



IN PARTNERSHIP WITH:
CNRS

**Ecole normale supérieure de
Lyon**

**Université Claude Bernard
(Lyon 1)**

Activity Report 2016

Project-Team NUMED

Numerical Medicine

IN COLLABORATION WITH: Unité de Mathématiques Pures et Appliquées

RESEARCH CENTER
Grenoble - Rhône-Alpes

THEME
**Modeling and Control for Life Sci-
ences**

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Project-Team NUMED

Creation of the Project-Team: 2009 January 01

Keywords:

Computer Science and Digital Science:

- 6. - Modeling, simulation and control
- 6.1. - Mathematical Modeling
- 6.2. - Scientific Computing, Numerical Analysis & Optimization
- 6.3. - Computation-data interaction

Other Research Topics and Application Domains:

- 1. - Life sciences
 - 1.1. - Biology
 - 1.2. - Ecology
 - 1.4. - Pathologies
- 2. - Health
 - 2.2. - Physiology and diseases
 - 2.2.2. - Nervous system and endocrinology
 - 2.2.3. - Cancer
 - 2.2.4. - Infectious diseases, Virology
 - 2.4.1. - Pharmacokinetics and dynamics
 - 2.4.2. - Drug resistance
 - 2.6.1. - Brain imaging

1. Members

Research Scientist

Vincent Calvez [CNRS, Researcher, HDR]

Faculty Members

Emmanuel Grenier [Team leader, ENS Lyon, Professor, HDR]

Marie Aimee Dronne [Univ. Lyon I, Associate Professor]

Paul Vigneaux [ENS Lyon, Associate Professor]

PhD Students

Mathilde Giacalone [Univ. Lyon]

Arthur Marly [ENS Lyon]

Alvaro Mateos Gonzalez [ENS Lyon]

Edouard Ollier [ENS Lyon]

Aziz Ouerdani [Inria, until May 2016]

Post-Doctoral Fellows

Thibault Bourgeron [ENS Lyon]

Christopher Henderson [Univ. Lyon, until Aug 2016]

Administrative Assistant

Sylvie Boyer [Inria]

2. Overall Objectives

2.1. Overall Objectives

The purpose of Numed is to develop new numerical methods and tools to simulate and parametrize complex systems arising in biology and medicine. Numed focuses on two axes:

- Thema 1: Modeling using complex models: how to deal with multiple spatial or temporal scales (theoretical study, numerical simulations)?

This covers several aims: design of models of propagation taking into account the microscopic phenomena and starting from small scale description, importance of mechanics in the growth of tissues, peculiarities of tumor tissues, nonlinear rheology, evolutionary perspectives.

Thema 1 may be split in three objectives.

- Multiscale propagation phenomena in biology
- Growth of biological tissues
- Multiscale models in oncology
- Thema 2: Parametrization of complex models: how to find parameters for complex models, with particular emphasis on population approaches and on computationally expensive models.

and two main axes of applications

- Thema 3: Stroke

Stroke is one of the major diseases in developed countries. Its modeling is very challenging and rich, involving imagery, cell death modeling, apoptosis, energy issues, inflammation, free radicals, anatomy, ...

- Thema 4: Cancer

The aim is to develop models of cancer growth in close link with clinical data.

3. Research Program

3.1. Multiscale propagation phenomena in biology

3.1.1. Project team positioning

The originality of our work is the quantitative description of propagation phenomena accounting for several time and spatial scales. Here, propagation has to be understood in a broad sense. This includes propagation of invasive species, chemotactic waves of bacteria, evolution of age structured populations ... Our main objectives are the quantitative calculation of macroscopic quantities as the rate of propagation, and microscopic distributions at the edge and the back of the front. These are essential features of propagation which are intimately linked in the long time dynamics.

Multiscale modeling of propagation phenomena raises a lot of interest in several fields of application. This ranges from shock waves in kinetic equations (Boltzmann, BGK, etc...), bacterial chemotactic waves, selection-mutation models with spatial heterogeneities, evolution in age-structured population or subdiffusive processes.

Earlier works generally focused on numerical simulations, hydrodynamic limits to average over the microscopic variable, or specific models with only local features, not suitable for most of the relevant biological situations. Our contribution enables to derive the relevant features of propagation analytically, and far from the hydrodynamic regime for a wide range of models including nonlocal interaction terms.

Our recent understanding is closely related to the analysis of large deviations in multiscale dispersion equations (e.g. PDMP), for which we gave important contributions too in collaboration with E. Bouin (CEREMADE Dauphine), E. Grenier (Inria NUMED) and G. Nadin (Univ. Paris 6).

These advances are linked to the work of other Inria teams (MAMBA, DRACULA, BEAGLE), and collaborators in mathematics, physics and theoretical biology in France, Austria and UK.

3.1.2. Recent results

Vincent Calvez has focused on the modelling and analysis of propagation phenomena in structured populations. This includes chemotactic concentration waves, transport-reaction equations, coupling between ecological processes (reaction-diffusion) and evolutionary processes (selection of the fittest trait, adaptation), evolution of age structured populations, and anomalous diffusion. As a main result, he could establish the existence of concentration waves of chemotactic bacteria *E. coli* in a fully coupled kinetic/reaction-diffusion system previously validated on experimental data.

In collaboration with a group of theoretical biologists at ISEM Montpellier (O. Ronce and O. Cotto), and J. Garnier (Univ. Savoie), Th. Lepoutre (Inria DRACULA), Th. Bourgeron (Inria NUMED) he has investigated quantitatively the maladaptation of an age-structured population in a changing environment. He has unravelled a striking phenomenon of severe maladaptation specific to age structure. This was observed on numerical simulations by biologists, but it has now a systematic mathematical comprehension.

He has also continued his work on the optimal control of monotone linear dynamical systems, using the Hamilton-Jacobi framework, and the weak KAM theory, in collaboration with P. Gabriel (UVSQ) and S. Gaubert (Inria MAXPLUS).

Alvaro Mateos Gonzalez has started his PhD on September 2014 under the supervision of Vincent Calvez, and Hugues Berry (BEAGLE). He has already collaborated fruitfully with Thomas Lepoutre (DRACULA) and Hugues Berry to investigate the long-time asymptotics of a degenerate renewal equation. This is a first step towards the mathematical analysis of anomalous diffusion processes. In collaboration with P. Gabriel (UVSQ) and V. Calvez (Inria NUMED) he has investigated large deviations of heterogenous continuous time random walks.

3.1.3. Collaborations

- Mathematical description of bacterial chemotactic waves:
 - **N. Bournaveas** (Univ. Edinburgh), **V. Calvez** (ENS de Lyon, Inria NUMED) **B. Perthame** (Univ. Paris 6, Inria BANG), **Ch. Schmeiser** (Univ. Vienna), **N. Vauchelet**: design of the model, analysis of traveling waves, analysis of optimal strategies for bacterial foraging.
 - **J. Saragosti**, **V. Calvez** (ENS de Lyon, Inria NUMED), **A. Buguin**, **P. Silberzan** (Institut Curie, Paris): experiments, design of the model, identification of parameters.
- Transport-reaction waves and large deviations:
 - **E. Bouin**, **V. Calvez** (ENS de Lyon, Inria NUMED), **E. Grenier** (ENS de Lyon, Inria NUMED), **G. Nadin** (Univ. Paris 6)
- Selection-mutation models of invasive species:
 - **E. Bouin** (ENS de Lyon, Inria NUMED), **V. Calvez** (ENS de Lyon, Inria NUMED), **S. Mirrahimi** (Inst. Math. Toulouse): construction of traveling waves, asymptotic propagation of fronts,
 - **E. Bouin** (ENS de Lyon, Inria NUMED), **V. Calvez** (ENS de Lyon, Inria NUMED), **N. Meunier**, (Univ. Paris 5), **B. Perthame** (Univ. Paris 6, Inria Bang), **G. Raoul** (CEFE, Montpellier), **R. Voituriez** (Univ. Paris 6): formal analysis, derivation of various asymptotic regimes.
- Age-structured equations for anomalous diffusion processes, and evolution

- **H. Berry** (Inria BEAGLE), **V. Calvez** (ENS de Lyon, Inria NUMED), **Th. Lepoutre** (Inria DRACULA), **P. Gabriel** (Univ. UVSQ), O. Ronce (ISEM Montpellier), O. Cotto (ISEM Montpellier), J. Garnier (Univ. Savoie).

3.2. Growth of biological tissues

3.2.1. Project-team positioning

The originality of our work is the derivation, analysis and numerical simulations of mathematical model for growing cells and tissues. This includes mechanical effects (growth induces a modification of the mechanical stresses) and biological effects (growth is potentially influenced by the mechanical forces).

This leads to innovative models, adapted to specific biological problems (*e.g.* suture formation, cell polarisation), but which share similar features. We perform linear stability analysis, and look for pattern formation issues (at least instability of the homogeneous state).

The biophysical literature of such models is large. We refer to the groups of Ben Amar (ENS Paris), Boudaoud (ENS de Lyon), Mahadevan (Harvard), etc.

Our team combines strong expertise in reaction-diffusion equations (V. Calvez) and mechanical models (P. Vigneaux). We develop linear stability analysis on evolving domains (due to growth) for coupled biomechanical systems.

Another direction of work is the mathematical analysis of classical tumor growth models. These continuous mechanics models are very close to classical equations like Euler or Navier Stokes equations in fluid mechanics. However they bring their own difficulties: Darcy law, multispecies equations, non newtonian dynamics (Bingham flows). Part of our work consist in deriving existence results and designing acute numerical schemes for these equations.

3.2.2. Recent results

We have worked on several biological issues. Cell polarisation is the main one. We first analyzed a nonlinear model proposed by theoretical physicists and biologists to describe spontaneous polarisation of the budding yeast *S. cerevisiae*. The model assumes a dynamical transport of molecules in the cytoplasm. It is analogous to the Keller-Segel model for cell chemotaxis, except for the source of the transport flux. We developed nonlinear analysis and entropy methods to investigate pattern formation (Calvez et al 2012). We are currently validating the model on experimental data. The analysis of polarization of a single cell is a preliminary step before the study of mating in a population of yeast cells. In the mating phase, secretion of pheromones induces a dialogue between cells of opposite types.

We also derive realistic models for the growth of the fission yeast *S. pombe*. We proposed two models which couple growth and geometry of the cell. We aim to tackle the issue of pattern formation, and more specifically the instability of the spherical shape, leading to a rod shape. The mechanical coupling involves the distribution of microtubules in the cytoplasm, which bring material to the cell wall.

Over the evaluation period, Paul Vigneaux developed expertise in modelling and design of new numerical schemes for complex fluid models of the viscoplastic type. Associated materials are involved in a broad range of applications ranging from chemical industry to geophysical and biological materials. In the context of NUMED, this expertise is linked to the development of complex constitutive laws for cancer cell tissue. During the period, NUMED used mixed compressible/incompressible fluid model for tumor growth and viscoelastic fluid model. Viscoelastic is one of the other types of complex fluid model which is usable in the field. Mathematically, it involves variational inequalities and the need for specific numerical methods.

3.2.3. Collaborations

- **V. Calvez** (ENS de Lyon, Inria NUMED), **Th. Lepoutre** (Inria DRACULA), **N. Meunier**, (Univ. Paris 5), **N. Muller** (Univ. Paris 5), **P. Vigneaux** (ENS de Lyon, Inria NUMED): mathematical analysis of cell polarisation, numerical simulations

- **V. Calvez** (ENS de Lyon, Inria NUMED), **N. Meunier**, (Univ. Paris 5), **M. Piel**, (Institut Curie, Paris), **R. Voituriez** (Univ. Paris 6): biomechanical modeling of the growth of *S. pombe*
- **D. Bresch** (Univ. Chambéry), **V. Calvez** (ENS de Lyon, Inria NUMED), **R.H. Khonsari** (King's College London, CHU Nantes), **J. Olivier** (Univ. Aix-Marseille), **P. Vigneaux** (ENS de Lyon, Inria NUMED): modeling, analysis and simulations of suture formation.
- **Didier Bresch** (Univ Chambéry), **Benoit Desjardins**(Moma group): petrology.

ANR JCJC project "MODPOL", *Mathematical models for cell polarization*, led by Vincent Calvez (ENS de Lyon, CNRS, Inria NUMED).

3.3. Multiscale models in oncology

3.3.1. Project-team positioning

Since 15 years, the development of mathematical models in oncology has become a significant field of research throughout the world. Several groups of researchers in biomathematics have developed complex and multiscale continuous and discrete models to describe the pathological processes as well as the action of anticancer anti-cancer drugs. Many groups in US (e.g. Alexander Anderson's lab, Kristin Swansson's lab) and in Canada (e.g. Thomas Hillen, Gerda de Vries), quickly developed and published interesting modeling frameworks. The setup of European networks such as the Marie Curie research and training networks managed by Nicolas Bellomo and Luigi Preziosi constituted a solid and fertile ground for the development of new oncology models by teams of biomathematicians and in particular Zvia Agur (Israel), Philip Maini (UK), Helen Byrne (UK), Andreas Deutsch (Germany), or Miguel Herrero (Spain).

3.3.2. Results

We have worked on the development of a multiscale system for modeling the complexity of the cancer disease and generate new hypothesis on the use of anti-cancer drugs. This model relies on a multiscale formalism integrating a subcellular level integrating molecular interactions, a cell level (integrating the regulation of the cell cycle at the levels of individual cells) and a macroscopic level for describing the spatio-temporal dynamics of different types of tumor tissues (proliferating, hypoxic and necrotic). The model is thus composed by a set of partial differential equations (PDEs) integrating molecular network up to tissue dynamics using lax from fluid dynamic. This formalism is useful to investigate theoretically different cancer processes such as the angiogenesis and invasion. We have published several examples and case studies of the use of this model in particular, the action of phase-specific chemotherapies (Ribba, You et al. 2009), the use of anti-angiogenic drugs (Billy, Ribba et al. 2009) and their use in combination with chemotherapies (Lignet, Benzekry et al. 2013). This last work also integrates a model of the VEGF molecular pathway for proliferation and migration of endothelial cells in the context of cancer angiogenesis (Lignet, Calvez et al. 2013).

If these types of models present interesting framework to theoretically investigate biological hypothesis, they however present limitation due to their large number of parameters. In consequence, we decided to stop the development of the multiscale platform until exploration of alternative modeling strategies to deal with real data. We focus our interest on the use of mixed-effect modeling techniques as classically used in the field of pharmacokinetic and pharmacodynamics modeling. The general principal of this approach lies in the integration of several levels of variability in the model thus allowing for the simultaneous analysis of data in several individuals. Nowadays, complex algorithms allow for dealing with this problem when the model is composed by few ordinary differential equations (ODEs). However, no similar parameter estimation method is available for models defined as PDEs. In consequence, we decided: 1. To develop more simple models, based on systems of ODEs, assuming simplistic hypothesis of tumor growth and response to treatment but with a real focus on model ability to predict real data. 2. To work alone the development of parameter estimation methods for PDE models in oncology.

3.4. Parametrization of complex systems

3.4.1. Project-team positioning

We focus on a specific problem: the "population" parametrization of a complex system. More precisely, instead of trying to look for parameters in order to fit the available data for one patient, in many cases it is more pertinent to look for the distribution of the parameters (assuming that it is gaussian or log gaussian) in a population of patients, and to maximize the likelihood of the observations of all patients. It is a very useful strategy when few data per patients are available, but when we have a lot of patients. The number of parameters to find is multiplied by two (average and standard deviation for each parameter) but the number of data is greatly increased.

This strategy, that we will call "population" parametrization has been initiated in the eighties by software like Nonmem. Recently Marc Lavielle (Popix team) made a series of breakthroughs and designed a new powerful algorithm, leading to Monolix software.

However population parametrization is very costly. It requires several hundred of thousands of model evaluations, which may be very long.

3.4.2. Results

We address the problem of computation time when the complex model is long to evaluate. In simple cases like reaction diffusion equations in one space dimension, the evaluation of the model may take a few seconds of even a few minutes. In more realistic geometries, the computation time would be even larger and can reach the hour or day. It is therefore impossible to run a SAEM algorithm on such models, since it would be much too long. Moreover the underlying algorithm can not be parallelized.

We propose a new iterative approach combining a SAEM algorithm together with a kriging. This strategy appears to be very efficient, since we were able to parametrize a PDE model as fast as a simple ODE model.

We are currently developing the corresponding software.

3.5. Models for the analysis of efficacy data in oncology

3.5.1. Project-team positioning

The development of new drugs for oncology patients faces significant issues with a global attrition rate of 95 percents and only 40 percents of drug approval in phase III after successful phase II. As for meteorology, the analysis through modeling and simulation (MS), of time-course data related to anticancer drugs efficacy and/or toxicity constitutes a rational method for predicting drugs efficacy in patients. This approach, now supported by regulatory agencies such as the FDA, is expected to improve the drug development process and in consequence the treatment of cancer patients. A private company, Pharsight, has nowadays the leader team in the development of such modeling frameworks. In 2009, this team published a model describing tumor size time-course in more than one thousand colorectal cancer patients. This model was used in an MS framework to predict the outcome of a phase III clinical trials based on the analysis of phase II data. From 2009 to 2013, 12 published articles address similar analysis of different therapeutic indications such as lung, prostate, thyroid and renal cancer. A similar modeling activity is also proposed for the analysis of data in preclinical experiments, and in particular, experiments in mice. Animal experiments represent critical stages to decide if a drug molecule should be tested in humans. MS methods are considered as tools to better investigate the mechanisms of drug action and to potentially facilitate the transition towards the clinical phases of the drug development process. Our team has worked in the development of two modeling frameworks with application in both preclinical and clinical oncology. For the preclinical context, we have worked on the development of models focusing on the process of tumor angiogenesis, i.e. the formation of intra-tumoral blood vessels. At the clinical level, we have developed a model to predict tumor size dynamics in patients with low-grade glioma.

At Inria, several project-teams have developed similar efforts. The project-team BANG has a solid experience in the development of age-structured models of the cell cycle and tissue regulation of tumors with clinical applications for chronotherapy. BANG is also currently applying these types of partial differential equation (PDE) models to the study of leukemia through collaboration with the project-team DRACULA. Project-team MC2 has recently shown that the analysis, through a simplified PDE model of tumor growth and treatment response, of 3D imaging, could lead to correct prediction of tumor volume evolution in patients with pulmonary metastasis from thyroid cancer. Regarding specifically the modeling of brain tumors, project-team ASCLEPIOS has brought an important contribution towards personalized medicine in analyzing 3D data information from MRI with a multiscale model that describes the evolution of high grade gliomas in the brain. Their framework relies on the cancer physiopathological model that was mainly developed by Kristin Swanson and her group at the university of Washington.

Outside from Inria, we wish to mention here the work of the group of Florence Hubert in Marseille in the development of models with an interesting compromise between mathematical complexity and data availability. A national ANR project led by the team is expected to support the development of an MS methodology for the analysis of tumor size data in patients with metastases.

3.5.2. Results

Regarding our contribution in preclinical modeling, we have developed a model to analyze the dynamics of tumor progression in nude mice xenografted with HT29 or HCT116 colorectal cancer cells. This model, based on a system of ordinary differential equations (ODEs), integrated the different types of tumor tissues, and in particular, the proliferating, hypoxic and necrotic tissues. Practically, in our experiment, tumor size was periodically measured, and percentages of hypoxic and necrotic tissue were assessed using immunohistochemistry techniques on tumor samples after euthanasia. In the proposed model, the peripheral non-hypoxic tissue proliferates according to a generalized-logistic equation where the maximal tumor size is represented by a variable called "carrying capacity". The ratio of the whole tumor size to the carrying capacity was used to define the hypoxic stress. As this stress increases, non-hypoxic tissue turns hypoxic. Hypoxic tissue does not stop proliferating, but hypoxia constitutes a transient stage before the tissue becomes necrotic. As the tumor grows, the carrying capacity increases owing to the process of angiogenesis (Ribba, Watkin et al. 2011). The model is shown to correctly predict tumor growth dynamics as well as percentages of necrotic and hypoxic tissues within the tumor.

Regarding our contribution in clinical oncology, we developed an ODE model based on the analysis of mean tumor diameter (MTD) time-course in low-grade glioma patients (Ribba, Kaloshi et al. 2012).

In this model, the tumor is composed of proliferative (P) and non-proliferative quiescent tissue (Q) expressed in millimeters. The proportion of proliferative tissue transitioning into quiescence is constant. The treatment directly eliminates proliferative cells by inducing lethal DNA damage while these cells progress through the cell cycle. The quiescent cells are also affected by the treatment and become damaged quiescent cells (k_{PQ}). Damaged quiescent cells, when re-entering the cell cycle, can repair their DNA and become proliferative once again (transition from Q_P to P) or can die due to unrepaired damages. We modeled the pharmacokinetics of the PCV chemotherapy using a kinetic-pharmacodynamic (K-PD) approach, in which drug concentration is assumed to decay according to an exponential function. In this model, we did not consider the three drugs separately. Rather, we assumed the treatment to be represented as a whole by a unique variable (C), which represents the concentration of a virtual drug encompassing the three chemotherapeutic components of the PCV regimen. We modeled the exact number of treatment cycles administered by setting the value of C to 1 (arbitrary unit) at the initiation of each cycle (T_{Treat}): $C(T = T_{Treat}) = 1$.

The resulting model is as follows:

$$\begin{aligned}
\frac{dC}{dt} &= -KDE \times C \\
\frac{dP}{dt} &= \lambda_P P \left(1 - \frac{P^\star}{K}\right) + k_{Q_p P} Q_p - k_{PQ} P - \gamma \times C \times KDE \times P \\
\frac{dQ}{dt} &= k_{PQ} P - \gamma \times C \times KDE \times Q \\
\frac{dQ_p}{dt} &= \gamma \times C \times KDE \times Q - k_{Q_p P} Q_p - \delta_{Q_p} Q_p
\end{aligned} \tag{1}$$

We challenged this model with additional patient data. In particular, MTD time-course information from 24 patients treated with TMZ (subset of the 120 patients from SH) and 25 patients treated with radiotherapy (SH). Note that exactly the same K-PD approach was used to model treatment pharmacokinetic (including for radiotherapy). This choice, though not really realistic was adopted for simplicity reasons: the same model can be indifferently applied to the three different treatment modalities of LGG patients.

3.5.3. Collaborations

François Ducray and Jérôme Honnorat (Pierre Wertheimer Hospital in Lyon)

External support: grant INSERM PhysiCancer 2012 and Inria IPL MONICA

3.6. Stroke

3.6.1. Project team positioning

Stroke is a major public health problem since it represents the second leading cause of death worldwide and the first cause of acquired disability in adults.

Numed is currently starting completely new issues with D. Rousseau (INSA) and his team. We have now at hand a large data base of clinical images. Our aim is to develop model which are able to predict the final size of the dead brain area as a function of the first two clinical data.

4. Highlights of the Year

4.1. Highlights of the Year

In the context of a long standing collaboration with Sanofi group, E. Grenier develops a software for the study of the stability of vaccines. This software has been used in a formal presentation of a new vaccine to the FDA (Food and Drug Administration).

4.1.1. Awards

Vincent Calvez has been award the prize of the European Mathematical Society (2016).

5. New Software and Platforms

5.1. Bingham flows

FUNCTIONAL DESCRIPTION

A 1D and 2D code with a new method for the computation of viscoplastic flows with free-surface. It essentially couples Optimization methods and Well-Balanced Finite-Volumes schemes for viscous shallow-water equations (induced by the viscoplastic nature of the fluid). Currently applied to avalanches of dense snow, it is a private code currently actively developed (in C++). One of the key feature is that its well-balanced property allows to obtained the stationary states which are linked to the stopping of the snow avalanche for this highly non-linear type of fluid.

- Contact: Paul Vigneaux

5.2. OptimChemo

FUNCTIONAL DESCRIPTION

OptimChemo is a userfriendly software designed to study numerically the effect of multiple chemotherapies on simple models of tumour growth and to optimize chemotherapy schedules.

- Participants: Emmanuel Grenier, Violaine Louvet, Paul Vigneaux and Ehouarn Maguet
- Contact: Emmanuel Grenier

5.3. SETIS

KEYWORDS: Health - DICOM - Medical imaging - Drug development

FUNCTIONAL DESCRIPTION

SETIS software is a GUI allowing to treat DICOM medical images to extract pathological data. These data can then be exported and used in a SAEM software (including Monolix (Inria et Lixoft)) for the parameters' estimation of models in the context of population approaches. As an example SETIS can be used to segment and compute the tumor size of a patients from MRI scans taken at different times. The software is sufficiently general to be used in various situations by clinicians (already done by colleagues in Lyon Hospital).

- Participants: Paul Vigneaux and Ehouarn Maguet
- Partner: ENS Lyon
- Contact: Paul Vigneaux

5.4. VAXSIMSTAB

KEYWORDS: Bioinformatics - Health - Drug development

FUNCTIONAL DESCRIPTION

VAXSIMSTAB is a modeler stability prediction of vaccine software.

- Participants: Benjamin Ribba, Emmanuel Grenier and Vincent Calvez
- Contact: Emmanuel Grenier

6. Bilateral Contracts and Grants with Industry

6.1. Bilateral Contracts with Industry

- Long standing contract with Sanofi company, on the stability of vaccines. This contract leads to the design and coding of a complete software devoted to the study of the degradation of vaccines. This software has been used in presentations of new vaccines to the FDA.
- Modeling of the quality of glass for a small French company.

7. Partnerships and Cooperations

7.1. European Initiatives

Vincent Calvez is the main investigator of an ERC.

7.1.1. FP7 & H2020 Projects

7.1.1.1. DDMoRE

Programm: FP7

Duration: February 2011 - January 2016

Coordinator: Pfizer

Inria contact: Marc Lavielle

7.2. International Research Visitors

7.2.1. Visits of International Scientists

Toan Nguyen (Penn State University) has visited Numed in June 2016.

8. Dissemination

8.1. Promoting Scientific Activities

8.1.1. Scientific Expertise

Emmanuel Grenier has been expert for an INSERM cancer call.

8.1.2. Research Administration

Emmanuel Grenier is member of the board of the LABEX Archimede (Marseille).

8.2. Teaching - Supervision - Juries

8.2.1. Teaching

Paul Vigneaux, Vincent Calvez and Emmanuel Grenier teach in L3, M1 and M2 at ENSL, including lectures on partial differential equations, modeling, analysis.

8.2.2. Supervision

Edouard Ollier and Mathilde Giacalone is supervised by Emmanuel Grenier, Arthur Marly by Paul Vigneaux and Alvaro Mateos Gonzalez by Vincent Calvez.

9. Bibliography

Publications of the year

Articles in International Peer-Reviewed Journals

- [1] H. BERRY, T. LEPOUTRE, Á. MATEOS GONZÁLEZ. *Quantitative convergence towards a self similar profile in an age-structured renewal equation for subdiffusion*, in "Acta Applicandae Mathematicae", 2016, n^o 145, pp. 15-45, in press, <https://hal.inria.fr/hal-01136667>
- [2] S. EUGENE, T. BOURGERON, Z. XU. *Effects of initial telomere length distribution on senescence onset and heterogeneity*, in "Journal of Theoretical Biology", January 2017, vol. 413, 8 p. , <https://hal.inria.fr/hal-01378596>

[3] E. GRENIER, C. HELBERT, V. LOUVET, A. SAMSON, P. VIGNEAUX. *Population parametrization of costly black box models using iterations between SAEM algorithm and kriging*, in "Computational and Applied Mathematics", April 2016, Accepted March, 24, 2016 [DOI : 10.1007/s40314-016-0337-5], <https://hal.archives-ouvertes.fr/hal-01224004>

[4] M. S. LEGUÈBE, M. G. NOTARANGELO, M. TWAROGOWSKA, R. NATALINI, C. POIGNARD. *Mathematical model for transport of DNA plasmids from the external medium up to the nucleus by electroporation*, in "Mathematical Biosciences", November 2016 [DOI : 10.1016/J.MBS.2016.11.015], <https://hal.inria.fr/hal-01412380>

Invited Conferences

[5] P. VIGNEAUX. *Numerical schemes for viscoplastic avalanches. A shallow - Bingham flow model*, in "SIMAI 2016", Milano, Italy, SIMAI, Politecnico di Milano, September 2016, <https://hal.archives-ouvertes.fr/hal-01376649>

[6] P. VIGNEAUX. *SAEM methods for statistical PDE parameters estimation and application to biology*, in "CIMPA School "Mathematical models in biology and medicine"", Moka, Mauritius, December 2016, <https://hal.archives-ouvertes.fr/hal-01419082>

Other Publications

[7] E. BOUIN, V. CALVEZ, E. GRENIER, G. NADIN. *Large deviations for velocity-jump processes and non-local Hamilton-Jacobi equations*, July 2016, working paper or preprint, <https://hal.archives-ouvertes.fr/hal-01344939>

[8] E. BOUIN, C. HENDERSON. *Super-linear spreading in local bistable cane toads equations*, March 2016, working paper or preprint, <https://hal.archives-ouvertes.fr/hal-01293988>

[9] V. CALVEZ. *Chemotactic waves of bacteria at the mesoscale*, July 2016, working paper or preprint, <https://hal.archives-ouvertes.fr/hal-01340375>

[10] V. CALVEZ, P. GABRIEL, Á. MATEOS GONZÁLEZ. *Limiting Hamilton-Jacobi equation for the large scale asymptotics of a subdiffusion jump-renewal equation*, September 2016, working paper or preprint, <https://hal.archives-ouvertes.fr/hal-01372949>

[11] V. CALVEZ, T. O. GALLOUËT. *Blow-up phenomena for gradient flows of discrete homogeneous functionals*, 2016, working paper or preprint, <https://hal.archives-ouvertes.fr/hal-01286518>

[12] E. GRENIER, F. HAMEL. *Large time monotonicity of solutions of reaction-diffusion equations in R^N* , June 2016, working paper or preprint, <https://hal.archives-ouvertes.fr/hal-01324533>

[13] H. HIVERT. *Numerical schemes for kinetic equation with diffusion limit and anomalous time scale*, October 2016, working paper or preprint, <https://hal.archives-ouvertes.fr/hal-01389100>