.7. This will be discussed at length in Section 3.3. Before we move to this, we shall present in the next section the standard design methods for exponential observers.

3.2. Extended Luenberger and Kalman Observers

Assume that the system (3.1) is exponentially observable and let us return to the observation scheme (3.2) :

$$\frac{d\hat{\xi}}{dt} = K\varphi(\hat{\xi}) - D\hat{\xi} - Q + F + \Omega(\hat{\xi})[\xi_1 - \hat{\xi}_1] \quad (3.2)$$

As we have already mentioned, the observer design problem is the problem of selecting the gain matrix $\Omega(\hat{\xi})$. Two standard solutions are the extended Luenberger observer and the extended Kalman observer, respectively, which are now presented.

3.2.1. The extended Luenberger observer

The design rule for Luenberger observers is to choose the matrix $\Omega(\hat{\xi})$ in such a way that $e = 0$ is an asymptotically stable equilibrium point (see Definition A2.1, Appendix 2) of the linear tangent error model (3.5). This is achieved by choosing $\Omega(\hat{\xi})$ such that :

a) the matrix $A(\hat{\xi}) - \Omega(\hat{\xi})L$ and its time derivative are bounded :

$$\|A(\hat{\xi}) - \Omega(\hat{\xi})L\| \leq C_1 \quad \forall \hat{\xi}$$

$$\left\| \frac{d}{dt} [A(\hat{\xi}) - \Omega(\hat{\xi})L] \right\| \leq C_2 \quad \forall \hat{\xi}$$

b) the eigenvalues of $A(\hat{\xi}) - \Omega(\hat{\xi})L$ have strictly negative real parts :

$$\operatorname{Re}\{ \lambda_i[A(\hat{\xi}) - \Omega(\hat{\xi})L] \} \leq C_3 < 0 \quad \forall \hat{\xi} \quad i = 1 \text{ to } N$$

Under these conditions, it can be shown that $e = 0$ is a stable equilibrium point of (3.5) provided C_2 is sufficiently small (see Theorem A.2.4, Appendix 2). A practical example of calculation of $\Omega(\hat{\xi})$ will be given in Section 3.2.3.

3.2.2. The extended Kalman observer

In a Kalman observer, the design is based on a "quadratic optimisation" approach. The problem is to find the gain matrix $\Omega(\hat{\xi})$ which minimises the mean square observation error :

$$E = \int_0^t \| \xi - \hat{\xi} \|^2 d\tau = \int_0^t \| e(\tau) \|^2 d\tau \quad (3.9.a)$$

under the constraint of the linear tangent error model (3.5).

The solution is as follows :

$$\Omega(\hat{\xi}) = R(\hat{\xi}) L^T \quad (3.9.b)$$

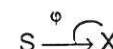
where the NxN square symmetric matrix $R(\hat{\xi})$ is generated by the Riccati equation :

$$\frac{dR}{dt} = -RL^T L R + RA^T(\hat{\xi}) + A(\hat{\xi})R \quad (3.10)$$

Note that this yields a time-varying gain Ω , even in those cases where A is independent of $\hat{\xi}$.

3.2.3. Example : Basic dynamics of microbial growth

Consider again the simple microbial growth process (1.33) :



Suppose that the reaction rate ϕ is governed by the "Contois law" (see (1.22)) :

$$\phi(X, S) = \frac{\mu^* XS}{K_c X + S} \quad (3.11)$$

where μ^* and K_c are constant kinetic coefficients. Then the state space model is written :

$$\frac{dS}{dt} = -k_1 \frac{\mu^* XS}{K_c X + S} - DS + DS_{in} \quad (3.12.a)$$

$$\frac{dX}{dt} = \frac{\mu^* XS}{K_c X + S} - DX \quad (3.12.b)$$

Assume that the substrate concentration S is measured on-line.

Hence, we are in the situation where :

$$N = 2 \quad q = 1 \quad \xi^T = [S \ X] \quad \xi_1 = S \quad L = [1 \ 0] \quad (3.13)$$

The matrix $A(\hat{\xi}) = A(\hat{S}, \hat{X})$ is as follows :

$$A(\hat{\xi}) = \begin{bmatrix} -k_1 & \frac{\partial \phi}{\partial S} \frac{\partial \phi}{\partial X} \Big|_{\xi=\hat{\xi}} \\ 1 & 0 \end{bmatrix} - D \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \quad (3.14.a)$$

$$= \begin{bmatrix} -k_1 \hat{\phi}_S - D & -k_1 \hat{\phi}_X \\ \hat{\phi}_S & \hat{\phi}_X - D \end{bmatrix} \quad (3.14.b)$$

$$\text{with } \hat{\phi}_S \stackrel{\Delta}{=} \frac{\partial \phi}{\partial S} \Big|_{\xi=\hat{\xi}} = \frac{\mu^* K_C \hat{X}^2}{(K_C \hat{X} + \hat{S})^2} \quad (3.15.a)$$

$$\hat{\phi}_X \stackrel{\Delta}{=} \frac{\partial \phi}{\partial X} \Big|_{\xi=\hat{\xi}} = \frac{\mu^* \hat{S}^2}{(K_C \hat{X} + \hat{S})^2} \quad (3.15.b)$$

The observer (3.2) is written :

$$\frac{d\hat{S}}{dt} = -k_1 \frac{\mu^* \hat{X} \hat{S}}{K_C \hat{X} + \hat{S}} - D \hat{S} + DS_{in} + \omega_1(\hat{X}, \hat{S})(S - \hat{S}) \quad (3.16.a)$$

$$\frac{d\hat{X}}{dt} = \frac{\mu^* \hat{X} \hat{S}}{K_C \hat{X} + \hat{S}} - D \hat{X} + \omega_2(\hat{X}, \hat{S})(S - \hat{S}) \quad (3.16.b)$$

The Luenberger and Kalman observers differ from one another by the way in which the gain matrix $\Omega^T(\hat{X}, \hat{S}) = [\omega_1(\hat{X}, \hat{S}) \ \omega_2(\hat{X}, \hat{S})]$ is computed.

In the case of the Luenberger observer one desires to assign to the eigenvalues of $A(\hat{X}, \hat{S}) - \Omega(\hat{X}, \hat{S})L$ some prespecified negative real values, say $\lambda_1, \lambda_2 (< 0)$.

The gains $\omega_1(\hat{X}, \hat{S})$ and $\omega_2(\hat{X}, \hat{S})$ can then be shown to be :

$$\omega_1(\hat{X}, \hat{S}) = -\lambda_1 - \lambda_2 - k_1 \hat{\phi}_S + \hat{\phi}_X - 2D \quad (3.17.a)$$

$$\omega_2(\hat{X}, \hat{S}) = \frac{1}{k_1 \hat{\phi}_X} \{-\lambda_1 \lambda_2 - (\lambda_1 + \lambda_2)(D - \hat{\phi}_X) - (D - \hat{\phi}_X)^2 + k_1 \hat{\phi}_X \hat{\phi}_S\} \quad (3.17.b)$$

Note that the estimated value \hat{S} must not be allowed to become zero in order to avoid division by zero in (3.17.b).

In the case of the Kalman observer, the gain $\Omega(\hat{X}, \hat{S})$ is calculated as follows :

$$R = \begin{bmatrix} R_1 & R_3 \\ R_3 & R_2 \end{bmatrix} \quad (3.18.a)$$

$$\frac{dR_1}{dt} = -R_1^2 - 2R_1(k_1 \hat{\phi}_S + D) - 2R_3 k_1 \hat{\phi}_X \quad (3.18.b)$$

$$\frac{dR_2}{dt} = -R_3^2 + 2R_3 \hat{\phi}_S + 2R_2(\hat{\phi}_X - D) \quad (3.18.c)$$

$$\frac{dR_3}{dt} = -R_1 R_3 - R_3(k_1 \hat{\phi}_S - \hat{\phi}_X + 2D) + R_1 \hat{\phi}_S - R_2 k_1 \hat{\phi}_X \quad (3.18.d)$$

$$\omega_1(\hat{X}, \hat{S}) = R_1 \quad \omega_2(\hat{X}, \hat{S}) = R_3 \quad (3.18.e)$$

Figs.3.1 and 3.2 illustrate the performances of both observers in a simulation performed under the following conditions :

- 1) $\mu^* = 0.3 \text{ h}^{-1}$, $K_C = 0.2$, $k_1 = 20$.
- 2) a square wave influent substrate concentration $S_{in}(t)$ (from 50 to 40 g/l)
- 3) a constant value for the dilution rate : $D(t) = 0.1 \text{ h}^{-1}$
- 4) $X(0) = 2.49 \text{ g/l}$, $S(0) = 0.25 \text{ g/l}$

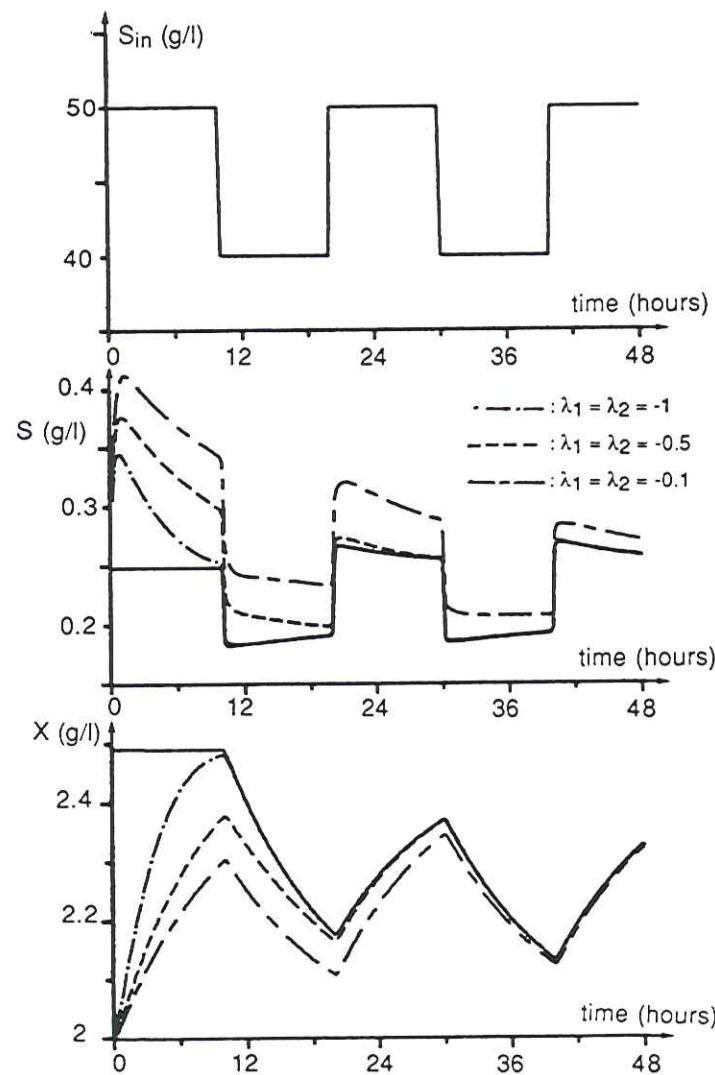


Fig. 3.1. State observation with an extended Luenberger observer

Fig.3.1 shows the simulation results of the extended Luenberger observer for three sets of eigenvalues λ_1 and λ_2 :

- a) $\lambda_1 = \lambda_2 = -1$
- b) $\lambda_1 = \lambda_2 = -0.5$
- c) $\lambda_1 = \lambda_2 = -0.1$

which correspond to decreasing response times.

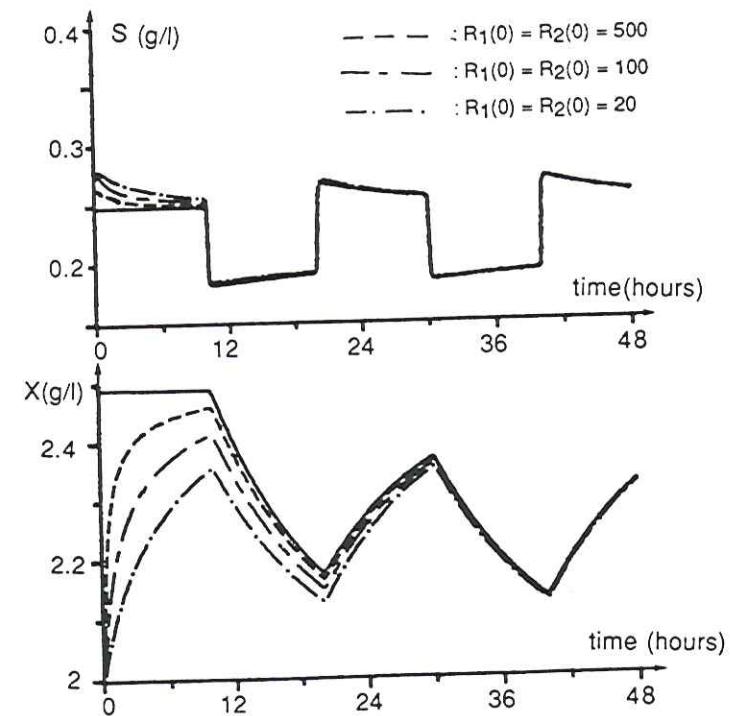


Fig.3.2. State observation with an extended Kalman filter

In Fig.3.2, the simulation results of the extended Kalman filter are presented under three sets of initial conditions :

- a) $R_1(0) = R_2(0) = 500, R_3(0) = 0$
- b) $R_1(0) = R_2(0) = 100, R_3(0) = 0$
- c) $R_1(0) = R_2(0) = 20, R_3(0) = 0$

which also result in decreasing response times.

The figures clearly illustrate the ability of the observers to guarantee an arbitrarily fast convergence.

3.3. Asymptotic Observers for State Estimation when the Reaction Rates are Unknown

In Section 3.2 we presented the design of state observers under two very restrictive conditions :

- the model (3.1) is exponentially observable
- the structure of the model is fully known.

However there are many simple processes of practical interest which are known not to be exponentially observable (see Example 2 in Section 3.1). Moreover, the requirement of a full knowledge of the process kinetics is too severe in most engineering applications, as was shown in Chapter 2. There is therefore a clear incentive to search for a category of observers which allows one to asymptotically reconstruct the missing states even when the process is not exponentially observable and the kinetics are unknown. In this section we present a design method of such *asymptotic* observers under the following conditions :

- the reaction rate function $\phi(\xi)$ is unknown

- the yield coefficients (matrix K) are known
- the number q of measured state variables is equal to or greater than the rank of the matrix K : $q = \dim(\xi_1) \geq p = \text{rank}(K)$

3.3.1. Statement of the asymptotic observer

From the basic structural property of Section 1.7, we know that there exists (at least) one partition (ξ_a, ξ_b) of the state, one $(N-p) \times p$ matrix A_0 , and one vector Z of dimension $N-p$ defined as the following linear combination of the state variables :

$$Z = A_0 \xi_a + \xi_b \quad (1.70) = (3.19)$$

and whose dynamics, given by (1.73), are independent of the reaction rate $\phi(\xi)$:

$$\frac{dZ}{dt} = -DZ + A_0(F_a - Q_a) + (F_b - Q_b) \quad (1.73) = (3.20)$$

Now, it is clear that we can rewrite this vector Z explicitly as a linear combination of the vectors ξ_1 and ξ_2 of measured and non-measured state variables :

$$Z = A_1 \xi_1 + A_2 \xi_2 \quad (3.21)$$

with appropriate definitions of the $(N-p) \times q$ and $(N-p) \times (N-q)$ matrices A_1 and A_2 .

Example : The anaerobic digestion process

We consider the simplified reaction scheme (1.86) obtained in Section 1.8.4 :



Suppose, furthermore, that we are not interested in the products P_1 and P_2 , so that we can omit them in the analysis (see Section 1.4.2). The reaction scheme reduces to :



According to the rules of Section 1.5, the state space model is as follows :

$$\frac{d}{dt} \begin{bmatrix} S_1 \\ X_1 \\ S_2 \\ X_2 \end{bmatrix} = \begin{bmatrix} -k_1 & 0 \\ 1 & 0 \\ k_3 & -k_2 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} \varphi_1 \\ \varphi_2 \end{bmatrix} - D \begin{bmatrix} S_1 \\ X_1 \\ S_2 \\ X_2 \end{bmatrix} + \begin{bmatrix} F_1 \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad (3.24)$$

The matrix K is clearly of rank 2. An admissible state partition is :

$$\xi_a = \begin{bmatrix} X_1 \\ X_2 \end{bmatrix} \quad \xi_b = \begin{bmatrix} S_1 \\ S_2 \end{bmatrix} \quad (3.25)$$

The vector Z is as follows :

$$Z = \begin{bmatrix} Z_1 \\ Z_2 \end{bmatrix} = A_0 \xi_a + \xi_b = \begin{bmatrix} k_1 & 0 \\ -k_3 & k_2 \end{bmatrix} \begin{bmatrix} X_1 \\ X_2 \end{bmatrix} + \begin{bmatrix} S_1 \\ S_2 \end{bmatrix} \quad (3.26)$$

If we assume that X_1 and S_2 are measured on-line, then :

$$\xi_1 = \begin{bmatrix} X_1 \\ S_2 \end{bmatrix} \quad \xi_2 = \begin{bmatrix} S_1 \\ X_2 \end{bmatrix} \quad (3.27)$$

and we can rewrite Z :

$$Z = A_1 \xi_1 + A_2 \xi_2 \quad (3.28)$$

with :

$$A_1 = \begin{bmatrix} k_1 & 0 \\ -k_3 & 1 \end{bmatrix} \quad A_2 = \begin{bmatrix} 1 & 0 \\ 0 & k_2 \end{bmatrix} \quad (3.29)$$

Similarly, if we assume that S_1 , X_2 , S_2 are measured on-line, then :

$$\xi_1 = \begin{bmatrix} S_1 \\ S_2 \\ X_2 \end{bmatrix} \quad \xi_2 = X_1 \quad (3.30.a)$$

$$A_1 = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & k_2 \end{bmatrix} \quad A_2 = \begin{bmatrix} k_1 \\ -k_3 \end{bmatrix} \quad (3.30.b)$$

The asymptotic observer

If the $(N-p) \times (N-q)$ matrix A_2 has a left inverse, the following asymptotic observer follows quite naturally from (3.20) and (3.21) :

Asymptotic observer

$$\frac{d\hat{Z}}{dt} = -D\hat{Z} + A_0(F_a - Q_a) + (F_b - Q_b) \quad (3.31.a)$$

$$\hat{\xi}_2 = A_2^+ (\hat{Z} - A_1 \xi_1) \quad (3.31.b)$$

where A_2^+ is a left inverse of A_2 . \hat{Z} and $\hat{\xi}_2$ denote on-line estimates of Z and ξ_2 respectively.

This algorithm is completely independent of $\phi(\xi)$ and can be used without any knowledge of the kinetics (i.e. of the reaction rates).

The convergence of this algorithm is proved by the following theorem :

Theorem 3.1 : If the dilution rate $D(t)$ is persistently exciting (see Appendix 3), i.e. if there exist positive constants δ and β_1 such that :

$$0 < \beta_1 \leq \int_t^{t+\delta} D(\tau) d\tau \quad \forall t \quad (3.32)$$

then :

$$\lim_{t \rightarrow \infty} \|\xi_2(t) - \hat{\xi}_2(t)\| = 0 \quad (3.33)$$

The proof of this theorem is immediate when one observes that, from (3.20), (3.21) and (3.31), the dynamics of the estimation error are as follows :

$$\frac{d}{dt} (\xi_2 - \hat{\xi}_2) = -D(\xi_2 - \hat{\xi}_2) \quad (3.34)$$

The assumption (3.32) simply implies that the dilution rate $D(t)$ does not remain equal to zero for excessively long periods of time. Hence, the convergence of the observer is valid only for fed-batch and continuous operating conditions. In batch reactors, any initial estimation error will persist throughout the estimation procedure.

Unlike the Luenberger and Kalman observers of Section 3.1, the speed of convergence of the estimation is completely determined by the experimental conditions (through the value of the dilution rate). This is why this algorithm is called an *asymptotic* observer. One consequence is that the accuracy of the initial estimate may be critical when the observer is implemented for a period of time which is not very long with respect to the residence time (i.e. the inverse of the dilution rate).

Example : The anaerobic digestion process (continued)

We return to the process described by the reaction scheme (3.23). We consider three different situations.

- 1) Suppose that X_1 and S_2 are measured on-line and that S_1 and X_2 need to be estimated.

The vectors ξ_a , ξ_b , Z , ξ_1 , ξ_2 and the matrices A_1 , A_2 have been defined above ((3.25), (3.26), (3.27), (3.29)).

Clearly the matrix A_2 is square and nonsingular. Hence its left inverse is :

$$A_2^+ = A_2^{-1} = \begin{bmatrix} 1 & 0 \\ 0 & k_2^{-1} \end{bmatrix} \quad (3.35)$$

The asymptotic observer (3.31) is as follows :

$$\frac{d}{dt} \begin{bmatrix} \hat{Z}_1 \\ \hat{Z}_2 \end{bmatrix} = -D \begin{bmatrix} \hat{Z}_1 \\ \hat{Z}_2 \end{bmatrix} + \begin{bmatrix} F_1 \\ 0 \end{bmatrix} \quad (3.36.a)$$

$$\begin{bmatrix} \hat{S}_1 \\ \hat{X}_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 0 & k_2^{-1} \end{bmatrix} \left(\begin{bmatrix} \hat{Z}_1 \\ \hat{Z}_2 \end{bmatrix} - \begin{bmatrix} k_1 & 0 \\ -k_3 & 1 \end{bmatrix} \begin{bmatrix} X_1 \\ S_2 \end{bmatrix} \right) \quad (3.36.b)$$

- 2) We now assume that S_1 , X_2 , S_2 are measured on-line.

The on-line estimation of Z_1 , Z_2 is obviously given by the same expression (3.36.a). The matrix A_2 is necessarily full rank, and its (left) pseudo-inverse is :

$$A_2 = \begin{bmatrix} k_1 \\ -k_3 \end{bmatrix} \quad A_2^+ = \frac{1}{k_1^2 + k_3^2} \begin{bmatrix} k_1 & -k_3 \end{bmatrix} \quad (3.37)$$

The on-line estimate of X_1 is :

$$\hat{X}_1 = \frac{1}{k_1^2 + k_3^2} [k_1(\hat{Z}_1 - S_1) - k_3(\hat{Z}_2 - k_2 X_2 - S_2)] \quad (3.38)$$

In this case, it is interesting to note that the observer provides an estimate which is in fact a weighted average between two estimates, which could be computed separately from S_1 and Z_1 on the one hand, and from S_2 , X_2 and Z_2 on the other.

- 3) A necessary condition for applying the asymptotic observer is that the number of measurements be equal to or greater than the rank of K : $q \geq p$. But this condition is not always sufficient. Suppose for instance that S_1 and X_1 are measured on-line. Then the matrices A_1 and A_2 are defined as follows :

$$A_1 = \begin{bmatrix} 1 & k_1 \\ 0 & -k_3 \end{bmatrix} \quad A_2 = \begin{bmatrix} 0 & 0 \\ 1 & k_2 \end{bmatrix} \quad (3.39)$$

It is clear that, although the number of measurements is sufficient ($q=p=2$), the matrix A_2 is singular and cannot be inverted : it is not possible to estimate $\xi_2 = [S_2, X_2]^T$ from $\xi_1 = [S_1, X_1]^T$ with an asymptotic observer of the form (3.31).

3.3.2. A simulation experiment : estimation of substrate and biomass concentration from synthesis product data

We consider the example 2 of Section 3.1, i.e. a process characterised by the following reaction scheme :



In Section 3.1 we showed that this process is not exponentially observable. But, as we shall see, it is asymptotically observable.

The dynamics of the process are described by the state space model (3.8). We choose the following state partition :

$$\xi_a = X \quad \xi_b = \begin{bmatrix} S \\ P \end{bmatrix} \quad (3.41)$$

Z and its time derivative are then equal to :

$$Z = \begin{bmatrix} Z_1 \\ Z_2 \end{bmatrix} = \begin{bmatrix} k_1 X + S \\ -k_2 X + P \end{bmatrix} \quad (3.42.a)$$

$$\frac{dZ_1}{dt} = -DZ_1 + DS_{in} \quad (3.42.b)$$

$$\frac{dZ_2}{dt} = -DZ_2 \quad (3.42.c)$$

Since $\text{rank}(K)$ is obviously equal to 1, the measurement of only one component is needed to estimate the other two. Assume that P is measured on-line. ξ_1, ξ_2, A_1, A_2 are then defined as follows :

$$\xi_1 = P \quad \xi_2 = \begin{bmatrix} S \\ X \end{bmatrix} \quad (3.43.a)$$

$$A_1 = \begin{bmatrix} 0 \\ 1 \end{bmatrix} \quad A_2 = \begin{bmatrix} 1 & k_1 \\ 0 & -k_2 \end{bmatrix} \quad (3.43.b)$$

The asymptotic observer (3.31) for the estimation of the substrate concentration S and the biomass concentration X is written :

$$\frac{d\hat{Z}_1}{dt} = -D\hat{Z}_1 + DS_{in} \quad (3.44.a)$$

$$\frac{d\hat{Z}_2}{dt} = -D\hat{Z}_2 \quad (3.44.b)$$

$$\hat{S} = \hat{Z}_1 + \frac{k_1}{k_2}(\hat{Z}_2 - P) \quad (3.44.c)$$

$$\hat{X} = \frac{-1}{k_2}(\hat{Z}_2 - P) \quad (3.44.d)$$

The behaviour of the observer is illustrated by a simulation experiment (Fig.3.3).

The kinetics of the "true" process are assumed to be governed by the following growth rate model (see Appendix 1)

$$\mu(t) = \mu^* \frac{S}{K_M + S + S^2/K_I} \frac{K_P}{K_P + P} \left(1 - \frac{P}{P_L}\right) \quad (3.45)$$

with the following set of parameter values :

$$\mu^* = 0.23 \text{ h}^{-1}, K_M = 0.26 \text{ g/l}, K_I = 297 \text{ g/l}, K_P = 7.77 \text{ g/l}, P_L = 85.81 \text{ g/l}$$

The simulation of Fig.3.3 was performed under the following conditions :

a) $X(0) = 0.365 \text{ g/l}$, $S(0) = 90 \text{ g/l}$, $P(0) = 5.1 \text{ g/l}$

$D(0) = 0.1 \text{ h}^{-1}$, $S_{in}(0) = 100 \text{ g/l}$

b) two different sets of initial conditions for Z_1 and Z_2 :

$\hat{Z}_1(0) = -1$ and 1 , $\hat{Z}_2(0) = 80$ and 110

c) a trapezoidal signal for $D(t)$ (from 0.1 to 0.05 h^{-1})

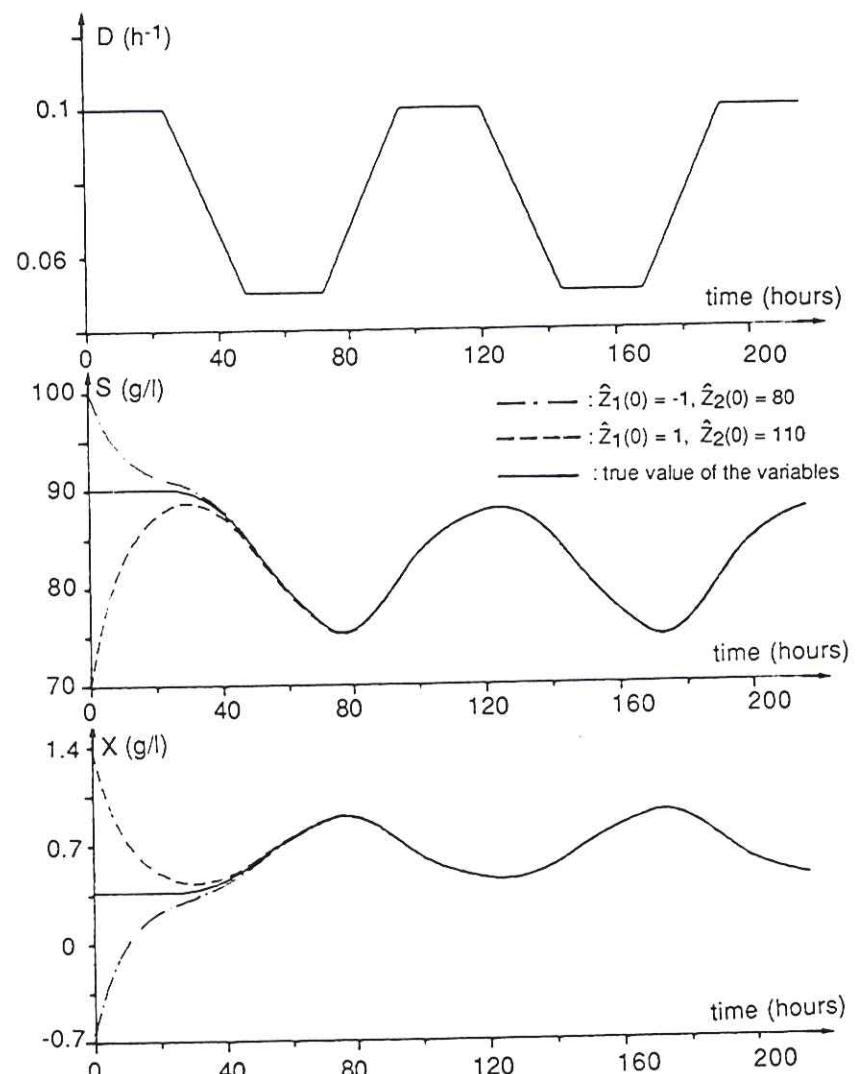
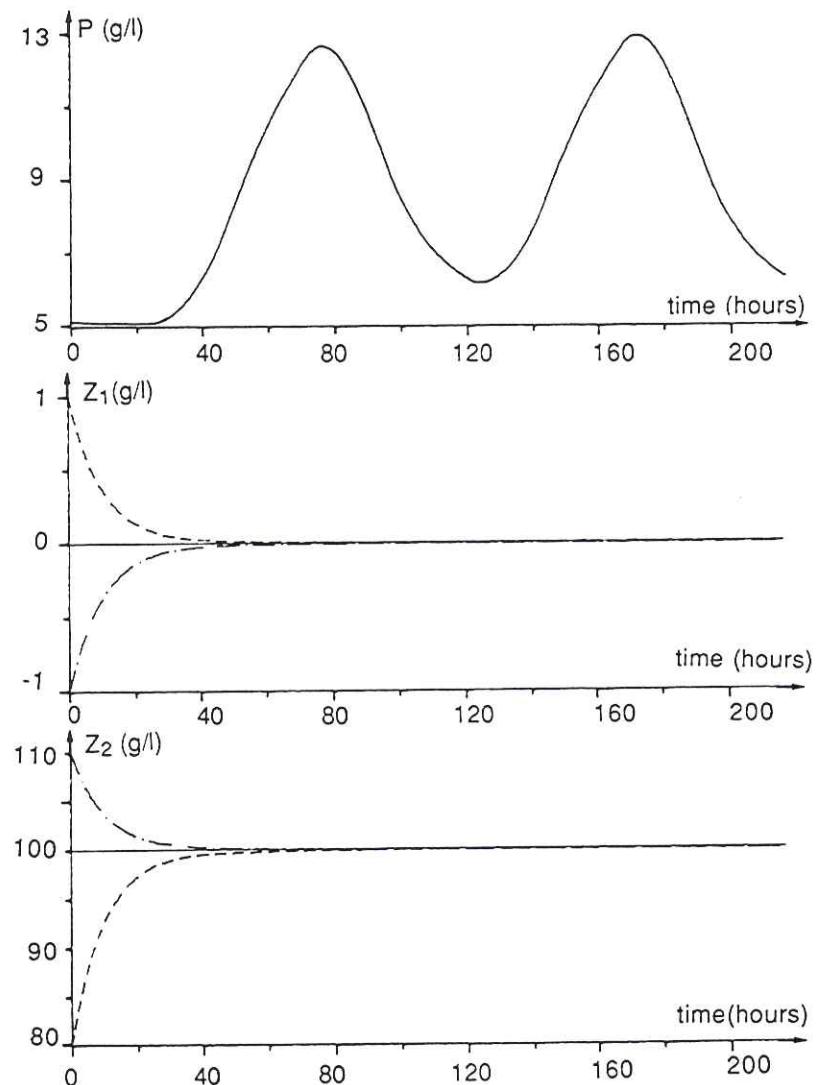


Fig.3.3.a. State observation with the asymptotic observer : simulation result



Comments

- 1) It is worth noting that the asymptotic observer (3.44) is extremely simple compared with the Luenberger and Kalman observers. Compare for instance (3.44) with (3.16) to (3.18).
- 2) Besides its simplicity, the asymptotic observer does not require any knowledge of the reaction rate structure (here the particular and quite complex structure (3.45) has been used to simulate the process, but clearly this structure is ignored by the observer) and, nevertheless, has a most acceptable behaviour. The drawback, however, is that the speed of convergence is fixed by the experimental conditions and cannot be manipulated by the user. In the simulation, convergence is achieved after about 40 hours.
- 3) Last but not least we know (see example 2, Section 3.1) that, in this example, the process is *not* exponentially observable, and therefore cannot be observed at an arbitrary exponential rate by using e.g. extended Luenberger or Kalman observers. However, as illustrated by Fig.3.3, the state is efficiently reconstructed with the simple asymptotic observer (3.44).

3.3.3. Real life experiment 1 : An anaerobic digestion process

The asymptotic observer (3.31) has been applied to a pilot-scale anaerobic digestion process for the on-line estimation of organic substrate concentration and of acidogenic and methanogenic bacterial concentrations. The results of this experiment (performed by the Unit of Bioengineering, Université Catholique de Louvain, Belgium) are now reported.

The process is assumed to be described by the simplified reaction scheme (1.86) :

Fig.3.3.b. State observation with the asymptotic observer : simulation result



with X_1 being the acidogenic biomass, S_1 the organic substrate, X_2 the methanogenic biomass, S_2 the acetate, P_1 the methane and P_2 the inorganic carbon.

The dynamics of the process are described by the model (1.85) which is rewritten as follows :

$$\frac{d}{dt} \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ -k_1 & 0 \\ 0 & 1 \\ k_3 & -k_2 \\ 0 & k_6 \\ k_4 & k_5 \end{bmatrix} \begin{bmatrix} \varphi_1 \\ \varphi_2 \end{bmatrix} - D \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} + \begin{bmatrix} 0 \\ F_1 \\ 0 \\ 0 \\ 0 \\ Q_1 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ Q_2 \end{bmatrix} \quad (3.46)$$

We choose the partition $\xi_a = [X_1, X_2]^T$, $\xi_b = [S_1, S_2, P_1, P_2]^T$ so that the auxiliary state Z is as follows :

$$\begin{bmatrix} Z_1 \\ Z_2 \\ Z_3 \\ Z_4 \end{bmatrix} = \begin{bmatrix} S_1 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} - \begin{bmatrix} -k_1 & 0 \\ k_3 & -k_2 \\ 0 & k_6 \\ k_4 & k_5 \end{bmatrix} \begin{bmatrix} X_1 \\ X_2 \end{bmatrix} \quad (3.47)$$

We are interested in the problem of estimating the biomass concentrations X_1 and X_2 and the substrate concentration S_1 from on-line measurements of S_2 (acetate concentration), $F_1 = DS_{1,in}$ (substrate feedrate) and Q_1 (methane gas flow rate). We know also that the dissolved methane concentration and its time derivative may be neglected (see Section 1.8.4) : $P_1 = dP_1/dt = 0$.

We immediately note that, for our purpose, the fourth auxiliary state Z_4 is superfluous and hence that the yield coefficients k_4 and k_5 are not required.

The asymptotic observer (3.31) is as follows :

$$\frac{d\hat{Z}_1}{dt} = -D\hat{Z}_1 + F_1 \quad (3.48.a)$$

$$\frac{d\hat{Z}_2}{dt} = -D\hat{Z}_2 \quad (3.48.b)$$

$$\frac{d\hat{Z}_3}{dt} = -D\hat{Z}_3 - Q_1 \quad (3.48.c)$$

$$\hat{X}_2 = -\frac{\hat{Z}_3}{k_6} \quad (3.48.d)$$

$$\hat{X}_1 = \frac{1}{k_3} \left(S_2 - \hat{Z}_2 - \frac{k_2}{k_6} \hat{Z}_3 \right) \quad (3.48.e)$$

$$\hat{S}_1 = \hat{Z}_1 - \frac{k_1}{k_3} \left(S_2 - \hat{Z}_2 - \frac{k_2}{k_6} \hat{Z}_3 \right) \quad (3.48.f)$$

Experimental results

This asymptotic observer has been implemented over 90 days on a 60 liter pilot bioreactor with the yield coefficients :

$$k_1 = 3.2 \quad k_2 = 28.3 \quad k_3 = 5.7 \quad k_6 = 27.3 \quad (3.49)$$

and the following three sets of initial conditions :

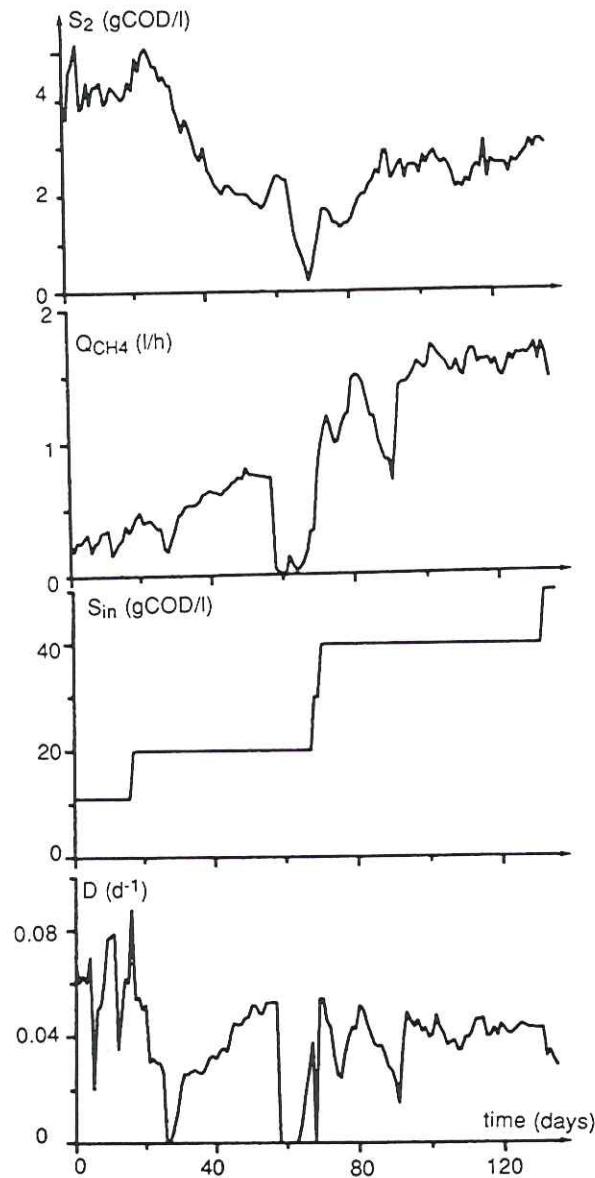


Fig.3.4. State observation in a continuous anaerobic digestion process :
on-line data

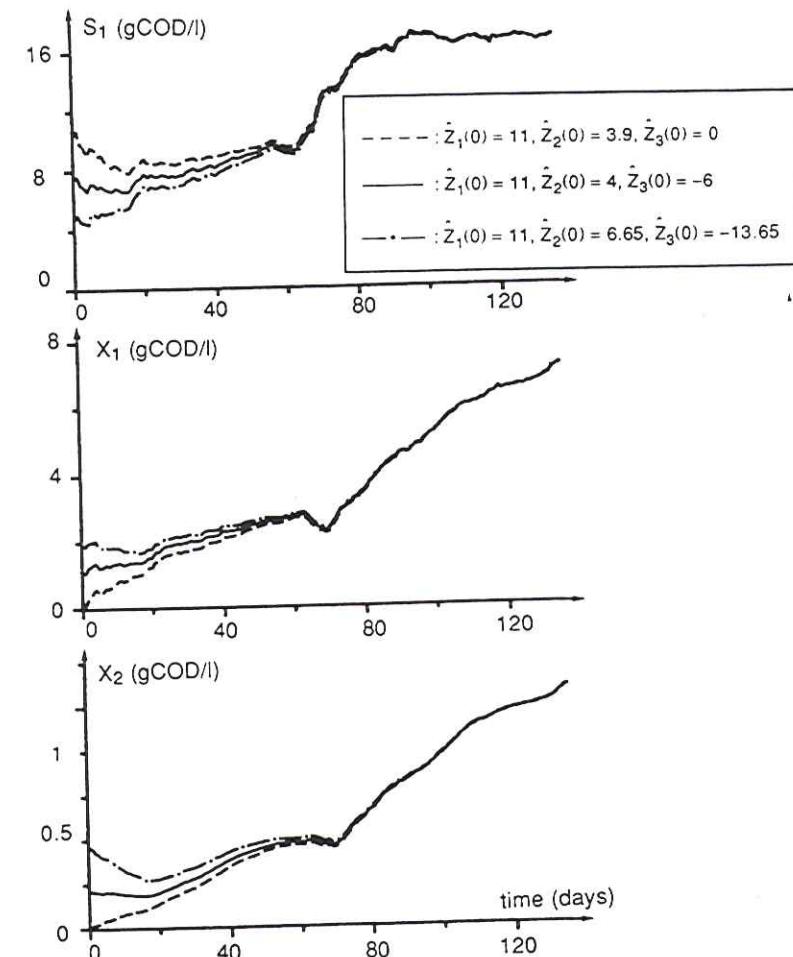


Fig.3.5. State observation in a continuous anaerobic digestion process :
estimation results

$$1) \hat{Z}_1(0) = 11, \hat{Z}_2(0) = 3.9, \hat{Z}_3(0) = 0 \quad (3.50.a)$$

$$2) \hat{Z}_1(0) = 11, \hat{Z}_2(0) = 4, \hat{Z}_3(0) = -6 \quad (3.50.b)$$

$$3) \hat{Z}_1(0) = 11, \hat{Z}_2(0) = 6.65, \hat{Z}_3(0) = -13.65 \quad (3.50.c)$$

The influent substrate concentration $S_{1,in}$, the dilution rate D and the measurements of S_2 (acetate) and Q_1 (methane gas) are shown in Fig.3.4.

The on-line estimates of X_1, X_2, S_1 are shown in Fig.3.5.

An *experimental validation* of the observer can be performed as follows. A measurement of the *total* biomass (i.e $X_1 + X_2$) in the reactor is also available : it is obtained from the difference between total COD and solubilised COD measurements. We can thus compare the estimated total biomass $\hat{X}_1 + \hat{X}_2$ with its actual value : this is done in Fig.3.6 where a very good agreement is found (after the initial transient). We see also that convergence is achieved within 70 days.

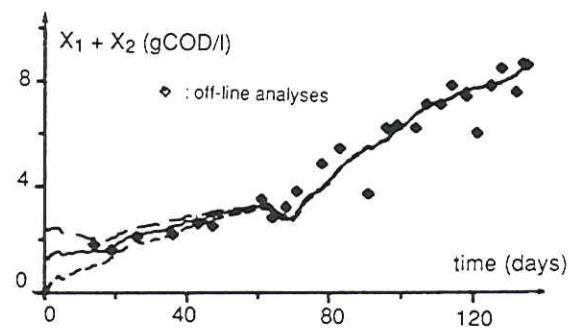


Fig. 3.6. State observation in a continuous anaerobic digestion process : experimental validation

3.3.4. Real life experiment 2 : A PHB production process

The dynamical model (1.66) of the intracellular production of PHB was described in Section 1.6. In this section an experimental validation (performed by the SOLVAY Company of Belgium) of the asymptotic observer (3.31) on a fed-batch PHB production pilot plant is reported.

The choice of useful measurements

In this pilot plant, both oxygen and carbon dioxide are available for on-line measurement. However, as we shall show, only one of these two components can be used for the implementation of the observer because the respiratory quotient (RQ) is equal to one ($RQ = 1$). The RQ is defined as follows :

$$RQ = \frac{\text{moles CO}_2 \text{ formed}}{\text{moles O}_2 \text{ consumed}}$$

This can be written in terms of our dynamical model as follows :

$$RQ = \left(\frac{1}{\gamma}\right)^{k_7\varphi_1+k_8\varphi_2} \quad (3.51)$$

where γ is a conversion factor from grams to moles.

However, since RQ is equal to 1 in *both* reactions, as can be checked experimentally, we necessarily have :

$$k_7 = \gamma k_4 \quad (3.52.a)$$

$$k_8 = \gamma k_6 \quad (3.52.b)$$

Suppose now that we try to estimate the state variables of the process from the measurements of oxygen (C) and carbon dioxide (P_2).

Since the matrix K is presently of rank 2, we can define ξ_a and ξ_b as follows :

$$\xi_a = \begin{bmatrix} X \\ P_1 \end{bmatrix} \quad \xi_b = \begin{bmatrix} S_1 \\ S_2 \\ C \\ P_2 \end{bmatrix} \quad (3.53)$$

Then, using (3.52), Z is equal to :

$$Z = \begin{bmatrix} (k_1 - k_3 k_5)X + k_5 P_1 + S_1 \\ k_2 X + S_2 \\ (k_4 - k_3 k_6)X + k_6 P_1 + C \\ -\gamma[(k_4 - k_3 k_6)X + k_6 P_1] + P_2 \end{bmatrix} \quad (3.54)$$

A priori, we could believe that the state of the process could be reconstructed using the asymptotic observer from the measurement of *any two* components. However, this is not true if the estimation is based on oxygen and carbon dioxide data. Indeed ξ_1 , ξ_2 , A_1 and A_2 would be defined as follows :

$$\xi_1 = \begin{bmatrix} C \\ P_2 \end{bmatrix} \quad \xi_2 = \begin{bmatrix} X \\ S_1 \\ S_2 \\ P_1 \end{bmatrix} \quad (3.55.a)$$

$$A_1 = \begin{bmatrix} 0 & 0 \\ 0 & 0 \\ 0 & 1 \\ 0 & 1 \end{bmatrix} \quad A_2 = \begin{bmatrix} k_1 - k_3 k_5 & 1 & 0 & k_5 \\ k_2 & 0 & 1 & 0 \\ k_4 - k_3 k_6 & 0 & 0 & k_6 \\ -\gamma(k_4 - k_3 k_6) & 0 & 0 & -\gamma k_6 \end{bmatrix} \quad (3.55.b)$$

A_2 is a square matrix but not full rank (lines 3 and 4 are proportional) and therefore not invertible : we cannot estimate the state of the PHB process from the measurements of O_2 and CO_2 . This is simply the mathematical

confirmation of the fact that, in view of the fact that $RQ = 1$, the measurements of O_2 and CO_2 do not give independent information on the state of the process. This highlights the fact that the measurements used for the state observation need to be carefully chosen.

The observer equations

In order to reconstruct the state of this PHB process, it is necessary either to have another component available for on-line measurement, or to look for additional prior knowledge on the process dynamics. As the first possibility was excluded from an operational point of view, we opted for the second one.

From the description of the process given in Section 1.4.3, it can be seen that the two biological paths of the PHB production are mutually exclusive. The first path (microbial growth (with a small growth-associated production) with rate φ_1) requires fructose *and* nitrogen as substrates. The second path (enzyme catalysed production with rate φ_2) requires fructose but is *completely inhibited* by nitrogen. The results, clearly, is that only one path is activated at each time.

In practice, the process was conducted in two successive steps :

- 1) During the first step the process is fed with the two substrates (fructose and ammonia) : this is a growth step without enzyme-catalysed production.
- 2) During the second step the process is fed with fructose only : this is a production step without growth.

This allows us to consider two different dynamical models to describe each step. Both are special cases of the general dynamical model (1.49).

MODEL A : Growth without production (in presence of nitrogen)

$$\xi^T = [X \ S_1 \ S_2 \ P_1 \ C \ P_2]$$

$$Q^T = [0 \ 0 \ 0 \ 0 \ 0 \ Q_1]$$

$$F^T = [0 \ DS_{1,in} \ DS_{2,in} \ 0 \ Q_{in} \ 0]$$

$$K^T = [1 \ -k_1 \ -k_2 \ k_3 \ -k_4 \ k_7]$$

$$G(\xi) = S_1 S_2 C X$$

MODEL B : Production without growth (absence of nitrogen)

$$\xi^T = [X \ S_1 \ P_1 \ C \ P_2]$$

$$Q^T = [0 \ 0 \ 0 \ 0 \ Q_1]$$

$$F^T = [0 \ DS_{1,in} \ 0 \ Q_{in} \ 0] \quad (3.57)$$

$$K^T = [0 \ -k_5 \ 1 \ -k_6 \ k_8]$$

$$G(\xi) = S_1 C X$$

In both models, the rank of matrix K is equal to 1, and the measurement of one component can be used for the state observation. We decided to use the on-line measurements of oxygen in preference to those of CO_2 because the oxygen sensors were in practice more reliable and less sensitive to pH variations.

Hence ξ_1 and ξ_2 are defined as follows :

$$\xi_1 = C$$

$$\text{model A : } \xi_2^T = [X \ S_1 \ S_2 \ P_1 \ P_2]$$

$$\text{model B : } \xi_2^T = [X \ S_1 \ P_1 \ P_2]$$

For both models, we choose the partition $\xi_a = \xi_1$ and $\xi_b = \xi_2$. Then :

$$A_0 = A_1 = \left[\begin{array}{ccccc} 1 & -k_1 & -k_2 & k_3 & \gamma \\ \frac{1}{k_4} & \frac{-k_1}{k_4} & \frac{-k_2}{k_4} & \frac{k_3}{k_4} & \gamma \end{array} \right]^T \quad (\text{model A}) \quad (3.58.a)$$

$$= \left[\begin{array}{ccccc} 0 & -\frac{k_5}{k_6} & \frac{1}{k_6} & \gamma \end{array} \right]^T \quad (\text{model B}) \quad (3.58.b)$$

$$A_2 = I \quad (3.58.c)$$

In this study, we were interested in reconstructing the time evolution of the biomass concentration X, the PHB concentration P_1 and the nitrogen concentration S_2 from the on-line measurement of C (dissolved oxygen), D (dilution rate), $S_{2,in}$ (influent nitrogen concentration), and Q_{in} (oxygen feed rate).

The following auxiliary variables are defined :

$$\text{Model A : } Z_1 = X + \frac{C}{k_4} \quad (3.59.a)$$

$$Z_2 = S_2 - \frac{k_2 C}{k_4} \quad (3.59.b)$$

$$Z_3 = P_1 + \frac{k_3 C}{k_4} \quad (3.59.c)$$

$$\text{Model B : } Z_4 = X$$

$$Z_5 = P_1 + \frac{C}{k_6} \quad (3.59.d)$$

The asymptotic observer (3.31) is as follows :

A. Whenever $\hat{S}_2 > 0$:

$$\frac{d\hat{Z}_1}{dt} = D\hat{Z}_1 + \frac{Q_{in}}{k_4} \quad (3.60.a)$$

$$\frac{d\hat{Z}_2}{dt} = -D\hat{Z}_2 + DS_{2,in} - \frac{k_2 Q_{in}}{k_4} \quad (3.60.b)$$

$$\frac{d\hat{Z}_3}{dt} = -D\hat{Z}_3 + \frac{k_3 Q_{in}}{k_4} \quad (3.60.c)$$

$$\hat{X} = \hat{Z}_1 - \frac{C}{k_4} \quad (3.60.d)$$

$$\hat{S}_2 = \hat{Z}_2 + \frac{k_2 C}{k_4} \quad (3.60.e)$$

$$\hat{P}_1 = \hat{Z}_3 - \frac{k_3 C}{k_4} \quad (3.60.f)$$

B. When $\hat{S}_2 = 0$

$$\frac{d\hat{Z}_4}{dt} = -D\hat{Z}_4 \quad (3.61.a)$$

$$\frac{d\hat{Z}_5}{dt} = -D\hat{Z}_5 + \frac{Q_{in}}{k_6} \quad (3.61.b)$$

$$\hat{X} = \hat{Z}_4 \quad (3.61.c)$$

$$\hat{P}_1 = \hat{Z}_5 - \frac{C}{k_6} \quad (3.61.d)$$

Note that, since the nitrogen concentration is not accessible from on-line measurement, we use the estimate \hat{S}_2 to switch from the first algorithm (3.60) to the second one (3.61).

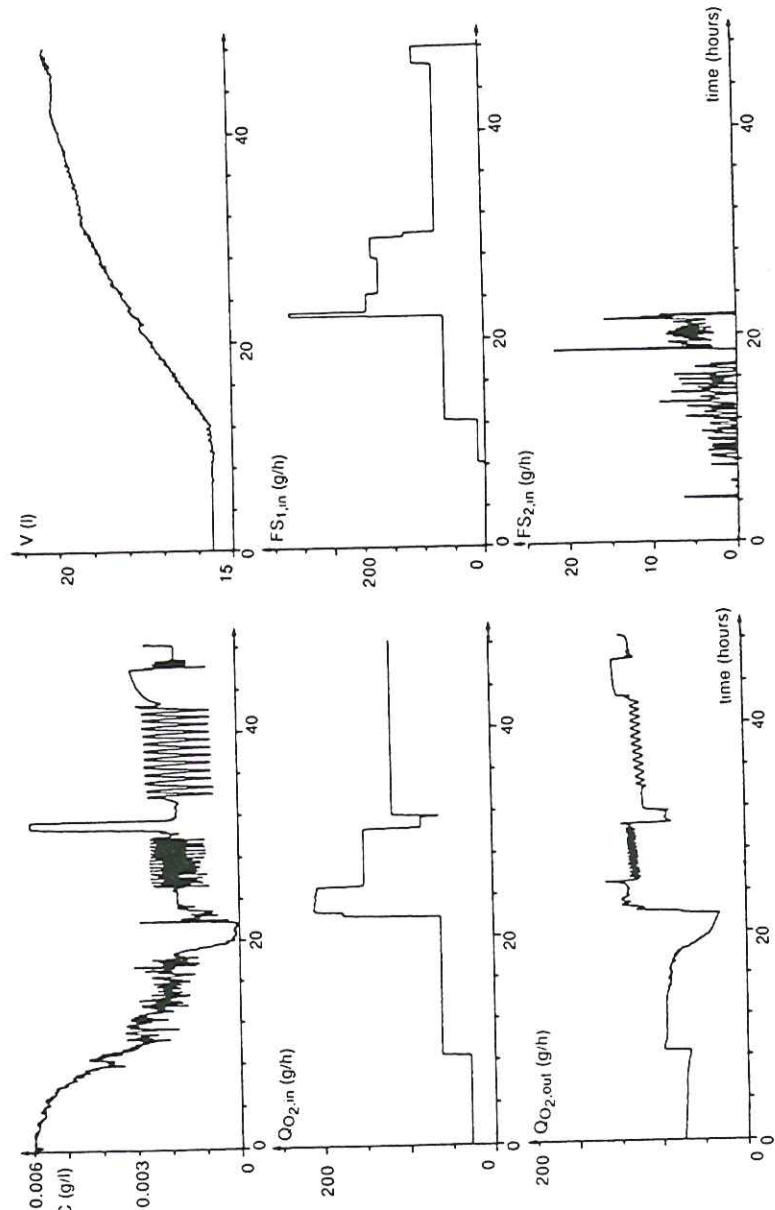


Fig.3.7. State observation in a PHB producing process : on-line data

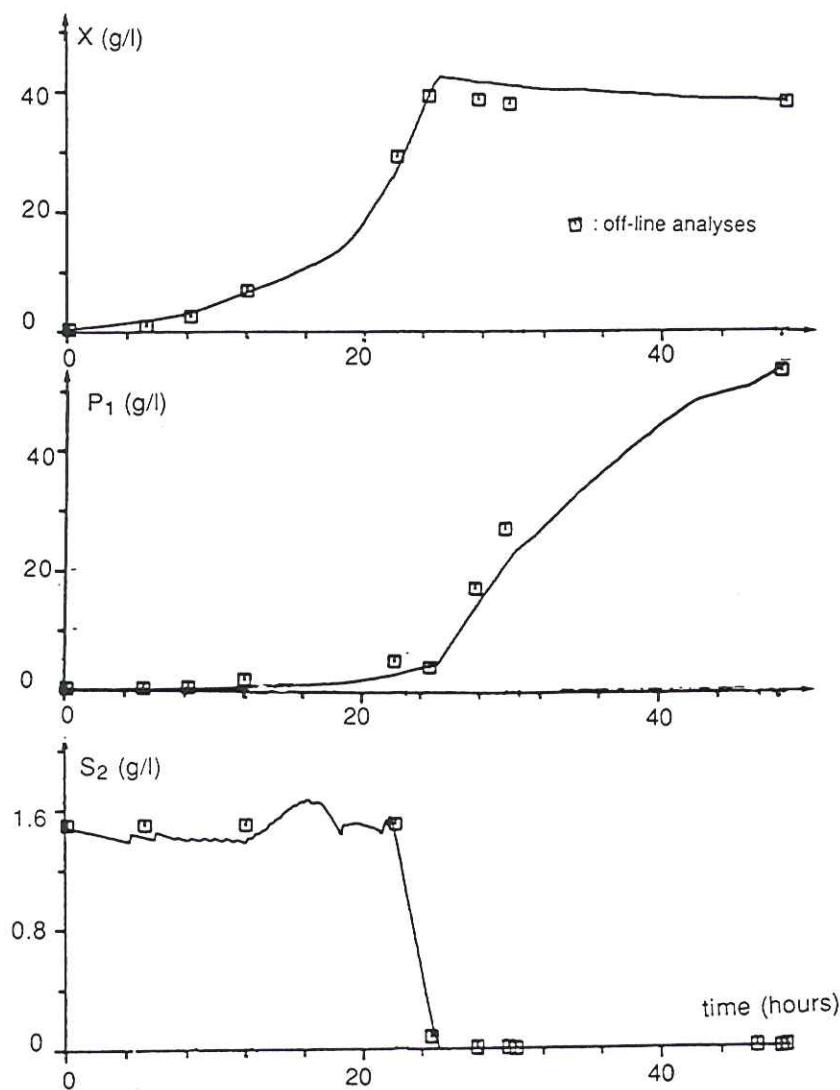


Fig.3.8. State observation in a PHB producing process : estimation results

Implementation on a fed-batch bioreactor

We present the estimation results on one experiment carried out by the SOLVAY Company (Belgium) on a 20 liter pilot bioreactor. The numerical values of the yield coefficients are as follows :

$$k_2 = 0.83, k_3 = 0.657, k_4 = k_6 = 0.769$$

The on line data are shown in Fig.3.7. (Note that $Q_{in} = Q_{O2,in} - Q_{O2,out}$). The estimates of X , S_2 and P are shown in Fig.3.8. The agreement between these estimates and off-line data from chemical analysis is evident. In addition, it can be observed that the switching from algorithm A to algorithm B is very efficiently driven by the estimate of the nitrogen substrate S_2 .

3.3.5. Practical aspects of implementation

Numerical implementation

Practical computer implementation of the asymptotic observer (3.31) requires that it be rewritten in a discrete-time form. This can be done simply by replacing the time derivative of Z by a finite difference (using a first order forward Euler approximation) :

$$\frac{d\hat{Z}}{dt} \rightarrow \frac{\hat{Z}_{t+1} - \hat{Z}_t}{T} \quad (3.62)$$

where T is the sampling period and t and $t+1$ are time indices.

The asymptotic observer (3.31) is then written as follows :

Discrete-time asymptotic observer

$$\hat{Z}_{t+1} = \hat{Z}_t - TD_t \hat{Z}_t + TF_{bt} - TQ_{bt} + A_0 T (F_{at} - Q_{at}) \quad (3.63)$$

Choice of the sampling period T

The switch from the continuous-time equation (3.31) to the discrete-time version (3.61) induces the presence of the sampling period T. The continuous-time equation (3.31) is unconditionally stable. For the discrete-time equation (3.63), the value of T plays an important role in the stability. In fact, if the dilution rate is bounded as follows :

$$0 \leq D(t) \leq D_{\max} \quad \forall t$$

then equation (3.63) will remain stable as long as the value of $T/2$ is smaller than D_{\max}^{-1} :

$$\frac{T}{2} \leq \frac{1}{D_{\max}} \quad (3.64)$$

This is easily shown by considering the following positive definite, decrescent candidate Lyapunov function :

$$W_t = (Z_t - \hat{Z}_t)^T (Z_t - \hat{Z}_t) \geq 0 \quad (3.65)$$

the time difference of which is equal to :

$$W_{t+1} - W_t = \{TD_t(TD_t - 2)\}(Z_t - \hat{Z}_t)^T (Z_t - \hat{Z}_t) \quad (3.66)$$

which is nonpositive definite, decrescent as long as inequality (3.64) holds.

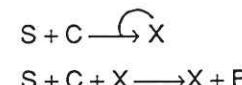
Matrix inversion and conditioning

The implementation of the asymptotic observer (3.31) requires the inversion of yield coefficient matrices in the computation of A_0 and A_2^+ . It is well known that, if the matrices to be inverted are ill-conditioned, the algorithm is extremely sensitive to any numerical error and its performance will be dramatically

degraded. The conditioning of a matrix is evaluated by the condition number. Ill-conditioning is characteristic of nearly singular matrices, i.e. matrices with one (or more) row (or columns) which are an almost exact linear combination of some of the other rows (or columns).

This is typical of reaction networks in which one reaction is almost indistinguishable from some of the others, or in which some components appear almost proportionally. The extreme situation is exact proportionality, which has been illustrated in the PHB example (Section 3.3.4).

As an illustration of matrix conditioning and condition number, let us consider the following reaction network :



The matrix K and the component vector ξ are defined as follows :

$$K = \begin{bmatrix} -k_1 & -k_2 \\ -k_3 & -k_4 \\ 1 & 0 \\ 0 & 1 \end{bmatrix} \quad \xi = \begin{bmatrix} S \\ C \\ X \\ P \end{bmatrix}$$

Let us choose a state partition (ξ_a, ξ_b) . As has already been pointed out, this choice is arbitrary. It is then usually possible, in the absence of any constraint, to select a state partition for which the matrix K_a is (almost) diagonal with "1" on the diagonal and for which inversion is easy. Here, if we choose $\xi_a = [X \ P]^T$ and $\xi_b = [S \ C]^T$, then

$$K_a = I$$

and it follows that A_0 is simply equal to $-K_b$:

$$A_0 = -K_b K_a^{-1} = -K_b$$

Assume now that the objective is to estimate X and P from the measurements of S and C. The implementation of the asymptotic observer (3.31) requires the inversion of A_2 :

$$A_2 = \begin{bmatrix} -k_1 & -k_2 \\ -k_3 & -k_4 \end{bmatrix}$$

The computation of A_2 is possible only if A_2 is of full rank, i.e. if its columns (or its rows) are linearly independent. Assume that A_2 is symmetric ($k_2 = k_3$) and that the yield coefficients k_1, k_2, k_3 and k_4 are such that they can be expressed as follows :

$$(k_1, k_3) = a(k_2, k_4 + b)$$

with $a \in \mathbb{R}$ and b a small positive real number. A_2 will be invertible as long as b is different from zero. However its condition number is highly dependent on b . In fact, due to the symmetry of A_2 , the condition number is simply the ratio of the maximum and minimum norm of the eigenvalues of A_2 :

$$CN(A_2) = \frac{\max |\lambda(A_2)|}{\min |\lambda(A_2)|}$$

The condition number is an expression of the propagation of numerical errors (arising from roundoff or experimental data for instance) from $\hat{Z}-A_1\xi_1$ to ξ_2 . It can be shown that, in our example, a relative error on $\hat{Z}-A_1\xi_1$, $\|\delta(\hat{Z}-A_1\xi_1)\|/\|\hat{Z}-A_1\xi_1\|$, will give a relative error on ξ_2 , $\|\delta\xi_2\|/\|\xi_2\|$, which is related to the preceding one by the condition number $CN(A_2)$ as follows :

$$\frac{\|\delta\xi_2\|}{\|\xi_2\|} \leq CN(A_2) \frac{\|\delta(\hat{Z}-A_1\xi_1)\|}{\|\hat{Z}-A_1\xi_1\|}$$

In our example, the condition number of A_2 is approximately equal to :

$$CN(A_2) = \frac{(k_1+k_4)^2}{2k_1b}$$

The performances of the estimation algorithm will fall off as b becomes smaller.

If, for instance, $k_1 = k_2 = k_3 = 1$ and $k_4 = 1.01$ (i.e. $a = 1$ and $b = 0.01$), the condition number $CN(A_2)$ is equal to :

$$CN(A_2) = 200$$

and any numerical error in $\hat{Z}-A_1\xi_1$ might propagate in ξ_2 with a factor equal to 200!

Further illustration of degraded performances of the estimation algorithm (3.31) in the presence of ill-conditioned matrices can be found in the references.

In order to avoid the degradation of the estimation performances in the presence of ill-conditioned matrices, it is clear that the estimation algorithm must be modified. In general, one possible solution consists in rearranging the reaction network. This may eventually lead to the suppression of some reactions which are almost redundant and can hardly be distinguished from the others. Or, as in the PHB process, the rearrangement can take advantage of additional a priori information and the practical operation of the process. As shown in the different examples of Section 3.3, there usually exists a state partition for which K_a is (almost) diagonal with "1" on the diagonal. We may therefore expect that the eigenvalues will be equal, or close, to 1, and the condition number for the inversion of K_a will then be small. However, if the ill-conditioning affects the matrix A_2 , a solution may be to look for other on-line measurements if available, so as to improve the conditioning of the inversion of A_2 .

3.4. On-line Estimation of Reaction Rates

So far in this chapter, we have dealt with the *state estimation* problem in bioreactors. In Section 3.3, this problem was considered in the case where the reaction rates $\phi(\xi)$ are unknown. In this section, we address the complementary question, namely the problem of estimating the reaction rates from on-line knowledge of the state variables (either from measurements or by means of asymptotic observers).

3.4.1. Statement of the estimation problem

We consider a biotechnological process described by the general state space model (1.43) :

$$\frac{d\xi}{dt} = K\phi(\xi) - D\xi - Q + F \quad (1.43) = (3.67)$$

We assume that :

- a) The yield coefficients (matrix K) are known.
- b) The dilution rate D , the feed rates F and the gaseous outflow rates Q are measured on-line.
- c) The vector of state variables ξ is known on-line either by measurement or by estimation via the asymptotic observer of Section 3.3.

We assume that the vector $\phi(\xi)$ of reaction rates is partially unknown and written as follows :

$$\phi(\xi) = H(\xi)\rho(\xi) \quad (2.13) = (3.68)$$

where $H(\xi)$ is an $M \times r$ matrix of *known* functions of the state and $\rho(\xi)$ a vector of *unknown* functions of ξ , with $\dim \rho(\xi) = r$.

Several examples of this representation of $\phi(\xi)$ have been given in Chapter 2. With this definition, the process dynamics (3.67) are rewritten :

$$\frac{d\xi}{dt} = KH(\xi)\rho(\xi) - D\xi - Q + F \quad (2.24) = (3.69)$$

We are concerned with the problem of estimating $\rho(\xi)$ from the on-line knowledge of D , F , Q and ξ .

Two different solutions to this problem are presented. The first one (Section 3.4.2) is called an *observer-based estimator* because it is based on the use of a variant of the state observers described in Section 3.1. The second one (Section 3.4.3) is based on a reformulation of the process model in a linear regression form.

3.4.2. An observer-based estimator

The basic idea is to use a state observer, not to estimate the state (since it is known) but to provide on-line information for the updating of the estimate of $\rho(\xi)$.

The estimation algorithm is as follows :

Observer-based estimator

$$\frac{d\xi}{dt} = KH(\xi)\hat{\rho}(t) - D\xi - Q + F - \Omega(\xi - \hat{\xi}) \quad (3.70.a)$$

$$\frac{d\hat{\rho}}{dt} = [KH(\xi)]^T \Gamma(\xi - \hat{\xi}) \quad (3.70.b)$$

where $\hat{\rho}$ denotes the on-line estimate of $\rho(\xi)$.

An intuitive justification for this algorithm is as follows. Equation (3.70.a) is clearly similar to the general state observer (3.2) but with three decisive modifications:

- The square matrix Ω may be dependent on ξ but must be stable for all $\xi(t)$.
- The actual value of the state ξ is used in the right hand side of the equation (terms $H(\xi)$ and $D\xi$).
- The actual value of $p(\xi)$, which is unknown, is replaced by an estimate \hat{p} which is updated by the second equation (3.70.b).

Γ is the gain matrix of the updating law (3.70.b); it must be chosen such that the matrix $\Omega^T\Gamma + \Gamma\Omega$ is negative definite.

This updating law (3.70.b) is in turn driven by the deviation $(\xi - \hat{\xi})$ which is supposed to reflect the mismatch between $\hat{p}(t)$ and $p(\xi)$.

Tuning the estimator

The matrices Ω and Γ are design parameters at the disposal of the user for the control of the stability and the tracking properties of the algorithm. A common choice is to take :

$$\Omega = \text{diag} \{ -\omega_i \}_{i=1,\dots,N} \quad \Gamma = \text{diag} \{ \gamma_j \}_{j=1,\dots,r} \quad \omega_i, \gamma_j \in \mathbb{R}^+ \quad (3.71)$$

With this choice, the condition on $\Omega^T\Gamma + \Gamma\Omega$ is automatically verified. In such a case the tuning of the estimator reduces to the calibration (by trial and error) of the $N + r$ scalar constants ω_i and γ_j . This issue will be further discussed and illustrated with the examples of Sections 3.4.5. and 3.4.7.

Analysis

Define the observation error e and the tracking error \tilde{p} as follows :

$$e = \xi - \hat{\xi} \quad \tilde{p} = p(\xi) - \hat{p} \quad (3.72)$$

Their dynamics are easily shown to be governed by the following linear time-varying system (obtained by subtracting (3.70.a) from (3.67)) :

$$\frac{d}{dt} \begin{bmatrix} e \\ \tilde{p} \end{bmatrix} = A(\xi) \begin{bmatrix} e \\ \tilde{p} \end{bmatrix} + v \quad (3.73.a)$$

with

$$A(\xi) = \begin{bmatrix} \Omega & KH(\xi) \\ -H^T(\xi)K^T\Gamma & 0 \end{bmatrix} \quad v = \begin{bmatrix} 0 & \frac{dp}{dt} \end{bmatrix}^T \quad (3.73.b)$$

Suppose that the assumptions of Section 1.9.1 hold, that Ω is constant with all its eigenvalues having strictly real parts, and that $p(\xi)$ is a differentiable function of ξ . Then it is a standard result of adaptive system theory that the error system (3.73) is stable if the matrix $KH(\xi)$ is persistently exciting, which is easily established from Theorem A2.6 (Appendix 2) and Theorem A3.2 (Appendix 3).

Numerical implementation

The numerical implementation of the estimator requires a discrete-time formulation. A forward Euler discretization of the continuous-time algorithm (3.70) gives :

Discrete-time observer-based estimator

$$\hat{\xi}_{t+1} = \hat{\xi}_t + T [KH(\xi_t)\hat{p}_t - D\xi_t - Q_t + F_t - \Omega(\xi_t - \hat{\xi}_t)] \quad (3.74.a)$$

$$\hat{p}_{t+1} = \hat{p}_t + T [KH(\xi_t)]^T \Gamma(\xi_t - \hat{\xi}_t) \quad (3.74.b)$$

where T denotes the sampling period.

As for the numerical implementation of asymptotic observers (Section 3.3), the switch from the continuous-time observer-based estimator (3.70) to the discrete-time version sets specific stability questions in which the sampling period T , the design parameters Ω and Γ and the regressor $KH(\xi_t)$ play an important role. This will be illustrated at the end of Section 3.4.5 with a simple example.

Remark

The observer-based estimator (3.70) and its discrete-time counterpart (3.74) are based on the full dynamical model of the process. In practice, however, this is not always necessary. It is often sufficient to select a subset of the state equations, provided they involve all the parameters $p(\xi)$ which need to be estimated.

In such a case, the entire theory presented in this chapter holds "mutatis mutandis". For instance, if we denote by ξ_S the selected part of the state and by (K_S, Q_S, F_S) the corresponding parts of (K, Q, F) , the observer-based estimator (3.70) is rewritten :

$$\frac{d\hat{\xi}_S}{dt} = K_S H(\xi) \hat{p}(t) - D\xi_S - Q_S + F_S - \Omega(\xi_S - \hat{\xi}_S) \quad (3.75.a)$$

$$\frac{d\hat{p}}{dt} = [K_S H(\xi)]^T \Gamma(\xi_S - \hat{\xi}_S) \quad (3.75.b)$$

This will be illustrated many times throughout the book, namely in the experimental applications of Sections 3.4.8 and 3.4.9.

3.4.3. A linear regression estimator

We present an alternative estimator of $p(\xi)$ based on a model reformulation in terms of linear regression.

Model reformulation

The solution of the differential equation (3.69) which describes the process dynamics can be shown to be written as follows :

$$\xi = \psi^T p + \psi_0 + \varepsilon$$

ψ , ψ_0 and ε are the outputs of the following linear filters :

$$\frac{d\psi^T}{dt} = \Omega\psi^T + KH(\xi) \quad (3.76.a)$$

$$\frac{d\psi_0}{dt} = \Omega\psi_0 - (\Omega + DI_N)\xi - Q + F \quad (3.76.b)$$

$$\frac{d\varepsilon}{dt} = \Omega\varepsilon - \psi^T \frac{dp}{dt} \quad (3.77)$$

with Ω an arbitrary stable symmetric matrix.

Introduce the notation :

$$y \stackrel{\Delta}{=} \xi - \psi_0 \quad (3.78)$$

It is then obvious that the process dynamics (3.69) are described by the following linear regression model :

$$y = \psi^T p + \varepsilon \quad (3.79)$$

where y is the output, ψ is the regressor, p is the unknown parameter to be estimated and ε is interpreted as an unknown additive disturbance.

Note that the output y and the regressor ψ can be calculated on-line from the available data (ξ, D, Q, F) with the aid of the filtering equations (3.76). The important point is that the linear regression model (3.79) allows us to use a standard least squares algorithm for the estimation of $p(\xi)$.

The least squares estimator

The principle of least squares estimation is the computation of the on-line estimate $\hat{p}(t)$ which minimises the following quadratic criterion :

$$J(\hat{p}) = \int_0^t e^{\lambda(t-\tau)} \| (y - \psi^T \hat{p}) \|^2 d\tau \quad (3.80)$$

where the parameter λ is called the *forgetting factor*.

The algorithm for the on-line computation of \hat{p} , involving the computation of ψ and ψ_0 via (3.76), is as follows :

Least squares estimator

$$\frac{d\psi^T}{dt} = \Omega\psi^T + KH(\xi) \quad (3.81.a)$$

$$\frac{d\psi_0}{dt} = \Omega\psi_0 - (\Omega + DI_N) \xi - Q + F \quad (3.81.b)$$

$$\frac{d\hat{p}}{dt} = \Gamma\psi(\xi - \psi_0 - \psi^T \hat{p}) \quad (3.81.c)$$

$$\frac{d\Gamma}{dt} = -\Gamma\psi\psi^T\Gamma + \lambda\Gamma \quad \Gamma(0) > 0 \quad (3.81.d)$$

Tuning the estimator

The matrix Ω and the forgetting factor λ are design parameters at the disposal of the user for the control of the stability and the tracking properties of the estimator.

The matrix Ω is commonly chosen as follows :

$$\Omega = \text{diag}_{i=1,\dots,N} \{-\omega_i\} \quad \omega_i \in \mathbb{R}^+ \quad (3.82)$$

Hence, as for the observer-based estimator, the tuning of the estimator reduces to the calibration (by trial and error) of the $n + 1$ scalar constants ω_i and λ .

Analysis

We define the tracking error \tilde{p} :

$$\tilde{p} = p(\xi) - \hat{p} \quad (3.83)$$

Then, from (3.77) and (3.81.c), the dynamics of the estimator are easily shown to be governed by the following linear time-varying system :

$$\frac{d}{dt} \begin{bmatrix} \varepsilon \\ \tilde{p} \end{bmatrix} = A(\xi) \begin{bmatrix} \varepsilon \\ \tilde{p} \end{bmatrix} + v \quad (3.84.a)$$

with :

$$A(\xi) = \begin{bmatrix} \Omega & 0 \\ -\Gamma\psi & -\Gamma\psi\psi^T \end{bmatrix} \quad v = [-\psi^T \ 1]^T \frac{dp}{dt} \quad (3.84.b)$$

Suppose that the assumptions of Section 1.9.1 hold, that Ω is constant and stable and that $p(\xi)$ is a differentiable function of ξ . It is a standard result of adaptive systems theory that the system (3.84) is stable if the matrix ψ is persistently exciting (from Theorem A2.6 (Appendix 2) and Theorem A3.1 (Appendix 3)).

Numerical implementation

The numerical implementation of the estimator (3.81) requires a discrete-time formulation. Euler discretization of the filters (3.81.a-b) which provide ψ and ψ_0 gives :

$$\psi_{t+1}^T = (I_N + \Omega T) \psi_t^T + T K H(\xi_t) \quad (3.85.a)$$

$$\psi_{0,t+1} = (I_N + \Omega T) \psi_{0,t} + T [(\Omega - D I_N) \xi_t - Q_t + F_t] \quad (3.85.b)$$

Moreover, the discrete-time least squares algorithm for the linear regression model (3.79) is written :

$$\hat{p}_{t+1} = \hat{p}_t + T \Gamma_t \psi_{t+1}^T [\xi_{t+1} - \psi_{0,t+1} - \psi_{t+1}^T \hat{p}_t] \quad (3.85.c)$$

$$\Gamma_{t+1} = \frac{\Gamma_t}{\lambda} [I - T^2 \psi_{t+1} \{ \lambda I + T^2 \psi_{t+1}^T \Gamma_t \psi_{t+1} \}^{-1} \psi_{t+1}^T \Gamma_t] \quad (3.85.d)$$

An interesting special case occurs when the matrix Ω is chosen as :

$$\Omega = - (T)^{-1} I_N \quad (3.86)$$

Indeed, in that case, the discrete-time algorithm reduces to :

Discrete-time least square estimator

$$\hat{p}_{t+1} = \hat{p}_t + T \Gamma_t K H(\xi_t) \{ \xi_{t+1} - \xi_t - T [K H(\xi_t) \hat{p}_t - D \xi_t - Q_t + F_t] \} \quad (3.87.a)$$

$$\Gamma_{t+1} = \frac{\Gamma_t}{\lambda} [I - T^2 H^T(\xi_t) K^T \{ \lambda I + T^2 K H(\xi_t) \Gamma_t H^T(\xi_t) K^T \}^{-1} K H(\xi_t) \Gamma_t] \quad (3.87.b)$$

This algorithm (3.87) is simply the recursive least squares algorithm obtained by applying a linear regression technique to the first order Euler discretized counterpart of the model equation (3.67).

As for the observer-based estimator, the influence of the sampling period T , of the design parameters Γ_t and λ , and of the regressor $K H(\xi_t)$ on the stability of the discrete-time least square estimator (3.87) will be illustrated in Section 3.4.5 with a simple example.

3.4.4. An example of convergence analysis

The stability and convergence properties of the estimators presented in the previous sections are closely related to so-called "persistence of excitation"

conditions (see Appendix 3). In this section we illustrate, with a particular example, how the full analysis can be carried out.

We consider the situation in which the reaction rates $\phi_j(\xi)$ are described by the multilinear model motivated in Section 1.5.2:

$$\phi_j(\xi) = \alpha_j \left[\prod_{n-j} \xi_n \right] \quad (1.47.a) = (3.88)$$

Here ξ_n denotes the *reactants* involved in the reaction with index j and α_j is the "specific reaction rate".

With this definition, the state space model of the process is written (equation (1.49)) :

$$\frac{d\xi}{dt} = KG(\xi)\alpha - D\xi + F - Q \quad (1.49) = (3.89.a)$$

with $G(\xi)$ being a diagonal matrix (equation (1.48.b)) :

$$G(\xi) = \text{diag} \left\{ \prod_{n-j} \xi_n \right\} \quad (1.48.b) = (3.89.b)$$

Several examples of this way of modelling were given in Section 1.6.

The reactor is supposed to be operating under assumptions A1 to A4 (Section 1.9.1) which guarantee the global input-output stability of the process, and in particular that the state variables have upper bounds (see Corollary 1.2) :

$$\xi_i(t) \leq r \frac{F_{\max}}{D_{\min}} \quad \forall i, \forall t \quad (3.90)$$

In addition, it is assumed that :

A5. The experimental conditions are such that the state variables are bounded away from zero :

$$0 < \xi_{\min} \leq \xi_i(t) \quad \forall i, \forall t \quad (3.91)$$

A6. The specific reaction rates α_j ($j=1, \dots, M$) are constant parameters.

A7. The matrix K of yield coefficients is full rank.

We address the problem of the on-line estimation of parameters α_j from the on-line knowledge of D, F, Q, ξ . We note that this estimation problem is stated in the format of Section 3.4.1 with the definitions :

$$H(\xi) = G(\xi) \quad p(\xi) = \alpha \quad (3.92)$$

We suppose that the linear regression estimator (3.81) is used for the estimation of α . In this particular case, the estimator is written as follows :

$$\frac{d\psi^T}{dt} = -\omega\psi^T + KG(\xi) \quad (3.93.a)$$

$$\frac{d\psi_0}{dt} = -\omega\psi_0 + (\omega - D)\xi - Q + F \quad (3.93.b)$$

$$\frac{d\hat{\alpha}}{dt} = \Gamma\psi (\xi - \psi_0 - \psi^T\hat{\alpha}) \quad (3.93.c)$$

$$\frac{d\Gamma}{dt} = -\Gamma\psi\psi^T\Gamma \quad \Gamma(0) > 0 \quad (3.93.d)$$

Note that we have chosen a scalar parametrization of the filters (parameter ω) and a zero forgetting factor ($\lambda = 0$) because the α_j are constant.

The convergence of this algorithm is established in the following theorem.

Theorem 3.2 : Under Assumptions A1 to A7,

$$\lim_{t \rightarrow \infty} \hat{\alpha}(t) = \alpha \quad (3.94)$$

Proof : The proof proceeds in 2 steps.

Step 1 : We establish that ψ is persistently exciting (Appendix 3).

It follows from Theorem 1.1 and Assumption A5 that the diagonal matrix $G(\xi)$ is positive definite for all t . This, in turn, implies from Assumption A7 that the matrix $G(\xi)K^T K G(\xi)$ is also positive definite, and hence that $K G(\xi)$ is persistently exciting (see Definition A3.1, Appendix 3). Since the filter (3.93.a) is state reachable, then ψ is persistently exciting (Theorem A.3.4, Appendix 3).

Step 2 : We define :

$$\varepsilon = \xi - \psi^T \tilde{\alpha} \quad \text{and} \quad \tilde{\alpha} = \alpha - \hat{\alpha} \quad (3.95)$$

It is easily shown that these quantities are governed by the following dynamics:

$$\frac{d}{dt} \begin{bmatrix} \varepsilon \\ \tilde{\alpha} \end{bmatrix} = \begin{bmatrix} -\omega I & 0 \\ -\Gamma \psi & -\Gamma \psi \psi^T \end{bmatrix} \begin{bmatrix} \varepsilon \\ \tilde{\alpha} \end{bmatrix} \quad (3.96)$$

The theorem follows immediately from step 1 (Theorem A3.1, Appendix 3).

Q.E.D

3.4.5. Case study : Estimation of microbial specific growth rates

In Sections 3.3.1 to 3.3.3, we presented a general theory for the estimation of reaction rates. In this section, the theory is extensively studied through a

simple application : the on-line estimation of the microbial growth rate in a simple biological culture which involves a single biomass growing on a single substrate and yielding a single product. This case study is carried out for two main reasons. First, the issue of tracking microbial growth rates, even in simple processes, is clearly a relevant problem by itself in many biotechnological applications. Secondly, the case study will serve to show the power of the theory and to illustrate its main features and variants, while keeping the mathematical derivations as simple as possible.

Process definition

We consider a process characterised by the following reaction scheme :



where S is the substrate, X the biomass and P a gasifiable synthesis product. The process dynamics are as follows :

$$\frac{d}{dt} \begin{bmatrix} X \\ S \\ P \end{bmatrix} = \begin{bmatrix} 1 \\ -k_1 \\ k_2 \end{bmatrix} \varphi - D \begin{bmatrix} X \\ S \\ P \end{bmatrix} + \begin{bmatrix} 0 \\ F_1 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ Q \end{bmatrix} \quad (3.98)$$

where F_1 is the substrate feed rate and Q is the gaseous outflow rate.

According to the usual approach in fermentation modelling, the reaction rate is assumed to be described as follows (see Section 1.5.3) :

$$\varphi = \mu(X, S, P)X \quad (3.99)$$

where $\mu(X, S, P)$ is termed "specific growth rate".

We note that φ is in the format of Section 3.4.1 with :

$$H(\xi) \stackrel{\Delta}{=} X \quad \text{and} \quad p(\xi) = \mu(X, S, P) \quad (3.100)$$

The problem is the on-line estimation of the time-varying specific growth rate μ .

Using the observer-based estimator

In this particular case, the observer-based parameter estimator (3.70) specialises as follows :

$$\frac{d\hat{X}}{dt} = \hat{\mu}X - DX + \omega_1(X - \hat{X}) \quad (3.101.a)$$

$$\frac{d\hat{S}}{dt} = -k_1\hat{\mu}X - DS + F + \omega_2(S - \hat{S}) \quad (3.101.b)$$

$$\frac{d\hat{P}}{dt} = k_2\hat{\mu}X - DP - Q + \omega_3(P - \hat{P}) \quad (3.101.c)$$

$$\frac{d\hat{\mu}}{dt} = \gamma_1 X(X - \hat{X}) - \gamma_2 k_1 X(S - \hat{S}) + \gamma_3 k_2 X(P - \hat{P}) \quad (3.101.d)$$

We remark that the design matrices have been chosen diagonal :

$$\Omega = \text{diag}\{-\omega_i\} \quad \Gamma = \text{diag}\{\gamma_i\} \quad (3.102)$$

The implementation of the estimator (3.101) requires full state measurement (X, S, P) as well as measurement of F and Q . Various alternatives, however, are possible in the case of incomplete measurements.

Incomplete state measurements

We know from Section 3.2 that only one state measurement is actually needed to design an asymptotic observer able to reconstruct the process state,

independently of the specific growth rate μ . In the case of incomplete state measurement, the solution is obviously to use this asymptotic observer to compute on-line estimates to replace the missing states in the algorithm (3.101). This is illustrated by an example.

Suppose the product concentration P is the only measurable state variable. Then, applying the theory of Section 3.2, we define the auxiliary variables :

$$Z_1 = X - \frac{1}{k_2} P \quad Z_2 = S + \frac{k_1}{k_2} P \quad (3.103)$$

for which we have the following asymptotic observer :

$$\frac{d\hat{Z}_1}{dt} = -D\hat{Z}_1 + \frac{1}{k_2} Q \quad (3.104.a)$$

$$\frac{d\hat{Z}_2}{dt} = -D\hat{Z}_2 + F \quad (3.104.b)$$

$$X_0 = \hat{Z}_1 + \frac{1}{k_2} P \quad (3.104.c)$$

$$S_0 = \hat{Z}_2 - \frac{k_1}{k_2} P \quad (3.104.d)$$

The "observed" states X_0 and S_0 provided by this observer are then used, in the algorithm (3.101), in place of the "true but unknown" states X and S .

A reduced order parameter estimator

If the substrate feed rate F or the gaseous outflow rate Q (or both) are not accessible on-line, it is nevertheless possible to derive an efficient estimator of

μ provided the biomass X is measured on-line. The solution is simply to drop, from the estimator, equation (3.101.b) which contains F or (and) equation (3.101.c) which contains Q , and to set γ_2 or (and) γ_3 to zero in the updating equation (3.102.d). In such a case, the observer-based estimator reduces to :

$$\frac{d\hat{X}}{dt} = \hat{\mu}X - DX + \omega(X - \hat{X}) \quad (3.105.a)$$

$$\frac{d\hat{\mu}}{dt} = \gamma X(X - \hat{X}) \quad (3.105.b)$$

Stability analysis of the reduced order estimator

The structural simplicity of the reduced order estimator (3.105) allows one to perform a full stability analysis with a moderate mathematical effort. The analysis will be carried out under the following assumptions :

- H1. The biomass data, denoted $X_m(t)$, are corrupted by an additive measurement noise $\varepsilon(t)$:

$$X_m(t) = X(t) + \varepsilon(t) \quad (3.106)$$

- H2. $X_m(t)$ is strictly positive for all t :

$$X_m(t) \geq \eta > 0 \quad (3.107)$$

- H3. The specific growth rate $\mu(t)$ is time-varying and bounded :

$$0 \leq \mu(t) = \hat{\mu}(X, S, P) \leq \mu^* \quad \forall t \quad (3.108)$$

- H4. The time derivative of the specific growth rate is bounded :

$$|\frac{d\mu}{dt}| < M_1 \quad \forall t \quad (3.109)$$

- H5. The measurement noise is bounded :

$$|\varepsilon(t)| < M_2 \quad \forall t \quad (3.110)$$

- H6. The dilution rate is bounded :

$$0 \leq D(t) \leq D_{\max} \quad \forall t \quad (3.111)$$

- H7. The substrate feed rate is expressed as (see Section 1.5.5) :

$$F_1 = DS_{in} \quad (3.112)$$

where S_{in} is the influent substrate concentration, assumed to be bounded for all t :

$$0 \leq S_{in}(t) \leq S_{\max} \quad (3.113)$$

- H8. The design parameter ω is chosen to be proportional to the biomass measurement :

$$\omega = \sigma \hat{X}_m \quad (3.114)$$

Under these assumptions the parameter estimator (3.105) is rewritten as follows :

$$\frac{d\hat{X}}{dt} = [\hat{\mu} - D + \sigma(X_m - \hat{X})] X_m \quad (3.115.a)$$

$$\frac{d\hat{\mu}}{dt} = \gamma X_m (X_m - \hat{X}) \quad (3.115.b)$$

If we define the errors $\tilde{X} = X - \hat{X}$ and $\tilde{\mu} = \mu - \hat{\mu}$, the following error system derives from (3.115) :

$$\frac{dx}{dt} = X_m Ax + v \quad (3.116)$$

with

$$x = \begin{bmatrix} \tilde{X} \\ \tilde{\mu} \end{bmatrix} \quad A = \begin{bmatrix} -\sigma & 1 \\ -\gamma & 0 \end{bmatrix}$$

$$v = \begin{bmatrix} (D - \mu - \sigma X_m)\varepsilon \\ -\gamma X_m \varepsilon + \frac{d\mu}{dt} \end{bmatrix}$$

Let v_1 and v_2 be the eigenvalues of A related (by definition) to σ and γ as follows :

$$\sigma = -(v_1 + v_2) \quad \gamma = v_1 v_2 \quad (3.117)$$

Assume that :

H9. The design parameters σ and γ are chosen such that A has real distinct eigenvalues : $v_2 < v_1 < 0$ (i.e $\gamma < \sigma^2/4$).

We have the following stability result.

Theorem 3.3. : Under assumptions H1 to H9, the estimation errors \tilde{X} and $\tilde{\mu}$ are bounded for all t and asymptotically bounded as follows :

$$\limsup_{t \rightarrow \infty} |\tilde{X}(t)| \leq \frac{1}{\eta} \left\{ \frac{M_1}{\gamma} + M_2^2 + \frac{S_{\max} M_2}{k_1} + \frac{2\beta_1 \delta M_2}{\sqrt{\sigma^2 - 4\gamma}} \right\} \quad (3.118)$$

$$\limsup_{t \rightarrow \infty} |\tilde{\mu}(t)| \leq \frac{1}{\eta} \left\{ \frac{\sigma}{\gamma} M_1 + \beta_1 M_2 + \sigma \left(M_2^2 + \frac{S_{\max} M_2}{k_1} \right) \right\} \quad (3.119)$$

with :

$$\beta_1 \stackrel{\Delta}{=} \max \left(D_{\max}, \mu^* + \sigma \left(\frac{S_{\max}}{k_1} + M_2 \right) \right) \quad (3.120.a)$$

$$\delta \stackrel{\Delta}{=} \left(\frac{v_2}{v_1} \right)^{\left(\frac{v_1}{v_1 - v_2} \right)} - \left(\frac{v_2}{v_1} \right)^{\left(\frac{v_2}{v_1 - v_2} \right)} \quad (3.120.b)$$

Proof : From Assumptions H5 and H7, the measured biomass concentration X_m has an upper bound, as follows from Corollary 1.3 :

$$X_m(t) \leq \frac{S_{\max}}{k_1} + M_2 \quad \forall t \quad (3.121)$$

Moreover, since $X_m(s) \geq \eta > 0$ for all s (Assumption H2), the following change of time scale :

$$dt = X_m(s) ds \quad (3.122)$$

leads to rewriting the system (3.116) as follows :

$$\frac{dx}{dt} = Ax + \frac{v}{X_m} \quad (3.123)$$

From Assumptions H3, H4, H5, H6, H7 and (3.121), the input v/X_m of this system is bounded. Hence, since A is a stable matrix, the state x is also bounded (see Theorem A2.6, Appendix 2) and the first part of the theorem (boundedness of \tilde{X} and $\tilde{\mu}$) follows.

The second part of the theorem follows from the technical Lemma A2.2 (Appendix 2) with the following definitions of B_1 and B_2 :

$$B_1 \stackrel{\Delta}{=} \frac{M_2}{\eta} \max \left\{ D_{\max}, \mu^* + \sigma \left(\frac{S_{\max}}{k_1} + M_2 \right) \right\} \quad (3.124.a)$$

$$B_2 \stackrel{\Delta}{=} \frac{1}{\eta} \left[M_1 + \gamma \left(\frac{S_{max}}{k_1} + M_2 \right) \right] \quad (3.124.b)$$

Q.E.D.

In the case of noise-free measurement of the biomass (i.e. $M_2 = 0$), the asymptotic upper bounds of \tilde{X} and $\tilde{\mu}$ are simplified as follows :

$$\lim_{t \rightarrow \infty} |\tilde{X}(t)| \leq \frac{M_1}{\eta \gamma} \quad (3.125)$$

$$\lim_{t \rightarrow \infty} |\tilde{\mu}(t)| \leq \frac{M_1 \sigma}{\eta \gamma} \quad (3.126)$$

An important consequence of these expressions is that the estimation errors $\tilde{X}(t)$ and $\tilde{\mu}(t)$ can be made asymptotically arbitrarily small, by choosing a sufficiently large design parameter γ . This means that, in the noise free case, a perfect tracking accuracy can be expected although the parameter $\mu(t)$ is time-varying. In practice, however, large values of γ will make the estimation sensitive to measurement noise. The choice of γ is thus a compromise between asymptotic accuracy and sensitivity to noise. The issue is discussed in the next paragraph.

Optimal values of the design parameters σ and γ

The characteristic polynomial of the matrix A (see (3.116)) is written :

$$s^2 + 2\zeta ws + w^2 \quad (3.127)$$

with the natural frequency $w = \sqrt{\gamma}$ and the damping coefficient $\zeta = \sigma/2\sqrt{\gamma}$.

The choice of the design parameters γ and σ is thus equivalent to the choice of ζ and w . A common engineering rule of thumb for the design of second order systems is to fix the damping coefficient ζ close to 1. Once ζ is fixed, optimal

values of σ and γ can be defined, both from the point of view of asymptotic accuracy as well as transient behaviour.

Asymptotic accuracy

The optimal value of σ is defined as the value which minimises the asymptotic upper bound (3.119) on the tracking error $\tilde{\mu}$:

$$\sigma_{opt} = \arg \min_{\sigma} \left\{ \limsup_{t \rightarrow \infty} |\tilde{\mu}| \right\} \quad (3.128)$$

This is easily shown to be :

$$\sigma_{opt} = 2\zeta \sqrt{\frac{k_1 M_1}{k_1 M_2^2 + M_2 S_{max}}} \quad (3.129)$$

The optimal value of γ follows from the definition of ζ :

$$\gamma_{opt} = \frac{\sigma_{opt}^2}{4\zeta^2} \quad (3.130)$$

Transient behaviour

The ingredient for the selection of optimal design parameters is the mean square tracking error over a given period of time :

$$J(\sigma) = \frac{1}{t_2 - t_1} \int_{t_1}^{t_2} |\tilde{\mu}(\tau)|^2 d\tau \quad (3.131)$$

The period of time ($t_2 - t_1$) may, for instance, be the duration of a standard fed-batch operation.

The optimal value of σ is defined as the value which minimises the criterion $J(\sigma)$. The optimal value of γ follows as in the previous case (3.130). The computation of these optimal values is illustrated in the next paragraph.

A simulation experiment

The reduced order estimator (3.115) is simulated under the following conditions.

1°) Figure 3.9 :

- a) The specific growth rate to be estimated is assumed to be a *Monod* growth rate (1.18) :

$$\mu = \frac{\mu^* S}{K_M + S}$$

with $\mu^* = 0.33 \text{ h}^{-1}$ and $K_M = 5 \text{ g/l}$.

- b) The influent substrate concentration is constant ($S_{in} = 5 \text{ g/l}$) but the dilution rate $D(t)$ is a square wave signal (Fig.3.9).

- c) The yield coefficient $k_1 = 2$.

- d) The process state and the estimation algorithm are initialised as follows :

$$X(0) = 2.054 \text{ g/l} \quad S(0) = 0.893 \text{ g/l} \quad \hat{\mu}(0) = 0.06 \text{ h}^{-1}$$

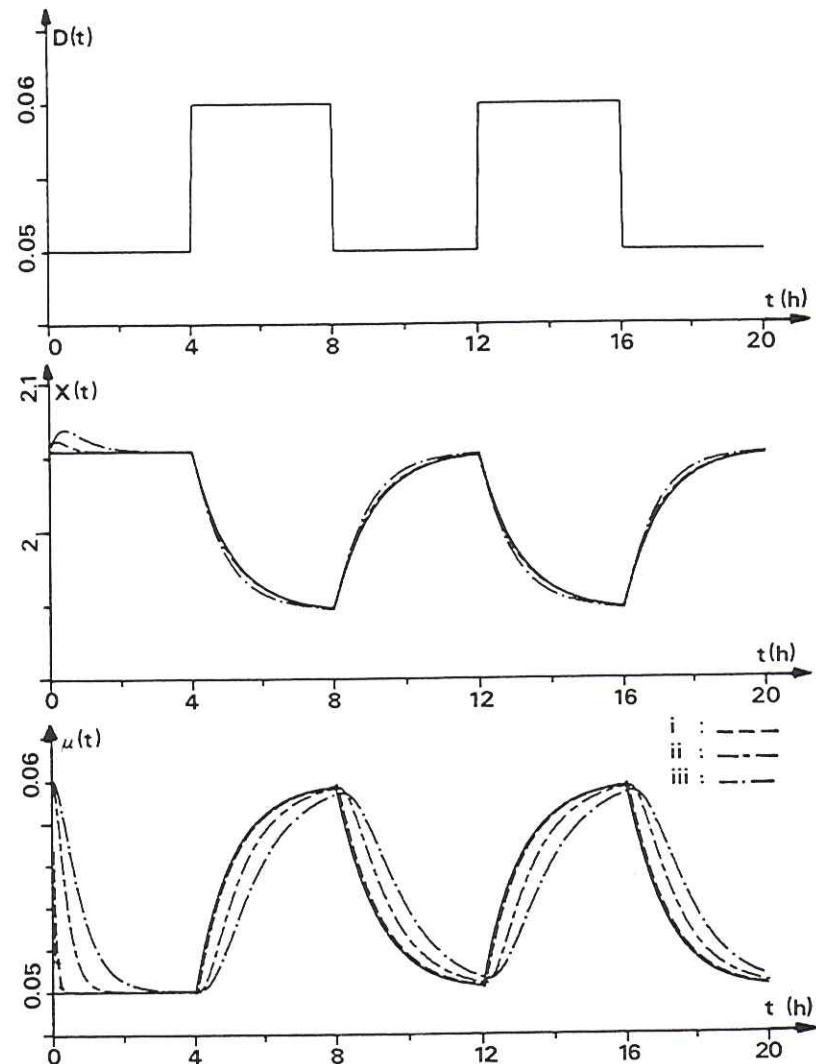


Fig.3.9. On-line estimation of μ from noise-free data of X

e) Three different sets of design parameters are considered :

- (i) $\sigma = 5, \gamma = 6$
- (ii) $\sigma = 1, \gamma = 0.24$
- (iii) $\sigma = 0.5, \gamma = 0.06$

which correspond to decreasing response times.

2°) Figure 3.10 :

a) The specific growth rate to be estimated is assumed to be a *Haldane* growth rate (1.20.a)

$$\mu = \frac{\mu^* S}{K_M + S + S^2/K_I}$$

with $\mu^* = 0.33 \text{ h}^{-1}$, $K_M = 5 \text{ g/l}$, $K_I = 25 \text{ g/l}$

b) The dilution rate is constant, $D = 0.05 \text{ h}^{-1}$, but the influent substrate concentration, $S_{in}(t)$, is a square wave signal (Fig.3.10.a).

c) The yield coefficient $k_1 = 2$.

d) The biomass data are corrupted by a measurement noise with a standard deviation of 0.04 (i.e. about 5% of the biomass mean value).

e) The process state and the estimation algorithm are initialised as follows :

$$X(0) = 2.05 \text{ g/l} \quad S(0) = 0.9 \text{ g/l} \quad \hat{\mu}(0) = 0.06 \text{ h}^{-1}$$

f) The design parameters are set to the following values :

$$\sigma = 1, \gamma = 0.24$$

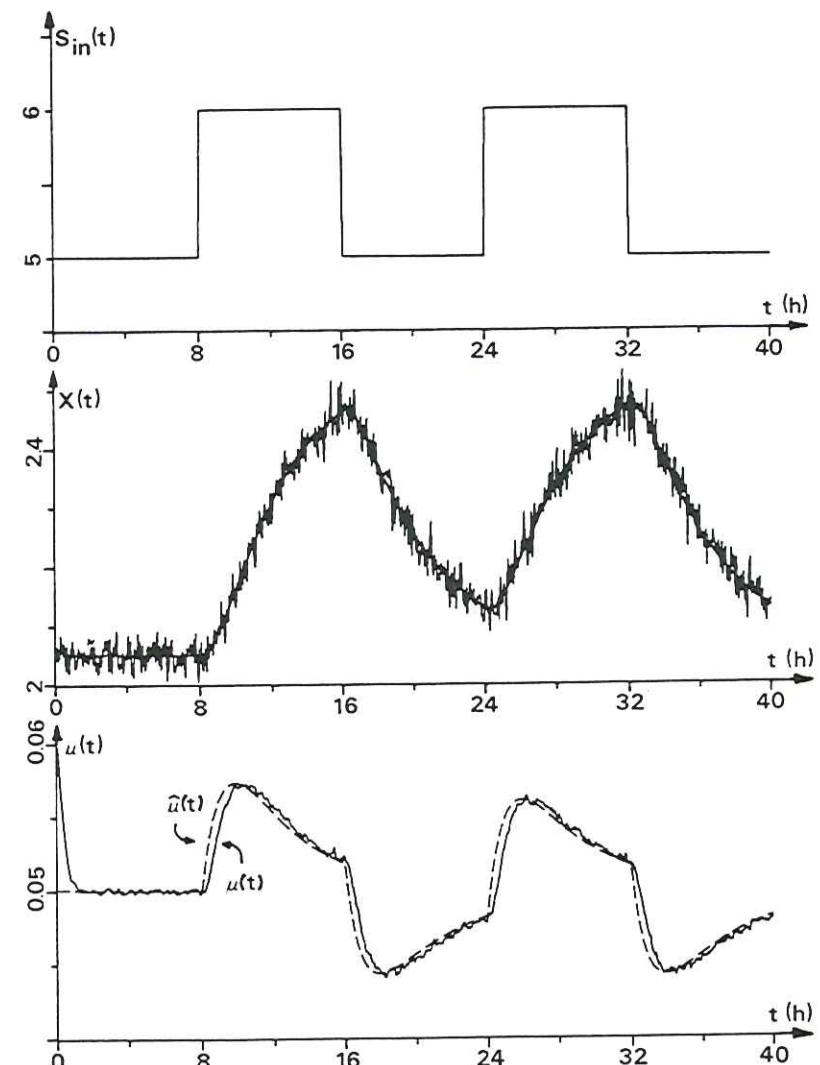


Fig.3.10. On-line estimation of μ from noisy data of X

The behaviour of the process and of the algorithm are shown in Figs.3.9 and 3.10. We note the excellent performance of the estimator, which is indeed able to track the specific growth rate, even in the presence of noisy measurements (Fig.3.10), without any knowledge of the Monod or Haldane structures.

The optimal choice of design parameters is illustrated in Fig.3.11. The criterion (3.131) is drawn with respect to σ for different values of ζ . The figure clearly shows the existence of an optimal value of σ for each ζ . In particular, for $\zeta = 1$, the optimal parameters are :

$$\sigma = 2.25 \quad \gamma = 1.27$$

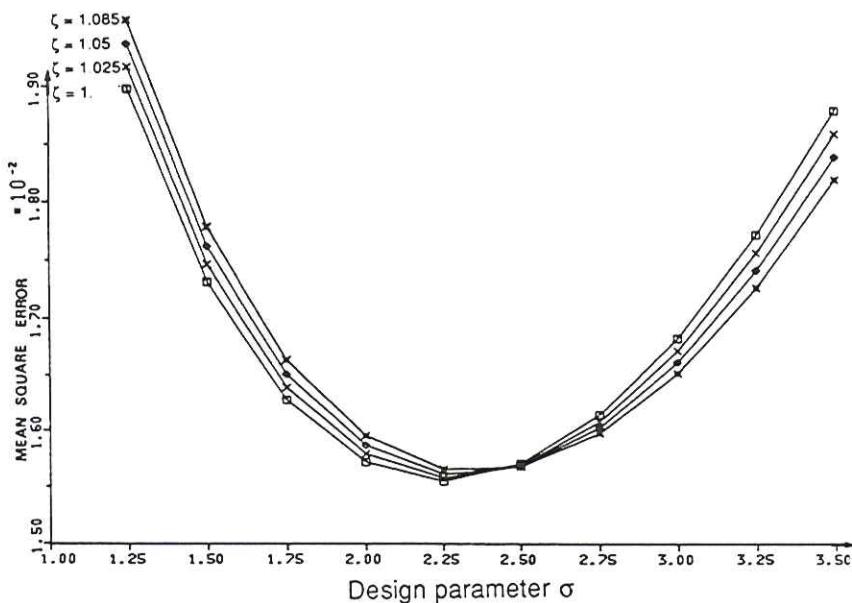


Fig. 3.11. Optimal values of σ for different values of ζ

Numerical implementation

Let us now briefly analyse the stability of the discrete-time versions of the two parameter estimators (observer-based (3.74) and least squares (3.87) algorithms) proposed in this section. For the continuous-time version, the choice of the design parameters is quite free : for instance, with diagonal gain matrices (see (3.71) and (3.82)), the estimators will be stable for any positive value of ω_i and γ_j . However, as for the asymptotic observer (see Section 3.3.5), the stability of the discrete-time version of the estimators depends on additional constraints, in which the sampling period T also plays an important role.

It should be pointed out that, basically, the values of the design parameters must be bounded proportionally to T^{-1} and $|KH(\xi)|^{-1}$ in order to keep the estimators stable.

We illustrate this with the on-line estimation of the specific growth rate from biomass measurements.

1) Let us begin with the observer-based estimator. The discrete-time version of (3.115) is written as follows :

$$\begin{cases} \hat{X}_{t+1} = \hat{X}_t + T\hat{\mu}_t X_t + T\sigma X_t(X_t - \hat{X}_t) \\ \hat{\mu}_{t+1} = \hat{\mu}_t + T\gamma X_t(X_t - \hat{X}_t) \end{cases}$$

Let us write the parameter γ as in Section 3.4.5 :

$$\gamma = \frac{\sigma^2}{4\zeta^2}$$

To simplify the analysis, we shall consider that $\zeta = 1$. The estimator equations are then equal to :

$$\begin{bmatrix} \hat{X}_{t+1} \\ \hat{\mu}_{t+1} \end{bmatrix} = A_t \begin{bmatrix} \hat{X}_t \\ \hat{\mu}_t \end{bmatrix} + b_t$$

with :

$$A_t = \begin{bmatrix} 1 - \sigma T X_t & T X_t \\ -\frac{\sigma^2}{4} T X_t & 1 \end{bmatrix} \quad b_t = T \sigma X_t^2 \begin{bmatrix} 1 \\ \frac{\sigma}{4} \end{bmatrix}$$

The *unforced* system

$$\begin{bmatrix} \hat{X}_{t+1} \\ \hat{\mu}_{t+1} \end{bmatrix} = A_t \begin{bmatrix} \hat{X}_t \\ \hat{\mu}_t \end{bmatrix}$$

is uniformly asymptotically stable if :

$$0 < \eta \leq X_t \leq X_{\max}$$

$$0 < \sigma < \frac{2}{T X_{\max}}$$

Indeed, A_t is bounded and the time difference of the following positive definite, decrescent candidate Lyapunov function W_t :

$$W_t = \sigma^2 \hat{X}_t^2 - 2\sigma \hat{X}_t \hat{\mu}_t + 2\hat{\mu}_t^2 = (\sigma \hat{X}_t - \hat{\mu}_t)^2 + \hat{\mu}_t^2 \geq 0$$

for the unforced system is equal to :

$$W_{t+1} - W_t = -\sigma T X_t \left(\hat{\mu}_t - \frac{3\sigma}{4} \hat{X}_t \right)^2 - \frac{\sigma^3 T X_t}{16} (6 - \sigma T X_t) \hat{X}_t^2$$

It is clearly decrescent and negative definite under the above assumptions. Hence, since b_t is bounded via boundedness of X_t and σ , the estimator is stable.

2) Let us now consider the linear regression estimator. The discrete-time least squares algorithm is written from (3.87) as follows :

$$\hat{\mu}_{t+1} = \hat{\mu}_t + T \gamma_t [X_{t+1} - X_t - T \hat{\mu}_t X_t + T D_t X_t]$$

$$\gamma_{t+1} = \frac{\gamma_t}{\lambda + T^2 X_t^2 \gamma_t}$$

It is easy to verify that $\hat{\mu}_t$ and γ_t will remain bounded under Assumptions H2 and H6 (Section 3.4.5), if λ and γ_0 are chosen as follows :

$$\max \left\{ 0, 1 - 2 \frac{\eta^2}{X_{\max}^2} \right\} < \lambda \leq 1 \quad \gamma_0 \leq \frac{1 - \lambda}{\lambda T^2 \eta^2}$$

Therefore, the values of the design parameters σ and γ_0 must remain even smaller as the sampling period T and the bounds on the regressor X , i.e. η and X_{\max} , are large.

3.4.6. Extended Kalman filtering for on-line estimation of reaction rates

In Section 3.1 we showed how extended Kalman observers can be designed for on-line state estimation when the model structure (and hence the kinetic structure) is fully known. The same technique can be used to solve the dual problem of estimating the reaction rates from full state measurement. This has given rise to numerous studies and applications (see the bibliography).

The basic idea is to consider the unknown parameter p as an additional unknown state of the process. The state space model (3.69) is therefore augmented as follows :

$$\frac{d}{dt} \begin{bmatrix} \xi \\ p \end{bmatrix} = \begin{bmatrix} K H(\xi) p & -D \xi + F - Q \\ w(t) \end{bmatrix} \quad (3.132)$$

where $w(t)$ is a completely unknown time-varying function.

A state observer, analogous to (3.2), is written for that system :

$$\frac{d}{dt} \begin{bmatrix} \hat{\xi} \\ \hat{p} \end{bmatrix} = \begin{bmatrix} KH(\hat{\xi})\hat{p} - D\hat{\xi} + F - Q \\ 0 \\ \Omega_1(\hat{\xi}, \hat{p}) \\ \Omega_2(\hat{\xi}, \hat{p}) \end{bmatrix} \begin{bmatrix} \xi - \hat{\xi} \\ p - \hat{p} \end{bmatrix} \quad (3.133)$$

We note that $w(t)$ is replaced by zero in the observer equation since it is an a priori unknown quantity.

The extended Kalman filtering (EKF) technique is then used to compute the gain matrices Ω_1 and Ω_2 on-line.

The linearised tangent approximation of (3.133) is written (compare with (3.5.a)) :

$$\frac{d}{dt} \begin{bmatrix} \xi - \hat{\xi} \\ p - \hat{p} \end{bmatrix} = \begin{bmatrix} A(\hat{\xi}, \hat{p}) - \Omega_1(\hat{\xi}, \hat{p}) & KH(\hat{\xi}) \\ -\Omega_2(\hat{\xi}, \hat{p}) & 0 \end{bmatrix} \begin{bmatrix} \xi - \hat{\xi} \\ p - \hat{p} \end{bmatrix} \quad (3.134)$$

$$\text{with } A(\hat{\xi}, \hat{p}) = K \left[\frac{\partial [H(\xi)\hat{p}]}{\partial \xi} \right]_{\xi=\hat{\xi}} - DI_N$$

The gain matrices Ω_1 and Ω_2 are computed in order to minimise the following quadratic criterion :

$$J(t) = \int_0^t \left\{ \left(\frac{d\hat{p}^T}{dt}(\tau) \right) \Sigma^{-1} \left(\frac{d\hat{p}}{dt}(\tau) \right) + \| \xi(\tau) - \hat{\xi}(\tau) \|^2 \right\} dt \quad (3.135)$$

under the constraint of the linearised tangent model (3.134)

This criterion is a weighted sum of two terms (weighting matrix Σ^{-1}) : the first term penalises rapid variations of the parameter estimate \hat{p} while the second term penalises excessively large deviations between the actual state value ξ and its estimate $\hat{\xi}$.

The solution of this optimisation is as follows. The time-varying symmetric matrix $R(t)$:

$$R(t) \stackrel{\Delta}{=} \begin{bmatrix} R_{11}(t) & R_{12}(t) \\ R_{12}(t) & R_{22}(t) \end{bmatrix} \quad (3.136)$$

is updated via the following Riccati equation :

$$\frac{dR}{dt} = -RE_0R + RA_0^T(\hat{\xi}, \hat{p}) + A_0(\hat{\xi}, \hat{p})R + \Sigma_0 \quad (3.137.a)$$

where

$$E_0 \stackrel{\Delta}{=} \begin{bmatrix} I_N & 0 \\ 0 & 0 \end{bmatrix} \quad \Sigma_0 \stackrel{\Delta}{=} \begin{bmatrix} 0 & 0 \\ 0 & \Sigma \end{bmatrix} \quad (3.137.b)$$

and $A_0(\hat{\xi}, \hat{p})$ is the coefficient matrix of the system (3.134).

The gains Ω_1 and Ω_2 are given by :

$$\Omega_1(\hat{\xi}, \hat{p}) = R_{11}(t) \quad (3.138.a)$$

$$\Omega_2(\hat{\xi}, \hat{p}) = R_{12}(t) \quad (3.138.b)$$

The EKF estimator thus consists of equations (3.133), (3.137) and (3.138). It appears to have a similar structure to that of the observer-based estimator (3.70). However the computational complexity is increased by the need to solve the Riccati equation (3.137) on-line.

An additional drawback of the EKF approach is that its stability and convergence properties are extremely difficult to analyse and, as far as we know, are still an open problem in the case (which is our concern) of parameter estimation in nonlinear systems. It is well known, however, that an EKF estimator may give biased estimates or may even diverge if it is not

carefully initialised (Ljung, 1979). Therefore, although the EKF estimator may often yields interesting results, there is no a priori guarantee as to its stability. This issue is illustrated with a simple example.

Example : EKF estimation of microbial specific growth rates

Our aim is to compare the EKF estimator with the reduced order observer-based estimator (3.105) for the on-line estimation of microbial specific growth rates in simple cultures. The process is assumed to be described by the equation :

$$\frac{dX}{dt} = \mu X - DX \quad (3.139)$$

Applying the EKF technique to this model yields the following algorithm :

$$\frac{d\hat{X}}{dt} = \hat{\mu}\hat{X} - D\hat{X} + r_{11}(X - \hat{X}) \quad (3.140.a)$$

$$\frac{d\hat{\mu}}{dt} = r_{12}(X - \hat{X}) \quad (3.140.b)$$

$$\frac{dr_{11}}{dt} = 2(\hat{\mu} - D)r_{11} + 2\hat{X}r_{12} - r_{11}^2 \quad (3.140.c)$$

$$\frac{dr_{12}}{dt} = (\hat{\mu} - D)r_{12} + \hat{X}r_{22} - r_{11}r_{12} \quad (3.140.d)$$

$$\frac{dr_{22}}{dt} = -r_{12}^2 + \sigma \quad (3.140.e)$$

where σ denotes the weighting factor of the associated quadratic criterion (3.135) and r_{11}, r_{12}, r_{22} are the entries of the matrix R :

$$R = \begin{bmatrix} r_{11} & r_{12} \\ r_{12} & r_{22} \end{bmatrix} \quad (3.141)$$

It immediately appears that this EKF algorithm is far more complex than the reduced order estimator (3.105).

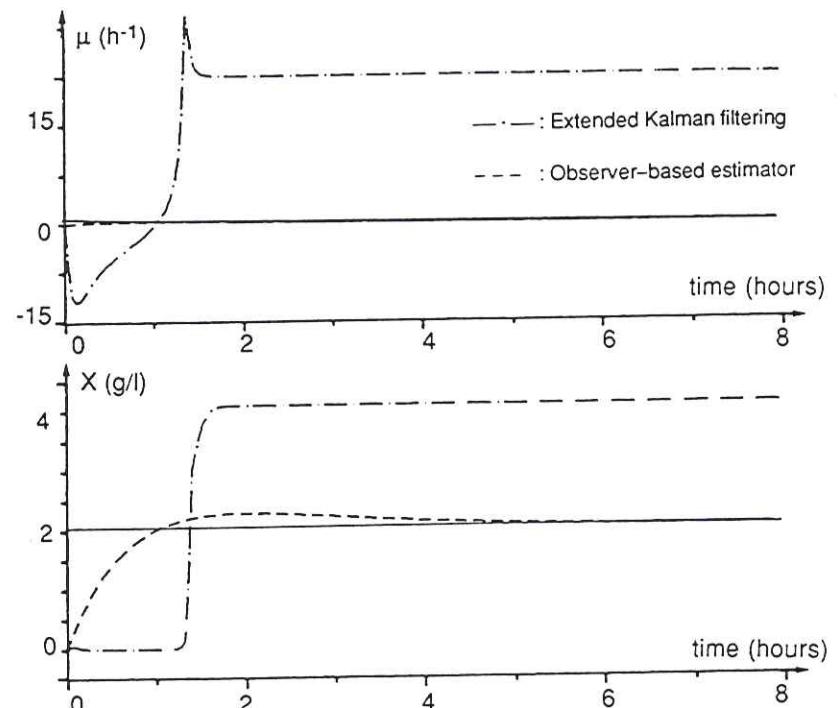


Fig.3.12. Comparison between the EKF and the observer-based estimator

A simulation experiment using this algorithm has been performed with the same process model as in Fig.3.10 and is shown in Fig.3.12. We examine the case in which the process is in a steady state. This implies that μ is constant

and hence $d\mu/dt = 0$. In addition, we assume noise-free measurements of X. Therefore $M_1 = M_2 = 0$ in expression (3.118) and (3.119), and we know from Theorem 3.2 that the estimate $\hat{\mu}(t)$ will converge to its true value with the reduced order estimator (3.105).

Both the reduced order estimator and the EKF estimator are initialised with :

$$\hat{\mu}(0) = 0 \text{ h}^{-1} \quad \hat{X}(0) = 0 \text{ g/l}$$

The design parameters of the reduced order estimator are $\sigma = 1$, $\gamma = 0.24$.

The design parameters of the EKF estimator are :

$$\sigma = 0.01 \quad r_{11}(0) = 1 \quad r_{12}(0) = -99 \quad r_{22}(0) = 10000$$

(with these values, the initial matrix R(0) is positive definite).

The estimation results are shown in Fig. 3.12. With the EKF estimator, the estimate $\hat{\mu}(t)$ converges to a biased value equal to 22 h^{-1} (i.e. a relative error of 4400 %), while with the simple reduced order estimator $\hat{\mu}(t)$ converges, as expected, to its true constant value ($\mu = 0.05 \text{ h}^{-1}$).

3.4.7. Experimental application 1 : Estimation of the specific growth rate in a fed-batch ethanolic fermentation process

In this section, we present an experimental application, on a laboratory pilot scale process, of the parameter estimator (3.101) which has been proposed for the on line estimation of the specific growth rate μ . The process under consideration is a yeast growth process assumed to be characterised by the reaction scheme (1.37). However the reactor is not aerated, so that only the second metabolic path (1.37.b) of the reaction is activated. Hence, the reaction scheme reduces to the following single reaction :



where S, X and P denote, respectively, the glucose, yeast and ethanol concentrations (we ignore, here, the CO_2 production).

We notice that this scheme is identical to (3.97). The dynamics of the process are then given by equations (3.98). We suppose that ethanol is the only component available for on-line measurement. Moreover, the feed rate F and the dilution rate D are known while the gaseous ethanol outflow rate Q is negligible. Therefore we can directly apply a discrete-time version of the estimation scheme (3.101) (3.103) (3.104) for the specific growth rate μ , i.e.:

$$\hat{Z}_{1t+1} = \hat{Z}_{1t} - TD_t \hat{Z}_{1t} \quad (3.142.a)$$

$$\hat{Z}_{2t+1} = \hat{Z}_{2t} - TD_t \hat{Z}_{2t} + TF_t \quad (3.142.b)$$

$$X_{0t+1} = \hat{Z}_{1t+1} + \frac{1}{k_2} P_{t+1} \quad (3.142.c)$$

$$S_{0t+1} = \hat{Z}_{2t+1} - \frac{k_1}{k_2} P_{t+1} \quad (3.142.d)$$

$$\hat{X}_{t+1} = \hat{X}_t + T\hat{\mu}_t X_{0t} - TD_t X_{0t} + \omega_1 T (X_{0t} - \hat{X}_t) \quad (3.142.e)$$

$$\hat{S}_{t+1} = \hat{S}_t - Tk_1 \hat{\mu}_t X_{0t} - TD_t S_{0t} + TF_t + \omega_2 T (\hat{S}_{0t} - \hat{S}_t) \quad (3.142.f)$$

$$\hat{P}_{t+1} = \hat{P}_t + Tk_2 \hat{\mu}_t X_{0t} - TD_t P_t + \omega_3 T (P_t - \hat{P}_t) \quad (3.142.g)$$

$$\hat{\mu}_{t+1} = \hat{\mu}_t + T\gamma_1 X_{0t} (X_{0t} - \hat{X}_t) - T\gamma_2 k_1 X_{0t} (S_{0t} - \hat{S}_t) + T\gamma_3 k_2 X_{0t} (P_t - \hat{P}_t) \quad (3.142.h)$$

The estimation algorithm (3.142) has been implemented on a fed-batch ethanolic bioreactor over a period of 44 hours (Fig.3.13) at the Unit of Bioengineering (Université Catholique de Louvain, Belgium). The reactor operated under the following conditions : the initial volume of culture was equal to 35 liters; the reactor was fed twice with a 5-minute pulse of glucose ($F = 600 \text{ mMol/h}$) and the volume was increased by 8 liters at each step to

finally reach 51 liters. Fig.3.13.a shows the evolution of the ethanol concentration P with time during the experiment.

The values of the yield coefficients are equal to :

$$k_1 = 0.18 \frac{\text{mMol}}{\text{NTU}} \quad k_2 = 0.3 \frac{\text{mMol}}{\text{NTU}} \quad (3.143)$$

(NTU : Normal Turbidimetry Units)

The result of the estimation of the specific growth rate μ with the algorithm (3.142) is shown in Fig.3.13.b. It was obtained under the following conditions :

$$\hat{\mu}_0 = 0.15 \text{ h}^{-1} \quad \hat{Z}_{10} = 13 \text{ NTU} \quad \hat{Z}_{20} = 54.7 \text{ mMol} \quad (3.144.\text{a})$$

$$\omega_1 = \sigma_1 X_{0t} \quad \omega_2 = \sigma_2 k_1 X_{0t} \quad \omega_3 = \sigma_3 k_2 X_{0t} \quad \gamma_i = \frac{\sigma_i^2}{4} (i=1,2,3) \quad (3.144.\text{b})$$

$$\sigma_1 = 0.018 \quad \sigma_2 = 0.086 \quad \sigma_3 = 0.086 \quad (3.144.\text{c})$$

Note that the form of $\omega_1, \omega_2, \omega_3$ is in line with the argument presented in Section 3.4.5 and Assumption H8. An experimental validation of this result has been carried out as follows. Off-line data on biomass X (via a turbidimeter) and on glucose S were available. The validation procedure is based on a comparison between estimates of X and S obtained via the estimated specific growth rate $\hat{\mu}$ and the *true* measured values of X and S .

Recall first that the dynamical equations governing X and S are :

$$\frac{dS}{dt} = -k_1 \mu X + F - DS \quad (3.145.\text{a})$$

$$\frac{dX}{dt} = \mu X - DX \quad (3.145.\text{b})$$

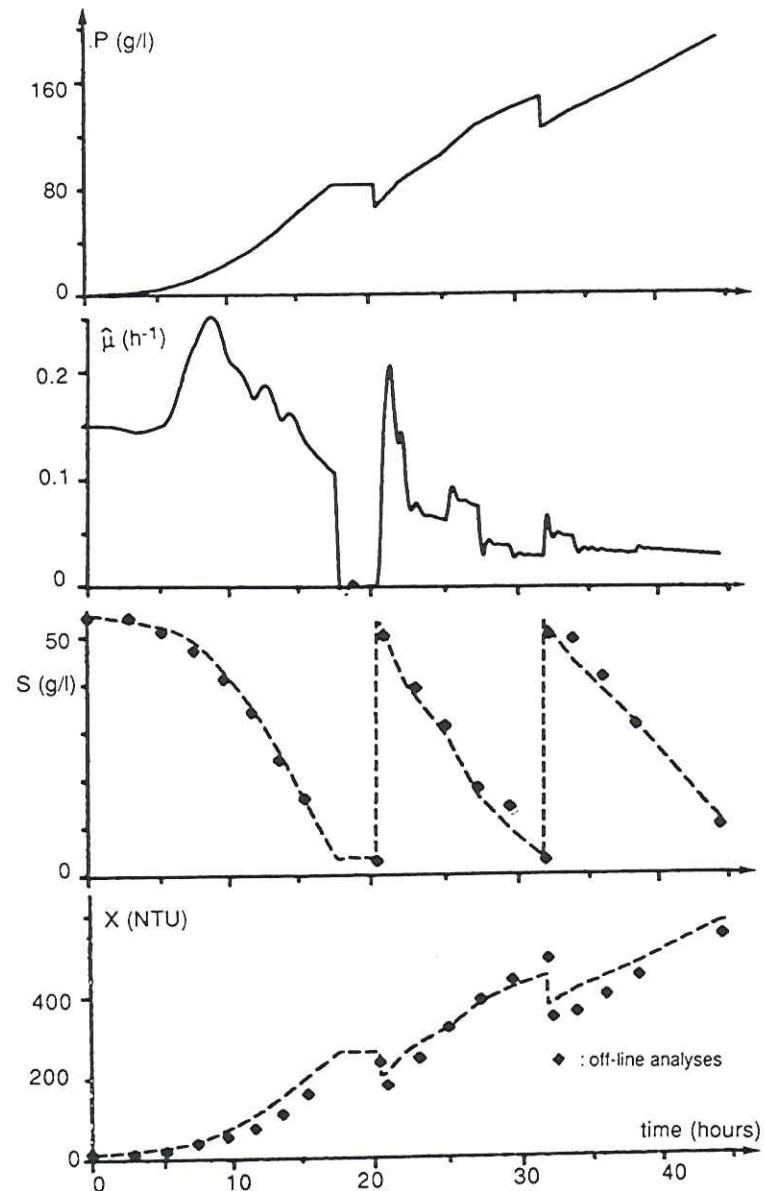


Fig.3.13. Estimation of μ in a fed-batch ethanolic fermentation process

We can compute on-line estimates of X and S by introducing the estimated specific growth rate $\hat{\mu}$, given by (3.142), into these equations, i.e. :

$$\frac{d\hat{S}_v}{dt} = -k_1 \hat{\mu} X_0 + F - D\hat{S}_v \quad (3.146.a)$$

$$\frac{d\hat{X}_v}{dt} = \hat{\mu} \hat{X}_v - D\hat{X}_v \quad (3.146.b)$$

where \hat{X}_v and \hat{S}_v denote the validation estimates of X and S . Discretization of (3.146) gives :

$$\hat{S}_{v,t+1} = \hat{S}_{v,t} - Tk_1 \hat{\mu}_t X_{0t} + TF_t - TD_t \hat{S}_{v,t} \quad (3.147.a)$$

$$\hat{X}_{v,t+1} = \hat{X}_{v,t} + T\hat{\mu}_t \hat{X}_{v,t} - TF_t - TD_t \hat{X}_{v,t} \quad (3.147.b)$$

Note that the use of X_0 in (3.146.a) makes both estimations (3.146.a) and (3.146.b) independent of one another.

The validation results are shown in Fig.3.13.c-d. They exhibit a very good agreement between the off-line data of S and X and their estimates provided through the estimated specific growth rate $\hat{\mu}$.

Calibration of the design parameters

In Section 3.3 we have used, when available, off-line data to validate the state observation performed by the asymptotic observer. Here again, as explained above and as will be true in the following applications, a similar experimental validation of the parameter estimation has been carried out. However, the validation results shown in Fig.3.13 are somewhat unfair. Actually, we used the experimental validation as a tool for choosing appropriate values for the design parameters. These are calibrated so as to obtain the reaction rate estimates which give rise to the best estimates of the unmeasured

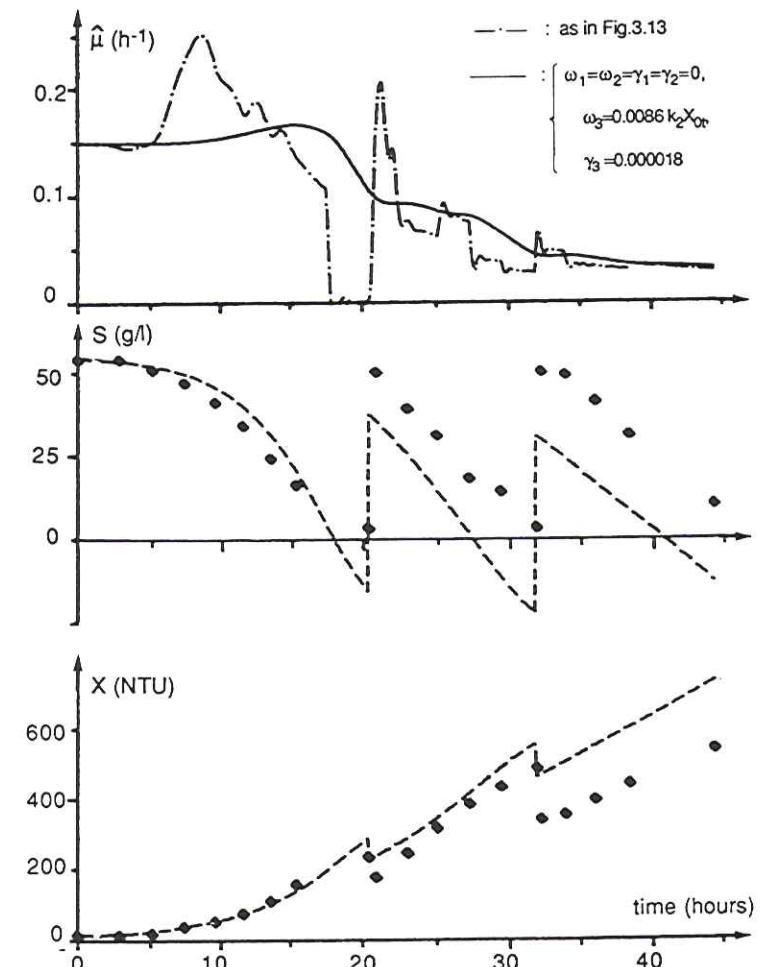


Fig 3.14. calibration of the design parameters : comparison between two sets of design parameters

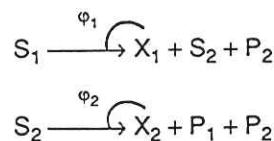
components for which there exist some off-line data. Fig.3.13 shows the estimation of the specific growth rate with a *good* set of design parameters, i.e. those which correctly validate the estimation of the substrate and biomass concentrations. For comparison purposes, Fig.3.14 shows what happens when the design parameters are not well calibrated. The estimation of the specific growth rate is performed under the same initial conditions as in Fig.3.13 but with a different set of design parameters : ω_1 , ω_2 , γ_1 and γ_2 are set to zero and ω_3 and γ_3 are divided by a factor of 10 and 100, respectively,

$$\omega_1 = \omega_2 = \gamma_1 = \gamma_2 = 0, \quad \omega_3 = \sigma_3 k_2 X_{ot}, \quad \gamma_3 = \frac{\sigma_3^2}{4}, \quad \sigma_3 = 0.0086$$

The values of ω_3 and γ_3 are clearly too low to make the estimator capable of tracking the rapid variations of the specific growth rate. $\hat{\mu}$ does not vary quickly enough from its initial value of 0.15 h^{-1} , and the experimental validation gives negative values for the substrate concentration S and excessively large values for the biomass concentration.

3.4.8. Experimental application 2 : Estimation of the reaction rates in a continuous anaerobic digestion process

In this section, we present an experimental application of the linear regression estimator proposed in Section 3.4.3, on the anaerobic digestion application already described in Section 3.3.3. The reaction scheme and the dynamics are as follows :



$$\frac{d}{dt} \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ -k_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ k_3 & -k_2 & 0 & 0 & 0 & 0 \\ 0 & k_6 & 0 & 0 & 0 & 0 \\ k_4 & k_5 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \varphi_1 \\ \varphi_2 \end{bmatrix} - D \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} + \begin{bmatrix} 0 \\ F_1 \\ 0 \\ 0 \\ 0 \\ Q_1 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ Q_2 \end{bmatrix}$$

with X_1 being the acidogenic biomass, S_1 the organic substrate, X_2 the methanogenic biomass, S_2 the acetate, P_1 the methane and P_2 the inorganic carbon.

We recall that :

- 1) the only components which are available from on-line measurements are the acetate S_2 and the methane P_1 ;
- 2) the biomass concentrations X_1 and X_2 and the organic substrate concentrations S_1 are given on-line by the asymptotic observer (3.48);
- 3) there are two unknown reaction rates : the acidogenesis reaction rate φ_1 , and the methanization reaction rate φ_2 , which can be expressed (see Section 1.5.3) by one of the following expressions :

$$\varphi_1 \stackrel{\Delta}{=} \mu_1 X_1 \stackrel{\Delta}{=} \alpha_1 X_1 S_1$$

$$\varphi_2 \stackrel{\Delta}{=} \mu_2 X_2 \stackrel{\Delta}{=} \alpha_2 X_2 S_2$$

We decide to design an algorithm for the estimation of :

$$p(\xi) = \begin{bmatrix} \mu_1 \\ \alpha_2 \end{bmatrix}$$

This choice of $H(\xi)$ and $p(\xi)$ illustrates the flexibility of our approach to the design of parameter estimators, since it will allow us jointly to estimate two

parameters of different dimensions : a specific growth rate μ_1 (time $^{-1}$) and a specific reaction rate α_2 (concentration $^{-1} \times$ time $^{-1}$).

As we have mentioned earlier (see the remark at the end of Section 3.4.2), the algorithm does not necessarily need to be based on the full dynamical model of the process. It may be sufficient to select a subset of the state equations, provided they involve all the parameters we want to estimate. Here we have selected the following two equations :

$$\frac{d}{dt} \begin{bmatrix} S_2 \\ P_1 \end{bmatrix} = \begin{bmatrix} k_3 & -k_2 \\ 0 & k_6 \end{bmatrix} \begin{bmatrix} X_1 & 0 \\ 0 & S_2 X_2 \end{bmatrix} \begin{bmatrix} \mu_1 \\ \alpha_2 \end{bmatrix} - D \begin{bmatrix} S_2 \\ P_1 \end{bmatrix} - \begin{bmatrix} 0 \\ Q_1 \end{bmatrix}$$

but, obviously, many other choices are possible.

The least squares discrete-time algorithm (3.87) is then written as follows for this model (in which the methane P_1 is assumed, as before, to be a low solubility product) :

$$\begin{bmatrix} \hat{\mu}_{1t+1} \\ \hat{\alpha}_{2t+1} \end{bmatrix} = \begin{bmatrix} \hat{\mu}_{1t} \\ \hat{\alpha}_{2t} \end{bmatrix} + T\Gamma_t \begin{bmatrix} k_3 \hat{X}_{1t} - k_2 S_{2t} \hat{X}_{2t} \\ k_6 S_{2t} \hat{X}_{2t} \end{bmatrix} Y_t$$

with :

$$Y_t = \begin{bmatrix} S_{2t+1} - S_{2t} \\ 0 \end{bmatrix} - T \begin{bmatrix} k_3 \hat{X}_{1t} - k_2 S_{2t} \hat{X}_{2t} \\ k_6 S_{2t} \hat{X}_{2t} \end{bmatrix} \begin{bmatrix} \hat{\mu}_{1t} \\ \hat{\alpha}_{2t} \end{bmatrix} - D \begin{bmatrix} S_{2t} \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ Q_{1t} \end{bmatrix}$$

and an appropriate equation (3.87.b) for the updating of the matrix Γ_t .

The estimates of \hat{X}_{1t} and \hat{X}_{2t} are provided by the asymptotic observer (3.48).

The algorithm (3.152) has been implemented on the same set of data as in Section 3.3.3 (Fig. 3.4) under the following conditions :

$$\Gamma_{10} = 0.01 \quad \lambda_1 = 0.9 \quad \hat{\mu}_{10} = 0.06 \text{ d}^{-1} \quad (3.153.a)$$

$$\Gamma_{20} = 0.01 \quad \lambda_2 = 0.9 \quad \hat{\alpha}_{20} = 0.01 \text{ l/g.d} \quad (3.153.b)$$

$$\hat{X}_{10} = 1.1 \text{ g/l} \quad \hat{X}_{20} = 0.22 \text{ g/l} \quad (3.153.c)$$

The results are presented in Fig.3.15.a-b.

An experimental validation of these results has been carried out as follows by using, as in Section 3.3, the off-line data of total biomass concentration X_T ($=X_1 + X_2$). The time derivative of X_T is equal to :

$$\frac{dX_T}{dt} = \frac{dX_1}{dt} + \frac{dX_2}{dt} \quad (3.154.a)$$

$$= \mu_1 X_1 + \alpha_2 S_2 X_2 - D(X_1 + X_2) \quad (3.154.b)$$

$$= \mu_1 X_1 + \alpha_2 S_2 X_2 - DX_T \quad (3.154.c)$$

It is then natural to compute an on-line estimate of X_T from the estimates of μ_1 and α_2 , as follows :

$$\frac{d\hat{X}_T}{dt} = \hat{\mu}_1 \hat{X}_1 + \hat{\alpha}_2 S_2 \hat{X}_2 - D \hat{X}_1 \quad (3.155)$$

or, in discrete time :

$$\hat{X}_{T,t+1} = \hat{X}_{T,t} + T \hat{\mu}_{1t} \hat{X}_{1t} + T \hat{\alpha}_{2t} S_2 \hat{X}_{2t} - TD \hat{X}_{T,t} \quad (3.156)$$

The successful comparison between the actual measured total biomass X_T and its estimate \hat{X}_T calculated with the aid of the parameter estimates $\hat{\mu}_1$ and $\hat{\alpha}_2$ is shown in Fig.3.15.c.

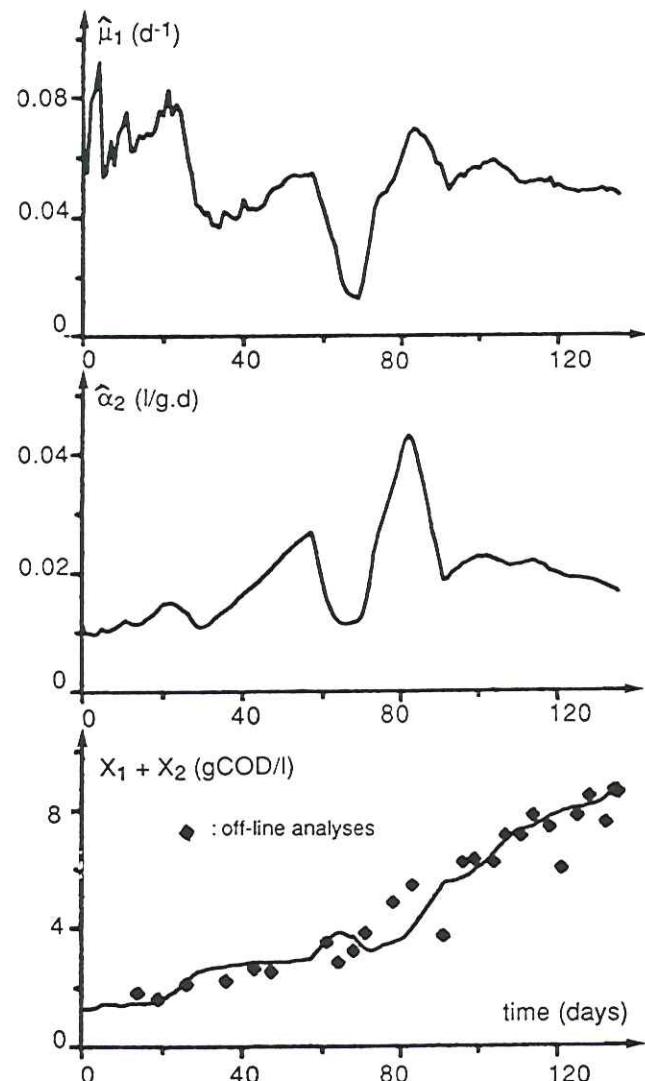


Fig.3.15. Estimation of the reaction rates in a continuous anaerobic digestion process

3.4.9. Experimental application 3 : Estimation of reaction rates in a batch process of lactic acid production

In this example, we illustrate the on-line estimation of the reaction rates φ_i on a lactic acid fermentation process (Laboratoire de Génie des Procédés Biotechnologiques et Agro-alimentaires, INRA, Grignon, France)(see Section 1.4 (1.40)). The process under study in this example is a pure culture of *Lactobacillus bulgaricus*, in which the yield of glucose consumption for biomass growth appears to be negligible. The process can then be described by the reaction schemes (1.40.a) and (1.40.e) :



where S, P₁, P₂, X₂ and P₅ are, respectively, the lactose, glucose, galactose, biomass and lactic acid.

The reactions take place in a 15 liter batch bioreactor maintained at a temperature of 44°C. pH is regulated at a value of 5.8 by addition of NaOH. From stoichiometric arguments, we know that the yield coefficients k₁₂, k₂₂ and k₁₃ are equal to :

$$k_{12} = 0.5, k_{22} = 1, k_{13} = 0.5$$

Taking into account that, here, F = Q = D = 0, the process dynamics are described by the following model :

$$\frac{d}{dt} \begin{bmatrix} S \\ P_1 \\ P_2 \\ X_2 \\ P_5 \end{bmatrix} = \begin{bmatrix} -1 & 0 & 0 & 0 & 0 \\ k_{12} & -k_{22} & 0 & 0 & 0 \\ 0 & 0 & k_{13} & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \varphi_1 \\ \varphi_2 \end{bmatrix}$$

Assume that we wish to estimate the reaction rates ϕ_1 and ϕ_2 from the glucose P_1 and lactic acid P_5 concentrations. Let us apply for instance the observer-based estimator. We consider a reduced order estimator based on the dynamical equations in P_1 and P_5 (i.e. with $\xi_S^T = [P_1, P_5]$ in (3.75)). If we choose diagonal gain matrices Ω and Γ , the estimator is written in discrete time (see (3.74)) :

$$\hat{P}_{1,t+1} = \hat{P}_{1,t} + Tk_{12}\hat{\phi}_{1,t} - Tk_{22}\hat{\phi}_{2,t} + \omega_1 T(P_{1,t} - \hat{P}_{1,t}) \quad (3.138.a)$$

$$\hat{P}_{5,t+1} = \hat{P}_{5,t} + T\hat{\phi}_{2,t} + \omega_2 T(P_{5,t} - \hat{P}_{5,t}) \quad (3.138.b)$$

$$\hat{\phi}_{1,t+1} = \hat{\phi}_{1,t} + \gamma_1 Tk_{12}(P_{1,t} - \hat{P}_{1,t}) \quad (3.138.c)$$

$$\hat{\phi}_{2,t+1} = \hat{\phi}_{2,t} - \gamma_2 Tk_{22}(P_{1,t} - \hat{P}_{1,t}) + \gamma_2 T(P_{5,t} - \hat{P}_{5,t}) \quad (3.138.d)$$

$$\Omega = \begin{bmatrix} -\omega_1 & 0 \\ 0 & -\omega_2 \end{bmatrix} \quad \Gamma = \begin{bmatrix} \gamma_1 & 0 \\ 0 & \gamma_2 \end{bmatrix}$$

In this application, glucose is measured on-line with a biosensor. Besides, NaOH essentially neutralises the lactic acid produced : as shown in Fig.3.16, NaOH addition and lactic acid concentration are proportional (with a proportionality coefficient of 6.5). Since NaOH is representative of lactic acid and easier to measure on-line, we used NaOH data (instead of lactic acid data) in the implementation of the estimation algorithm (3.158).

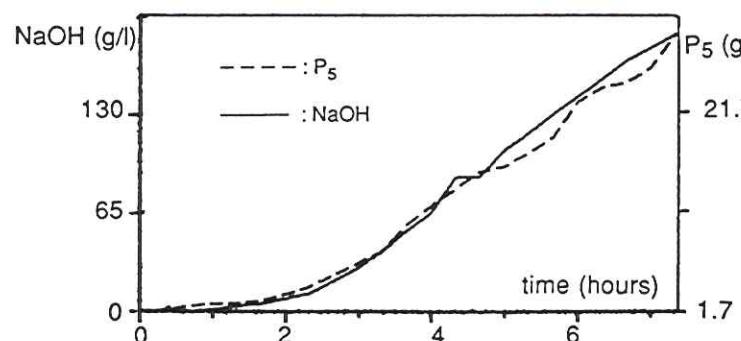


Fig.3.16. Lactic acid fermentation : NaOH and lactic acid data

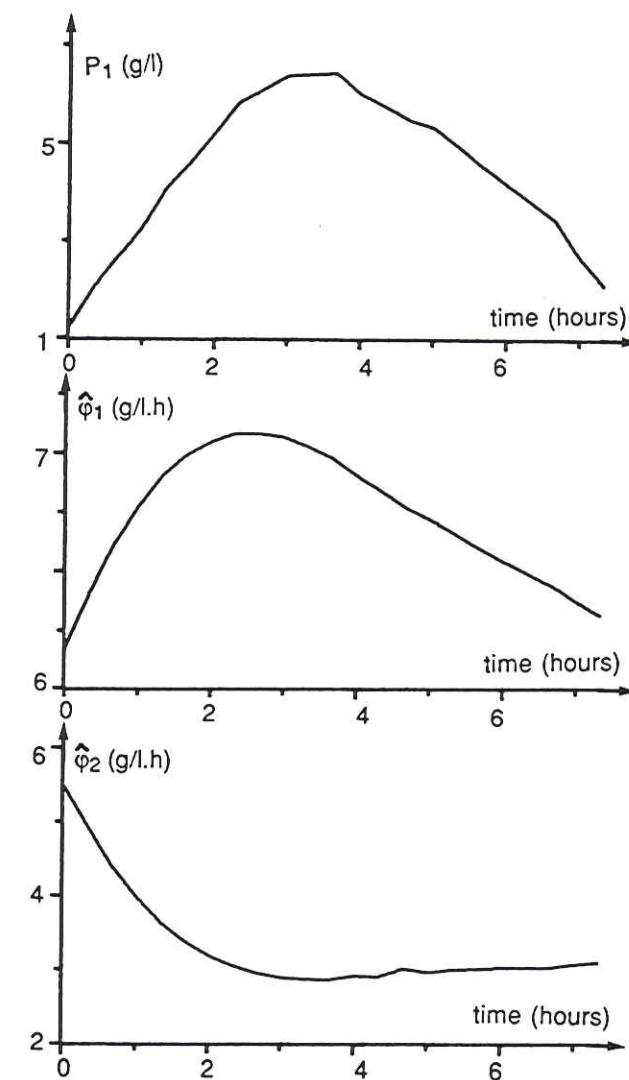


Fig.3.17. Estimation of the reaction rates in a batch lactic fermentation process : on-line data and estimation results

Estimation results of ϕ_1 and ϕ_2 are shown in Fig.3.17. They were obtained under the following conditions :

$$\begin{array}{ll} \omega_1 = 2 & \omega_2 = 1 \\ \hat{\phi}_{10} = 6 \text{ l/g.h} & \hat{\phi}_{20} = 6 \text{ l/g.h} \end{array} \quad \begin{array}{ll} \gamma_1 = 2 & \gamma_2 = 0.25 \\ \hat{P}_{10} = P_{10} & \hat{P}_{50} = P_{50} \end{array} \quad T = 1/3\text{h}$$

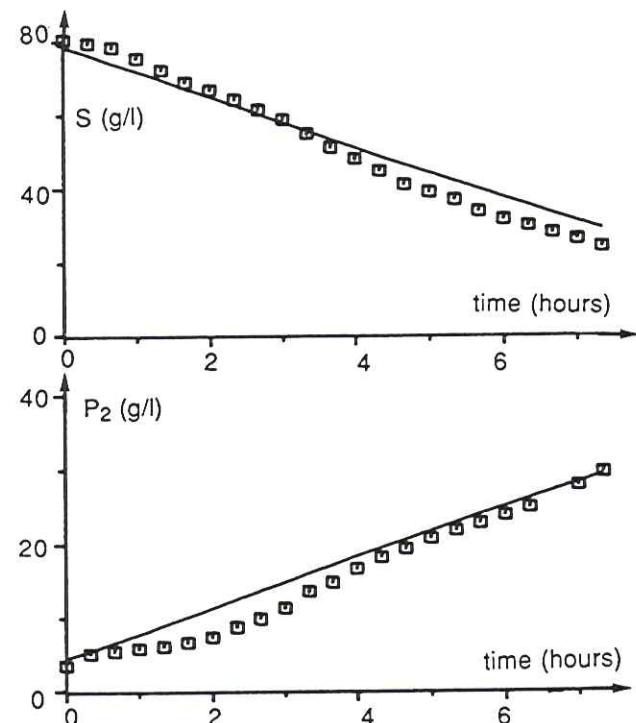


Fig.3.18. Estimation of the reaction rates in a batch lactic fermentation process: experimental validation

As in Sections 3.4.7 and 3.4.8, the experimental validation of the reaction rate estimation was carried out on the remaining components, i.e. lactose S and galactose P_2 , i.e. :

$$\hat{S}_{t+1} = \hat{S}_t + T\hat{\phi}_{1,t}$$

$$\hat{P}_{2,t+1} = \hat{P}_{2,t} + k_{13}\hat{\phi}_{1,t}T$$

where \hat{S}_0 and $\hat{P}_{2,0}$ were set to :

$$\hat{S}_0 = S_0 \quad \hat{P}_{2,0} = P_{2,0}$$

The experimental validation results are shown in Fig.3.18. Note here again the good fit between experimental data and estimated values of S and P_2 .

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CHAPTER 4

STATE AND PARAMETER ESTIMATION WITH UNKNOWN YIELD COEFFICIENTS

4.0. Introduction

Chapter 4 is a natural extension of Chapter 3. In the preceding chapter we have considered different estimation problems when the yield coefficients are known. Here we shall concentrate on the same estimation problems but when the yield coefficients are (partially) *unknown*.

In Section 4.1 we address the on-line estimation problem of the specific reaction rates. We first examine the conditions under which one can derive an alternative dynamical model of the process from which the unknown yield coefficients have disappeared. When this is possible, it is straightforward to extend the observer-based and the linear regression algorithms of Chapter 3 to perform on-line estimation of the kinetic related parameter vector $\rho(\xi)$, independently of the unknown yield coefficients. The issue is discussed in Sections 4.1.1 and 4.1.2 and illustrated with practical applications (ethanolic fermentation and anaerobic digestion) in Sections 4.1.3 and 4.1.4.

The approach proposed in Section 4.1 can be followed only if *some* of the yield coefficients are unknown. Therefore, in Section 4.2, we examine the situation where *all* the yield coefficients are unknown and we explore the possibility of simultaneous on-line estimation of both specific reaction rates

and yield coefficients from full state measurement (Section 4.2.1) and partial state measurement (Section 4.2.2).

It is a natural extension to investigate the possibility of jointly estimating the yield coefficients, the specific reaction rates and the missing states. Algorithms designed for that purpose are briefly presented in Section 4.3. They are called *adaptive observers* because they are state observers, as defined in Chapter 3, which are made adaptive by introducing on-line parameter estimation.

When the yield coefficients are unknown, the simplest method may be to try to estimate them from experimental data before going on to implement state observers or on-line parameter estimators. The problem of estimating the yield coefficients independently of the reaction rates, from full state measurement, is therefore considered in Section 4.4.

Unknown parameters can also be hidden in the transport dynamics part of the General Dynamical Model (1.43) (see Section 1.2), for which the estimation methods presented in this book also apply. Two such issues are briefly treated in Section 4.5 : estimation of specific liquid-gas transfer rates (Section 4.5.1) and estimation of oxygen related parameters (Section 4.5.2).

4.1. On-line Estimation of the Specific Reaction Rates

We consider a biotechnological process described by the general state space model (2.24) :

$$\frac{d\xi}{dt} = -D\xi + KH(\xi)\rho(\xi) + F - Q \quad (2.24) = (4.1)$$

i.e. where the reaction rate vector $\varphi(\xi)$ is expressed as the product of an $M \times r$ matrix $H(\xi)$ of known functions of ξ and a vector $\rho(\xi)$ of unknown functions of ξ ($\dim \rho(\xi) = r$) :

$$\varphi(\xi) = H(\xi)\rho(\xi)$$

In addition, we suppose now that (some of) the yield coefficients (matrix K) are unknown.

In this section we examine under what conditions the estimation of the parameter vector $\rho(\xi)$ could be performed independently of the unknown yield coefficients. It is obvious that this will be possible only if an alternative state space representation exists which is independent of these unknown yield coefficients.

Let us begin with an example.

4.1.1. Example 1 : Simple microbial growth

Consider the simple microbial growth process with a single limiting substrate (1.33) :



the dynamical model of which is as follows :

$$\frac{dS}{dt} = -k_1\alpha SX - DS + DS_{in} \quad (4.3.a)$$

$$\frac{dX}{dt} = \alpha SX - DX \quad (4.3.b)$$

Assume that the substrate concentration S is measured on-line (as well as the dilution rate D and the influent substrate concentration S_{in}). Define the parameter ρ as follows :

$$\rho = \alpha$$

It is immediately apparent that, in this simple example, $(\xi_a = X, \xi_b = S)$ is a nice partition, so that the auxiliary state :

$$Z = S + k_1 X \quad (4.4)$$

has dynamics :

$$\frac{dZ}{dt} = -DZ + DS_{in} \quad (4.5)$$

independent of the yield coefficient k_1 and the specific reaction rate α .

We know from the structural property of Section 1.7 that the dynamics (4.3.a-b) of the process are equivalently represented by equations (4.3.b) and (4.5). By substituting S in equation (4.3.b) by its expression in (4.4) (i.e. $S = Z - k_1 X$), the equivalent state space model (4.3.b)(4.5) is written as follows :

$$\frac{dX}{dt} = \alpha(Z - k_1 X)X - DX \quad (4.6.a)$$

$$\frac{dZ}{dt} = -DZ + DS_{in} \quad (4.6.b)$$

We note, however, that this system representation explicitly depends on the yield coefficient k_1 , and is useless for our purpose since it involves the state X which is *not* measured.

But it is clear that equations (4.3.a) and (4.5) constitute an alternative equivalent dynamical model. This one is explicitly written as follows by replacing $k_1 X$ by its expression in (4.4) (i.e. $k_1 X = Z - S$) :

$$\frac{dS}{dt} = -\alpha S(Z - S) - DS + DS_{in} \quad (4.7.a)$$

$$\frac{dZ}{dt} = -DZ + DS_{in} \quad (4.7.b)$$

This model is now independent of the yield coefficient k_1 and involves the measured state S . It is clear that, as a consequence, it can be used for on-line estimation of the parameter α *independently of k_1* . By way of example, if we choose for instance an observer-based estimator (Section 3.4.2), the estimation of α will be carried out as follows :

$$\frac{d\hat{Z}}{dt} = -D\hat{Z} + DS_{in} + \omega(S - \hat{S}) \quad (4.8.a)$$

$$\frac{d\hat{S}}{dt} = -\hat{\alpha}S(\hat{Z} - S) - DS + DS_{in} + \omega_1(S - \hat{S}) \quad (4.8.b)$$

$$\frac{d\hat{\alpha}}{dt} = \gamma_1 S(S - \hat{Z})(S - \hat{S}) \quad (4.8.c)$$

where ω, ω_1 and γ_1 are positive design parameters.

This example suggests an argument for the estimation of ρ independently of K which is presented in the next paragraph.

4.1.2. Conditions for estimating ρ independently of the unknown yield coefficients

Recall that the dynamics of the vector Z :

$$Z = A_0 \xi_a + \xi_b \quad (1.70) = (4.9)$$

defined in the structural property of Section 1.7 are equal to :

$$\frac{dZ}{dt} = -DZ + A_0(F_a - Q_a) + (F_b - Q_b) \quad (1.73) = (4.10)$$

Assume that, in line with Section 3.3.1, the $(N-p)$ vector Z can be expressed as a linear combination of the vectors ξ_1 and ξ_2 of measured and non measured variables, i.e. :

$$Z = A_1 \xi_1 + A_2 \xi_2$$

(4.11)

The dynamics of the measured variables ξ_1 are equal to :

$$\frac{d\xi_1}{dt} = K_1 H(\xi_1, \xi_2) p(\xi_1, \xi_2) - D \xi_1 + F_1 - Q_1 \quad (4.12)$$

The kinetics term $K_1 H(\xi_1, \xi_2) p(\xi_1, \xi_2)$ is in general a function of some of the unknown components of ξ_2 (and not necessarily of all of them, see e.g. example 2 below). Assume that these components can be expressed from (4.11) as functions of ξ_1 and Z only (in the particular situation when *all* the components of ξ_2 appear explicitly in $K_1 H(\xi_1, \xi_2) p(\xi_1, \xi_2)$, this means that then A_2 must be left invertible, as been shown in Section 3.3.1). Then the kinetic term $K_1 H(\xi_1, \xi_2) p$ can be rewritten in terms of the measured states ξ_1 and of the auxiliary states Z :

$$K_1 H(\xi_1, \xi_2) p = \Phi(\xi_1, Z) p \quad (4.13)$$

where $\Phi(\xi_1, Z)$ is a qxM matrix which is a function of ξ_1 and Z . (Recall, for instance, that in example 1, $\Phi(\xi_1, Z)$ was equal to $S(S - Z)$).

Assume also that F and Q are known.

In conclusion, the parameter vector p can be estimated independently of the unknown yield coefficients under the two following conditions :

- C1. There exists a state transformation Z (4.9) whose dynamics (4.10) are independent of the unknown yield coefficients.
- C2. The reformulation (4.13) of the kinetic term $K_1 H(\xi_1, Z) p(\xi_1, Z)$ is such that the matrix $\Phi(\xi_1, Z)$ is independent of the unknown yield coefficients.

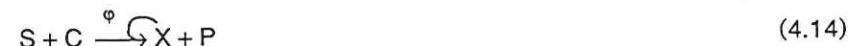
Remark

Note that the nice partition (i.e. with $F_a - Q_a = 0$) is a particular case of condition C1, since then the dynamics of the auxiliary state vector Z are independent of *all* the yield coefficients.

Let us now introduce two more examples by way of illustration.

4.1.3. Example 2 : Estimation of the specific growth rate independently of the yield coefficients

We shall here extend the first example to a single aerobic biochemical reaction with two reactants (substrate S and oxygen C), one biomass X and one (possibly gasifiable) product P, i.e. :



with $\varphi = \mu X$.

The dynamical model of the system is then written as follows :

$$\frac{dX}{dt} = \mu X - DX \quad (4.15.a)$$

$$\frac{dS}{dt} = -k_1 \mu X - DS + F \quad (4.15.b)$$

$$\frac{dC}{dt} = -k_2 \mu X - DC + Q_{in} \quad (4.15.c)$$

$$\frac{dP}{dt} = k_3 \mu X - DP - Q \quad (4.15.d)$$

We shall now study the on-line estimation of the specific growth rate μ (i.e. $\rho = \mu$) from the measurements of *one* of the process components X, S, C or P, independently of the yield coefficients k_1 , k_2 and k_3 .

If the biomass X is measured on-line, equation (4.15.a) is the relevant special case of (4.12) with $\rho = \mu$ and $\Phi(\xi_1, Z) = X$. This equation is clearly independent of the k_i s. The on-line estimation of μ with this equation has been quite exhaustively treated in Chapter 3 (Section 3.4.5).

Consider now the estimation of μ from one of the other three components S, C or P.

$(\xi_a = X, \xi_b = [S, C, P]^T)$ is a nice partition with the following associated state transformation :

$$\begin{bmatrix} Z_1 \\ Z_2 \\ Z_3 \end{bmatrix} = \begin{bmatrix} k_1 \\ k_2 \\ -k_3 \end{bmatrix} X + \begin{bmatrix} S \\ C \\ P \end{bmatrix} \quad (4.16)$$

The dynamics are equal to :

$$\frac{d}{dt} \begin{bmatrix} Z_1 \\ Z_2 \\ Z_3 \end{bmatrix} = -D \begin{bmatrix} Z_1 \\ Z_2 \\ Z_3 \end{bmatrix} + \begin{bmatrix} F \\ Q_{in} \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ Q \end{bmatrix} \quad (4.17)$$

They are independent of the yield coefficients k_1 , k_2 and k_3 . Therefore, condition C1 is fulfilled.

Now let us see how to replace the unknown component ξ_2 by a function of ξ_1 and Z in the kinetic term $K_1 H(\xi_1, \xi_2) \rho$ of equation (4.12). Note that here the kinetic term does not explicitly depend on *all* the unknown components of ξ_2 . Suppose, for instance, that S is the only measured component. The kinetic term $K_1 H(\xi_1, \xi_2) \rho$ is equal to :

$$K_1 H(\xi_1, \xi_2) \rho = -k_1 \mu X \quad (4.18)$$

which can be rewritten as follows by using the first component Z_1 of the auxiliary vector (4.16) :

$$K_1 H(\xi_1, \xi_2) \rho = \mu(S - Z_1) \quad (4.19)$$

i.e. with $\Phi = S - Z_1$.

We see that we do not have to invert the matrix A_2 in order to write (4.19).

The same reasoning can be used if the measured component ξ_1 is C or P. As a matter of fact, it is straightforward to see that, in each situation, the dynamical equation of the measured variable ξ_1 (which is alternatively S, C or P) may be written as follows :

$$\frac{d\xi_1}{dt} = \mu(\xi_1 - Z) - D\xi_1 + F_1 - Q_1 \quad (4.20)$$

but with a different auxiliary variable Z and a different meaning for F_1 and Q_1 depending on which component is accessible for on-line measurement (see Table 4.1).

ξ_1	Z	F_1	Q_1
S	$S + k_1 X$	F	0
C	$C + k_2 X$	Q_{in}	0
P	$P - k_3 X$	0	Q

Table 4.1. Estimation of μ from S, C or P

The dynamics of the scalar variable Z appearing in (4.20) are given by the following equation :

$$\frac{dZ}{dt} = -DZ + F_1 - Q_1 \quad (4.21)$$

Note that equations (4.20) and (4.21) are independent of the yield coefficients k_1 , k_2 and k_3 . Condition C2 is then fulfilled and these equations can be used to estimate the specific growth rate independently of k_1 , k_2 and k_3 from any of the component S, C or P. The observer-based estimator is, for instance, written here as follows :

$$\frac{d\hat{Z}}{dt} = -D\hat{Z} + F_1 - Q_1 + \omega(\xi_1 - \hat{\xi}_1) \quad (4.22.a)$$

$$\frac{d\hat{\xi}_1}{dt} = \hat{\mu}(\xi_1 - \hat{Z}) - D\xi_1 + F_1 - Q_1 + \omega_1(\xi_1 - \hat{\xi}_1) \quad (4.22.b)$$

$$\frac{d\hat{\mu}}{dt} = \gamma_1(\xi_1 - \hat{Z})(\xi_1 - \hat{\xi}_1) \quad (4.22.c)$$

with ω , ω_1 and γ_1 positive design parameters.

Experimental application : estimation of the specific growth rate μ in a batch ethanolic bioreactor

The estimation algorithm has been implemented on an ethanolic fermentation bioreactor described (as in Section 3.4.7) by the following reaction scheme :



where S, X and P are glucose, yeast and ethanol, respectively.

The only difference from the scheme (4.14) is that there is no dissolved oxygen C because the reaction is anaerobic. It is easy to see that, in this case, the algorithm (4.22) remains valid for estimating the specific growth rate μ from measurements of the ethanol concentration P.

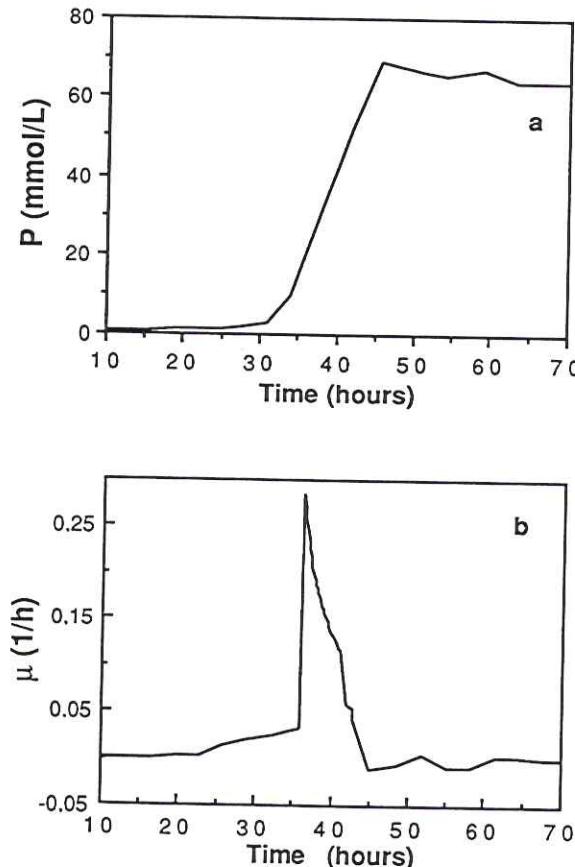


Fig.4.1. On-line estimation of the specific growth rate in an ethanolic batch bioreactor

The process was operated in a batch reactor (Unit of Bioengineering, Catholic University of Louvain, Belgium). Considering that the process operates in batch mode ($D = 0$) and that the presence of ethanol P in the gas phase is negligible, a discrete-time version of (4.22) is written as follows :

$$\hat{Z}_{t+1} = \hat{Z}_t + \omega T(P_t - \hat{P}_t) \quad (4.24.a)$$

$$\hat{P}_{t+1} = \hat{P}_t + \hat{\mu}_t T(P_t - \hat{Z}_t) + \omega_1 T(P_t - \hat{P}_t) \quad (4.24.b)$$

$$\hat{\mu}_{t+1} = \hat{\mu}_t + \gamma_1 T(P_t - \hat{Z}_t)(P_t - \hat{P}_t) \quad (4.24.c)$$

The data of the ethanol concentration P and the estimates of the specific growth rate μ , obtained with (4.24), are shown in Figs.4.1.a and 4.1.b, respectively. The estimation was carried out under the following conditions :

$$\hat{Z}_0 = 0 \text{ mmol/L}, P_0 = 0 \text{ mmol/L}, \hat{\mu}_0 = 0 \text{ h}^{-1} \quad (4.25.a)$$

$$\omega = 0, \omega_1 = 3.8(P_t - \hat{Z}_t) \text{ h}^{-1}, \gamma_1 = 3.9 \text{ L}^2/\text{mmol}^2 \cdot \text{h}^2 \quad (4.25.b)$$

The calibration of the design parameters was performed (Fig.4.2) by comparing some off-line yeast concentration data X (measured by cell counting) and an estimate calculated from the estimate of μ with a discrete-time version of the dynamical equation of X in (4.15) with $D = 0$, as follows :

$$\hat{X}_{t+1} = \hat{X}_t + T\hat{\mu}_t \hat{X}_t \quad (4.26)$$

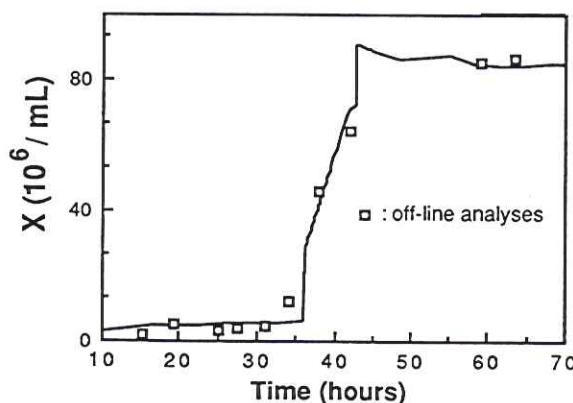


Fig.4.2. Experimental validation of the on-line estimation of μ

Note the good fit between the few off-line data of X and its estimate in Fig.4.2.

Comment

A similar application of the estimation of the specific growth rate has already been treated in Section 3.4.5. The advantage of the estimation scheme (4.24) compared to (3.101)-(3.104) is that it does not require any knowledge of the yield coefficients. The drawback, however, is that it does not take advantage of data on substrate feed rate F , which are usually available on-line.

Correlation between μ and the glucose concentration

In Chapter 2 we mentioned that there are three advantages to the consideration of the parameters $p(\xi)$ as unknown time-varying parameters to be estimated on-line :

- 1) it avoids the difficult choice of an analytical expression for $p(\xi)$;
- 2) it avoids the identifiability difficulties inherent in the expression chosen ;
- 3) it allows, once the estimation has been processed, a search for possible correlations between $p(\xi)$ and the factors which are capable of influencing it. For instance, how does the substrate concentration influence $p(\xi)$? Is there any inhibition effect which can be emphasised?

We now illustrate this idea. In the experimental application, some off-line glucose concentration data were also available. In Fig.4.3 the glucose concentration values have been drawn with respect to the corresponding specific growth rate estimates $\hat{\mu}$ (calculated with the algorithm (4.24)). It is clear from this figure that the dependence between the specific growth rate and the glucose concentration appears to be "Monod-like", i.e. μ is an increasing function of the glucose concentration until a certain saturation level is reached. It is worth noting that, in order to emphasise this dependence, we

do not need to formulate any *a priori* assumption about the analytical structure of μ . Moreover, Fig.4.3 does not mean that this dependence is a Monod law. In fact, any equivalent mathematical expression (such as the models of Blackman or Tessier (see Appendix 1), for instance) could as well be used to represent it.

The purpose when carrying out such an analysis does not consist of finding the "best" analytical relationship between the specific growth rate and the biochemical and physico-chemical variables. It is more specifically aimed at emphasising possible correlations. In practice, this means that the above procedure does not necessarily imply the mathematical formulation of the correlation (with, as a consequence, the calibration of the kinetic coefficients). In a process "modelling" context (or rather a process description context), this has the advantage of avoiding the hazardous interpretation of uncertain coefficients of the model (see Section 2.1).

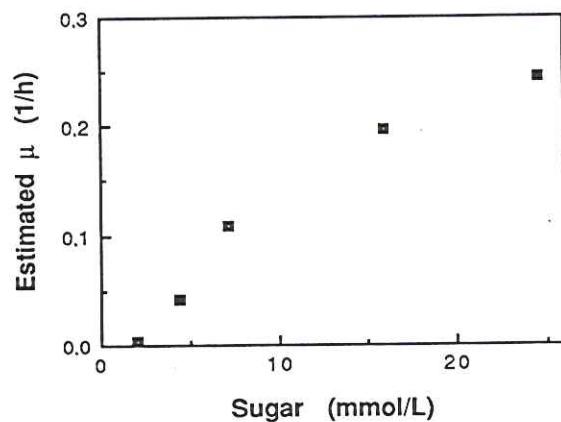


Fig.4.3. Correlation between the estimated specific growth rate and the glucose concentration

4.1.4. Example 3 : Estimation of the specific reaction rates in an anaerobic digestion process

In this example, we shall show that the existence of a nice partition is not enough to estimate the specific reaction rates independently of the (unknown) yield coefficients.

Consider the same example as in Section 3.3.1, i.e. the simplified scheme of the anaerobic digestion without the two products P_1 and P_2 (see (3.23)) :



The dynamical model is defined as follows :

$$\frac{d}{dt} \begin{bmatrix} S_1 \\ X_1 \\ S_2 \\ X_2 \end{bmatrix} = \begin{bmatrix} -k_1 & 0 \\ 1 & 0 \\ k_3 & -k_2 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} S_1 X_1 & 0 \\ 0 & S_2 X_2 \end{bmatrix} \begin{bmatrix} \alpha_1 \\ \alpha_2 \end{bmatrix} - D \begin{bmatrix} S_1 \\ X_1 \\ S_2 \\ X_2 \end{bmatrix} + \begin{bmatrix} DS_{in} \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad (4.28)$$

Assume that the substrate concentrations S_1 and S_2 are measured on-line.

We can define the following state transformation which corresponds to a nice partition :

$$Z = \begin{bmatrix} Z_1 \\ Z_2 \end{bmatrix} = \begin{bmatrix} k_1 & 0 \\ -k_3 & k_2 \end{bmatrix} \begin{bmatrix} X_1 \\ X_2 \end{bmatrix} + \begin{bmatrix} S_1 \\ S_2 \end{bmatrix} \quad (4.29.a)$$

$$\frac{dZ}{dt} = -DZ + F_1 \quad (4.29.b)$$

$$\text{with } F_1 = \begin{bmatrix} DS_{in} \\ 0 \end{bmatrix}$$

But the dynamical behaviour of ξ_1 ($= [S_1 \ S_2]^T$) does not become independent of the yield coefficients with the introduction of the above state transformation. In fact, $K_1 H(\xi_1, Z)$ is equal to :

$$K_1 H(\xi_1, Z) = \begin{bmatrix} S_1(S_1 - Z_1) & 0 \\ \frac{k_3}{k_1} S_1(Z_1 - S_1) & S_2\left(S_2 - Z_2 + \frac{k_3}{k_1}(S_1 - Z_1)\right) \end{bmatrix} \quad (4.30)$$

Therefore, a knowledge of the yield coefficients k_1 and k_3 (but not k_2) is necessary to perform the on-line estimation of α_1 and α_2 with one of the algorithms of Section 3.4. More precisely, the specific reaction rate α_1 can be estimated independently of the yield coefficients, while the estimation of α_2 with the above formulation requires the knowledge of k_3/k_1 (which, as a matter of fact, is the yield coefficient from S_1 into S_2 , i.e., in the two-step anaerobic digestion example, from organic matter into acetate).

4.2. Joint Estimation of Yield Coefficients and Specific Reaction Rates

The issue of estimating the reaction rates $\phi(\xi)$ (or related quantities like $\rho(\xi)$, $\alpha(\xi)$, $\mu(\xi)$) has been already addressed in this book. A general method was described in Chapter 3 (Section 3.4) in the case in which the yield coefficients (i.e. the matrix K) are known. Later on, in Section 4.1, we discussed the case in which some of the yield coefficients are unknown but can be eliminated from the estimation procedure by appropriate model transformations. In this section, we shall examine the situation in which all the yield coefficients are unknown. We explore the possibility of simultaneous on-line estimation of both specific reaction rates $\alpha(\xi)$ and yield coefficients (matrix K), from full state measurement (Section 4.2.1) and partial state measurement (Section 4.2.2).

4.2.1. Full state measurement

We consider biotechnological processes described by the state space model (1.49) :

$$\frac{d\xi}{dt} = KG(\xi)\alpha - D\xi + F - Q \quad (1.49) = (4.31)$$

We assume that :

- 1) the full state ξ is measured on-line;
- 2) the dilution rate D , the feed rates F and the gaseous outflow rates are known on-line;
- 3) the yield coefficients (matrix K) and the specific reaction rates α are unknown.

The problem is to design an estimator of K and α .

Recall that N denotes the number of components and M the number of reactions involved in the process. The first point to notice, then, is that the matrix K necessarily contains M nonzero entries which may be freely assigned by the user and are usually set to "1" as was discussed in Section 1.5.6.

If we denote by N_j the number of components involved in the reaction with index j , it is then easy to see that the total number m of unknown yield coefficients in K (denoted k_1, k_2, \dots, k_m) is given by :

$$m = \sum_{j=1}^M (N_j - 1) \quad (4.32)$$

Moreover, there are obviously M parameters α_j ($j = 1, \dots, M$) in the model (4.31). Hence the total number of unknown parameters is :

$$m + M = \sum_{j=1}^M N_j \quad (4.33)$$

Now, due to its particular structure, the vector $KG(\xi)\alpha$ may be rewritten in a linear regression form as follows :

$$KG(\xi)\alpha \stackrel{\Delta}{=} \Phi(\xi)\theta \quad (4.34)$$

In this expression, $\Phi(\xi)$ is a $N \times (m+M)$ matrix of known *multilinear* combinations of the state variables. $\theta^T = [\theta_1, \theta_2, \dots, \theta_{m+M}]$ is a vector of *bilinear* combinations of the unknown parameters k_i ($i = 1, \dots, m$) and α_j ($j = 1, \dots, M$). It is formally written as follows :

$$\theta = f(\alpha, k) \quad (4.35)$$

The definitions of Φ and θ will be soon illuminated by several examples. An important point is that the function f in (4.35) is *invertible*, that is α and k can be computed uniquely from θ :

$$\begin{bmatrix} \alpha \\ k \end{bmatrix} = f^{-1}(\theta) \quad (4.36)$$

With the definition (4.34), the process model (4.31) is rewritten as follows :

$$\frac{d\xi}{dt} = \Phi(\xi)\theta - D\xi + F - Q \quad (4.37)$$

Since the unknown parameter θ enters linearly in (4.37), a natural solution is to estimate it with algorithms similar to those of Chapter 3 (Section 3.4), and then to recover α and k with the inverse function (4.36). The algorithms are written as follows :

Observer-based Estimator

$$\frac{d\hat{\xi}}{dt} = \Phi(\xi)\hat{\theta} - D\xi + F - Q - \Omega(\xi - \hat{\xi}) \quad (4.38.a)$$

$$\frac{d\hat{\theta}}{dt} = \Phi^T(\xi) \Gamma(\xi - \hat{\xi}) \quad (4.38.b)$$

$$\begin{bmatrix} \hat{\alpha} \\ \hat{k} \end{bmatrix} = f^{-1}(\hat{\theta}) \quad (4.38.c)$$

Linear Regression Estimator

$$\frac{d\psi^T}{dt} = \Omega\psi^T + \Phi(\xi) \quad (4.39.a)$$

$$\frac{d\psi_0}{dt} = \Omega\psi_0 + (\Omega - D I_N) \xi - Q + F \quad (4.39.b)$$

$$\frac{d\hat{\theta}}{dt} = \Gamma\psi(\xi - \psi_0 - \psi^T\hat{\theta}) \quad (4.39.c)$$

$$\frac{d\Gamma}{dt} = -\Gamma\psi\psi^T\Gamma + \lambda\Gamma \quad (4.39.d)$$

$$\begin{bmatrix} \hat{\alpha} \\ \hat{k} \end{bmatrix} = f^{-1}(\hat{\theta}) \quad (4.39.e)$$

Example : basic microbial growth process

Consider the basic process (1.33) :

$$S \xrightarrow{\quad} X \quad (4.40)$$

whose dynamics are written :

$$\frac{d}{dt} \begin{bmatrix} X \\ S \end{bmatrix} = \begin{bmatrix} SX & 0 \\ 0 & -SX \end{bmatrix} \begin{bmatrix} \alpha \\ \alpha k_1 \end{bmatrix} - D \begin{bmatrix} X \\ S \end{bmatrix} + \begin{bmatrix} 0 \\ DS_{in} \end{bmatrix} \quad (4.41)$$

We notice that we have here :

$$M = 1 \quad m = 1 \quad \dim(\theta) = m + M = 2 \quad (4.42)$$

$$\theta = \begin{bmatrix} \theta_1 \\ \theta_2 \end{bmatrix} = \begin{bmatrix} \alpha \\ \alpha k_1 \end{bmatrix} = f(\alpha, k_1) \quad \Phi(\xi) = \begin{bmatrix} SX & 0 \\ 0 & -SX \end{bmatrix} \quad (4.43)$$

The function f is inverted as follows :

$$\begin{bmatrix} \alpha \\ k_1 \end{bmatrix} = f^{-1}(\theta) = \begin{bmatrix} \theta_1 \\ \theta_2 \\ \frac{\theta_2}{\theta_1} \end{bmatrix} \quad (4.44)$$

If we choose diagonal matrices for Ω and Γ_1 , the observer-based estimator (4.38) resolves to :

$$\frac{d\hat{X}}{dt} = SX\hat{\theta}_1 - DX + \omega_1(X - \hat{X}) \quad (4.45.a)$$

$$\frac{d\hat{S}}{dt} = -SX\hat{\theta}_2 - DS + DS_{in} + \omega_2(S - \hat{S}) \quad (4.45.b)$$

$$\frac{d\hat{\theta}_1}{dt} = \gamma_1 SX(X - \hat{X}) \quad (4.45.c)$$

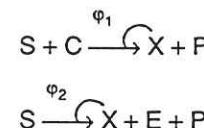
$$\frac{d\hat{\theta}_2}{dt} = -\gamma_2 SX(S - \hat{S}) \quad (4.45.d)$$

$$\hat{\alpha} = \hat{\theta}_1 \quad (4.45.e)$$

$$\hat{k}_1 = \frac{\hat{\theta}_2}{\hat{\theta}_1} \quad (4.45.f)$$

Example : Yeast fermentation process

Consider a yeast fermentation described by the reaction scheme (1.37). Suppose, however, that the reaction of respiratory growth on ethanol is not activated. Hence the reaction scheme reduces to :



with X being biomass, S glucose, C oxygen, E ethanol and P carbon dioxide.

The associated dynamical model is as follows :

$$\frac{d}{dt} \begin{bmatrix} X \\ S \\ E \\ C \\ P \end{bmatrix} = \begin{bmatrix} k_1 & k_2 \\ -k_3 & -k_4 \\ 0 & XS \\ 0 & k_5 \\ -k_6 & 0 \\ 1 & 1 \end{bmatrix} \begin{bmatrix} XSC & 0 \\ 0 & XS \end{bmatrix} \begin{bmatrix} \alpha_1 \\ \alpha_2 \end{bmatrix} - D \begin{bmatrix} X \\ S \\ E \\ C \\ P \end{bmatrix} + \begin{bmatrix} 0 \\ DS_{in} \\ 0 \\ Q_{in} \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ Q_1 \end{bmatrix}$$

Expression (4.34) is written here :

$$\Phi(\xi)\theta = \begin{bmatrix} XSC & XS & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & XSC & XS & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & XS & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & XSC & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & XSC & XS \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \theta_1 \\ \theta_2 \\ \theta_3 \\ \theta_4 \\ \theta_5 \\ \theta_6 \\ \theta_7 \\ \theta_8 \end{bmatrix}$$

with the reparametrization $\theta = f(\alpha, k)$:

$$\begin{aligned}\theta_1 &= k_1\alpha_1 & \theta_2 &= k_2\alpha_2 & \theta_3 &= -k_3\alpha_1 & \theta_4 &= -k_4\alpha_2 \\ \theta_5 &= k_5\alpha_2 & \theta_6 &= -k_6\alpha_1 & \theta_7 &= \alpha_1 & \theta_8 &= \alpha_2\end{aligned}$$

which is clearly invertible.

4.2.2. Partial state measurement

We shall now reconsider the problem of joint estimation of yield coefficients and specific reaction rates, but when only a part of the state is measured online.

We assume that :

- 1) the subset of measured state variables is denoted ξ_1 ; the set of remaining non measured states is denoted ξ_2 , so that (ξ_1, ξ_2) is a state partition which in turn induces the similar partitions (K_1, K_2) , (F_1, F_2) , (Q_1, Q_2) as before;
- 2) there exists a *nice* state partition (ξ_a, ξ_b) , with an associated auxiliary state Z (see sections 1.7 and 3.3.1) :

$$Z = A_0\xi_a + \xi_b = A_1\xi_1 + A_2\xi_2 \quad (4.46)$$

which obeys the following dynamics :

$$\frac{dZ}{dt} = -DZ + F_b - Q_b \quad (4.47)$$

- 3) the matrix A_2 is left invertible.

Under these assumptions, the state space model (4.31) is equivalent to :

$$\frac{d\xi_1}{dt} = K_1G(\xi_1, A_2^+(Z - A_1\xi_1))\alpha - D\xi_1 + F_1 - Q_1 \quad (4.48.a)$$

$$\frac{dZ}{dt} = -DZ + F_b - Q_b \quad (4.48.b)$$

Now, as in the previous section, it is easily seen that the term $K_1G(\xi_1, A_2^+(Z - A_1\xi_1))\alpha$ may be rewritten as :

$$K_1G(\xi_1, A_2^+(Z - A_1\xi_1))\alpha \stackrel{\Delta}{=} \Phi(\xi_1, Z)\theta \quad (4.49)$$

The structures of Φ and θ , however, are slightly different from the previous ones. $\Phi(\xi_1, Z)$ is now a matrix of known *polynomial* combinations of the measured states ξ_1 and the auxiliary state Z . θ is a vector of polynomial combinations of some of the unknown parameters k_i and α_j , denoted as before in (4.35):

$$\theta = f(\alpha, k) \quad (4.50)$$

It may arise, however, that this function f is not completely invertible. Then, in contrast with the previous case, only a few k_i and α_j can be recovered from θ . This is illustrated in the examples below.

With the *reparametrization* (4.49), the model (4.48) is rewritten :

$$\frac{d\xi_1}{dt} = \Phi(\xi_1, Z)\theta - D\xi_1 + F_1 - Q_1 \quad (4.51.a)$$

$$\frac{dZ}{dt} = -DZ + F_b - Q_b \quad (4.51.b)$$

On the grounds of our previous discussions, the solution to the estimation problem readily appears : it suffices to combine a parameter estimator for θ (Section 4.2.1) with an asymptotic observer for Z (Section 3.3.1). For instance, an observer-based estimator is written as follows :

Observer-based Estimator

$$\frac{d\hat{Z}}{dt} = -D\hat{Z} + F_b - Q_b \quad (4.52.a)$$

$$\frac{d\hat{\xi}_1}{dt} = \Phi(\xi_1, \hat{Z})\hat{\theta} - D\xi_1 + F_1 - Q_1 - \Omega_1(\xi_1 - \hat{\xi}_1) \quad (4.52.b)$$

$$\frac{d\hat{\theta}}{dt} = \Phi^T(\xi_1, \hat{Z})\Gamma(\xi_1 - \hat{\xi}_1) \quad (4.52.c)$$

Example 1. Simple microbial growth process

Consider the basic microbial growth process (1.33) :



the dynamics of which are written :

$$\frac{d}{dt} \begin{bmatrix} X \\ S \end{bmatrix} = \begin{bmatrix} SX & 0 \\ 0 & -SX \end{bmatrix} \begin{bmatrix} \alpha \\ \alpha k_1 \end{bmatrix} - D \begin{bmatrix} X \\ S \end{bmatrix} + \begin{bmatrix} 0 \\ DS_{in} \end{bmatrix} \quad (4.54)$$

Assume that only the biomass concentration X is measured on-line. Hence, we have :

$$\xi_1 = X \quad \xi_2 = S \quad (4.55.a)$$

$$K_1 = 1 \quad K_2 = -k_1 \quad (4.55.b)$$

$$Z = S + k_1 X \quad (A_0 = A_1 = k_1, \quad A_2 = 1) \quad (4.55.c)$$

The equivalent model (4.51) is written here :

$$\frac{dX}{dt} = [ZX \quad -X^2] \begin{bmatrix} \alpha \\ \alpha k_1 \end{bmatrix} - DX \quad (4.56.a)$$

$$\frac{dZ}{dt} = -DZ + DS_{in} \quad (4.56.b)$$

That is :

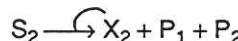
$$\Phi(\xi_1, Z) = [ZX \quad -X^2] \quad (4.57.a)$$

$$\theta = \begin{bmatrix} \theta_1 \\ \theta_2 \end{bmatrix} = \begin{bmatrix} \alpha \\ \alpha k_1 \end{bmatrix} \quad (4.57.b)$$

We notice that, in this example, the parameter θ is identical to that which was identifiable when both S and X were measured (example 1 of Section 4.2.1).

Example 2. Anaerobic digestion process

We consider the simplified reaction scheme (1.86) obtained in Section 1.8.4 :



We suppose, furthermore, that we are not interested in the products P_1 and P_2 , so that we can omit them in the analysis. Then the state space model is as follows :

$$\frac{d}{dt} \begin{bmatrix} S_1 \\ X_1 \\ S_2 \\ X_2 \end{bmatrix} = \begin{bmatrix} -k_1 & 0 \\ 1 & 0 \\ k_3 & -k_2 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} S_1 X_1 & 0 \\ 0 & S_2 X_2 \end{bmatrix} \begin{bmatrix} \alpha_1 \\ \alpha_2 \end{bmatrix} - D \begin{bmatrix} S_1 \\ X_1 \\ S_2 \\ X_2 \end{bmatrix} + \begin{bmatrix} F_1 \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad (4.58)$$

We assume that the substrates S_1, S_2 are measured on-line :

$$\xi_1 = [S_1 \ S_2]^T \quad \xi_2 = [X_1 \ X_2]^T \quad (4.59)$$

We notice that $(\xi_a = \xi_2, \xi_b = \xi_1)$ constitutes a nice partition of the state.

The auxiliary state Z is as follows :

$$Z = \begin{bmatrix} Z_1 \\ Z_2 \end{bmatrix} = \xi_b + A_0 \xi_a = A_1 \xi_1 + A_2 \xi_2 = \begin{bmatrix} S_1 \\ S_2 \end{bmatrix} + \begin{bmatrix} k_1 & 0 \\ -k_3 & k_2 \end{bmatrix} \begin{bmatrix} X_1 \\ X_2 \end{bmatrix} \quad (4.60)$$

Clearly the matrix A_2 is full rank. Straightforward calculations then lead to the following expressions :

$$\Phi(\xi_1, Z) = \begin{bmatrix} S_1(S_1 - Z_1) & 0 & 0 & 0 \\ 0 & S_1(S_1 - Z_1) & S_2(S_2 - Z_2) & S_2(S_1 - Z_1) \end{bmatrix} \quad (4.61.a)$$

$$\theta = \begin{bmatrix} \theta_1 \\ \theta_2 \\ \theta_3 \\ \theta_4 \end{bmatrix} = \begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \alpha_1 k_3 / k_1 \\ \alpha_2 \\ k_3 / \alpha_2 k_1 \end{bmatrix} \quad (4.61.b)$$

We notice that the new model is now "underparametrized" in the sense that it contains only four parameters $\theta_1, \theta_2, \theta_3, \theta_4$, although the initial system contained five unknown parameters, $\alpha_1, \alpha_2, k_1, k_2, k_3$. Therefore, as appears clearly from (4.61), there is no hope to recover all the α_i and k_i from θ .

On the other hand, if we consider the same example, but assume that the measured state is $\xi_1 = [X_1 \ X_2]$, then the calculations lead to the following expressions for Φ and θ :

$$\Phi(\xi_1, Z) = \begin{bmatrix} X_1 Z_1 - X_1^2 & 0 & 0 & 0 \\ 0 & 0 & X_2 Z_2 & X_1 X_2 - X_2^2 \end{bmatrix} \quad (4.62.a)$$

$$\theta^T = [\theta_1 \ \theta_2 \ \theta_3 \ \theta_4 \ \theta_5]^T = [\alpha_1 \ \alpha_1 k_1 \ \alpha_2 \ \alpha_2 k_3 \ \alpha_2 k_2] \quad (4.62.b)$$

In this case, the reparametrization θ is identical to that which would be used when the full state is measured (Section 4.2.1). Therefore, it is clearly invertible:

$$\alpha_1 = \theta_1 \quad k_1 = \frac{\theta_2}{\theta_1} \quad \alpha_2 = \theta_3 \quad k_3 = \frac{\theta_4}{\theta_3} \quad k_2 = \frac{\theta_5}{\theta_3}$$

Comments

- 1) The equivalent model (4.51) has been introduced under the condition that the matrix A_2 is left invertible. There are however particular situations in which a suitable model of the form (4.51) can be derived even if the matrix A_2 is not left invertible. This issue has been already discussed in Section 4.1.
- 2) As in Chapter 3, the convergence of the parameter estimators presented above is guaranteed only if the regressor matrix $\Phi(\xi)$ or $\Phi(\xi_1, Z)$ is persistently exciting (see Appendix 3). This condition is easily fulfilled when the yield coefficients are known (see for example Theorems 3.2 and 3.3). But the problem is dramatically more difficult when the yield coefficients are unknown. Actually the problem of deriving sufficient experimental conditions so as to assure the persistency of excitation of regressors in nonlinear systems is at the time of writing still an open question in the field of control science. Only very limited results are available. As a matter of illustration, it can be shown for example, that the following conditions are sufficient to guarantee that the regressor (4.57.a) of example 1 (simple microbial growth) is persistently exciting :

C1. The dilution rate is positive and constant :

$$0 < D = \text{constant}$$

C2. The influent substrate concentration S_{in} is :

- persistently exciting of order 2 (see Appendix 3)

- piecewise continuous

- bounded as follows :

$$0 < 2D \frac{\theta_{2\max}}{\theta_{1\min}} \leq S_{in} \leq S_{\max}$$

where $\theta_{1\min}$ and $\theta_{2\max}$, respectively, are known lower and upper bounds on θ_1 and θ_2 such that $2\theta_{2\max} \geq \theta_{1\min}$.

Simulation result

Fig.4.4 shows a simulation result of the estimation problem of example 1 (simple microbial growth). The simulation has been performed under the following conditions :

$$\begin{array}{ll} \alpha = 0.4 \text{ l/g.d} & k_1 = 0.25 \\ X(0) = 0.7 \text{ g/l} & S(0) = 0.25 \text{ g/l} \\ D(0) = 0.1 \text{ d}^{-1} & S_{in}(0) = 2 \text{ g/l} \end{array}$$

This means that a Blackman model (see Appendix 1) in limiting conditions has been chosen :

$$\mu = \alpha S$$

with $\alpha = \text{constant}$

Random amplitude step functions of the inputs D and S_{in} have been applied to the process (Fig. 4.4.a&b).

A discrete-time least squares estimation algorithm has been implemented to estimate θ_1 and θ_2 . It specialises here as follows :

$$\hat{Z}_{t+1} = \hat{Z}_t - TD_t \hat{Z}_t + TD_t S_{in,t} \quad (4.63.a)$$

$$\begin{bmatrix} \hat{\theta}_{1t+1} \\ \hat{\theta}_{2t+1} \end{bmatrix} = \begin{bmatrix} \hat{\theta}_{1t} \\ \hat{\theta}_{2t} \end{bmatrix} + T \Gamma_t \hat{\phi}_t^T (X_{t+1} - X_t + TD_t X_t - \hat{\theta}_{1t} T \hat{Z}_t X_t + \hat{\theta}_{2t} T X_t^2) \quad (4.63.b)$$

$$\Gamma_{t+1} = \frac{\Gamma_t}{\lambda} \left(I - \frac{\hat{\phi}_t^T \hat{\phi}_t \Gamma_t^T}{\lambda + T^2 \hat{\phi}_t^T \Gamma_{t-1} \hat{\phi}_t} \right) \quad (4.63.c)$$

$$\text{with } \Gamma_t = \begin{bmatrix} \gamma_{11t} & \gamma_{12t} \\ \gamma_{21t} & \gamma_{22t} \end{bmatrix} \quad (4.63.d)$$

$$\hat{\phi}_t = [\hat{Z}_t X_t \quad -X_t^2] \quad (4.63.e)$$

$$0 < \lambda \leq 1 \quad (4.63.f)$$

A sampling period T of 1 hour has been chosen. The following initial conditions and forgetting factor have been used in the estimator :

$$\hat{\theta}_{10} = \hat{\theta}_{20} = 0 \quad \hat{Z}_0 = 2 \text{ g/l} \quad \Gamma_0 = 10^7 * I \quad \lambda = 1$$

Fig.4.4.c&d show the convergence of the estimates of θ_1 and θ_2 to their true constant values. From (4.45.e), we know that the estimation of the specific reaction rate α is directly given by $\hat{\theta}_1$:

$$\alpha_1 = \hat{\theta}_{1t}$$

Fig.4.4.e shows the reconstruction (4.45.f) of the yield coefficient k_1 from the estimates of θ_1 and θ_2 :

$$\hat{k}_{1t} = \frac{\hat{\theta}_{2t}}{\hat{\theta}_{1t}}$$

Note that, in the simulation of Fig.4.4, both the influent substrate S_{in} , as well as the dilution rate D , fulfill the first requirement of condition C2 (persistence of excitation of order 2). It has been observed in practical implementation that a time-varying dilution rate $D(t)$ induces more excitation to the estimator and therefore improves the convergence rate of the algorithm.

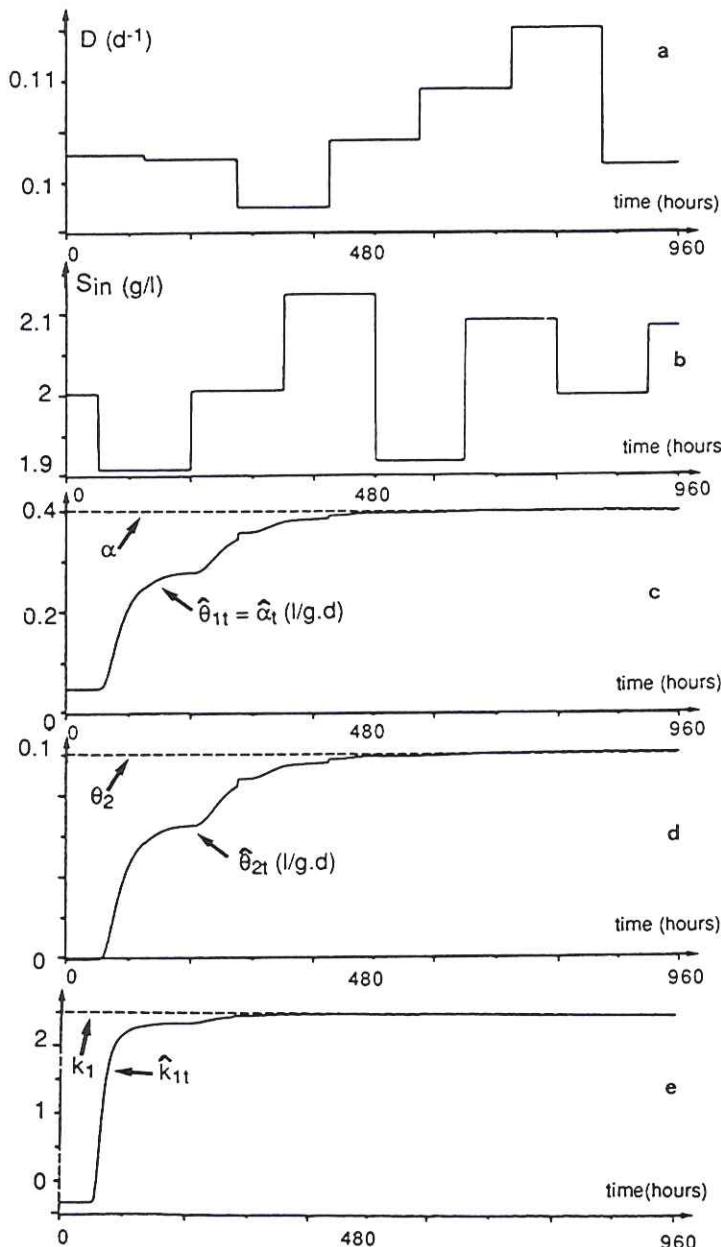


Fig.4.4. On-line estimation of the specific reaction rate and the yield coefficient in a basic microbial growth process

4.3. Adaptive Observers

In Section 4.2.2 we examined the problem of joint estimation of the yield coefficients k_i and the specific reaction rates α_j from partial state measurement ξ_1 . It is a natural extension to investigate the possibility of jointly estimating the yield coefficients, the specific reaction rates and the missing states. Algorithms designed for that purpose are called *adaptive observers* because these are state observers as defined in Chapter 3, which are made adaptive by introducing on-line parameter estimation. The design of adaptive observers for nonlinear systems in general is still, nowadays, a matter of intense research. It is beyond the scope of this book to report on the state-of-the-art of that topic. We limit ourselves to a review of three possible solutions, without further comment.

Extended Luenberger adaptive observer

A first solution is the combination of a Luenberger observer (3.2) with the observer-based parameter estimator (4.52). The adaptive observer is as follows :

Extended Luenberger adaptive observer

$$\frac{d\hat{\xi}}{dt} = \Phi(\hat{\xi})\hat{\theta} - D\hat{\xi} + F - Q + \Omega(\xi - \hat{\xi}) \quad (4.64.a)$$

$$\frac{d\hat{\theta}}{dt} = \Phi^T(\hat{\xi})\Gamma(\xi_1 - \hat{\xi}_1) \quad (4.64.b)$$

Extended Kalman filtering

As we have discussed in Chapter 3, extended Kalman filtering can be used either for state estimation (Section 3.2.2) or for parameter estimation (Section

3.4.6). Obviously, it can also be used for both together. In that case, the adaptive observer is written as follows (compare with (3.133)) :

Extended Kalman filter

$$\frac{d\hat{\xi}}{dt} = \Phi(\hat{\xi}, \hat{\theta})\hat{\theta} - D\hat{\xi} + F - Q + \Omega_1(\hat{\xi}, \hat{\theta})(\xi_1 - \hat{\xi}_1) \quad (4.65.a)$$

$$\frac{d\hat{\theta}}{dt} = \Omega_2(\hat{\xi}, \hat{\theta})(\xi_1 - \hat{\xi}_1) \quad (4.65.b)$$

where Ω_1 and Ω_2 are updated by an appropriate Riccati equation.

An asymptotic adaptive observer

A third solution, which is more closely related to the results of Section 4.2.2, is the following one. We suppose that all the yield coefficients involved in A_1 and A_2 (equation (4.46)) can be calculated from θ . An adaptive observer is then readily obtained by augmenting the observer based parameter estimator (4.52) as follows :

Asymptotic adaptive observer

$$\frac{d\hat{Z}}{dt} = -D\hat{Z} + F_b - Q_b \quad (4.66.a)$$

$$\frac{d\hat{\xi}_1}{dt} = \Phi(\xi_1, \hat{Z})\hat{\theta} - D\xi_1 + F_1 - Q_1 - \Omega_1(\xi_1 - \hat{\xi}_1) \quad (4.66.b)$$

$$\frac{d\hat{\theta}}{dt} = \Phi^T(\xi_1, \hat{Z})\Gamma(\xi_1 - \hat{\xi}_1) \quad (4.66.c)$$

$$\hat{\xi}_2 = \hat{A}_2^+(\hat{Z} - \hat{A}_1\xi_1) \quad (4.66.d)$$

where \hat{A}_2^+ and \hat{A}_1 respectively denote the matrices A_2^+ and A_1 whose nonzero entries are substituted by the corresponding estimates.

Example : simple microbial growth process

Let us return to example 1 of Section 4.2.2. The Luenberger adaptive observer is written :

$$\frac{d\hat{X}}{dt} = \hat{S}\hat{X}\hat{\theta}_1 - D\hat{X} + \omega_1(X - \hat{X}) \quad (4.67.a)$$

$$\frac{d\hat{S}}{dt} = -\hat{S}\hat{X}\hat{\theta}_2 - D\hat{S} + DS_{in} + \omega_2(X - \hat{X}) \quad (4.67.b)$$

$$\frac{d\hat{\theta}_1}{dt} = \gamma_1\hat{S}\hat{X}(X - \hat{X}) \quad (4.67.c)$$

$$\frac{d\hat{\theta}_2}{dt} = -\gamma_2\hat{S}\hat{X}(X - \hat{X}) \quad (4.67.d)$$

The asymptotic adaptive observer is written :

$$\frac{d\hat{Z}}{dt} = -D\hat{Z} + DS_{in} \quad (4.68.a)$$

$$\frac{d\hat{X}}{dt} = \hat{Z}\hat{X}\theta_1 - X^2\theta_2 - DX + \omega(X - \hat{X}) \quad (4.68.b)$$

$$\frac{d\hat{\theta}_1}{dt} = \gamma_1\hat{Z}X(X - \hat{X}) \quad (4.68.c)$$

$$\frac{d\hat{\theta}_2}{dt} = -\gamma_2X^2(X - \hat{X}) \quad (4.68.d)$$

$$\hat{S} = \hat{Z} - \frac{\hat{\theta}_2}{\hat{\theta}_1}X \quad (4.68.e)$$

Simulation result

Fig.4.5 shows the complementary simulation result of Fig.4.4, i.e. the adaptive observation of the substrate concentration S with equation (4.68.e) where $\hat{\theta}_1$ and $\hat{\theta}_2$ are given by (4.63.b) as shown in Fig.4.4.c&d.

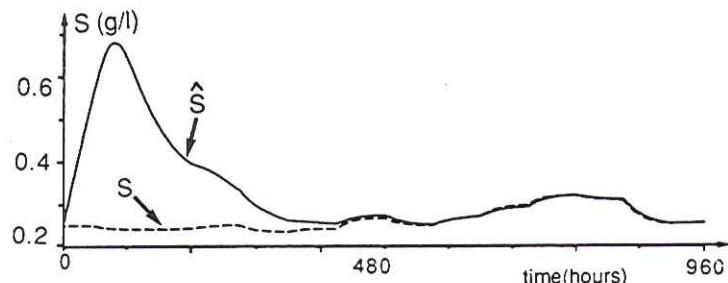


Fig.4.5. Adaptive observation of S

4.4. Estimation of Yield Coefficients

4.4.1. The estimation problem

In this section we shall address the problem of estimating the yield coefficients independently of the reaction rates. We consider biotechnological processes described by the general dynamical model (1.43) :

$$\frac{d\xi}{dt} = K\phi(\xi) - D\xi + F - Q \quad (1.43) = (4.69)$$

under the following conditions :

- 1) the yield coefficients (matrix K) are *unknown*;
- 2) the reaction rates $\phi(\xi)$ are unknown;
- 3) the full state ξ is measured;

- 4) the substrate feed rates F, the gaseous outflow rates Q and the culture volume V are measured.

On this basis, we investigate the possibility of estimating the yield coefficients independently of the reaction rates. In a first step we derive a linear regression form equivalent to the model (4.69) but independent of the reaction rates $\phi(\xi)$.

4.4.2. A linear regression form

We consider a partition of the model (4.69), as defined in Section 1.7 :

$$\frac{d\xi_a}{dt} = K_a\phi(\xi) - D\xi_a + F_a - Q_a \quad (1.68) = (4.70)$$

$$\frac{d\xi_b}{dt} = K_b\phi(\xi) - D\xi_b + F_b - Q_b \quad (1.69) = (4.71)$$

with $\dim(\xi_a) = p = \text{rank}(K)$ and $\dim(\xi_b) = N-p$

We define the auxiliary time-varying quantities :

$$\eta_a(t) \stackrel{\Delta}{=} V(t)\xi_a(t) - V(0)\xi_a(0) + \int_0^t [F_{out}\xi_a + V(Q_a - F_a)]d\tau \quad (4.72)$$

$$\eta_b(t) \stackrel{\Delta}{=} V(t)\xi_b(t) - V(0)\xi_b(0) + \int_0^t [F_{out}\xi_b + V(Q_b - F_b)]d\tau \quad (4.73)$$

where V denotes the culture volume and F_{out} the effluent flow rate (see Section 1.1). Note in the integral of expressions (4.72) and (4.73) that the first term ($F_{out}\xi_a$ and $F_{out}\xi_b$, respectively) is equal to zero in batch and fed-batch reactors and that the second term ($V(Q_a - F_a)$ and $V(Q_b - F_b)$, respectively) represents the cumulated mass of feed introduced and of gas produced.

Then, according to the structural property of Section 1.7, straightforward calculations and integration lead to the following relationship between $\eta_a(t)$ and $\eta_b(t)$:

$$\eta_b(t) = -A_0 \eta_a(t) \quad (4.74)$$

where A_0 is the solution of the matrix equation (1.71) :

$$A_0 K_a + K_b = 0 \quad (4.75)$$

Most often, K_a is a square $M \times M$ nonsingular matrix, such that $A_0 = -K_b K_a^{-1}$ and (4.74) is rewritten :

$$\eta_b(t) = (K_b K_a^{-1}) \eta_a(t) \quad (4.76)$$

Let us now denote by $\theta = [\theta_1, \dots, \theta_l]^T$ ($\dim(\theta) = l$) the vector of the entries of the matrix A_0 which are not identically zero. Expression (4.76) is rewritten in the following linear regression form :

$$\eta_b(t) = R^T(\eta_a(t))\theta \quad (4.77)$$

where $R^T(\eta_a(t))$ is a $(N-p) \times l$ matrix, function of $\eta_a(t)$.

It is worth noting that this form is independent of the kinetics.

4.4.3 Example 1 : PHB acid production process

Consider the state space model (1.66) for intracellular production of PHB acid, with the following state partition :

$$\xi_a = \begin{bmatrix} X \\ S_1 \end{bmatrix} \quad \xi_b = \begin{bmatrix} S_2 \\ P_1 \\ C \\ P_2 \end{bmatrix} \quad (4.78)$$

with X being biomass, S_1 fructose, S_2 ammonia, P_1 PHB acid, P_2 carbon dioxide, and C oxygen. The corresponding partition of the matrix K is written :

$$K_a = \begin{bmatrix} 1 & 0 \\ -k_1 & -k_5 \end{bmatrix} \quad K_b = \begin{bmatrix} -k_2 & 0 \\ k_3 & 1 \\ -k_4 & -k_6 \\ k_7 & k_8 \end{bmatrix} \quad (4.79)$$

The matrix $-A_0 = K_b K_a^{-1}$ is calculated as follows :

$$K_b K_a^{-1} = \begin{bmatrix} -k_2 & 0 \\ k_3 \frac{k_1}{k_5} & \frac{-1}{k_5} \\ -k_4 + \frac{k_1 k_6}{k_5} & \frac{k_6}{k_5} \\ k_7 \frac{k_1 k_8}{k_5} & \frac{-k_8}{k_5} \end{bmatrix} \quad (4.80)$$

We see that this matrix contains $l = 7$ nonzero entries, so that we define the vector $\theta = [\theta_1, \dots, \theta_7]^T$:

$$\begin{aligned} \theta_1 &= -k_2 & \theta_2 &= -k_3 - \frac{k_1}{k_5} & \theta_3 &= k_4 - \frac{k_1 k_6}{k_5} & \theta_4 &= k_7 - \frac{k_1 k_8}{k_5} \\ \theta_5 &= -\frac{1}{k_5} & \theta_6 &= \frac{k_6}{k_5} & \theta_7 &= -\frac{k_8}{k_5} \end{aligned} \quad (4.81)$$

Finally the matrix $R^T(\eta_a)$ is defined as follows :

$$R^T(\eta_a) = \begin{bmatrix} \eta_{a1} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \eta_{a1} & 0 & 0 & \eta_{a2} & 0 & 0 \\ 0 & 0 & \eta_{a1} & 0 & 0 & \eta_{a2} & 0 \\ 0 & 0 & 0 & \eta_{a1} & 0 & 0 & \eta_{a2} \end{bmatrix} \quad (4.82)$$

where :

$$\eta_a = \begin{bmatrix} \eta_{a1} \\ \eta_{a2} \end{bmatrix} = \begin{bmatrix} V(t)X(t) - V(0)X(0) + \int_0^t F_{out}X d\tau \\ V(t)S_1(t) - V(0)S_1(0) + \int_0^t [F_{out}S_1 - F_{in}S_{1,in}] d\tau \end{bmatrix} \quad (4.83)$$

4.4.4. Estimators of the parameter vector θ

Suppose that measurements of ξ , F and Q have been collected during a time interval $[0, t_f]$. Obviously, expression (4.77) naturally suggests the use of a linear regression technique to estimate θ independently of the reaction rates $\varphi(\xi)$. The standard least squares algorithm is written as follows in this case :

$$\hat{\theta} = \left\{ \int_0^{t_f} [R(\eta_a)R^T(\eta_a)] d\tau \right\}^{-1} \int_0^{t_f} [R(\eta_a)\eta_b] d\tau \quad (4.84)$$

The matrix inversion can be avoided by using a recursive form of this algorithm (compare, for instance, with (4.39)) :

$$\frac{d\hat{\theta}}{dt} = \Gamma R(\eta_a)[\eta_b - R^T(\eta_a)\hat{\theta}] \quad (4.85.a)$$

$$\frac{d\Gamma}{dt} = -\Gamma R(\eta_a) R^T(\eta_a) \Gamma \quad (4.85.b)$$

4.4.5. Example 2 : Basic microbial growth process with a synthesis product

Consider a basic microbial growth process with a synthesis product P :



Its dynamics are described by the following model :

$$\frac{d}{dt} \begin{bmatrix} S \\ X \\ P \end{bmatrix} = \begin{bmatrix} -k_1 \\ 1 \\ k_2 \end{bmatrix} \varphi - D \begin{bmatrix} S \\ X \\ P \end{bmatrix} + \begin{bmatrix} DS_{in} \\ 0 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ Q \end{bmatrix} \quad (4.87)$$

Consider for instance the following state partition (ξ_a, ξ_b) :

$$\xi_a = P \quad \xi_b^T = [S, X] \quad (4.88)$$

Then A_0 is clearly equal to :

$$A_0 = \begin{bmatrix} \frac{k_1}{k_2} \\ -1 \\ \frac{-1}{k_2} \end{bmatrix} \quad (4.89)$$

Equation (4.76) specialises here as follows :

$$\eta_b = \begin{bmatrix} \theta_1 \\ \theta_2 \end{bmatrix} R(\eta_a) \quad (4.90)$$

with :

$$\begin{bmatrix} \eta_b \\ \eta_a \end{bmatrix} = \begin{bmatrix} V(t)S(t) - V(0)S(0) + \int_0^t [F_{out}S - F_{in}S_{in}]d\tau \\ V(t)X(t) - V(0)X(0) + \int_0^t F_{out}Xd\tau \end{bmatrix} \quad (4.91.a)$$

$$R(\eta_a) = -\eta_a(t) = -V(t)P(t) + V(0)P(0) - \int_0^t [F_{out}P + VQ]d\tau \quad (4.91.b)$$

$$\begin{bmatrix} \theta_1 \\ \theta_2 \end{bmatrix} = \begin{bmatrix} k_1 \\ k_2 \\ -1 \\ \frac{k_1}{k_2} \end{bmatrix} \quad (4.91.c)$$

The above relation is obviously invertible :

$$k_2 = -\frac{1}{\theta_2} \quad (4.92.a)$$

$$k_1 = -\frac{\theta_1}{\theta_2} \quad (4.92.b)$$

And the yield coefficient k_1 and k_2 can be estimated from S , X and P .

If X is not available for measurement, but only S and P , we can still estimate $\theta_1 = k_1/k_2$, which is the expression of the yield from S to P . This is now illustrated with a real-life experiment.

Real-life implementation on an anaerobic digestion pilot reactor

Consider a two-step anaerobic digestion process in which the methanization phase is assumed to be rate-limiting. The process can then be described by the reaction scheme (4.86) where S is the organic matter and P the methane.

The estimation of k_1/k_2 has been implemented on a 60 liter CSTR pilot reactor (Unit of Biogineering, Catholic University of Louvain, Belgium) over a period of 14 days by using a discrete-time least square estimation algorithm.

By taking account of the low solubility of the methane (see Section 1.8.4), a discrete-time version of the estimator (4.85) specialises here as follows (with an additional forgetting factor) :

$$\hat{\theta}_{1,t+1} = \hat{\theta}_{1,t} + \gamma_t R(\eta_{at})[\eta_{bt} - \hat{\theta}_{1,t}R(\eta_{at})] \quad (4.93.a)$$

$$\gamma_t = \frac{\gamma_{t-1}}{\lambda + \gamma_{t-1}R(\eta_{at})^2} \quad 0 < \lambda \leq 1 \quad \gamma_0 > 0 \quad (4.93.b)$$

$$R(\eta_{at}) = -\int_0^t VQd\tau \quad (4.93.c)$$

$$\eta_{bt} = V(t)S(t) - V(0)S(0) + \int_0^t [FS - FS_{in}]d\tau \quad (4.93.d)$$

with $F = F_{out} = F_{in} = DV$ (since the bioreactor is a CSTR).

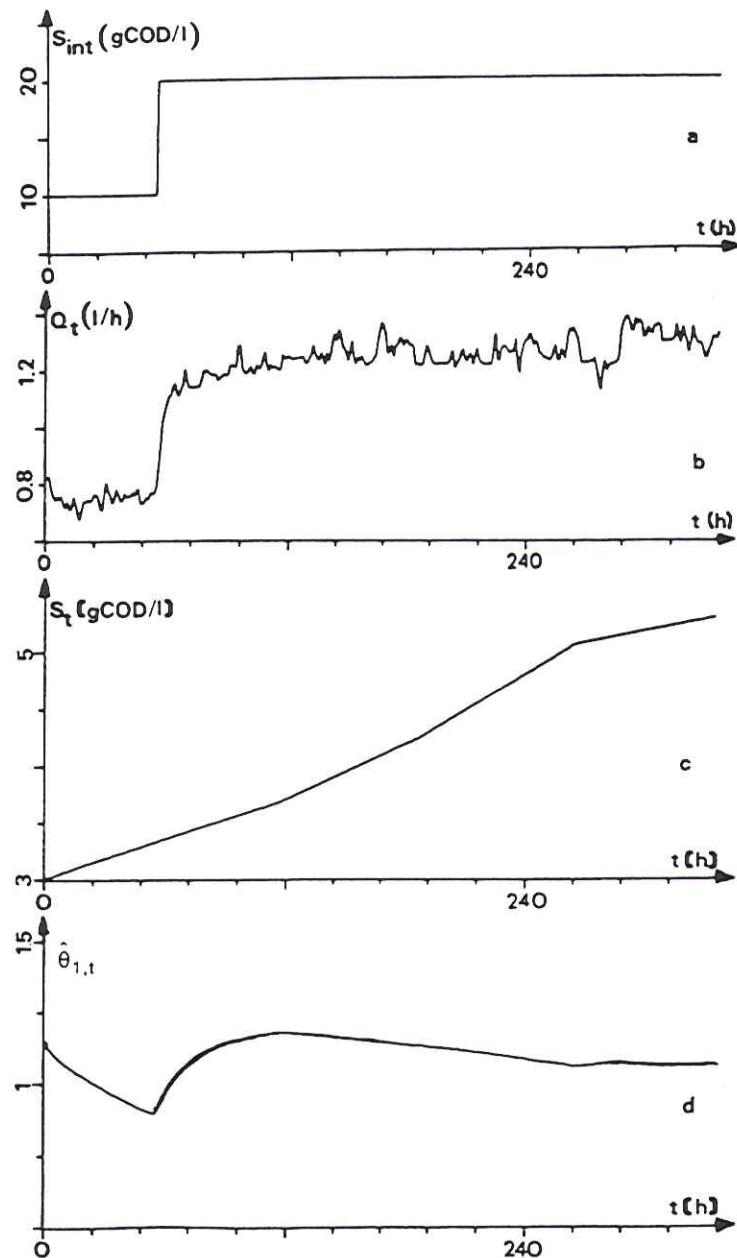
The reactor was operated under the following conditions. The dilution rate D was set to 0.1 d^{-1} and a step of influent substrate concentration S_{in} (from 10 to 20 gCOD/l) was applied during the second day of the experiment (Fig.4.6.a). The on-line measurements of the methane gas flow rate Q and of the substrate concentration S are shown in Fig.4.6.b-c. The sampling period T is equal to 1 hour. The estimation of θ_1 shown in Fig.4.6.d was performed under the following conditions :

$$\hat{\theta}_{1,0} = 1.15, \gamma_0 = 0.3, \lambda = 0.99 \quad (4.94)$$

Note that $\hat{\theta}_1$ converges to a value close to 1.1, which corresponds to the following physical value.

Simple calculation of k_1/k_2

An approximate value of the yield coefficient $\theta_1 = k_1/k_2$ can be deduced by using the following line of reasoning.

Fig.4.6. Estimation of θ_1

It is usually considered that in an anaerobic digestion process, when 1 g COD is decomposed, in the mean 0.1 g is used for the production of acidogenic bacteria and 0.9 g for the production of volatile acids (VA). Of this 0.9 g, 0.02 g is used for the production of methanogenic bacteria and 0.88 g under the form of methane gas CH₄.

$$1 \text{ g COD} \rightarrow 0.1 \text{ g COD : } X_{\text{acidogenic}}$$

$$\rightarrow 0.9 \text{ g COD : VA} \rightarrow 0.02 \text{ g COD } X_{\text{methanogenic}}$$

$$\rightarrow 0.88 \text{ g COD CH}_4$$

At a temperature T = 35°C and a pressure p = 1 atm (which corresponds to the physical operating conditions), 1 mole of CH₄ correspond to 64 g COD and 25.3 l CH₄.

$$1 \text{ mole CH}_4 \rightarrow 64 \text{ g COD} \rightarrow 25.3 \text{ l CH}_4$$

This gives a conversion ratio CH₄/COD equal to 2.53 g COD/l CH₄. A mean theoretical value of θ_1 can then be deduced :

$$\theta_1 = \frac{2.53 \times 24}{0.88 \times 60} = 1.15 \frac{\text{g COD} \times \text{h}}{\text{l CH}_4 \times \text{day} \times \text{l reactor}}$$

The term 24/60 is introduced in order to take account of the fact that the methane gas flow rate is expressed in h⁻¹ (instead of day⁻¹ × 1 reactor) (the volume of the reactor is here equal t°60 l).

4.4.6. Structural identifiability of the yield coefficients

With the algorithm (4.84), we have a tool for estimating the parameter θ . But our goal is actually to estimate the yield coefficients, i.e. the vector $k = k_1, k_2, \dots, k_m$). Clearly, as illustrated with (4.81), θ is a nonlinear rational function of k , which we write formally as follows :

$$\theta = f(k)$$

Therefore the question arises whether k can be calculated from a knowledge of θ or not. This is called the *structural identifiability* issue. It is evidently of interest to be able to detect beforehand those models which are not identifiable whatever the experimental conditions. A first trivial condition is obviously that the number of unknown yield coefficients cannot be larger than the number of parameters θ_i . For example the yield coefficients of the PHB adipic production process are certainly not identifiable (independently of the kinetics) since the number of unknowns is eight while there are only seven parameters θ_i (see (4.81)). (For further details on the structural identifiability issue of the yield coefficients k_i , see the bibliography.)

4.5. Other Parameter Estimation Issues in Bioreactors

At this stage, we would like to remind the reader of the important remark which we made in Section 1.5.2, regarding the general dynamical model (1.43) :

$$\frac{d\xi}{dt} = K\varphi(\xi) - D\xi + F - Q \quad (1.43) = (4.95)$$

This model is a combination of two terms : $K\varphi(\xi)$ describes the process kinetics while $-D\xi + F - Q$ represents the mass transport (or dilution) dynamics.

In Chapters 3 and 4, we have focused either on the real time estimation of the state ξ or on the estimation of the parameters related to the kinetics $K\varphi(\xi)$. But unknown parameters can also be hidden in the transport dynamics, for which the methods followed so far may easily be extended. Two such issues are briefly examined in this section.

4.5.1. Estimation of specific liquid gas transfer rates

In Section 1.5.4 we argued that it is legitimate to consider that the gaseous outflow rates Q_i are proportional to the concentrations ξ_i in the liquid phase :

$$Q_i = \beta_i \xi_i$$

as long as ξ_i is lower than the saturation level. The parameters β_i are termed *specific liquid-gas transfer rates*. Define the vector β containing those parameters β_i . It is then clear that the model (4.95) can be rewritten as follows:

$$\frac{d\xi}{dt} = \Phi(\xi)\theta - D\xi + F - \Psi(\xi)\beta \quad (4.96)$$

where $\Psi(\xi)$ is an $N \times \text{dim}(\beta)$ matrix which depends linearly on ξ .

If we define :

$$\Phi^*(\xi) = [\Phi(\xi), \Psi(\xi)] \quad \theta^* = \begin{bmatrix} \theta \\ \beta \end{bmatrix} \quad (4.97)$$

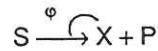
this model (4.96) can also be written :

$$\frac{d\xi}{dt} = \Phi^*(\xi)\theta^* - D\xi + F \quad (4.98)$$

It is then evident that the augmented parameter θ^* can be estimated by any of the algorithms which have been built for θ , only replacing Φ by Φ^* and θ by θ^* . It is, however, necessary that the augmented regressor Φ^* is persistently exciting. A simple example illustrates the definitions.

Example

Consider the process :



where S is the substrate, X the biomass and P a gasifiable product (e.g. CO₂).

The dynamical model is as follows :

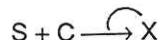
$$\frac{d}{dt} \begin{bmatrix} X \\ S \\ P \end{bmatrix} = \underbrace{\begin{bmatrix} SX & 0 & 0 \\ 0 & -SX & 0 \\ 0 & 0 & SX \end{bmatrix}}_{\Phi(\xi)} \underbrace{\begin{bmatrix} \alpha \\ -k_1\alpha \\ k_2\alpha \end{bmatrix}}_{\theta} - D \begin{bmatrix} S \\ X \\ P \end{bmatrix} + \begin{bmatrix} 0 \\ DS_{in} \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ P \end{bmatrix} \underbrace{\beta}_{\Psi(\xi)}$$

Hence the augmented regressor and parameter are defined :

$$\Phi^*(\xi) = \begin{bmatrix} SX & 0 & 0 & 0 \\ 0 & -SX & 0 & 0 \\ 0 & 0 & SX & P \end{bmatrix} \quad \theta^* = \begin{bmatrix} \alpha \\ -k_1\alpha \\ k_2\alpha \\ \beta \end{bmatrix}$$

4.5.2. Estimation of oxygen related parameters

Another typical application, which has given rise to numerous studies (see the bibliography), concerns the parameters related to the dissolved oxygen concentration, which is often the most easily measurable state. Consider an aerobic process described by the following scheme :



with S the substrate, X the biomass and C the dissolved oxygen. The biomass and dissolved oxygen dynamics are written (see Section 1.5.5) :

$$\frac{dX}{dt} = \mu X - DX \quad (4.99.a)$$

$$\frac{dC}{dt} = -k_2\mu X - DC + k_L a(C_S - C) \quad (4.99.b)$$

where $k_L a$ and C_S denote the mass transfer coefficient and the saturation concentration, respectively. These equations may be reformulated as follows :

$$\begin{aligned} \frac{d}{dt} \begin{bmatrix} X \\ C \end{bmatrix} &= \begin{bmatrix} X & 0 & 0 & 0 \\ 0 & -X & 1 & -C \end{bmatrix} \begin{bmatrix} \mu \\ k_2\mu \\ k_L a C_S \\ k_L a \end{bmatrix} - D \begin{bmatrix} X \\ C \end{bmatrix} \\ &\stackrel{\Delta}{=} \Phi^*(\xi) \theta^* - D \xi \end{aligned}$$

with

$$\Phi^*(\xi) = \begin{bmatrix} X & 0 & 0 & 0 \\ 0 & -X & 1 & C \end{bmatrix} \text{ and } \theta^* = \begin{bmatrix} \theta_1 \\ \theta_2 \\ \theta_3 \\ \theta_4 \end{bmatrix} = \begin{bmatrix} \mu \\ k_2\mu \\ k_L a C_S \\ k_L a \end{bmatrix}$$

The model is thus clearly in the correct format for parameter estimation. We notice, in addition, that the reparametrization θ^* is invertible (see the discussion in Section 4.2.1), that is estimates of μ , k_2 , $k_L a$ and C_S can be recovered as follows :

$$\hat{\mu} = \hat{\theta}_1 \quad \hat{k}_2 = \frac{\hat{\theta}_2}{\hat{\theta}_1} \quad \hat{k}_L a = \hat{\theta}_4 \quad \hat{C}_S = \frac{\hat{\theta}_3}{\hat{\theta}_4}$$

In addition, an on-line estimate of the *oxygen uptake rate* OUR (see Section 1.2) is given by :

$$\hat{\text{OUR}} = \hat{\theta}_2 \hat{\text{X}}$$

Numerous variants for the estimation of oxygen related parameters in aerobic processes have been proposed in the literature (see the bibliography). For instance, one can assume that the mass transfer coefficient $k_L a$ is proportional to the aeration flow rate (see Section 1.5.5) :

$$k_L a = k_0 F_g$$

and hence one can rewrite (4.99) as follows :

$$\frac{dC}{dt} = [-1 \quad F_g \quad -CF_g] \begin{bmatrix} \text{OUR} \\ k_0 C_s \\ k_0 \end{bmatrix} - DC$$

i.e., one can proceed directly to the estimation of the oxygen uptake rate OUR, together with the parameters k_0 and C_s .

4.6. References and Bibliography

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Several examples of the on-line estimation of the specific growth rates independently of the yield coefficients are presented in the following paper :

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Narendra K.S. and A.M. Annaswamy (1989). *Stable Adaptive Systems*. Prentice-Hall, Englewood Cliffs.

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Section 4.5

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- Holmberg A. (1983b). A microprocessor-based estimation and control system for the activated sludge process. In A. Halme (Ed.), *Modelling and Control of Biotechnical Processes*, Pergamon, Oxford, 111-120.
- Holmberg U. and G. Olsson (1986). Simultaneous on-line estimation of oxygen transfer rate and respiration rate. In A. Johnson (Ed.), *Modelling and Control of Biotechnological Processes*, Pergamon, Oxford, 205-209.
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- Marsili-Libelli S., R. Giardi and M. Lasagni (1985). Self-tuning control of the activated sludge process. *Environmental Technology Letters*, **6** (12), 576-583.

CHAPTER 5

ADAPTIVE CONTROL OF BIOREACTORS

5.0. Introduction

We are concerned in this chapter with the control of state variables in bioprocesses. Roughly speaking, the purpose of control is to keep some process state variable (or some function of the state variables) close to a prespecified reference value, in spite of disturbances and variations in process kinetics. In the special case where the reference value is *constant*, it is termed a *set point* and control is called *regulation*. A computer controlled bioreactor is schematically represented in Fig.5.1. The feedback loop is clearly apparent : it involves successively the reactor, a set of sensors and measuring devices, the computer and an actuator (here a valve). The *closed loop* system is defined as the combination of the process and the controller within the feedback loop. The process is thus controlled by the computer through the manipulation of the feed rate of one external substrate. The task of the control algorithm, implemented on the computer, is to determine, at each instant, the control action, on the basis of information collected in real time by the sensors or provided by the user via the keyboard. As we see in Fig.5.1, the regulator may also incorporate information from state observers and parameter estimators such as those which were described in Chapters 3 and 4. Our main concern in this chapter will be the design of control *algorithms* for bioreactors. Depending on the context, a control algorithm will also be called a control law, controller or regulator. Before embarking on this, we would like to discuss briefly the significance of control in bioreactors.

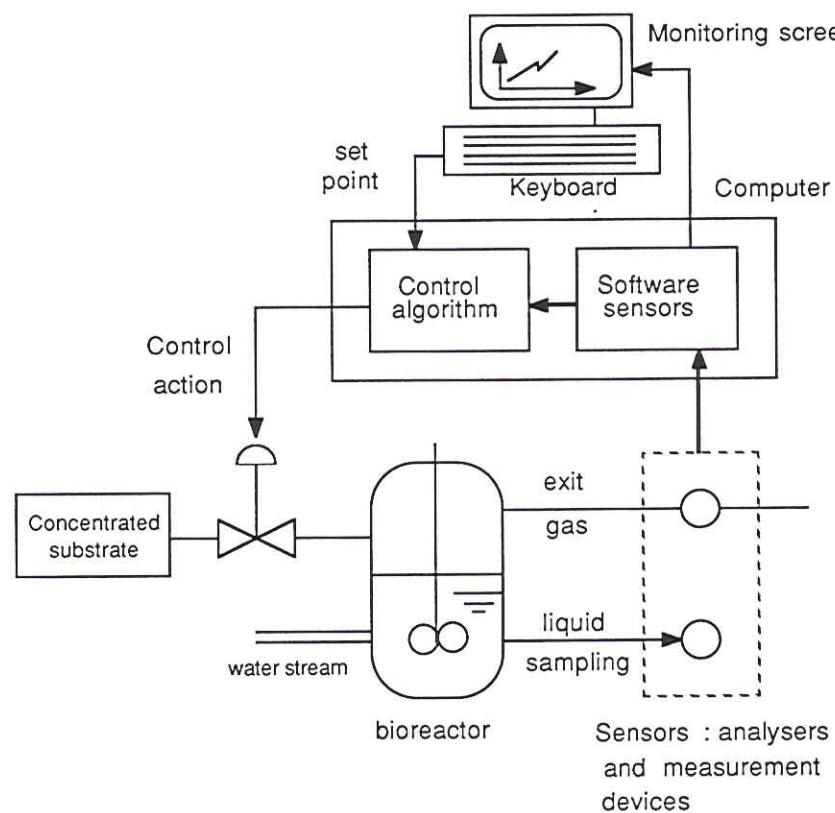


Fig.5.1 Computer control system for bioreactors

demonstrate in this chapter) that significant performance improvements (in terms of yield and/or productivity) may be expected from the control of the biological variables themselves (such as biomass, substrate or synthesis product). The following examples are typical.

- 1) *Regulation of substrate concentration* in the case where biomass growth is inhibited by high substrate concentrations (see Section 1.3). The challenge is twofold : first, feedback regulation may be needed to stabilise the process, which is intrinsically unstable in open loop (see Section 1.9.3); secondly, a good choice of the set point may contribute to the optimisation of the biomass production as will be discussed in Section 5.7. Moreover, in biological waste water treatment processes, regulation of the substrate concentration is equivalent to controlling the pollution level in the effluent of the plant.
- 2) *Regulation of dissolved oxygen concentration*. In aerobic bioprocesses this concentration must be maintained sufficiently high to guarantee microbial activity. But excessive aeration is undesirable from an economic viewpoint (oxygen in excess is just lost to the atmosphere) and, in addition, can induce biomass settling problems in activated sludge processes.
- 3) *Regulation of product concentration* (e.g. ethanol in yeast fermentation processes). Fed-batch biotechnological processes are often characterised by a conflict between yield and productivity (see Section 5.7). In many instances regulation of the product concentration is an attractive method to maintain the process at an operating point which corresponds to a good trade-off between yield and productivity (see also Section 5.2.4).
- 4) *Regulation of gaseous outflow rates* : for example regulation of the methane flow rate in a biomethanization plant in order to achieve a match between gas production and energy demand (see Section 5.8).

Significance of control in bioreactors

The control of bioreactors, in industrial applications, is usually restricted to the regulation of pH and temperature at constant values which are supposed to be favourable to the microbial growth. However, it should be clear (as we shall

Why adaptive control ?

As we shall see throughout the chapter, the control design problem is solved by appropriate algebraic manipulations of the general dynamical model (1.43) of the process under consideration. The design, however, is carried out as if the process kinetics were known exactly. But, as we have argued many times in this book, since the kinetics are most often poorly known, they are replaced in the control law by suitable on-line estimates provided by one of the various parameter estimators which have been described in Chapters 3 and 4, or others which will be specifically designed in this chapter. Such a controller, equipped with parameter estimation (see Fig.5.1), is called an *adaptive controller* because it has the potential to adapt itself to variations in the kinetics.

Why not conventional control techniques ?

Various conventional control techniques such as PID control or minimum variance control have been used many times (even by the authors of this book) to regulate biological variables in bioreactors. Several relevant references are listed at the end of this chapter. However, these techniques will not be presented here because, in our view, they suffer from the drawback of being based on linear tangent model approximations (see Section 1.9.3) or even on linear "black box" models.

Yet, as we have discussed at length in Chapter 1, we have a crucial prior knowledge of the nonlinear dynamics of the processes, formalised in the general dynamical model (1.43) and its variants. Therefore, improved control performance can be expected from an exploitation of the nonlinear structure of the model in solving the control design problem. In this chapter we shall follow such a nonlinear control approach by repeatedly using a design technique which is called *Exact Linearizing Control*. The difference between this technique and conventional control lies in the way that linearization is introduced in the problem. In a standard approach, one first calculates a

linearized approximation of the model, and then one designs a *linear controller* for this approximate model. But, the *closed loop* remains *nonlinear*

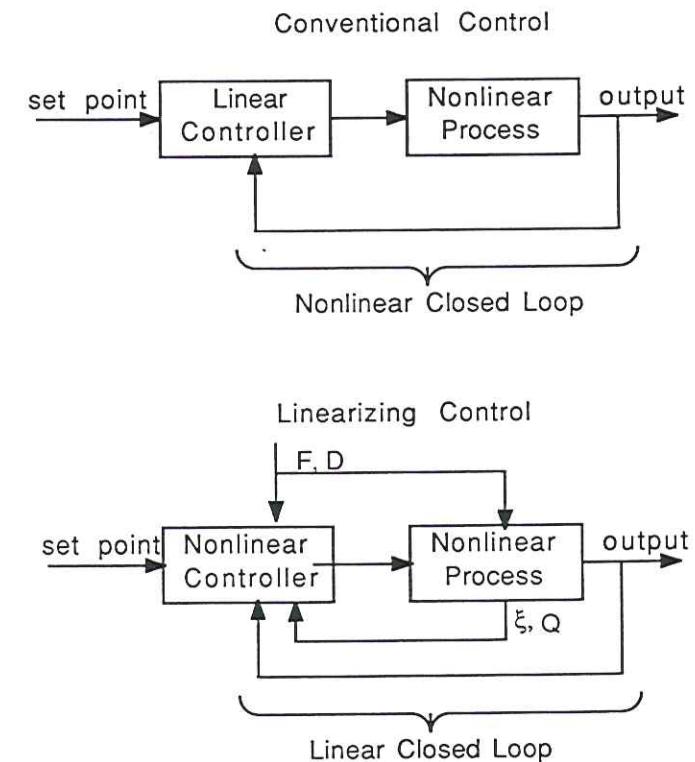


Fig.5.2. Conventional and linearizing control schemes

and is guaranteed to be stabilised only locally but not over a wide range of operating points or around the transient trajectory in fed-batch operation. In the exact linearizing control approach we obtain a *nonlinear controller* which is precisely designed to achieve a *linear closed loop* which is unconditionally stable whatever the operating point or the transient fed-batch trajectory. This is summarized in Fig.5.2.

Outline of the chapter

The control objective and the principle of linearizing control are presented, formalised and illustrated with simple examples in Section 5.1. Some basic notations and definitions used in the sequel and an essential remark on the closed loop stability are also given.

In Section 5.2 we address the linearizing control problem of bioreactors when the kinetics $\phi(\xi)$ are unknown but can be alleviated by a systematic application of the singular perturbation technique. The theory is presented first. Then its motivation is discussed and illustrated with three applications : depollution control, propionate regulation in anaerobic digestion, and ethanol regulation in yeast fermentation. Adaptive implementation is described and real life experiment is reported.

In Section 5.3 we treat the adaptive linearizing control problem when the lack of knowledge of the kinetics $\phi(\xi)$ is explicitly taken into account (by incorporating on-line parameter estimation in the control law) but under the assumption that the yield coefficients are known. Two particular cases are considered : substrate control and product control.

A general solution to the problem is also presented in Section 5.4 for a class of CST bioreactors. The concept of relative degree is introduced.

In Section 5.5, we treat the adaptive linearizing control problem in the case where *both* reaction rates $\phi(\xi)$ and yield coefficients are unknown. The price to pay, however, is that more restrictive structural assumptions are to be considered.

In Section 5.6 we discuss some practical implementation aspects of the proposed control laws.

In Section 5.7 a first case study is carried out in detail : it concerns the adaptive linearizing control of fed-batch bioreactors. The goal is to give a concrete illustration of the design procedure and to emphasize the benefit to be expected from using adaptive control in practical engineering applications, in particular when a yield-productivity conflict occurs. A comparison with optimal control is also presented.

In Section 5.8 a second case study is considered : the adaptive linearizing control of gaseous outflow rates. It is an extension of the preceding adaptive linearizing laws to the regulation of a nonlinear combination of the process variables (not of one process component). We also introduce a modification of the linearizing control algorithm in order to avoid possible division by zero.

5.1. Principle of Linearizing Control and Remarks on Closed Loop Stability

In this chapter, as we have mentioned in the introduction, we shall concentrate on a particular control strategy which is called *state feedback linearizing control* and which is formalised in the present section.

We consider biotechnological processes described by the general dynamical model (1.43) :

$$\frac{d\xi}{dt} = K\phi(\xi) - D\xi + F - Q \quad (1.43) = (5.1)$$

with $\dim(\xi) = N$ and $\dim(\phi) = M$.

The objective is to control a scalar output variable which is a measured linear combination of the state variables :

$$y = \sum_{i=1}^N c_i \xi_i = C^T \xi \quad (5.2)$$

where $C^T = [c_1, c_2, \dots, c_N]$ is a vector of known constants.

The control input (denoted by "u", as is usual in control science terminology) is the feed rate of *one* external substrate of the process (i.e. a substrate which is introduced to the reactor from the outside). This is denoted as follows :

$$\begin{aligned} u &= F_i \text{ for some } i \\ F &= bu + f \\ b^T &= [b_1, b_2, \dots, b_N] \quad b_i = 1, \quad b_j = 0 \quad \forall j \neq i \\ f^T &= [f_1, f_2, \dots, f_N] \quad f_i = 0, \quad f_j = F_j \quad \forall j \neq i \end{aligned} \quad (5.3)$$

With this definition the model (5.1) is rewritten :

$$\frac{d\xi}{dt} = K\phi(\xi) - D\xi + bu + f - Q \quad (5.4)$$

Throughout the chapter it will be assumed that f and Q are measured on-line and that ξ is known on-line either by measurement or from an asymptotic observer (Section 3.3).

The various notations and definitions are illustrated by an example.

Example : Depollution control

Consider an anaerobic digestion process used for the depollution control. Suppose that the dynamics of the process are suitably described by the model (1.85.a-e), (1.88) :

$$\frac{d}{dt} \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 & \varphi_1 \\ -k_1 & 0 & \varphi_2 \\ 0 & 1 & 0 \\ k_3 & -k_2 & 0 \\ 0 & k_6 & 0 \\ k_4 & k_5 & 0 \end{bmatrix} \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} - D \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} + \begin{bmatrix} 0 \\ F_1 \\ 0 \\ 0 \\ 0 \\ Q_1 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ Q_2 \end{bmatrix} \quad (5.5)$$

where X_1 is the acidogenic biomass, S_1 the organic substrate, X_2 the methanogenic biomass, S_2 the acetate, P_1 the methane and P_2 the carbon dioxide.

Clearly, the output pollution level (expressed in COD (Chemical Oxygen Demand) units for instance) is defined as :

$$y = c_1 S_1 + c_2 S_2 \quad (5.6)$$

where c_1 and c_2 are the unit conversion constants from (g/l) to (g COD/l).

Suppose, in addition, that the influent feed rate F_1 is the control input. It is easy to check that, in this example :

$$\begin{aligned} C^T &= [0 \ c_1 \ 0 \ c_2 \ 0 \ 0] \\ b^T &= [0 \ 1 \ 0 \ 0 \ 0 \ 0] \\ f &= 0 \end{aligned}$$

5.1.1. Principle of linearizing control

The control objective is to track a reference output signal denoted $y^*(t)$. In the special case of a constant reference, $y^*(= \text{constant})$ is called the *set point*, and control is called *regulation*.

The principle of linearizing control is to find a *control law* $u(\xi, Q, f, y^*)$ which is a multivariable nonlinear function of ξ, Q, f, y^* such that the tracking error ($y^* - y$) is governed by a prespecified *stable linear* differential equation called a *reference model*.

Linearizing control design is a three-step procedure.

Step 1. The first task is to derive an *input/output model* (abr.: *I/O model*) by appropriate manipulations (e.g. successive differentiations) of the general dynamical model (5.4). This model takes the form of a δ^{th} order differential equation:

$$\frac{d^\delta y}{dt^\delta} = f_0(t) + u(t)f_1(t) \quad (5.7.a)$$

where δ is called the *relative degree*. The way to derive input/output models will be illustrated many times in this chapter. At this stage, let us just emphasise that:

- depending on the application, $f_0(t)$ and $f_1(t)$ may be highly complex functions of ξ, Q, F and their successive derivatives;
- as a consequence of the specific structure of the general dynamical model (5.4), the input/output model (5.7.a) is *linear* with respect to the control input $u(t)$.

Step 2. A *stable linear reference model* of the tracking error ($y^*(t) - y(t)$) is selected as follows:

$$\sum_{j=0}^{\delta} \lambda_{\delta-j} \frac{d^j}{dt^j} [y^*(t) - y(t)] = 0 \quad \lambda_0 = 1 \quad (5.7.b)$$

It is a model of how we want the tracking error to decrease (Fig.5.3). The coefficients $\lambda_{\delta-j}$ are arbitrary except that they have obviously to be chosen so that the differential equation (5.7.b) is stable. The reference model is independent of the particular process operating point.

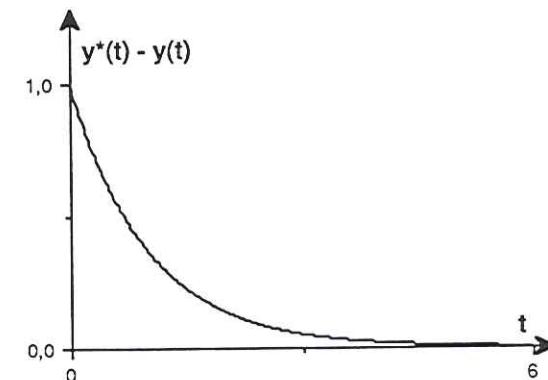


Fig. 5.3. Reference model of the tracking error

Step 3. Finally the control design consists of calculating the control action $u(t)$ such that the input/output model (5.7.a) exactly matches the reference model (5.7.b). This is achieved by eliminating $(d^\delta y / dt^\delta)$ between both equations. The solution, as can readily be seen, is written:

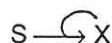
Linearizing Control Law

$$u(t) = \frac{1}{f_1(t)} \left[-f_0(t) + \sum_{j=0}^{\delta-1} \lambda_{\delta-j} \frac{d^j}{dt^j} [y^*(t) - y(t)] + \frac{d^\delta y^*}{dt^\delta} \right] \quad (5.7.c)$$

In this chapter we shall examine three ways of solving the linearizing control problem for bioprocesses described by the model (5.4). They are arranged according to the complexity of the assumptions regarding the prior knowledge available. We first give some simple examples.

Examples of linearizing control :

We consider the basic microbial growth process (1.33) :



for which the dynamical model (1.52)-(1.55) holds :

$$\frac{dX}{dt} = \mu(X, S)X - DX \quad (5.8.a)$$

$$\frac{dS}{dt} = -k_1\mu(X, S)X - DS + F \quad (5.8.b)$$

Case 1. Suppose that we want to regulate the substrate concentration $S = y$ at a given constant value S^* . Notice that (5.8.b) is an input/output model with $\delta=1$. We select a first order reference model for the regulation error :

$$\frac{d}{dt}(S^* - S) + \lambda_1(S^* - S) = 0$$

which also implies (since $dS^*/dt = 0$ because $S^* = \text{constant}$) :

$$\lambda_1(S^* - S) = \frac{dS}{dt}$$

Now, by substituting (5.8.b) in this equation, we obtain :

$$\lambda_1(S^* - S) = -k_1\mu(X, S)X - DS + F$$

The linearizing control law is the expression of the feed rate F which satisfies this equation, that is :

$$F = \lambda_1(S^* - S) + k_1\mu(X, S)X + DS \quad (5.8.c)$$

Case 2. Suppose now that the feed rate F is expressed as follows (see Section 1.5.5) :

$$F = DS_{in}$$

and that we want to use the dilution rate D as the control action. It is straightforward to see that the linearizing control law is written :

$$D = \frac{\lambda_1(S^* - S) + k_1\mu(X, S)X}{S_{in} - S}$$

Case 3. Suppose, finally, that we want to regulate the biomass concentration $X = y$ at a constant value X^* and the dilution rate is constant. Clearly the first model equation (5.8.a) is not suitable for deriving the linearizing control law since it does not explicitly express the connection between the feed rate F and the biomass X (which is to be regulated). This apparent difficulty is solved as follows. We differentiate (5.8.a) :

$$\frac{d}{dt}\left(\frac{dX}{dt}\right) = \frac{d^2X}{dt^2} = \frac{\partial \varphi}{\partial X} \frac{dX}{dt} + \frac{\partial \varphi}{\partial S} \frac{dS}{dt} - D \frac{dX}{dt}$$

where $\varphi(X, S) = \mu(X, S)X$ as usual.

Then, substituting (5.8.a) and (5.8.b) for (dX/dt) and (dS/dt) in this equation, we obtain :

$$\frac{d^2X}{dt^2} = \left(\frac{\partial \varphi}{\partial X} - k_1 \frac{\partial \varphi}{\partial S} - D \right) \mu X - D \left(\frac{\partial \varphi}{\partial X} X + \frac{\partial \varphi}{\partial S} S - DX \right) + \frac{\partial \varphi}{\partial S} F$$

This equation is an input/output model, that is an explicit differential relationship between the control F and the controlled output X . Because it is a second order differential equation, we have also to select a second order reference model for the regulation error :

$$\frac{d^2}{dt^2}(X^* - X) + \lambda_1 \frac{d}{dt}(X^* - X) + \lambda_2(X^* - X) = 0$$

or equivalently, since X^* is assumed to be constant :

$$\frac{d^2X}{dt^2} + \lambda_1 \frac{dX}{dt} = \lambda_2(X^* - X)$$

Straightforward calculations then lead to the linearizing control law :

$$F = \left(\frac{\partial \varphi}{\partial S} \right)^{-1} \left[\lambda_2(X^* - X) + \lambda_1(DX - \mu X) - \left(\frac{\partial \varphi}{\partial X} - k_1 \frac{\partial \varphi}{\partial S} - D \right) \mu X + D \left(\frac{\partial \varphi}{\partial X} X + \frac{\partial \varphi}{\partial S} S - DX \right) \right]$$

5.1.2. An essential remark regarding closed loop stability

It is generally claimed in control textbooks that the main objective of feedback control is plant stabilisation. It is very important to draw the reader's attention on the fact that, in *fed-batch* biotechnological processes, the objective is actually to destabilise the plant. Let us explain this apparent paradox.

A fed-batch bioreactor is, by definition, operated during a finite time. The goal is generally to exponentially accumulate some reaction product, which is harvested at the end of the operation. In mathematical terms, this means that some state variable follows an exponentially growing trajectory, which is characteristic of an unstable behaviour. As a matter of fact, in many instances, this exponential trajectory can be made more or less optimal by regulating some other state variables at appropriate reference values. Hence the goal is

clearly *not* to stabilise the process globally but rather to keep an unstable trajectory under control. This issue, which has also been pointed out by other authors (see the bibliography), will be illustrated in depth in Section 5.7.

In contrast, it is obviously clear that, for CST bioreactors, the global stability of the closed loop is a primary requirement which has to be checked in advance by the control designer. Unfortunately, depending on the particular form of the kinetics, the same method of designing a linearizing controller may produce a stable as well as an unstable closed loop. Furthermore, checking the stability beforehand with the aid of a process model is hazardous in our context of minimal modelling of the kinetics, since our aim is precisely to propose adaptive feedback control strategies when the kinetics are poorly known and hence when a full process model is not available. Our best recommendation is therefore to experiment very carefully with new controllers on bioreactors.

Let us illustrate this point with an example.

Example

Consider the basic microbial growth process (5.8.a-b) with the linearizing control law (5.8.c) to regulate the substrate concentration S at the constant set point S^* .

Suppose first that the specific growth rate $\mu(S)$ depends only on the substrate. Then it can be easily checked that, if $\mu(S^*) > D$, there is no equilibrium state in closed loop. The dynamics of the biomass growth tend asymptotically to :

$$\frac{dX}{dt} = [\mu(S^*) - D]X > 0$$

Hence the biomass concentration is exponentially increasing without limit. If the process operates in the fed-batch mode, with a view to biomass production, this unstable behaviour is exactly the desired objective. But if the

process operates in the continuous mode this is obviously a completely unacceptable behaviour.

On the other hand, if the specific growth rate $\mu(X, S)$ depends on both biomass X and substrate S , then the closed loop has an equilibrium state defined by :

$$\bar{S} = S^* \quad \text{and} \quad \bar{X} \text{ such that } \mu(\bar{X}, S^*) = D$$

which can even be globally attractive, depending on the shape of the function $\mu(X, S)$.

Hence we see that the same control law applied to the same process may give either a globally stable or a completely unstable behaviour: it is just a matter of how the kinetics depend on the biomass concentration, an issue which is very poorly known in most practical applications.

5.2. Singular Perturbation Design of Linearizing Controllers

In this section we shall establish a general method for the design of linearizing controllers based on so-called "fully reduced" models which are obtained by a systematic application of the singular perturbation technique (Section 1.8). The theory is presented first. Its biological motivation is then discussed and illustrated with three typical examples.

5.2.1. Theory

A "fully reduced model" is defined as follows :

a) there exists a state partition $\xi^T = [\xi_s^T, \xi_f^T]$, $K^T = [K_s^T, K_f^T]$ with $\dim(\xi_f) = M$ and K_f full rank. The components of ξ_s are referred to as the "slow" components and those of ξ_f are the "fast" components.

b) the dynamics of ξ_f are supposed to be sufficiently fast to allow singular perturbation reduction to a set of algebraic equations, so that the model is written :

$$\frac{d\xi_s}{dt} = K_s \varphi - D \xi_s + F_s - Q_s \quad (5.9.a)$$

$$K_f \varphi + F_f - Q_f = 0 \quad (5.9.b)$$

c) the controlled output y is a combination of the slow states only :

$$y = C_s^T \xi_s \quad (5.9.c)$$

Since K_f is supposed to be full rank, it follows from (5.9.b) that the vector $\varphi(\xi)$ of reaction rates can be written :

$$\varphi(\xi) = -K_f^{-1}(F_f - Q_f) \quad (5.10)$$

Substituting (5.10) into (5.9.a) gives :

$$\frac{d\xi_s}{dt} = -D \xi_s + [I_{N-M} - K_s K_f^{-1}] (F - Q) \quad (5.11)$$

Denoting $J = [I_{N-M} - K_s K_f^{-1}]$, the dynamics of y are written :

$$\frac{dy}{dt} = -Dy + C_s^T J(F - Q) \quad (5.12)$$

We now turn to the control design problem. Substituting (5.3) into (5.12), we get the following *input/output fully reduced model* :

$$\frac{dy}{dt} = -Dy + C_s^T J b u + C_s^T J (f - Q) \quad (5.13)$$

We suppose that :

$$C_S^T J b \neq 0$$

We select a first order reference model for the tracking error (see the definition (5.7.b)) :

$$\frac{d}{dt} (y^* - y) + \lambda_1 (y^* - y) = 0 \quad (5.14)$$

According to the principle of linearizing control, we have to find a control law $u(y, y^*, f, Q)$ such that the linear reference equation (5.14) is satisfied (with (dy/dt) given by (5.13)). This control law is readily obtained by substituting (5.13) into (5.14), as follows :

Linearizing control law by singular perturbation design

$$u(y, y^*, f, Q) = (C_S^T J b)^{-1} \left[\frac{dy^*}{dt} + \lambda_1 (y^* - y) + Dy + C_S^T J(Q - f) \right] \quad (5.15)$$

We notice that this control law involves a feedforward compensation of the feed rates f , which are not used to control the process.

The theory will now be illustrated by three examples.

5.2.2. Depollution control in an anaerobic digestion process

The process is described by the model (5.5)-(5.6) which is clearly not "fully reduced" although it already results from a reduction by singular perturbation (see Section 1.8.4). In order to perform the full reduction, we select the following state partition :

$$\xi_s = \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \end{bmatrix} \quad \xi_f = \begin{bmatrix} P_1 \\ P_2 \end{bmatrix} \quad (5.16)$$

We notice that the "slow" state ξ_s involves the two substrate concentrations S_1 and S_2 , a combination of which is to be controlled, since (5.6) :

$$y = c_1 S_1 + c_2 S_2 \quad (5.6) = (5.17)$$

The induced partition of K is as follows :

$$K_s = \begin{bmatrix} 1 & 0 \\ -k_1 & 0 \\ 0 & 1 \\ k_3 & -k_2 \end{bmatrix} \quad K_f = \begin{bmatrix} 0 & k_6 \\ k_4 & k_5 \end{bmatrix} \quad (5.18)$$

We observe that K_f is invertible :

$$K_f^{-1} = \begin{bmatrix} -k_5 & 1 \\ \frac{k_5}{k_4 k_6} & \frac{1}{k_4} \\ \frac{1}{k_6} & 0 \end{bmatrix} \quad (5.19)$$

In this particular situation, equation (5.10) is then written :

$$\begin{bmatrix} \varphi_1 \\ \varphi_2 \end{bmatrix} = K_f^{-1} \begin{bmatrix} Q_1 \\ Q_2 \end{bmatrix} = \begin{bmatrix} -k_5 & 1 \\ \frac{k_5}{k_4 k_6} & \frac{1}{k_4} \\ \frac{1}{k_6} & 0 \end{bmatrix} \begin{bmatrix} Q_1 \\ Q_2 \end{bmatrix} \quad (5.20)$$

Substituting (5.20) in the first four equations of the model (5.5) leads to the "fully reduced model" (compare with (5.11)) :

$$\frac{d}{dt} \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \end{bmatrix} = -D \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \end{bmatrix} + \underbrace{\begin{bmatrix} 0 \\ F_1 \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 & 0 \\ -k_1 & 0 \\ 0 & 1 \\ k_3 & -k_2 \end{bmatrix} \begin{bmatrix} Q_1 \\ Q_2 \end{bmatrix}}_{J(F-Q)}$$

We verify that $C_S^T J b = c_1 \neq 0$.

The equation expressing output dynamics is then written as follows (compare with (5.13)) :

$$\frac{dy}{dt} = -Dy + c_1 u + [\theta_1 \ \theta_2] \begin{bmatrix} Q_1 \\ Q_2 \end{bmatrix}$$

\downarrow

$$C_S^T J b \quad C_S^T (f - Q)$$
(5.21.a)

with :

$$\theta_1 \triangleq \frac{c_1 k_1 k_5 - c_2 (k_3 k_5 + k_2 k_4)}{k_4 k_6} \quad (5.21.b)$$

$$\theta_2 \triangleq \frac{c_1 k_1 + c_2 k_3}{k_4} \quad (5.21.c)$$

Hence, the linearizing control law (5.15) is specialised as follows :

$$u = F_1 = c_1^{-1} \left(\frac{dy^*}{dt} + \lambda_1 (y^* - y) + Dy - \theta_1 Q_1 - \theta_2 Q_2 \right) \quad (5.22)$$

It is worth noting that this control law not only makes use of the measured output y (which is the pollution level we want to control) but also of the other

available on-line measurements, namely methane gas Q_1 and carbon dioxide Q_2 flow rates.

5.2.3. Propionate control in an anaerobic digestion process

Motivation

Anaerobic digestion is well known to exhibit unstable equilibrium states (see Section 1.9.3) and feedback control is therefore required to stabilise the process. In Section 5.2.2, a control algorithm has been designed with a view to depollution control. Our purpose, in this section, is to show how linearizing control can be designed with a specific objective of stabilization. The issue of analysing the sources of instability of anaerobic digestors has received much attention in the scientific literature (see the references). Propionate accumulation is often described as one of the main symptoms. This implies a twofold hypothesis regarding the process model :

- a) propionate is an inhibiting factor for the growth of methanogenic bacteria;
- b) propionate degradation is considered to be a critical limiting reaction for the process (otherwise propionate accumulation would not be possible).

It is therefore relevant to try to stabilise the process by regulation of the propionate concentration in the reactor. And the fact that propionate degradation is presumed to be limiting makes the fully reduced model approach adequate for control design.

The fully reduced model

We consider that the process is described by the model (1.65) and we select the following set of fast state variables :

$$\xi_f = [S_1, S_2, S_4, P_1]^T$$

where we recall that S_1 is the influent organic substrate, S_2 is the acetic acid, S_4 is the hydrogen and P_1 is the methane.

The important point is that the propionate S_3 is not involved in ξ_f : propionate is considered as a "slow" state according to the assumption that propionate degradation is limiting.

The corresponding matrix K_f is as follows :

$$K_f = \begin{bmatrix} -k_{21} & 0 & 0 & 0 \\ k_{41} & -k_{42} & k_{43} & 0 \\ k_{81} & 0 & k_{83} & -k_{84} \\ 0 & k_{02} & 0 & k_{04} \end{bmatrix} \quad (5.23)$$

The controlled output is :

$$y = S_3 = C^T \xi \quad (5.24)$$

while the control input is :

$$u = F_1 \quad (5.25)$$

Then the (fairly tedious) calculations of the fully reduced model lead to the following input/output dynamics if Q_3 is assumed to be negligible :

$$\frac{dy}{dt} = -Dy + \theta_1 Q_1 + \theta_2 u \quad (5.26.a)$$

with :

$$\theta_1 = -k_{63} \left(k_{83} + \frac{k_{02}k_{84}k_{43}}{k_{04}k_{42}} \right)^{-1} \left(\frac{k_{84}}{k_{04}} \right) \quad (5.26.b)$$

$$\theta_2 = \frac{k_{61}}{k_{21}} + k_{63} \left(k_{83} + \frac{k_{02}k_{84}k_{43}}{k_{04}k_{42}} \right)^{-1} \left(\frac{k_{81}}{k_{21}} + \frac{k_{02}k_{84}k_{41}}{k_{21}k_{04}k_{42}} \right) \quad (5.26.c)$$

The control law

From (5.26), the control law is derived as follows :

$$u = F_1 = \frac{(dy^*/dt) + \lambda_1(y^* - y) + Dy - \theta_1 Q_1}{\theta_2} \quad (5.27)$$

5.2.4. Ethanol regulation in a yeast fermentation process

Motivation

Fed-batch yeast fermentation processes are known to be characterised by a conflict between yield and productivity. This can be roughly explained as follows. A high glucose feed rate will generally induce high biomass productivity but with a low yield due to the additional production of ethanol which inhibits glucose respiration. The converse is obviously true for low glucose feeding. Simulation studies have shown that ethanol regulation in the process (with glucose feed rate as control action) allows to maintain the process to be maintained at operating points which correspond to a good trade-off (from an economic viewpoint) between yield and productivity. This section is therefore devoted to the design of a linearizing regulator of the ethanol concentration.

The fully reduced model

We suppose that the process is described by the model (1.64) and we select the following set of "fast" state variables :

$$\xi_f = [S, C, P]^T \quad (5.28)$$

with S being the glucose concentration, C the dissolved oxygen concentration and P the dissolved CO_2 concentration.

We notice that ethanol concentration E , which is the state variable to be regulated, does not belong to ξ_f . The corresponding matrix K_f is as follows :

$$K_f = \begin{bmatrix} -k_1 & -k_2 & 0 \\ -k_5 & 0 & -k_6 \\ k_7 & k_8 & k_9 \end{bmatrix} \quad (5.29)$$

The controlled output is $y = E$ while the control input is $u = F_1$. The calculations lead the following fully reduced input/output model :

$$\frac{dy}{dt} = -Dy + \theta_1 Q_1 + \theta_2 Q_{in} + \theta_3 F_1 \quad (5.30.a)$$

with Q_1 the CO_2 gaseous outflow rate, Q_{in} the oxygen transfer rate and :

$$\theta_1 = \left(\frac{k_1 k_4}{k_2} - \frac{k_3 k_5}{k_6} \right) \Theta \quad (5.30.b)$$

$$\theta_2 = \left(\frac{k_1 k_4 k_9}{k_2 k_6} - \frac{k_3 k_5 k_9}{k_6^2} \right) \Theta - \frac{k_3}{k_6} \quad (5.30.c)$$

$$\theta_3 = \left(\frac{k_1 k_4 k_8}{k_2^2} - \frac{k_3 k_5 k_8}{k_2 k_6} \right) \Theta + \frac{k_4}{k_2} \quad (5.30.d)$$

$$\Theta = \left(k_7 - \frac{k_5 k_9}{k_6} - \frac{k_1 k_8}{k_2} \right)^{-1} \quad (5.30.e)$$

Control law

From (5.30), the linearizing control law (5.15) is written :

$$u = F_1 = \theta_3^{-1} \left\{ \frac{dy^*}{dt} + \lambda_1(y^* - y) + Dy - \theta_1 Q_1 - \theta_2 Q_{in} \right\} \quad (5.31)$$

5.2.5. Direct adaptive linearizing control

The practical implementation of the control law (5.15) requires the knowledge of the yield coefficients which are present in the matrix $J = [I_{N-M} \ -K_S K_f^{-1}]$. It may arise, however, that some of these coefficients are either badly known or time-varying and, hence, that the linearizing controller is not well adapted to the process. The remedy offered by control science in that case is known as *Adaptive Control*. It is a design methodology which provides controllers or regulators capable of adapting themselves to modelling uncertainties.

We consider the nonzero unknown components of the vector $C_S^T J$ as a set of unknown parameters, denoted θ . This means that $C_S^T J$ can be factorised as follows :

$$C_S^T J = \theta^T J_0 \quad (5.32)$$

with J_0 being a known matrix.

The model (5.13) is then rewritten :

$$\frac{dy}{dt} = -Dy + \theta^T J_0(bu + f - Q) = -Dy + \theta^T \phi(F, Q) \quad (5.33)$$

where $\phi(F, Q) \stackrel{\Delta}{=} J_0(bu + f - Q)$ is a so-called linear regressor.

Examples of such parametrization have been given above for anaerobic digestion and yeast fermentation processes (equations (5.21), (5.26), (5.30)).

This implies that the linearizing control law (5.15) is reformulated as :

$$u = (\theta^T J_0 b)^{-1} \left(\frac{dy^*}{dt} + \lambda_1 (y^* - y) + Dy + \theta^T J_0 (Q - f) \right) \quad (5.34)$$

An *adaptive control law* is then obtained by replacing the true unknown parameter θ in (5.34) by a time-varying parameter value $\hat{\theta}(t)$ calculated on-line with a so-called adaptation law. The adaptive control law is written :

Adaptive linearizing control law

$$\frac{d\hat{\theta}}{dt} = h(y, F, Q) \quad (5.35)$$

$$u = (\hat{\theta}^T J_0 b)^{-1} \left(\frac{dy^*}{dt} + \lambda_1 (y^* - y) + Dy + \hat{\theta}^T J_0 (Q - f) \right) \quad (5.36)$$

Equation (5.35) is the adaptation law. The design problem consists of selecting a suitable function $h(y, F, Q)$ for the adaptation law, which guarantees the closed loop stability of the control system despite the lack of knowledge of the true parameter θ . So called *direct* and *indirect* adaptive algorithms can be formulated. In a direct scheme the parameter adaptation is driven by the tracking error ($y^* - y$). In an indirect scheme it is driven by an auxiliary observation error. The direct scheme obtained from a Lyapunov design is now presented. The indirect one is the subject of the next section.

Lyapunov design

The direct adaptive control technique is based on Lyapunov stability theory (see Appendix 2).

We thus suppose that an adaptive control law (5.35)-(5.36) is applied to the process (5.33). We select the following candidate Lyapunov function :

$$W(t) = \frac{1}{2} [(y^* - y)^2 + (\theta - \hat{\theta})^T \Gamma^{-1} (\theta - \hat{\theta})] \quad (5.37)$$

where Γ is an arbitrary positive definite matrix.

Taking the time derivative of $W(t)$ and using (5.33) and (5.35), we obtain :

$$\frac{dW}{dt} = -\lambda_1 (y^* - y)^2 - (\theta - \hat{\theta})^T [\Gamma^{-1} h(y, F, Q) + \phi(F, Q) (y^* - y)] \quad (5.38)$$

If the adaptation function $h(y, F, Q)$ is chosen as follows :

$$h(y, F, Q) \stackrel{\Delta}{=} -\Gamma \phi(F, Q) (y^* - y) \quad (5.39)$$

and if we substitute (5.39) into (5.38), we find that dW/dt is semi-negative definite along the system trajectory since it reduces to :

$$\frac{dW}{dt} = -\lambda_1 (y^* - y)^2 \quad (5.40)$$

Thus the direct adaptive control law (5.35)-(5.36) is written as follows :

Direct adaptive linearizing control law

$$\frac{d\hat{\theta}}{dt} = -\Gamma \phi(F, Q) (y^* - y) \quad (5.41.a)$$

$$u = (\hat{\theta}^T J_0 b)^{-1} \left(\frac{dy^*}{dt} + \lambda_1 (y^* - y) + Dy + \hat{\theta}^T J_0 (Q - f) \right) \quad (5.41.b)$$

Example : Depollution control

If we apply the above theory to example 5.2.2 with a diagonal matrix $\Gamma = \text{diag}\{\gamma_1, \gamma_2\}$, straightforward calculations lead to the following adaptive counterpart of the control law (5.22) :

$$\frac{d\hat{\theta}_1}{dt} = \gamma_1 Q_1 (y^* - y) \quad (5.42.a)$$

$$\frac{d\hat{\theta}_2}{dt} = \gamma_2 Q_2 (y^* - y) \quad (5.42.b)$$

$$u = c_1^{-1} \left(\frac{dy^*}{dt} + \lambda_1 (y^* - y) + Dy - \hat{\theta}_1 Q_1 - \hat{\theta}_2 Q_2 \right) \quad (5.42.c)$$

Although the theory may seem rather involved to those who are not familiar with adaptive systems, it is worth noting that it leads to a very simple control structure in practice, as is illustrated by this example.

5.2.6. Indirect adaptive linearizing control

Indirect adaptive control is based on the idea of using a parameter estimator as the adaptation law. The two different estimators (observer-based and linear regression), which have been presented and discussed several times in this book, can be used. In this section we analyse in detail the design of an adaptive controller with an observer-based estimator as the adaptation law. The use of linear regression (least squares algorithm) will be illustrated on the basis of the experimental application of Section 5.2.8.

An observer-based estimator, similar to (3.70), is written as follows from the fully reduced model (5.33) :

$$\frac{d\hat{y}}{dt} = -Dy + \hat{\theta}^T \phi(F, Q) - \omega(y - \hat{y}) \quad \hat{y}(0) = y(0) \quad (5.43.a)$$

$$\frac{d\hat{\theta}}{dt} = \gamma \phi(F, Q) (y - \hat{y}) \quad (5.43.b)$$

with ω and γ being scalar design parameters (which play the same role as the matrices Ω and Γ in (3.70)).

It is interesting to notice that the adaptation law (5.43.b) is quite parallel to the preceding one (5.41.a), the only difference being that the tracking error ($y^* - y$) is replaced by the observation error ($y - \hat{y}$).

The corresponding adaptive control law is then just obtained by using (5.36) but with $\hat{\theta}$ provided by (5.43.b).

Indirect adaptive linearizing control law

$$\frac{d\hat{y}}{dt} = -Dy + \hat{\theta}^T \phi(F, Q) - \omega(y - \hat{y}) \quad \hat{y}(0) = y(0) \quad (5.43.a)$$

$$\frac{d\hat{\theta}}{dt} = \gamma \phi(F, Q) (y - \hat{y}) \quad (5.43.b)$$

$$u = (\hat{\theta}^T J_0 b)^{-1} \left(\frac{dy^*}{dt} + \lambda_1 (y^* - y) + Dy + \hat{\theta}^T J_0 (Q - f) \right) \quad (5.36)$$

Stability analysis

The stability analysis of indirect adaptive control is carried out under the following realistic assumptions.

A.5.1. The reference signal y^* , its time derivative dy^*/dt and the measured signals F and Q are continuous bounded functions of time t .

A.5.2. The initial parameter estimate $\hat{\theta}(0)$ belongs to a closed ball $B_\theta \subset \mathbb{R}^{dim \theta}$, centered on θ , such that each $\bar{\theta} \in B_\theta$ has all nonzero components.

This latter assumption, which is fairly technical, is illustrated in Fig.5.4.

Lemma 5.1. For the parameter estimator (5.43), under Assumptions A.5.1, A.5.2,

a) the observation error $e = y - \hat{y}$ and the parameter error $\tilde{\theta} = \theta - \hat{\theta}$ are bounded as follows :

$$|e(t)| \leq \sqrt{\gamma^{-1}} \|\tilde{\theta}(0)\| \quad \|\tilde{\theta}(t)\| \leq \|\tilde{\theta}(0)\| \quad \forall t \geq 0 \quad (5.44)$$

b) the observation error converges asymptotically to zero :

$$\lim_{t \rightarrow \infty} |e(t)| = 0 \quad (5.45)$$

Proof (Lyapunov analysis). The following candidate Lyapunov function is considered :

$$W(e, \tilde{\theta}) = \frac{1}{2} (\gamma e^2 + \tilde{\theta}^T \tilde{\theta}) \quad (5.46)$$

The time derivative of W along the trajectories of (5.43) is easily shown to be :

$$\frac{dW}{dt} = -\omega \gamma e^2 \quad (5.47)$$

which is clearly a semi-negative definite function. Hence $W(e, \tilde{\theta})$ is a positive decreasing function. Since $e(0) = y(0) - \hat{y}(0) = 0$ (see 5.43.a), we have :

$$W(e(t), \tilde{\theta}(t)) \leq W(e(0), \tilde{\theta}(0)) = \|\tilde{\theta}(0)\|^2 \quad (5.48)$$

Part a) follows.

On the other hand, (5.47) and (5.48) also imply :

$$\int_0^t |e(\tau)|^2 d\tau \leq W(0) - W(t) \leq \|\tilde{\theta}(0)\|^2 \quad (5.49)$$

From Assumption A.5.1 and (5.44), $\phi(F, Q)$ and hence (de/dt) are bounded. Therefore $e(t)$ is continuous and (5.49) implies part b).

QED.

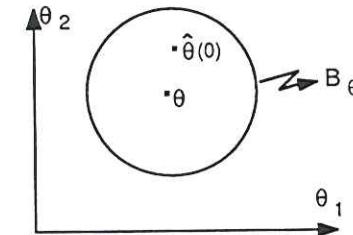


Fig.5.4. B_θ

It can now be shown by straightforward calculation that the adaptive control law (5.36) with the parameter estimator (5.43) applied to the system (5.33) leads to the following expression of the closed loop dynamics :

$$\frac{d}{dt}(y^* - y) + \lambda_1(y^* - y) = \frac{de}{dt} + \omega e \quad (5.50)$$

That is the tracking error ($y^* - y$) is the output of a stable linear filter driven by the observation error e . Then the convergence of e to zero (Lemma 5.1) necessarily implies the convergence of ($y^* - y$) to zero as stated in the following theorem.

Theorem 5.1. For the adaptive control law (5.36) with the parameter estimator (5.43) applied to the system (5.33), under Assumptions A.5.1 and A.5.2, the tracking error ($y^* - y$) converges asymptotically to zero :

$$\lim_{t \rightarrow \infty} |y^*(t) - y(t)| = 0 \quad (5.51)$$

Example : Depollution control

If we apply the foregoing theory to Example 5.2.2, we obtain the following adaptive control law :

$$\frac{d\hat{y}}{dt} = -Dy + c_1 u + \hat{\theta}_1 Q_1 + \hat{\theta}_2 Q_2 + \omega(y - \hat{y}) \quad (5.52.a)$$

$$\frac{d\hat{\theta}_1}{dt} = \gamma Q_1 (y - \hat{y}) \quad (5.52.b)$$

$$\frac{d\hat{\theta}_2}{dt} = \gamma Q_2 (y - \hat{y}) \quad (5.52.c)$$

$$u = c_1^{-1} \left(\frac{dy^*}{dt} + \lambda_1(y^* - y) + Dy - \hat{\theta}_1 Q_1 - \hat{\theta}_2 Q_2 \right) \quad (5.52.d)$$

This indirect control law has to be compared to that obtained by the direct method (5.42).

5.2.7. Using the dilution rate D as control action

So far, we have supposed that the process control input $u = F_i$ (see (5.3)) is the feed rate of some external substrate which is introduced into the reactor *independently* of the dilution water stream. An alternative (see Fig.1.10), which is common in industrial practice, is to suppose that the feeding substrate is diluted in the water stream and to use the *dilution rate* as the manipulated variable to control the process (Fig.5.5). In that case, the derivation of the control algorithm is a direct consequence of our previous theory. Indeed, the I/O fully reduced model, (5.12), is simply rewritten :

$$\frac{dy}{dt} = D(C_S^T J S_{in} - y) - C_S^T J Q \quad (5.53)$$

where $F = DS_{in}$ according to (1.62).

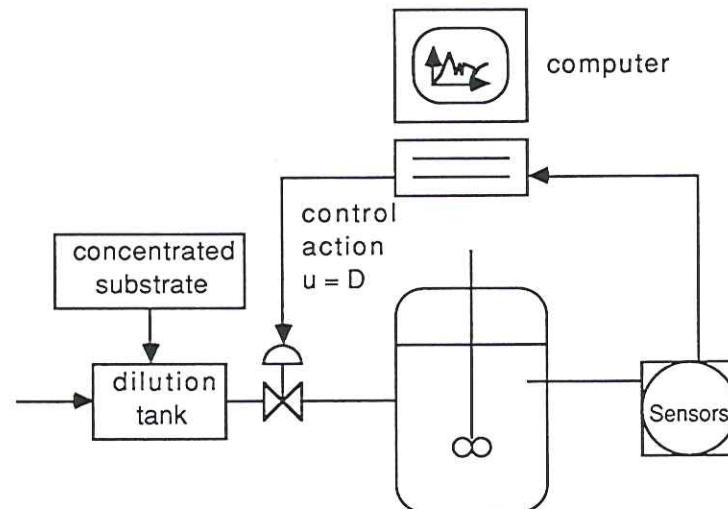


Fig.5.5. Computer control system for bioreactors with the dilution rate as the control action

The principle of linearizing control then produces the following control law (compare with 5.15) :

Linearizing control law with D as control action

$$D = (C_S^T J S_{in} - y)^{-1} \left[\frac{dy^*}{dt} + \lambda_1(y^* - y) + C_S^T J Q \right] \quad (5.54)$$

or, using the parametrization θ (5.32) :

$$D = (\theta^T J_0 S_{in} - y)^{-1} \left[\frac{dy^*}{dt} + \lambda_1(y^* - y) + \theta^T J_0 Q \right] \quad (5.55)$$

Adaptive versions of (5.55) are simply obtained by replacing θ by the parameter estimates $\hat{\theta}$ provided either by the direct adaptation law (5.41.a) or the observer-based adaptation law (5.43).

5.2.8. Experimental application. Adaptive regulation of propionate concentration in an anaerobic digestion pilot plant

Adaptive regulation of propionate concentration, as described in Section 5.2.3, has been implemented on a pilot-scale anaerobic digestion process by the unit of Bioengineering (Université Catholique de Louvain, Belgium). The dilution rate D was used as control action so that (as explained in the previous paragraph), the control law (5.27) was rewritten :

$$D = \frac{\lambda_1(S_3 - S_{3,t}) - \theta_1 Q_1}{\theta_2 S_{in} - S_3} \quad (5.56)$$

where S_3 is the propionate regulation which is to be regulated at the set point S_3^* , S_{in} is the influent substrate concentration and Q_1 is the methane gas outflow rate.

The process has been operated during more than 150 days under an indirect adaptive version of the control law (5.56). However the parameter adaptation was applied only to the parameter θ_2 because the value of θ_1 was known from a preliminary identification study :

$$\theta_1 = -0.94 \text{ gr.COD/lit} \quad (5.57)$$

The adaptation of θ_2 was performed by a discrete-time least squares estimator, analogous to (3.87), written as follows :

$$\hat{\theta}_{2,t-1} = \hat{\theta}_{2,t} + T \gamma_t S_{in,t} D_t \{S_{3,t+1} - S_{3,t} - T[\theta_1 Q_{1,t} - D_t S_{3,t} + \hat{\theta}_{2,t} D_t S_{in,t}]\} \quad (5.58)$$

$$\gamma_{t+1} = \frac{\gamma_t}{\lambda + (TD_t S_{in,t})^2 \gamma_t} \quad (5.59)$$

The forgetting factor λ was set to 0.9 while a sampling period $T = 2$ days was used. The adaptive controller was thus constituted by the control law (5.56) rewritten in discrete time as follows :

$$D_t = \frac{\lambda_1(S_3 - S_{3,t}) - \theta_1 Q_{1,t}}{\hat{\theta}_{2,t} S_{in,t} - S_{3,t}} \quad (5.60)$$

combined with the parameter adaptation law (5.58)-(5.59).

An excerpt of the experimental results is shown in Fig.5.6 from which the following conclusions are drawn :

- 1) During the first part of the experiment (until the 65th day), we observe an excellent behaviour of the control system which keeps the actual propionate concentration S_3 very close to the set point. The regulation is robust against a big step of influent organic matter on day 38, from 40 g COD/l to 50 g COD/l (Fig.5.6.a).
- 2) On day 66, the regulator has been switched off and the process operates in open loop with a slightly increasing dilution rate. We see that the process is rapidly destabilised and that propionate is exponentially increasing.
- 3) On day 82, the regulator is switched on again and brings the propionate concentration S_3 back to the set point.
- 4) The control law (5.60) takes advantage of the on-line measurement of the methane gas flow rate Q_1 (Fig.5.6.d) which gives valuable on-line information on the biomass activity.

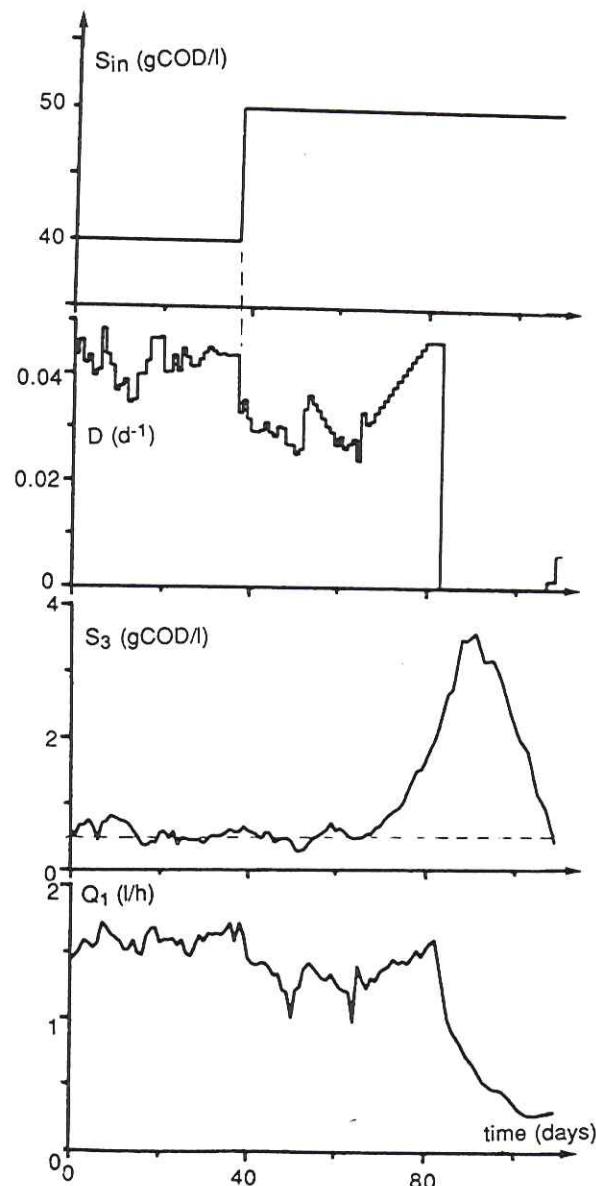


Fig.5.6. Adaptive regulation of propionate concentration in an anaerobic pilot plant.

5.3. Adaptive Linearizing Control (Known Yield Coefficients)

In Section 5.2 we have discussed the design of linearizing controllers for bioreactors when a (fairly drastic) model reduction is authorised (on the basis of available prior knowledge).

In the present section we are concerned with adaptive control in bioreactors when such a model reduction is not desirable but, however, the yield coefficients are known (either from stoichiometry or preliminary parameter identification, see Chapter 4). The case where the yield coefficients are unknown will be treated in the next section.

5.3.1. Statement of the adaptive control problem

We consider biotechnological processes described by the state space model (1.49) :

$$\frac{d\xi}{dt} = KG(\xi)\alpha - D\xi + F - Q \quad (1.49) = (5.61)$$

where it is recalled that $G(\xi)$ is a diagonal matrix depending only on the reactants in the bioreactor, while $\alpha(\xi, t)$ is a set of time-varying, state dependent *specific reaction rates*.

As in Section 5.2, we suppose that the objective is to control a scalar output variable $y = CT\xi$ by using some external substrate feedrate as control action. Using (5.3) it is then convenient to rewrite the model (5.61) as follows :

$$\frac{d\xi}{dt} = KG(\xi)\alpha - D\xi + bu + f - Q \quad (5.62)$$

Assumption : throughout this section, we assume that :

- f and Q are measured on-line;

- ξ is known on-line either by measurement or from an asymptotic observer (Section 3.2);
- the specific reaction rates α are *unknown*.

Crucial comment :

The reader is advised to notice that, in this section (unlike in the previous one) we suppose from the beginning that the process model is parametrized by a set of unknown parameters α . This motivates an immediate search for adaptive controllers, i.e. controllers which are able to cope with parameter uncertainty and nonstationarity.

The control design problem

The problem is to find an adaptive control law $u(\xi, f, Q, \hat{\alpha})$, which is a function of the measurements ξ , f , Q and of on-line estimates $\hat{\alpha}$, such that the dynamics of the tracking error ($y^* - y$) are governed, at least asymptotically and in the neighbourhood of the reference trajectory y^* , by stable linear dynamics. This is called *the adaptive linearizing control problem*.

The derivation of a general solution to this problem is extremely involved and has not yet received a complete answer for nonlinear systems in general. Therefore, we shall be content to examine three particular situations, which nevertheless cover a wide range of potential applications.

The first situation, presented in Section 5.3.2, is termed "substrate control" because it relies on the assumption that one of the components involved in the output y is precisely the external substrate which is used as control input.

The second situation, presented in Section 5.3.3, is termed "product control" because it relies on the assumption that the output y involves only liquid products (including internal substrates).

Finally, the third situation concerns a particular class of continuous stirred tank bioreactors. It will be presented in Section 5.4.

5.3.2. Substrate control

Here we suppose that one of the components involved in the controlled output y is precisely the external substrate which is used as control input. That is the vectors b and C are such that : $C^T b \neq 0$.

From the state space model (5.62), we readily derive the following I/O dynamics :

$$\frac{dy}{dt} = C^T K G(\xi) \alpha - D y + C^T b u + f - Q \quad (5.63)$$

A straightforward application of the linearizing control principle leads to the following control law :

$$u = (C^T b)^{-1} \left[\frac{dy^*}{dt} + \lambda_1 (y^* - y) - C^T K G(\xi) \alpha + D y - C^T (f - Q) \right] \quad (5.64)$$

which necessarily exists, since $C^T b \neq 0$ by assumption, and which guarantees the stable linear dynamics of the tracking error :

$$\frac{d}{dt} (y^* - y) + \lambda_1 (y^* - y) = 0 \quad (5.65)$$

if the parameter α is known. But our hypothesis is precisely that α is unknown. Then (5.64) is transformed into an adaptive control law by using one of the parameter estimators which have been proposed in Chapter 3. For instance the linear regression estimator (3.93), with a forgetting factor λ :

$$\frac{d\psi^T}{dt} = -\omega\psi^T + KG(\xi) \quad (3.93.a) = (5.66.a)$$

$$\frac{d\psi_0}{dt} = -\omega\psi_0 + (\omega - D)\xi - Q + F \quad (3.93.b) = (5.66.b)$$

$$\frac{d\hat{\alpha}}{dt} = \Gamma\psi(\xi - \psi_0 - \psi^T\hat{\alpha}) \quad (3.93.c) = (5.66.c)$$

$$\frac{d\Gamma}{dt} = -\Gamma\psi\Gamma + \lambda\psi \quad \Gamma(0) > 0 \quad (3.93.d) = (5.66.d)$$

The full adaptive controller is thus the combination of the control law (5.64) and the parameter estimator (5.66) with α substituted by $\hat{\alpha}$.

Example : Depollution control

Again, we come back to Example 5.2.2. The process model is as follows :

$$\begin{aligned} \frac{d}{dt} \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} &= \begin{bmatrix} 1 & 0 \\ -k_1 & 0 \\ 0 & 1 \\ k_3 & -k_2 \\ 0 & k_6 \\ k_4 & k_5 \end{bmatrix} \begin{bmatrix} X_1S_1 & 0 \\ 0 & X_2S_2 \end{bmatrix} \begin{bmatrix} \alpha_1 \\ \alpha_2 \end{bmatrix} - D \begin{bmatrix} X_1 \\ S_1 \\ X_2 \\ S_2 \\ P_1 \\ P_2 \end{bmatrix} + \begin{bmatrix} 0 \\ F_1 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ Q_1 \\ Q_2 \end{bmatrix} \quad (5.67.a) \\ y &= c_1S_1 + c_2S_2 \quad (5.67.b) \end{aligned}$$

We notice that in this example :

$$C^T b = c_1 \neq 0 \quad (5.68)$$

The I/O dynamics are written (compare to (5.63)) :

$$\frac{dy}{dt} = [(c_2k_3 - c_1k_1)X_1S_1 - c_2k_2X_2S_2] \begin{bmatrix} \alpha_1 \\ \alpha_2 \end{bmatrix} - Dy + c_1u \quad (5.69)$$

$C^T KG(\xi)$

so that the linearizing control law is written :

$$u = \frac{dy^*}{dt} + \lambda_1(y^* - y) + Dy - (c_2k_3 - c_2k_1)X_1S_1\alpha_1 + c_2k_2X_2S_2\alpha_2 \quad (5.70)$$

Practical implementation

Let us suppose that the output pollution level y , the acetic acid concentration S_2 and the methane gas flow rate Q_1 are the only measurements which are available on-line. We shall see how to implement an adaptive version of (5.70) by using the algorithmic tools which have been proposed in the preceding chapters. First of all we have, from (5.67.b) :

$$S_1 = \frac{y - c_2S_2}{c_1} \quad (5.71)$$

Then we use the asymptotic observer (3.48) to compute on-line estimates of X_1 and X_2 :

$$\frac{d\hat{Z}_2}{dt} = -D\hat{Z}_2 \quad (5.72.a)$$

$$\frac{d\hat{Z}_3}{dt} = -D\hat{Z}_3 - Q_1 \quad (5.72.b)$$

$$\hat{X}_2 = -\frac{\hat{Z}_3}{k_6} \quad (5.72.c)$$

$$\hat{X}_1 = \frac{1}{k_3} \left(S_2 - \hat{Z}_2 + \frac{k_2}{k_6} \hat{Z}_3 \right) \quad (5.72.d)$$

We then use the parameter estimator (5.66) to compute on-line estimates of $\hat{\alpha}_1$ and $\hat{\alpha}_2$.

As we mentioned in Chapter 3, we can apply this parameter estimator to a subset of the state equations, provided they involve the two unknown parameters α_1 and α_2 . We select the dynamics of S_1 and S_2 :

$$\frac{dS_1}{dt} = -k_1 X_1 S_1 \alpha_1 - DS_1 + F_1$$

$$\frac{dS_2}{dt} = k_3 X_1 S_1 \alpha_1 - k_2 X_2 S_2 \alpha_2$$

Then the algorithm (5.66) is specialised as follows :

$$\frac{d\psi_1}{dt} = -\omega\psi_1 + \hat{X}_1 S_1 \quad (5.73.a)$$

$$\frac{d\psi_2}{dt} = -\omega\psi_2 + \hat{X}_2 S_2 \quad (5.73.b)$$

$$\frac{d\psi_{01}}{dt} = -\omega\psi_{01} + (\omega - D) S_1 + F_1 \quad (5.73.c)$$

$$\frac{d\psi_{02}}{dt} = -\omega\psi_{02} + (\omega - D) S_2 \quad (5.73.d)$$

$$\frac{d}{dt} \begin{bmatrix} \hat{\alpha}_1 \\ \hat{\alpha}_2 \end{bmatrix} = \Gamma \begin{bmatrix} -k_1\psi_1 & k_3\psi_1 \\ 0 & -k_2\psi_2 \end{bmatrix} \begin{bmatrix} S_1 - \psi_{01} + k_1\psi_1\hat{\alpha}_1 \\ S_2 - \psi_{02} - k_3\psi_1\hat{\alpha}_1 + k_2\psi_2\hat{\alpha}_2 \end{bmatrix} \quad (5.73.e)$$

$$\frac{d\Gamma}{dt} = -\Gamma\psi\psi^T\Gamma + \lambda\Gamma \quad (5.73.f)$$

with :

$$\psi^T = \begin{bmatrix} -k_1\psi_1 & 0 \\ k_3\psi_1 & -k_2\psi_2 \end{bmatrix} \quad (5.73.g)$$

Finally, the full adaptive controller is made up of the combination of (5.71), (5.72), (5.73) with the control law (5.70) rewritten :

$$u = \frac{dy^*}{dt} + \lambda_1(y^* - y) + Dy - (c_2k_3 - c_2k_1)\hat{X}_1 S_1 \hat{\alpha}_1 + c_2k_2\hat{X}_2 S_2 \hat{\alpha}_2 \quad (5.74)$$

5.3.3. Product control

We suppose now that the output $y = C^T\xi$ involves only liquid products (including internal substrates as we shall see in the example hereafter). We notice immediately that this implies :

$$C^T(F - Q) = 0 \text{ and, in particular, } C^T b = 0 \quad (5.75)$$

We assume in addition that at least one of these products is produced by a reaction to which the control substrate also belongs. This is formalised by assuming that the following quantity is not identically zero :

$$C^T K \frac{\partial}{\partial \xi} [G(\xi)\alpha] b \neq 0 \quad (5.76)$$

Under these assumptions, it can be observed that :

$$\frac{dy}{dt} = C^T KG(\xi)\alpha - Dy \quad (5.77)$$

This equation does not involve the control input u so that it is useless for the design of a linearizing control law. Now, if we differentiate (5.77), we obtain, thanks to (5.75) :

$$\begin{aligned} \frac{d^2y}{dt^2} &= -\frac{dD}{dt}y - D \frac{dy}{dt} + C^T K \frac{\partial}{\partial \xi} [G(\xi)\alpha] \frac{d\xi}{dt} + C^T KG(\xi) \frac{d\alpha}{dt} \\ &= -\frac{dD}{dt}y - D [C^T KG(\xi)\alpha - Dy] + C^T KG(\xi) \frac{d\alpha}{dt} \\ &\quad + C^T K \frac{\partial}{\partial \xi} [G(\xi)\alpha] \{KG(\xi)\alpha - D\xi + bu + (f - Q)\} \end{aligned} \quad (5.78)$$

Clearly, this equation now contains an explicit relation between u and y . To simplify the notation, (5.78) is rewritten :

$$\frac{d^2y}{dt^2} = g_0\left(\xi, \alpha, \frac{d\alpha}{dt}\right) + g_1(\xi, \alpha)(f - Q) + g_1(\xi, \alpha)b u \quad (5.79.a)$$

with

$$\begin{aligned} g_0\left(\xi, \alpha, \frac{d\alpha}{dt}\right) &= -\frac{dD}{dt}y - D[C^T KG(\xi)\alpha - Dy] + C^T K \frac{\partial}{\partial \xi} [G(\xi)\alpha] \{KG(\xi)\alpha - D\xi\} \\ &\quad + C^T KG(\xi) \frac{d\alpha}{dt} \end{aligned} \quad (5.79.b)$$

$$g_1(\xi, \alpha) = C^T K \frac{\partial}{\partial \xi} [G(\xi)\alpha] \quad (5.79.c)$$

We select a second order linear reference model :

$$\frac{d^2}{dt^2}(y^* - y) + \lambda_2 \frac{d}{dt}(y^* - y) + \lambda_1(y^* - y) = 0 \quad (5.80)$$

The principle of linearizing control requires the calculation of the control law $u\left(\xi, \alpha, \frac{d\alpha}{dt}\right)$ in such a way that (5.80) is satisfied with dy/dt and d^2y/dt^2 , respectively, given by (5.77) and (5.78). The solution is as follows :

$$\begin{aligned} u\left(\xi, \alpha, \frac{d\alpha}{dt}\right) &= [g_1(\xi, \alpha)b]^{-1} \left[\frac{d^2y^*}{dt^2} + \lambda_2 \frac{dy^*}{dt} + \lambda_1(y^* - y) \right. \\ &\quad \left. - \lambda_2(C^T KG(\xi)\alpha - Dy) - g_0\left(\xi, \alpha, \frac{d\alpha}{dt}\right) - g_1(\xi, \alpha)(f - Q) \right] \end{aligned} \quad (5.81)$$

We see that this control law not only depends, as before, on the unknown value of the specific reaction rates α , but also on their derivatives $d\alpha/dt$. This apparent difficulty, however, is easily resolved : we replace α by an on-line estimate $\hat{\alpha}$, and $d\alpha/dt$ by $d\hat{\alpha}/dt$ (see 5.66.c) in order to make the control law adaptive.

Example : Ethanol control in a yeast production process

In Section 5.2.4, we derived a linearizing controller based on a fully reduced model of the yeast fermentation process. We shall now derive an alternative controller using the theory presented above. The process dynamics (1.54) are as follows :

$$\frac{d}{dt} \begin{bmatrix} X \\ S \\ E \\ C \\ P \end{bmatrix} = \begin{bmatrix} 1 & 1 & 1 \\ -k_1 & -k_2 & 0 \\ 0 & k_4 & -k_3 \\ -k_5 & 0 & -k_6 \\ k_7 & k_8 & k_9 \end{bmatrix} \begin{bmatrix} XSC & 0 & 0 \\ 0 & XS & 0 \\ 0 & 0 & XEC \end{bmatrix} \begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \alpha_3 \end{bmatrix} - D \begin{bmatrix} X \\ S \\ E \\ C \\ P \end{bmatrix} + \begin{bmatrix} 0 \\ F_g \\ 0 \\ 0 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ Q_1 \end{bmatrix} \quad (5.82)$$

The goal is to regulate the ethanol concentration :

$$y = C^T \xi = E \text{ with } C^T = [0 \ 0 \ 1 \ 0 \ 0] \quad (5.83)$$

The control action is the glucose feed rate F_g :

$$u = F_g \quad \text{i.e.} \quad b^T = [0 \ 1 \ 0 \ 0 \ 0] \quad (5.84)$$

According to (5.75), we verify that $C^T(F - Q) = 0$ and $C^T b = 0$, and also that, according to (5.76) : $C^T K \frac{\partial}{\partial \xi} [G(\xi)\alpha] b = k_4 X \alpha_2 \neq 0$.

Equations (5.77) and (5.78) are specialised as follows :

$$\frac{dE}{dt} = k_4 X S \alpha_2 - k_3 X E C \alpha_3 - D E \quad (5.85)$$

$$\frac{d^2E}{dt^2} = g_0\left(\xi, \alpha, \frac{d\alpha}{dt}\right) + g_1(\xi, \alpha)[f - Q + bu] \quad (5.86.a)$$

with :

with

$$\begin{aligned} g_0\left(\xi, \alpha, \frac{d\alpha}{dt}\right) &= (\alpha_2 k_4 S - \alpha_3 k_3 E C) (XSC\alpha_1 + XS\alpha_2 + XEC\alpha_3 - DX) \\ &\quad + \alpha_2 k_4 X (-k_1 XSC\alpha_1 - k_2 XS\alpha_2 - DS) \\ &\quad - \alpha_3 k_3 XE (-k_5 XSC\alpha_1 - k_6 XEC\alpha_3 - DC) \\ &\quad - (D + \alpha_3 k_3 XC) (\alpha_2 k_4 XS - \alpha_3 k_3 XEC - DE) \\ &\quad + k_4 XS \frac{d\alpha_2}{dt} - k_3 XEC \frac{d\alpha_2}{dt} - E \frac{dD}{dt} \end{aligned} \quad (5.86.b)$$

$$g_1(\xi, \alpha)[f - Q + bu] = \alpha_2 k_4 X F_g - \alpha_3 k_3 X E Q_{in} \quad (5.86.c)$$

The computation of the control law (5.81) follows.

Comment

In contrast to Section 5.2, we have designed a linearizing adaptive controller without model reduction, i.e. a controller which is able to compensate for the full process nonlinearities. Expressions (5.81) and (5.86) show that the price to pay is, however, a much greater complexity of the controller equations as compared to (5.27).

5.4. A General Solution to the Linearizing Control Problem for a Class of CST Bioreactors

Several particular ways of deriving linearizing controllers for bioreactors have been introduced, either through model simplification by singular perturbations (Section 5.2) or under specific structural assumptions regarding the link between the control action u and the component which is to be regulated y (Section 5.3). In this section, we would like to give an idea of the way in which the theory of nonlinear control systems can be applied to solve the problem in

general. However, in order to limit the mathematical complexity, we introduce some simplifying hypotheses.

Model description

We consider a class of bioreactors described by the state space model (1.49), with the particular model of the gaseous outflow rates given by (1.57), that is :

$$\frac{d\xi}{dt} = KG(\xi)\alpha - D\xi - B\xi + F \quad (5.87)$$

We suppose that :

- 1) the dilution rate D is *constant* ;
- 2) the specific reaction rates α are *constant* ;
- 3) the specific liquid-gas transfer rates β_i (see Section 1.5.4) are *constant*. Hence the matrix $B = \text{diag}\{\beta_i\}$ is also *constant* ;
- 4) the process involves only one external substrate such that the vector F is written (compare to (5.3)) :

$$F = bu \quad (5.88)$$

Under these assumptions, the model is rewritten in the following convenient, compact form :

$$\begin{aligned} \frac{d\xi}{dt} &= g(\xi) + bu \\ y &= C^T \xi \end{aligned} \quad (5.89)$$

with $g(\xi) \stackrel{\Delta}{=} KG(\xi)\alpha - D\xi - B\xi$

Technical definitions

Let $h(\xi) : \mathbb{R}^N \rightarrow \mathbb{R}^N$ denote a real valued vector function. The *gradient* of h , denoted ∇h , is the following matrix :

$$\nabla h \triangleq \frac{\partial h}{\partial \xi} = \begin{bmatrix} \frac{\partial h_1}{\partial \xi_1} & \dots & \frac{\partial h_1}{\partial \xi_N} \\ \vdots & \ddots & \vdots \\ \frac{\partial h_N}{\partial \xi_1} & \dots & \frac{\partial h_N}{\partial \xi_N} \end{bmatrix} \quad (5.90)$$

The gradient of h , along an N -vector g , is itself the vector obtained by multiplying ∇h and g . This is denoted :

$$\nabla_g h \stackrel{\Delta}{=} (\nabla h)g \quad (5.91)$$

The components of this vector are thus defined as follows :

$$\sum_{i=1}^N \frac{\partial h_j}{\partial \xi_i} g_i \quad j = 1, \dots, N \quad (5.92)$$

It is remarkable that the notation (5.91) can be used recursively :

$$\nabla_g^k h = \nabla_g (\nabla_g^{k-1} h) \quad (5.93)$$

Moreover, the vector g can itself be a real valued vector function :

$$g(\xi) : \mathbb{R}^N \rightarrow \mathbb{R}^N \quad (5.94)$$

We then notice that, with these definitions, the model (5.89) can be rewritten :

$$\frac{d\xi}{dt} = \nabla_g \xi + bu \quad (5.95.a)$$

$$y = C^T \xi \quad (5.95.b)$$

The *relative degree* δ of the model is the smaller integer δ such that :

$$C^T \nabla_b (\nabla_g^\gamma \xi) = 0 \quad \gamma = 1, 2, \dots, \delta-2 \quad (5.96.a)$$

$$C^T \nabla_b (\nabla_g^{\delta-1} \xi) \neq 0 \quad (5.96.b)$$

Derivation of an input/output model

The next step is to derive an input/output model in order to be able to apply the linearizing control principle. This is done as follows. We first differentiate the output equation (5.95.b) :

$$\frac{dy}{dt} = C^T \frac{d\xi}{dt} \quad (5.97)$$

Substituting (5.95.a) gives :

$$\frac{dy}{dt} = C^T \nabla_g \xi + C^T bu = C^T \nabla_g \xi + (C^T \nabla_b \xi)u \quad (5.98)$$

If $C^T b = C^T \nabla_b \xi$ is not identically equal to zero :

$$C^T b = C^T \nabla_b \xi \neq 0$$

(which corresponds to a relative degree $\delta = 1$, see (5.96.b)), (5.98) is a convenient input/output model and the derivation procedure has come to an end. But, if the relative degree $\delta > 1$, $C^T b = 0$ and (5.98) reduces to :

$$\frac{dy}{dt} = C^T \nabla_g \xi \quad (5.99)$$

which does not involve an explicit connection between u and y . Then we proceed by differentiating (5.99) further to obtain :

$$\frac{d^2y}{dt^2} = C^T \nabla_g^2 \xi + C^T \nabla_b (\nabla_g \xi) u \quad (5.100)$$

As before, if $\delta = 2$, (5.100) is convenient for linearizing control design. Otherwise, we continue the differentiation up to the relative degree δ of the model, to obtain :

$$\frac{d^\delta y}{dt^\delta} = C^T \nabla_g^\delta \xi + C^T \nabla_b (\nabla_g^{\delta-1} \xi) u \quad (5.101)$$

We see that the meaning of the concept of relative degree δ is that we have to differentiate the output y δ times before terms involving the input u appear on the right hand side of the input/output model (5.101).

Linearizing control design

With the input-output model (5.101) at hand, we are in a position to design the control law. We adopt a reference model (5.7) of order δ , that is :

$$\frac{d^\delta}{dt^\delta} (y^* - y) + \lambda_1 \frac{d^{\delta-1}}{dt^{\delta-1}} (y^* - y) + \dots + \lambda_\delta (y^* - y) = 0 \quad (5.102)$$

Then substituting the expressions (5.99) to (5.101) of the successive derivatives of y into (5.102) readily yields the linearizing control law :

$$u(\xi, \alpha) = [C^T \nabla_b (\nabla_g^{\delta-1} \xi)]^{-1} \left[\frac{d^\delta y^*}{dt^\delta} - C^T \nabla_g^\delta \xi + \sum_{j=1}^{\delta} \lambda_j \left(\frac{d^{\delta-j} y^*}{dt^{\delta-j}} - C^T \nabla_g^{\delta-j} \xi \right) \right] \quad (5.103)$$

As will by now be familiar to the reader, an adaptive version of this control law is obtained by replacing the non-measured states and the parameter α by on-line estimates provided by the algorithms described in Chapter 3.

5.5. Adaptive Linearizing Control (Unknown Yield Coefficients)

5.5.1. Introduction and basic assumptions

In Section 5.2 we addressed the problem of the (adaptive) linearizing control of bioreactors when the reaction rates $\phi(\xi)$ are unknown, but can be alleviated by using singular perturbations. In Sections 5.3 and 5.4 we addressed the problem in which the lack of knowledge of the reaction rates explicitly taken into account (by incorporating on-line parameter estimation in the control law) but under the assumption that the yield coefficients (matrix K) are known. In this section, we shall deal with the case where *both* reaction rates $\phi(\xi)$ and yield coefficients (matrix K) are unknown. The price to pay, however, is that more restrictive structural assumptions have to be considered.

We suppose that the bioreactor dynamics are described by the general state space model (1.49) :

$$\frac{d\xi}{dt} = KG(\xi)\alpha - D\xi - Q + F \quad (1.49) = (5.104)$$

under the following assumptions :

- 1) There exists a state partition $\xi = (\xi_1, \xi_2)$ where ξ_1 is a set of measured states while ξ_2 is the complementary set of non measured states. The partition (ξ_1, ξ_2) induces similar partitions $(K_1, K_2), (Q_1, Q_2), (F_1, F_2)$ as usual.
- 2) The output to be controlled is a linear combination of the measured states :

$$y = C_1^T \xi_1 \quad (5.105)$$

- 3) On the other hand, there exists a nice partition (ξ_a, ξ_b) and an auxiliary state (see Sections 1.7 and 3.3.1) :

$$Z = A_0 \xi_a + \xi_b = A_1 \xi_1 + A_2 \xi_2 \quad (5.106)$$

4) The matrix A_2 is left invertible. The left inverse is denoted A_2^+ .

Under these assumptions, it follows that the state space model (5.104) is equivalent to :

$$\frac{d\xi_1}{dt} = K_1 G(\xi_1, A_2^+(Z - A_1 \xi_1)) \alpha - D \xi_1 + F_1 - Q_1 \quad (5.108.a)$$

$$\frac{dZ}{dt} = -DZ + F_b - Q_b \quad (5.108.b)$$

The problem is to control the system (5.108) with K_1 , α and Z being unknown. As we have argued in Chapter 4 (Section 4.2.2), the term $K_1 G \alpha$ in (5.108.a) can be reparametrized as follows :

$$K_1 G(\xi_1, A_2^+(Z - A_1 \xi_1)) \alpha \stackrel{\Delta}{=} \Phi(\xi_1, Z) \theta \quad (5.109)$$

where $\Phi(\xi_1, Z)$ is a matrix of *known* functions of ξ_1 and Z while θ is an *unknown* parameter vector which is itself a nonlinear combination of the yield coefficients k_i and the specific rates α_j . Several examples have been given in Chapter 4, see for instance (4.19).

With the reparametrization (5.109), the model (5.108) is rewritten :

$$\frac{d\xi_1}{dt} = \Phi(\xi_1, Z) \theta - D \xi_1 + F_1 - Q_1 \quad (5.110.a)$$

$$\frac{dZ}{dt} = -DZ + F_b - Q_b \quad (5.110.b)$$

The technique for constructing this model (5.110) will be illustrated in Section 5.7 with a simple practical example.

5.5.2. Adaptive control design : the relative degree one case

We now suppose that the control input is the feed rate of one external substrate chosen so that :

$$F_1 = b_1 u + f_1 \text{ with } C_1^T b_1 \neq 0 \quad (5.111)$$

This means that the system has relative degree one and, therefore, that the input/output model is obtained from (5.105) and (5.110) as follows :

$$\frac{dy}{dt} = C_1^T \Phi(\xi_1, Z) \theta - Dy + C_1^T b_1 u + C_1^T (f_1 - Q_1) \quad (5.112)$$

According to the linearizing control principle, we select first order linear dynamics for the tracking error :

$$\frac{d}{dt}(y^* - y) + \lambda_1(y^* - y) = 0 \quad (5.113)$$

The linearizing control law is then calculated by substituting (5.112) into (5.113) :

$$u(\xi, \theta) = \left[\frac{dy^*}{dt} + C_1(y^* - y) + Dy - C_1^T \Phi(\xi_1, Z) \theta + C_1^T (f_1 - Q_1) \right] (C_1^T b_1)^{-1} \quad (5.114)$$

In practice, the auxiliary state Z and the parameter vector θ are unknown. As before, they will be replaced by on-line estimates so as to make the control law (5.114) adaptive. On the grounds of Chapter 3, a natural asymptotic observer for the on-line estimation of Z is obtained as follows from (5.110.b) :

$$\frac{d\hat{Z}}{dt} = -D\hat{Z} + F_b - Q_b \quad (5.115)$$

On the other hand, both direct and indirect parameter adaptation laws can be derived, which are similar to the ones of Sections 5.2.5 and 5.2.6.

Direct adaptive control

By analogy with (5.41.a), the parameter adaptation law is written :

$$\frac{d\hat{\theta}}{dt} = \Gamma\Phi(\xi_1, \hat{Z})(y^* - y) \quad (5.116)$$

It can be justified by using exactly the same Lyapunov function (5.37) as before.

Indirect adaptive control

In this case, the solution is clearly to use one of the parameter estimators (4.38) (4.39) which were introduced in Section 4.2 for the design of adaptive observers. Here also, the closed loop stability may be demonstrated by an argumentation similar to that of Section 5.2.6.

5.5.3. Adaptive control design : relative degrees higher than one

In the case where the control feed rate is chosen in such a way that condition (5.109) is not satisfied, it is clear that the system has a relative degree higher than one. The solution is then to extend the theory which has been developed in Sections 5.3 and 5.4 when the yield coefficients are known. It will not be pursued here.

5.6. Practical Aspects of Implementation

We would like in this section to draw the reader's attention to some practical problems which may arise in the implementation of adaptive linearizing control laws in bioreactors.

5.6.1. Saturation of the control input

A practical control limitation, which is not specific to adaptive linearizing control schemes but is usually present in any controller, is the saturation of the control input. Throughout the chapter, we have considered a flow rate (a feed rate F_i or the dilution rate D) as the command input. It is obvious that, in practice, the flow rate which is physically applied to the bioreactor will be bounded; it must be positive and upper bounded :

$$0 \leq u(t) \leq u_{\max} \quad (5.117)$$

In presence of bounds on the control input, the performances of the closed loop system may be degrading with respect to the ideal case of unbounded inputs. The effect may even be disastrous in some instances, as will be illustrated in Sections 5.6.3 and 5.8. Ideally, an exhaustive theoretical stability analysis should take their influence into account. An example of such an analysis is mentioned in the bibliography. However, in general, an analysis taking account of the input saturation is fairly involved and is beyond the scope of this book. Usually, careful simulation studies constitute a useful tool for the analysis of the influence of the input bounds on the control performances. In the case study of Section 5.7 we also emphasise theoretical conditions on the choice of the design parameters which avoid setting the control input to zero.

5.6.2. Introduction of an integral action in the control law

The introduction of integral action in control laws is a very important and commonly used technique for eliminating steady-state errors in the closed loop system. It is worth noting that, in our case, integral action is introduced naturally in the linearizing control laws proposed in the preceding sections via the parameter adaptation algorithms. Indeed, as appears in (5.41.a) and (5.43.b), these equations are in integral form. Our preference is for the introduction of the integral action via the adaptive law (and not for the simple addition of an integrator into the controller) for the following reasons. First of all, in the adaptive control schemes, the integrator is incorporated within a control framework for which the theoretical stability and convergence has been carefully studied. Second, the adaptation algorithm will give extra information about the uncertain process parameters, which can be very valuable to the process operator.

Let us also mention one classical problem of integral control in the presence of bounded inputs : the reset windup. When the input reaches the bounds, the integrator still integrates the regulation error : this may lead to undesirable oscillations and degradation of the control performance. This problem can be easily avoided by using an *antireset windup* mechanism. Let us give an example.

Example : basic microbial growth process with a synthesis product

Consider the following bioprocess :



characterised by the following dynamics :

$$\frac{d}{dt} \begin{bmatrix} S \\ X \\ P \end{bmatrix} = \begin{bmatrix} -k_1 \\ 1 \\ k_2 \end{bmatrix} \varphi - D \begin{bmatrix} S \\ X \\ P \end{bmatrix} + \begin{bmatrix} F \\ 0 \\ 0 \end{bmatrix} \quad (5.119)$$

$$\text{with } \varphi = \alpha SX$$

Let us follow the procedure of Section 5.2.7 to derive a direct adaptive linearizing controller of the substrate concentration S with the dilution rate D as the control action. If S^* denotes the set point of S and the parameter θ is defined as follows :

$$\theta = k_1 \alpha X \quad (5.120)$$

the discrete-time version of the direct adaptive linearizing controller, with input saturation and antireset windup mechanism, is written as follows :

$$D_t^0 = \frac{\lambda_1(S^* - S_t) + \hat{\theta}_t S_t}{S_{in,t} - S_t} \quad (5.121.a)$$

$$D_t = \begin{cases} D_t^0 & \text{if } 0 \leq D_t^0 \leq D_{\max} \\ 0 & \text{if } D_t^0 < 0 \\ D_{\max} & \text{if } D_t^0 > D_{\max} \end{cases} \quad (5.121.b)$$

$$(5.121.c)$$

$$(5.121.d)$$

$$\hat{\theta}_{t+1} = \hat{\theta}_t + \gamma T S_t (S^* - S_t) + (D_t - D_t^0) \frac{S_{in,t} - S_t}{S_t} \quad (5.121.e)$$

In the above equations, D_t^0 is the value of the dilution rate which is *calculated* by the control law (5.120) and D_t is the value which is effectively *applied* to the bioreactor. The last term of the adaptation equation (5.121.e) is the antireset windup mechanism : when the input D_t saturates, the integral adaptation law is reset to a value that gives 0 or D_{\max} , respectively.

5.6.3. Control of a product or biomass with the dilution rate D

It is straightforward to see from the general dynamical model (5.1) that, for any process component, the relative degree is always equal to one when the dilution rate D is chosen as the control input. Therefore it appears a priori very attractive to directly use, for the synthesis of the linearizing control law, the dynamical equation of the component to be controlled. Due to the presence of the input bounds, this might easily give disastrous results when the controlled variable is a product or a biomass, as we now illustrate.

Let us consider the example of basic microbial growth with a synthesis product (5.118) already considered above. From (5.119) we can directly synthesise the following linearizing control law for the regulation of P with D as the control input :

$$D^o = \frac{\lambda_1(P^* - P) - k_2\phi}{-P} \quad (5.122)$$

where P^* is the reference value of P. In practice, we must take account of the bounds (5.121.b,c,d).

The problem is that this controller may be diverging. As a matter of fact, if at some instant, the reference P^* becomes larger than $P + k_2\phi/\lambda_1$, then D^o is negative and D is set to zero. The process is set to a batch operation : if there is not enough substrate available to make $P + k_2\phi/\lambda_1$ larger than P^* , it will remain in batch mode and P will never be able to reach the desired value P^* . This is illustrated in Fig.5.7 which shows a simulation performed under the following conditions :

$$\phi = \frac{\mu^* S X}{K_M + S} \text{ (Monod model) with } \mu^* = 0.4 \text{ h}^{-1} \text{ and } K_M = 1 \text{ g/l}$$

$$k_1 = 2, k_2 = 0.5$$

$$S_{in}(0) = 5 \text{ g/l}, D(0) = 0.2 \text{ h}^{-1}, S(0) = 1 \text{ g/l}, X(0) = 2 \text{ g/l}, P(0) = 1 \text{ g/l}$$

$$\lambda_1 = 1$$

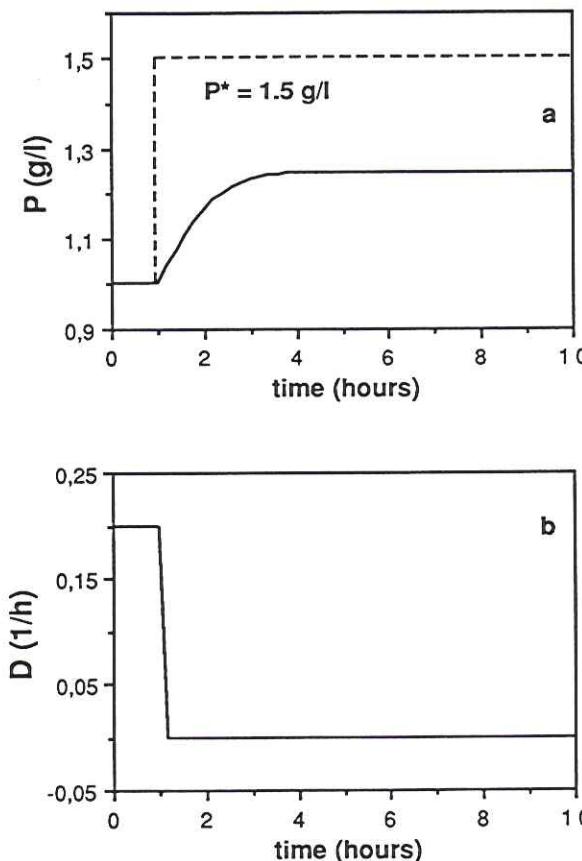


Fig.5.7. Effect of input saturation on the linearizing control of P with D

The process is initially in open loop. At time $t = 1$ hour the influent substrate concentration S_{in} is set to 7 g/l. The loop is closed with the control algorithm (5.122)(5.121.b,c,d). P^* has been set to 1.5 g/l. Note that this set point is a priori accessible, since it corresponds, with the new value of S_{in} equal to 7 g/l, to a stable equilibrium point, defined by the following input and state variable values :

$$D = 0.2 \text{ h}^{-1}, S_{in} = 7 \text{ g/l}, P = 1.5 \text{ g/l}, X = 3 \text{ g/l}, S = 1 \text{ g/l}$$

However, the controller appears to be unable to drive the process to it. Indeed, the control input D is instantaneously set to zero (Fig.5.7.b); there is an increase of the product concentration which stops when all the substrate which remained in the bioreactor has been consumed. By that time, φ has become equal to zero since S is equal to zero. Because the increase of P is not large enough, D^* remains negative, the batch operation ($D = 0$) goes on and P will never reach the desired value P^* .

Another example will be given in Section 5.8, showing the control of the production rate of a gaseous product.

One solution to this problem has been suggested in the literature (see the references): it consists of trying to reach the final set point P^* step-by-step by introducing intermediate reference values within a "setpoint definition" mechanism. Another possible approach is to change the control law either by choosing a feed rate F_i (and not the dilution rate D) as the control input, or to follow the procedure proposed in Section 5.2.7, i.e. to derive a controller with an external substrate F_i as the input and then rewrite it by choosing the dilution rate D as the manipulated variable. By comparing (5.121.a) with (5.122), we see that (5.122) contains an explicit feedforward term S_{in} and that its denominator is usually positive.

5.6.4. Division by zero

It is obvious that, in practice, it is undesirable in the computation of the control law to divide by zero (or by values close to zero). Rapid inspection of equation (5.54) shows that the problem of division by zero will be present if the controlled output y is equal to $C_S^T S_{in}$ (note that this will not happen with the controller (5.15), i.e. when the input is a feed rate F_i).

It is therefore important to check (theoretically and/or by simulation) if the operation of the bioreactor might possibly lead the controlled output y to a value close to $C_S^T S_{in}$. In many practical situations division by zero is most unlikely. For instance, in the example of the regulation of S (5.121.a), the bioreactor is usually operated in regions where S is strictly smaller than S_{in} . But there may exist control situations where division by zero is more likely to appear. We shall give an example in Section 5.8 and we shall then show how to modify the controller so as to deal with that problem.

5.7. Case Study : Adaptive Linearizing Control of Fed-Batch Reactors

Our purpose in this section is to highlight the issue of the adaptive control of bioreactors by discussing in detail its application to a specific class of simple fed-batch processes. The aim is not only to describe the design procedure but also to emphasize the benefit which is to be expected from using adaptive control in practical engineering applications.

5.7.1. Process description

We consider a microbial growth process with an associated enzyme-catalysed product described by the reaction scheme (1.36) :



According to the modelling assumptions of Section 1.5.3, we suppose that the reaction rates φ_g and φ_c are expressed as follows :

$$\varphi_g = \mu(S)X = \alpha(S)SX \quad (5.124)$$

$$\varphi_c = v(S)X = \beta(S)SX \quad (5.125)$$

The corresponding dynamical model is written :

$$\frac{dX}{dt} = \mu(S)X - DX \quad (5.126.a)$$

$$\frac{dS}{dt} = -k_1\mu(S)X - k_2v(S)X - DS + DS_{in} \quad (5.126.b)$$

$$\frac{dP}{dt} = v(S)X - DP \quad (5.126.c)$$

We suppose, in addition, that the yield of substrate consumption for product formation is negligible. Therefore, $k_2 = 0$ in the model (5.126), which is rewritten in matrix form, with the definitions (5.124)-(5.125) :

$$\frac{d}{dt} \begin{bmatrix} X \\ S \\ P \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ -k_1 & 0 & 0 \\ 0 & 1 & 0 \end{bmatrix} \begin{bmatrix} SX & 0 \\ 0 & SX \end{bmatrix} \begin{bmatrix} \alpha \\ \beta \end{bmatrix} - D \begin{bmatrix} X \\ S \\ P \end{bmatrix} + \begin{bmatrix} 0 \\ DS_{in} \\ 0 \end{bmatrix} \quad (5.127)$$

We now explicitly adopt assumptions 1) to 4) of Section 5.5 in this particular case.

1) We suppose that only the substrate S is measured on-line. That is :

$$\xi_1 = S \quad \xi_2 = [X \ P]^T \quad (5.128.a)$$

$$K_1 = [-k_1 \ 0] \quad K_2 = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} \quad (5.128.b)$$

$$F_1 = DS_{in} \quad F_2 = [0 \ 0]^T \quad (5.128.c)$$

2) Consequently, the substrate S is also the controlled output :

$$y = \xi_1 = S \quad c_1 = 1 \quad (5.129)$$

3) Clearly, the model (5.127) exhibits a nice partition :

$$\xi_a = [X \ P]^T \quad \xi_b = S \quad (5.130)$$

$$Z = S + k_1 X \quad (5.131)$$

$$\frac{dZ}{dt} = -DZ + DS_{in} \quad (5.132)$$

4) The unmeasured state X can be recovered from the auxiliary state Z as follows :

$$X = \frac{Z - S}{k_1} \quad (5.133)$$

5.7.2. Adaptive control design

From (5.127) and (5.133), the input/output dynamics are written (recall that $y = S$) :

$$\frac{dS}{dt} = -S(Z-S)\alpha - DS + DS_{in} \quad (5.134)$$

Notice that this equation is in the format of the model (5.112) with :

$$\Phi(\xi_1, Z) = -S(Z-S) \quad \theta = \alpha \quad (5.135)$$

We suppose that the dilution rate $D(t)$ is imposed by the experimental conditions, that the control input is the influent substrate concentration S_{in} :

$$u = S_{in} \quad (5.136)$$

and that the control objective is to regulate the substrate concentration at a constant desired value S^* (the "set point"). Then, the linearizing control principle (see (5.114)) gives the following linearizing control law :

$$S_{in}(Z, \alpha) = \frac{1}{D} [\lambda_1(S^*-S) + DS + S(Z-S)\alpha] \quad (5.137)$$

where λ_1 is a design parameter.

Since the reaction rate α is presumed to be unknown and Z is not measured on-line, an adaptive version of the above control law (5.137) is implemented :

$$S_{in}(\hat{Z}, \hat{\alpha}) = \frac{1}{D} [\lambda_1(S^*-S) + DS + S(\hat{Z}-S)\hat{\alpha}] \quad (5.138)$$

where \hat{Z} is updated as follows :

$$\frac{d\hat{Z}}{dt} = -D\hat{Z} + DS_{in} \quad (5.139)$$

and $\hat{\alpha}$ is computed according to the following direct adaptation scheme (Lyapunov design, see (5.116)) :

$$\frac{d\hat{\alpha}}{dt} = \gamma_1 S(\hat{Z}-S)(S^*-S) \quad (5.140)$$

except if $\hat{\alpha}=0$ and $S^*< S$, then $\frac{d\hat{\alpha}}{dt}=0$
(in order to avoid negative values of $\hat{\alpha}$)

Comment

The full adaptive controller is thus constituted by equations (5.138)-(5.140). It is obtained by a straightforward implementation of the Lyapunov design technique presented in Section 5.2.5, but with a slight additional modification

to force the positivity of $\hat{\alpha}$, which is critical to guaranteeing the control convergence established in the next subsection.

5.7.3. Convergence analysis

The convergence analysis of the above adaptive controller is based on Lyapunov stability theory (Appendix 3).

We define the following candidate Lyapunov function :

$$W(\tilde{S}, \tilde{\alpha}, \tilde{Z}) = \tilde{S}^2 + \gamma_1^{-1}\tilde{\alpha}^2 + \tilde{Z}^2 \quad (5.141)$$

with : $\tilde{S} = S^*-S$, $\tilde{\alpha} = \alpha - \hat{\alpha}$, $\tilde{Z} = Z - \hat{Z}$

and the domain of attraction \mathcal{D} :

$$\mathcal{D} = \{\tilde{S}, \tilde{\alpha}, \tilde{Z} \mid W(\tilde{S}, \tilde{\alpha}, \tilde{Z}) \leq C_0, C_0 > 0\} \quad (5.142)$$

We introduce the following assumptions :

H1. The specific reaction rate α is constant.

H2. The dilution rate D has a lower bound :

$$0 < D_{min} \leq D(t) \quad \forall t$$

(recall that the process is operated in the fed-batch mode).

H3. The minimum dilution rate D_{min} , the design parameter λ_1 and the constant C_0 are chosen such that :

$$\frac{\alpha^2(S^*+C_0)^2}{4D_{min}} < \lambda_1 < D_{min} \quad (5.143)$$

(it is easy to check that such a choice is necessarily possible).

H4. The initial estimate of Z is chosen such that :

$$\hat{Z}(0) \geq S(0) \quad (5.144)$$

We have the following convergence result.

Theorem 5. Under assumptions H1 to H4, if

$$\{\tilde{S}(0), \tilde{\alpha}(0), \tilde{Z}(0)\} \in \mathbb{D}$$

then : $\{\tilde{S}(t), \tilde{\alpha}(t), \tilde{Z}(t)\} \in \mathbb{D} \quad \forall t$ (5.145)

$$\lim_{t \rightarrow \infty} (\tilde{Z} - \hat{Z}) = 0 \quad \lim_{t \rightarrow \infty} S(t) = S^* \quad (5.146)$$

Proof. First, it can easily be shown that the upper bound in H3 and H4 (together with the positivity of $\hat{\alpha}$) implies that the influent substrate concentration $S_{in}(t)$ is positive for all t . Straightforward calculations then show that the time derivative of the Lyapunov function $W(\tilde{S}, \tilde{\alpha}, \tilde{Z})$ can be bounded as follows :

$$\begin{aligned} \frac{dW}{dt} &\leq -\lambda_1 \tilde{S}^2 - D \tilde{Z}^2 + \alpha \tilde{S} \tilde{Z} \\ &\leq -[\tilde{S}, \tilde{Z}] \left[\begin{array}{cc} \lambda_1 & -\frac{\alpha(S^* + C_0)}{2} \\ -\frac{\alpha(S^* + C_0)}{2} & D_{min} \end{array} \right] [\tilde{S}, \tilde{Z}] \end{aligned} \quad (5.147)$$

which is a negative definite quadratic form by assumption H3. The theorem follows (see Appendix 2).

QED.

5.7.4. Yield-productivity conflict in fed-batch reactors

So far in this section we have been concerned with the design and analysis of an adaptive regulator of substrate concentration for fed-batch reactors characterized by the reaction scheme (5.123). Now the question arises : why choose substrate regulation in fed-batch processes? There are several answers to that question. One of them relies on the fact that substrate regulation can constitute an efficient tool to manage the yield-productivity conflict which occurs in many practical applications. We shall illustrate this point with an example. Bacterial production of amino acids (e.g. lysine) is known to be inhibited by high substrate concentration. The dynamics of such processes are described in the literature (see the references) by the state space model (5.127), with a Monod model for the specific growth rate :

$$\mu(S) = \frac{\mu^* S}{K_m + S} \quad (5.148)$$

and a parabolic specific production rate :

$$v(S) = \begin{cases} S(v_0 - v_1 S) & 0 \leq S \leq \frac{v_0}{v_1} \\ 0 & S > \frac{v_0}{v_1} \end{cases} \quad (5.149.a)$$

$$S > \frac{v_0}{v_1} \quad (5.149.b)$$

According to (5.124)-(5.125), the corresponding specific reaction rates are as follows, for $0 \leq S \leq v_0/v_1$:

$$\alpha(S) = \frac{\mu^*}{K_m + S} \quad \beta(S) = v_0 - v_1 S \quad (5.150)$$

Suppose now that the fed-batch operation has a fixed duration T . We define the productivity as the final product quantity per unit of time :

$$PR \triangleq \frac{P(T) V(T)}{T} \quad (5.151)$$

and the yield as the ratio of the final product quantity to the amount of substrate which has been consumed :

$$YI \triangleq \frac{P(T)V(T)}{\int_0^T DS_{in} dt} \quad (5.152)$$

These parameters PR and YI are plotted in Fig.5.8 with respect to the set point S^* , for a series of simulations, performed with the model (5.127), (5.150), under the adaptive control (5.138)-(5.140). From this figure it clearly appears that the set point S^* (and obviously the associated adaptive controller) can be viewed as a means to modulate the process between productivity maximization (but with a low yield) obtained with $S^*=1$, and yield maximization (with a low productivity) obtained with $S^*=2$.

It must be clear that this conclusion holds even if the analytical models of $\mu(S)$ and $v(S)$ are unknown to the user, provided that they have the same shape as in Fig.5.9. In that case, the optimization procedure should consist of looking, over successive fed-batch experiments, for the best set point S^* ; that is, the set point which corresponds, from the user's viewpoint, to the best trade-off between yield and productivity.

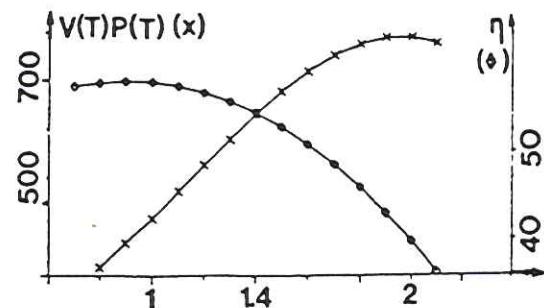


Fig.5.8. Final product quantity $V(T)P(T)$ (x) and yield YI (◊) vs set point S^*

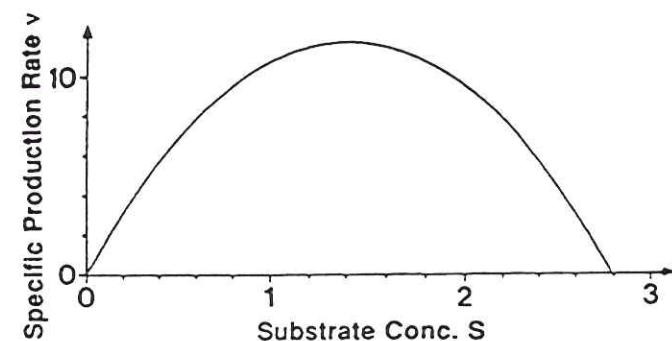


Fig.5.9. Specific production rate $v(S)$

5.7.5. Comparison with optimal control

We now consider the case where the biomass growth itself is inhibited by high substrate concentration. We assume that the specific growth rate $\mu(S)$ is suitably described by a Haldane law (1.20) :

$$\mu(S) = \frac{\mu_0 S}{K_M + S + S^2/K_I} \quad \text{with } \mu_0 = \mu^* \left[1 + \sqrt{K_M/K_I} \right] \quad (5.153)$$

A simulation experiment is shown in Fig.5.10 for the following set of parameters:

$$K_I = 1 \quad K_M = 10 \quad K_I = 0.1 \quad \mu^* = 5$$

and the following initial and operating conditions :

$$S(0) = 1 \quad X(0) = 0.1 \quad V(0) = 10 \quad S_{in}(0) = 3.5$$

$$F_0 = 0.1 \quad V_{max} = 12$$

$$\lambda_1 = 10 \quad \gamma_1 = 10 \quad \hat{\alpha}(0) = 0.2 \quad \hat{Z}(0) = S(0)$$

Fig.5.10 compares closed loop and open loop operations of the fed-batch process. In both cases, the reactor is fed with the same amount of substrate. In open loop, a constant input concentration $S_{in}(t)$ is used while, in closed loop, $S_{in}(t)$ is computed by the control algorithm (5.138)-(5.140). One hour after the end of the feeding period, $X(t)$ has already reached its maximum value. In open loop the substrate concentration $S(t)$ increases rapidly to high values which inhibits the growth and the final biomass concentration remains below 10% of the value reached in closed loop.

It is interesting to compare this result with that which would be obtained by using optimal control theory. In this application, the optimal control problem is the problem maximizing the final biomass production ($X(T)V(T)$) under the constraint of the dynamical model (5.127).

It can be shown that, if :

$$S(0) = \sqrt{K_M K_I} \quad (5.154)$$

the optimal control is written :

$$S_{in} = \sqrt{K_M K_I} + k_1 \frac{v}{F_0} \frac{\mu^* \sqrt{K_M K_I}}{2K_M + \sqrt{K_M K_I}} X \quad (5.155)$$

with V and X computed from :

$$\frac{dV}{dt} = F_0 \quad \frac{dX}{dt} = \frac{\mu^* \sqrt{K_M K_I}}{2K_M + \sqrt{K_M K_I}} X - \frac{F_0}{V} X \quad (5.156)$$

In contrast with the adaptive regulator (5.138)-(5.140) which just requires the choice of the set point S^* , it appears that the main drawback of this optimal control is the need for a knowledge of the specific growth rate structure and, in particular, of the constants μ^* , K_M and K_I .

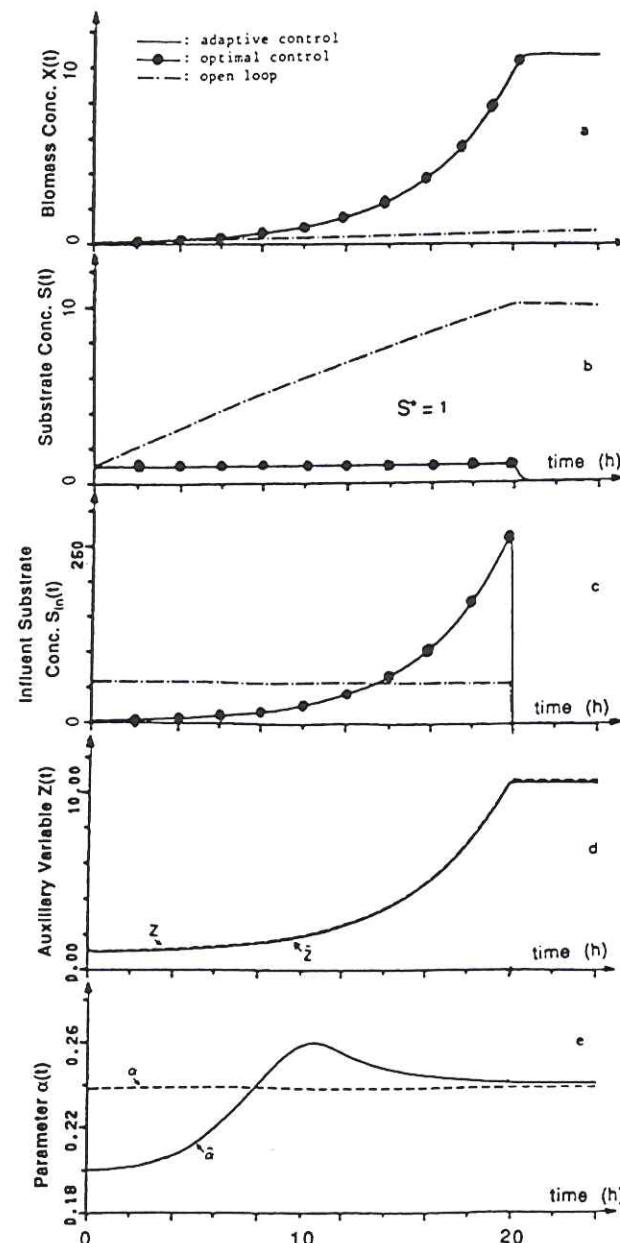


Fig.5.10. Adaptive control of fed-batch reactors : maximization of $X(t)$

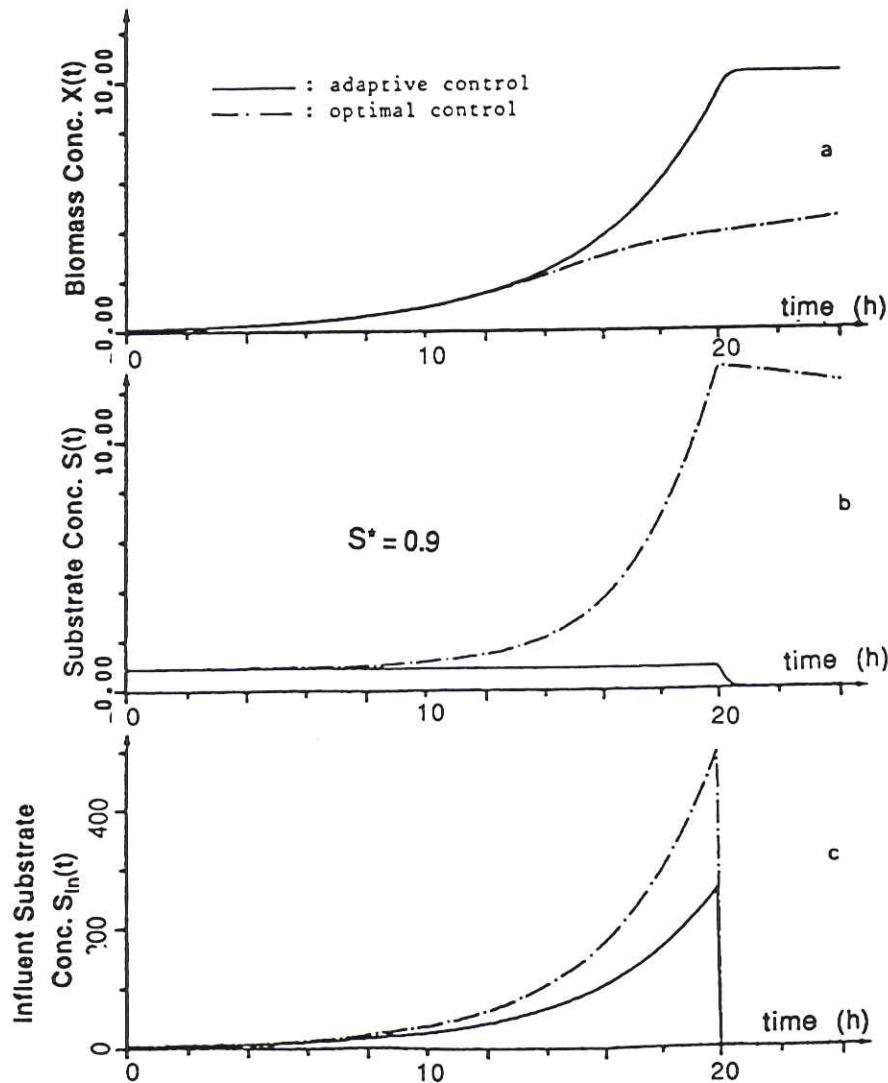


Fig.5.11. Comparison adaptive control - optimal control : robustness with respect to model inaccuracies

Besides, as shown in Fig.5.10, the behaviour of the adaptive controller is so close to the optimal one that no significant discrimination between both trajectories can be made, despite the initial errors in the estimates $\hat{Z}(0)$ and $\hat{\alpha}(0)$.

Obviously, the quasi-optimality of the adaptive controller relies critically on a precise knowledge of the set point S^* which maximizes the specific growth rate. It is therefore relevant to study the sensitivity of the control performance with respect to the value of S^* . In Fig.5.11 we have considered that the "best" value of S^* was known with a 10% error. This means that, in our simulations, the adaptive controller (5.138)-(5.140) has been implemented with a desired set point $S^* = 0.9$ (while the true $S^* = 1$). Accordingly, the value of K_M has been set to 8.1 (instead of 10) in the optimal control law (5.150) because :

$$S^* = \sqrt{K_M K_I} = 0.9 \rightarrow K_M = \frac{(S^*)^2}{K_I} = 8.1$$

Fig.5.11 shows the better robustness of the adaptive controller towards that inaccuracy. Although the biomass production is no more optimal, it remains very close to the optimum, while the (open loop) optimal controller diverges completely from the optimal trajectory, which induces a loss of more than 50% of the production.

5.8. Case Study : Adaptive Control of the Gaseous Production Rate of a Synthesis Product

Throughout the chapter we have discussed the control of an output which is a linear combination of the process variables. We shall now illustrate how to extend the methodology to the control of variables which are complex nonlinear combinations of the process variables. We shall also see, in Section 5.8.4 how to modify the linearizing control law in order to avoid division by zero.

5.8.1. Description of the process

Consider a single substrate, single biomass process with a low solubility product P :



By considering the singular perturbation approximation for P (Section 1.8), the dynamical equations of the process are given by :

$$\frac{d}{dt} \begin{bmatrix} X \\ S \end{bmatrix} = \begin{bmatrix} 1 \\ -k_1 \end{bmatrix} \phi + \begin{bmatrix} 0 \\ DS_{in} \end{bmatrix} - D \begin{bmatrix} X \\ S \end{bmatrix} \quad (5.158.a)$$

$$Q = k_2 \phi \quad (5.158.b)$$

where Q is the gaseous outflow rate of the synthesis product P and where the reaction rate ϕ can be expressed as follows according to (1.53) (1.54) :

$$\phi = \mu X \quad (5.159.a)$$

$$= \alpha SX \quad (5.159.b)$$

Assume that the objective here is to regulate the gaseous production rate Q at a desired level Q^* by acting on the dilution rate D.

5.8.2. Example : anaerobic digestion process

A typical example is anaerobic digestion. In the preceding sections we have discussed the application of anaerobic digestion processes in wastewater treatment. Another possible application, potentially combined with the first one, is methane production. Methane may then be used as an energy supply to feed e.g. gas ovens in industry or as a fuel for light or heating purposes on farms. If the process is used for methane production, there is a clear incentive to optimize its production rate Q and to have a methane production that fits the

energy demand. As a matter of fact, we can expect that the optimal desired value Q^* will be an increasing function of the available influent substrate concentration $S_{in}(t)$, as illustrated in Fig.5.12. The control objective consists here of regulating the methane production rate Q at a desired value Q^* by acting on the dilution rate D. S_{in} may be chosen so as to define an "optimal" value of Q^* , which itself corresponds to the energy demand.

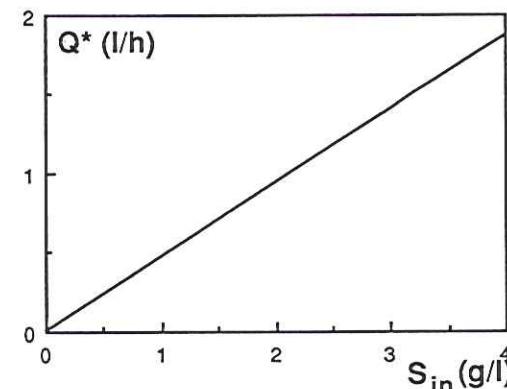


Fig.5.12. $Q^* = f(S_{in})$

Let us now describe two different control algorithms.

5.8.3. Control algorithm #1

It is clear from equation (5.159.b) that the production rate Q is a nonlinear function of the state (X, S). Moreover, its time evolution is described explicitly by a differential equation in the model (5.158). In order to synthesise a linearizing controller, let us first calculate its time derivative.

A bad solution consists of using equation (5.159.a) (which does exhibit the explicit dependence with respect to S) as a basis for the time derivation. Indeed, we then obtain :

$$\frac{dQ}{dt} = \theta Q - DQ \quad (5.160)$$

with :

$$\theta = \mu + \frac{1}{\mu} \frac{d\mu}{dt} \quad (5.161)$$

This equation is similar to the dynamical equation of the biomass in a basic microbial growth process (with θ instead of μ). As has been pointed out in Section 5.6.2, the linearizing control directly based on this equation is not a good solution since, as a result of input saturation, the control may diverge. This is illustrated in the simulation of Fig.5.13.

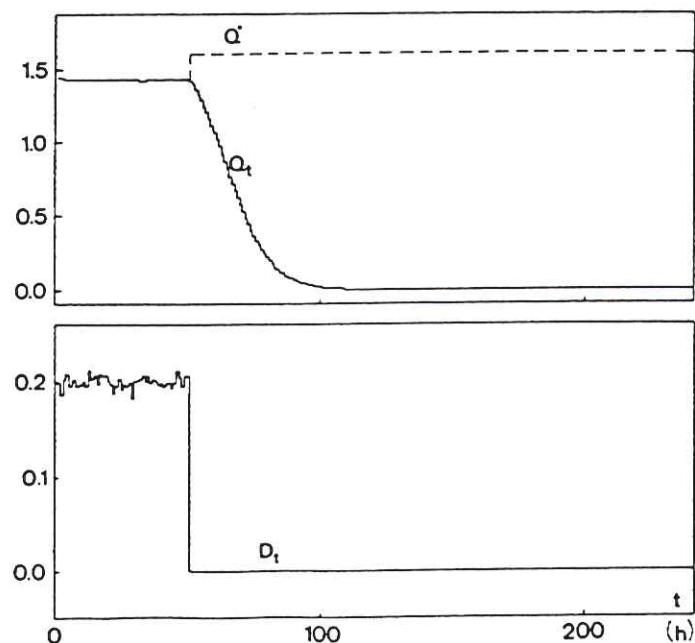


Fig.5.13. Divergence of the controller due to the input saturation

The simulation has been performed under the following conditions. A Monod model (1.18) has been chosen for the specific growth rate μ :

$$\mu = \frac{\mu^* S}{K_M + S} \quad (5.162)$$

with $\mu^* = 0.4 \text{ d}^{-1}$ and $K_M = 0.4 \text{ g/l}$

The initial conditions have been set to :

$$X(0) = 0.095 \text{ g/l}, S(0) = 0.4 \text{ g/l}, S_{in}(0) = 3 \text{ g/l}, D(0) = 0.2 \text{ d}^{-1}$$

and the yield coefficients are :

$$k_1 = 27.3 \quad k_2 = 75 \text{ l}^2\text{d/g.h}$$

The upper bound on the input D is :

$$D_{max} = 0.39 \text{ d}^{-1}$$

The process is initially operated in open loop (without control) with a white noise input signal $D(t)$. At time $t = 72$, S_{in} has been set to 3.4 g/l , and according to Fig. 5.12, Q^* has been set to 1.58 l/h . The gain of the controller λ_1 is equal to 1 h^{-1} . The dilution rate is instantaneously set to zero. It remains at this bound and Q tends to zero (since S , and therefore $\mu(S)$, tends to zero).

Therefore we propose to use equation (5.159.b) to compute the time derivative of Q . This gives :

$$\frac{dQ}{dt} = \theta_1 S Q - \theta_2 \frac{Q^2}{S} + \theta_3 Q + DQ \left[\frac{S_{in}}{S} - 2 \right] \quad (5.163)$$

with :

$$[\theta_1, \theta_2, \theta_3] = \left[\alpha, \frac{k_1}{k_2}, \frac{1}{\alpha} \frac{d\alpha}{dt} \right] \quad (5.164)$$

The adaptive linearizing adaptive control law then specialises here as follows :

$$D^0 = \frac{\lambda_1(Q^* - Q) - \hat{\theta}_1 S Q + \hat{\theta}_2 Q^2 / S - \hat{\theta}_3 Q}{Q[S_{in}/S - 2]} \quad (5.165)$$

In practice, we have to take account of the physical bounds on the flow rate and the control law is then implemented as follows :

$$D = \begin{cases} D^0 & \text{if } 0 \leq D^0 \leq D_{\max} \\ 0 & \text{if } D^0 < 0 \\ D_{\max} & \text{if } D^0 > D_{\max} \end{cases} \quad (5.166.a)$$

$$(5.166.b)$$

$$(5.166.c)$$

In (5.165) and (5.166) D^0 is the value of the control input *calculated* by the computer, and D is the input value which is effectively *applied* at the control value.

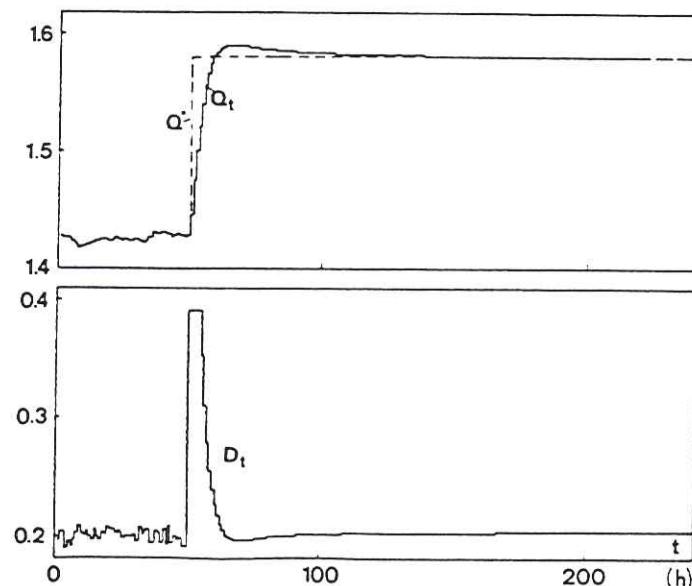


Fig.5.14. Adaptive control of the production rate Q

This control law (5.165) appears to be more effective. This is mainly due to the explicit dependence of Q on the limiting substrate S . This is illustrated in Fig.5.14, which shows the performance of the controller (5.165) in the same experiment as in Fig.5.13.

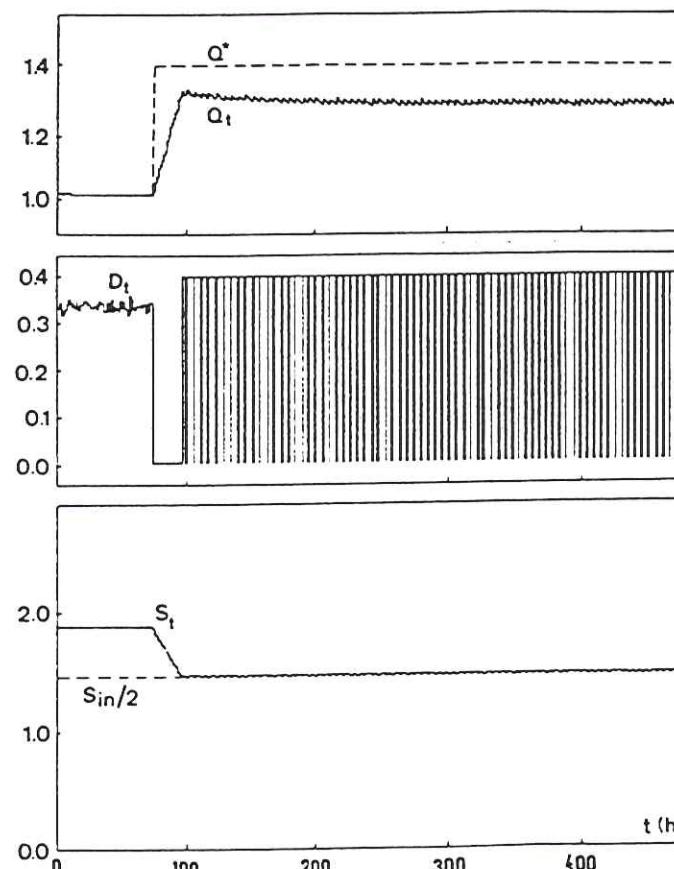


Fig.5.15. Problems of division by zero

However, the drawback of the controller (5.165) is the possibility of the occurrence of a division by zero. Indeed it is obvious that values of the

substrate concentration S close to $S_{in}/2$ are possible in practice. This is illustrated in Fig.5.15. At time $t = 72$, the desired value Q^* has been set to 1.4 l/h (S_{in} is equal to 3 g/l). The control input D is oscillating between its lower and upper bounds, and the controller is able to drive the output Q to its desired value Q^* .

The simulation has been performed in almost similar conditions as before but with the following initial conditions :

$$X(0) = 0.04 \text{ g/l}, S(0) = 1.9 \text{ g/l}, S_{in}(0) = 3 \text{ g/l}, D(0) = 0.33 \text{ d}^{-1}$$

5.8.4. Control algorithm #2

In order to avoid division by zero which arises when S is equal to $S_{in}/2$, we suggest the use of the following dynamic control law :

$$\frac{dD^0}{dt} = \frac{-g^2}{\omega + g^2} D^0 + \frac{g}{\omega + g^2} \left[\lambda_1(Q^* - Q) - \hat{\theta}_1 SQ + \hat{\theta}_2 \frac{Q^2}{S} - \hat{\theta}_3 Q \right] \quad (5.167)$$

where ω is an arbitrary positive constant ($\omega > 0$) and g is the denominator of (5.165), i.e. :

$$g = Q \left[\frac{S_{in}}{S} - 2 \right] \quad (5.168)$$

It is clear that for values of ω different from zero, division by zero is avoided.

Note that, in the steady-state ($dD^0/dt = 0$), the control law (5.168) reduces to the preceding one (5.165).

It is also worth noting that (5.168) with $\lambda_1 = 1$ is a continuous time equivalent of the generalized minimum variance (GMV) controller.

By way of comparison, Fig.5.16 reproduces the same simulation experiment as in Fig.5.15 but with the application of the controller (5.168) (with $\omega = 0.16$) and shows its ability to avoid division by zero and reach the desired set point Q^* .

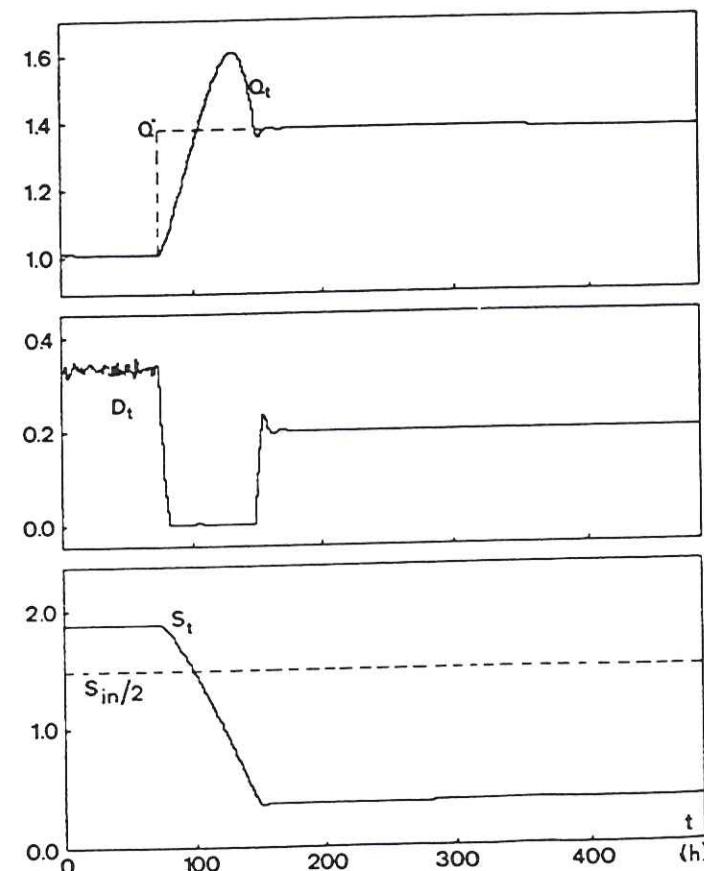


Fig.5.16. Dynamic control of the production rate Q

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APPENDIX 1

MODELS OF THE SPECIFIC GROWTH RATE

1. Dependence on the Substrate Concentration : $\mu(S)$

Monod (1942)

$$\mu(S) = \frac{\mu^* S(t)}{K_M + S(t)}$$

Blackman (1905)

$$\mu(S) = \begin{cases} \frac{\mu^*}{K_M} S(t) & \text{if } S(t) \leq K_M \\ \mu^* & \text{if } S(t) > K_M \end{cases}$$

Tessier (1942)

$$\mu(S) = \mu^* \left(1 - \exp \left[-\frac{S(t)}{K_M} \right] \right)$$

Haldane (Andrews, 1968)

$$\mu(S) = \frac{\mu_0 S(t)}{K_M + S(t) + S^2(t)/K_I}$$

Moser (1958)

$$\mu(S) = \frac{\mu^* S^\lambda(t)}{K_M + S^\lambda(t)}$$

with $\lambda > 0$

Powell (1967)

$$\mu(S) = \frac{\mu^*}{2 K_M} \left[K_M + S(t) - \sqrt{K_M + S(t)^2 - 4 K_M S} \right]$$

with $K_M > 0$

Konak (1974)

$$\frac{d\mu}{dS} = K_M (\mu^* - \mu)^\lambda$$

with $\lambda > 0$

Aborhey and Williamson (1977)

a) $\frac{d\mu}{dt} = k \left[\mu^* S(t) - \mu [S(t) + K_M] \right]$

b) $\frac{d\mu}{dt} = k \left[\frac{\mu^* S(t)}{K_M + S(t)} - \mu \right]$

with k : constant

Takamatsu et al. (1983)

$$\mu_B(S) = K_B (S(t) - S_B)$$

$$\mu_F(S) = K_F (S(t) - S_F)$$

with $\mu_B(S)$: bulking sludge specific growth rate

$\mu_F(S)$: floc-forming sludge specific growth rate

K_B, S_B, K_F, S_F : constants

Axelsson et al (1984)

$$\mu(S) = \frac{\mu^* S(t)}{K_M + S(t)} + Y \pi^-(S(t))$$

with Y : yield coefficient

$\pi^-(S(t))$: negative part of $\pi \cong p(S - S_c)$

S_c : critical substrate concentration.

Hoppe and Hansford (1982)

$$\mu(S) = \frac{\mu^* S(t)}{K_M + S(t)} \frac{K_M}{K_M + Y[S_{in} - S(t)]}$$

with K_M, Y : constants

Chen and Hashimoto (1978)

$$\mu(S) = \frac{\mu^* S(t)}{K[S_{in} - S(t)] + S(t)}$$

with K : constant

Yue (Roques et al., 1982)

$$\mu(S) = \frac{\mu^* S(t)}{K[S_{in} - S(t)] + K_M + S(t)}$$

Jost et al (1973)

$$\mu(S) = \frac{\mu^* S(t)^2}{(K_{m1} + S(t))(K_{m2} + S(t))}$$

with K_{m1}, K_{m2} : saturation constants

Shehata and Marr (1971)

$$\mu(S) = \frac{\mu_1^* S(t)}{K_{m1} + S(t)} + \frac{\mu_2^* S(t)}{K_{m2} + S(t)}$$

with $\mu_1^* + \mu_2^* = \mu^*$

Sokol and Howell (1981)

$$1) \mu(S) = \frac{K_1 S}{K_2 + S^2}$$

$$2) \mu(S) = \frac{K_1 S}{K_2 + S^{K_3}}$$

Ming et al (1988)

$$\mu(S) = \mu^* \frac{S^2}{K_1 + S^2}$$

2. Dependence on the Biomass Concentration : $\mu(X)$

Verhulst (1838)

$$\mu(X) = \mu^* \left(1 - \frac{X}{X_M}\right)$$

with X_M : constant

Kono and Asai (1969)

$$\mu(X) = K_X \Phi$$

with K_X = growth rate constant

Φ = apparent coefficient of growth activity

$\Phi = 0$, induction phase

$\Phi = \varphi$, $0 < \varphi < 1$, transient phase

$$\varphi = \alpha t$$

$\Phi = 1$ exponential phase

$$\Phi = \frac{C_{XC}}{C_{XM} - C_{XC}} \quad \frac{C_{XM} - C_X}{C_X}$$

with C_{XC} : critical cell concentration

C_{XM} : maximum cell concentration

C_X : cell concentration

3. Dependence on the Substrate Concentration $S(t)$ and on the Biomass Concentration $X(t)$: $\mu(S,X)$

Contois (1959)

$$\mu(S,X) = \frac{\mu^* S(t)}{K_C X(t) + S(t)}$$

with K_C : saturation constant

Nihtilä and Virkkunen (1977)

$$\mu(S,X) = K_1 \frac{C(t)}{X(t)}$$

$$\frac{dC}{dt} = K_2 S(t)[X(t) - C(t)] - K_3 C(t)$$

with $C(t)$: cell-substrate complex

K_1, K_2, K_3 : constants

Kishimoto et al (1983)

$$\mu(S, X) = \bar{\mu} + Q_1(X(t) - \bar{X}) + Q_2(S(t) - \bar{S})$$

with $\bar{\mu}$, \bar{X} , \bar{S} : mean arithmetic values
of $\mu(t)$, $X(t)$, $S(t)$

Q_1 , Q_2 : partial regression coefficients

Staniskis and Levisauskas (1984)

$$\mu(S, X) = K_1 S(t) - K_2 X(t)$$

with K_1 , K_2 : constants

4. Dependence on the Product Concentration $P(t)$: $\mu(P)$

Hinshelwood (1946)

$$\mu(P) = \mu^* - K_1 [P(t) - K_2]$$

with K_1 , K_2 : positive constants

Aiba et al (1968)

$$\mu(P) = \mu^* e^{-K_1 P(t)}$$

with K_1 : constant

Jerusaliwski and Engambergediev (1969)

$$a) \mu(P) = \frac{\mu^* P(t)}{K_P + P(t)}$$

with K_P : saturation constant

$$b) \mu(P) = \frac{\mu^* K_P}{K_P + P(t)}$$

Levenspiel (1980)

$$\mu(P) = \mu^* \left[1 - \frac{P(t)}{P_L} \right]^n$$

with P_L : limiting product concentration
 n : toxic power

Hägglund (1983)

$$\mu(P) = K_1 - K_2 \frac{P}{K_3 + P}$$

5. Dependence on the Substrate Concentration $S(t)$ and the Product Concentration $P(t)$: $\mu(S, P)$

Ghose and Tyagi (1979)

$$\mu(S, P) = \frac{\mu_0 S(t)}{K_M + S(t) + S^2(t)/K_i} \left(1 - \frac{P(t)}{P_L} \right)$$

Jin et al (1981)

$$\mu(S, P) = \mu^* \frac{S(t)}{K_M + S(t)} \exp \{-K_1 P(t) - K_2 S(t)\}$$

with K_1 , K_2 : constants

Sevely et al (1981)

$$\mu(S, P) = \mu^* \frac{S(t)}{K_M + S(t)} \frac{K_P}{K_P + P(t)} \left(1 - \frac{P(t)}{P_L} \right)$$

Aborhey and Williamson (1977)

$$a) \mu(S, P) = \mu^* \frac{S(t)}{K_M + S(t)} \frac{P(t)}{K_P + P(t)}$$

$$b) \mu(S, P) = \mu^* \frac{S(t)}{K_M + S(t)} \frac{S(t)}{S(t) + K_P P(t)}$$

with K_P : constant

Dourado and Calvet (1983)

$$\mu(S, P) = \mu^* \frac{S(t)}{K_M + S(t) + S^2(t)/K_i} \frac{K_P}{K_P + P(t)} \left(1 - \frac{P(t)}{P_L} \right)$$

Moulin et al (1980)

$$\mu(S, P) = \mu^* \exp\{-K_1 P(t) + K_2 (S(t) - K_3) - K_4 P(t) (S(t) - K_3)\}$$

with K_1, K_2, K_3, K_4 : constants

Aiba et al (1968)

$$\mu(S, P) = \mu^* \frac{S(t)}{K_M + S(t)} \exp\{-K_1 P(t)\}$$

Bazua and Wilke (1977)

$$\mu(S, P) = \mu^* - \frac{K_1 P(t)}{K_2 - P(t)} \frac{S(t)}{K_M + S(t)}$$

6. Dependence on the Substrate Concentration $S(t)$ and the Dissolved Oxygen Concentration $C(t)$: $\mu(S, C)$

Olsson (1976)

$$\mu(S, C) = \mu^* \frac{S(t)}{K_M + S(t)} \frac{C(t)}{K_C + C(t)}$$

with K_C : saturation constant

Peringer et al. (1972)

$$\mu = \mu_1^* \frac{S(t)}{K_M + S(t)} \left[\frac{C(t)}{K_C + C(t)} + \frac{1}{1 + K_1 C(t)} \right] + \mu_2^*$$

with K_1 : constant

μ_2^* : specific endogenous respiration rate

$$2 \mu_1^* + \mu_2^* = \mu^*$$

7. Dependence on the Substrate Concentration $S(t)$, the Dissolved Oxygen Concentration $C(t)$ and the Product Concentration $P(t)$: $\mu(S, C, P)$

Williams et al. (1984)

$$\mu(S, C, P) = \left\{ \frac{K_1 S(t)}{K_M + S(t)} + \frac{K_2 P(t)}{K_P + P(t)} \right\} \left\{ \frac{C(t)}{K_C + C(t)} + K_3 C(t) - K_4 \right\}$$

with K_1, K_2, K_3, K_4 : constants

8. Dependence on the Substrate Concentration $S(t)$ and the Inhibitory Metabolite Concentration $I(t)$: $\mu(S, I)$

Kishimoto et al (1983)

$$a) \mu(S, I) = K_1 + K_2 S(t) + K_3 I(t)$$

with K_1, K_2, K_3 : constants

$I(t)$: inhibitory metabolite concentration

$$b) \mu(S, I) = \frac{\mu^* S(t)}{K_M + S(t)} \cdot \frac{1}{1 + I^2(t)}$$

9. Dependence on the pH : $\mu(pH)$

Andreyeva and Biryukov (1973)

$$\mu(pH) = \alpha pH^2 + \beta pH + \gamma$$

with α, β, γ : constants

10. Dependence on the pH and the Temperature : $\mu(pH, T)$

Cheruy and Durand (1979)

$$\mu(pH) = \alpha pH^2 + \beta pH (\delta + T) + \gamma$$

with $\alpha, \beta, \gamma, \delta$: constants

11. Dependence on the pH and the Substrate Concentration $S(t)$: $\mu(pH, S)$

Andreyeva and Biryukov (1973)

$$a) \mu(pH, S) = \frac{\mu^* SH^+}{K_M + SH^+ + (SH^+)^2/K_i}$$

with H^+ : hydrogen ion concentration

pH : $-\log H^+$

$$b) \mu(pH, S) = \frac{\mu^* S}{K_M \left(1 + \frac{K_a}{H^+} + \frac{H^+}{K_b} \right) + S}$$

with K_a, K_b : constants

$$c) \mu(pH, S) = \frac{\mu^* S}{K_M \left(1 + \frac{K_a}{H^+} + \frac{H^+}{K_b} \right) + S \left(1 + \frac{K'_a}{H^+} + \frac{H^+}{K'_b} \right)}$$

with K'_a, K'_b : constants

$$d) \mu(pH, S) = \frac{\mu^* S}{K_M + S} \cdot \frac{K_H}{K_H + H^+}$$

with K_H : constant

$$e) \mu(pH, S) = \frac{\mu^* S}{K_M + S} \cdot \frac{K_{OH}}{K_{OH} + 1/H^+}$$

with K_{OH} : constant

$$f) \mu(pH, S) = \frac{\mu^* S}{K_M + S} \cdot \frac{K_H}{K_H + H^+} \cdot \frac{K_{OH}}{K_{OH} + 1/H^+}$$

$$g) \mu(pH, S) = \frac{\mu^* S}{K_M \left(1 + \frac{K_a}{H^+} + \frac{H^+}{K_b} \right) + S} \frac{K_H}{K_H + H^+} \frac{K_{OH}}{K_{OH} + 1/H^+}$$

$$h) \mu(pH, S) = \frac{\mu^* S}{K_M \left(1 + \frac{K_a}{H^+} \right) + S} \frac{K_H}{K_H + H^+} \frac{K_{OH}}{K_{OH} + 1/H^+}$$

Jackson and Edwards (1975)

$$\mu = \frac{\mu^* S}{\left(1 + \frac{K_2}{H^+} + \frac{H^+}{K_1} \right) (K_M + S + S^2/K_i [1 + K_3/H^+])}$$

with K_1, K_2, K_3 : constants

12. Dependence on the Temperature T : $\mu(T)$

Topiwala and Sinclair (1971)

$$\mu(T) = A_1 e^{-E_1/RT} + A_2 e^{-E_2/RT} - A_3$$

with A_1, A_2, A_3 : constants

E_1, E_2 : activation energies

R : gas constant

Hashimoto (1982)

$$\mu(T) = \alpha T - \beta$$

with α, β : constants

13. Dependence on the Temperature T and the Biomass Concentration X(t) : $\mu(T, X)$

Constantinides (1970)

$$\mu(T, X) = b_1(T) \left(1 - \frac{X(t)}{b_2(T)} \right)$$

$$b_1(T) = K_1 - K_2 (T(t) - K_3)^2$$

$$b_2(T) = K_4 - K_5 (T(t) - K_6)^2$$

with $K_1, K_2, K_3, K_4, K_5, K_6$: constants

14. Dependence on the Light Intensity I(t) and the Biomass Concentration X(t) : $\mu(I, X)$.

Tamiya et al (1953)

$$\mu(I, X) = \frac{\mu^*}{Z \varepsilon X(t)} \ln \frac{\mu^* + C I_0}{\mu^* + C I_0 \exp[-\varepsilon Z X(t)]}$$

with ε : extinction coefficient of the micro-organisms

Z : culture's depth

I_0 : incident intensity.

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APPENDIX 2

ELEMENTS OF STABILITY THEORY

In this appendix we present an elementary and intuitive presentation of the stability theory of nonlinear and linear time-varying systems. The reader is referred to the books listed in the references for a comprehensive treatment of the subject.

A2.1. Nonlinear Systems

Consider a nonlinear system described by the differential equation :

$$\frac{dx}{dt} = f(x) \quad x \stackrel{\Delta}{=} (x_1, x_2, \dots, x_n) \in \mathbb{R}^n \quad \forall t \geq 0 \quad (\text{A2.1})$$

Suppose that $x \equiv 0$ is an equilibrium state of the system :

$$f(0) \equiv 0 \quad (\text{A2.2})$$

Definition A2.1

The equilibrium state $x = 0$ is asymptotically stable (a.s.) if there exists a positive constant $\varepsilon_1 > 0$ such that, if $\|x(0)\| \leq \varepsilon_1$, then :

$$\lim_{t \rightarrow \infty} \|x(t)\| = 0 \quad (\text{A2.3})$$

The Lyapunov methods are techniques for testing the stability of an equilibrium state of a nonlinear system without having to calculate the trajectories $x(t)$.

Definition A2.2

A Lyapunov function $W(x)$ for the system (A2.1) is defined as follows :

- a) $W(x)$ is a continuously differentiable scalar function of x
- b) $W(x)$ is positive definite, i.e. $W(x) \geq 0 \forall x$, $W(x) = 0$ if $x = 0$
- c) $\frac{d}{dt}W(x) = \frac{\partial W(x)}{\partial x}f(x)$ is negative-definite along the solutions of (A2.1).

Theorem A2.1 (Direct Lyapunov's method)

If there exists a positive constant $\varepsilon_1 > 0$ such that, if $\|x(0)\| < \varepsilon_1$, there exists a Lyapunov function for the system (A2.1), then $x \equiv 0$ is an asymptotically stable equilibrium state.

Definition A2.3

The equilibrium state $x \equiv 0$ is exponentially stable if there exist three positive constants ε_1 , C_1 , C_2 such that, for all $\|x(0)\| \leq \varepsilon_1$, the solution $x(t)$ of (A2.1) is bounded as follows :

$$\|x(t)\| \leq C_1 \exp(-C_2 t) \|x(0)\| \quad \forall t \geq 0 \quad (\text{A2.4})$$

(Notice that exponential stability implies asymptotic stability).

Theorem A2.2 (First Lyapunov method)

Consider the matrix : $\Delta = \left(\frac{\partial f}{\partial x} \right)_{x=0}$ (A2.5)

- If all the eigenvalues of the matrix Δ have negative real parts, then the equilibrium state $x \equiv 0$ is exponentially stable.
- If any of the real parts of the eigenvalues of Δ are positive, then the equilibrium state $x \equiv 0$ is unstable.
- No conclusion may be drawn in case of eigenvalues having zero real parts.

Total stability

Suppose that the system (A2.1) is perturbed as follows :

$$\frac{dx}{dt} = f(x) + g(x,t) \quad (\text{A2.6})$$

where $g(x,t)$ is a continuously differentiable perturbation function.

Definition A2.4

The equilibrium state of (A2.1) is totally stable if there exist two positive constants ε_1 and ε_2 such that, if $\|x(0)\| \leq \varepsilon_1$ and $\|g(x,t)\| \leq \varepsilon_2$, then the solution $x(t)$ of (A2.6) is bounded for all t .

Theorem A2.3

If the equilibrium state $x \equiv 0$ of (A2.1) is exponentially stable, then it is totally stable.

Remark A2.1. A special case of (A2.6) occurs when the perturbation $g(x,t) = g(x)u(t)$ with $u(t)$ an external input. In such a case, total stability is also called BIBS (for Bounded Input Bounded State) stability.

A2.2. Linear Time-Varying Systems

Consider a linear time-varying system described by the following non stationary differential equation :

$$\frac{dx}{dt} = A(t)x(t) \quad t \geq t_0 \quad (A2.7)$$

with $x \stackrel{\Delta}{=} (x_1, x_2, \dots, x_n) \in \mathbb{R}^n$.

and $A(t)$ a square $n \times n$ real valued matrix of continuously differentiable bounded time functions.

We notice that $x \equiv 0$ is necessarily an equilibrium state of the system (A2.7). Furthermore, it is an isolated equilibrium state if $A(t)$ is nonsingular for some t .

Definition A2.5

The equilibrium state $x \equiv 0$ of system (A2.7) is exponentially stable (synonymous : uniformly asymptotically stable), if there exist two positive constants C_1 and C_2 , independent of t_0 and $x(t_0)$, such that $x(t)$ is bounded as follows for all t_0 and $x(t_0)$:

$$\|x(t)\| \leq [C_1 \exp(-C_2(t - t_0))] \|x(t_0)\| \quad \forall t \geq t_0 \quad (A2.8)$$

Theorem A2.4

If there exists a positive constant ε_1 , such that for each $t \geq 0$, the eigenvalues of $A(t)$ all have real parts less than or equal to $-\varepsilon_1$, then there exists another constant ε_2 such that the equilibrium state $x \equiv 0$ of the system (A2.7) is exponentially stable whenever :

$$\left\| \frac{dA(t)}{dt} \right\| \leq \varepsilon_2 \quad \forall t \geq 0 \quad (A2.9)$$

where $\|\cdot\|$ is the matrix norm induced by the vector norm used in (A2.8)

Definition A2.6

A scalar function $W(x,t)$ is decrescent in a closed region S of the x -space containing the origin $x \equiv 0$, if a positive definite function $W_1(x)$ exists such that, for all x in S and all t ,

$$|W(x,t)| \leq W_1(x)$$

Theorem A2.5

If the matrix $A(t)$ is bounded, then the equilibrium state $x \equiv 0$ of system (A2.7) is uniformly asymptotically stable if and only if there exists a time-varying, quadratic, positive definite, decrescent Lyapunov function whose derivative along the solutions of (A2.7) has a time-varying negative definite decrescent quadratic form.

BIBS (Bounded Input Bounded State) Stability

Consider a linear time-varying system with an external input $u(t)$ described by the following differential equation :

$$\frac{dx}{dt} = A(t)x(t) + B(t)u(t) \quad (A2.10)$$

Theorem A2.6

If the equilibrium state $x \equiv 0$ of (A2.7) is exponentially stable, if the matrix $B(t)$ is bounded ($\|B(t)\| \leq M_1$), if the input $u(t)$ is bounded ($\|u(t)\| \leq M$), then the state of the system (A2.10) is bounded as follows :

$$\|x(t)\| \leq C_1 \|x(0)\| + \frac{MC_1M_1}{C_2} \quad \forall t \geq 0$$

Second Order Systems

Technical Lemma A2.1

If $\lambda_2 < \lambda_1 < 0$, then

$$\int_0^t |\lambda_2 \exp(\lambda_1 s) - \lambda_2 \exp(\lambda_2 s)| ds \\ = \exp(\lambda_1 t) - \exp(\lambda_1) + 2[\exp(\lambda_1 \sigma^*) - \exp(\lambda_2 \sigma^*)] \quad (\text{A2.11})$$

$$\text{with } \sigma^* = \frac{\ln(\lambda_2/\lambda_1)}{\lambda_1 - \lambda_2} \quad \text{for all } t \geq \sigma^* \quad (\text{A2.12})$$

Proof : the value σ^* defined by (A2.12) is clearly the unique value such that :

$$\lambda_1 \exp(\lambda_1 \sigma^*) = \lambda_2 \exp(\lambda_2 \sigma^*) \quad (\text{A2.13})$$

Then it is easy to see that :

$$\int_0^t |\lambda_1 \exp(\lambda_1 s) - \lambda_2 \exp(\lambda_2 s)| ds \\ = \int_0^{\sigma^*} [\lambda_1 \exp(\lambda_1 s) - \lambda_2 \exp(\lambda_2 s)] ds \\ + \int_{\sigma^*}^t [\lambda_1 \exp(\lambda_1 s) - \lambda_2 \exp(\lambda_2 s)] ds \quad (\text{A2.14})$$

and expression (A2.11) follows readily.

QED

Consider the second order system :

$$\frac{dx(t)}{dt} = Ax(t) + b(t) \quad (\text{A2.15})$$

$$\text{with } x(t) = \begin{bmatrix} x_1(t) \\ x_2(t) \end{bmatrix} \quad (\text{A2.16})$$

$$A = \begin{bmatrix} -C_1 & 1 \\ -C_2 & 0 \end{bmatrix} \quad (\text{A2.17})$$

$$b(t) = \begin{bmatrix} b_1(t) \\ b_2(t) \end{bmatrix} \quad (\text{A2.18})$$

Technical Lemma A2.2

Assume that $b_1(t)$ and $b_2(t)$ are bounded :

$$|b_1(t)| \leq B_1 \quad |b_2(t)| \leq B_2 \quad (\text{A2.19})$$

and that A has real distinct eigenvalues $\lambda_2 < \lambda_1 < 0$ (i.e. $C_2 < C_1^2/4$).

Then :

$$\limsup_{t \rightarrow \infty} |x_1(t)| \leq \frac{2B_1}{\lambda_1 - \lambda_2} \left\{ \left[\frac{\lambda_1}{\lambda_2} \right]^{(\lambda_1/\lambda_1 - \lambda_2)} - \left[\frac{\lambda_1}{\lambda_2} \right]^{(\lambda_2/\lambda_1 - \lambda_2)} \right\} + \frac{B_2}{\lambda_1 \lambda_2} \quad (\text{A2.20})$$

$$\limsup_{t \rightarrow \infty} |x_2(t)| \leq B_1 - \frac{\lambda_1 + \lambda_2}{\lambda_1 \lambda_2} B_2 \quad (\text{A2.21})$$

Proof : the solution $x(t)$ of A2.15 may be written as follows :

$$x(t) = P J(t) P^{-1} x(0) = \int_0^t P J(t-\tau) P^{-1} b(\tau) d\tau \quad (\text{A2.22})$$

$$\text{with } P = \begin{bmatrix} 1 & 1 \\ -\lambda_2 & -\lambda_1 \end{bmatrix} : \text{the eigenvector matrix of A}$$

$$P^{-1} = \frac{1}{\lambda_1 - \lambda_2} \begin{bmatrix} \lambda_1 & 0 \\ -\lambda_2 & -1 \end{bmatrix}$$

$$J(t) = \begin{bmatrix} \exp(\lambda_1 t) & 0 \\ 0 & \exp(\lambda_2 t) \end{bmatrix}$$

For sufficiently large t (i.e. after the effect of initial conditions has disappeared), the solution of (A2.15) is :

$$\begin{aligned} x_1(t) &= \frac{1}{\lambda_1 - \lambda_2} \int_0^t \{ [\lambda_1 \exp(\lambda_1 [t-\tau]) - \lambda_2 \exp(\lambda_2 [t-\tau])] b_1(\tau) \\ &\quad + [\exp(\lambda_1 [t-\tau]) - \exp(\lambda_2 [t-\tau])] b_2(\tau) \} d\tau \end{aligned} \quad (\text{A2.23})$$

$$\begin{aligned} x_2(t) &= \frac{1}{\lambda_1 - \lambda_2} \int_0^t \{ \lambda_1 \lambda_2 [\exp(\lambda_2 [t-\tau]) - \exp(\lambda_2 [t-\tau])] b_1(\tau) \\ &\quad + [\lambda_1 \exp(\lambda_1 [t-\tau]) - \lambda_2 \exp(\lambda_2 [t-\tau])] b_2(\tau) \} d\tau \end{aligned} \quad (\text{A2.24})$$

It is then easy to see that :

$$\exp(\lambda_1 [t-\tau]) - \exp(\lambda_2 [t-\tau]) > 0 \quad (\text{A2.25})$$

$$\text{and } \lambda_1 \exp(\lambda_1 [t-\tau]) - \lambda_2 \exp(\lambda_2 [t-\tau]) > 0 \quad (\text{A2.26})$$

We now examine $x_1(t)$ and $x_2(t)$ separately. Using (A2.12) (A2.26) and the Cauchy-Schwartz inequality, we have from (A2.23) :

$$\begin{aligned} |x_1(t)| &+ \frac{1}{\lambda_1 - \lambda_2} \int_0^t \{ B_1 |\lambda_1 [\exp(\lambda_1 [t-\tau]) - \lambda_2 \exp(\lambda_2 [t-\tau])]| \\ &\quad + B_2 [\exp(\lambda_1 [t-\tau]) - \exp(\lambda_2 [t-\tau])] \} d\tau \end{aligned} \quad (\text{A2.27})$$

and from Technical Lemma A2.1 :

$$\begin{aligned} |x_1(t)| &< \frac{1}{\lambda_1 - \lambda_2} \{ B_1 [\exp(\lambda_2 t) - \exp(\lambda_1 t) + 2\{\exp(\lambda_1 \sigma^*) \\ &\quad - \exp(\lambda_2 \sigma^*)\}] + B_2 \left[\frac{1}{\lambda_1} \exp(\lambda_1 t) - 1 - \frac{1}{\lambda_2} (\exp(\lambda_2 t) - 1) \right] \} \end{aligned} \quad (\text{A2.28})$$

with σ^* given by (A2.12).

Hence taking the limit of the RHS of (A2.28) for $t \rightarrow \infty$, we obtain inequality (A2.20) after some simple manipulations.

In an analogous way, using (A2.25) and (A2.26), we have from (A2.11) :

$$\begin{aligned} |x_2(t)| &< \frac{1}{\lambda_1 - \lambda_2} \{ B_1 \lambda_1 \lambda_2 \left[\frac{1}{\lambda_1} \left(\exp(\lambda_1 t) - 1 - \frac{1}{\lambda_2} (\exp(\lambda_2 t) - 1) \right) \right. \right. \\ &\quad \left. \left. + B_2 \left[\frac{\lambda_1}{\lambda_2} (\exp(\lambda_2 t) - 1) - \frac{\lambda_2}{\lambda_1} (\exp(\lambda_1 t) - 1) \right] \right] \} \end{aligned} \quad (\text{A2.29})$$

Hence taking the limit of (A2.29) for $t \rightarrow \infty$, we obtain inequality (A2.21).

Then expression (A2.20) and (A2.21) hold and the lemma is proved.

QED

Corollary A2.1

If C_2 is chosen such that :

$$C_2 = \alpha C_1^2 / 4, \quad 0 < \alpha < 1$$

then expression (A2.20)(A2.21) can be rewritten as follows :

$$\limsup_{t \rightarrow \infty} |x_1(t)| \leq \frac{2B_1}{C_1\sqrt{1-\alpha}} \left[\left\{ \frac{1-\sqrt{1-\alpha}}{1+\sqrt{1-\alpha}} \right\}^{-[(1-\sqrt{1-\alpha})/2\sqrt{1-\alpha}]} - \left\{ \frac{1-\sqrt{1-\alpha}}{1+\sqrt{1-\alpha}} \right\}^{-(1+\sqrt{1-\alpha})/2\sqrt{1-\alpha}} \right] + \frac{4B_2}{\alpha C_1^2} \quad (\text{A2.30})$$

$$\limsup_{t \rightarrow \infty} |x_2(t)| \leq B_1 + \frac{4}{\alpha C_1} B_2 \quad (\text{A2.31})$$

Proof : straightforward by noting that :

$$\lambda_1 = \frac{-C_1}{2} [1 - \sqrt{1-\alpha}]$$

$$\lambda_2 = \frac{-C_1}{2} [1 + \sqrt{1-\alpha}]$$

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APPENDIX 3

PERSISTENCE OF EXCITATION. CONVERGENCE OF ADAPTIVE ESTIMATORS

In this appendix we introduce several definitions and theoretical results concerning the persistence of excitation of regressors which is a key concept for the analysis of adaptive estimators such as those which are described in Chapters 3 and 4 of this book.

Definition A3.1

An $m \times n$ matrix $\Phi(t)$, $t \geq 0$, of continuously differentiable bounded time functions is persistently exciting if there exist positive constants α and ε such that :

$$\alpha I \leq \int_t^{t+\varepsilon} \Phi(\tau) \Phi^T(\tau) d\tau \quad \forall t \geq 0 \quad (\text{A3.1})$$

Convergence of adaptive estimators

Definition A3.2

If the equilibrium state $x \equiv 0$ of the time-varying linear system (A2.7) is exponentially stable, then by extension the system itself is said to be exponentially stable.

Theorem A3.1

If $\Phi(t)$ is persistently exciting, if Γ is a constant $m \times m$ positive definite matrix, then the following linear time-varying system is exponentially stable :

$$\frac{d\tilde{\theta}}{dt} = -\Gamma\Phi(t)\Phi^T(t)\tilde{\theta} \quad (\text{A3.2})$$

Theorem A3.2

If $\Phi(t)$ is persistently exciting, if $A(t)$ is a stable $n \times n$ matrix of bounded piecewise continuous-time functions, if $P(t)$ is a symmetric positive definite matrix of bounded continuous-time functions such that $dP/dt + PA + A^TP$ is negative definite, then the following linear time-varying system is exponentially stable :

$$\frac{d}{dt} \begin{bmatrix} x \\ \tilde{\theta} \end{bmatrix} = \begin{bmatrix} A(t) & -\Phi^T(t) \\ \Phi(t)P(t) & 0 \end{bmatrix} \begin{bmatrix} x \\ \tilde{\theta} \end{bmatrix} \quad (\text{A3.3})$$

Transfer of excitation

The above theorems are useful for demonstrating the convergence of adaptive estimators if the "regressor" $\Phi(t)$ is the state of stable linear filter. In such a case, the following results are relevant.

Let $\phi(t)$ denote one arbitrary column of the matrix $\Phi(t)$. Let $u(t)$ be a scalar, real valued, time-varying, continuously differentiable signal.

Definition A3.3

The signal $u(t)$ is said to be sufficiently rich of order m if the following vector :

$$W(t) = \left[u, \frac{du}{dt}, \frac{d^2u}{dt^2}, \dots, \frac{d^{m-1}u}{dt^{m-1}} \right]^T \quad (\text{A3.4})$$

is persistently exciting.

Theorem A3.4

If each column of $\Phi(t)$ is generated by a linear stable time invariant filter

$$\frac{d\phi}{dt} = A\phi(t) + Bu(t) \quad \phi \in \mathbb{R}^m \quad (\text{A3.5})$$

If the following matrix is full rank :

$$[B \ AB \ A^2B \ \dots \ A^{m-1}B] \quad (\text{A3.6})$$

If $u(t)$ is sufficiently rich of order m , then $\Phi(t)$ is persistently exciting.

Remark : when the matrix (A3.6) is full rank, the system (A3.5) is said to be "state reachable".

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NOMENCLATURE

A : bioreactor cross-section (Section 1.10)
A(ξ) : state matrix of the linear tangent model
a,b,c,a₁, a₂ : constants
A₀, A₁, A₂ : (yield coefficient nonlinear combination) matrices
B : diagonal matrix of the specific liquid-gas transfer rates
b,f : feed rate vectors
C : dissolved oxygen (concentration); output matrix (Chapter 4)
C_i ($i = 1,2,3$) : constants (Chapter 3)
C_S : oxygen saturation constant
D : dilution rate
E : enzyme
E₁, E₂ : activation energies
F : flow rate (Sections 1.1 and 5.7) or feed rate vector
F_g : aeration feed rate
F_r : substrate feed rate
H : matrix of known functions of the state
h : adaptation law
I : inhibitor concentration
J : cost function
K : yield coefficient matrix
K_C, K_P : specific growth rate constants of the models
k_d : death coefficient
k_i, k_{ij} ($i,j \in N$) : yield coefficient
k_La : mass transfer coefficient
K_M : Michaelis-Menten constant
k_m : maintenance coefficient

L : bioreactor length (Section 1.10); light intensity (Section 1.3);
 output matrix (Chapter 3)
 M_1, M_2 : constant
 M : number of reactions
 N : number of components
 α : observability matrix
 OTR : oxygen transfer rate
 OUR : oxygen uptake rate
 p : dimension of the matrix K
 P : product (concentration)
 pH : pH
 P_{sat} : product saturation concentration
 q : number of measured components
 Q : gaseous flow rate
 R : ideal gas constant; symmetric matrix (Kalman filter)
 r_{11}, r_{12}, r_{22} : elements of R
 R_i ($i = 1$ to 3) : elements of R
 RQ : respiratory quotient
 S : substrate (concentration)
 T : sampling period; temperature (Chapter 1)
 t : time
 V : volume
 v : vector
 w : natural frequency ($= \sqrt{\gamma}$)
 W : Lyapunov function
 X : biomass (concentration)
 y : output

Greek letters

α : specific reaction rate (vector)
 β : specific liquid-gas transfer rate

ε : singular perturbation variable (Section 1.8) or linear filter output (Section 3.4.2)
 Φ : regressor matrix
 Γ : gain matrix
 $\gamma_1, \gamma_2, \gamma_3$: elements of Γ
 η, δ : constants
 ϕ : reaction rate
 λ : forgetting factor
 μ : specific growth rate
 μ^* : maximum specific growth rate
 μ_0 : Haldane growth rate parameter
 v : specific production rate
 v_1, v_2 : eigenvalues of the 2×2 matrix A
 Π : P/P_{sat} (Section 1.8)
 θ : unknown parameter vector
 ρ : non-growth associated specific production rate (Section 1.3) or vector of unknown functions
 σ : design parameter
 Ω : gain matrix
 ω, γ : tuning parameters
 ω_1, ω_2 : elements of Ω
 ξ : biochemical reaction component (vector)
 ψ, ψ_0 : linear filter output
 ζ : damping coefficient
 Σ^{-1} : weighting matrix

Subscripts

t : time index
 in : influent
 out : effluent
 i, j : number indices
 a, b, s, f : partition indices

min, max : minimum, maximum

m : measured

R : recycle

T : total

W : waste

Superscripts

T : transposed matrix or vector

: estimate

\sim : error

$*$: desired

Mathematical notations

Σ : sum

Π : product

\forall : for all

$\lim_{t \rightarrow \infty}$: limit for time tending to infinity

min : minimum

max : maximum

sup : supremum

diag{.} : diagonal matrix

$\sum_{j=1}^i$: summation on the reactions with index j which involve the component with index i

\in : belongs to

$\frac{d}{dt}$: time derivative

$\frac{\partial}{\partial t}, \frac{\partial}{\partial z}$: partial derivative with respect to time t and length z

$\arg \min_x F(x)$: value of the argument x for which $F(x)$ is minimum with respect to x

elementary matrix : matrix which contains only terms equal to 1 or 0

A^{-1} : inverse of the (square) matrix A, i.e. such that $AA^{-1} = A^{-1}A = I$ (where I is the identity matrix)

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