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Project-Team MERE

Modelling and Water Resources

Sophia Antipolis - Méditerranée

THEME BIO

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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”, launched after a 2006 INRIA 3+3 call for proposal (see Section 8.1.5) has been renewed for two additional years. It now benefits from several financial support from its partners and from the European IRSES COADVISE project (cf. http://www.lapinsonniere.fr/3plus3/index.php?rubrique=treasure).
2. MERE is a partner of the ANR SYSCOMM project MODECOL (2009-2011) – “Using mathematical modelling to improve ecological services of prairial ecosystems” – for computational modeling of terrestrial prairial plant communities for purifying water from extra nitrate and pesticides (partners: UMR Ecobio, INRIA, Universities of La Rochelle, Houston and Berkeley).
3. The cooperation with researchers in Chili has led to the publication of two papers [21], [22].
4. CAFE is a new large scale European project, in which the team is involved in modeling and control batch processes for wine fermentation.
5. The team has published four papers in international journals of biology or ecology [24], [40], [25], [27].

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 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 spatio-temporal 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 [64] [66]. They are intensively used in Bayesian inference: “Markov chain Monte Carlo” (MCMC) in the static context [68] and “sequential Monte Carlo” (SMC, also called “particle filter”) in the dynamic context [62]. In the non-Bayesian approach, Monte Carlo techniques are used to explore likelihood functions [69]. They also gave rise to general algorithmics [65]. 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 [63].

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 [67], 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 versus 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 quite a 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*.

Agro-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 renewable resources assessment, for forestry applications. We adopted the Markovian formalism presented in Section 3.2. The hierarchical structure of these models allows for an efficient simulation-based inference of the a posteriori distribution law of the latent variables given the observation data.We recently considered the dynamics of tropical forests (see Section 6.2.5). 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. 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 6.1.7.
See the web page http://wwwlisc.clermont.cemagref.fr/Labo/MembresEtPagesIntermediaires/pagesperso/membres_actuels/mabrouk/index.html.

5.2. JPADE

Participant: Nabil Mabrouk.

JPADE is a simulator for two-dimensional biofilms grown on a planar surface. The simulator is written in Java and solves a system of three diffusion-reaction equations for the substrate, the bacteria and a product excreted by the bacteria [58].

The substrate consumption rate is modeled using a Monod equation. A fraction of the consumed substrate is supposed to be released back on the form of a product whereas the remaining part is transformed to biomass. The biomass, the substrate and the excreted product are allowed to diffuse. The diffusion factors may be constant or may depend on other variables. For instance, the simulator has been used for simulating the spatial patterns that arise is Pseudomonas Aeruginosa biofilms grown in flow chamber when the diffusion of the biomass is reduced by the accumulation of the self-excreted product.

The model parameters and the simulation results are displayed using a Graphical User Interface. JPADE is available on demand under the General Public License issued by the Free Software Foundation.

5.3. FORSIMS

Participants: Fabien Campillo, Nicolas Desassis.

In the context of the INRIA Collaborative research initiatives “MICR”, two software tools have been developed. They aim the simulation of spatio-temporal models of forest dynamics (FORSIMS, for forest simulations). Both are individual-based models (IBM) where each individual in the population is explicitly represented in the model as well as each mechanisms acting on each individual tree. The first one, in MATLAB, takes into account natural death, death by competition, birth/dissemination and growth. The second, developed in JAVA with a graphical user interface, does not take into account the growth phenomenon. These two software tools are available on http://www-sop.inria.fr/mere/personnel/campillo/computer.html

6. New Results

6.1. Theoretical results

6.1.1. Control 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).

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 [43].

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. 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 [56]. 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 [36], 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 stabilize a *predefined* oscillating behavior. Notice also that our control laws possess the required properties of positiveness and boundedness.

While significant, the results of [36] is limited to the case where the full state of the system (namely, the level of the limiting substrate and the species concentrations) is available for measurement and where there is no uncertainty in the model. To try to overcome these limitations, an alternative class of output feedbacks (depending only on an arbitrary linear combination of the species levels but not the individual species levels themselves) has been developed that stabilized prescribed equilibria in two species chemostats with actuator errors and Monod growth rates. These results are given in [35]. The results provide feedback stabilizers that yield input-to-state stability with respect to appropriately small disturbances acting on the dilution rate and input nutrient concentration controllers. The bounds on the admissible disturbances can be computed explicitly from the known parameters of the model.

6.1.2. Designs under Matrosov's conditions and robust adaptive control

Participant: Frédéric Mazenc.

In [35] (see also [55]) is the design of explicit global strict Lyapunov function constructions is performed under conditions of Matrosov-type. The advantages of [35] are (a) the results are simpler than the known constructions relying on the Matrosov's approach (b) the Lyapunov functions are locally lower bounded by positive definite quadratic functions for a large class of systems (c) they only require a non-strict *positive definite* function whose derivative along the trajectories is nonpositive instead of a (radially unbounded) nonstrict Lyapunov function. The motivation for (c) is that for biological models, one can frequently find non-strict Lyapunov-like functions which are not proper. Another useful property of [35] is that it yields some robustness results. The paper also uses the results to construct a strict Lyapunov function and prove robustness for a wastewater treatment process stabilized through adaptive feedback. This illustrates the value added by strict Lyapunov functions for biological models.

One difficulty in applying the known Matrosov theorems is that one needs to know the auxiliary functions to build the global Lyapunov function. This was overcome in [53] (which is a preliminary version of a submitted paper) for the special case of the tracking error dynamics for adaptively controlled nonlinear systems that are affine in the unknown parameter. The main assumption was a classical persistence of excitation (PE)

condition. PE establishes that a necessary (and sometimes sufficient) condition for parameter identification is that the reference trajectory be *sufficiently rich* so that the regressor satisfies a PE inequality along the reference trajectory. For large classes of systems, PE implies that tracking error convergence can only happen when the adaptation law identifies the actual parameters.

The contribution of [53] involved (a) constructing explicit auxiliary functions for adaptive controlled error dynamics and (b) extending the resulting global Lyapunov function construction to cases where the unknown parameter also has additive time-varying uncertainty. This made it possible to explicitly quantify the effects of the uncertainty using ISS, provided the regressor satisfies an additional affine growth condition. The results in [53] apply under general adaptation laws that could include, for example, projection operators, least-squares estimators, and prediction-error-based estimators. The practical interest of this work is that it leads to uniform global asymptotic stability of the error dynamics by constructing explicit, global, strict Lyapunov functions.

Another challenging problem which has been addressed is the construction of explicit Lyapunov functions for time-varying hybrid systems. Hybrid systems naturally arise in a variety of important engineering applications e.g. temperature control models where there are continuous temperature changes from heating or cooling as well as on-off switching between modes of operation such as a furnace turning on or off. Most of the known results for the hybrid model concern the existence of stabilizing feedback, reachability sets, and necessary and sufficient conditions for stability in terms of the existence of a hybrid Lyapunov function.

The work [34] uses the hybrid system model developed by Andrew Teel and his school in which there are continuous and discrete subsystems and addressed the complementary problem of establishing a robustness property called Input to State Stability of hybrid systems through the explicit construction of hybrid ISS Lyapunov functions. The constructions are new even for the special case of discrete time systems, since the constructions involve finite sums of the persistence of excitation parameters from the nonstrict decay estimate, instead of the infinite sums that were used in the earlier results.

6.1.3. Systems with delays

Participant: Frédéric Mazenc.

In the work [37] is provided new explicit constructions of Lyapunov-Krassovski functionals for control affine time-varying systems with feedback delays. As a byproduct, the work gave explicit upper bounds on the possible feedback delays that yield input-to-state stability with respect to actuator errors. The work applied to important examples that are beyond the scope of the standard treatments of feedback delayed systems such as control affine systems with unbounded vector fields that are not necessarily locally exponentially stable. Observe that [37] addresses the realistic scenario where there are different delays in the different components of the feedbacks and where the delays themselves are time varying. In addition, the delays considered in [37] are not required to be bounded. In fact, the feedback delays can be made as large as desired (while maintaining stability) for a significant class of examples where the system has no drift and where the given Lyapunov function for the undelayed system is independent of time.

In [54], a model of the Gleevec treatment for chronic myelogenous leukemia is studied. This model is a nonlinear system with a pointwise delay which admits three equilibria, whose local analysis is performed first. Next, through a change of coordinates which gives a triangular structure to the equations which eases the understanding and analysis, existence of unbounded solutions is established. The work ends with comments on how the conditions based on initial cell concentrations that guarantee unbounded solutions can serve to predict whether the Gleevec treatment will result in a sustained remission.

A central result of the theory of the chemostat is the Competitive Exclusion Principle. It states that for a chemostat model with several species with increasing growth rates at most one competitor can survive when there is a single limiting resource. However, this result is valid only in the absence of delays in the equations. But delay occur naturally in biological models and in particular chemostats models with delays in the dynamics of the species concentrations are more realistic than models without delays. In [21] it is proved that, for models of this type, the competitive exclusion principle still holds true, provided that the delays are smaller than an upper bound for which an explicit expression is given. The proof is established through the construction of Lyapunov-Krasovskii functional.

6.1.4. Optimal control of fed-batch reactors

Participant: Alain Rapaport.

The problem of feeding in minimal time a batch reactor with one reaction involving one substrate and one biomass has been originally 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.
We have carried on a work initiated in 2006 within the cooperation program with Chile (see Section 8.1.3). Two kinds of extensions have been considered:

- 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. This approach has been inspired by recent theoretical results on turnpike optimality in calculus of variations problems [46]. 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.

This year, we have generalized our first results to situations for which singular arcs may touch the target (in these cases, we have shown that the optimal trajectory has the leave the singular arc before the reactor is full, for reaching the target in minimal time). The complete solution of the problem appears in the paper [22].

6.1.5. Modeling and identification of batch processes

Participants: Miled El Hajji, Alain Rapaport.

We have analyzed a model of batch reactor with with an explicit compartment of inactive (or dead) micro-organisms and nutrient recycling.

$$\begin{aligned} \dot{S} &= -\mu(S)X/Y + \alpha m X \ ;, \\ \dot{X} &= \mu(S)X - mX \ , \\ \dot{X}_d &= (1-\alpha)m \ . \end{aligned}$$

The trajectories of this model fit qualitatively the data from experiments performed at INRA Dijon, in the framework of El Hajji's PhD thesis. The online observation made on this system are the concentration S and an optical density assumed to be proportional to the total biomass $M = X + X_d$. As one can check, parameters (m, α, Y) are not identifiable at steady state. We have proposed a practical observer of X, X_d and the three parameters, based on particular time transformation, for reconstructing the unknown parameters and variables of the model. This is part of the ongoing PhD work of M. El Hajji.

6.1.6. 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.

6.1.7. Models of competition for one resource

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

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).
We pursue our systematic approach of a better understanding of this general model under various particular assumptions listed below.

6.1.7.1. Two species in a chemostat.

This is the particular case where $f(s) = D(S_{in} - s)$, $\mu_i(s,x) = \mu_i(s)$ and $N = 2$. Under these assumptions the competitive exclusion principle holds and one of the species eliminate the other, but this can eventually take a long time [19]. If we add extra assumptions (which changes the model) such as:

1. Delay in the functional response,
2. Control devices,
3. Cascades of reactors,
4. Periodic forcing,

persistence of species at any time can be proved. Case (1) is addressed in [21], case (2) in [37], [43], case (3) in [18], [42] and case (4) in [36].

6.1.7.2. Many species in the chemostat.

Motivated by the fact that "finger print" technics tell us that the number of species present in a reactor is usually very large (10^3) we start to investigate the case where N in system (1) is very large. Our first published result in this direction is [40].

6.1.8. DNA-based techniques in microbial ecology

Participant: Bart Haegeman.

Microbial ecologists use a wide range of DNA-based techniques to monitor the composition of microbial communities, like reassociation kinetics, microbial fingerprinting, and molecular inventories. Extracting quantitative information from such measurements is difficult due to (1) the inherent biases of molecular techniques and (2) the high diversity of microbial communities. A detailed estimation of the microbial community composition is therefore often impossible. Our strategy has been to look for global, averaged quantities, defined on the microbial community as a whole, which might be possible to estimate accurately in spite of technical biases and complex communities.

In recent years this approach has been successfully applied to fingerprinting techniques, for which we established that a quantity called the Simpson diversity index is accurately encoded in fingerprinting profiles. This work has now been extended to another technique, namely DNA reassociation kinetics. The time needed for a mixture of denatured (i.e., single-stranded) DNA to renaturatre (i.e., to form double strands) is used as a measure of the microbial diversity present in the mixture. We showed that not only the Simpson diversity can be obtained from this type of measurement, but also a range of other quantities called the Renyi diversity indices. This work has been published in a major general ecology journal [27].

6.1.9. Neutral community models 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, remarkable agreement between neutral model predictions (species-abundance distributions and species-area relationships) and empirical observations has been reported for some, mostly rather diverse, ecological communities.

There is some evidence that also certain aspects of microbial communities can be well described by the neutral model. Highly diverse microbial communities have been difficult to deal with using more traditional modeling approaches from community ecology. The neutrality assumption could lead to an effective global description, without requiring quantitative species data (growth characteristics, interaction strengths, etc). We are actively participating in the development of such microbial community models.

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, the so-called zero-sum assumption. This assumption is often unacceptable for microbial systems, e.g., to describe the recovery of a microbial community from a toxic contamination. We have extended the neutral model by replacing the zero-sum assumption with a community-level density dependence. Some preliminary results on the mathematical properties of this model have been reported in [24].

A second modification of Hubbell's neutral model concerns its dynamical aspects. Most non-microbial communities have dynamical time scales that are much longer than observation times. Model comparisons are therefore often exclusively based on the stationary aspects of the neutral model. The situation is quite different for the much faster evolving microbial communities. Model comparisons will therefore most probably involve the dynamics of the neutral model. We have published a number of dynamical model predictions in terms of the Simpson diversity index [45], which can be accurately measured on microbial communities (see Sect. 4.4).

The neutral model framework is close in spirit to certain modeling approaches in statistical mechanics. Many individual contributions (organisms in ecology, particles in physical systems) yield some global, averaged system behavior (a community in ecology, a gas or a solid in physics). The model outcome on this global level is often rather insensitive to the modeling assumptions on the detailed level. This mapping between global and detailed level can be formulated as a so-called entropy maximization problem. The paper [26] attempts to clarify the similarities and differences between the entropy maximization approach as used in physics and in ecology.

6.1.10. Monte Carlo approximation

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 more robust 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 [13], [14] 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.

MCMC are primarily applied to parameter estimation problem. In this context, an alternate approach is to adapt sequential Monte Carlo methods (also known particle filters) to the tracking of static parameter. In [15] we propose an algorithm where the variance of the proposal kernel adapt its variance to to the signal-to-noise ratio.

The differences between the two approaches in the context of Bayesian inference have been considered in [16].

6.2. Applications

6.2.1. Modeling and control of Anaerobic Membrane BioReactors (AMBR)

Participants: Claude Lobry, Jérôme Harmand.

To circumvent the problem of separating treated water from sludge and to maximize the biomass concentration inside bioreactors, membranes can be used. They can be installed either inside or in a separate module and form a physical barrier to microorganisms. In such a configuration, the main limitation is the risk of membrane clogging. One of the main challenges is to modify the actual models in order to be able to predict clogging and to act on the process early before it appears. In order to better understand this phenomenon, a lot of research is going on. It is necessary to better understand the links between the characteristics of the membrane and the microorganisms. On aerobic processes, it has been shown that Soluble Microbial Products (or SMP) that are molecules produced when a cell dies could play a major role. The reason is that in MBR, the biomass retention time is important when compared to classical Activated Sludge Processes. Thus, when modeling the biological process, the biomass mortality terms can no longer be neglected (because small with respect to the dilution rate) as usually assumed and the turnover of the matter coming from the dead cell must be taken into account. Working with AMBRs, we face many challenges: i) evaluating whether these SMP can explain, as in the aerobic case, the discrepancies observed between classical anaerobic model predictions and experimental data and ii) how to link these SMP to membranes characteristics in order to be able to better predict clogging events and iii) how the microbial ecosystem is affected by the membranes. Amine Charfi (ENIT-LAMSIN, Tunis, Tunisia) and Boumediene Benyahia (Univ. Tlemcen, Tlemcen, Algeria) are just beginning their PhD on this subject within the TREASURE network under the co-advisoring of J. Harmand, cf. Section 8.1.5.

6.2.2. Observers for the investigating microbial ecology problems

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 into ecological problems of interest for wastewater treatment technology. In particular, within the thesis of Maxime Dumont, new observers have been proposed to assign a given function of an ecosystem to a specific species identified using data from molecular biology.

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 the 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 [26], 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 control of cascade biosystems to mimic batch wine making processes

Participants: Jérôme Harmand, Alain Rapaport.

Within the European CAFE project within which the LBE-INRA is involved, a multi-steps continuous pilot plant located in Montpellier at the UMR SPO ("Sciences Pour l'Oenologie") will be modeled and controlled. This process is used to mimic batch processes used for wine making. The challenge of the research is to link metabolic pathways modeling together with macro mass balance modeling of the system and to control it in order to automatically change the desired steady state point in minimal time.

6.2.5. Modeling and inferring ago-ecological dynamics

Participants: Fabien Campillo, Nicolas Desassis, Khader Khadraoui, Abdel Dkhissi.

This work is part of an INRIA Cooperative Research Initiative (see Section 8.3), and is done in collaboration with CIRAD Montpellier ("Dynamics of Natural Forests" unit). This work aims at developing individual-based Markovian models of forest dynamics with competition for the access to nutrients or light. We propose models derived from the work of Sylvie Méléard and co-authors. The model combines pure jump mechanisms as birth/dissimination, natural death (natural and by competition) together with a continuous mechanism of growth [47], [48].

In collaboration with Marc Joannides (Université Montpellier 2, Research Mathematics and Modelling Institute of Montpellier), we started the analysis of such individual-based Markovian models.

A simpler version of this model has been studied in [59]. F. Campillo, N. Dessasis and Abdel Dkhissi (the first two for the conception, the last two for the programming) developped a `Java` interface for this simplified model (see Section 5.3). We also proposed an algorithm to tune an aggregation index to a prescribed value. The tuning is achieved through a Kiefer-Wolfowitz stochastic approximation technic.

6.2.6. Modeling and inferring agricultural dynamics

Participants: Fabien Campillo, Angelo Rahenirina.

This work is supported by the SARIMA program and AUF (see Section 8.1.1) and is done in collaboration with the University of Fianarantsoa in Madagascar and with Dominique Hervé (IRD, Fianarantsoa, Madagascar).

We consider a Markov model for agricultural successions. The applicationof Markov models to agricultural succession problems is not new, but relatively new tools of numerical Bayesian inference allow us to test general prior laws. In addition to the maximum likelihood estimate, we consider the Jeffreys prior (non-informative), and calculate the associated Bayesian estimator with a Metropolis-Hastings approximation procedure. We study the capabilities and limitations of thisapproach [61], [49].

7. Contracts and Grants with Industry

7.1. TREASURE

Participants: Jérôme Harmand, Claude Lobry, Tewfik Sari.

The TREASURE network benefits from financial support from INRIA, INRA and African partners of about 20 Keuros/year for the next three years (2009-2011). In addition, a European IRSES (called COADVISE) project has been accepeted and includes 42 man months available for exchanging PhD and postdoc students within the next 48 months.

7.2. CAFE

Participants: Jérôme Harmand, Alain Rapaport.

The Large Scale European Project CAFE has begun in September 2008. The financial support obtained by the LBE-INRA includes 70 Keuros of consumables and travel expenses and one 18 month postdoc (this grant is expected to be converted in a 1/2 PhD grant for a chilean PhD student) to be located in the UMR ASB from March 2009.

7.3. DIMIMOS

Participants: Jérôme Harmand, Alain Rapaport.

The ANR Project DIMIMOS has just been accepted: it will begin next January for 4 years (2009-2012). The financial support obtained by the MERE project includes about 5000 euros of travel expenses and two 6 month training periods for engineers.

7.4. MODECOL

Participant: Fabien Campillo.

The ANR SYSCOMM Project MODECOL has just been accepted: it will be launched next January for 3 years (2009-2011) and will involve three INRIA projects (MERE, MAESTRO and TOSCA) with the UMR Ecobio (Rennes, France), the University of La Rochelle and the Universities of Houston and Berkeley. The aim of the MERE project is to propose individual-based models for terrestrial prairial plant communities' dynamics in the context of water purifying from nitrate and pesticides

8. Other Grants and Activities

8.1. International cooperations

8.1.1. 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.
- Within the SARIMA program (support for research activities in computer science and mathematics in Africa) supported by INRIA and MAE (Ministère des Affaires Etrangères): C. Lobry is a member of the Steering Committee and Fabien Campillo is the INRIA representative for scientific relations with Madagascar. 2008 was dedicated to the completion and evaluation of this program. F. Campillo, C. Lobry and T. Sari participate in a working group in charge of the setting up of the SARIMA 2. This program will follow the SARIMA 1 program but on a wider scale.
- Fabien Campillo is the INRIA representative for scientific relations with Madagascar, within the SARIMA program. 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 planned for 2009. 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.
- The team has also a close relationship with the LANI (Laboratoire d'Analyse Numérique et Informatique de l'Université Gaston Berger de Saint-Louis du Sénégal).

8.1.2. Cooperation with Maghreb countries

Tewfik Sari is the leader of the project 05MDU641B (2005-2008) on 'Dynamical systems and Geometries', with the University of Algiers (USTHB). This project is part of the H. Curien program Tassili. Tewfik Sari is invited to the "Colloque d'Evaluation et de prospective du programme Tassili: 25 ans de coopération scientifique algéro-française", Algiers 16-17/12/2008 to present the scientific report of the projet.
Claude Lobry and Tewfik Sari are involved in the program Aires-Sud "Epuration des eaux par procédés membranaires : Modélisation et Commande" under the direction of Brahim Cherki University of Tlemcen, Algeria. This program also associates the University of Saint Louis, Senegal.

8.1.3. 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' (2005-2007), on estimation of unknown inputs (with G. Acuna, University of Santiago) and optimal impulsive control for fed-batch reactors [22] (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. The project has been reconducted for 2008 and 2009 under the name 'ECOLOMICRO2'.

8.1.4. 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 (five journal papers this year). F. Mazenc also paid a visit in November 2008 to Jiang Zhong Ping (Professor in the Polytechnic Institute of New York) with a view to prepare future collaborations with him.

In collaboration with M. Malisoff, F. Mazenc is currently preparing a monograph. This book, entitled "Construction of Strict Lyapunov Functions" and geared to advanced graduate students and researchers , would be published in the Springer Communications and Control Engineering Series.

8.1.5. 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 . 2008 has been the year of reinforcement of this network with getting a number of national as well as international financial supports. "Anaerobic Membranes BioReactors (AMBR) for the treatment of water and its reutilization in agriculture under semi arid climates" have been chosen as the main theme of the research program. Since 2006, we have organized several secientific meetings and schools in partners countries. The acronym TREASURE stands for **Trea**tment 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
- University of Tlemcen, Tlemcen, Algeria
- UCL, Louvain-la-Neuve, Belgium
- POLIMI, Milano, Italy
- University of Provence, IRD, Marseille, France
- University of Santiago de Compostella, Spain

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 into 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 wastewater 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. For more information, see the web page http://www.treasure.fr.

8.2. European collaborations

The team has strong connections with the CESAME, Univ. Louvain-la-Neuve, Belgium. Professeur D. Dochain visit regularly 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).

8.3. National initiatives

- J. Harmand and A. Rapaport, with the 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).
- J. Harmand and A. Rapaport are partners of the ANR DIMIMOS (Relationship between microbial diversity and organic matter turn-over in agricultural soils), launched in fall 2008 within the national SYSTERRA program.
- J. Harmand and A. Rapaport are co-leader with E. Dubreucq (SupAgro Montpellier) of the project BioInh (Modeling and optimization of bioconversion of plant materials in inhomogeneous media) within the program “Computational Plants and Eco-Systems” lauched by the Agropolis Fondation.
- 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. http://www-sop.inria.fr/mere/personnel/campillo/micr/

8.4. Visits

- Denis Dochain, CESAME, University of Louvain, Belgium, 15–18 January and 27–31 october.
- Mieczyslaw Metzger, Silesian Technical University, Gliwice, Poland, 21–25 January and 15–19 September.
- Rampal Etienne, Center of Evolutionary and Ecological Studies, University of Groningen, The Netherlands, 25–30 April.
- Pedro Gajardo, Departamento de Matemática Universidad Técnica Federico Santa María, Chile, 18–29 september.
- Hector Ramirez, Departamento de Ingeniería Matemática, Universidad de Chile, Santiago, Chile, 18–29 september, funded by INRIA/CONYCIT project ’ECOLOMICRO2’.
- Gonzalo Ruiz, Escuela de Ingeniería Bioquímica, U. Católica de Valparaíso, Chile, 18–29 september, funded by INRIA/CONYCIT project ’ECOLOMICRO2’.

9. Dissemination

9.1. Leadership with scientific community

Fabien Campillo and Claude Lobry are members of the Scientific Committee of the 9th African Conference on Research in Computer Science and Applied Mathematics.

Fabien Campillo was member of an INRA selection board for the selection of junior scientists (statistics and modeling).

Alain Rapaport was member of an CIRAD selection board for the selection of scientists (dynamical systems and modeling).

Claude Lobry was President of an AERES evaluation committee; he was President of an evaluation committee of the University of Saint-Louis du Sénégal.

Frédéric Mazenc is member of the COST (Scientific and Technological Orientation Council) in the team GTAI (Groupe de travail Actions Incitatives). The main mission of the GTAI: organization, selection and supervision of INRIA's incentive initiatives, such as the Cooperative Research Initiatives (ARC) of the Scientific Management and the Software Development Operations (ODL) and Standardization operations of the Department of Development and Industrial Relations.

T. Sari is in charge of the monitoring of projects co-funded by INRIA and Agropolis Foundation (RTRA Agronomie Montpellier).

9.2. Teaching

The team started a long term collaboration of teaching with LAMSIN in Tunis (20h of master course in mathematical system theory) and LBS in Sfax (20h of master course in Biological control processes).
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 is in charge of a two-week 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).
In collaboration with R. Rakotozafy (University of Fianarantsoa, Madagascar), F. Campillo gave a course on "Markov modelling" in the CIMPA-UNESCO-MADAGASCAR school on "Mathematical and Computer oriented Methods for Landscape Modelling", September 15-30 (4h30).
J. Harmand is in charge of a two-week lecture "Modélisation des procédés biologiques de dépollution" within the master "Biotechnologie de l'Environnement" at the University of Sfax, Sfax, Tunisia.

9.3. Ongoing thesis

- Maxime Dumont (Grant from INRA-MIA and INRA-MICA departments) has begun his thesis in 2005. He will defend it on December the 17th in Montpellier. He aims at confronting concepts of the theoretical ecology to experimental data. His work consisted in proposing a number of experiments with model ecosystems commonly used in biological wastewater plants, such as the nitrification process, in order to investigate whether the fact that mutualism among individuals and species promotes diversity holds true or not. The first experiments have been run at the end of 2005 and have continued until October 2008. His findings include a new generic method to assign a species to a given function of an ecosystem and the evaluation from experimental data of a functional model of a wastewater treatment plant including interactions between species. Two conference proceedings papers have been published and two journal papers are now under evaluation.
- 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. Nabil will defend his thesis by the end of 2008.
- Miled El Hajji is preparing a PhD thesis since December 2007, under the supervision of A. Rapaport and L. Ranjard (INRA Dijon). 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. One journal paper on "practical coexistence" of two species in a chemostat has been accepted [19].
- Ihab Haidr is funded by the French Ministry of Research (MESR grant) since November 2008, for preparing a PhD thesis under the supervision of A. Rapaport and F. Gerard (INRA Montpellier). His research subject focuses on coupling geochemical models of soil with microbial dynamical models.
- The PhD thesis of Diagne Mamadou Lamine is co-directed by Prof. Mary Teuw Niane (Saint Louis Sénégal) and Tewfik Sari on the subject "Modélisation mathématique de la dynamique de prolifération du Typha dans le Parc National du Djoudj".
- Boumediene Benyahia has just begun his PhD Thesis in September 2008 within the TREASURE network (cf. 8.1.5). His thesis aims at evaluating classical anaerobic process models for AMBRs. In close cooperation with Amine Charfi (cf. herebelow) and all partners of the TREASURE network, he will try to modify such models to link their variables to those used to characterize the membranes. The final objective is to be able to predict and control the clogging of membranes. The first work to be realized is the modeling of an AMBR working in the Biotechnological Center of Sfax (CBS, Sfax, Tunisia). At the same time, he will be in charge of the design and the building of an AMBR pilot plant in Tlemcen which should begin soon.
- Amine Charfi will begin his PhD soon within the TREASURE network (cf. 8.1.5). His thesis aims at characterizing the membranes used in AMBRs in order to link their characteristics to biological compartment of bioprocess models. In close cooperation with Boumediene Benyahia and all partners of the TREASURE network, he will conceive and realize experiments on membranes modules both with and without biomass in order to better understand chemical and physical properties of the membranes and its capacity to clog. The first work to be realized is, on the one side, an extensive literature survey on the membrane models, and, on the other side, on classical models of anaerobic bioreactors.

9.4. Participation to thesis committees

- T. Sari (advisor) : K. Yadi, "Perturbations singulières : approximations, stabilité pratique et application à des modèles de compétition." Univ. de Tlemcen et de Mulhouse.

- C. Lobry (referee) : K. Yadi, “Perturbations singulières : approximations, stabilité pratique et application à des modèles de compétition.” Univ. de Tlemcen et de Mulhouse (Advisor : T. Sari).
- F. Campillo (referee) : A. Totohasina, “Contribution à l´étude des mesures de la qualité des règles d’association: normalisation sous cinq contraintes et cas de MGK”, thèse d’Habilitation à Diriger des Recherches, Univ. d’Antsiranana.
- F. Campillo (referee) : T. Romary, “Inversions des modèles stochastiques de milieux hétérogènes”, Univ. Paris VI (Advisor : J. Jacod).
- T. Sari (referee) : B. Ettaoui, “Problèmes métriques dans les espaces projectifs et dans les espaces de Grassmann”, thèse d’Habilitation à Diriger des Recherches, Univ. de Mulhouse.

9.5. Conferences, Invited conferences

Bart Haegeman has presented a talk on “Neutral community models for microbial ecology” at the NERN Annual Meeting 2008 in Lunteren, The Netherlands. He was invited to participate in the ESF workshop on theoretical microbial ecology in Glasgow, UK, where he gave a presentation entitled “Microbial diversity and the neutral chemostat”.
Bart Haegeman has been visiting the Theoretical Ecology Laboratory of Prof. Michel Loreau at McGill University, Montreal from Sept 24 to Dec 19. He was financed by the INRIA program “Explorateur”.
Bart Haegeman has been invited to give a seminar at the Dept. of Biology, McGill University (Montreal, Oct 9) entitled “Limitations of entropy maximizations in ecology”.
F. Mazenc has delivered a lecture in the *workshop* “*Delays, Feedbacks and Interconnections: From Simple Structures to Complex Networks*” of the *IFAC World Congress* 2008 (workshop organized by Silviu Niculescu and Joono Cheong).
A. Rapaport has been invited to give a talk at the Control and Power Seminars, Dept. of Electrical & Electronic Engineering, Imperial College (London, May 7, 2008) on “About minimal time impulse control of sequential batch reactors with one or more species”.
A. Rapaport has been invited to give a presentation at the International Conference dedicated to the Centennial Anniversary of L. S. Pontryagin (Moscow, June 2008), in an invited session organized vy Professor Veliov.
A. Rapaport has been invited to give a presentation at the conference of the GDR MABEM “Modélisation bioinformatique en biologie et médecine” (Nice, October 2008).
J. Harmand has presented a talk on “Observers for Microbial Ecology – How Including Molecular Data into Bioprocess Modeling?“ at the 16th Mediterranean Conference on Control and Automation, Ajaccio, Corsica, June 25-27, 2008.
C. Lobry has been invited to give a plenary lecture at the First Conference of the SM2A (Société marocaine de Mathématiques Appliquées), Rabat, Feb. 6-8.
F. Campillo gave lectures at the “Rencontres Statistiques au Sommet de Rochebrune” (Meugève), April 30-March 04; the 9th African Conference on Research in Computer Science and Applied Mathematics 27-30 October 2008, Rabat, Morocco; the XIVth International Biometric Conference, University College Dublin (UCD), Ireland July 13th to 18th.
Tewfik Sari has presented a talk on “Delayed loss of stability in a biological model” at the Second International Symposium on Dynamical Systems in Alger-Boussaada-Msila, October, 18–22, 2008.
Claude Lobry and Tewfik Sari were invited to the Reunion of the ANR “ANAR” (Analyse Non linéaire et Application aux Rythmes du vivant) in La Rochelle 26-28/11/2008 where they gave two presentations, based on joint work with Alain Rapaport, entitled “Coexistence in a Chemostat with a slowly varying whashout rate”.
Tewfik Sari was the scientific editor, with Hamidou Toure and Gauthier Sallet of the special volume 9 of ARIMA, 2008, the Proceedings of the International Conference in Honor of Claude Lobry, held in Saint-Louis, Sénégal, 10–14/09/2007 (http://www.lmia.uha.fr/ConferenceStLouis/).

9.6. 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 [14], [52], [33], [54], [46], [31], [30], [39].

Bart Haegeman, Jérôme Harmand, Nabil Mabrouk and Alain Rapaport have presented the activities of the team at the Salon Européen de la Recherche et de l'Innovation - Paris, 5– 7 june 2008.

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