



IN PARTNERSHIP WITH:
INRA

Activity Report 2014

Project-Team MODEMIC

Modelling and Optimization of the Dynamics of Ecosystems with MICro-organisms

IN COLLABORATION WITH: Mathématiques, Informatique et STatistique pour l'Environnement et l'Agronomie

RESEARCH CENTER
Sophia Antipolis - Méditerranée

THEME
Modeling and Control for Life Sciences

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Project-Team MODEMIC

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2. Overall Objectives

2.1. Introduction

Modemic is a joint Inria-Inra team with the Inra-Supagro Mistea Research Unit, settled at the “Campus de La Gaillarde”, Montpellier.

In complex processes of material and energy transformations on Earth, the microbial compartment is an essential link for major biochemical cycles that sustain life on Earth and regulate the climate. There are presently growing social demands for preservation of water quality, regeneration or soil fertility or development of new ecosystem services for the environment, for which the role of micro-organisms is fundamental. Micro-organisms are also responsible of fermentation processes that can be found specifically in food production. Knowledge, control and management of microbial ecosystems appear then to be essential to satisfy the expectations of our society. Aside observations and experiments, modeling and computer simulations have to play an important role in the fields of microbiology and microbial ecology.

In this context, MODEMIC aims at cross-fertilizing Inra and Inria researchers' competences for developing, analyzing and simulating new models of microbial ecosystems as efficient tools to understand, explore, pilot and manage natural or industrial bio-processes. Being a joint team with the MIA (Applied Mathematics and Informatics) Department of Inra, an important issue for the team is to develop relevant and useful techniques for scientists and engineers in biology, micro-biology, microbial ecology and agronomy.

For this purpose, we study mathematical and/or computer models of the dynamics of populations of micro-organisms. These models can be complex or reduced ones. We carry simulations and possibly mathematical analyses. We put an emphasis on the understanding of the dynamical behaviors out of equilibrium, because most of real processes represented by these models are either not stationary, or one needs to drive them out of an equilibrium.

For concrete applications in laboratory and/or within industrial perspectives, we also study control strategies and identification techniques of these models, based on tools from Automatic Control.

Our objective is twofold: on the one hand to build, simulate and analyze models of microbial ecosystems; on the other hand to develop methods for the identification, the control and the optimization of microbial ecosystems.

2.2. Build, simulate and analyze models of microbial ecosystems

We investigate different models of microbial ecosystems at various scales, depending on the observations reported by biologists and questions of interest. The models we intend to develop and study cover the usual three scales of ecology: the individual in its community, the community in interaction with its environment and the overall ecosystem.

The main questions we address concern the roles of biotic and abiotic interactions on the coexistence or exclusion of species, the behavior of transient dynamics and the performances of bio-processes.

For this purpose, we build population models both deterministic (differential equations) and stochastic (stochastic differential equations, birth and death processes), as well as individual-based models (usually stochastic). We study their dynamical properties combining mathematical analysis (determination of equilibria and their stability, construction of Lyapunov functions, analysis of limit cycles, weak convergence between models...) and numerical simulations (Monte-Carlo techniques, Gillespie-like algorithms...). Some of our models include spatial considerations, with explicit (transport and/or diffusion terms) or implicit (compartments or "gradostat"-like equations) representations.

We aim at determining the validity and the effective limits of these models, and at developing tools for change of scales (e.g. from an individual-based model to a deterministic macroscopic model and vice-versa). We consider also multi-scale modeling, for instance in biofilm simulations for which the scale of micro-organisms and the scale of the exo-polymer matrix impact each other. The scope of our research program stops at the individual level as its smallest level. We do not intend to model the mechanisms inside micro-organisms but rather to focus on populations, and especially on the effects of large numbers of individuals sharing the same environment.

2.3. Identification, control and optimization of microbial ecosystems

Biologists have often to deal with data and use statistical tools to reveal or quantify variables correlations. We focus on situations for which models can bring complementary knowledge or lightning over these statistical treatments. In many practical cases, the state variables of the dynamical models (nutrient concentrations, composition of the biomass...) are not all accessible through direct observations. Instead, indirect effects of the internal states are observed with time by way of the system outputs. State observers or filters, that are built on the precise knowledge of a dynamical model and its outputs, allow on-line reconstruction of unknown state variables or parameters, and could in principle replace missing sensors. Moreover, knowing the system state is often necessary to solve many control problems (for instance stabilizing a system using state feedback) that we describe below. In practice, several obstacles due to model non-linearity, imperfect measurements, disturbances or simply lack of observability appear when one tries to apply the usual constructions of state estimators. We aim at proposing and studying reconstruction methods dedicated to the family of models we are considering in Objective 2.2, with the possible considerations of multi-valued systems or probabilistic estimations.

Among most of our collaborations about real life bio-processes (waste-water treatments, food fermentation...), we also often met questions related to the driving, design or supervision, that we aim at considering at both methodological and practical scopes. Our objective is to look for state or output feedback strategies for stabilizing bio-processes, or optimizing paths with respect to a given criterion such as minimum time. We focus on the derivation of global controllers based on the nature of non-linearity and input constraints (such as positivity of the manipulated variables), and investigate how these realizations can be applied under uncertainties on both model and measurements. Our final goal is to provide satisfactory solutions (optimal or sub-optimal) relevant to be implemented on real processes that possesses a limited number of sensors.

3. Research Program

3.1. Modeling and simulating microbial ecosystems

The chemostat model is quite popular in microbiology and bioprocess engineering [60], [62]. Although the wording “chemostat” refers to the experimental apparatus dedicated to continuous culture, invented in the fifties by Monod and Novick & Szilard, the chemostat model often serves as a mathematical representation of biotic/abiotic interactions in more general (industrial or natural) frameworks of microbial ecology. The team carries a significant activity about generalizations and extensions of the classical model (see Equation (1) and Section 3.1.1) which assumes that the sizes of the populations are large and that the biomass can be faithfully represented as a set of deterministic continuous variables.

However recent observations tools based notably on molecular biology (e.g. molecular fingerprints) allow to distinguish much more precisely than in the past the internal composition of biomass. In particular, it has been reported by biologists that minority species could play an important role during transients (in the initialization phase of bio-processes or when the ecosystem is recovering from disturbances), that cannot be satisfactorily explained by the above deterministic models because the size of those populations could be too small for these models to be valid.

Therefore, we are studying extension of the classical model that could integrate stochastic/continuous macroscopic aspects, or microscopic/discrete aspects (in terms of population size or even with explicit individually based representation of the bacteria), as well as hybrid representations. One important question is the links between these chemostat models (see Section 3.1.2).

3.1.1. About the chemostat model

The classical mathematical chemostat model:

$$\begin{aligned} \dot{s} &= - \sum_{j=1}^n \frac{1}{y_j} \mu_j(s) x_j + D (s_{in} - s) \\ \dot{x}_i &= \mu_i(s) x_i - D x_i \quad (i = 1 \cdots n) \end{aligned} \quad (1)$$

for n species in concentrations x_i competing for a substrat in concentration s , leads to the so-called “Competitive Exclusion Principle”, that states that generically no more species than limiting resources can survive on a long term [61]. Apart some very precise laboratory experiments that have validated this principle, such an exclusion is rarely observed in practice.

Several possible improvements of the model (1) need to be investigated, related to biologists’ knowledge and observations, in order to provide better interpretations and predictive tools. Various extensions have already been studied in the literature (e.g. crowding effect, inter-specific interactions, predating, spatialization, time-varying inputs...) to which the team has also contributed. This is always an active research topic in bio-mathematics and theoretical ecology, and several questions remains open or unclear, although numerical simulations guide the results to be proven.

Thanks to the proximity with biologists, the team is in position to propose new extensions relevant for experiments or processes conducted among the application partners. Among them, we can mention: intra and inter-specific interactions terms between microbial species; distinction between planktonic and attached biomass; effects of interconnected vessels; consideration of maintenance or variable yield in the growth reactions; coupling with membrane fouling mechanisms.

Our philosophy is to study how complex or not very well known mechanisms could be represented satisfactorily by simple models. It often happens that these mechanisms have different time scales (for instance the flocculation of bacteria is expected to be much faster than the biomass growth), and we typically use singular perturbations techniques to produce reduced models.

3.1.2. Stochastic and multi-scale models

Comparatively to deterministic differential equations models, quite few stochastic models of microbial growth have been worked out in the literature. Nonetheless, numerous problems could benefit from such an approach (dynamics with small population sizes, persistence and extinction, random environments...).

For example, the need to clarify the role of minority species conducts to revisit thoroughly the chemostat model at a microscopic level, with birth and death or pure jump processes, and to investigate which kind of continuous models it raises at a macroscopic scale. For this purpose, we consider the general framework of Markov processes [59].

It also happens that minority species cohabit with other populations of much larger size, or fluctuate with time between small and large sizes. There is consequently a need to build new “hybrid” models, that have individual-based and deterministic continuous parts at the same time. The persistence (temporarily or not) of minority species on the long term is quite a new questioning spread in several applications domains at the Inra Institute.

Continuous cultures of micro-organisms often face random abiotic environments, that could be considered as random switching between favorable or unfavorable environments. This feature could lead to non-intuitive behaviors in long run, concerning persistence or extinction of populations. We consider here the framework of piecewise deterministic Markov processes [58].

3.1.3. Computer simulation

The simulation of dynamical models of microbial ecosystems with the features described in Section 3.1.2 raises specific and original algorithmic problems:

- simultaneous presence in the same algorithms of both continuous variables (concentration of chemicals or very large populations) and discrete (when the population has a very small number of individuals),
- simultaneous presence in the same algorithms of stochastic aspects (for demographic and environmental noises) and deterministic ones (when the previous noises are negligible at macroscopic scales)
- use of individual-based models (IBM) (usually for small population sizes).

We believe that these questions must be addressed in a rigorous mathematical framework and that their solutions as efficient algorithms are a formidable scientific challenge.

3.2. Identification and control

3.2.1. Models identification and state estimation

Growth kinetics is usually one of the crucial ingredients in the modeling of microbial growth. Although the specific growth rate functions and their parameters can be identified in pure cultures (and can be estimated with accuracy in laboratory experiments), it is often an issue to extrapolate this knowledge in industrial setup or in mixed cultures. The parameters of these functions could change with their chemical and physical environment, and species interactions could inhibit or promote a strain that is expected to dominate or to be dominated in a multi-species ecosystem. Moreover, we need to estimate the state variables of the models.

We aim at developing effective tools for the on-line reconstruction of growth curves (and of their parameters) and/or state variables, along with the characteristics of microbial ecosystems:

- It is not always possible to drive a biological system for exploring a large subset of the state space, and open-loop dynamics could be unstable when far from locally stable equilibria (for instance under inhibition growth).
- The number of functional groups of species and the nature of their interactions (competition, mutualism, neutral) are not always known a priori and need to be estimated.

We look for observers or filters based methods (or alternatives), as well as estimation procedures, with the typical difficulty that for biological systems and their outputs it is rarely straightforward to write the models into a canonical observation form. However, our objective is to obtain an adjustable or guaranteed speed of convergence of the estimators.

3.2.2. Optimal design and control

For practitioners, an expected outcome of the models is to bring improvements in the design and real-time operation of the processes. This naturally leads to mathematical formulations of optimization, stabilizing control or optimal control problems. We distinguish two families of problems:

- *Process design and control within an industrial setup.* Typically one aims at obtaining small residence times for given input-output performances and (globally) stable processes. The design questions consist in studying on the models if particular interconnections and fill strategies allow to obtain significant gains. The specificity of the models and the inputs constraints can lead to systems that are not locally controllable, and thus the classical linearizing techniques do not work. This leaves open some problems for the determination of globally stabilizing feedback or optimal syntheses.
- *Design and control for resource preservation in natural environments (such as lakes, soil bio-remediation...).* Here, the spatial heterogeneity of the resource might be complex and/or not well known. We look for sparse spatial representations in order to apply finite dimensional tools of state-space systems.

In both cases, one faces model uncertainty and partial measurements that often require to couple the techniques developed in Section 3.2.1.

4. Application Domains

4.1. Wastewater treatment systems

The water resources of our planet are limited, and today the quality of drinking water is considered to be responsible of more human deaths than malnutrition. Pollution and over-exploitation of water resources affect almost all the water reservoirs on Earth. Preserving the quality of water has thus become a worldwide problem. The industry of decontamination is thus a necessity, but waste-water treatment is costly and requires large plants. It relies on the use of micro-organisms that concentrate toxic soluble substances into sludge (that can be used as a fertilizer in agriculture). Today, a water decontamination plant costs about 1000 to 5000 euros per inhabitant. 30 to 40% of its running costs are devoted to the energy necessary for pool ventilation.

The waste-water treatment industry use software to optimize the plant design (number, size, interconnections of tanks), but design and improvements of bio-processes remain costly. This is why modelling allows numerical simulations of *virtual* bio-processes that can save substantial amount of money, avoiding tests at a real scale.

There is presently a growing need to conceive treatment systems in a more global framework, including the valorization of the “outputs” such as:

- the biogas production,
- the reuse of treated water for agriculture or dam refill in case of drought.

This requires to re-think the use of the models or to couple them with other models with new outputs and novel criteria to be optimized.

This is our most important domain of transfer and dissemination.

4.2. Environmental microbiology

Chemostat-like models (see Section 3.1.1) are also quite popular in theoretical marine ecology or in soil bio-chemistry, because micro-organisms play again a crucial role in the bio-geo-chemical cycles on Earth. Questioning are here a bit different than the ones depicted in Section 4.1, because it is much more oriented towards comprehension and prediction than decision making (at the present time). Grasping the role of the microbial biodiversity appears to be an everlasting and common important question among scientists of various domains.

Nevertheless, mathematical models are quite similar but with some specificity (much more resources are available in marine microbiology; the spatial heterogeneity play a crucial role in underground processes).

A recent trend of considering natural microbial ecosystems on Earth to be able to delivering new 'eco-systemic services' has emerged, especially in terms of bio-remediation. Modelling and simulating tools are much relevant as in site experiments are quite costly and time-consuming.

4.3. Bioprocesses industry

Several industries use micro-organisms or yeasts to product substances of commercial interest (in pharmaceuticals, green biotechnology, food making...). Novel investigation techniques in microbiology (such as multistage continuous bioreactors) brings new insights on the metabolic functioning of the various strains. This conducts to revisit old models such as Monod's one, and to look for new estimation and piloting strategies. Those questions are quite closed from the ones studied in 4.1 and 4.2, although the ecological dimension is less present (most of the culture are pure ones). The team is naturally solicited to contribute together with the specialists about problems related to modelling, simulation and control of these bio-processes.

5. New Software and Platforms

5.1. Action Depollution

Participant: Alain Rapaport.

Action Depollution is a “serious” game for learning how to purify fast and well a water reservoir, such as lakes. In the scope of the international initiative Mathematics of Planet Earth, this game shows an application of mathematics related to environmental education and sustainable development. The player can act as a researcher, that compares different strategies and looks for the best solution. The conception has been achieved with the Inria project-team LEMON, and the realization with the help of the start-up Funkadelichik, sponsored by the french consortium Cap'Maths.

This work is in connection with the INRA/Inria patent [47] that has been deposited jointly with LEMON Team.

5.2. VITELBIO (VIRtual TELluric BIOreactors)

Participants: Jérôme Harmand, Alain Rapaport.

Vitelbio is a simulator of the microbial activity in soils, for which the spatialization is represented as a network of interconnected reservoirs. The software allows to draw an interconnections graph, that respects the constraint of the maximum flow, and to choose the biological characteristics of various bacterial species in competition for a single nutrient. The simulator computes the time evaluations of the different populations in each compartment, and compares the overall yielding of the ecosystem in terms of bio-conversion of the substrate. This software has been developed in the framework of the INRA/Inria project VITELBIO (VIRtual TELluric BIOreactors), with the help of the company ITK. It is today mainly used for educational purposes (in MSC and PhD lectures).

5.3. Mass-structured chemostat simulators

Participants: Fabien Campillo, Coralie Fritsch.

We developed in Python two pieces of software. The first one aims at simulating a chemostat dynamics with a mass-structured bacterial population: first with an IBM approach, second with a integro-differential equation. The latter approach is using uncentered difference scheme; the former one is stochastic and so needs numerous runs to built empirical representation of the distribution law [27].

The second piece of software is a graphical user interface for the previous one, allowing for runs on remote number cruncher and graphical post-treatment of runs.

The need of reusability of these codes leads us to develop them in an oriented programming framework. This work was done with the help of MISTEA (P. Neveu) and I3M (P. Pudlo).

6. New Results

6.1. Highlights of the Year

Yeasts play a central role in the wine making process. To study the yeasts in a stable environment and physiological state, a Multi-Stage Continuous Fermentor (MSCF) has been designed by the research Unit SPO (Sciences For Oenology). This device mimics the steps of the batch fermentation process. In this paper, the problem of the control of the sugar concentrations in each of the four reactors of the MSCF is considered. The cascade structure of the device leads to a constraint on the input flow rates (the control variables). A control strategy based on a linearizing control law coupled with a state observer and an anti windup component is proposed and finally implemented on the experimental process (see also 6.3.2).

BEST PAPER AWARD :

[41] **Control of a Multi-Stage Continuous Fermentor for the study of the wine fermentation in 19th IFAC World Congress 2014.** C. CASENAVE, D. DOCHAIN, J. HARMAND, M. PEREZ, A. RAPAPORT, J.-M. SABLAYROLLES.

6.2. Mathematical models for microbial ecology

6.2.1. Differential equations models

Participants: Céline Casenave, Jérôme Harmand, Claude Lobry, Alain Rapaport, Alejandro Maximiliano Rojas.

Anaerobic digestion refers to the transformation of biodegradable material by micro-organisms in absence of oxygen (it can be found in waste-water treatments or industrial fermentation, and occurs naturally in soils). It receives an increasing consideration due to recent technological advances, but also because it is a source of renewable energy (bio-gas, fuel...). The anaerobic digestion is a complex set of bio-processes, for which there is a strong expectation of tractable models. We have proposed and studied new mathematical models that takes into account the following features:

- The available anaerobic digestion models used for control purposes do usually only consider soluble matter. In fact, part of the pollutants are not soluble but are under a particulate form. In order to establish whether adding the dynamics of such matter into the models is important for the system behavior or not, we have studied new models and established that depending on the kinetics of this additional reaction step, the qualitative behavior of the process may be significantly modified [26].
- Microbial food chains are present in anaerobic digestion where the different reaction steps can be seen as such: the waste products of the organisms at one trophic level (i.e. one reaction step) are consumed by organisms at the next trophic level (i.e. the next reaction step). In [55] we study a model of a two-tiered microbial ‘food chain’ with feedback inhibition, which was recently presented [63] as a reduced and simplified version of the anaerobic digestion model ADM1 of the International Water Association (IWA). It is known that in the absence of maintenance (or decay) the microbial ‘food chain’ is stable. In [63], using a purely numerical approach and ADM1 consensus parameter values, it was shown that the model remains stable when decay terms are added. In [55] we prove that introducing decay in the model preserves stability whatever its parameters values are and for a wide range of kinetics.

For the study of spatial heterogeneity in the models, we have carried on mathematical analyses of the properties of interconnected chemostats, in particular when growth rates present a substrate inhibition. In addition to the stabilizability properties discovered last year on “buffered” interconnections [33], we have studied this year yielding performances at steady state for the stabilizing configurations and characterized the set of the most efficient ones. For such configurations, we have shown that under certain circumstances, a “by-pass” of the main tank could be the best solution to ensure a global stabilization.

We have also analyzed two kinds of models, suited to specific characteristics of the microbial activity in soils:

- In [30], we have studied analytically and numerically a piece-wise linear model of carbon mineralization by two functional groups of micro-organisms in view of predicting the “priming effect” in soil ecosystems. The conclusion is that under a climate change, the augmentation of $C0^2$ will not affect to primary production and carbon storage when the plants are limited by nitrogen, but surprisingly a higher carbon input in soil should lead to a deplete of sequestered carbon and the increase of nitrogen release.
- In collaboration with Géosciences Rennes (Jean-Raynald de Dreuzy, Tristan Babey) and in the scope of the co-supervision of the PhD of Alejandro Rojas (also in the collaboration within the associated team with Chile), we investigate the equivalence between networks that represent interconnections of mobile/immobile zones in mass transfer models for soil ecosystems. For Structured INteracting Continua (SINC) models, that are described as the combination of a finite number of diffusion-dominated interconnected immobile zones exchanging with an advection-dominated mobile domain, we have proved an equivalence with Multi-Rate Mass Transfer (MRMT) and proposed a method for the identification of the equivalent MRMT model [14]. Moreover, we have shown the role of the controllability properties of a sub-system, in addition to the irreducibility of the network graph, for the input/output equivalence between several representations (work in preparation).

6.2.2. Stochastic and hybrid discrete-continuous dynamical models

Participants: Fabien Campillo, Bertrand Cloez, Coralie Fritsch.

Hybrid mass-structured chemostat models

Within the context of Coralie Fritsch thesis [12], we adopt a new modeling approach where instead of focusing on one type of model we propose different models and their interconnections, on the numerical viewpoint as well as the analytical one. Namely we propose an hybrid model of the chemostat where the population of bacteria is individually-based, each individual being described by its mass, and the substrate concentration is represented as a classic differential equation. We proved the convergence of this model in high population size toward an integro-differential system [20]. We proposed specific numerical schemes for the two approaches (see 5.3) [27].

Evolutionary invasion analysis and simulation for the chemostat

Still in the context of Coralie Fritsch thesis [12] and following her last year stay at the University of Helsinki in Otso Ovaskainen's Research Group, we consider an hybrid mass-structured mass-structured chemostat models with trait. The trait could for example be the factor of mass dissymmetry in the binary fission of a bacteria. In this context we proved an equivalence between invasion fitness for the hybrid-IBM model and the integro-differential system. We also numerically exhibit an evolutionarily singular strategy: with this given trait a monomorphic resident population cannot be invaded by a mutated population; the result is true for the two models.

PDE and stochastic models

In collaboration with M. Joannides and I. Larramendy-Valverde (I3M, University of Montpellier) we consider a stochastic growth model for which extinction eventually occurs almost surely. The associated complete Fokker-Planck equation describing the law of the process is established and studied. In dimension one, e.g. for the stochastic logistic model this equation combines a PDE and an ODE (paper under revision); in dimension two, e.g. for the stochastic chemostat model this equation combines a 2D PDE and a 1D PDE [22]. We then design a finite differences numerical scheme under a probabilistic viewpoint.

6.2.3. Other modeling approaches

Participants: Anne Bisson, Jérôme Harmand, Alain Rapaport.

A collaboration with the UMR Eco & Sols has led to the development of a (static) probabilistic model for inferring nature and number of interactions in communities assembly [29]. This model has brought new insights on a data set from reconstituted soil ecosystems. Because of the curse of dimensionality, we have begun this year to extend this approach to “assembling motifs” instead of considering all the possible assemblages (paper in preparation).

In [28], ecological trade-offs between species are studied to explain species coexistence in ecological communities. In our model, plant species compete for sites where each site has a fixed stress condition. Species differ both in stress tolerance and competitive ability. We derive the deterministic discrete-time dynamical system for the species abundances. We prove the conditions under which plant species can coexist in a stable equilibrium. We compare our model with a recently proposed, continuous-time dynamical system for a tolerance-fecundity trade-off in plant communities, and we show that this model is a special case of the continuous-time version of our model.

6.3. Analysis and supervision of bioprocesses

6.3.1. Models development and identification

Participants: Fabien Campillo, Amine Charfi, Yessmine Daoud, Jérôme Harmand, Sonia Hassam, Guilherme Pimentel, Alain Rapaport.

Membrane bioreactors combine a filtration process (with a membrane) and a suspended growth rate bioreactor. This recent technology present many advantages compared to conventional ones, but is more sophisticated and requires refined control because of the fouling process. We have proposed new modeling approaches of such bioreactors, where a fouling mechanism is explicitly described:

- Membrane bioreactors allow a perfect separation of biomass and treated waters. However, membranes are subject to clogging - also called fouling - by large organic molecules and solids (biomass, suspended solids, etc...). This phenomenon represents the main problem that limits the development of membranes bioreactors. It is well documented but very studies tried to formalize it under the form of dynamical model, even more under anaerobic conditions. This is what we did in the framework of Amine Charfi's PhD [11]: he contributed to a better understanding of membrane fouling dynamics and proposed a number of strategies to avoid irreversible clogging [24], [25].
- In the scope of the PhD supervision of Guilherme Pimentel, we have proposed a simple three time scales model in view of the control of the cake formation [13], [37]. This model has been validated on real data from a pilot plant at Univ. Mons (Belgium).

As already mentioned in 6.2.1, anaerobic bioreactors are able to produce valuable energy. However, they are subject to destabilization in case of organic overload. It is thus necessary to develop appropriate models dedicated to the synthesis of stabilizing control feedbacks. Two strategies are followed to obtain such models. Either simple models are proposed from the knowledge we have about the process, either reduced models are obtained from more complex ones. Yessmine Daoud just began her PhD thesis following the first strategy: more precisely, we study simple inhibition models of the anaerobic digestion and tries to establish simple equivalence between these models and the well known ADM1 model. Sonia Hassam, in her PhD, works within the framework of the second strategy to propose simple models obtained in reducing complex ones like the ADM1.

As already proposed last year, we have set a methodology to identify from data observed on a chemostat plant a multi-specific model that suits better than a mono-specific one, when data from molecular biology are available. In [35], we combine molecular fingerprints obtained at some discrete times (such as the ones provides by the DGGE or SSCP techniques) with on-line macroscopic measurements. In a similar spirit, within the framework of a collaboration with the LOMIC at Banyuls, we have analysed molecular data obtained via SSCP technique to monitor the structure of microbial communities. It was shown that aerial transport of bacteria from desert into the sea influenced its bacterial diversity [32], [31].

As far as stochastic approaches are concerned, the thesis of Mohsen Chebbi aims at developing stochastic models of membrane bioreactors following the approach proposed in [57]. A mathematical and simulation framework has been established, as well as the bases of vectorial simulation techniques in `Matlab`. Developments of Monte Carlo techniques for the identification of bioprocesses are investigated in the thesis of Oussama Hadj-Abdelkader, improving classical particle filtering approaches (sequential Monte Carlo) by integrating MCMC (Monte Carlo Markov Chain) procedures. A software approach has been adopted in `C++`.

6.3.2. *Synthesis of control laws*

Participants: T erence Bayen, Walid Bouhafs, C eline Casenave, Amel Ghouali, J er me Harmand, Zeyneb Khedim, Claude Lobry, Alain Rapaport, Victor Riqueleme, Matthieu Sebbah.

We investigate two kinds of bioprocesses to be controlled, arising in industrial biotechnology (digesters, wastewater purification...) or in the bioremediation of natural environments (lakes, landfill...).

6.3.2.1. *Industrial biotechnology*

As it is often the case in industry, we distinguish two kinds of process operating: continuous processes, for which the volumes of the bio-reactors are constant, and fed-batch processes, for which the filling rate is the control.

We tackle several optimal control problems related to the maximization of productivity of continuous bioprocesses:

- As far as anaerobic digestion is concerned, we have considered an optimal control problem for the chemostat model with substrate inhibition. The originality of this problem relies on the fact that the quantity to be maximized is not simply a state of the model (the substrate or the biomass) but the volume of biogas produced (which is a nonlinear function of the state) within a given time interval. Optimal strategies have been proposed for a class of initial conditions of the system (PhD thesis of Amel Ghouali). Other optimal control problems are studies by Walid Bouhafis to establish the optimality of controls initially proposed by Djalel Mazouni, a former PhD candidate supervised by the team. Using a tricky projection of the problem into another state space, he has shown that the problem of optimizing the degradation of two different substrates by two antagonist bacterial communities could be solved in a very general sense as the minimization of a specific functional for a very large class of nonlinear systems [19].
- The work [15] arises in the context of selection of species (widely used in agriculture and biotechnology in order to improve productivity). For microorganisms, the selection process can be based on genetic tools. Our methodology in [15] is to drive the competition between species in a chemostat. We consider a two species chemostat model with one limiting substrate, and our aim is to optimize the selection of the species of interest. Thanks to the Pontryagin Maximum Principle, we introduce a singular feeding strategy which allows to reach the target, and we prove that the feedback control provided by this strategy is optimal. The optimal synthesis of the problem in presence of more than two species will be investigated in a future work.
- In [38], we study the problem of minimal time for a chemostat system with one limiting substrate and one species. Given a target point, the problem consists in finding an optimal feeding strategy steering any initial condition of the system to this target. This is typically of interest whenever the input substrate concentration changes yielding in a new steady state. We consider the case where the growth rate function is of Haldane type implying the existence of a singular arc that is non-necessary admissible everywhere. We provide an optimal synthesis of the problem using tools from optimal control theory.
- The work [16] studies the coupling of a culture of micro-algae limited by light and an anaerobic digester in a two-tank bioreactor (the model combines a periodic day-night light for the culture of micro-algae and a classical chemostat model for the digester). We first prove the existence and attraction of periodic solutions of this problem for a one day period. Then, we study the optimal control problem of optimizing the production of methane in the digester during a certain time frame, the control on the system being the dilution rate (the input flow of micro-algae in the digester). We also investigate the dependence of the optimal cost with respect to the volume ratio of the two tanks.

In collaboration with researchers of the unit SPO (Sciences For Oenology), we have proposed a control law of a multi-stage continuous fermentor (MSCF) designed for the study of the wine fermentation, that has been implemented on the experimental process [41]. We have also finalized the controllability analysis and minimal time feedback synthesis of models of cascade of continuous bioreactors under input constraints [18], [40] (that is also related to the control of MSCF).

As far as fed-batch processes are concerned, an extension of former results of the team about the minimal time control of fed-batch processes with impulse controls is presented in [34],

The paper [17] is devoted to the study of the minimal time problem of a fed-batch reactor, under the presence of a saturation point on the singular locus (this typically occurs whenever the growth rate function is of Haldane type and when typically the maximum input flow rate is not high enough to maintain the substrate concentration constant). This brings non-intuitive issues for the optimal synthesis (existence of switching curve and point of prior saturation).

6.3.2.2. Bioremediation of natural environments

In the scope of the associated team with Chile and the supervision of the postdoctoral stay of Matthieu Sebbah in Chile, we have addressed a new model of landfill remediation when controlling the leachate recirculation [53]. We have applied the same methodological approach than the one for the work [18], [40] mentioned in the previous section, which consists in characterizing first the sub-domains for which the target can be optimally reached with a constant extreme control (no recirculation or maximal speed of recirculation), and further the nature of optimal commutations outside these sets. This analysis provides information for the practitioners on the benefit to implement sensors and real-time controllers.

Also in the scope of the associated team with Chile (see 7.3.2.1) and the co-supervision of the PhD of Victor Riquelme, we have carried on the study of optimal syntheses for the minimal time treatment of natural water reservoirs (such as lakes) [52]. We have proved that the minimal time strategy consists in a most-rapid approach to homogeneous concentrations, even though the optimal control problem is non convex. Moreover, we have shown that a large diffusion increases the treatment time when the resource is everywhere highly polluted, while it can at the opposite be beneficial when only part of the resource is polluted. This feature should serve the practitioners in the choice of pumps positioning in a originally clean water resource that is suddenly affected by a local pollution. This work is in connection with the INRA/Inria patent [47] that has been deposited jointly with LEMON Team.

6.4. Other application domains

Participants: Fabien Campillo, Céline Casenave.

Semi-Markov land use dynamic

With IRD (GRED Montpellier) and the Univ. of Fianarantsoa (Madagascar) we pursued our study on land use dynamics models corresponding to parcels located on the edge of the forest corridor, Madagascar. We use semi-Markov chain to infer the land-use dynamics. In addition to the empirical and maximum likelihood methods, we estimate the semi-Markov kernel by a Bayesian approach [21].

Ice cream crystallization

We study the problem of the control of an ice cream crystallization process, part of the European CAFE project, in collaboration with CESAME (Univ. Catholique de Louvain-la-neuve), Irstea Antony and AgroParisTech. The goal is to control the viscosity of the ice cream at the outlet of the continuous crystallizer. On the basis of a population balance equation describing the evolution of the crystal size distribution of the ice cream, and an energy balance equation, we have proposed an input-output reduced order model of the process, that has been identified and validated on experimental data [23]. A nonlinear control strategy based on an adaptive linearizing control law coupled with a Smith predictor to account for the measurement delay has been proposed, and validated on the experimental pilot plant (paper in preparation).

7. Partnerships and Cooperations

7.1. Regional Initiatives

7.1.1. Labex Numev

Within the Labex Numev (Solutions Numériques, Matérielles et Modélisation pour L'Environnement et le Vivant ¹), the team is the coordinator since 2012 of a working group on Modelling and numerical probabilities for ecology and biology with Univ. Montpellier II, Univ. Montpellier I and CNRS ISEM.

A one day workshop on "Stochastic Models for Biology" has been organized in January with Pierre Pudlo (Univ. Montpellier II). The invited speakers were Nicolas Champagnat (Inria/Institut Élie Cartan), Jean-François Delmas (Ecole des Ponts ParisTech – CERMICS), and Michel Benaïm (Université de Neuchâtel).

¹<http://www.lirmm.fr/numev>

7.1.2. Inter-teams seminar

J. Harmand is the coordinator of the inter-teams seminar about the modelling of bioprocesses ², involving the labs INRA-LBE (Narbonne), UMR LISPB (Toulouse) and the two Inria project teams BIOCORE and MODEMIC.

A. Rapaport has been invited to participate to the “Séminaire au vert” of BIOCORE team in November 2014.

7.2. National Initiatives

7.2.1. RNSC project “MnMs”

The MnMs ³ (Numerical Models for Microbial ecosystems) project has been funded by the RNSC (National Network on Complex Systems) in 2013 for two years.

It aims at studying how to articulate existing models (discrete, continuous, deterministic, stochastic...) in a multi-scale framework with interactions between various scales. The team has been the coordinator and the other partners were Irstea LISC (Clermont-Ferrand) and CNRS/UMPC LPMTIC (Paris VI).

7.2.2. Inria Project Lab “Algae in Silico”

MODEMIC is a partner of the proposal of the Inria Project Lab *Algae in Silico* launched last year by BIOCORE Inria project-team.

7.2.3. INRA-CEPIA project “New perspectives for the MSCF”

The project entitled *Multi-Stage Continuous Fermentor (MSCF): Study of fermentation with disturbances, and development of a control law* has been funded in 2013 by the INRA Dept. CEPIA for two years, in which the Montpellier Units SPO and Mistea are involved.

It is the continuation of the work initiated within the former European CAFE project about the control of a wine fermentation process. The goal of this project is to study the fermentation with nitrogen addition. From a control point of view, we study how to regulate both the sugar concentration and the CO_2 production rate in a series of four tanks of a MSCF, that mimics in continuous culture four important physiological states of a batch fermentation.

7.2.4. PGMO “OPTIBIO”

OPTIBIO (New challenges in the optimal control of bioprocesses) is a new project funded by the french Foundation FMJH (Fondation Mathématique Jacques Hadamard) in 2014 for three years, within the program PGMO (Gaspard Monge Program for Optimization and operations research).

The project is coordinated by T. Bayen (ACSIOM, Univ. Montpellier II) and the other partners are: MODEMIC, Univ. Limoges, EPI COMMANDS (Saclay) and EPI BIOCORE (Sophia Antipolis).

The overall objective of this project is to address the optimization of bioprocesses over an *infinite horizon*. Infinite horizon optimal control is well suited for every problem where the time horizon is uncertain and can be expected to be large: e.g. economics models related to optimal growth and sustainable development, biological models such as the optimal control of interacting species and pest control, stabilization of controlled mechanical systems...The recent expectations of sustainable development raise new optimization problems that take into account auxiliary outputs, such as biogas production, that were neglected in the past. It appears that mathematical problems that come from the modelization of these processes are often difficult to solve, and one objective of the proposal is to develop new mathematical methods in order to address these issues. More precisely, the objective of the project is to study the following issues:

- Optimization of bioprocess over an infinite horizon.
- Development of accurate methods in order to deal with uncertainties that affects the chemostat model (uncertainties come from unknown parameters or noise from the measurements).
- Stabilization of the chemostat model including delay in the system.

²<https://sites.google.com/site/journeesthematiquesdulbe/>

³<http://www-sop.inria.fr/members/Fabien.Campillo/projects/mnms>

7.2.5. INRA-MIA methodological networks

The team is involved in two new networks of the MIA (Applied Mathematics and Informatics) Department of INRA:

- MEDIA ⁴ (Modèles d'Équations Différentielles et Autres systèmes dynamiques pour l'écologie),
- REM ⁵ (RÉduction de Modèles),

that have been launched this year.

7.3. International Initiatives

7.3.1. Inria International Labs

Within the BioNature ⁶ operation program of CIRIC Center (Inria Chile), the team participates to the axis *Modeling, control and optimization of waste-water treatment processes and biogas production*, and more specifically to the research lines

- automation and control of anaerobic digestion,
- innovative technologies and modeling on wastewater and residues treatment.

In this framework, the team has co-supervised the postdoctoral stay of. M. Sebbah in Chile.

7.3.2. Inria Associate Teams

7.3.2.1. DYMECOS2

Title: Modelling of microbial ecosystems, bioprocesses control and numerical simulations

International Partner (Institution - Laboratory - Researcher):

Departamento de Ingeniería Matemática (DIM), Universidad de Chile

Centro de Modelamiento Matemático (CMM), UMi CNRS/ Universidad de Chile

Departamento de Matematica, Universidad Tecnica Federico Santa Maria (UTFSM), Valparaiso (Chile)

Bionature, CIRIC, Inria Chile

Duration: 2014-2016

See also: <https://sites.google.com/site/eadymecos/>

The objective is to develop, from expert knowledge and experimental observations, models of microbial ecosystems that are simple enough to carry out the determination of explicit "control laws", and realistic enough to represent real bio-processes. One of the difficulties is to identify the limits of the validity of these models, in terms of spatial heterogeneity and microbial population size.

We aim also outcomes of the modeling for the optimal design of waste-water treatment plants.

7.3.3. Inria International Partners

7.3.3.1. Declared Inria International Partners

LIRIMA NuWat ⁷ 2013-... (Tlemcen, Algeria and Tunis, Tunisia). NuWat focuses on the numerical Modeling and simulation of microbial ecosystems and their application in biotechnology with a focus on solutions considered as promising for countries of the Maghreb, for instance in waste-water treatment systems and its reuse in agriculture under semi-arid climates. NuWat handles the two following related topics: (1) the elaboration of numerical hybrid models for simulation of bacterial ecosystems combining discrete models (for small size populations) and continuous models (for large size populations, substrate and environment); (2) the systematic numerical and software development for biotechnology process control. The project was initially developed in collaboration with the Univ. of Tlemcen but is now extended to the ENIT in Tunis, with an extension of the domain of application to system biology and biotechnologies.

⁴<http://www.netvibes.com/reseaumiamedia>

⁵<https://sites.google.com/site/reseaurem2/>

⁶<http://www.bionature.cl>

⁷<https://project.inria.fr/nuwat/>

7.3.3.2. Informal International Partners

CESAME, Univ. Louvain, Belgium : D. Dochain
 3BIO, Univ. Mons, Belgium : A. Vande Wouwer
 Univ. Neuchâtel, Switzerland : M. Benaim
 MOMAT, Univ. Madrid, Spain : B. Ivorra
 Univ. Newcastle, U.K. : M. Wade

7.3.4. Participation In other International Programs

7.3.4.1. CIB (Centre Interfacultaire Bernoulli)

Program: Bernoulli workshops

Title: The role of mathematics and computer science in ecological theory

Inria principal investigator: MODEMIC (C. Lobry),

Partners: EPFL, Lausanne (Switzerland).

Duration: July 1 to December 31, 2014

Abstract: A former collaboration of Inria with ecologists (the COREV network presently animated by R. Arditi) initiated (at the beginning of the 90s) by J-L. Gouzé and C. Lobry within the framework of the Inria project team COMORE, pursued then by MERE and COMORE raised an important event: the half-year *Mathematics and computer sciences in theoretical ecology* which we co-organize with R. Arditi (associated with D. de Angelis and L. Ginzburg) at the Federal Polytechnical School of Lausanne (Centre Interfacultaire Bernoulli).

The program lasted from July 1 to December 31, 2014. It gathered about 90 participants among them very well known scientists from Theoretical Ecology (S. Allesina, D. de Angelis, P. Chesson, J. Damuth, L. Ginzburg, R. Holt...) and from Mathematics (M. Benaïm, N. Berglund, M. and F. Diener, M. Krupa, A. Lam, W.M. Ni...).

Six one-week workshops were organized (one each month) on the following topics:

- Non-adaptive selection: explaining macroscopic laws in ecology and evolution (Organizers: L. Ginzburg, R. Arditi, L.-F. Bersier).
- Dispersal and competition of populations and communities in spatially inhomogeneous environments (Organizer: D. DeAngelis).
- Validation of uncertain ecological models with imprecise data (Organizer : S. Ferson)
- Discrete, explicit simulations versus continuous, aggregated models (Organizers: R. Arditi, C. Lobry, Y. Tyutyunov).
- Multi-scale models, slow-fast differential equations, averaging in ecology (Organizers: M. Desroches, O. Faugeras, C. Lobry, T. Sari).
- Microbial ecology and mathematical modelling (Organizers : R. Arditi, J.J. Godon, J. Harmand, C. Lobry)

The third workshop was organized in collaboration with O. Faugeras (EPI Neuromathcomp, Sophia-Antipolis) and M. Desroches (EPI MYCENAE, Rocquencourt) and tried to find connections between neurosciences and theoretical ecology through mathematical models.

Web-site: <http://mathcompecol.epfl.ch/>

7.3.4.2. TREASURE

Program: **Euromediterranean 3+3**

Title: Treatment and Sustainable Reuse of Effluents in semiarid climates

Inria principal investigator: MODEMIC (J. Harmand),

Partners: Centre de Biotechnology de Sfax, Department of environmental engineering (Tunisia), Ecole Nationale des Ingénieurs de Tunis, Dept. de Mathématiques (Tunisia), Institut National de la Recherche Agronomique, Dept. EA, MICA et MIA (France), National Research Center, Water Pollution Control (Egypt), University of Patras, Process Control Laboratory (Greece), University of Tlemcen, Automatic control (Algeria), University of santiago de compostella, Environmental engineering (Spain) Université Cadi Ayyad de Marrakech, Faculté des Sciences de Semlalia, Dépt. de Mathématiques (Morocco), Centre National de Recherche sur l'Eau et l'Energie, Université Française d'Egypte (Egypt)

Duration: Jan 2012 - Dec 2015

Abstract: The TREASURE network aims at integrating knowledge on the modelling, the control and the optimization of biological systems for the treatment and reuse of waste-waters in countries submitted to semi-arid climates under both socio-economical and agronomic constraints within the actual context of global changes. A special focus of the actual project concerns the integration of technical skills together with socio-economical and agronomic studies for the integrated solutions developed within the network to be evaluated and tested in practice in the partner's countries and, as possible as it may be within the context of the actual research network, valorizing these proposed technologies with the help of industrial on site in partners from South.

Web-site: <https://project.inria.fr/treasure>

7.3.4.3. TASSILI

Program: Hubert Curien Program

Title: Procédés membranaires pour le traitement anaérobie des eaux usées - Modélisation, commande et optimisation

Inria principal investigator: MODEMIC (J. Harmand),

Partners: LBE-INRA (Narbonne), Univ. Tlemcen (Algeria)

Duration: 3 years

Abstract: This project aims at promoting collaborations with our historical Algerian partners of the department of automatic control of the University of Tlemcen. The objectives of the project are to develop research on the modeling and the control of anaerobic systems through the co-advising of Zeyneb Khedim (PhD 'co-tutelle' between UM2 and Univ. Tlemcen).

7.4. International Research Visitors

7.4.1. Visits of International Scientists

Imme Van Den Berg

Subject: Construction, analysis and simulation of population dynamics models

Date: until Feb. 2014

Institution: Univ. of Evorra (Portugal)

7.4.1.1. Internships

Moshen Chebbi

Subject: Stochastic modeling for membrane bioreactors

Date: from Sep 2014 until Nov 2014

Institution: ENIT, Tunis (Tunisia)

Alejandro Rojas-Palma

Subject: Study of some problems related to modelling and optimization of bioprocesses

Date: from Oct 2014 until dec 2014

Institution: Univ. of Chile

Victor Riquelme

Subject: Optimal control for the preservation of exploited water resources

Date: from Nov 2014 until Jan 2015

Institution: Univ. of Chile

7.4.2. Visits to International Teams

7.4.2.1. Research stays abroad

C. Lobry has spent one semester (July-December 2014) at CIB, EPFL (Lausanne, Switzerland) for the co-organization of the Bernoulli workshop on the role of mathematics and computer science in ecological theory (see 7.3.4.1).

B. Cloez has spent one month (November-December) in Switzerland at Univ. Neuchâtel and at CIB-EPFL, Lausanne.

8. Dissemination

8.1. Promoting Scientific Activities

8.1.1. Scientific events organization

8.1.1.1. member of the organizing committee

C. Lobry has been coordinator of six one-week “Bernoulli” workshops (see 7.3.4.1).

F. Campillo was co-organiser of a workshop on “Stochastic Models for Biology”, see Section 7.1.1.

C. Casenave and F. Campillo were in the organizing committee of the meeting of the MIA⁸ Division of INRA in March 2014, and have organized a session on “spatio-temporal models and methods”.

8.1.2. Scientific events selection

8.1.2.1. reviewer

European Control Conference, IFAC World Congress, IEEE Conference on Decision and Control.

8.1.3. Journal

8.1.3.1. reviewer

Automatica, BioMath, Bulletin of Mathematical Biology, Computers and Mathematics with Applications, Differential Equations and Dynamical Systems, J. of Advances Research in Differential Equations, J. of Biological Dynamics, J. of Process Control, Math. Biosciences and Eng.

8.2. Teaching - Supervision - Juries

8.2.1. Teaching

Engineering degree

A. Rapaport, “Introduction to modelling”, 12 hours, 1st year, SupAgro Montpellier.

Master

F. Campillo, “Stochastic modelling of ecosystems”, 20 hours, Master 2 in Biostatistics, Univ. Montpellier II.

A. Rapaport, “Practical Mathematics”, 27 hours, Master 1 in Mathematics, Univ. Montpellier II.

PhD

⁸<http://www.mia.inra.fr/>

F. Campillo and C. Fritsch, “Object oriented programming: probabilistic modeling and statistical numerics for biology”, 20 hours, Doctoral lectures, Univ. Montpellier II.

C. Casenave and A. Rapaport, “Modelling for biology and ecology, mathematical and computational methods”, 20 hours, Doctoral lectures, Univ. Montpellier II.

8.2.2. Supervision

Amine Charfi

PhD: Etude d’un procédé membranaire de traitement des eaux usées : effet des paramètres biotiques et abiotiques sur le colmatage de la membrane.

Univ. Carthage, Dec. 2014.

Advisors: N. Ben Amar (ENIT-LAMSIN, Tunis) and J. Harmand.

Coralie Fritsch

PhD: Simulation et analyse de modèles individu-centrés d’écosystèmes bactériens pour des procédés biotechnologiques.

Univ Montpellier II, dec. 2014.

Advisors: F. Campillo and J. Harmand.

Walid Bouhafs

PhD in progress: Commande optimale des réacteurs biologiques séquentiels discontinus.

ENIT (Tunis), since 2010.

Advisors: N. Abdellatif (ENIT-LAMSIN, Tunis), F. Jean (ENSTA) and J. Harmand.

Sonia Hassam

PhD in progress: Réduction de modèles biotechnologiques : application à la digestion anaérobie.

Univ. Tlemcen, since 2011.

Advisors: B. Cherki (Univ. Tlemcen) and J. Harmand.

Amel Ghouali

PhD in progress: Analyse et commande optimale d’un bioréacteur de dépollution des eaux usées

cotutelle Univ Montpellier II/Univ. Tlemcen (Algeria), since Nov. 2011.

Advisors: J. Harmand and T. Sari (UMR ITAP, Montpellier).

Guilherme Pimentel

PhD in progress: Modélisation dynamique, analyse et supervision d’un réacteur membranaire.

cotutelle Univ. Montpellier II/Univ. Mons (Belgique), since Nov. 2011. Defense scheduled in Feb. 2015.

Advisors: A. VandeWouwer (Univ. Mons) and A. Rapaport.

Victor Riqueleme

PhD in progress: Commande optimale pour la préservation de ressources hydriques exploitées.

cotutelle Univ. Montpellier II/Univ. Chile, since Sept. 2013.

Advisors: H. Ramirez (Univ. Chile) and A. Rapaport.

Alejandro Rojas-Palma

PhD in progress: Etude de quelques problèmes dans la modélisation et l’optimisation de bioprocédés.

cotutelle Univ. Montpellier II/Univ. Chile, since Sept. 2014.

Advisors: H. Ramirez (Univ. Chile) and A. Rapaport.

Yessmine Daoud

PhD in progress: Analyse de modèles de la digestion anaérobie : application à l'optimisation de la production du biogaz.

cotutelle ENIT (Tunis)-Univ. Montpellier II, since sep. 2014.

Advisors: N. Abdellatif (ENIT, Tunis) and J. Harmand.

Mohsen Chebbi

PhD in progress: Modélisation stochastique de procédés membranaires de traitement des eaux usées.

ENIT (Tunis) , since sep. 2014.

Advisors: S. Toumi (ENIT, Tunis) and F. Campillo.

Oussama Hadj-Abdelkader

PhD in progress: Filtrage particulaire pour le chemostat.

Univ. Tlemcen, since sep. 2014.

Advisors: A. Hadj-Abdelkader (Univ. Tlemcen) and F. Campillo.

Zeyneb Khedim

PhD in progress: Modélisation et contrôle de la digestion anaérobie : vers une meilleure prise en compte des phénomènes d'inhibition.

cotutelle Univ. Tlemcen - Univ. Montpellier II, since nov. 2014.

Advisors: B. Benyahia (Univ. Tlemcen) and J. Harmand.

Anne Bisson

PhD in progress: Modélisation probabiliste du fonctionnement d'écosystèmes considérés comme des assemblages de communautés.

Univ. Montpellier II, since Dec. 2014.

Advisors: B. Jaillard (UMR Eco & Sols, Montpellier) and A. Rapaport.

The team has supervised the MsC and Engineering School internships [49], [50], [51], [54], [56].

8.2.3. *Juries*

M. Abouzlam. "Optimisation d'un procédé de traitement des eaux par ozonation catalytique", Thèse de Doctorat, Univ. Poitiers, Jan. 2014 (referee : J. Harmand).

Y. Chen. "Inférence bayésienne dans les modèles de croissance de plantes pour la prévision et la caractérisation des incertitudes", Thèse de Doctorat, Ecole Centrale, Paris, Jun. 2014 (referee : F. Campillo).

H. Sedrakyan. "Comportement limite des systèmes singuliers et les limites de fonctions valeur en contrôle optimal", Thèse de Doctorat, Université Paris VI, Dec. 2014 (referee : T. Bayen).

G. François. "Optimisation en temps Réel : Optimiser les Performances des Procédés Chimiques malgré l'Incertain et les Erreurs de Modélisation", Habilitation à diriger des recherches, Univ. Lorraine, Dec. 2014 (referee : A. Rapaport).

S. Martin. "D'oxymore en oxymore : du développement durable au contrôle complexe." Habilitation à diriger des recherches, Univ. B. Pascal, Jan 2015 (referee : A. Rapaport).

8.3. Popularization

Jointly with Inria project-team LEMON, MODEMIC has participated to the elaboration of a "serious" game for learning how to purify fast and well a water reservoir, in the scope of the international initiative Mathematics of Planet Earth and the french consortium Cap'Maths (see 5.1).

8.4. Institutional commitment

F. Campillo is member of the NICE Inria committee (long term invited scientists selection); deputy elected member of the Inria Scientific Council; member of the internal communication working group of Inria for the redesign of the national intranet; member the “support group to researchers” of Inria Sophia Antipolis.

J. Harmand is member of the steering committee of the Inra/MEM meta-program (Métagénomique des écosystèmes microbiens); member of the EA department of Inra; member of the “commissions scientifiques spécialisées” STEA-Inra.

A. Rapaport is member of the scientific committee of BIOS dept. of CIRAD, and is member of the scientific committee of Ecotechnologies department of Irstea.

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