IN PARTNERSHIP WITH:
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Activity Report 2013

Project-Team MODEMIC

Modeling 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
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THEME
Modeling and Control for Life Sciences

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Project-Team MODEMIC

Keywords: Microbial Ecology, Population Dynamics, System Analysis And Control, Multiscale Models, Individual-based Models

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

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2. Overall Objectives

2.1. Introduction

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.

2.4. Highlights of the Year

A lectures program submitted by the team and R. Arditi (AgroParis Tech) entitled “Mathematics, Computer sciences and Theoretical Ecology” has been accepted by the “Centre Interfacultaire Bernoulli” at EPFL (Lausanne, Switzerland) for a semester in 2014 (see Section 7.4.3.2).

A patent has been deposited jointly with Moise/Lemon Inria project-team concerning an algorithm for “intelligent” pumps, that provides an efficient treatment of natural water resources [69].

3. Research Program

3.1. Modeling and simulating microbial ecosystems

The chemostat apparatus is quite popular in microbial ecology and bio-process engineering [79], and well adapted to modeling. 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 hybride representations. One important question is the interconnection between these chemostat models (see Section 3.1.2) ([1]).

3.1.1. About the chemostat model

The classical mathematical chemostat model:

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

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 [78]. 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...) 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, mutation...). 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. We adopt the approach proposed by Ethier and Kurtz [76].

[1] Modemic tends to use the term "chemostat" (or chemostat model) for the mathematical/computer models to avoid confusion with the biotechnological apparatus also known as chemostat, that we will call chemostat apparatus or device in this activity report.

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.

3.1.3. Simulation algorithms

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 an 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 modeling 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 biogaz production, and 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 heterogeneities play a crucial role in underground processes).

A recent trend of considering natural microbial ecosystems on the Earth to be able to delivering new “eco-systemic services” has emerged, especially in terms of bio-remediation. Modeling 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 pharmaceutics, green biotechnology, food making...). Novel investigation techniques in microbiology (such as multistage continuous bioreactors) bring new insights on the metabolic behavior 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 to those studied in Sections 4.1 and 4.2, although the ecological aspct is less present (most of the culture are pure ones). The team is naturally asked to contribute together with the specialists to problems related to modeling, simulation and control of these bio-processes.

5. Software and Platforms

5.1. SMC Demos (Sequential Monte Carlo demos)

Participant: Fabien Campillo.

SMC Demos proposes a set of demonstration Matlab procedures for nonlinear filtering approximation via particle filtering (sequential Monte Carlo): bearing-only tracking with obstacles, tracking in digital terrain model, track-before-detect in a sequence of digital picture, mobile phone tracking based on the signal strength to nearby antenna. This software is deposited with the "Agence pour la Protection des Programmes" (APP, 7/7/2009) [[2]].

5.2. IBM Cellulose

Participant: Fabien Campillo.

In the context of the DISCO/ANR and MnMs/RNSC projects (see Sections 7.2.1 and 7.2.2), in collaboration with Ariane Bize (Irstea), the team has developed an individual-based model for the degradation of one cellulose bead (dozens of micrometers in diameter) by cellulolytic bacteria [[3]].

5.3. VITELBIO (VIrtual TELluric BIOreactors)

Participants: Jérôme Harmand, Alain Rapaport.

VITELBIO is a simulation tool for studying networks of interconnected chemostat models with the objective of mimicking microbial activities in heterogeneous media, such as the soil. This software, that has been developed with the help of ITK Company, is accessible on a server from any web navigator [[4]] and makes use of Flex for the user interface and Octave for the numerical integration. It is is no longer maintained but serves as a teaching support.

6. New Results

6.1. Macroscopic models

6.1.1. About species coexistence

Participants: Fabien Campillo, Jérôme Harmand, Claude Lobry, Alain Rapaport, Tewfik Sari.

The so called "Principle of Competitive Exclusion" states that in the chemostat model, in presence of p substrates only p species can coexist. By contrast, in a bioreactor used for decontamination, hundreds to thousand different species are observed in presence of just very few substrates. Actually the classical chemostat models rely on assumptions: perfect mixing, substrate-dependent growth rate, constant environment, only asymptotic results are considered, deterministic continuous models...

A long term objective since Mere Inria project-team is to revisit the chemostat model in the absence of one or more of these hypotheses having in view the question of coexistence. In our "major publications" we proved coexistence in absence of the second hypothesis [6] or during long transient [9]. In [57], we consider the case where the environment (in some sense) is periodic in time. Our results concerning non continuous and/or stochastic models (see Section 6.2.3) are also a first step in avoiding the fifth hypothesis.

6.1.2. Modeling and analysis of bioprocesses

Participants: Boumédiène Benyahia, Radhouane Fekih-Salem, Jérôme Harmand, Claude Lobry, Guilherme Pimentel, Alain Rapaport, Tewfik Sari.

[2] http://www-sop.inria.fr/members/Fabien.Campillo/software/smc-demos/
[3] http://www-sop.inria.fr/members/Fabien.Campillo/software/ibm-cellulose/
[4] https://sites.google.com/site/vitelbio/logiciel

Within the supervision of the PhD thesis of R. Fekih-Salem, we have studied a chemostat model where the species are present in two forms, isolated and aggregated individuals, such as attached bacteria in biofilm or bacteria in flocks [22]. We show that our general model contains a lot of models that were previously considered in the literature [77]. Assuming that flocculation and deflocculation dynamics are fast compared to the growth of the species, we construct and analyse a reduced chemostat-like model in which both the growth functions and the apparent dilution rate depend on the density of the species.

Within the framework of the PhD thesis of B. Benyahia, we have included the fouling dynamics of membranes into the AM2 (or AMOCO) model and we have analyzed the resulting model (called the AM2b) [15]. In particular, we have integrated into this model the production and the degradation of Soluble Microbial Products (SMP), which are known to play an important role in the membrane fouling phenomenon. We show that under some general assumptions, the AM2b model has the same number of equilibria as the AM2 model and can exhibit bi-stability. However, under certain operating conditions or if biological parameters values are slightly modified, the AM2b model exhibits equilibria bifurcations and multi-stability properties.

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 anaerobic models and established that depending on the kinetics of this additional reaction step, the qualitative behavior of the process may be significantly modified [44].

This year, G. Pimentel as started a PhD co-supervised with the University of Mons, about modeling of the membrane fouling in bioreactors in view of control. The objective is to represent cake formation and air cross-flow as a manipulated variable in the models, in view of future studies of control strategies for improving the efficiency of MBR processes [35], [47], [52], [53].

6.1.3. Ecosystem functioning in heterogeneous environments

Participants: Céline Casenave, Jérôme Harmand, Alain Rapaport.

This year, we have carried out a study of particular spatial interconnections such as “buffered” configurations, and its ecological impacts in terms of setup of a species in environments that are unfavorable when perfectly mixed. We have extended our previous results about the design of configurations for obtaining a global stability [28]. New conditions have been obtained for a species to setup when it is impossible in a perfectly mixed environment. At the opposite, we have characterized configurations that could destabilize bioprocesses.

With UMR Géosciences (Univ. of Rennes 1), we have carried on our analysis of the equivalence of two soil fracture models in terms of transfer functions [19]: the MINC (Multiple INteractiong Continua) and MRMT (Multiple Rate Mass Transfer) models that are quite popular in soil hydrodynamics. We have shown that a strict equivalence can be obtained if one considers different volumes in the discretization of the MINC model. For the moment, this study concerns the transfer of abiotic substances only.

In soil ecosystems, it often happens that several functional groups can be detected to operate concomitantly. We have investigated the mathematical properties of a relatively simple model that has been proposed by the UREP lab (Inra Clermont), that distinguishes explicitly two functional groups of micro-organisms: the decomposers of SOM (soil organic mater) and the producers of SOM, and compared it with a single microbial compartment model in terms of prediction of the so-called “priming effect” [27].

Together with agronomists of the UMR Eco & Sols (Cirad, Inra, IRD, Montpellier SupAgro) and the supervision of the MSc thesis of C. Droin, we have proposed and started to study a new model of consumer/resource for soil microbial ecosystems, in which we explicitly distinguish available and recalcitrant resources [71].

6.2. Stochastic and hybrid models

6.2.1. Stochastic macroscopic models

Participants: Fabien Campillo, Marc Joannides.

We continued our study of stochastic modeling of the chemostat. In a first study we establish the Fokker-Planck equation of the law of the diffusion process. This equation features relevant boundary condition for the washout. We propose specific finite difference schemes to account for this feature [18]. In a second work we adopt the same approach to more accurately study the logistic model [64] which allowed us to propose estimation procedures to take into account the extinction (see Section 6.3.2).

6.2.2. From microscopic models to macroscopic laws

Participants: Fabien Campillo, Coralie Fritsch, Jérôme Harmand, Claude Lobry.

We proposed a chemostat model where the bacterial population is individually-based (IBM), each bacterium is explicitly represented and has a mass evolving continuously over time, and where the substrate concentration is represented as a conventional ordinary differential equation. These two components are coupled with the bacterial consumption. Mechanisms acting on the bacteria are explicitly described (growth, division and uptake). Bacteria interact via consumption. We set the exact Monte Carlo simulation algorithm of this model and its mathematical representation as a stochastic process. We prove the convergence of this process to the solution of an integro-differential equation (IDE) when the population size tends to infinity. The IDE is discretized with the help of finite differences, with simulation as well as the IBM are developed in `Python` with the help of the Gamma-Team (UMR Mistea) [63].

Finally with O. Ovaskainen (Univ. of Helsinki) we developed an evolution model for the chemostat.

6.2.3. Simulation and analysis of hybrid models and the atto-fox problem

Participants: Fabien Campillo, Claude Lobry, Alain Rapaport.

We proposed a new "hybrid" model for the simulation of biofilm growth in a plug flow bioreactor, that combines information from three scales: a microscopic one for the individual bacteria, a mesoscopic or "coarse-grained" one that homogenizes at an intermediate scale the quantities relevant to the attachment/detachment process, and a macroscopic one in terms of substrate concentration. In contrast to existing partial differential equations models, this approach is based on a description of biological mechanisms at the individual scale, thus bringing in a biological justification of the attachment/detachment process responsible for the macroscopic behavior [20].

We pursue our study of the "atto-fox" question in the classical Rosenzweig-MacArthur model for a resource-consumer relationship: for certain values of parameters the system has a limit cycle such that the smallest value reached by the resource on this cycle is so small that the model validity is jeopardized [65].

6.3. Identification and control

6.3.1. Reconstruction methods of kinetics functions

Participant: Alain Rapaport.

A collaboration with Sisyphe Inria project-team has led to the development of a new identification method of the kinetics function in the chemostat model, without any a priori on the monotonicity of the function (thus allowing the consideration of bio-processes that are unstable in open loop) [29]. An extension of this method, that is based on singular perturbations, has been proposed for the extremum seeking problem with only two times scale (instead of three for the usual extremum seeking techniques [75]) [50].

6.3.2. Parameter estimation and particle filtering

Participants: Amine Boutoub, Fabien Campillo, Jérôme Harmand, Marc Joannides.

We consider a stochastic logistic growth model involving both birth and death rates in the drift and diffusion coefficients for which extinction eventually occurs almost surely. We then use the numerical integration of the Fokker-Planck equation presented in Section 6.2.1 to build a likelihood function for the unknown model parameters, when discretely sampled data is available. The existing estimation methods need adaptation in order to deal with the extinction problem. We propose such adaptations, based on the particular form of the Fokker-Planck equation, and we evaluate their performances with numerical simulations [64].

We develop particle approximation methods for the nonlinear filtering and parameter estimation with the help of the chemostat model [70].

6.3.3. Functional assignments methods

Participants: Jérôme Harmand, Alain Rapaport.

Following the philosophy of the work that was achieved within the framework of the former PhD thesis of M. Dumont [3], we have applied part of the proposed methodology for a better understanding of the dynamics of specific species of the anaerobic digestion [30], with Chilean collaborators (see Sections 7.4.1.1 and 7.4.2).

Using a combinatorial approach, we have also developed together with UMR Eco & Sols (Cirad, Inra, IRD, SupAgro – Montpellier) a new method to study the role of the interactions within bacterial species on the performance of an ecosystem. More precisely, based on the specific characteristics of the species of a community and the way they interact between each other, we propose a method to predict the behavior of the ecosystem with respect to its biodiversity [34], [25].

6.3.4. Stabilizing strategies for bioprocesses

Participants: Céline Casenave, Jérôme Harmand, Guilherme Pimentel, Alain Rapaport.

We have carrying on developments of stabilizing strategies for bio-processes, with specific characteristics:

- In [48], it has been shown how the buffered configuration of two chemostat models studied in Section 6.1.3 provides an efficient way to stabilize bioprocesses with inhibition. In the same spirit, its has been shown how the consideration of a "passive" buffer (i.e. without biological reaction) can play the role of a delay and enlarge the attraction basin of stable equilibria [49].
- If often happens in bio-processes that measurements are delayed. In [46], a new stabilizing strategy have been proposed to robustly cope with such delays for single chemostats with inhibition.
- For the stabilization of a series of reactors with multiple inputs, a control strategy based on a linearizing control law coupled with a state observer and an anti windup component has been proposed [66], [67], in view of its application in wine fermentation processes. The originality and difficulty of this multi-inputs problem are due to the inputs constraint that imposes that the manipulated dilution rate of each tank has to be less or equal than the one of the previous tank.

6.3.5. Optimal syntheses for bioprocesses control

Participants: Térence Bayen, Amel Ghouali, Jérôme Harmand, Claude Lobry, Alain Rapaport, Tewfik Sari.

We have continued our activities related to the development of optimal control laws for the optimization of bio-processes, notably in taking advantage of the presence of T. Bayen in the team in 2013. Three kinds of results, depending on the kind of processes under interest, were obtained.

a. Control of batch processes. Sequencing Batch bioReactors can be used to efficiently treat water containing both carbonaceous and nitrogenous pollutants. In such a case, an efficient control that can be used is the oxygen concentration. In such systems, oxic and anoxic bacterial are in competition for certain substances. For a simplified version of this complex situation, we have investigated the optimal strategies in order to minimize the energy to be introduced into the system under performance constraints. The originality of the approach lies in the fact that the original problem is transformed into a very general form. Thus, the optimal control problem is formulated and solved for a very general class of systems of ecological relevance [16].

b. Control of fed-batch processes. References [13], [36], [60] are devoted to the study of a bioreactor which is operated in fed-batch mode. We aim at finding an optimal control in feedback form (i.e. depending of the state) that steers the system in a minimal amount of time to a target (which typically has several interests in wastewater treatment). Finding an optimal control in feedback form is crucial from a practical point of view. In [13], previous works on the subject are extended to the case where the growth function depends on an additional product of the reaction. In the references [36], [60], we provide an optimal control in feedback form whenever mortality and recycling rates are considered, and in the case where the maximum dilution rate is not large enough to compete the growth of the species (in the latter case, this implies that the singular arc is non-necessary controllable implying difficulties in determining optimal controls). References [58], [61] are devoted to the study of optimal control problem governed by a chemostat-type model. In [58], an optimal feedback control law is provided in order to optimize the selection of a species in a chemostat model with one limiting substrate and two species. This brings an interesting issue in order to extend this result to the case where the number of species is larger than 3.

c. Coupled dynamics. References [59], [60] give the results of the study of an optimal control problem of a system coupling a culture of micro-algae limited by light and an anaerobic digester. The mathematical model for the dynamics of the reactors takes into account a periodic day-night model of the light in the culture of micro-algae and a chemostat model for the digester. Our aim is to optimize the production of methane in the digester during a certain number of days with respect to the dilution rate. In [59], some preliminary results on this problem are given for an optimal control problem governed by a one-dimensional Kolmogorov equation. In [60], the full system is analyzed by combining direct methods and indirect methods based on Pontryagin's Principle. In [62], we provide a complete characterization of optimal controls for a minimal time control problem where the system describes a two tanks gradostat model under a cascade inputs constraint. This model allows to create a gradient of resources that is expected to be more realistic to mimic real environment for studying micro-organisms growth.

6.4. Distributed delay systems

Participant: Céline Casenave.

In microbial ecosystems, time delays are often present. For a long time (especially with V. Volterra), distributed delay models (or integro-differential equations) have been proposed to take into account these delays in population models. Some dynamic problems dealing with integro-differential models can be tackled in an original way by using the methodology called "diffusive representation". Some works, which began during the PhD thesis of Céline Casenave, are still under development.

In [26], a new formulation of an integro-differential model of a porous media is proposed, based on this methodology. From this formulation, the dissipative and passive features of the porous wall are established, and numerical simulations are performed. A reduced order model is also proposed which summarizes the boundary behavior of the porous wall ([5]).

This work is done in collaboration with LAAS (Univ. Toulouse III) and the Gipsa-lab (CNRS, Grenoble-INP, Univ. Joseph Fourier, Univ. Stendhal). In the future, these works could be adapted to the case of microbial ecosystems.

6.5. Applications to wastewater treatment

Participants: Térence Bayen, Fabien Campillo, Radhouane Fekih-Salem, Amel Ghouali, Jérôme Harmand, Claude Lobry, Alain Rapaport, Tewfik Sari.

If an important part of our work has been done with the final objective of confronting models to data, the studies realized this year are rather theoretical (cf. research achieved within the framework of PhD theses by B. Benyahia, R. Fekih Salem, S. Hassam and G. Araujo Pimentel). In fact, they can be considered as prerequisites before being applied to real systems which, as for most Anaerobic MBRs, are still often found only at pilot scale and not yet applied on real sites.

Concerning the study of membrane fouling, we collaborate with our colleagues of the University Montpellier 2 within the framework of A. Charfi to characterize membrane fouling [43], [54], [42].

In association with the "Laboratoire d'Automatique de Tlemcen" (Univ. Aboubekr Belkaid) and the Gamma Team (UMR Mistea), Modemic launch the NuWat project (Numerics for water treatment research) in the Lirima network (see Section 7.4.2). The first visit of colleagues from the LAT allowed to make choices on the establishment of teachings for the Master in Tlemcen of general trainings and to define research priorities.

[5] Two journal articles dealing with the identification of integro-differential models, and the controllability of some SISO Volterra models are still under revision.

The collaboration with Moise Inria project-team has led to a patent application about an algorithm for "intelligent" pumps for the efficient treatment of large water resources [69]. The method relies on an extension of a former work [4] coupled with faithful simulations of the hydrodynamics of the resource and the pollutant dispersion. This typically applied for Chilean lakes, an application that we plan to launch within a common project with CIRIC Inria-Chile.

6.6. Applications to environmental microbiology

Participants: Céline Casenave, Jérôme Harmand, Alain Rapaport.

We have several ongoing works on the modeling of soil microbial ecosystems. The main characteristics of the models we develop with these partners, compared to aquatic microbial ecosystems, concern the availability of the resources, in terms of:

- spatial distribution and transfer of resources, using simple space representations, with the UMR Eco & Sols (Cirad, Inra, IRD, SupAgro – Montpellier) and the UMR Géosciences (Rennes). See Section 6.1.3 and references [28], [19];
- consideration of recalcitrant forms and recycling of nutrients, with UMR Eco & Sols (Cirad, Inra, IRD, SupAgro – Montpellier) and Inra UREP (Clermont). See Section 6.1.3 and [27], [71].

We have also proposed, together with the UMR Eco & Sols (Cirad, Inra, IRD, SupAgro – Montpellier), a new methodology to deduce from the observation of the performances of several assembling of reconstituted ecosystems, the number and the nature of species interactions (see Section 6.3.3 and [34], [25]).

The organization of a "research school" dedicated to the biologists of the marine research station of Banyuls (see Section 8.1) has led to a primary work about variable yield in marine microbial populations.

6.7. Applications to wine fermentation

Participants: Térence Bayen, Céline Casenave, Jérôme Harmand, Alain Rapaport.

We study the problem of the control of a Multi-State Continuous Fermentor (MSCF) composed of 4 reactors connected in series (the experimental pilot plant is located at Montpellier, in the UMR SPO (INRA, Montpellier SupAgro, Univ. Montpellier 1)). The goal is to control the sugar concentration of the four reactors with, as control inputs, the input flow rates of the four reactors. The originality of the problem comes from the cascade structure of the device which leads to a constraint on the control inputs. Two control strategies have been studied.

An output stabilizing control strategy. The linearizing control law proposed in [66], [67] (see Section 6.3.4) has been validated on numerical simulations, and then has been implemented (Labview-Matlab interface) on the experimental process. The obtained results are convincing; others experiments are scheduled in 2014 to refine the control law.

A minimal time state feedback strategy. The optimal state feedback studied in [62] (see Section 6.3.5) is of completely different nature, as it relies on bang-bang controls and singular arcs. We plan to couple this control law when far from the target with the previous stabilizing law when close from the target, in order to provide a practical sub-optimal strategy.

The first part of this work was conducted as a part of the European CAFE project (Computer-Aided Food processes for control Engineering) described in Section 7.3.1, in collaboration with CESAME (Univ. Catholique de Louvain-la-neuve), and UMR SPO.

A new project, see Section 7.2, in which the UMR SPO and the Unit Mistea are involved has begun in 2013. Preliminary work has been performed during the MSc thesis of S. Sekkat [74] about the modeling of the fermentation with addition of nitrogen in the MSCF.

6.8. Applications to micro-algae

Participants: Térence Bayen, Matthieu Sebbah.

An originality developed within the Biocore Inria project-team is to couple a bioreactor that cultivate micro-algae with an anaerobic digester, that uses micro-algae as a substrate that is then converted into valuable bio-gaz (methane). As micro-algae are micro-organisms whose growth is limited by light, one has to take into account periodic day-night model of the light. In [59], [61], control laws that maximize the biogaz production in this periodic framework have been proposed (see Section 6.3.5). In the framework of the Inria Project Lab "Algae in Silico" (see Section 7.2) and the Inria-CIRIC Center in Chile (see Section 7.4), several extensions and collaborations with Biocore Inris project-team are scheduled for the coming year.

6.9. Other results

This section contains some theoretical as well as applied results, that are not directly connected to the main field of the team.

Theoretical ecology
Participant: Tewfik Sari.

In [24], 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.

Calculus of variations
Participant: Térence Bayen.

The work [37] is devoted to the study of necessary and sufficient optimality conditions for weak and strong minima for optimal control problems governed by semi-linear parabolic equations; whereas in the field of calculus of variation, these conditions (such as Euler-Lagrange equation, Legendre's condition, Weierstrass's condition) have been deeply investigated, the study of strong solutions for optimal control problems of partial differential equations is new.

Ice cream crystallization
Participant: Céline Casenave.

We study the problem of the control of an ice cream crystallization process (the experimental pilot plant is located at Irstea Antony). The goal is to control the viscosity of the ice cream at the outlet of the continuous crystallizer. The problem has been studied in two steps.

Modeling, model reduction and parameter identification. On the basis of a population balance equation describing the evolution of the crystal size distribution (CSD) of the ice cream, and an energy balance equation, we have proposed an input-output reduced order model of the process, which is based on physical assumptions. The parameters of the model have been identified and the model has been validated from experimental data [68].

Design of the control law. Based on the reduced order model, 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 [41], [66], [67]. The control has been implemented (Labview-Matlab interface) and then validated on the experimental pilot plant. During the industrial conference which has been organized in February 2013 by the European CAFE project (see Section 7.3.1), and which representatives of several industries in food processing attended, a live demonstration of the designed control law has been performed.

This work was conducted as a part of the European CAFE project, described in Section 7.3.1, in collaboration with CESAME (Univ. Catholique de Louvain-la-neuve), Irstea Antony and AgroParisTech.

Semi-Markov land use dynamic
Participant: Fabien Campillo, Angelo Raherinirina.

We pursued the development of semi-Markov model for the inference of land use dynamic from data proposed by IRD. The thesis of A. Raherinirina was defended in August 2013 [12]. Later in the year during the stay of A. Raherinirina in Montpellier we completed an article accepted by the journal ARIMA and that will be published in 2014 [17].

7. Partnerships and Cooperations

7.1. Regional Initiatives

7.1.1. Numev

Within the Labex Numev (Solutions Numériques, Matérielles et Modélisation pour L'Environnement et le Vivant [[6]]), the team is the coordinator since 2012 of a working group on Modeling and numerical probabilities for ecology and biology with the team EPS of I3M (Univ. Montpellier 2) [[7]].

7.1.2. LBE

An new interlab seminar about the modeling of bioprocesses has been launched in July 2013 under the responsibility of J. Harmand, involving Biocore and Modemic Inria project-teams [[8]].

7.2. National Initiatives

7.2.1. ANR project "DISCO"

DISCO (Multi-scale modeling bioDIversity Structure COupling in biofilms) is a project funded by the ANR SYSCOMM since the end of 2009, that ended in May 2013. Modemic has been the coordinator and other partners were Irstea LISC (Clermont-Ferrand), Irstea HBAN (Antony), Inra LBE (Narbonne) and CNRS/UMPC LPMTC (Paris VI). The objectives were to develop and study computational and mathematical models of biofilm dynamics, taking into account the biodiversity (distribution of bacteria species) and the spatial structure. The project had a strong multi-disciplinary dimension, gathering specialists of IBM study and reduction techniques, mathematical analysis of ecosystems modeling, multi-scale modeling of complex structures and dynamics, wastewater engineering and biodiversity measurements through DNA fingerprints, and solid waste biodegradation and microscopic biofilm structure imaging. During the project, several kinds of models (individual-based up to deterministic continuous) have be developed and confronted to experimental data at both micro and macroscopic scales. For the closing of the projet, the team has organized a one day meeting in Paris, combining a project restitution and and international workshop [[9]].

7.2.2. RNSC project "MnMs"

This year, a partial support of the continuation of the ANR DISCO has been been funded for two years by the RNSC (National Network on Complex Systems). The MnMs (Numerical Models for Microbial ecosystems) project [[10]] aims at studying how to articulate existing models (discrete, continuous, deterministic, stochastic...) in a multi-scale framework with interactions between various scales. The team is the coordinator and the other partners are Irstea LISC (Clermont-Ferrand) and CNRS/UMPC LPMTC (Paris VI).

We organized a joint seminar with the project DyLeRBio of the RNSC (M. Desroches, Sisyphe/Mycenae projet-team) in Montpellier (September 30, October 1-2 2013) [[11]].

[6] http://www.lirmm.fr/numev
[7] http://www-sop.inria.fr/members/Fabien.Campillo/gt-modelisation/
[8] https://sites.google.com/site/journeesthematiquesdulbe/home
[9] https://sites.google.com/site/anrdisco/
[10] http://www-sop.inria.fr/members/Fabien.Campillo/mnms/
[11] http://www-sop.inria.fr/members/Fabien.Campillo/projects/mnms/

7.2.3. Inra-MEM program project “ENOC”

Since 2012, the team is the coordinator of the ENOC project with the LBE lab (Inra Narbonne) [[12]], funded the by Inra meta-program MEM (metagenomics of microbial ecosystems). This two-years project proposes a multidisciplinary approach shared by microbial ecologists and mathematicians for the reverse modeling of metagenomic data for microbial resource management. The final objective is to develop a generic approach for predicting ecosystem performance from an unknown inoculum.

7.2.4. Inra-CEPIA project “New perspectives for the MSCF”

A new project submitted to the Inra Dept. CEPIA, entitled “New perspectives for the Multi-Stage Continuous Fermentor (MSCF): Study of fermentations with disturbances, and development of a control law”, in which the Montpellier Units SPO and Mistea are involved has been accepted in 2013 and will last 2 years. It is the continuation of the work made within the CAFE project (see Section 7.4) about the control of a wine fermentation process. The goal of the project is to study the fermentations with addition nitrogen. From the control point of view, we will study the control of both the sugar concentration and the CO_2 production rate in each of the 4 reactors of a MSCF.

7.2.5. CNRS-PEPS project “ASYDE”

The team participates to the CNRS PEPS “ASYDE” (Analyse de systèmes de digesteurs biologiques) launched in 2013 for two years, with the objective to develop tools for the analysis and reduction of the models (flat systems, Lyapunov functions, delayed equations...) in microbial ecology. The project is coordinated by the L2S (CNRS/Supélec, Gif-sur-Yvette), with Modemic, LBE (Inra Narbonne) and MIA (Inra Jouy) as partners.

7.2.6. Inria Project Lab “Algae in Silico”

Modemic is a partner of the proposal of the Inria Project Lab “Algae in Silico” launched by Biocore Inria project-team.

7.3. European Initiatives

7.3.1. FP7 Projects

Program: Food, Agriculture and Fisheries, and Biotechnology (Theme 2)
Project acronym: CAFE
Project title: Computer-Aided Food processes for control Engineering
Duration: 2009-2013
Coordinator: CESAME, UCL (Louvain-la-Neuve, Belgium)
Other partners: Alctra, BIV SA, C-Tech Innovation, Irstea, Consejo Superior de Investigaciones Cientificas (CSIC), Wageningen Univ. and Research centre, Institut des Sciences et Industries du Vivant et de l’Environnement Agro Paris Tech, Inra, Povltavske Mlekarny AS, Psutec SPRL, Societa di Progettazione Elettronica e Software S.C.R.L. SPES, Telstar Technologies SLU, The Univ. of Manchester, Univ. Degli Studi di Roma Tor Vergata, X-Flow BV.
Abstract: This is a Large collaborative project, whose objective is to provide new paradigms for the smart control of food processes, on the basis of four typical processes in the areas of bio-conversion, separation, preservation and structuring (resp. wine making, micro-filtration of food beverages, freeze-drying of lactic acid bacteria and ice cream crystallization. The novelty of the project lies in the capacity of combining PAT (Process Analytic Technology) and sensing devices with models and simulation. The team works on the control of multi-stage bioreactors (for wine making) and the regulation of ice quality (ice cream crystallization).
Web-site: http://www.cafe-project.org/

The CAFE project ended in March 2013 (see deliverables [66], [67], [68]). An industrial conference has been organized by the consortium in February 2013 at Irstea (Antony, France),. During the conference, which representatives of several industries in food processing attended, a live demonstration of the designed control law has been performed.

[12] https://sites.google.com/site/enocprojetreversemodelling/

7.4. International Initiatives

7.4.1. Inria International Partners

7.4.1.1. Declared Inria International Partners

From 2010 to 2012, the Inria associated-team Dymecos (DYnamical Microbial and Environmental eCOSystems) has associated the team with three main partners in Chile: UMR CNRS CMM (Santiago), Math. Dept. of UTFSM (Valparaiso) and EIB-PUCV (Valparaiso). A continuation of this associated-team has been submitted for 2014. Within the Inria CIRIC Center in Chile, the team has co-supervised in 2013 the postdoctoral stay of M. Sebbah (part-time in Chile, part-time in France).

7.4.1.2. Informal International Partners

The team has a long term collaboration with Prof. D. Dochain from CESAME (Univ. Louvain-la-Neuve).

7.4.2. Inria International Labs

Lirima STIC-Mada [[13]] since 2010 (Madagascar). The purpose of the project was to develop land use dynamical models corresponding to plots located on the edge of the forest corridor linking the two national parks of Ranomafana and Andringitra in Madagascar. We use both Markov and semi-Markov models to infer the land-use dynamics. The main contribution was the co-advising of a PhD student, Angelo Raherinirina who defended his thesis in August 2013. This work is done in collaboration with IRD in Madagascar.

Lirima NuWat (Numerics for water treatment research) [[14]] 2013-... (Tlemcen, Algeria and Gamma Team/UMR Mistea). 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.

CIRIC-Chile. The future of our collaboration with Chile within the BIONATURE line is not entirely in our hands and relies much on CIRIC's policy regarding fundamental research. Anyway we shall try to continue our fruitful collaboration in modeling and optimal control within the CIRIC project, and ficus more on transfer applications.

7.4.3. Participation In other International Programs

7.4.3.1. TREASURE (Treatment and Sustainable Reuse of Effluents in semiarid climates)

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), Univ. of Patras, Process Control Laboratory (Greece), Univ. of Tlemcen, Automatic control (Algeria), Univ. 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

[13] http://www.Lirima.uninet.cm/index.php/recherche/equipes-de-recherche/stic-mada
[14] https://project.inria.fr/nuwat/

Abstract: The TREASURE network aims at integrating knowledge on the modeling, the control and the optimization of biological systems for the treatment and reuse of wastewater 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

7.4.3.2. CIB (Centre Interfacultaire Bernoulli)

A very old 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 Comore Inria project-team, pursued then by Mere and Comore raised very recently an important success: 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 organization of this half-year (in July-December 2014) and the preparation of the acts will mobilize a great part of our activity for the coming two years. It should gather around sixty specialists during a half-dozen workshops. If additional funds are obtained from other sponsors we hope to welcome for the totality of the semester half a dozen post-doc.

7.5. International Research Visitors

Imme Van Den Berg (Univ. of Évora, Portugal) from Oct. 2013 until Feb. 2014: Construction, analysis and simulation of population dynamics models.

Nihel Ben Amar (ENIT, Tunis, Tunisia) from September 2013 to October 2013: Bioprocess modeling.

Boumédiène Benyahia (Univ. Tlemcen, Algeria) from January 2013 to October 2013: Bioprocess modelling.

Abdoudramane Guiro (Univ. Ougadougou, Burkina Fasso) from October 2013 to December 2013: Construction, analysis and simulation of dynamical models of populations.

7.5.1. Visits to International Teams

Coralie Fritsch as obtained a grant in the context of the Agreenium program [[15]] to visit Pr. Otso Ovaskainen's mathematical biology group (Univ. of Helsinki) from September to December 2013.

8. Dissemination

8.1. Scientific Animation

C. Casenave has been an "outstanding reviewer" for IEEE Transactions on Automatic Control in 2013.

The team has organized a one day international workshop on biofilm modeling (May, Paris) [[16]].

The team has organized a "research school" of one week in June dedicated to the biologists of the marine research station of Banyuls [[17]].

[15] http://www.agreenium.org
[16] https://sites.google.com/site/anrdisco/meetings/workshop-may-2013
[17] http://lomic.obs-banyuls.fr/fr/test/ecole_chercheur_chemostat.html

F. Campillo was invited to give a lecture on stochastic modeling and simulation at CNRS/Génopôle Thematic School on “Advances in Systems and Synthetic Biology” at La Colle sur Loup (France), March 25 to 29. Fabien Campillo was invited to give a lecture on particle filtering at the Univ. of Mons at the "Dynamical systems, control and optimization" (DYSCO) of the Interuniversity Attraction Poles, May 24.

C. Casenave and F. Campillo are in the organizing committee of the MIA Division national meeting to be held in March 2014.

C. Casenave is in charge of the Modemic Seminar.

From the 15th to the 18th April, the team had its annual meeting in the “Hameau de l’Etoile”.

8.2. Teaching - Supervision - Juries

8.2.1. Teaching

F. Campillo and M. Joannides, “Stochastic modeling of ecosystem”, 20 hours, Master 2 in Biostatistics, Univ. Montpellier 2.

A. Rapaport, “Practical Mathematics”, 25 hours, Master 1 in Mathematics, Univ. Montpellier 2.

C. Casenave and A. Rapaport, “Advanced mathematical modeling”, 18 hours, Master 2 STIC - Environnement, Univ. Montpellier 2.

A. Rapaport, “About modeling and numerical simulations of dynamical systems”, 9 hours, Master 1 in Ecosystems, Univ. Montpellier 2.

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

C. Casenave, F. Campillo and A. Rapaport, “modeling for biology and ecology, mathematical and computational methods”, 20 hours, Doctoral lectures, Univ. Montpellier 2.

8.2.2. Masters supervision

Supervision:

A. Boutoub [70], supervisor: F. Campillo.

C. Droin [71], supervisor: C. Casenave.

S. Sekkat [74], supervisor: C. Casenave.

Co-supervision:

M. Chebbi: “Modélisation et approximation stochastique appliquées en écologie”, Master of Applied Mathematics, ENIT/LAMSIN, Tunis, co-supervisors: S. Toumi and F. Campillo.

Y. Dadoud: “Contrôle Optimal d’un procédé biologique séquentiel discontinu : approche par simulations”, Master of Applied Mathematics, ENIT/LAMSIN, Tunis, co-supervisors: N.a Abdellatif and F. Campillo.

Z. Khedim: “Réalisation d’une interface Matlab pour la simulation des bioprocédés : Application au modèle ADM1”, Master of Automatic Control, Univ. Aboubekr Belkaid, Tlemcen, Algeria, co-supervisors: B. Benyahia and J. Harmand.

M. Crespo: “Modelling unhomogeneous biorectors”, Master of Applied Mathematics, Univ. Madrid., co-supervisors: B. Ivorra, A. Rapaport

8.2.3. PhD's supervision

M. Radhouane Fekih-Salem, "Modèles mathématiques pour la compétition et la coexistence d' espèces microbiennes dans un chémostat, co-tutelle Univ. Montpellier 2/ENIT-LAMSIN, Tunis (Tunisia), defended in Sep. 2013 (co-directors: A. Rapaport and T. Sari) [11].

M. Angelo Raherinirina,"Modélisation markovienne des dynamiques d'usages des sols. Cas des parcelles situées sur le bord du corridor forestier Ranomafana-Andringitra", Univ. Fianarantsoa (Madagascar), defended in Aug. 2013 (director: F. Campillo) [12].

Ms Coralie Fritsch, "Simulation et analyse de modèles individu-centrés d'écosystèmes bactériens pour des procédés biotechnologiques", Univ Montpellier 2, since Oct. 2011 (director: F. Campillo).

Ms Amel Ghouali, "Analyse et commande optimale d'un bioréacteur de dépollution des eaux usées", cotutelle Univ Montpellier 2/Univ. Tlemcen (Algeria), since Nov. 2011 (director: J. Harmand).

M. Guilherme Pimentel, "Modélisation dynamique, analyse et supervision d'un réacteur membranaire", cotutelle Univ. Montpellier 2/Univ. Mons (Belgique), since Sept. 2013 (Co-directors: A. Vande Wouver and A. Rapaport).

8.2.4. Juries

M. Benjamin Ivorra, "Méthodes et techniques de modélisation, simulation et optimisation appliquées à divers problèmes industriels", thèse d'Habilitation à Diriger des Recherches, Univ. Montpellier 2, Fev. 2013 (examiner: A. Rapaport).

M. Derdei Bichara, "Etude de modèles épidémiologiques: stabilité, observation et estimation de paramètres", Univ. Metz, Fev. 2013 (referee: A. Rapaport).

M. Mickael Teixeira Alves, "Des interactions indirectes entre les proies: modélisation et influence du comportement du prédateur commun, Univ. Nice Sophia Antipolis, Jan. 2013 (referee: T. Sari).

M. Sihem Kouloughli, "Optimisation de systèmes automatisés de stockage/déstockage multi allées et à racks glissants", Univ. of Tlemcen, Algeria, Jun. 2013 (referee: T. Sari).

M. Térence Bayen, "Etude du quelques problèmes de contrôle optimal issus des EDP et des EDO", Habilitation à diriger des recherches, Univ. Montpellier 2, Dec. 2013 (examiner: A. Rapaport).

8.3. Popularization

The team has participated to the writing of a blog [73], [72] for the MPT2013, french edition of Mathematics of the Planet Earth 2013.

The team has participated to the writing of two articles [31], [32] in the TDC magazine dedicated to teachers in secondary classes.

8.4. Community services

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.

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; member of the selection board in case of selection of a Professor of probability at the Univ. of Montpellier 2.

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.

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