MATHEMATICAL MODELLING
OF COMPLEX SYSTEMS

An international conference on mathematical modelling in social sciences and life sciences, statistics and complexity

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Confirmed speakers
F. Bach, H. Berestycki,
G. Bernot, A. Bertozzi,
A. Boudaoud, A. Carbone,
J. A. Carrillo, T. Coolen, V. Danos,
V. Fromion, D. Holcman, C. Matias,
B. Maury, S. Méléard, S. Robin,
G. Toscani, V. Volpert.

Organizing committee
F. Abergel, M. Aiguier, P-H. Cournède, G. Faÿ, P. Laffite

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Invited Talks

Large-Scale Optimization for Machine Learning
Francis Bach

Propagation in Non Homogeneous Media
Henri Berestycki

An extension of Hoare logic to identify the parameters of a gene regulatory network
Gilles Bernot

Mathematics of Crime
Andrea Bertozzi

Stochasticity in Plant Growth and Morphogenesis
Arezki Boudaoud

Conservation and Co-Evolution: from Sequence Analysis to Protein-Protein Interactions
Alessandra Carbone

Stability and Pattern formation in Nonlocal Interaction Models
Jose Antonio Carrillo

Solvable Model of an Immune Network on a Finitely Connected Heterogeneous Graph with Extensively Many Short Loops
Anthony C. C. Coolen

Thermodynamic Graph-Rewriting
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Constraint-Based Approaches as a Promising Tool to Handle the Complexity of Life: the Bacterium as an Example
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Invited Talks
Large-Scale Optimization for Machine Learning

Francis Bach

INRIA - Sierra team, Laboratoire d’Informatique de l’Ecole Normale Supérieure, Paris, France
(Joint work with Nicolas Le Roux, Eric Moulines and Mark Schmidt)

Many machine learning and signal processing problems are traditionally cast as convex optimization problems. A common difficulty in solving these problems is the size of the data, where there are many observations ("large n") and each of these is large ("large p"). In this setting, online algorithms which pass over the data only once, are usually preferred over batch algorithms, which require multiple passes over the data. In this talk, I will present several recent results, showing that in the ideal infinite-data setting, online learning algorithms based on stochastic approximation should be preferred, but that in the practical finite-data setting, an appropriate combination of batch and online algorithms leads to unexpected behaviors, such as a linear convergence rate with an iteration cost similar to stochastic gradient descent.
Diffusion phenomena in heterogeneous environments arise in many different contexts of modelling. A fine description of epidemics spreading such as the black death plague of the 14th century, biological invasions in ecological systems or in medicine lead to this kind of problems. Likewise, contagions of ideas as well as the diffusion of social norms all involve this type of problems. They lead to new questions from a mathematical point of view. What is the role of heterogeneity in blocking propagation? What is the effect of roads with fast diffusion in the global invasion? These are examples of such questions. In this talk I will review some of these questions and models in the framework of reaction-diffusion equations and report on recent progress.
An extension of Hoare logic to identify the parameters of a gene regulatory network

Gilles Bernot

Laboratoire d’Informatique, Signaux et Systèmes Complexes de Sophia-Antipolis (I3S), Université de Nice-Sophia Antipolis and CNRS, Sophia-Antipolis, France

The main difficulty when modeling biological networks is the identification of the numerous parameters that govern the dynamics. After the pioneering works of the SMBioNet and BIOCHAM teams, temporal logic has become a standard formal tool to identify these parameters when applied to discrete models. We propose here a new formal way to identify parameters, which is easier to apply when using data from biological traces, such as transcriptomic data. We will firstly explain the framework of genetic network models defined by R. Thomas. Then, we define a method inspired from Hoare logic, properly extended to genetic state graphs, that is able to extract the weakest precondition on parameters that copes with a given set of observed traces.
Mathematics of Crime

Andrea Bertozzi

Department of Mathematics, UCLA, Los Angeles, CA, USA

There is an extensive applied mathematics literature developed for problems in the biological and physical sciences. Our understanding of social science problems from a mathematical standpoint is less developed, but also presents some very interesting problems, especially for young researchers. This lecture uses crime as a case study for using applied mathematical techniques in a social science application and covers a variety of mathematical methods that are applicable to such problems. We will review recent work on agent based models, methods in linear and non-linear partial differential equations, variational methods for inverse problems and statistical point process models. From an application standpoint we will look at problems in residential burglaries and gang crimes. Examples will consider both "bottom up" and "top down" approaches to understanding the mathematics of crime, and how the two approaches could converge to a unifying theory.
Stochasticity in Plant Growth and Morphogenesis

Arezki Boudaoud

Reproduction et Développement des Plantes, ENS Lyon, Lyon, France

How do organisms cope with natural variability to achieve well-defined morphologies and architectures? We address this question by combining experiments with live plants and analyses of stochastic models. This leads us to counterintuitive results on the role of noise in plant development.
Protein-protein interactions (PPI) are at the heart of the molecular processes governing life and constitute an increasingly important target for drug design. Given their importance, it is vital to determine which protein interactions have functional relevance and to characterize the protein competition inherent to crowded environments, as the cytoplasm or the cellular organelles. Given a family of protein sequences and the associated distance tree, we shall explain how to predict important information on protein binding sites and on protein interactions by using a fine reading of the conservation and co-evolution signals between residues in the sequences. This information is helpful to identify protein-protein interaction networks and describe them at the molecular level.
Stability and Pattern formation in Nonlocal Interaction Models

Jose Antonio Carrillo

*Department of Mathematics, Imperial College London, London, UK*

I will review some recent results for first and second order models of swarming in terms of patterns, stationary states, and qualitative properties. I will discuss the stability of these patterns for the continuum and discrete particle cases. These non-local models appear in collective behavior for animals, control engineering, and molecular structures among others. We first concentrate in the spatial shape of these patterns and the dynamics when inertia terms are neglected. The mathematical question behind consists in finding properties about local minimizers of the total interaction energy. Concerning 2nd order models, we will discuss particular properties of two patterns: flocks and mills. We will discuss the stability of these patterns in the discrete case. In both cases, we will describe the properties obtained for the continuum limits.
The immune system can recall and execute a large number of memorized defense strategies in parallel. The explanation for this ability turns out to lie in the topology of immune networks. We studied a statistical mechanical immune network model with 'coordinator branches' (T-cells) and 'effector branches' (B-cells), and show how the finite connectivity enables the system to manage an extensive number of immune clones simultaneously, even above the percolation threshold. The model is solvable using replica techniques, in spite of the fact that the network has an extensive number of short loops.
Thermodynamic Graph-Rewriting

Vincent Danos

School of Informatics, University of Edinburgh, UK
(Joint work with Russ Harmer and Ricardo Honorato-Zimmer)

We develop a new ’thermodynamic’ approach to stochastic graph-rewriting. The ingredients are a finite set of reversible graph-rewriting rules $G$ (called generating rules), a finite set of connected graphs $P$ (called energy patterns), and an energy cost function $\varepsilon : P \to \mathbb{R}$. The idea is that $G$ defines the qualitative dynamics by showing which transformations are possible, while $P$ and $\varepsilon$ specify the long-term probability $\Pi$ of any graph reachable under $G$. Given $G$, $P$, we construct a finite set of rules $GP$ which (i) has the same qualitative transition system as $G$, and (ii) when equipped with suitable rates, defines a continuous-time Markov chain of which $\Pi$ is the unique fixed point. The construction relies on the use of site graphs and a technique of ‘growth policy’ for quantitative rule refinement which is of independent interest. The ’division of labour’ between the qualitative and the long-term quantitative aspects of the dynamics leads to intuitive and concise descriptions for realistic models. It also guarantees thermodynamical consistency (aka detailed balance), otherwise known to be undecidable, which is important for some applications. Finally, it leads to parsimonious parameterizations of models, again an important point in some applications.
Constraint-Based Approaches as a Promising Tool to Handle the Complexity of Life: the Bacterium as an Example

Vincent Fromion

INRA, UR1077, Mathématique Informatique et Génomé, Jouy-en-Josas, France
(Joint work with A. Goelzer (INRA-MIG) and the partners of the BaSynTech EU project)

Growth is a highly optimized process in bacteria since the battle for the conquest of ecological niches is tough. Understanding the key elements governing the growth rate management of bacteria is then crucial to further understand and predict the bacterium behavior with respect to various environmental conditions. In this context, the constraint-based approaches integrating the whole metabolic network of an organism such as Flux Balance Analysis successfully predicted the maximum growth rate reachable in various conditions. However, limitations exist since FBA fail to predict a number of commonly observed metabolic strategies, showing implicitly that constraints are missing. In particular, we have recently shown that the sharing of proteins between the cellular processes intrinsically and structurally limits the growth rate. More generally, we have formalized the problem of protein allocation at the cell scale as a (quasi) convex optimization problem. The resolution of this convex optimization problem allows to estimate for a given medium composition of (i) the maximal growth rate reachable; (ii) the concentrations of ribosomes, the concentration of proteins involved in the metabolic network and more generally the resource allocation between all the cell components; (iii) the flux distribution. More fundamentally, this new method allows to predict the emergence of functional modules in the metabolic network regulation.

The aim of this talk is then to present this new framework, so-called Resource Balance Analysis (RBA), and its recent validation with respect to biological data on the model bacterium Bacillus subtilis.
Bursting in Small and Large Neuronal Networks: from Physiology to Analysis

David Holcman

Ecole Normale Supérieure, IBENS, Paris, France

Neuronal network activity can generate complex patterns that depend on membrane properties of individual neurons as well as functional synapses. To analyze the complex behavior of neuronal network, we study the transient response from neuronal ensembles of small (between 5-30 cells in a restricted space) and large sizes (acute hippocampal slice). Interestingly, in both cases a single stimulation generated a synchronous long lasting bursting activity. Based on electrophysiological recordings, we derive a stochastic dynamical system that characterizes this bursting activity in these neuronal populations. We compute the bursting time analytically. We further found a regime of Up- and Down-states characterized by an unstable limit cycle. Surprisingly, the distribution of escape times from the basin of attraction cycle is not Poissonian, as previously shown in the classical escape problem, but presents quantized peaks. We obtain a full characterization of these peaks from the analysis of the Fokker-Planck equation, associated with the stochastic equation.

The present study shows that synaptic properties and network connectivity shape the mean burst duration, which persisted across various network scales. Thus synchronization is an inherent property of sufficiently connected neural networks driven by synaptic depression-facilitation.
Stochastic Blockmodels for Random Graphs

Catherine Matias

Laboratoire Statistique et Génome, Evry, France

We will discuss in details the stochastic blockmodel that allows to capture heterogeneity in random graphs, its properties and applications.
The Respiratory System from all Sides

Bertrand Maury

*Laboratoire de Mathématiques d'Orsay, Université Paris Sud, Orsay, France*

The modeling of complex systems can be undertaken from two sides. The Top Down approach consists in identifying a small number of relevant parameters and relations between them, and in progressively integrating more and more complexity to the description in order to reach a satisfying description of the global behavior. On the other side, the Bottom Up approach consists in starting from the finest level at which the reality can be described by basic and unquestionable laws (like Newton’s law for mechanical systems). From this microscopic description of subsystems, an attempt can be made to build “the big picture”, i.e. a model that mimics the overall functioning of the system.

We shall illustrate these considerations in the context of lung modeling, by focusing on the notion of resistance of the respiratory system. Measuring this quantity is common medical practice (Top Down standpoint), whereas its actual signification covers a wide range of complex phenomena (Bottom Up). Merging both standpoints, i.e. obtaining similar numerical values by the two different approaches and build a hierarchy of mutually consistent models, is the holy grail for applied mathematicians involved in the modeling process of complex systems. We shall present different aspects of this lengthy process, which calls for constant back and forth moves between the two sides.
Stochastic Modeling of Darwinian Evolution

Sylvie Méléard

CMAP, Ecole Polytechnique, Palaiseau, France

We consider stochastic models describing the Darwinian evolution of a polymorphic population with mutation and selection. The interactions between individuals occur by way of competition for resources whose concentrations depend on the current state of the population. Our aim is to model the successive fixations of successful mutants in the population and further its diversification on an evolutionary time scale. We prove, starting from a birth and death model, that, when advantageous mutations are rare and the population size large enough, the population process behaves on the mutation time scale as a jump process moving between successive equilibria. The main idea is a time scale separation. The model explains a possible diversification into specialized species more adapted to consume some specific resources. Essential technical ingredients are the study of a generalized system of ODE’s modeling a finite number of biological populations in a competitive interaction due to multi-resources and a fine description of the invasion and fixation of mutants using branching processes.
Modelling Heterogeneity in Interaction Networks

Stéphane Robin\textsuperscript{1,2}

\textsuperscript{1} INRA, UMR 518 MIA, Paris, France, \textsuperscript{2} AgroParisTech, UMR 518 MIA, Paris, France

Network analysis has become a very active field of statistics within the last decade. Several models have been proposed to describe and understand the heterogeneity observed in real networks. We will present here several modelling involving latent variables. We will discuss the issues raised by their inference, focusing on the stochastic block model and on the graphon model. The presentation will be illustrated with several applications.
Kinetic and Fokker-Planck Models for Goods Exchange in Microeconomics

Giuseppe Toscani

University of Pavia, Department of Mathematics, Pavia, Italy
(Joint work with Stefano Demichelis and Carlo Brugna, from the University of Pavia)

We introduce various kinetic equations able to describe the exchange of goods among a huge population of agents. The leading idea is to describe the exchange by means of some fundamental rules in microeconomics, in particular by using Cobb-Douglas utility functions for the binary exchange, and the Edgeworth box for the description of the common exchange area in which utility is increasing for both agents. In presence of uncertainty, it is shown that the solution develops Pareto tails, where the Pareto index depends on the ratio between the gain and the variance of the uncertainty. Among others, the result holds true for a linearized Boltzmann-like equation, whose solution is shown to converge to the solution of a drift-diffusion equation of a Fokker-Planck type.
On the Emergence and Evolution of Biological Species

Vitaly Volpert

Université de Lyon, UMR CNRS 5208, Institut Camille Jordan, Villeurbanne, France

Darwin illustrated his theory about emergence and evolution of biological species with a diagram. It shows how species exist, evolve, appear and disappear. The goal of this presentation is to give a mathematical interpretation of this diagram and to show how it can be reproduced in mathematical models. It appears that conventional models in population dynamics are not sufficient, and we introduce new models which take into account local, nonlocal and global consumption of resources, and models with space and time dependent coefficients.
Poster Presentations
A non-linear version of the wave equation in a string of a guitar

Elisabete Alberdi Celaya¹, Juan José Anza Aguirrezabala²

¹Department of Applied Mathematics, EUIT de Minas y Obras Públicas, Universidad del País Vasco UPV/EHU, Spain
²Department of Applied Mathematics, ETS de Ingeniería de Bilbao, Universidad del País Vasco UPV/EHU, Spain

The non-linear Partial Differential Equation (PDE) which corresponds to a non-linear version of a string of a guitar has been modelled. Real data have been used for the length, the diameter and the section of the string, as well as for the frequency and for the tension. The first mode of vibration has been considered and a time interval of five linear periods, which corresponds to the linear behaviour with small deformations.

After applying the Finite Element Method (FEM) approximation to this problem a non-linear Ordinary Differential Equations (ODE) system is obtained. This system is solved by the trapezoidal rule, the MATLAB odesolver ode15s and the HHT-α method and the differences observed in the different solutions are reported.

References

Heat content asymptotic propagation in compact domains with discontinuous transmission boundary conditions

Claude Bardos¹, Anna Rozanova-Pierrat²

¹ Laboratory Jacques Louis Lions, University of Paris 6, Pierre et Marie Curie, France
² Laboratory of Applied Mathematics and Systems, Ecole Centrale Paris, France

We consider a heat problem posed in \( \mathbb{R}^n \) with discontinuous coefficients over \( \partial \Omega \) and discontinuous boundary transmission conditions with a resistance coefficient \( \lambda \):

\[
\begin{align*}
\partial_t u^+ - \text{div}(D_+(x) \nabla u^+) &= 0 & x \in \mathbb{R}^n, \ t > 0, \\
u^+|_{t=0} &= 1, \ u^-|_{t=0} = 0, \\
D_-(x) \frac{\partial u^-}{\partial n} |_{\partial \Omega} &= -\lambda(x) (u^+ - u^-)|_{\partial \Omega}, \\
D_+(x) \frac{\partial u^+}{\partial n} |_{\partial \Omega} &= D_-(x) \frac{\partial u^-}{\partial n} |_{\partial \Omega},
\end{align*}
\]

where \( \Omega \) represents a “hot body” and \( \mathbb{R}^n \setminus \overline{\Omega} \) is a “cold” one, \( D_+ \in C^2(\overline{\Omega}), D_- \in L_\infty(\mathbb{R}^n \setminus \Omega) \cap C(\mathbb{R}^n \setminus \Omega), \lambda > 0 \) for all \( x \in \partial \Omega \) and \( \lambda \in C^1(\partial \Omega) \). We obviously suppose that \( D_-|_{\partial \Omega} \neq D_+|_{\partial \Omega} \), what excludes the case of continuous metric \( g_-|_{\partial \Omega} = g_+|_{\partial \Omega} \) considered in [1]. Let notice that for \( \lambda = 0 \) conditions (3)–(4) give the Neumann boundary condition, and hence \( u^- \equiv 0 \), but for \( \lambda = +\infty \) we have the continuity of \( u_+ = u_- \) on the boundary \( \partial \Omega \).

For this problem, which is well-posed, we show that for all compact connected domains \( \Omega \) in \( \mathbb{R}^n \) (\( \text{Vol}(\Omega) < \infty \)) the heat content

\[
N(t) = \int_{\mathbb{R}^n \setminus \Omega} u(x,t) \, dx = \text{Vol}(\Omega) - \int_{\Omega} u(x,t) \, dx
\]

has the following asymptotic expansion for \( t \to 0 \):

\[
N(t) = \sqrt{t} \int_{\partial \Omega} \frac{\lambda(\sigma)}{2 \sqrt{D_+(\sigma)}} \text{Vol}(\Omega_2 \sqrt{D_+(\sigma)}) \, d\sigma [1 + O(\sqrt{t})] + O(t^2),
\]

where for a fixed \( \sigma \in \partial \Omega \)

\[
\Omega_2 \sqrt{D_+(\sigma)} = \{ x \in \Omega \mid \text{dist}(x,\sigma) < 2 \sqrt{D_+(\sigma)} \}.
\]

Expansion (6) is actually an approximation of the following asymptotic formula

\[
N(t) = 2 \sqrt{t} \int_{\Omega} \frac{\lambda(\sigma)}{\sqrt{D_+(\sigma)}} \int_0^{+\infty} e^{2\lambda(\sigma)\alpha(\sigma)\sqrt{t} + \lambda^2(\sigma)\alpha^2(\sigma)} \, d\sigma \, dz + O(t^2),
\]

where \( \alpha = \frac{1}{\sqrt{D_+(\sigma)}} + \frac{1}{\sqrt{\sigma}}. \)

In particular, for a domain with a regular boundary, (6)–(7) give

\[
N(t) = t \int_{\Omega} \lambda(\sigma) \, d\sigma + O(t^2),
\]

and for a fractal boundary we replace \( \text{Vol}(\Omega_2 \sqrt{D_+(\sigma)}) \) by the volume of the interior Minkowski sausage which was estimated in [2].

References


Dynamics of Trust in Networks and Systemic Risk

João da Gama Batista\textsuperscript{1}, Damien Challet\textsuperscript{1} and Jean-Philippe Bouchaud\textsuperscript{2,3}

\textsuperscript{1}École Centrale Paris
\textsuperscript{2}Capital Fund Management and \textsuperscript{3}École Polytechnique

The feeling of confidence or trust is widely considered a crucial “macro” variable to describe the dynamics of the financial markets. It is driven both by objective information (e.g.: the state of the economy) and interaction between the agents. Moreover, it is highly sensitive to expectations about what other people expect, which is one of the fundamental feedback loops for self-fulfilling prophecies. Sudden evaporation of trust tends to reinforce financial crises, for instance by causing liquidity breakdowns. In contrast to more static approaches, we model both the creation and destruction of the network over time, with a mutual feedback between one’s links to one’s trustworthiness. In this model, losing trust is a faster phenomena than gaining trust, triggering panic avalanches which cause the sudden disintegration of the network for specific parameter values. This research project is part of the pan-European initiative CRISIS \cite{1}.

References

\cite{1} Complexity Research Initiative for Systemic Instabilities: http://www.crisis-economics.eu
Pattern Formation in a Generalized Phyllotactic System

Robert Beyer¹, Jürgen Richter-Gebert²

¹ Laboratory of Applied Mathematics and Systems, Ecole Centrale Paris, France
² Zentrum Mathematik, Technische Universität München, Germany

Based on Hofmeister’s hypothesis [1] on the time \( t \) and position \( x \) of the formation of a new primordium on the apical ring of a plant’s shoot, [2] present a variation of the iterative model

\[
t_{n+1} = t_n + \lambda \\
x_{n+1} = \arg\min_{x \in S^n} \sum_{i=1}^{n} \|x - (1 + t_n + \lambda - t_i) \cdot x_i\|^{-2}
\]

(1)

where \( \mathbb{R}^2 \) represents the plant’s surface, \( S^1 \) its apical ring and \( \lambda > 0 \) the plastochrone. For any \( \lambda \) and well-behaved initial conditions, the divergence angle \( \delta_n(\lambda) = \angle x_{n+1}, x_n \) converges for \( n \to \infty \). The model generalizes straightforwardly to \( \mathbb{R}^m \) when replacing the unit circle in iteration (1) by \( S^{m-1} \). In order to describe the emerging patterns we generalize the divergence angle to

\[
\delta_n(j)(\lambda) = \angle \text{span}(x_{n+j}, \ldots, x_{n+1}), \text{span}(x_{n+j-1}, \ldots, x_{n}), \quad j = 1, \ldots, m - 1
\]

We simulated the case \( m = 3 \): For all large \( \lambda \), both divergence angles converge to \( \pi \) and primordia form at two poles of \( S^2 \). With decreasing \( \lambda \), at first the limit of \( \delta_n(1)(\lambda) \) decreases continuously while that of \( \delta_n(1)(\lambda) \) remains \( \pi \), Fig. 1(a). In this parameter range, primordia form on a great circle of \( S^2 \). For even smaller \( \lambda \), \( \delta_n(2)(\lambda) \) continuously deviates from \( \pi \) and alternates (in the limit \( \delta_{2n}(2)(\lambda) = 2\pi - \delta_{2n-1}(2)(\lambda) \)), Fig. 1(a), corresponding to primordia forming on two parallel small circles of \( S^2 \). Further decreasing \( \lambda \) initiates fluctuations in the divergence angle sequence – increasing in amplitude with decreasing \( \lambda \) (Fig. 1(b)) – reminiscent of overlapping sinusoids, Fig. 1(c). The set of positions on \( S^2 \) where primordia are formed for these \( \lambda \) reminds of sines as well. For even smaller \( \lambda \), no structure whatsoever is apparent, the sequences seem to be chaotic.

Figure 1: (a) Limits of \( \delta_n(1)(\lambda) \) (blue) and \( \delta_n(2)(\lambda) \) (green) against those \( \lambda \) for which they converge. Light blue points correspond to \( \delta_n \) in 2D which (merely) converges for any \( \lambda > 0 \). (b) sup \( \inf \delta_{2n}(1,2) \), \( \inf \delta_{2n}(1,2) \) and the means of the regularly fluctuating sequences. shown in (c) for \( \lambda = 0.198 \).

References


Substance Abuse via Legally Prescribed Drugs: The Case of Vicodin in the United States

Wendy K. Caldwell\textsuperscript{1}, Benjamin Freedman\textsuperscript{2}, Luke Settles\textsuperscript{3}, Michael M. Thomas\textsuperscript{4}
\textsuperscript{1} Department of Mathematics, University of Tennessee, Knoxville, USA
\textsuperscript{2} Department of Mathematics, Bucknell University, USA
\textsuperscript{3} Department of Mathematics and Statistics, Southern Illinois University Edwardsville, USA
\textsuperscript{4} Department of Mathematics and Statistics, Kennesaw State University, USA

Among medically accessible pain relievers, Vicodin is the most widely prescribed in the United States [1]. Although it comprises 4\% of the world’s population, the United States uses 99\% of the world’s supply of hydrocodone, the narcotic agent in Vicodin [2]. Research indicates that the most common path to becoming a Vicodin abuser begins with a prescription [3]. We develop and analyze two mechanistic mathematical models for a population introduced to Vicodin by prescription and their dynamics and transition through the stages of medical use, drug abuse, and treatment. We model relapse into the abuse compartment in two ways: a non-linear Social Interaction with Abuse-Dependent Prescription Rate (SIAD, Figure 2) Model incorporating social interaction and one linear Compartmental Vicodin Transition (CVT, Figure 1) Model without it.

\textbf{Figure 2: CVT Model}

\textbf{Figure 3: SIAD Model}

Sensitivity analyses are conducted varying the rates of success of these intervention methods measured by the parameters to determine which strategy has the greatest impact on controlling the population of Vicodin abusers. These results give insight into the most effective method of reducing the number of people who abuse Vicodin. From these models, we determine that manipulating parameters tied to prevention measures has a greater impact on reducing the population of abusers than manipulating parameters associated with treatment. We also note that increasing the rate at which abusers seek treatment affects the population of abusers more than the success rate of treatment itself.

References


Detection of Correlations with Adaptive Sensing

Rui M. Castro¹, Gábor Lugosi², Pierre-André Savalle³

¹ Eindhoven University of Technology, ² Pompeu Fabra University, ³ ENS Cachan & Ecole Centrale Paris

The problem of detecting correlations from samples of a high-dimensional Gaussian vector has recently received a lot of attention. In most existing work, detection procedures are provided with a full sample. However, following common wisdom in experimental design, the experimenter may have the capacity to make targeted measurements in an on-line and adaptive manner. In this work, we investigate such adaptive sensing procedures for detecting positive correlations. It is shown that, using the same number of measurements, adaptive procedures are able to detect significantly weaker correlations than their non-adaptive counterparts. We also establish minimax lower bounds that show the limitations of any procedure.

References


Holographic Coding of Non-optic Information for Data Compression

Shlomi Dolev¹, Sergey Frenkel²

¹ Dept. of Computer Science; Ben-Gurion University of the Negev, Israel
² Institute of Informatics Problems, Russia

Unique property of holograms is that the original image may be reconstructed from any of the hologram portions as a "blurred" image, and the "blurredess" (quality) depends only on the size and the number of the portions. These properties are resulted from known optical laws (diffraction, interference etc.). It is no wonder, that such attractive features try to use also for non-optical objects. Holographic memories providing large storage capacity and fast data access is an example. In fact, in modern theory of Locally Detectable Codes (LDC) some holographic features also are exploited, namely, the using of techniques enabling to correct the codes by examining only a few bits. The features of the hologram portions mentioned above are a way of lossy compression of the original information, where information about original object is retained in the portion but in a "blurred" manner. Thereby, these features can be expressed in terms of different spectral transformations. Recently [1] we have showed a way to holographic-based compression/encoding for arbitrary integer arrays. First of all, we showed that in this case Walsh-Hadamard spectral transformation (WHT) has benefits over the Fourier transformation for integer arrays. We proposed to randomize the data so that the coefficients of the Walsh-Hadamard code will ensure, with high probability, a monotonic gain of information, then the array can be represented by a set of spectral Walsh-Hadamard coefficients that have holographic properties. Namely, any portion of the set of coefficients defines a 'blurry' image of the original data. The values of the coefficients of the Walsh-Hadamard transformation are distributed approximately normally when the information is randomized. Moreover the randomization of the original information yields robust code that is able to cope with missing coefficients. We estimate each bit \( b_i \) of the randomized sequence \( b \) by Walsh-Hadamard Transformation mentioned above as \( \tilde{b}_i = \sum_{j=0}^{\ell} c_j W(j,i) \). 'j' is the ordered index of the first \( \ell \) large coefficients. We suggested a metric that captures the difference of the bits \( b_i \) and \( \tilde{b}_i \). Each coefficient \( c_i \) is transmitted/stored with its index \( i \) in the WHT matrix, namely the pairs \( (c_i; i) \) are stored as the representation of the data.

In spite of suitable effectiveness of the WHT based coding [1] for compression, this is only lossy compression method. The lossless algorithms provide the compression of a file to the values dependent asymptotically on entropy of a source modeling the file generation [2]. It would be interesting to consider a relationship between the entropy and the holographic property of the WHT based codes. In this presentation we will show such relationship. For example, well-known compression algorithm of Lempel and Ziv (LZ77) gives asymptotically optimal compression ratios for sequences, that is asymptotically equivalent to Shannon’s entropy as the size of the sequence goes to infinity. Namely, the less entropy of WHT coefficients set of a file \( F \) previously randomized as mention above, the more compression rate of this set can be provided by LZ77 algorithm. In particular, the more WHT coefficients are zero-valued the more compression is provided, and on the other hand, the less entropy (of \( \ell \) order [2]) the coefficients set has. As the coefficients are normally distributed with zero expected value, we may expect such low entropy property.

References


Cellular automata and L-Systems are well-known formal models to describe the behaviour of biological processes. They are discrete dynamical systems, each of which can have complex and varied behaviour. Here, we study a class of substitutive systems incorporating properties of both cellular automata and L-systems, that exhibits self-reproducing behaviour. A one-dimensional array of cells is considered, which might loosely be thought of as a model for algae. Each cell has a set of modes or states which are determined by a number from $\mathbb{Z}/n\mathbb{Z}^*$ ($n$ prime). The behaviour of a cell depends on the states of its neighbours and obeys to an additive rule. It has also a cell-division mode, which allows the line of cells to grow. The behaviour of such a model can be complex, but, using algebraic techniques, we prove that it can describe a reproducing system.

References

Small World Picture of Worldwide Seismic Events

Douglas S. R. Ferreira\textsuperscript{1,2}, Andrés R. R. Papa\textsuperscript{2,3}, Ronaldo Menezes\textsuperscript{4}

\textsuperscript{1} Instituto Federal de Educação, Ciência e Tecnologia do Rio de Janeiro, Paracambi, RJ, Brazil
\textsuperscript{2} Geophysics Department, Observatório Nacional, Rio de Janeiro, RJ, Brazil
\textsuperscript{3} Instituto de Física, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil
\textsuperscript{4} BioComplex Laboratory, Computer Sciences, Florida Institute of Technology, Melbourne, USA

The understanding of long-distance relations between seismic activities has for long been of interest to seismologists and geologists. In this paper we have used data from the world-wide earthquake catalog for the period between 1972 and 2011, to generate a network of sites around the world for earthquakes with magnitude $m \geq 4.5$ in the Richter scale. Figure 1 depicts a toy example of a network being formed.

After the network construction, we have analyzed the results under two viewpoints. Firstly, in contrast to previous works [1], which have considered just small areas, we showed that the best fitting for networks of seismic events is not a pure power law, but a power law with exponential cutoff. We also have found that the global network presents small-world properties [2]. Secondly, we have found that the time intervals between successive earthquakes have a cumulative probability distribution well fitted by nontraditional functional forms [3]. The implications of our results are discussed. We also sketch some future trends of our work.

References


Indirect Influences in the international trade

Laura Gómez Bermeo

Universidad Sergio Arboleda, Colombia

Using the theory of complex networks, indirect influences and the PWP method, we compute and study indirect influences in international trade. We construct the international trade graph by taking countries as nodes and connecting two nodes by an edge if one exports or imports to the other. Our main goal is to understand the difference between direct influences, represented by the direct trade graph, and indirect influences. For A and B countries, represented by nodes in the trade graph, we define an equation that computes the weight of the edge, if any, from A to B in the matrix of direct influences. The equation represents the direct influence in trade from the country A to the country B and computes the percentage of the total trade with the world that depends on the country B. To use this equation we collect data of exports and imports between countries, the GDP and the totals of exports and imports of each country. Then we calculate with the PWP method the indirect influences between countries and compare with the direct influences. Our results yield two rankings among nations, by direct influences and by indirect influences in international trade. Comparing both rankings we analyze relevant changes in economics terms and consider them through the use of applied mathematics.

References

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Multiscale DNA Modeling and Birod Mechanics

Alexandre Grandchamp, Jaroslow Glowacki, John H. Maddocks

Laboratory for Computation and Visualization in Mathematics and Mechanics (LCVMM), EPFL, Switzerland

A standard description of DNA fragments is provided by the Kratky-Porod model of bending and twisting, which corresponds in continuum mechanics language to an inextensible and unshearable elastic rod [1, 2]. Classical rod theory, which is useful in applications over a wide range of length scales, e.g. from polymers to plant tendrils and wire ropes, allows one to describe more complex mechanical behaviours involving shear and extension, which are also pertinent to DNA [3, 4]. However, at short scales, strand separation is central to the function of DNA, which requires a continuum mechanics theory of interacting double-stranded filaments: called the birod theory [5].

Figure 2: Sketch of Multiscale DNA Modeling

We will show that birod equilibrium configurations are solutions of non-canonical Hamiltonian evolution equations in arc-length. Moreover, we will present how a multiscale DNA modeling approach can be built by parametrizing the birod Hamiltonian in a sequence-dependent way starting from coarse grained rigid base models, which are in turn parameterized by finer grain molecular dynamic simulations [6]. Finally, we will show how birod two-point boundary value problems can be solved numerically, using a parameter continuation method, in order to investigate features of DNA equilibrium probability distributions that can be probed experimentally.

References

Multi-channel Analysis of Micro-cracks in Reinforced Concrete

Thomas A. Lampert¹, Asher Perez², Anatoli Babchenko³

¹ ICube, UMR 7357 Université de Strasbourg, Strasbourg, France
² Département de Physique, Université de Strasbourg, Strasbourg, France
³ Optical Physics Department, Jerusalem College of Technology, Jerusalem, Israel

The detection of cracks in concrete is a problem with wide ranging safety applications. A novel approach is to embed optical fibers within the concrete, to model their optical properties and subsequently detect changes that indicate a structural failure. We are currently able to clearly record signal changes caused by external pressure upon external optical fibers. Our research is focused on providing a means to detect pressure signals along both internal and external optical fibers, to detect possible failures in the surrounding concrete. Furthermore, we are researching the embedding of multiple fibers in a matrix structure, to allow for the detection of the failure’s position. Our research shows that this can be achieved using several signal features that can be detected asynchronously (hits, time of flight etc.). The noise level inherent in this problem is high and therefore a high level of precision is required. Our research has shown that accurate detection may be achieved using a fast photo-diode device that enables sub-meter precision, where such a device has been designed within our laboratory.
Numerical Acceleration Techniques for a Multiscale Model of Tumor Growth
Annelies Lejon, Giovanni Samaey, Dirk Roose
Scientific Computing, KU Leuven, Belgium

Introduction
Cancer is currently one of the most important causes of death in the western society. The WHO estimates 7.6 million people died of cancer in 2008. Tumour growth is a complex multiscale phenomenon (with cellular and intracellular effects affecting the tissue level). Thus its simulation using detailed (microscopic) models is computationally very expensive with classical techniques. This poster discusses numerical techniques to accelerate multiscale simulations of tumour growth.

Methods
One can describe tumour growth on different levels. The most common are (i) a macroscopic continuum description (usually a set of PDEs) and (ii) a microscopic particle-based description (usually a set of ODEs per cell or a cellular automaton). Clearly, the macroscopic description is cheap compared to the microscopic one, whereas the microscopic model is very detailed. Additionally, we use a mesoscopic description based on kinetic equations. This work will study three acceleration techniques. The first component is a domain decomposition technique such that the detailed model is only used in the active zones of the tumour. Second, we use variance reduction techniques to reduce the variance on the microscopic simulation. As a consequence, we need fewer particles to obtain the same level of accuracy. Finally, we also use a specific technique - called projective integration [1] - that allows us to accelerate the simulation of the mesoscopic, kinetic level. Since the system evolution involves multiple time scales, the resulting kinetic equation is very stiff. Classical explicit integration schemes would force us to use a very small time step to satisfy the stability condition. We further developed a projective integration scheme [2], which first takes a few microscopic time steps, and then extrapolates the result over a large projective time step.

Results
Using the numerical acceleration techniques described above, we aim at obtaining an acceleration of the simulation of a factor 10-100, depending on the specific tumor. This should make it possible to use in silico models as an extra tool to develop drugs more efficiently. We will outline the approach and illustrate with numerical results. As a first result, we already demonstrated that, by using projective integration for multiscale kinetic equations, we were able to accelerate the simulation at the mesoscopic level. We are currently extending a variance reduction approach for a particle-based simulation that couples a microscopic ODE-model [3] with the kinetic model.

References
A Model of Cell Polarisation

Nicolas Muller

Université Paris Descartes, France

In this work, we focus on the modelling of cell polarisation during the mating of yeast. We use a convection-diffusion model with a non-linear and non-local drift [1, 2, 3] to describe the distribution of molecular markers responsible of the cell polarisation. This model is similar to the Keller-Segel model, the source of the attractive potential comes from the boundary of the domain. Biological observations show that there is a critical value on pheromone concentration at which cells polarize, we find a similar behaviour in our numerical simulations in two dimensions [4]. In a more realistic model, we consider a dynamical exchange of molecular markers with the membrane. The similarity in the behaviour of our numerical results with experimental results provided by Mr. Piel allows us to estimate the biological data with the model [1]. This validation requires adding a dynamical noise in our numerical simulations [5]. Indeed, numerical simulations [4] done in an uniform field allow us to fix the free parameters. In a gradient of pheromone, the behaviour of the numerical cell, with the same parameters chosen in the uniform field, is similar to the behaviour observed by M. Piel for yeast cells.

Although the main mechanisms of polarization are known precisely, but the way cells communicate with each other remains unexplained. The choice of sexual partner is an issue that raises many research interests in biology. We set, through a simplification, a first criterion ensuring cell discussion, involving mainly the distance between cells [5]. By using a numerical simulation, we show that the distance between cells seems to be an important element also in determining the choice of partner.

References

Population Model for Tumor Cells with Influence of D-factor

T.R. Myrzakul\(^1\), J.J. Yermekbayeva \(^2\)

\(^1\) Eurasian International Center for Theoretical Physics, Department of General Theoretical Physics, Eurasian National University, Astana, Kazakhstan

\(^2\) Department of System Analysis and Management, Eurasian National University, Astana, Kazakhstan

Currently, malignant tumors are the subject of active research of biologists and chemists, but also mathematicians and physicists. As the supply of biologists and chemists model can not fully predict the progression of the tumor, and accordingly offer the most appropriate treatment in this particular case. In this regard were created huge number of mathematical and physical models, whose main aim is to describe the process of the emergence and growth of tumor cells, that is, the dynamics of tumor cells and reset the most appropriate clinical treatment \(^1\).

In this work we investigate the mathematical model of tumor growth taking into account the interaction of tumor cells with two types of cells responsible for the organism’s resistance against the tumor growth \(^2\). Our model is:

\[
\begin{align*}
\dot{x} &= j - \beta xy - y^3 + \frac{\alpha xy}{1+y} - (x^3 + y^3 + k_1 xy - k_2 y + k_3 x) \\
\dot{y} &= y - \frac{\mu y}{1+y} - xy - (y^3 + x^3 + k_1 y x - k_2 x + k_3 y) 
\end{align*}
\]  

(1)

Here \(x\) is the concentration of free cells (effector cells), \(y\) is the concentration of tumor cells, \(j\) is the growth rate of effector cells, \(\beta xy\) is the death rate of effector cells due to their interactions with tumor cells, \(xy\) is the death rate of tumor cells due to their interactions with effector cells, \(\gamma\) controls the growth rate of effector cells due to interactions with tumor cells, \(\alpha\) controls the growth rate of tumor cells, \(\mu\) controls the natural death rate of effector cells, and \(\delta\) controls the natural death rate of tumor cells. The \(-x^3 - y^3 - k_1 xy + k_2 y + k_3 x\) is hyperbolic umbilic catastrophe or D-factor which is a function of three parametric structurally steady mappings. D-factor can be described, explained, as some sort of type of treatment, such as chemotherapy, radiation therapy and etc. The negative signs of D-factor means the specific effect on the organism and \(k_1, k_2, k_3\) are control values. Check whether our system is stable or not, as well as the stability conditions can be found by using Lyapunov function \(^2\). Through this method can also be found stability equilibrium of the system. For the dynamical system (1) the total derivative of the Lyapunov function is:

\[
W(x_1, x_2) = - \left[ j - \beta x_1 x_2 - y^3 + \frac{\alpha x_1 x_2}{x_2 + 1} - x^3 - y^3 - k_1 y x + k_2 y - k_3 x \right]^2 - \left[ x_2 - \frac{\mu x_2}{\delta x_2 + 1} - x_1 x_2 - y^3 - x^3 - k_1 y x + k_2 x - k_4 y \right]^2
\]

We can see that \(W(x_1, x_2, ..., x_n) \leq 0\). For asymptotic stability derivative is negative function, ie \(W(x_1, x_2, ..., x_n) < 0\) at all points except at the point \(x = 0\). The proposed results can be used in theoretical studies to stabilize the immune system at predicted level. These results are particularly relevant as a new method of mathematical modeling and as well as applied method for prevention and early diagnosis of cancer and to recovery of a health.

References


A Lax Representation and Equivalent Counterpart for one Heisenberg Ferromagnet Equation in (1+1)-Dimension

Gulgassyl Nugmanova\(^1\), Galiya Mamyrbekova\(^2\)

\(^1\)Department of Mathematical and Computer Modelling, L.N.Gumilyov Eurasian National University, Kazakhstan
\(^2\)Department of General and Theoretical Physics, L.N.Gumilyov Eurasian National University, Kazakhstan

In this work we study one integrable Heisenberg Ferromagnet Equation with self-consistent potentials called Myrzakulov-XCIX equation (M-XCIX equation) which is given as [1]-[4]

\[ S_t + 0.5\varepsilon_1 S \wedge S_{xx} + \frac{2}{\omega} S \wedge W = 0, \]  \hspace{1cm} (1)

\[ W_t + 2\omega S \wedge W = 0, \]  \hspace{1cm} (2)

where \(\wedge\) denotes a vector product and

\[ S = (S_1, S_2, S_3), \quad W = (W_1, W_2, W_3). \]  \hspace{1cm} (3)

Here \(S^2 = S_1^2 + S_2^2 + S_3^2 = 1\), \(S_i\) and \(W_i\) are some real functions, \(\omega\) and \(\varepsilon_i\) are real constants.

We have constructed a Lax representation for the M-XCIX equation which shows the integrability of this equation by the Inverse Scattering Method:

\[ \Phi_x = U\Phi, \]  \hspace{1cm} (4)

\[ \Phi_t = V\Phi, \]  \hspace{1cm} (5)

where

\[ U = -i\lambda S, \]  \hspace{1cm} (6)

\[ V = \lambda^2 V_2 + \lambda V_1 + \frac{i}{\lambda + \omega} V_{-1} - \frac{i}{\omega} V_0. \]  \hspace{1cm} (7)

Here

\[ V_2 = -i\varepsilon_1 S, \quad V_1 = 0.25\varepsilon_1 [S, S_1], \quad V_{-1} = V_0. \]

Also, the equivalent counterpart of the M-XCIX equation, which is a nonlinear Schrödinger type equation, is derived as

\[ i\phi_t + \varepsilon_1 (0.5\phi_{xx} + |\phi|^2\phi) - 2ip = 0, \]  \hspace{1cm} (8)

\[ p_x - 2i\omega p - 2\eta \phi = 0, \]  \hspace{1cm} (9)

\[ \eta_x + \phi^* p + \phi p^* = 0. \]  \hspace{1cm} (10)

References


Prospective Analysis of Large and Complex Partially Observed Temporal Social Networks

Zoran Obradović

Data Analytics and Biomedical Informatics Center, Computer and Information Sciences Department, Statistics Department Temple University, PA, USA

Challenge: The analysis of social networks often assumes a time invariant scenario, while in practice actor attributes and links in such networks evolve over time and are inextricably dependent on each other. In addition, the temporal graph is just partially observed, multiple kinds of links exist among actors, various actors have different temporal dynamics, and environmental influence can be both positive and negative. This project is closely examining the hypothesis that a unified approach of jointly modeling these and related problems is beneficial for prospective analysis of large-scale partially observed temporal multimodal graphs.

Application: Our project is aimed at solving a set of high impact applications related to predictive modeling of massive evolving graphs of information networks, climate and human health.

Method: This objective is addressed by developing a structured learning Gaussian conditional random field (GCRF) model, which is shown to be more accurate than several unstructured alternatives in forecasting dynamics of evolving graphs. Efficient methods are developed by our team for scalable distributed modeling of large evolving graphs by GCRF. Some of our results presented here are recently published [1, 2, 3] while other manuscripts are under review.

References


In this work, we aim at modelling crowd motion in emergency situations. We propose a macroscopic model (where people are represented as a density) following two basic principles. First, each individual has a spontaneous velocity (typically, the one which leads to the nearest exit) which would be fulfilled in the absence of other people. On the other hand, the crowd has to respect a congestion constraint, and its density must remain underneath a critical value. This constraint prevents people from following their desired velocity. The actual velocity we consider is the closest, in a mean square sense, to the desired one, among the velocities which respect the maximal density constraint.

The mathematical formulation writes as a transport equation which cannot be studied with classical methods, since the real velocity field has no a priori regularity, even if the desired velocity is smooth. Thanks to the optimal transport theory, we prove an existence result, first in the case where the desired velocity is the gradient of a given function, and then in the general framework. We also propose a numerical scheme which follows the catching-up principle: at each time step, we move the density according to the spontaneous velocity, and then project it onto the space of admissible densities. The numerical results we obtain reproduce qualitatively the experimental observations.

Figure 1: Up: example of geometry. Down: evacuation of the Stade de France.

References


Community Detection in Temporal Networks

Vsevolod Salnikov, Renaud Lambiotte

University of Namur, NaXys, Belgium

The field of community detection has attracted much attention in recent years. If efficient methods exit for overlapping or non-overlapping communities in static networks, the problem of finding communities in temporal networks is still a challenge. Basic approaches consider the temporal system as a sequence of static networks where standard methods can be used. Alternative approaches represent the system by a tensor to be clustered.

In this work we have developed a statistical approach taking advantage of the temporal correlations between edges in order to uncover overlapping, synchronized communities in networks. Our approach has the advantage of allowing for the use of existing methods for static networks after minor modifications. As a benchmark, we have converted two widely used partitioning methods (Louvain [2] and Map Flow equation methods [1]) and tested their performance on a benchmark with a tuneable parameter, lambda, corresponding to the strength of the communities. The accuracy of the methods is assessed by comparing the exact solution with the partition of edges produced by the algorithm [3]. Results are presented in Fig. 1.

Figure 1: Methods performance with respect to the strength of communities

References


Direction of Technical Change, Endogenous Fertility, and Patterns of Growth

Mehdi Senouci

1 LGI, Ecole Centrale Paris, France & Paris School of Economics

What type of technical progress is able to increase income per capita, instead of merely translating into higher fertility? To investigate this question, this paper first sets up an OLG growth model with capital, land and endogenous fertility. At each date, children compete with physical capital as a means of saving for the young. This framework is then put into motion by continuous neutral and investment-specific technical change. Neutral technical change leads to well-known Malthusian dynamics and cannot make the wage rate grow asymptotically. On the contrary, investment technology alters the relative price of capital and children and so also affects the households’ accumulation/fertility decisions. If capital and labor are strict substitutes in the production function, continuous investment-specific technical change results in long-term growth of per capita income. When the direction of technical change is made endogenous, the agents most often tend to undertake R&D that increases neutral productivity, leading to stagnation of per capita income. The theory is used to interpret some evidence on the first steps of the Industrial Revolution.