INRIA

INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET EN AUTOMATIQUE

Project-Team MERE

Modelling and Water Resources

Sophia Antipolis

THEME BIO

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1. Team

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2. Overall Objectives

2.1. Overall Objectives

Biological WasteWater Treatment Plants (WWTP) are used to transform organic compounds present in wastewater in soluble form (also called substrates) into solids (micro-organisms or biomass also called sludge). In more general terms, such a system where a micro-organism is used to transform substrates into others is called a bioreactor. In the context of wastewater treatment, substrates are consumed by the biomasses under adequate environmental conditions. Once the substrate concentrations have reached normative constraints, the solids (the biomass) and the clean water are separated: the liquid is rejected to the natural environment while the sludge is either incinerated, used in agriculture or, until recently, stored in wetlands. The treatment industry can be considered as the first industry in terms of matter to be processed. Therefore, the design, the control and in more general terms, the optimization of treatment processes are real challenges. Our objective is to better understand these processes in order to optimize their functioning in the presence of uncertainty and of unknown and unmeasured external disturbances. To do so,

1. we approach the problems at two levels: the microscopical scale (the micro-organism) and the macroscopical one (the plant),
2. we use macroscopical modeling and control system science tools to develop new design rules, estimation techniques and control systems that we calibrate on real biological pilot plants.

Our methodology consists in the development of mathematical models of the biological reactions and transports in the reactor. At this stage, we have very strong interactions with micro-biologists. After that we analyze the model with the available mathematical tools or/and through computer simulations. Our main emphasis is put on the effects of the spatial distribution of the biomass. This questioning can be understood at various scales.

- At the macroscopic level we compare the performances of various designs, from infinitely stirred reactors to purely non-mixed reactors through cascade of reactors.
- At the microscopic level we are interested in the growth process of the biomass, limitations caused by the diffusion of the substrate, the role of the biofilms.

We are interested in fundamental questions of microbial ecology, like biodiversity of biomasses, competition and predation since they are at the roots of the understanding of biological wastewater treatment and, at the same time we address very practical questions like the minimization of the size of the bioreactors.

3. Scientific Foundations

3.1. Scientific Foundations

Keywords: *(theoretical) ecology*, *control systems*, *environment*, *mathematical modeling*, *observers*, *process engineering*.

The chemostat is a laboratory device which goes back to the second world war, with the work of Monod and Szilard. It is used to study the growth of micro-organisms. The principle is simple: a continuous flow rate through a constant volume reactor provides nutrients to a population or a community of micro-organisms. At equilibrium the growth-rate must equal the artificial mortality induced by the outflow of the reactor. A simple model, for the case where the reactor is perfectly stirred, is given by a set of two differential equations, one for the variations of the nutrient concentration, the other one for the biomass concentration. This model is based on the classical law of mass action used in the modeling of chemical kinetics: the rate of a reaction is proportional to the product of the concentrations of the two reactants. In the case of population growth this means that the growth-rate of a population depends on the nutrient concentration. This system of two equations has been perfectly well-understood for more than half a century.

The chemostat model is a good first approximation of the running of a wastewater treatment plant. From this simple model one can develop models which incorporate more realistic assumptions like:

- Existence of a complicated trophic chain in the digestion process,
- Consideration of non-perfect mixing inducing diffusion processes,
- Consideration of mass transport in plug-flow reactors,
- Parallel or cascade connections of reactors,
- Re-circulation of the biomass,
- Aggregation of micro-organisms in flocs,
- Constitution of biofilms,

which lead to complicated systems of coupled partial differential equations of transport-diffusion type. Due to the presence of non-monotonic kinetics the theory of equations of this type is not yet perfectly understood. Determination of stable stationary solutions is often a question of current research and numerical simulations are used. Moreover the control of industrial plants addresses new questions in the domain of robust control and observers.

Since a Waste Water plant is a microbial ecosystem, microbial ecology is fundamental for the understanding of our processes. An ecosystem is a system in which various populations of different species are interacting between them and reacting to the environmental abiotic parameters. Concepts of competition, predation, symbiosis are used to describe these interactions and try to understand important questions like the biodiversity and the productivity of the ecosystem. The biodiversity is related to the number of species which is supported by the ecosystem. There are many ways of quantifying the biodiversity of a microbial ecosystems. The most intuitive measurement of diversity is the richness which simply is the number of species. The productivity measures the rate at which abiotic resources are transformed into biomass. An old prediction of theoretical population models says that, in a constant environment, an ecosystem with n different kinds of resources can support at most n different species (different means that the ways two species use resources are different). This prediction is not realized in wastewater treatment plants where it was demonstrated, using tools of molecular biology (SSCP), that a small number of resources (maintained at a constant level) is able to maintain a huge number of species. This shows that the classical model of the perfectly stirred reactor is no longer valid if one wants to model the biodiversity in the reactor. We explore alternative models based on the consideration of growth-rates which are not solely nutrient-dependent, but are also density-dependent, which means that the growth rate may depends not only on the nutrient concentration but also on the density of biomass. More specifically, based on physical arguments, we currently work with models where the growth rates decrease with the biomass concentration. A special case of density-dependence is the ratio dependence which was much discussed recently.

Since a density-dependent model is a macroscopic model, it is important to understand how the density-dependence is a consequence of the microscopic behaviors of individuals. Since direct observation of the behavior of bacteria is difficult, mathematical modeling is of great help. The hypotheses, at the microscopic level, are expressed in terms of partial differential equations or in terms of individually based models so that macroscopic consequences are derived, either by using mathematical reasonings or computer simulations. Finally, mathematical analysis is the starting point for the design of new experiments which could validate hypotheses of the theoretical models. But conducting biological experiments require time, energy and qualified people for rigorous validation (many protocols have to be checked for ensuring that contamination or side-effects do not alterate the results).

4. Application Domains

4.1. Design of Wastewater treatment plants

The question of the **optimal design** of chemical or biochemical systems has been addressed by several authors during the last thirty years. An important effort has been made by the chemical engineering community to synthesize plants with the smallest possible volume in order to minimize the investment cost. This task turns out to be much more complex in the case of biological systems. One reason for that is the difficulty of finding simple and yet accurate models to represent all the important dynamics of living organisms interacting in a bio-system.

A plant that is made of a cascade of homogeneous Continuous Stirred Tank Reactors (CSTR or chemostats) has a particular practical interest: in most cases, it allows to approximate the behavior of diffusive systems (also called Plug Flow Reactors or PFR) which usually exhibit better performances than a single CSTR. In other terms, a given conversion rate can be obtained with a PFR of smaller volume than the one of a CSTR. However, a PFR is very difficult to operate in practice while CSTR operability and reliability are better.

Biological processes can usually be classified into two classes of systems: micro-biological and enzymatic reactions. In simple terms, micro-biological-based reactions define (bio)reactions where a substrate degradation is associated with the growth of certain organisms while the second, the enzymatic reaction, may be viewed as a chemical reaction with specific kinetic functions.

Given a model of a series of CSTRs, representing either enzyme or micro-biological reactions, and a flow rate to be treated, the problem of determining optimal conditions for a steady-state operation has been studied. In particular, conditions have been proposed to minimize the Total Retention Time (TRT) required to attain a given conversion rate $1 - S_N/S_0$ (here S_0 and S_N denote respectively the input and output substrate concentrations), or equivalently to minimize the total volume of the plant given that the flow rate to be treated is constant.

4.2. Observation and control of wastewater treatment plants

Control problems frequently arise in the context of the study of biological systems such as wastewater treatment plants. In general, in order to cope with disturbances, modeling errors or uncertainty of parameters, one has to take advantage of robust nonlinear control design results. These results are based on central theories of modern non-linear control analysis, like for instance those based on the input-to-state stable (ISS) notion and the back-stepping and the forwarding techniques. Observe that most of these results are based on the construction of families of Control Lyapunov Functions.

Waste water treatments plants are often unstable as soon as bacteria growths exhibit some inhibition. Typically, under a constant feed rate, the wash-out of the reactor (i.e. when biomass is no longer present) becomes an attracting but **undesirable equilibrium point**. Choosing the dilution rate as the manipulated input is usually a mean for the stabilization about a desired set point, but the most efficient control laws often require a perfect knowledge of the state variables of the system, namely the online measurement of all the concentrations, which are generally not accessible (for technical or economical reasons). Most often, only a few sensors are available.

A popular way to achieve stabilization of a control dynamical system under partial knowledge of the state is to first design an “observer” or “software sensor” for the reconstruction of the unobserved variables, and then to couple this estimate with a stabilizing feedback control law, if some “separation principle” is satisfied. Unfortunately, in industrial operating conditions, one cannot thoroughly trust the models that were developed and identified in well-controlled environments such as in laboratory experiments. Engineers have to deal with several uncertainties on parts of the model, as well as on the output delivered by the sensors. During the initialization stage or hitches on the process, the system can be far away from the nominal state, where few empirical data are available. Generally, probabilistic hypotheses cannot be justified regarding the nature of the uncertainty for stochastic models to be considered. On the opposite, reasonable bounds on the unknown parts of the models are available, so that uncertainties can be considered as unknown deterministic inputs.

Consequently, robust observers and control laws need to be developed to cope with the particularities of the uncertainty on the models.

4.3. Control of sequencing batch reactors

From an engineering point of view, biological reactors are classified according to the way they are fed. When treating industrial as well as urban waste-waters, batch processes present a number of advantages with respect to continuous ones. In particular, the reaction rates are usually faster and the separation step, during which the biomass is separated from the effluent to be finally rejected into the environment, is much easier to control than during continuous operation. A **batch process** operates in a sequential mode (this is why they are called Sequencing Batch Reactors or SBR): the water to be treated is first introduced into a closed tank. Then, the reaction takes place (the biomass degrades the substrates), the biomass settles and the supernatant (clean water) is finally discharged from the process before another cycle begins.

A classical objective for improving the functioning of these processes is the **minimal time fedbatch strategy** for a SBR treating both the organic carbon and nitrogen. To do so, two different operating conditions are needed: one aerated period (also called the "aerobic phase") and one without aeration (also called the "anoxic phase"). Depending on the initial concentrations of the different components (biomasses and substrates), the objective is to find the switching instants (from the aerobic phase to the anoxic one or conversely from the anoxic phase to the aerobic one) such that the total reaction time is minimized. From the mathematical point of view, the models are very closed from the CSTR ones. Nevertheless, because several components and biological reactions are simultaneously present in the different reaction phases, the problem is far from being completely solved. A rigorous study has been conducted within the framework of the European project EOLI, and new challenging open questions (both from the mathematical and practical sides) have been raised.

4.4. Interpretation of molecular fingerprint profiles

The SSCP (Single Strand Conformation Polymorphism) is a very recent molecular analysis technique which allows us to estimate the relative abundance of a given species in a complex ecosystem at a given time t. This kind of (very rich) information is becoming to change completely the vision of an ecosystem, traditional given by macroscopic measurements (biomass density, gas production,...). The access to the knowledge of the relative abundance is about to be a “small revolution” in the micro-biology world. Nevertheless, these techniques are not completely satisfactory at the moment, because the knowledge is so rich and so intricate that nobody does clearly know what is really observed... More precisely, the result of such analyses are delivered under the form of a graphic in which the x-axis is related to the species while the y-axis gives the relative abundance of the corresponding species. Ideally, under the assumption that two different species do not respond on the same abscissa, a SSCP spectrum would be a succession of rays, the heights of which would correspond to the abundances of these species. From a technical point of view, the method is based on the fact that regions of the DNA remain unchanged during the cellular division, or at least that the variation rate of these regions is very low. Thus, these regions (called 16S) are assumed to be constant and have been designated as being a real signature for a given species. Being able to detect, to mark and to specifically amplify these regions using the PCR (Polymerase Chain Reaction) technique, it has become possible - for about ten years now - to specify "who is there?" in a complex microbial ecosystem. After the PCR, in adequate conditions, the RNA strands are separated on a gel by electrophoresis. The size of the strands and their spatial conformations allow them to be discriminated with respect to the time it takes for each of them to reach a laser detector, the intensity of which depends on the actual quantity of strands (it gives the relative abundance of the corresponding species). Because the detector is not perfect and because the strands of a given species do not move exactly together, the result is not a succession of rays but rather the sum of individual Gaussian-like curves. Furthermore, a real microbial ecosystem may comprise hundreds of species and it is expected that a number of DNA16S strands almost responds at the same time (and thus they are very close in the x-axis of the SSCP spectrum). These facts introduce an important bias about the analysis of such signals...

Until now, the micro-biologists analyze their SSCP profile in the following way. Usually, they empirically identify the visible peaks as being the responses of species which are major quantities in the ecosystem. The height of the peak is used as a measure of its relative abundance into the ecosystem. However, with respect to the uncertainty sources described above, it is straightforward to see that the picture cannot be considered as so simple. For instance, imagine that two species respond on the same x-axis: only one peak (the sum of all DNA16S detected at a given instant by the detector) will be visible on the spectrum and it will be concluded that one species is present at an abundance that is directly related to the magnitude of the peak while, in reality, this peak is due to two (or why not even to a greater number) species. And indeed, our preliminary works show that the results given by these molecular techniques under the form of spectra must be carefully analyzed in order not to draw wrong conclusions. Our objective is to better understand what exactly happens during the analysis in order to identify, characterize and extract the correct information given by this technique.

Many challenging signal processing and dynamical modeling questions are today wild open, and the team aims at investigating more deeply this field in the near future.

4.5. Experimentation in ecology

Mathematics and simulations show that substrate dependent models of competition and density-dependent models have radically different predictions in terms of extinction of species. A substrate dependent model is likely to be a reasonably good model for the case of low densities of biomass, the density-dependent model being a good one for high densities. The mathematical treatment on realistic parameters predicts outcomes which are to be tested. In connection with micro-biologists (among whose J.J. Godon, INRA-LBE) and ecologists (in particular R. Arditi, INAPG), we are currently working on this subject.

5. Software

5.1. Softwares

We produce our own software for the simulations we are currently doing. These softwares are, most of the time, uniquely designed for research purposes. However it might sometimes happen that some software has some wider interest. In that case we try to design it in such a way that it is useful for a larger community.

6. New Results

6.1. Theoretical results

6.1.1. Steady states in a certain class of reaction diffusion-transport equation

Participants: Abdou Khadry Dramé, Claude Lobry, Frédéric Mazenc, Alain Rapaport.

In a previous work ([1]) we showed that the asymptotic behavior of the system of two partial differential equations:

$$\begin{array}{l}
\frac{\partial S}{\partial t} = -\frac{q}{\sigma(z)}\frac{\partial S}{\partial z} + d\frac{\partial^2 S}{\partial z^2} - \mu(S)X \\
\frac{\partial X}{\partial t} = -\frac{q}{\sigma(z)}\frac{\partial X}{\partial z} + d\frac{\partial^2 X}{\partial z^2} + \mu(S)X \\
d\frac{\partial S}{\partial z}(t,0) = \frac{q}{\sigma(0)}(S(t,0) - S_{in}), \quad d\frac{\partial S}{\partial z}(t,l) = 0 \\
d\frac{\partial X}{\partial z}(t,0) = \frac{q}{\sigma(0)}(X(t,0) - X_{in}), \quad d\frac{\partial X}{\partial z}(t,l) = 0
\end{array}$$

(which models a single biomass growing in a bioreactor which is not well-stirred) is the same as the asymptotic behavior of the single equation:

$$\begin{array}{l}
\frac{\partial S}{\partial t} = -\frac{q}{\sigma(z)}\frac{\partial S}{\partial z} + d\frac{\partial^2 S}{\partial z^2} - \mu(S)(M - S) \\
\frac{q}{\sigma(0)}(S(t,0) - S_{in}), \quad d\frac{\partial S}{\partial z}(t,l) = 0
\end{array}$$

The growth rate $\mu(s)$ is supposed to be positive and non-monotonic (increasing, having a maximum, decreasing). Our purpose is to first determine equilibria and next to analyze their stability properties. The two point boundary value problem is solved using asymptotic methods for small and large values of d, which correspond respectively to the plug flow reactor and the perfectly stirred reactor. We prove that, under a mild condition on the growth rate, there exist at most two stable and one unstable solutions. More precisely we have the following : It is known that, under mild conditions, the perfectly stirred reactor has two stable solutions and one unstable. We show that it is the same if d is large (which is not a surprise !) and that, on the opposite side, when d is small (near the perfect plug flow reactor) the stationary solution is unique. For intermediate values of d the analysis is done through computer simulations and the bifurcation diagram is experimentally determined .

6.1.2. Multiple steady states in a cascade of well-stirred reactors with non-monotonic growth-rate

Participants: Abdou Khadry Dramé, Claude Lobry, Frédéric Mazenc, Alain Rapaport.

We prove that a cascade of well-stirred reactors with a non-monotonic growth-rate may present a complex set of stable equilibria which join together in a unique equilibrium when the number of reactors tends to infinity. The proof is very simple but uses a graphical representation which is not usual. The result is qualitative in the sense that it does not only apply in the case when the growth-rate admits a specific form but also for general non-monotonic growth-rates [12].

6.1.3. *Interconnection of bioreactors*

Participants: Abdou Khadry Dramé, Claude Lobry, Jérôme Harmand, Alain Rapaport.

Almost all the literature on the optimization of WWTP is related to unitary processes. However, it should be noticed that a WWTP is precisely composed of a number of different tanks connected together by the way of pipes, valves and pumps. And it is well known in chemical engineering that optimizing independently two connected processes is not equivalent to optimizing the overall process viewed as only one complex system composed of interconnected tanks.

As already mentioned, a cascade of chemostats presents a number of practical interests:

- Non homogeneous systems (also called tubular or plug flow reactors) may exhibit better performances than homogeneous ones. However, operating a real plug flow system is almost impossible in practice. In such a case, the use of a cascade of homogeneous reactors allows us, in adequate conditions, to approximate the behavior of the plug flow system.
- The presence of a gaseous phase usually increases the homogeneity of the mixed liquid phase. If a spatialization of phenomena is required (for instance to get better performances), then separating the reaction scheme between several reactors can be useful to attain this objective.
- When operating a tubular reactor, a continuous biomass sow is necessary in order to initiate the biological reaction at the entrance of the process. In other terms, it is necessary to have some biomass in the input flow rate. The use of a recirculation can be appropriate.

As a consequence, the study of interconnected biological systems is of particular theoretical as well as of practical importance.

In the project, we have more particularly studied mono-fed and multi-fed cascades of homogeneous bioreactors for which we have analyzed the role of the recirculation on the performances of the system. In the recent years, these studies have led to the proposition of an equivalence principle: conditions have been derived under which there exists an infinity of equivalent systems (of identical volumes) and that only differ from the way they are fed and by the way they are connected together via a recirculation loop.

Until now, these studies were related to static optimization : the design was performed in order to get performances at the equilibrium. However, it is recognized that a WWTP rarely operates around an equilibrium. On the contrary, it is always excited by input disturbances in both fluxes and concentrations. It is then desirable to study such interconnected systems in dynamical conditions. In order to dynamically optimize a cascade of uncertain bioprocesses, the theory of optimum seeking has been proposed (cf. [35]). In addition, we have proposed a number of new algorithms for observing and controlling bioreactors through the use of the recirculation loop (cf. [17] and [43]).

Finally, we actually work on the links between the microscopic and the macroscopic modeling approaches we have introduced in the introduction section. To do so, part of our results concern the use of interconnected reactors for studying the coexistence of several micro-organisms in competition on a single substrate. We have derived conditions under which two different species can coexist in such systems and established that it never happens in most optimally designed complex biosystems (ongoing work).

6.1.4. *Control and observation of biological systems*

Participants: Jérôme Harmand, Frédéric Mazenc, Alain Rapaport.

The control of most of the biological systems poses challenging robust control problems. Indeed, the parameters of the biological models are generally not well-known and delays or unknown dynamics are frequently present. Recall that Lyapunov functions are of paramount importance in nonlinear control theory and especially in robust nonlinear control theory. It is most of the time very beneficial to have a continuously differentiable Lyapunov function, whose derivative along the trajectories of the system can be made negative definite by an appropriate choice of feedback. For instance, many proofs of nonlinear disturbance-to-state L^p stability properties rely on Lyapunov functions. More precisely, control-Lyapunov function (CLF) based control designs guarantee robustness to different types of deterministic and stochastic disturbances, and to unmodeled dynamics. Moreover recent advances in the stabilization of nonlinear delay systems are based on knowledge of continuously differentiable Lyapunov functions. This motivates the problem of constructing strict Lyapunov functions for families of nonlinear systems. We addressed it in several works. In [27] we constructed CLF for systems satisfying conditions of a Jurdjevic-Quinn type. In [7] (Major publication), we explicitly construct strict Lyapunov functions for systems satisfying the stability conditions of the Matrosov theorem. Observe that Lotka-Volterra systems with a globally asymptotically stable equilibrium point usually satisfy these sufficient conditions. Some of our papers, written before 2005 and [22] are devoted to systems with delay. In particular, we used a Lyapunov function approach to determine bounded control laws which globally asymptotically stabilize linear systems with bounded and delayed inputs and, in [22], the recursive Lyapunov technique called back-stepping (one of the most popular nonlinear techniques of construction of control laws) is adapted to the case where there is an arbitrarily large delay in the input. In [21], we addressed the problem of establishing some robustness properties of hybrid systems through the explicit construction of Lyapunov functions. The techniques consists in transforming given non-strict Lyapunov functions for the discrete and continuous subsystems into strict Lyapunov functions. This leads to strict hybrid Lyapunov functions from which one can deduce a strong robustness property called ISS property. Observe that hybrid systems naturally arise in many important engineering applications and in particular in microbial ecology.

We have obtained recently further results on time-varying systems. For rapidly time-varying systems and for slowly time-varying systems, two techniques of construction of strict Lyapunov functions are presented in [26], [28]. In [38], for a model of chemostat with one species a time-varying dilution rate is designed so that the solutions converge to a prescribed periodic solution. This means that, no matter what positive initial levels for the species concentration and the nutrient are selected, the long term species concentration and substrate levels closely approximate a prescribed oscillatory behavior. This is significant because it reproduces the realistic ecological situation where the species and substrate concentration oscillate. besides, we have shown that the stability is maintained when the model is augmented by additional species that are being driven to extinction. We also gave robustness result for this system for cases where there are small perturbations acting on the dilution rate and initial substrate concentration.
The team has proposed last year a new control strategy for the regulation of a continuous stirred bioreactor [3] (Major publication). It consists in using by-pass and recirculation loops as control variables instead of the input dilution rate, traditionally used as the manipulated variable. In practice, this approach has the advantage to do not require an upstream storage tank, and has revealed good robustness properties with respect to unknown disturbances on the input rate as well as uncertainties on the growth function. Nevertheless, our feedback law requires a perfect knowledge of the input concentration.

In absence of measurement of the input concentration, we have recently proposed the design of an observer of the input concentration which guarantees a practical stabilization when coupled with the former feedback law [43]. The convergence is only “practical” (i.e. for each neighborhood of the desired reference of the output, there exists a tuning of the observer that guarantees the convergence towards the neighborhood) because the system is not exactly observable in the usual sense. The existence of “bad inputs” imposes constraints on the convergence speed of the estimator for inputs closed to the bad ones.

More generally, the question of reconstruction of concentration inputs in bioprocesses is most of the time crucial for the design of efficient control laws or observers of state variables. This refers to the “unknown inputs” problems in the control theoretic community. Exact rejection or L_2 attenuation of unknown inputs has been mainly studied in the literature. In the framework of bioprocesses, the hypothesis of unknown inputs belonging to L_2 is questionable. Usually, unknown inputs are bounded but with known bounds, and the team has proposed in the past several estimators in terms of "interval observers" [2] (Major publication) guaranteeing dynamical bounds of the unobserved variables, depending on bounds on unknown inputs. We are searching now how to take into account additional knowledge on the unknown inputs, such as bounded derivatives or periodic signals, for better estimations.

6.1.5. Analysis of an SSCP profile

Participants: Jérôme Harmand, Patrice Loisel.

Because of the complexity and the reduction of information due to the analysis, we can at most hope to identify the majority species (species representing a significant percentage). By construction, a majority species generates a peak, but to any peak we cannot systematically associate a majority species. Indeed, a preliminary simulated study showed that for a mixture made up of a very high number of minority species (as it is the case in nature, typically 5000 species with 0.01%) and without any majority species, the SSCP analysis provides a curve with peaks of significant amplitude.

The required goal being to determine the majority species, it is necessary to find a criterion to trust the information given by a peak. A first criterion is the width of the peak (standard deviation for Gaussian's). This idea comes from the following observations:

- the variance of the peak of an isolated species does not depend on the species but on specific materials used to make analysis SSCP.
- if, in a mixture of n minority species (with n large), one adds some majority species, one notes that the variance of the peak corresponding to the majority species is of the same order as the variance of an isolated species. On the other hand, for the peaks resulting from contributions of the minority ones, the variance is doubled (or more) with respect to the variance of an isolated species.

The details of this work are reported in [20].

6.1.6. Models of competition for one resource

Participants: Claude Lobry, Frédéric Mazenc, Alain Rapaport, Jérôme Harmand, Bart Haegeman.

We consider the system:

$$\begin{aligned}\dot{S} &= f(S) - \sum_{i=1}^{n} h_i(S,X_1,\cdots,X_n)X_i\\ \dot{X}_i &= (h_i(S,X_1,\cdots,X_n)-D_i)\,X_i \qquad (i=1,\cdots,n)\end{aligned}$$

under the general following assumptions :

- $f(S)$ is continuous positive between zero and a certain value K and is negative after.
- $\frac{\partial h_i}{\partial s} \geq 0$
- $\frac{\partial h_i}{\partial x_j} \leq 0$,

This system represents a general competition model for one resource including density dependence of the growth rates h_i. A challenging (theoretical) question is too understand how intra-specific dependency play a role in the persistence or exclusion of the species. In this completely general form, the system is too difficult to be fully understood and analyzed. For the moment, we have investigated simpler particular cases, which have some relevance in ecology and obtained new results, which may sound surprising for such an old subject.

- Assume that, for any j different from i, we have

$$\frac{\partial h_i}{\partial x_j} = 0$$

(which means that each h_i depends only on S and X_i) and that each h_i tends to zero when x_i tends to infinity. Then every equilibrium such that $f'(S_e)$ is strictly negative is locally exponentially stable. Under mild conditions, many species, or even all the species, are present in this stable equilibrium [4] (Major publication).

- Assume moreover that f is decreasing. Then the system admits one and only one positive equilibrium point. Then, under technical assumptions, still reasonable from the (theoretical) ecology point of view, this equilibrium is globally asymptotically stable [24]. If f is not decreasing, we can exhibit systems with a locally stable limit cycle (which was already known for competition of two species).
- Assume that $f(S) = D(S_{in} - S)$ and $d_i = D$, which is the case of the chemostat, then the unique equilibrium is globally asymptotically stable [4] (Major publication), [13].
- To some extent, the preceding results are valid for the general case when $\frac{\partial h_i}{\partial x_i}$ is large compared to $\frac{\partial h_i}{\partial x_j}$, which means that the intra-species competition is large with respect to the inter-species competition.
- In [25] a general family of systems is considered. The function f is supposed to be decreasing but is not necessarily linear and the removal rates D_i are constant but not necessarily all the same. Sufficient conditions ensuring the uniqueness of a positive rest point and its global asymptotic stability are given. The technique of proof relies on the fact that, in well-chosen coordinates, the system rewrites

  $$\dot{X} = A(X)X$$

  where , for any vector X, the matrix $A(X)$ is Hurwitz i.e. all these eigenvalues have a negative real part.

Observe that, when each h_i depends only on S, it is well-known that the “competitive exclusion principle” holds. Thus our results can be considered as a contribution to the understanding of the role of the intra-species competition in the persistence of species.

6.2. Applications

6.2.1. Advanced automatic control for SBRs

Participants: Jérôme Harmand, Djalel Mazouni, Alain Rapaport.

Monitoring and estimation techniques for the SBRs

One of the most important problems when dealing with biological processes is the quasi-systematic lack of sensors able - at a reasonable cost - to deliver on-line information about the composition of the matter to be processed. This is why the development of "software sensors" (observation techniques) are of particular interest in this field of research. When dealing with the optimal time control of SBRs, it was assumed that the entire state of the system was measured on-line. In reality, only parts of the state can be measured and an important experimental work [31], [33], [10], [34], [36], [44] has been realized

1. to generate data that are rich enough to be used for the modeling of a 200 liters SBR pilot plant,
2. to design estimators that use the available on-line information to reconstruct unmeasured state variables,
3. to validate these sensors that will be used for the time-optimal control of the SBR.

Optimal control design

The time optimal control of fed-batch chemostats with one reaction involving one substrate and one biomass has been solved by J. Moreno in 1999 using a technique based on Green’s theorem. The optimal trajectories correspond to “most rapid approach paths” towards

- the target, when the growth function is a monotonic function,
- a singular arc, when the growth presents an inhibition for large concentrations of nutrient.

The optimal controls are of two possible types: “bang-bang” (i.e. no feeding or feeding at the maximal rate) and singular ones. This year, we have considered two kinds of extensions :

- the consideration of unbounded or “impulsive”controls [45]. A bounded measurable control can be assimilated to a device that tunes the speed of a pump over a certain range, while an unbounded control can be assimilated to an arbitrary fast dilution with respect to the biological time scale,
- the consideration of several species of micro-organisms in competition for a single substrate.

Contrary to the one species case, we have shown that with more than one reaction, the optimal trajectories are not necessarily most rapid approach paths. This can be explained by the fact that the argumentation based of Green’s theorem is valid only for planar systems. Instead, we have proposed a characterization of the optimal solution in terms of a set of two variational inequalities of Hamilton-Jacobi-Bellman type. This approach has been inspired by recent theoretical results on turnpike optimality in calculus of variations problems. For monotonic growth functions, the optimal solution consists in an “immediate one impulse” or an “delayed one impulse” strategy. As a particular case, we generalize the result of Moreno with one species to the impulsive framework. The determination of the optimal solutions for non-monotonic growth functions is still open and will be the matter of our research program for the coming year.

6.2.2. Physical bases of density-dependence in the chemostat

Participants: Bart Haegeman, Jérôme Harmand, Claude Lobry, Nabil Mabrouk.

We saw that intra-specific competition is a major ingredient in possible explanation on violations of the principle of competitive exclusion. We try to understand whether this hypothesis of intra-specific competition can be supported by some physical reasons. One idea is to consider that the process of absorption of the substrate is limited by diffusion [18]. This idea is made more precise when one considers flocculation.

The flocculation process is of major importance in wastewater treatment plants. On one hand, the presence of flocs limits the access of the substrate to the biomass. On the other hand, floc formation permits the separation of the biomass from the effluent by decantation. We proposed an effective way to include flocculation in existing models ([14]), and showed that under certain conditions, this leads to a density-dependent growth function. This establishes the link between the limited access to the substrate inside the flocs, and the growth characteristics of the biomass on the level of the bioreactor.

6.2.3. Software design

Participants: Bart Haegeman, Jérôme Harmand, Patrice Loisel, Nabil Mabrouk.

A software for the analysis of SSCP profiles is currently designed (see above).

We developed an individual-based model for simulating floc-forming bacteria. It includes the aggregation and breakage processes of the flocs, together with the dilution dynamics of the reactor. Local nutrient concentration heterogeneities surrounding the flocs are explicitly taken into account. Our goal is to compare the predictions of this model with more macroscopic approaches as presented above.

7. Other Grants and Activities

7.1. International cooperations

The MERE project-team is very actively involved in cooperation with Africa in different but related ways.

- C. Lobry, as a former director of CIMPA, has been involved for a long time in cooperation with African mathematical teams. He visits Africa very often and delivers lectures in summer schools or universities.
- The team has a close relationship with the LANI (Laboratoire d’Analyse Numérique et Informatique de l’Université Gaston Berger de Saint-Louis du Sénégal).

- The team obtained a financial support from INRIA in order to initiate a collaboration Between teams from the south and the north of Mediterranean sea. We have currently Made connections with two teams in Maghreb, one in Tunisia, one in Algeria and one in Italy. A workshop will be held in Tlemcen by the end of December in order to formalize this cooperation.
- The team has a close relationship with the Department of Mathematics and the Department of Mechanical Engineering of the Louisiana State University. F. Mazenc is member of the Project "Research in Nonlinear Control Systems Theory: Lyapunov Functions, Stabilization, and Engineering Applications" which has obtained the NSF Standard Grant 0424011 ([23], [21], [27], [28], [26]).
- The MERE project-team interacts with researchers of CMM (Centro de Modelamiento Matematico, UMR CNRS Santiago de Chile) thanks to the INRIA-Conycit project 'ECOLOMICRO' (2006-2008), on estimation of unknown inputs (with G. Acuna, University of Santiago) and optimal impulsive control for fed-batch reactors (with P. Gajardo, chilean project leader, CMM, and H. Ramirez, University of Chile). The copper industry in Chile produces contaminated water, that can be depolluted by well-selected bacteria [47], [45], [46].

8. Dissemination

8.1. Teaching

The team has organized with J.J. Godon (INRA Narbonne) a workshop on "sensors in microbial ecology", sponsored by the INRIA COLOR program. More than fifty researchers have participated to this workshop. The team is preparing an autumn school in 2007 with the help of INRA.

C. Lobry delivered courses in Operational Research (16h), mathematical models of bioreactors (20h) and dynamical population models (20h) at Nice University, Institut National d'Agronomie (Paris) and University of Tlemcen (Algeria).

A. Rapaport has given lectures on optimal control theory for Master-2 "research" degree at Université Montpellier II (12h), and on operational research at Polytech'Montpellier (50h).

A. Rapaport is in charge of a two-weeks lectures "Mathématiques pour la gestion de ressources renouvelables" at Ecole Nationale Supérieure d'Agronomie de Montpellier. J. Harmand and A. Rapaport deliver each year several lectures and training periods on modeling, estimation and control of biosystems.

The team has organized with the ENIT-LAMSIN (Laboratoire de Modélisation Mathématique et Numérique dans les Sciences de l'Ingénieur, Tunis) a one week lecture series on dynamic systems (French lecturers : J. Harmand, C. Lobry and F. Mazenc).

The team has organized with the CMM (Centro de Modelamiento Matematico, UMR CNRS, Santiago de Chile) a one week lecture series on modeling for biological system (French lecturers : J.J. Godon, B. Haegeman, J. Harmand, F. Mazenc and A. Rapaport).

The team was invited to write a paper in the wide audience scientific European journal "Biofutur" [15].

8.2. Ongoing thesis

- Ilse Callens has started her PhD on November 2006 on “modeling soil ecosystems with dynamical systems approach” under the supervision of A. Rapaport and L. Ranjard (micro-biologist, INRA Dijon). Microbial communities of soil ecosystems appear to possess some similitude with waste-water ecosystems that worth being studied more deeply. The experience of the team collaborating with micro-biologists of Narbonne could be exploited in a new collaboration with micro-biologists from Dijon.
- Maxime Dumont began his PhD Thesis on November the first of 2005. His thesis aims at confronting concepts of the theoretical ecology to experimental data. His work will consist in proposing a number of experiments with model ecosystems commonly used in biological wastewater plants, such as the nitrification process, in order to validate, or to invalidate the fact that mutualism among individuals and species promotes diversity. The first experiments have been run at the end of 2005 and continue today. Three nitrification reactors are now operated under different environmental conditions and microbial analyses are on the way. The first results show that a simplified ecosystem has taken place but that some oscillations undergo.
- Nabil Mabrouk started his PhD thesis in March 2006, co-financed by CEMAGREF Clermont-Ferrand and INRIA Sophia-Antipolis. The goal is to explore multi-scale modeling in the context of bacterial interactions. He will investigate the link between models at different scales (from the reactor scale down to the bacteria scale) to better understand microbial processes, especially in the context of wastewater treatment. The initial focus is on the flocculation process, see 6.2.2. A first computer model, using a so-called individual-based approach, was developed, capable of simulating 1000 bacteria and their interactions (both substrate consumption and mutual interactions like flocculation) in a two-dimensional domain of size 1mm by 1mm. As a validation step, he is comparing this model with less detailed but analytical models. He is also working on the extension to three dimensions, and more realistic and efficient implementation of the physical and biological processes.
- Djalel Mazouni is preparing his PhD at the LBE. He will defend his PhD on December the 21st. He was granted by the LBE within the framework of the European EOLI project dedicated to the modeling and the optimization, through the development of control and supervision algorithms, of aerobic SBRs able to treat a large class of wastewater. During these last three years, his work was more particularly devoted to the generation of experimental data (he has started up and has been operating a 200 liters SBR pilot plant since the beginning of the project in 2002), the design of estimation techniques and the development and the validation of a number of innovative time-optimal control laws able to minimize the reaction period lengths.

8.3. Participation to thesis committees

C. Lobry (referee) : Dimi J-L "Analyse de modèles épidémiologiques - Applications à des modèles parasitaires et à la fièvre hémorragique Ebola".
C. Lobry (referee) : Ndiaye T. H. "Modélisation de la dynamique de population des moustiques *Aedes vexans arabiensis*, vecteur de la Fièvre de la Vallée du Rift en Afrique de l’Ouest".
F. Mazenc (referee): Khoi B. Ngo, "Control of Constrained Nonlinear Systsems: Applications in Aerospace and Robotics", Australian National University (Director: R. Mahony).

8.4. Conferences, Invited conferences

Claude Lobry : CIMOD 06 (Pointe à Pitre, 18-21 Avril 2006) *Construction of persistent systems of species competing for one resource*
Claude Lobry : 60 MF Conference in the honnor of the 60-th birthday of M. Fliess (Paris 30- 31 March 2006)
Claude Lobry : CARI 06 (Cotonou 6-9 November 2006) *Mathematics, computer sciences and microbial ecology*.

2006 Transactions on Control Systems Technology Best Paper Award for the work : K. Pettersen, F. Mazenc, H. Nijmeijer. *Global Uniform Asymptotic Stabilization of an Underactuated Surface Vessel: Experimental Results.* IEEE Transactions on Control Systems Technology, Vol. 12, No. 6, pp. 891-903, Nov. 2004.

9. Bibliography

Major publications by the team in recent years

[1] A. DRAMÉ. *A semilinear parabolic boundary-values problem in bioreactors theory*, in "Electronic Journal of Differential Equations,", n° 129, 2004, p. 1–13.

[2] J.-L. GOUZÉ, A. RAPAPORT, Z. HADJ-SADOK. *Interval observers for uncertain biological systems*, in "Ecological Modelling", vol. 133, n° 1, 2000, p. 45–561.

[3] J. HARMAND, A. RAPAPORT, F. MAZENC. *Output tracking of continuous bioreactors through recirculation and by-pass*, in "Automatica", vol. 42, n° 6, 2006, p. 1025–1032.

[4] C. LOBRY, F. MAZENC, A. RAPAPORT. *Persistence in ecological models of competition for a single resource*, in "Comptes Rendus de l'Académie des Sciences, Série Mathématiques", vol. 340, 2005, p. 199–204.

[5] P. LOISEL, J. HARMAND, O. ZEMB, E. LATRILLE, C. LOBRY, J. DELGENES, J. GODON. *DGE and SSCP molecular fingerprintings revisited by simulation and used as a tool to measure microbial diversity*, in "Environmental Microbiology", vol. 8, n° 4, 2006, p. 720–731.

[6] F. MAZENC, D. NESIC. *Strong Lyapunov functions for systems satisfying the conditions of La Salle*, in "IEEE Trans. Aut. Contr.", vol. 49, n° 6, 2004, p. 1026–1030.

[7] F. MAZENC, D. NESIC. *Lyapunov functions for time varying systems satisfying generalized conditions of Matrosov theorem*, in "44th IEEE Conference on Decision and Control and European Control Conference", Seville, Spain, 2005.

[8] A. RAPAPORT, J. HARMAND. *Robust regulation of a class of partially observed nonlinear continuous bioreactors*, in "Journal of Process Control", vol. 12(2), 2002, p. 291–302.

Year Publications

Doctoral dissertations and Habilitation theses

[9] D. MAZOUNI. *Modélisation et Commande en temps Minimum de Récateurs Biologiques Séquentiels Discontinus*, PhD thesis, Univ. Claude Bernard – Lyon I, December 2006.

Articles in refereed journals and book chapters

[10] F. CIAPPELLONI, D. MAZOUNI, J. HARMAND, L. LARDON. *On-line supervision and control of an aerobic SBR process*, in "Water Science and Technology", vol. 53, n° 1, 2006, p. 169–177.

[11] D. DESCHRIJVER, B. HAEGEMAN, T. DHAENE. *Orthonormal Vector Fitting: A Robust Macromodeling Tool for Rational Approximation of Frequency Domain Responses*, in "IEEE Transactions on Advanced Packaging", to appear, 2006.

[12] A. DRAMÉ, J. HARMAND, A. RAPAPORT, C. LOBRY. *Multiple steady state profiles in interconnected biological systems*, in "Mathematical and Computer Modelling of Dynamical Systems", vol. 12, n^{o} 5, 2006, p. 379–393.

[13] F. GROGNARD, F. MAZENC, A. RAPAPORT. *Polytopic Lyapunov functions for persistence analysis of competing species*, in "Discrete and Continuous Dynamical Systems - Serie B", to appear, 2006.

[14] B. HAEGEMAN, C. LOBRY, J. HARMAND. *An effective model for flocculating bacteria with density-dependent growth dynamics*, in "American Institute of Chemical Engineering Journal", to appear, 2006.

[15] J. HARMAND, C. LOBRY, A. RAPAPORT, J.-J. GODON. *La modélisation des écosystèmes microbiens : une nécessité pour la recherche et l'industrie*, in "Biofutur (dossier Ecologie microbienne des sols)", n^{o} 268, 2006, p. 54–57.

[16] J. HARMAND, L. PAULOU, J. DESMOUTIERS, L. GARRELLY, P. DABERT, J. GODON. *The microbial signature of potable waters : myth or reality*, in "Water Science and Technology", vol. 53, n^{o} 1, 2006, p. 259–266.

[17] J. HARMAND, A. RAPAPORT, F. MAZENC. *Output tracking of continuous bioreactors through recirculation and by-pass*, in "Automatica", vol. 42, n^{o} 6, 2006, p. 1025–1032.

[18] C. LOBRY, J. HARMAND. *A new hypothesis to explain the coexistence of N species in the presence of a single resource*, in "Comptes Rendus de l'Académie des Sciences, Série Biologie", n^{o} 329, 2006, p. 40–46.

[19] C. LOBRY, A. RAPAPORT, F. MAZENC. *Sur un modèle densité-dépendant de compétition pour une ressource*, in "Comptes Rendus de l'Académie des Sciences, Série Biologie", n^{o} 329, 2006, p. 63–70.

[20] P. LOISEL, J. HARMAND, O. ZEMB, E. LATRILLE, C. LOBRY, J. DELGENES, J. GODON. *DGE and SSCP molecular fingerprintings revisited by simulation and used as a tool to measure microbial diversity*, in "Environmental Microbiology", vol. 8, n^{o} 4, 2006, p. 720–731.

[21] M. MALISSOFF, F. MAZENC. *Constructions of strict Lyapunov functions for discrete time and hybrid time-varying systems*, in "Journal of Nonlinear Analysis", to appear, 2006.

[22] F. MAZENC, P. BLIMAN. *Backstepping Design for Time-Delay Nonlinear Systems*, in "IEEE Trans. on Automatic Control", vol. 51, n^{o} 2, 2006, p. 149–154.

[23] F. MAZENC, M. DE QUEIROZ, M. MALISSOFF, F. GAO. *Further Results on Active Magnetic Bearing Control with Input Saturation*, in "IEEE Transactions on Control Systems Technology", vol. 14, n^{o} 5, 2006, p. 914–919.

[24] F. MAZENC, C. LOBRY, A. RAPAPORT. *Persistence in Ratio-Dependent Models of Consumer-Resource Dynamics*, in "Electronic Journal of Differential Equations", to appear, 2006.

[25] F. MAZENC, C. LOBRY, A. RAPAPORT. *Stability Analysis of an Ecological Model*, in "Lecture Notes in Control and Information Sciences (Positive Systems)", vol. 341, 2006, p. 113–120.

[26] F. MAZENC, M. MALISSOFF, M. DE QUEIROZ. *Further Constructions of Strict Lyapunov Functions for Rapidly Time-Varying Nonlinear Systems*, in "Automatica", vol. 43, n^{o} 10, 2006, p. 1663–1671.

[27] F. MAZENC, M. MALISSOFF. *Further Constructions of Control-Lyapunov Functions and Stabilizing Feedbacks for Systems Satisfying the Jurdjevic-Quinn Conditions*, in "IEEE Trans. on Automatic Control", vol. 51, n^{o} 2, 2006, p. 360–365.

[28] F. MAZENC, M. MALISSOFF. *Lyapunov Function Constructions for Slowly Time-Varying Systems*, in "Mathematics of Control, Signals, and Systems", to appear, 2006.

[29] A. RAPAPORT, P. CARTIGNY. *Nonturnpike Optimal Solutions and Their Approximations in Infinite Horizon*, in "Journal of Optimization, Theory and Applications", to appear, 2006.

[30] A. RAPAPORT, J. TERREAUX, L. DOYEN. *Viability analysis for the sustainable management of renewable resources*, in "Mathematical and Computer Modelling", vol. 43, 2006, p. 466-484.

Publications in Conferences and Workshops

[31] M. BETANCUR, D. MAZOUNI, J. HARMAND, J. MORENO. *Optimal control of biological SBRÕs for the treatment of dairy and toxic wastewater*, in "5th MATHMOD VIENNA, IMACS Symposium on Mathematical Modelling", Vienna, Austria, 2006.

[32] S. BONELLI, N. FIOCCHI, E. FICARA, R. CANZIANI, F. CIAPPELLONI, P. RATINI, M. PIRANI, S. MARIANI, J. HARMAND. *Assessing influent toxicity to nitrification by an automatic set-point Titrator*, in "Colloque STIC and Environement", Narbonne, France, 2006.

[33] J. BOUVIER, M. BEKRI, D. MAZOUNI, O. SCHOEFS, J. HARMAND, A. PAUSS. *Mesure en ligne de nitrate, nitrite et DCO soluble par déconvolution spectrale de spectres UV, dans un procédé Biologique Séquentiel Discontinu (SBR)*, in "Colloque STIC and Environement", Narbonne, France, 2006.

[34] R. CANZIANI, E. FICARA, N. FIOCCHI, P. RATINI, M. PIRANI, S. MARIANI, A. PAUSS, T. RIBEIRO, O. SCHOEFS, J. BOUVIER, J. HARMAND, D. MAZOUNI. *Development Of Hardware Sensors For The On-Line Monitoring Of SBR Used For The Treatment Of Industrial Wastewaters*, in "5th MATHMOD VIENNA, IMACS Symposium on Mathematical Modelling", Vienna, Austria, 2006.

[35] D. DOCHAIN, M. GUAY, J. HARMAND. *Dynamical optimization of a configuration of multi-fed interconnected bioreactors by optimum seeking*, in "IEEE Conference on Decision and Control", San Diego (California), USA, 2006.

[36] H. FIBRIANTO, D. MAZOUNI, M. IGNATOVA, M. HERVEAU, J. HARMAND, D. DOCHAIN. *Dynamical modelling, identification and software sensors for SBRs*, in "5th MATHMOD VIENNA, IMACS Symposium on Mathematical Modelling", Vienna, Austria, 2006.

[37] M. MALISSOFF, F. MAZENC. *On Control-Lyapunov Functions for Hybrid Time-Varying Systems*, in "IEEE Conference on Decision and Control", San Diego (California), USA, 2006.

[38] F. MAZENC, P. DE LEENHEER, M. MALISSOFF. *Stabilizing a Periodic Solution in the Chemostat: A Case Study in Tracking*, in "IEEE Conference on Decision and Control", San Diego (California), USA, 2006.

[39] F. MAZENC, C. LOBRY, A. RAPAPORT. *Stability Analysis of an Ecological Model*, in "International Symposium on Positive Systems: Theory and Applications (POSTA 06)", Grenoble, France, 2006.

[40] F. MAZENC, M. MALISSOFF, M. DE QUEIROZ. *Further Constructions of Strict Lyapunov Functions for Rapidly Time-Varying Nonlinear Systems*, in "American Control Conference", Minneapolis (Minesota), USA, 2006.

[41] F. MAZENC, M. MALISSOFF. *Constructions of Strict Lyapunov Functions for Discrete Time and Hybrid Time-Varying Systems*, in "International Conference of Hybrid Systems and Applications", Lafayette (Louisina), USA, 2006.

[42] F. MAZENC, M. MALISSOFF. *Lyapunov Function Constructions for Slowly Time-Varying Systems*, in "IEEE Conference on Decision and Control", San Diego (California), USA, 2006.

[43] A. RAPAPORT, F. MAZENC, J. HARMAND. *Output tracking of bioprocesses through recirculation with unknown input concentration*, in "IFAC International Symposium on Advanced Control of Chemical Processes", Gramado, Brazil, 2006.

[44] P. RATINI, M. PIRANI, S. MARIANI, L. LUCCARINI, D. MAZOUNI, J. HARMAND. *Development of an integrated system for the optimisation of SBRs*, in "5th MATHMOD VIENNA, IMACS Symposium on Mathematical Modelling", Vienna, Austria, 2006.

Internal Reports

[45] A. GAJARDO, H. RAMIREZ, A. RAPAPORT. *About minimal time impulsive control of sequential batch reactors with several species*, Technical report, UMR CNRS CMM, Santiago, Universidad de Chile, 2006.

[46] F. MAZENC, A. GAJARDO, H. RAMIREZ. *Competitive exclusion principle in a model of chemostat with delays*, Technical report, UMR CNRS CMM, Santiago, Universidad de Chile, 2006.

[47] A. PIAZZA, A. RAPAPORT. *About optimal management of renewable resources with alternative use*, Technical report, UMR CNRS CMM, Santiago, Universidad de Chile, 2006.