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INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET EN AUTOMATIQUE

Project-Team MERE

Modelling and Water Resources

Sophia Antipolis - Méditerranée

THEME BIO

Table of contents

1. Team

MERE is a joint research team INRIA and INRA (UMR INRA/SupAgro "Analyse des Systèmes et Biométrie", Montpellier, France).

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2. Overall Objectives

2.1. Microbial ecology for environmental preservation

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 micro-organisms are 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 uncertainties and of unknown and unmeasured external disturbances. To do so,

1. we approach the problems at two levels: the microscopic scale (the micro-organism) and the macroscopic one (the plant),
2. we use macroscopic 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 bio-films.

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.

2.2. Highlights of the year

1. The EuroMéditerranée project “Treasure” has been launched (see Section 7.1.4).
2. A patent has been licensed with INRA (see Section 7.4).
3. The team was associated by D. Dochain (CESAME, Louvain-la-Neuve, Belgium) to his invited “keynote” (semi-plenary session) at the 10th Computer Applications in Biotechnology (CAB 2007), Cancun, Mexico [52].

3. Scientific Foundations

3.1. Bioprocess engineering and mathematical ecology

Keywords: *(theoretical) ecology*, *biology*, *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 variations of 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 flocks,
- Constitution of bio-films,

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 consists in evaluating 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 depend not only on the nutrient concentration but also on the density of the 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 requires time, energy and qualified people for rigorous validation (many protocols have to be checked for ensuring that contamination or side-effects do not degrade the results).

3.2. Markovian modeling, simulation-based inference and decision

Keywords: *Bayesian estimation*, *Markov Chain Monte Carlo (MCMC)*, *Markov models*, *Monte Carlo (MC) methods*, *Monte Carlo maximum likelihood (MCML)*, *hidden Markov models (HMM)*, *interacting particles methods*, *maximum likelihood estimation*, *particle filtering*, *sequential Monte Carlo (SMC)*.

The Mathematical modeling of systems exposed to randomness is of particular interest whenever we seek for an in depth understanding of complex stochastic phenomena or if we wish to infer noise-corrupted data. The underlying system can be static or dynamic. The state variables, the parameters and the observations can be finite, continuous, hybrid (continuous/discrete), graphical, time varying, pathwise, etc.

The first step in modeling is to describe the dependency graph connecting the different variables and parameters. Note that in the Bayesian networks framework this graph can be inferred from the data. The Markovian hypothesis is made in order to limit the complexity of the model and to allow for tractable algorithms. It consists in supposing that the dependency graph is limited to local connections. It appears in dynamic contexts (Markov random processes), in static contexts (Markov random field), as well as in spatiotemporal frameworks. From a statistical point of view, Markovian models can also feature hidden variables.

The Monte Carlo (MC) methods have expanded considerably over the past two decades, and have been successful in many areas.

In MC approaches, the quantity of interest is formulated in a probabilistic way as a functional of the distribution law of a stochastic process (or simply a random variable). By sampling independent trajectories of this process, we empirically approximate the underlying targeted distribution law. The convergence of this procedure is provided by the law of large numbers and the speed of convergence by central limit theorems.

MC approaches can be used for numerical approximation of complex systems distribution laws through empirical approximations [55] [57]. They are intensively used in Bayesian inference: "Markov chain Monte Carlo" (MCMC) in the static context [59] and "sequential Monte Carlo" (SMC, also called "particle filter") in the dynamic context [53]. In the non-Bayesian approach, Monte Carlo techniques are used to explore likelihood functions [60]. They also gave rise to general algorithmics [56]. Monte Carlo methods are also used to approximate deterministic quantity of interest, usually represented as the expected value of a functional of a process trajectory. This quantity can also be the probability that a given event has occurred. Finally, simulation-based approaches allow for approximating Markov decision problems in random and partially observed situations [54].

MC methods can lead to very poor results because trajectories are generated blindly. Classically, adequacy to the specific problem or to data, is handled afterwards by weighting the different trajectories: the higher the weight, the more the trajectory matches the targeted phenomenon or data. Some of these weights could be negligible, in which case the corresponding trajectories will not contribute to the estimator, i.e. computing power has been wasted. Recent advances, like sequential Monte Carlo or population Monte Carlo, focus on mutation-selection mechanisms that automatically concentrate MC simulations, i.e. the available computing power, into regions of interest of the state space.

Markovian modeling and algorithmics are applied successfully in numerous fields, a reason for this is its strong theoretical background. The limit behaviors of Markov processes are reasonably well identified [58], allowing for precise analyses of the asymptotic behavior of the proposed models, as well as convergence properties of the simulation-based inference algorithms. The development of these sophisticated MC methods, together with the associated mathematical analysis, which we can summarize as Markovian engineering, represents one of the major breakthroughs in applied probability.

4. Application Domains

4.1. Design of wastewater treatment plants

Keywords: *biology*, *environment*, *mathematical modeling*, *optimization*, *process engineering*.

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

Keywords: *biology*, *environment*, *feedback stabilization*, *observers*, *process engineering*, *robust control*, *unknown inputs*.

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, such as disturbance attenuation of 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 on-line 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

Keywords: *biology*, *environment*, *impulse control*, *optimal control*, *process engineering*.

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. When only one biological reaction in involved, and furthermore its growth law is monotonic, the optimal solution is well-known : it consists in filling the tank as fast as possible and waiting. For more complex cases (i.e. non-monotonic growths or several species in competition on the same substrate to be degraded), the optimal solution is most of time far less simple, because of the presence of singular arcs. In these cases, a true feedback is required to achieved the optimal trajectory, but the problem of determining optimal syntheses is still widely opened.

4.4. Interpretation of molecular fingerprint profiles

Keywords: *biodiversity*, *biology*, *environment*, *molecular fingerprints*, *signal processing*.

Dynamical studies of bioreactors as used in wastewater treatment are hampered by the lack of measurement techniques to assess the microbial community structure. Typically only global system variables (biomass and substrate densities, gas production, etc) are measured, so that the community dynamics as such cannot be followed in any detail. Nevertheless, it is commonly believed that monitoring the microbial composition in bioreactors is crucial for their performances (in terms of efficiency and stability). Accurate, rapid and inexpensive techniques to estimate microbial community properties are therefore of crucial importance.

Molecular fingerprinting techniques seem to be good candidates to fill this gap. They are based on a small region (so-called 16S ribosomal DNA) present in all bacterial genomes. This region varies very slowly in time (compared to other parts of the genome), so that it can be used as a signature of a bacterial species. The fingerprinting protocol then consists in, first, extracting all the DNA of the microbial community, next, selecting and amplifying the genomic region of interest (using the PCR (polymerase chain reaction) technique), and finally, separating the PCR products belonging to different species by electrophoresis migration. Compared to other molecular techniques (such as cloning/sequencing), fingerprinting is rapid and inexpensive, and therefore well suited to follow microbial community dynamics.

A quantitative interpretation of fingerprints is however troublesome. Under the assumption that all species are perfectly separated in the migration step, the fingerprinting profile would consist of a succession of sharp rays, each one corresponding to a species, and with ray heights proportional to the abundance of the corresponding species. In this ideal scenario, the complete community structure could be read off from the profile. Unfortunately, due to biases in the different experimental steps (DNA extraction + PCR amplification + electrophoresis migration), real profiles are composed of a number of peaks, all with more or less the same width, where some species can occasionally contribute several peaks, and with peak heights only approximately proportional to the species abundance. Moreover, as soon as the community is somehow diverse, different peaks overlap each other, resulting in a complex profile.

Although one cannot hope to recuperate the complete community structure from such complex profiles, partial community information is still encoded in them. Our objective is to develop quantitative methods to extract this information from the profiles. Given a single profile, the genetic diversity of the microbial community is contained in the fingerprint. How this diversity estimation should proceed in practice, is one of our central research questions. Given a sequence of profiles, additional information can be obtained by comparing successive profiles. Once this information is extracted, it can be coupled to mathematical models describing the dynamics of microbial communities. We are investigating how to rationally tackle this signal processing problem.

4.5. Experimentation in ecology

Keywords: *biodiversity*, *biology*, *ecology*, *environment*, *experimentation*.

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.

In September 2006, we started experiments in five chemostats performing nitrification within the framework of the PhD thesis of Maxime Dumont realized at the LBE. Maxime's thesis aims at studying intra vs inter-specific relationships within different species in a complex (i.e. natural) ecosystem. The nitrification process has been chosen because it is a well known biological process. On the one hand it is simple enough for molecular techniques to give a quite clear view of major species (the natural diversity of this process is known to be limited : only 5 or 6 major species are commonly detected within such a process). On the other hand, it is a natural process and not a reconstituted (artificial) ecosystem. In addition, it is of great interest because of its fundamental role within the nitrogen bio-geochemical cycle. The phenomenological observations together with molecular data that have been obtained are now going to be used as inputs of dynamical systems - in conjunction with nonlinear observers - in order to link functional and population diversity concepts. The first results obtained recently allowed us to propose a new procedure for identifying the functional group of unknown micro-organisms within the nitrification process. Perspectives of the work include the refinement of macroscopic models that have been obtained in order to better understand the role on diversity of inter vs intra-competition in such complex bio-systems. In order to extend these results to more complex ecosystems (and in particular to study the role of the space on the ecosystem functioning), experiments on reconstituted ecosystems isolated from soils are conducted simultaneously with colleagues from INRA in Dijon within the framework of another PhD thesis.

4.6. Modeling and inference of ecological and environmental dynamics

Keywords: *Bayesian estimation*, *Markov chain Monte Carlo (MCMC)*, *Metropolis-Hastings*, *interacting Monte Carlo methods*, *particle methods*.

Ecological and environmental dynamics are at the heart of some of today's leading issues (greenhouse effect, global warming, deforestation, loss of biodiversity, natural resources assessment etc.). For more than a decade, biologists and ecologists have been increasingly using computation modeling for a deeper understanding of the intricacies of these complex dynamics. This approach allows for improved assessments, accurate predictions and effective decision-making. Crucially, random effects need to be considered in this domain.

Most of the dynamical problems considered here are contrasted with the classical applications of hidden Markov models, such as automated speech recognition, target tracking or DNA sequence analysis. Indeed, the measurement data are highly noise-corrupted, acquired at very low frequencies, and on short time series (e.g. one measurement per year for several decades).

From the statistical point of view, the poor quality of data is an argument for using the Bayesian approach. The knowledge of ecological and environmental scientists allows for the choice of model used, as well as its structure. The Markovian framework offers a wide spectrum of possible models adapted to the Bayesian inference (see Section 3.2). Hence, in this context, we are drawn toward a model-driven approach.

Our first studies focused on the assessment of fishery resources. We adopted the Markovian formalism presented in Section 3.2. The evolution of the total biomass and the relative abundance indexes are represented as a hidden Markov model. The hierarchical structure of this model allows for an efficient simulation-based inference of the a posteriori distribution law of the latent variables (state vector and parameter), given the observation data (catches and abundance indexes).

We recently considered the dynamics of tropical forests (see Section 6.2.4). Beyond "simple" economic production issues, recent developments in this area incorporate the concerns of biodiversity conservation and sustainable management. In this context, the need for spatial-temporal models becomes essential. Again, the Markovian framework offers many possibilities. In a statistical point of view, the main difficulty is to strike a compromise between the complexity of the model and the limitations of available data.

5. Software

5.1. SAFUM (Statistical Analysis of Fingerprints Using Molecular biology)

Participants: Bart Haegeman, Jérôme Harmand.

A software tool to analyze SSCP fingerprinting patterns has been developed by the microbiology group at INRA-LBE [32]. The participation of our team has been two-fold: on one hand, some parts of the code have been implemented by team members; on the other hand, the software implements our work on diversity estimation from SSCP profiles (Section 6.1.4), making it readily accessible to the scientific community of microbial ecologists. See the web page http://www.montpellier.inra.fr/narbonne/francais/equipes/equipe-em/safumaccueil.htm.

5.2. BACSON (BACteria & maSON)

Participants: Nabil Mabrouk, Bart Haegeman, Claude Lobry.

We developed an individual-based model for simulating flock-forming bacteria. It includes aggregation and breakage processes of the flocks, together with the dilution dynamics of the reactor. Local nutrient concentration heterogeneities surrounding the flocks are explicitly taken into account. Our goal is to compare the predictions of this model with more macroscopic approaches as presented in Section 6.1.6.
See the web page http://wwwlisc.clermont.cemagref.fr/Labo/MembresEtPagesIntermediaires/pagesperso/membres_actuels/mabrouk/nabil%20mabrouk%20pageperso.htm.

6. New Results

6.1. Theoretical results

6.1.1. Control and observation of continuous bioreactors

Participants: Jérôme Harmand, Frédéric Mazenc, Alain Rapaport.

The team has worked these past years on several approaches for the control of perfectly stirred bioreactor. The stabilization is often achieved with the help of the dilution rate as a manipulated variable (which requires the use of an upstream tank).

Last year, the team has proposed to stabilize reactors with the help of by-pass and recirculation loops as control variables instead of the input dilution rate (see the main contribution [4]). This year, the team has investigated the stabilization of an unstable process under constant dilution rate, considering the addition of a new species (”biological control”). A well chosen species can make the new system globally asymptotically stable on the positive orthant (i.e. the new species needs to be present at initial time, but is asymptotically washed-out). The team has obtained a new result under different removal rates, which typically occurs in reactors with membranes.

Most of the time, the concentration of input nutrient is supposed to be known (possibly time varying), which is not realistic from an applied point of view. This year, the team has proposed a new kind of *unknown inputs observers* for the reconstruction of the input concentration, when only the biomass or the substrate concentration inside the tank is measured. The unknown input is assumed to be piecewise constant or periodic with known period. The proposed observer possesses variable gains and its convergence is established with the help of Lyapunov transformations. This is a work pursued in cooperation with Professors G. Acuna (Universidad de Santiago, Chile) and D. Dochain (CESAME, Louvain-la-Neuve, Belgium).

The team has also worked on an important class of problems involving the tracking of prescribed trajectories in the chemostat model with one limiting substrate. In [24], a prescribed oscillatory behavior for a chemostat with *one species* is generated by an appropriate choice of a time-varying dilution rate, and the global uniform asymptotic stability of the behavior is proved by a Lyapunov approach. In [40], new tracking results for chemostats with *two species*, based on Lyapunov function methods, have been presented. In particular, in a first step, we used a linear feedback control of the dilution rate and an appropriate time-varying substrate input concentration to produce a locally exponentially stable oscillatory behavior. In a second step, we generated a globally stable oscillatory reference trajectory for the species concentrations, using a nonlinear feedback control depending on the dilution rate and the substrate input concentration. This guarantees that all trajectories for the closed loop chemostat dynamics are attracted to the reference trajectory. Finally, we constructed an explicit Lyapunov function for the corresponding global error dynamics.

Notice that our works differ from the earlier results because we use Lyapunov function methods to globally feedback stabilizing a *predefined* oscillating behavior. Notice also that our control laws possess the required properties of positiveness and boundedness.

6.1.2. Optimal control of fed-batch reactors

Participant: Alain Rapaport.

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" toward

- 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.
When the growth function presents more than one inhibition, we have proposed a numerical technique for the approximation of the optimal trajectories. This technique is based on a regularization of the problem with an additional control such that the optimal solution admits a regular synthesis, that can be determined numerically by the Maximum Principle. The solution of the original problem may present several singular arcs [49].
We have also carried out a work initiated last year within the cooperation program with Chile (see Section 7.1.2). Two kinds of extensions have been considered in this work :

- the consideration of unbounded or "impulsive"controls. 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 [43]. This approach has been inspired by recent theoretical results on turnpike optimality in calculus of variations problems [29]. For monotonic growth functions, the optimal solution consists of an "immediate one impulse" or a "delayed one impulse" strategy. As a particular case, we generalize the result of Moreno with one species to the impulsive framework, but the determination of an optimal synthesis for non-monotonic growth functions is still an open problem.

6.1.3. Optimal design of bio-processes

Participants: Jérôme Harmand, Alain Rapaport.

Optimal interconnections of bioreactors have been widely studied in the literature during these five last years, in terms of minimizing the total retention time at steady state. Most of the studies deals with single species.

The team investigates the link between optimal configurations and its ability to sustain a biodiversity, for instance in presence of an "invader". More precisely, the coexistence of several species of microorganisms in an interconnected bioreactor composed of two tanks in series has been studied in [30]. It has been shown that at most only one species could survive in an optimally designed bio-system. In the presence of an invader only two cases may arise: either the invader takes the place of the actual species or the invader simply cannot survive and is washed out. This result may have important consequences in medical or agro-food systems in which it is expected that the processes cannot be invaded by pathogen species.

6.1.4. Analysis of an SSCP profile

Participants: Bart Haegeman, Jérôme Harmand, Patrice Loisel.

Fingerprinting profiles yield snapshots of the microbial community structure. Extracting quantitative information from them has turned out to be a non-trivial task. In particular, microbial communities with a large diversity, such as those used for wastewater processing, have complex profiles, consisting of a broad background with a number of sharp peaks on top of it. We established previously that the relative importance of the background signal contains crucial diversity information, although this background is often neglected in the current analysis of fingerprints. This result, obtained from a simulation study of fingerprinting profiles, was extended in different steps:

1. We found that different communities all with a given diversity index have a similar background signal. This index is the so-called Simpson diversity index, defined as the sum of the squares of the relative abundances, and which can be interpreted as the probability of finding individuals of the same species when randomly sampling two individuals from the community. This result suggests that the Simpson diversity index is clearly encoded in the profiles, and should be easy to extract.
2. Next, we constructed an estimator for the Simpson diversity index from fingerprinting profiles. Its performance was tested on simulated fingerprints, and compared to existing diversity estimators (for the number of species, for the Shannon diversity index and for the Simpson diversity index). Whereas the latter estimators all exhibit saturation characteristics, the Simpson diversity index estimator has linear characteristics up to the highest diversity levels observed experimentally (see next item).
3. We applied the Simpson diversity index estimator to several hundreds of experimental fingerprinting profiles. The estimated diversity values allow to distinctly classify microbial communities based on their origin: (from low to high diversity:) aquatic systems, digestive systems (human, animal), bioreactors, microbial systems in soil. Moreover, the logarithmic scale of the Simpson diversity index spreads evenly the classes of communities, indicating that this scale is particularly practical.
4. We developed an application of the Simpson diversity index for metagenomic studies. Metagenomics looks at a microbial community as a huge pool of genes with possibly interesting functionality. By repeatedly sampling genes and checking their properties, one tries to encounter these interesting genes. We showed that the Simpson diversity index allows us to estimate the number of samples where the probability of finding previously checked genes becomes appreciable. The Simpson diversity index estimator could therefore be used for the judicious selection of the most interesting communities for metagenomic studies.

6.1.5. Neutral community model for microbial ecology

Participant: Bart Haegeman.

Hubbell's neutral model describes the dynamics of an ecological community in terms of random birth, death and immigration events, attributing equivalent characteristics to all species. Although the absurd simplicity of these assumptions, the model predictions of species-abundance and species-area relationships are remarkably accurate for some ecosystems. The neutral model seems to capture some essential features of community dynamics, without requiring quantitative information about species behavior, unlike other ecological models (Lotka-Volterra equations, chemostat model, ...). This is particularly attractive for microbial ecology, as quantitative data (interaction strengths, growth functions, ...) about the thousands of species making up the community is completely missing.

However, Hubbell's model as such cannot be applied in microbial ecology. First, the model assumes that the number of individuals does not vary as a function of time. This would exclude, e.g., the description of a microbial community recovering after the addition of a toxic substance. We have proposed a model extension that deals with this shortcoming. Next, as species abundances cannot be estimated for microbial communities, models should be expressed in terms of global static or dynamical properties, like diversity or divergence. We have computed the dynamics of the Simpson diversity index under neutral dynamics. In this way, we have obtained a theoretical framework based on Hubbell's model, but appropriately modified to be testable on microbial communities.

6.1.6. Models of competition for one resource

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

We are interested by the system :

$$\left\{\begin{array}{lcl} \dfrac{ds}{dt} & = & f(s) - \displaystyle\sum_{i=1}^{N} \mu_i(s,x)x_i, \\ \dfrac{dx_i}{dt} & = & [\mu_i(s,x) - d_i]x_i \quad \text{where} \quad x = (x_1, \cdots, x_i, \cdots, x_N), \quad (i = 1, \cdots N) \end{array}\right. \tag{1}$$

which represents the competition of N consumers on one resource. The variables x_i represent the concentration of the consumers and s the concentration of the resource. The growth rate $\mu_i(s,x)$ is "density dependent" which means that it depends not only of the resource s but also of the concentration of the various consumers ; the function $s \to \mu_i(s,x)$ is increasing and the functions $x_j \to \mu_i(s, x_1, x_2, ..., x_j, ...x_N)$ are decreasing ; this last assumption expresses some kind of competition exerted by the species j on the species i. The function f represents the dynamics of the resource alone and the d_i's are "disparition" terms caused either by mortality and/or migration out of the system under consideration. Under these general assumptions not much is known on system (1).

In the note [5] we proved that, in the particular case (corresponding to the chemostat model) :

$$\left\{\begin{array}{lcl} \dfrac{ds}{dt} & = & d(S_{in} - s) - \displaystyle\sum_{i=1}^{N} \mu_i(s,x_i)x_i, \\ \dfrac{dx_i}{dt} & = & [\mu_i(s,x_i) - d]x_i, \quad (i = 1, \cdots N) \end{array}\right. \tag{2}$$

there exists a unique Globally Asymptotically Stable (G.A.S.) equilibrium $[s_e, x_e]$ and :

$$s_i^* > s_e \Rightarrow x_{ie} > 0$$

where the "growth threshold" s_i^* is defined as the first value of s such that the supremum of the function $x_i \to \mu_i(s,x_i)$ is greater than d.

We conjecture that this result is still true under the weakest assumption that :

- the function $f(\cdot)$ is strictly decreasing,
- the "growth threshold" s_i^* is the first value of s such that the supremum of the function $x_i \to \mu_i(s,x_i)$ is greater than d_i

and this conjecture is strongly supported by simulations. In the paper [23] we give sufficient conditions for a unique G.A.S. equilibrium which relax some assumptions (the function f is just decreasing, but assumptions on the μ_i's are not very natural) and show that f decreasing is essential. The paper [20] gives a new set of sufficient conditions which confirms the conjecture. Paper [15] gives an alternative proof for G.A.S. under the hypothesis of the note [5].
We are currently studying for the model :

$$\left\{\begin{array}{lcll} \dfrac{ds}{dt} & = & d(S_{in} - s) - \displaystyle\sum_{i=1}^{N} \mu_i(s)x_i, & \\ \dfrac{dx_i}{dt} & = & [\mu_i(s) - d]x_i - \rho_i(x_i)v_i, & (i = 1, \cdots N) \\ \dfrac{dv_i}{dt} & = & [\rho_i(x_i) - d]v_i, & \end{array}\right. \tag{3}$$

where the v_i's represent a species of virus specific of each species of bacteria. Some results are already present in the literature but we are mainly interested in the case where the number N of species is very large, which seems to be new.

6.1.7. Markov chain Monte Carlo

Participants: Fabien Campillo, Nicolas Desassis.

Markov chain Monte Carlo (MCMC) algorithms allow us to draw samples from a probability distribution π known up to a multiplicative constant. They consist in sequentially simulating a single Markov chain whose limit distribution is π. Many techniques exist to speed up the convergence towards the target distribution by improving the mixing properties of the chain. An alternative is to run many Markov chains in parallel. The simplest multiple chain algorithm would be to make use of parallel independent chains. The recommendations concerning this idea seem contradictory in the literature, as shown by the many short runs vs. one long run debate. It can be noted that independent parallel chains may be a poor idea: among these chains some may not converge. Therefore one long chain could be preferable to many short ones. Moreover, many parallel independent chains can artificially exhibit a robuster behavior, which does not correspond to a real convergence of the algorithm.

In practice, one however makes use of several chains in parallel. It is then tempting to exchange information between these chains to improve mixing properties of the MCMC samplers. A general framework of population Monte Carlo (PMC) has been proposed in this respect. In the present work [10] we propose an interacting method between parallel chains, which provides an independent sample from the target distribution. Contrary to PMC, the proposal law in our work is given and does not adapt itself to the previous simulations. Hence, the problem of the choice of this law still remains.

6.2. Applications

6.2.1. Advanced automatic control for SBRs

Participants: Jérôme Harmand, Djalel Mazouni, Alain Rapaport.

Within the framework of former European project EOLI, a SBR pilot has been designed at INRA Narbonne, treating both the organic carbon and nitrogen (PhD thesis of Djalel Mazouni). 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 best 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. Because several components and biological reactions are simultaneously present in the different reaction phases, the optimal solution is not obvious and has required a rigorous mathematical analysis. A complete attainability study and the determination of the optimal switchings have been achieved, with the help of Maximum Principle. A synthesis of the work realized within the PhD thesis of D. Mazouni is to be published [28] while, in collaboration with our Chilean colleagues at the CMM (cf. Section 7.1.2), we try to extend these results in order to take into account for the oxygen, giving to our results much more realism [36].

6.2.2. Observers for determining the major species

Participants: Maxime Dumont, Jérôme Harmand, Alain Rapaport.

The use of molecular fingerprinting techniques is about to induce major changes in the modeling of bio-processes. Indeed, under the condition that the ecosystem under interest is dominated by a limited number of species (for instance, it is typically the case in the nitrification process), it becomes possible to monitor the relative abundances of the major species. Viewed as real new sensors, the use of these data pose new problems to modelers : they can be used either as new inputs into models or as data useful to design and validate new ecological models. Among interesting problems for dynamical systems theory, one finds the need for new observers that are needed to recover a number of unmeasured variables of these new models of complex systems. These observers are tunable and insensitive to model uncertainty while allowing us

to classify - in terms of function - the major species which can be observed through molecular techniques. These molecular tools together with these new observers give insights to ecological problems of interest for wastewater treatment technology.

6.2.3. Physical bases of density-dependence in the chemostat

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

The flocculation process is of major importance in wastewater treatment plants. On one hand, the presence of flocks limits the access of the biomass to the substrate. On the other hand, flock formation permits the separation of the biomass from the effluent by clarification. We proposed an effective way to include flocculation in existing models [16], [17], 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 flocks, and the growth characteristics of the biomass on the level of the bioreactor.

6.2.4. Modeling and inferring of ecological and environmental dynamics

Participants: Fabien Campillo, Nicolas Desassis.

As mentioned in Section 4.6, most of ecological and environmental data could be treated in a batch way. We could therefore make use of iterative inference techniques (non-sequential), as the Markov Chain Monte Carlo (MCMC), as well as non-iterative methods (sequential), like sequential Monte Carlo (SMC). In the last case, the data are scanned only once, while in the first one, they are scanned as many times as needed for convergence. Thus, in the MCMC methods, the issues of convergence and convergence criterion are crucial.

Both MCMC and SMC methods can exploit the hierarchical structure of the distribution law of the underlying dynamic system; this structure is derived from the Markovian modeling approach (see Section 4.6).

We have investigated two different possibilities:

- The non-sequential approach - We propose to run many interacting MCMC's in parallel. Each chain independently proposes candidates to all others chains: this induces a mixing effect that improves the convergence properties of the global MCMC [10].
- The sequential approach - SMC scans sequentially the data through a prediction/correction updating process. The prediction step can be improved considerably by using a few iterations of MCMC, see [46] for details.

This work is part of an INRIA Cooperative Research Initiative (see Section 7.3), of the SARIMA program (see Section 7.1.1) and is done in collaboration with CIRAD Montpellier ("Dynamics of Natural Forests" unit) and the University of Fianarantsoa in Madagascar.

7. Other Grants and Activities

7.1. International cooperations

7.1.1. Cooperation with African countries

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).

- Fabien Campillo is the INRIA representative for scientific relations with Madagascar, within the SARIMA program (support to research activities in computer science and mathematics in Africa) supported by INRIA and MAE (Ministère des Affaires Etrangères). He develops collaborations with the universities of Antananarivo and Fianarantsoa in the field of probabilistic modeling and numerical statistical inference for environmental sciences and development. Within this program, Rivo Rakotozafy (university of Fianarantsoa, Madagascar) is preparing a HDR (habilitation à diriger les recherches) under the supervision of Fabien Campillo. This HDR defense is planed for 2008. Fabien Campillo was one of the organizers of a training course on software "R" held in Antananarivo in January. He also organized a one-week workshop "Probability, Statistics, Scilab" held in Fianarantsoa in May. In October, Fabien Campillo spent ten days in Madagascar to plan next year's SARIMA activities.

7.1.2. Cooperation with Latin America

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 [43] (with P. Gajardo, Chilean project leader, University of Valparaiso, and H. Ramirez, University of Chile). The copper industry in Chile produces contaminated water, that can be depolluted by well-selected bacteria.

7.1.3. Cooperation with North America

The MERE project-team interacts with researchers of the Department of Mathematics of the Louisiana State University in Baton Rouge in the framework of the NSF/DMS Grants 0424011 and 0708084. In particular, in collaboration with M. Malisoff and M.S. de Queiroz, papers have been written in the past few years (four journal papers this year). F. Mazenc delivered a lecture in the "Workshop on Control Theory and Mathematical Biology" organized by Michael Malisoff (July 2007) LSU, Baton Rouge.

7.1.4. The TREASURE network

Within the INRIA program "EuroMéditerranée", the team received since 2006 the financial support for the constitution of a "trans- Méditerranée" research network . "Membranes reactors" has been chosen as the main theme of the research program. After two initial meetings in Milano (Italy) and Tlemcen (Algeria), the network has been officially launched at Nice in October 2007 the 26th, under the acronym

TREASURE

Treatment and **Su**stainable **R**euse of **E**ffluents

in Semi-arid Climates

The following teams belong to the network

- MERE project, Montpellier, France (INRIA, coordinator)
- LBE-INRA, Narbonne, France
- CBS, Sfax, Tunisia
- LAMSIN, Tunis, Tunisia
- Universite de Tlemcen, Tlemcen, Algeria
- UCL, Louvain-la-Neuve, Belgium
- POLIMI, Milano, Italy

The Scientific objectives are the following. Nowadays, the drastic economical constraints of waste-water treatments lead the main actors to consider more and more often the biological depollution. The principle consists in the transformation in solid of liquid organic matter produced by the main bio-geochemical cycles (of carbon or nitrogen), with the help of micro-organisms (that constitutes the so-called “biomass”). As far as waster-water treatment is concerned, the principle can be synthesized in two steps. First, in adequate environmental conditions of pH, temperature, presence of oxygen,..., polluted liquids and biodegradable solids are transformed into biomass and gas by the micro-organisms. In a second stage, liquid and solid phases are separated in order to reject the purified liquid phase only. It should be noticed that such a process acts as a concentrator of pollution into biomass, and that the smallest biomass production is a main research objective. The network will focus on the following main directions.

- conception and elaboration of new processes,
- optimization of the operation of current processes.

Contribution to fundamental and applied research on the subject is the first objective. The second one is to contribute to the share of knowledge between members of the network and help its diffusion all over Mediterranean countries.

7.2. European collaborations

The team has strong connections with the CESAME, Univ. Louvain-la-Neuve, Belgium. During his last sabbatical period, Professeur D. Dochain has been invited by the project to stay three months at Montpellier among the team.
J. Harmand is a participant of a Large Scale Collaborative European Project, called "CAFE" for "Computer-Aided Food processes for control Engineering", coordinated by Denis Dochain, UCL, Louvain-la-Neuve, Belgium that has just been accepted for the next 4 years (2008-2012). This project aims at developing an integrated solution for the robust monitoring and control of food processes. INRA is an important partner through the participation of four labs and one Experimental Unit (UMR GMPA, Grignon, UMA ASB and SPO, Montpellier, LBE, Narbonne and UE Pech Rouge, Gruissan).

7.3. National initiatives

- J. Harmand and A. Rapaport, with teh help of J.J. Godon (INRA LBE, Narbonne) are the animators of the INRA methodology network “Populations microbiennes, modèles et systèmes dynamiques”, supported by several INRA Departments (MIA, EA, MICA). In this framework, a researcher school has been organized (see Section 8.2).
- J. Harmand and A. Rapaport are partners of the ANR “Microbio-géographie à l’échelle de la France par l’application d’outils moléculaires au réseau français de mesures de la qualité des sols”, launched in 2006 within the national Biodiversity program. The subject of thesis of I. Callens and M. Hajji (see Section 8.3) belongs to this framework.
- F. Campillo is the leader of the INRIA Cooperative Research Initiative MICR (Modélisation stochastique, Inférence numérique et Contrôle pour l’évaluation et la gestion de Ressources renouvelables), which is an interdisciplinary partnership comprising INRIA teams (MERE, ASPI, Virtual Plant in Montpellier and Rennes), the “Laboratoire d’Ecologie Halieutique” (Agrocampus Rennes), the INRA unit “Systems Analysis and Biometrics” (Montpellier), the CIRAD Unit “Dynamics of natural forests” (Montpellier), the CERMICS/ENPC (Marne La Vallée). The MICR action intersects two scientific axes: the renewable resources assessment studies and probabilistic modeling with statistical inference.

7.4. Patent

A patent entitled “A method for measuring the biological diversity of a sample” has been licensed by INRA. The inventors are B. Haegeman (INRIA, 40%), J. Hamelin (INRA, 30%), J.-J. Godon (INRA, 20%), J.

Harmand (INRA, 5%) and P ; Loisel (INRA, 5%). The abstact says that *this invention concerns a computer-implemented method for estimating diversity in a sample, which can apply to any sample, and in particular to a sample whom species distribution is unknown. The method of the invention comprises steps essentially involving two components, (a) a migration of a sample comprising molecules on a surface area, whereby molecules migrate on a surface area according to their nucleotide or amino-acid sequence and (b) method steps for the diversity measurement, which are preferably performed through the working of one or several computer program(s).*

8. Dissemination

8.1. Leadership with scientific community

Fabien Campillo is a member of the "conseil de laboratoire" of IRISA (UMR 6074) and of the "conseil de l'école doctorale de physique, modélisation et sciences pour l'ingénieur de Marseille".

8.2. Teaching

In October, the team has organized with the help of the educative support of INRA, a one week researcher school at La Grande Motte (France) on "mathematical modeling for microbial ecology" with a particular emphasis on dynamical systems. The aim of the school was to gather micro-biologists and mathematicians interested in modeling microbial ecosystems of particular interests in agronomy (waste-water, soil, digestion, fermentation, ...). It has been financially supported by INRA.
A. Rapaport has given lectures on operational research at Polytech'Montpellier (50h).
A. Rapaport is in charge of a two-weeks lecture "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 bio-systems.
F. Campillo gave a course on "Markov models, hidden Markov models, filtering and particle filtering" at Université de Sud Toulon–Var, within the Master's degree "Mathématiques (Filtrage et traitement des données)" and the Master's degree "Sciences et Technologies (Sciences de la mer, environnement, systèmes)" (24 hours).
The team was invited to write a paper in the wide audience scientific for Interstice [50]. See the web page http://interstices.info/depollution.

8.3. Ongoing thesis

- Ilse Callens has started a 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), but has decided to resign in July 2007. Another PhD student, Miled El Hajji has entered a PhD position on the same subject, following her.
- Miled El Hajji has begun his PhD in December 2007, under the supervision of A. Rapaport and L. Ranjard. Microbial communities of soil ecosystems appear to possess some similitude with waste-water ecosystems that are worth being studied more deeply, which is the main purpose of this thesis, granted by INRA. An originality of the work relies on experiments on simple ecosystems conducted at INRA Dijon.

- Maxime Dumont has begun his PhD Thesis in November 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 analyzes are on the way. The first results show that a simplified ecosystem has taken place but that some oscillations take place. The first results obtained for identifying the functional group of unknown micro-organisms within the nitrification process have been presented at the AFEM (association francophone d'écologie microbienne) 2007 conference held in La Grande Motte [48].
- Nabil Mabrouk develops individual-based computer models for bacterial communities, taking spatial structure (like flocks and bio-film) into account. The simulator has been validated by comparison with analytical models, which under certain conditions approximate the individual-based models quite accurately. In particular, the behavior of a population-balance model for bacterial flocculation has been reproduced. This work has been communicated at the M2M (model to model) conference in Marseille [37], and at the STATPHYS conference in Genova [51]. Moreover, a bio-film model has been proposed where bacteria belonging to the bio-film keep some mobility in a polymeric substance. This work has been communicated at the Complex Systems conference in Dresden [38].

8.4. 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", Univ. Metz (Advisor : G. Sallet).
- 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", Univ. Saint-Louis du Sénégal et Univ. Metz (Advisors : D. Bicout, G. Sallet et M.-T. Niane).
- C. Lobry (president) : Hamelin F. "Jeux dynamiques en écologie du comportement", Univ. de Nice Sophia-Antipolis (Advisor : P. Bernhard)
- F. Mazenc (referee): Khoi B. Ngo, "Control of Constrained Nonlinear Systems: Applications in Aerospace and Robotics", Australian National University (Advisor : R. Mahony).
- F. Mazenc (referee): Ahmad Hably, "Approches bornées pour la commande des drones" GIPSA-lab - Control Systems department, CNRS, (Advisors : M. Alamir and N. Marchand).
- A. Rapaport (referee) : Moisan M. "Synthèse d'observateurs par intervalles pour des systèmes biologiques mal connus", Univ. de Nice Sophia-Antipolis (Advisor : O. Bernard).
- F. Campillo (member) : Verdier G., "Supervision de procédés de dépollution biologique: Tests statistiques et estimation non paramétrique pour la détection et le diagnostic de pannes", Univ. Montpellier II (Advisor : J.P. Vila)

8.5. Conferences, Invited conferences

F. Campillo, J. Harmand, C. Lobry and A .Rapaport have delivered lectures at the International Conference in honor of Claude Lobry, which has been held at Saint-Louis, Sénégal in September 2007 [45], [52]. See the web page http://www.lmia.uha.fr/ConferenceStLouis/indexA.html
At the 2007 STATPHYS conference in Genova, D. Vanpeteghem and B. Haegeman have presented a poster on the "The dynamics of microbial diversity" (Section 6.1.5) and N. Mabrouk, G. Deffuant and C. Lobry a poster on "Population balance versus spatially explicit modelling of flock-forming bacteria dynamics" [51].
M. Dumont has delivered a lecture at the AFEM (association francophone d'écologie microbienne) 2007 conference held in La Grande Motte [48].
The team was associated by D. Dochain (CESAME, Louvain-la-Neuve, Begique) to his invited "keynote" (semi-plenary session) at the 10th Computer Applications in Biotechnology (CAB 2007), Cancun, Mexico [52].

C. Lobry has been invited to give a plenary lecture at the 5th Conference STIC & Environnement, Lyon, November 2007.
F. Campillo has given talks at
- the Montpellier Statistical Working group seminar (February 2nd)
- the INRA-IRD mathematical days (“Mathématiques pour les Ressources Renouvelables”, Montpellier, March 12-14)
- the International Operational Modal Analysis conference (IOMAC, Copenhagen, May 1-2) [33]
- the Cooperative Research Initiatives’ national days (IRISA-Rennes, Oct. 1-2)
- CIRAD (Montpellier, Oct. 12).
F. Campillo has participated in the workshop “New Directions in Monte Carlo methods” (June 25-29, Fleurance, France).
F. Mazenc has participated to the workshop “Séminaire Contrôle et Optimisation” (September 6-9, Valleraugue, France).

8.6. Miscellaneous

MERE is a very interdisciplinary team. Members are engineers in automatic control, physicists or mathematicians. We think that, in order to stay a good professional in ones speciality, it is necessary to publish technical (methodological) papers which are not directly connected to the main objectives of the project. Such are the papers [11], [12], [13], [21], [22], [26], [27], [29], [31] and communications [33], [41].

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