Workshop on

Theoretical Approaches and Related Mathematical Methods
in Biology, Medicine and Environment

Scientific Programme

Workshop on

Theoretical Approaches and Related Mathematical Methods in Biology, Medicine and Environment

THE PROGRAMME AT GLANCE

SOCIETÀ ITALIANA DI MATEMATICA APPLICATA E INDUSTRIALE

	04.04.2013	05.04.2013	06.04.2013
09:00-09:30		**Filippo Castiglione** *Bridging Computational Biology and Bioinformatics*	**Alberto D'Onofrio** *The pharmacodynamics of p53-targeted drug Nutlin: a hybrid stochastic model*
09:30-09:35		break	break
09:35-09:55		**Federico Vaggi** *Cell Polarity in Fission Yeast*	**Giuseppe Pontrelli** *Drug delivery in biological tissues: a semi-analytical study*
09:55-10:15		**Deborah Lacitignola** *Toward an environmental low-impact electroplating: mathematical and experimental study of forcing voltage effects on electrochemical growth dynamics*	**Giorgio Guzzetta** *Hope-Simpson's progressive immunity hypothesis explains Herpes Zoster incidence data Running head: Progressive immunity hypothesis explains Zoster*
10:15-10:30		**Claudio Gaz** *A popolution model for the pancreatic production of insuline*	**Simone Palamara** *Patient-specific computational generation of the Purkinje fibers network driven by clinical measuraments*
10:30-11:00		COFFEE BREAK	COFFEE BREAK
11:00-11:20		**Edoardo Beretta** *Global stability properties for an SEIR epidemic model with two delaysy*	**Laura Fumanelli** *Inferring the Structure of Social Contacts from Demographic Data in the Analysis of Infectious Diseases Spread*
11:20-11:40		**Bruno Buonomo** *Nonlinear aspects of epidemic models in behavioral epidemiology*	**Stefano Merler** *Determinants of the Spatiotemporal Dynamics of the 2009 H1N1 Pandemic in Europe: Implications for Real-Time Modelling*
11:40-12:00		**Eleonora Messina** *Numerical stability theory for Volterra Integral Equations*	**Piero Poletti** *The impact of varicella vaccination on the epidemiology of Herpes Zoster*
12:00-12:15		**Marco Ajelli** *The impact of demographic changes on the epidemiology of infectious diseases*	**Pamela Moschini** *A semi-discrete model for the West Nile virus*
12:15-12:30		**Luca Ferreri** *Modeling epidemic spreading in star-like networks*	**Manuela Ciddio** *A spatially explicit model of endemic cholera in Bangladesh: the role of hydroclimatological forcings*
12:30-14:00	Registration	LUNCH	**CONCLUSIONS**
14:00 - 14:05	Silvio Ghilardi, Director of Department of Mathematics *Welcome*	**Marco Scianna** *A measure-theoretic approach to cell migration and organization*	
14:05-14:15	Vincenzo Capasso - Director of CIMAB *What is CIMAB?*		
14:15-14:20	Luigi Preziosi President of CIMAB - Coordinator SIMAI GASVA		
14:20-14:25	*The SIMAI working group GASVA*	**Paola Causin** *Mathematical modeling of retinal circulation: fundamental mechanisms and impact on retinal diseases*	
14:25-14:30	Break		
14:30-14:40	**Mimmo Iannelli- Alessandra Micheletti** *To jump or not to jump: implicazioni ecologiche del salto della quaglia*	**Vincenzo Capasso** *Randomness and Angiogenesis*	
14:40-15:00			
15:00-15:10		Break	
15:10-15:20	Presentazione dell'Unità del Politecnico di Torino	**Fabio Lamantia** Evolution of competition and cooperation in fish wars	
15:20-15:30	Presentazione Unità dell'Università Firenze		
15:30-15:40	Presentazione Unità dell'Università Napoli	**Davide Radi** *Multi-species exploitation with evolutionary switching of*	
15:40-15:45	Presentazione Unità dell'Università Urbino		
15:45-15:50		**Serena Spina** **A Jump Stochastic Gompertz Model for an Intermittent**	
15:50-16:00	Presentazione Università dell'Università di Trento		
16:00-16:30	Coffe Break	Coffe Break	
16:30-16:40	Presentazione dell'Università IASI- CNR	**Michele Piana** *Estimation of the whole bone marrow asset in humans by integrated nuclear medicine and X-ray tomography data*	
16:40-16:50	Presentazione dell'Università IAC- CNR		
16:50-17:00	Presentazione Unità dell' Universiversità di Torino	**Alberto Sorrentino** *Sequential Monte Carlo samplers for multi-dipole estimation in Magnetoencephalography*	
17:00-17:10	Presentazione Unità dell'Università di Milano		
17:10-17:15	Break	**Cristina Campi** *Cortical constraints for particle filtering in Magnetoencephalography*	
17:15-17:30	**Antonio Fasano** *Modeling High Flux Hollow Fibers Dialyzers.*		
17:30-17:35		**Thierry Nieus** *Investigating the interplay between intrinsic and evoked*	
17:35:17:50	**Angiolo Farina** *A Model for Ultrafiltration in Kidney Glomeruli*		
17:50-17:55		**Sara Gambarino** *A computational approach to compartmental analysis of nuclear medicine data based on maximum-likelihood: application to renal* physiology	
17:55:18:05	**Armando Bazzani** *A Simple model for mutation dynamics in a bacteria population subject to external stress*		
18:05-18:15		**Anna Cattani** *FitzHugh-Nagumo to Model a Large Number of Diffusive Coupled Neurons*	
18:15-10:20	**Chiara Giverso** *Influence of nucleus mechanical properties on cell entry into ECM channels.*		
18:20-18:30		**Elisa Benedetto** *A non parametric estimator for neural firing rate in presence of dependent Interspike Intervals.*	
18:30-18:35	**Chiara Lelli** *A mathematical model of mechano-physiological processes regulating in vitro tissue growth*		
18:35-18:45			
20:00-23:00		SOCIAL DINNER - Restaurant BELLUCCIO's	

April 4, 2013 - Afternoon

12:30-14:00	Registration
	CHAIRMAN: Giovanni Naldi
14:00 - 14:05	**Silvio Ghilardi**, Director of Department of Mathematics *Welcome*
14:05-14:15	**Vincenzo Capasso**, - Director of CIMAB *What is CIMAB?*
14:15-14:25	**Luigi Preziosi,** President of CIMAB - Coordinator SIMAI GASVA *The SIMAI working group GASVA*
14:25-14:30	Break
14:30-15:10	**Mimmo Iannelli - Alessandra Micheletti** To jump or not to jump: implicazioni ecologiche del salto della quaglia
15:10-15:20	Presentazione dell'Unità del Politecnico di Torino
15:20-15:30	Presentazione Unità dell'Università Firenze
15:30-15:40	Presentazione Unità dell'Università Napoli
15:40-15:50	Presentazione Unità dell'Università Urbino
15:50-16:00	Presentazione Unità dell'Università di Trento
16:00-16:30	Coffe Break
16:30-16:40	Presentazione dell'Università IASI- CNR
16:40-16:50	Presentazione dell'Università IAC- CNR
16:50-17:00	Presentazione Unità dell' Universiversità di Torino
17:00-17:10	Presentazione Unità dell'Università di Milano
17:10-17:15	Break
	CHAIRMAN: Gian Italo Bischi
17:15-17:35	**Antonio Fasano** *Modeling High Flux Hollow Fibers Dialyzers.*
17:35-17:55	**Angiolo Farina** *A Model for Ultrafiltration in Kidney Glomeruli*
17:55-18:15	**Armando Bazzani** *A Simple model for mutation dynamics in a bacteria population subject to external stress*
17:15:18:30	**Chiara Giverso** *Influence of nucleus mechanical properties on cell entry into ECM channels.*
18:30-18:45	**Chiara Lelli** *A mathematical model of mechano-physiological processes regulating in vitro tissue growth*

April 5, 2013 - Morning

	CHAIRMAN: Vincenzo Capasso
09:0-09:30	**Filippo Castiglione** *Bridging Computational Biology and Bioinformatics*
09:30-09:35	Break
	CHAIRMAN: Bruno Buonomo
09:35-09:55	**Federico Vaggi** *Cell Polarity in Fission Yeast*
09:55-10:15	**Deborah Lacitignola** *Toward an environmental low-impact electroplating: mathematical and experimental study of forcing voltage effects on electrochemical growth dynamics*
10:15-10:30	**Claudio Gaz** *A popolution model for the pancreatic production of insuline*
10:30-11:00	COFFEE BREAK
	CHAIRMAN: Vincenzo Capasso
11:00-11:20	**Edoardo Beretta** *Global stability properties for an SEIR epidemic model with two delaysy*
11:20-11:40	**Bruno Buonomo** *Nonlinear aspects of epidemic models in behavioral epidemiology*
11:40-12:00	**Eleonora Messina** *Numerical stability theory for Volterra Integral Equations*
12:00-12:15	**Marco Ajelli** *The impact of demographic changes on the epidemiology of infectious diseases*
12:15-12:30	**Luca Ferreri** *Modeling epidemic spreading in star-like networks*
12:30-14:00	LUNCH

April 5, 2013
Afternoon

CHAIRMAN: Luigi Preziosi

14:00 - 14:20 **Marco Scianna**
A measure-theoretic approach to cell migration and organization

14:20-14:40 **Paola Causin**
Mathematical modeling of retinal circulation: fundamental mechanisms and impact on retinal diseases

14:40-15:00 **Vincenzo Capasso**
Randomness and Angiogenesis

15:00-15:30 **Fabio Lamantia**
Evolution of competition and cooperation in fish wars

15:30-15:40 **Davide Radi**
Multi-species exploitation with evolutionary switching of harvesting strategies

15:45-16:00 **Serena Spina**
A Jump Stochastic Gompertz Model for an Intermittent Treatment in Cancer Growth

16:00-16:30 Coffe Break

16:30-16:50 **Michele Piana**
Estimation of the whole bone marrow asset in humans by integrated nuclear medicine and X-ray tomography data

16:50-17:10 **Alberto Sorrentino**
Sequential Monte Carlo samplers for multi-dipole estimation in Magnetoencephalography

17:10-17:30 **Cristina Campi**
Cortical constraints for particle filtering in Magnetoencephalography

17:30-17:50 **Thierry Nieus**
Investigating the interplay between intrinsic and evoked activities in cultured neuronal networks by dimensional reduction techniques

17:50-18:05 **Sara Gambarino**
A computational approach to compartmental analysis of nuclear medicine data based on maximum-likelihood: application to renal physiology

18:05-18:20 **Anna Cattani**
FitzHugh-Nagumo to Model a Large Number of Diffusive Coupled Neurons

18:20-18:35 **Elisa Benedetto**
A non parametric estimator for neural firing rate in presence of dependent Interspike Intervals.

20:00-23:00 SOCIAL DINNER - Restaurant BELLUCCIO's

April 6,2013
Morning

CHAIRMAN: Alberto Gandolfi

09:00-09:30 **Alberto D'Onofrio**
The pharmacodynamics of p53-targeted drug Nutlin: a hybrid stochastic model

09:30-09:35 break

09:35-09:55 **Giuseppe Pontrelli**
Drug delivery in biological tissues: a semi-analytical study

09:55-10:15 **Giorgio Guzzetta**
Hope-Simpson's progressive immunity hypothesis explains Herpes Zoster incidence data
Running head: Progressive immunity hypothesis explains Zoster

10:15-10:30 **Simone Palamara**
Patient-specific computational generation of the Purkinje fibers network driven by clinical measuraments

10:30-11:00 COFFEE BREAK

CHAIRMAN: Andrea Pugliese

11:00-11:20 **Laura Fumanelli**
Inferring the Structure of Social Contacts from Demographic Data in the Analysis of Infectious Diseases Spread

11:20-11:40 **Stefano Merler**
Determinants of the Spatiotemporal Dynamics of the 2009 H1N1 Pandemic in Europe: Implications for Real- Time Modelling

11:40-12:00 **Piero Poletti**
The impact of varicella vaccination on the epidemiology of Herpes Zoster

12:00-12:15 **Pamela Moschini**
A semi-discrete model for the West Nile virus

12:15-12:30 **Manuela Ciddio**
A spatially explicit model of endemic cholera in Bangladesh: the role of hydroclimatological forcings

12:30-14:00 **CONCLUSIONS**

ABSTRACTS

Marco Ajelli
Fondazione Bruno Kessler

The impact of demographic changes on the epidemiology of infectious diseases

Despite a long history of immunization programs, measles and pertussis are still circulating in Europe. We review their epidemiological history in Italy, and examine the extent to which elimination would have been possible. Making use of a disease transmission model informed with longitudinal basic demographic data, we show that the demographic history of the population has determined changes in transmission potential, incidence and serological profiles over time, with remarkable shifts in age distribution of susceptible individuals and age at infection. Our results show that these induced epidemiological changes are responsible for the partial failure of routine immunization programs and that short-medium term effects of vaccination programs can be drastically different from those predicted by the standard theory. From the public health perspective, our results claim for an urgent intervention to protect individuals currently aged 15-30 years, given the partial failure of standard immunization programs aimed at targeting infants. More in the general, our results call for the introduction of a new class of models which, as the one proposed, deviate the age structure of the population from stationary equilibrium solutions by accounting for the demographic history of the population, to evaluate short-medium term effects of mass vaccination programs, notably in developing countries which are undergoing dramatic demographic changes.

Armando Bazzani,
Università di Bologna

A Simple model for mutation dynamics in a bacteria population subject to external stress

We study a possible modelization for the mutation process of a bacteria population under environmental stress. On one hand we take advantage from the fitness landscape approach on which one can visualize the mutation process by a generalized random walk. On the other hand we analyze the results of experimental data where the number of mutants of a given population were measured as a function of the umerousness of the initial population and the external stress. Our point of view is to propose the existence of generic assumptions that allow to define a minimal model able to interpret the experimental results. Therefore we suggest possible average scaling laws related to evolution dynamics of bacteria.

Elisa Benedetto, Federico Polito, Laura Sacerdote
Department of Mathematics, University of Torino

A non parametric estimator for neural firing rate in presence of dependent Interspike Intervals.

An important feature of the neural code is its firing rate. Mathematically, the firing rate corresponds to the hazard rate function of the point process associated to the spike train. In the literature there are many examples of hazard rate estimators. When the point process is a Poisson or a general renewal process, there exist various estimators for the hazard rate (see e.g. [2], [3], [4], [5]). However such assumptions are too strong to model data from neurons. Indeed several experimental data show that interspike intervals can be dependent. Our aim is to relax the hypothesis of independence and provide a uniform strong consistent estimator for the firing rate of a single neuron. In 2001 Brown, Barbieri et al. [1] obtained a maximum likelihood estimator of the hazard rate function of a single neuron modelled with a given known interspike intervals distribution. Here we focus our attention on a non-parametric estimation of the firing rate. Hence we assume that the interspike intervals belong to a Markov and ergodic stochastic process. Under these hypotheses we propose a non-parametric uniform strong consistent hazard rate estimator. Then we validate our estimate with a specific statistical test. Finally, we illustrate our method on some examples with simulated data.

References:

[1] E.N. Brown, R. Barbieri, V. Ventura, R.E. Kass and L.M. Frank, The time rescaling theorem and its application to neural spike train data analysis., Neural Computation 14, 325-346 (2001).
[2] B.L.S. Prakasa Rao, and J. Van Ryzin, Asymptotic theory for two estimators of the generalized failure rate., Statistical Theory and Data Analysis, ed. K. Matusita, North Holland, Amsterdam, 547-563 (1985).
[3] J. Rice and M. Rosenblatt, Estimation of the log survivor function and hazard function., Sankhya Ser. A, 38, 60-78 (1976).
[4] G.S. Watson and M.R. Leadbetter, Hazard analysis I, Biometrika, 51, 175-184 (1964).
[5] G.S. Watson and M.R. Leadbetter, Hazard analysis II, Sankhya Ser. A, 26, 110-116 (1964).

Edoardo Beretta
University of Urbino

Global stability properties for an SEIR epidemic model with two delaysy

The two constant delays are the latency time taken by the infected individuals "E" to become infectious individuals "I" (i.e. capable to infect the susceptibles S) and respectively the infectious period after which the infectious individuals are recovered. We assume that the recovered individuals " R " acquire permanent immunity and that the infection incidence rate is a saturated function of " I ". The model presents two non-negative equilibria : the disease-free equilibrium E_0 and the positive equilibrium E_+ , which is feasible iff the basic reproduction number R_0 is larger than one, where R_0 is dependent upon both delays. By describing the model through the age-infection density " $i(t, a)$ " of infected individuals that at time " t " have an infection-age " a " and by the construction of suitable Lyapunov functionals it is possible to prove that: *i*) whenever $R_0>1$ the equilibrium E_+ is globally asymptotically stable; *ii)* if $R_0 \leq 1$ the equilibrium E_0 is globally attractive and if $R_0< 1$ it is globally asymptotically stable. It may be interesting to question if the above results remain true even in the case of distributed delays which mean values are coincident with the two discrete delays in the model.

References

E.Beretta, D.Breda : An SEIR epidemic model with constant latency time and infectious period. Math. Biosci. and Eng.ng, Vol. 8, n.4, 931-952, 2011.
G.Huang, E.Beretta, Y.Takeuchi : Global stability for an epidemic model with constant latency time and infectious period. Math. Biosci. and Eng.ng, Vol. 9, n.2, 297-312, 2012. ……

Bruno Buonomo
Department of Mathematics, University of Naples "Federico II"

Nonlinear aspects of epidemic models in behavioral epidemiology

A nonlinear analysis of some behavioral-epidemic models (i.e. epidemic systems including feedbacks that the information about an infectious disease has on its spreading) is performed. Two important feedbacks are explicitly considered: the pseudo-rational exemption to vaccination and the information-related changes in contact patterns by healthy subjects. The analysis includes the global stability of steady states and the detection of oscillating behavior. In particular, we show that the vaccinating behavior depending on current information can trigger oscillations for diseases characterized by a latency time, differently from the case of SIR diseases, where an information delay is needed to induce oscillations.

Cristina Campi
SPIN- CNR, Genova

Cortical constraints for particle filtering in Magnetoencephalography

The last years have seen the rise of a new neuroimaging technique working thanks to superconductivity, Magnetoencephalography (MEG). MEG is able to record, outside the head, the weak magnetic field induced by neural currents inside the brain. Its temporal resolution is so fine to guarantee the possibility to follow the evolution of the neural activity producing the measured data. This advanced technique is employed both for clinical studies and for basic research. To infer information from the recorded data it is necessary to solve the severely unstable inverse problem of recovering the current density in the brain from the induced magnetic field measured in a point outside the skull. The analysis of these data is made difficult by several causes and sophisticated methods for the solution of the problem have been proposed. In particular, we have recently implemented a Bayesian approach for the analysis of MEG data allowing a dynamic localization of neural sources with no a priori assumption on their number, position and size. In this framework both the data and the unknowns are modeled as Markov processes, and the unknowns, i.e. the neural sources, are assumed to be a small set of dipoles. This talk describes a development of this approach, whereby morphological constraints are introduced, based on the segmentation of MRI images characterized by high spatial resolution. Specifically, we will constrain the dipoles to belong to the cortical mantle and we will impose different kinds of orientation constraints inspired by neurophysiological considerations. Applications will be concerned with MEG data evoked by somatosensory stimulations.

Vincenzo Capasso, Daniela Morale
Dipartimento di Matematica, Università di Milano

Randomness and Angiogenesis

We consider angiogenesis as a case study for analyzing the role of randomness in the formation of biological patterns. The mathematical description of the formation of new vessels is presented, based on a system of stochastic differential equations, coupled with a branching process, both of them driven by a set of relevant chemotactic underlying fields. A discussion follows about the possible reduction of complexity of the above approach, by mean field approximations of the underlying fields. The crucial role of randomness at the microscale is observed in order to obtain nontrivial realistic vessel networks.

Filippo Castiglione
IAC - CNR, Roma

Bridging computational biology and Bioinformatics

Immunoinformatics provides tools for analysing genomic and proteomic data in the immunological domain. Computational Immunology provides models to analyse population dynamics at the cellular scale. We present a new approach to the study of the immune system that combines techniques of both research fields. At the population level the interaction among cells is modelled by an agent-based simulator whereas at the molecular level we use amino acid strings. In order to make them working together we equipped the resulting model with data-driven bioinformatics methods to predict antigenic epitopes and to model receptor binding to determine antigenic immunogenicity. The combination of omic- information with simulation of the dynamics of the immune system, in one single tool, is a novelty that can offer new perspectives for a better understanding of the immune system dynamics in the field of vaccine design or immunotherapy.

Anna Cattani
Department of Mathematics, Politecnico of Torino

FitzHugh-Nagumo to Model a Large Number of Diffusive Coupled Neurons

The last years have seen the rise of a new neuroimaging technique working thanks to superconductivity, Magnetoencephalography (MEG). MEG is able to record, outside the head, the weak magnetic field induced by neural currents inside the brain. Its temporal resolution is so fine to guarantee the possibility to follow the evolution of the neural activity producing the measured data. This advanced technique is employed both for clinical studies and for basic research. To infer information from the recorded data it is necessary to solve the severely unstable inverse problem of recovering the current density in the brain from the induced magnetic field measured in a point outside the skull. The analysis of these data is made difficult by several causes and sophisticated methods for the solution of the problem have been proposed. In particular, we have recently implemented a Bayesian approach for the analysis of MEG data allowing a dynamic localization of neural sources with no a priori assumption on their number, position and size. In this framework both the data and the unknowns are modeled as Markov processes, and the unknowns, i.e. the neural sources, are assumed to be a small set of dipoles. This talk describes a development of this approach, whereby morphological constraints are introduced, based on the segmentation of MRI images characterized by high spatial resolution. Specifically, we will constrain the dipoles to belong to the cortical mantle and we will impose different kinds of orientation constraints inspired by neurophysiological considerations. Applications will be concerned with MEG data evoked by somatosensory stimulations.

Paola Causin
Department of Mathematics, University of Milano

Mathematical modeling of retinal circulation: fundamental mechanisms and impact on retinal diseases

Ocular circulation is a delicate mechanism, charged to maintain the homeostasis of retinal function in response to physiological stimuli. It is crucial to understand the processes underlying the regulation of ocular circulation in physiological conditions. Their impairment causes severe retinal disorders, affecting millions of people worlwide.

Mathematical and computational models based on the physical principles of mechanics, fluid-dynamics, mass transport and electrochemistry can help unraveling the cause-effect mechanisms acting as key factors in the regulation of functioning of the retinal microvasculature. The results can provide a rationale beyond correlations shown by clinical data. In particular, in this talk we will address the critical question, which is still debated, whether ocular haemodynamic alterations are primary cause (and not a secondary effect) to retinal diseases, focusing in particular on the glaucoma pathology.

Manuela Ciddio, Lorenzo Mari, Lorenzo Righetto
Politecnico di Milano

A spatially explicit model of endemic cholera in Bangladesh: the role of hydroclimatological forcings

Cholera is a disease transmitted especially through exposure to contaminated water. River networks thus represent one of the major pathways of disease spreading. Here we propose a spatially explicit model for cholera and apply it to Bangladesh, where the disease is endemic. The data structure designed for the application of the model is based on the hydrological connectivity network, as well as on the spatial distribution of the population and on the connections that regulate human mobility among communities. In this region, cholera incidence exhibits two annual peaks, although the main environmental drivers (precipitation and temperature) peak once per year during the monsoon season (from June to September). The proposed model attempts to explain these particular dynamics taking into account the annual fluctuations of water availability and considering hydro-climatological forcings as inputs of the model. For this purpose, a compartmental SIRB (Susceptible-Infected-Recovered-Bacteria) epidemiological model is integrated with a hydrological model. Results show that the introduction of two terms of transport (hydrological transport and human mobility) allows to generate spatial cholera prevalence patterns that confirm the bimodal pattern typically observed in this region.

Alberto D'Onofrio , Alberto Gandolfi, Krysztof Puszynski
European Institute of Oncology, Milan

The pharmacodynamics of p53-targeted drug Nutlin: a hybrid stochastic model

P53 is a so important oncosuppressor gene that it has been named the *guardian of the genome* [1] because it activates when the DNA is damaged in order to prevent damaged DNA replication by cell cycle arrest, DNA damage repair processes initiation and, if this fails, by apoptosis triggering. Under-expression of p53, thus, may lead to cancer, also in absence of mutation of p53. Indeed, in many tumor p53 is wild-type but p53 protein has low level due to over-expression (for example due to gene ampli_cation) of the competitor Mdm2. A key to restore physiologic levels of p53 protein might be, thus, to inhibit the binding of Mdm2 to p53. Nutlins are a family of small molecules, discovered by Vassilev et al. [2], that have this property . Indeed, they may occupy the binding sites of Mdm2 where normally p53 binds. It is thus of interest to investigate a model of Nutlin pharmacodynamics. This model has to be i) quite complete to take into the account the main players of the p53 network, such as p53 itself, of course, but also Mdm2 and PTEN, and the various active/inactive, cytoplasmic/nuclear and ubiquitinated forms (including complexes); ii) stochastic in order to take into the account the strong transcritional noise [3] a_ecting the above-mentioned biomolecules, due to the random activation-deactivation of the involved genes. This led us to formulate an hybrid stochastic/deterministic model [4] that includes large part of the main bioprocesses currently known for both p53 network and for Nutlin. As such, our model is quite complex, but it allowed us to _t experimental data by Vassilev et al. [2] concerning the e_ects of Nutlins on some important cancer cells lines. Based on these numerical results, we also considered some experiments of virtual therapies in order to simulate the *in-vivo* e_ect of Nutlins by considering time-varying concentrations, which are due to the pharmacokinetics of the drug.

References

[1] D.P. Lane *p53, guardian of the genome,* Nature, 358, 15{16 (1992)
[2] L.T. Vassilev et al. . *In vivo activation of the p53 pathway by small-molecule antagonists of MDM2,* Science, 303 (5659), 844{848 (2004)
[3] T. Lipniacki et al. *Transcriptional stochasticity in gene expression,* J Theor Biol., 238(2),348{67 (2006)
[4] K. Puszy_nski, A. Gandol_ and A. d'Onofrio *Submitted,* (2013)

Angiolo Farina,
Department of Mathematics, University of Firenze

A Model for Ultrafiltration in Kidney Glomeruli

The model describes the blood flow through fenestrated capillaries, with application to the ultrafiltration process that occurs in kidney glomerulus.

At the scale of capillaries the presence of a large volume fraction of Red Blood Cells makes the composite nature of blood quite visible, so that blood can hardly be identified with a fluid. We propose a model in which blood flow is a quasi-steady translation of plasma elements confined between RBC's, accompanied by mechanical power dissipation in a thin highly sheared plasma boundary layer. Applying just mass conservation and momentum balance (equivalent to the balance of the driving force due to pressure gradient and to the drag force arising from friction), we deduce a governing set of partial differential equations allowing to compute all the relevant quantities (hematocrit profile, hydrostatic and oncotic pressure profiles, plasma flow through the capillary wall).

Antonio Fasano
Università di Firenze

Modeling High Flux Hollow Fibers Dialyzers.

We present a mathematical model for hollow fibers hemodialyzers based on an upscaling technique. The model is being developed in cooperation with the Department of Nephrology at Vicenza Hospital, directed by prof. Ronco. It stems from previous studies by A. Farina, I. Borsi and myself with the aim of connecting the complex differential system governing the machine to the phenomena going on in the patient's body as a reaction to dialysis.

Luca Ferreri, Paolo Bajardi, Mario Giacobini

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Università di Torino

Modeling epidemic spreading in star-like networks

Our source of inspiration is the spreading of vector-borne pathogens with a particular focus on non-systemic transmission. Such transmission, known as cofeeding, occurs between vectors feeding on the same host simultaneously without the host becoming viremic. For instance, the Tick-Borne Encephalitis virus (TBEv) is mainly maintained by this transmission route in a natural cycle involving as vectors ticks of Ixodes species, and as hosts different animal species, in particular rodents. However, TBEv is also of interest for the human health since it causes the most important arboviral infection of the human central nervous system in Europe and Russia, which can result in long-term sequelae and, in some cases, to death. We model this transmission process using a Susceptible-Infectious-Susceptible model (SIS) on a dynamical contact network. Specifically, to describe and analyze cofeeding dynamics we consider a bipartite network composed by a collection of disconnected star-like structures. In such network, nodes are divided in two sets, A and B, that, in our biological source of inspiration represent rodents and ticks, respectively. Nodes of set B, B-nodes, are tied only with an A-node that represents the center of star-like structure. Moreover, in these bipartite structures, we specify the degree, i.e. the number of neighbors, of an A-node by p, a probability density function. A-nodes are not susceptible to the pathogen, while B-nodes are divided in susceptible and infectious according to their status. Thus, the pathogen spreading may occur only between B-nodes and only if connected through a common A-node. The transmission between an infectious individual and a susceptible one occurs with probability b, while the recovery takes place with probability m. At each iteration t we take into account the fraction of infected nodes of type B - i.e. the prevalence among set B - which is function of the prevalence at time t-1, of the transmission probability b, of the recovery probability m and of the degree probability function p. To model the dynamical nature of this network model, at every time step B-nodes are reshuffled and are randomly connected to A-nodes keeping the star-like structure (in our source of inspiration the reshuffling of ticks over rodents). By studying the system of differential equations describing both the dynamical star-like contact network and the epidemiological dynamics over the B-nodes, we analytically depict a necessary condition for which the pathogen remains endemic among B-nodes. The necessary transmission probability for the pathogen to reach endemicity is proportionally inverse to the second moment of the degree probability function. In other words, the larger the heterogeneity of the degree distribution the smaller transmission probability is needed by the pathogen to be endemic.
Furthermore, we confirm our results by stochastically simulating the epidemic spreading on a number of synthetic networks generated using several degree probability distributions.
It is worth to stress that this is the first time that such result is found out on the peculiar star-like networks. For the non-systemic transmission of vector-borne diseases it means that the larger the heterogeneity in the number of vectors feeding on a host (i.e. the greater is the aggregative behavior of ticks on hosts) is, the higher the probability that the disease becomes endemic through the vector population. However, such result could be extended to other transmission processes. For instance, the spreading occurring among people using transport means could be modeled by the approach just described. In such scenario passengers become B-nodes and means of transportation become A-nodes. Once again, a larger the heterogeneity among the number of passengers results in a lower the probability transmission needed for the pathogen to be maintained in the population.

Laura Fumanelli
Dipartimento Matematica Università di Trento

Inferring the Structure of Social Contacts from Demographic Data in the Analysis of Infectious Diseases Spread

Social contact patterns among individuals encode the transmission route of infectious diseases and are a key ingredient in the realistic characterization and modeling of epidemics. Unfortunately, the gathering of high quality experimental data on contact patterns in human populations is a very difficult task even at the coarse level of mixing patterns among age groups- Here we propose an alternative route to the estimation of mixing patterns that relies on the construction of virtual populations parametrized with highly detailed census and demographic data. We present the modeling of the population of 26 European countries and the generation of the corresponding synthetic contact matrices among the population age groups. The method is validated by a detailed comparison with the matrices obtained in six European countries by the most extensive survey study on mixing patterns. The methodology presented here allows a large scale comparison of mixing patterns in Europe, highlighting general common features as well as country-specific differences. We find clear relations between epidemiologically relevant quantities (reproduction number and attack rate) and socio-demographic characteristics of the populations, such as the average age of the population and the duration of primary school cycle.This study provides a numerical approach for the generation of human mixing patterns that can be used to improve the accuracy of mathematical models in the absence of specific experimental data.

Sara Gambarino
Dipartimento di Matematica Università di Genova and CNR - SPIN, Genova

A computational approach to compartmental analysis of nuclear medicine data based on maximum-likelihood: application to renal physiology

Positron Emission Tomography (PET) is an imaging technique capable of detecting pico-molar quantities of a labeled tracer with temporal resolution of the order of seconds. FDG-PET is a PET modality in which 18F-fluoro-2-deoxy-D-glucose (FDG) is used as a tracer to evaluate glucose metabolism and to detect diseases in many different organs. From a computational viewpoint, PET (and, specifically, FDG-PET) experiments involve two kinds of problems. First, signal processing techniques are applied to reconstruct the time dependence of location and concentration of tracer from the measured radioactivity. Second, these dynamic PET data can be processed to estimate physiological parameters that describe the functional behavior of the inspected tissues. This talk focuses on this second aspect and, specifically, on the analysis of tracer kinetics in tissues with the aim of estimating transmission coefficients between different functional compartments. Our approach represents a generalization of the classical graphical approaches to compartmental analysis. Specifically, we combine the ordinary differential equations modeling the forward problem in such a way to obtain a linear system in which the data vector components are realizations of a Poisson process. Then an iterative maximum-likelihood algorithm is implemented, able to reconstruct the set of unknown transmission coefficients by exploiting the statistical characteristics of the measurements. We describe an application to renal physiology utilizing nuclear data measured by a PET device for small animal models.

Claudio Roberto Gaz, Andrea De Gaetano
Politecnico di Torino

Un modello di popolazione per la produzione pancreatica di insulina.

Il rilascio di insulina da parte del pancreas, indotto da uno stimolo glicemico, è il fondamentale meccanismo responsabile dell'omeostasi del glucosio: qualora questo meccanismo non sia perfettamente funzionante, si ha una situazione clinica di Diabete Mellito. I dettagli dell'anello di controllo che controlla la glicemia attraverso la secrezione di insulina, sono stati un importante oggetto di analisi, anche a fini modellistici, da decadi. In questo talk verrà considerato un modello di popolazione recentemente pubblicato, il cui scopo è quello di replicare "in silico" differenti fenomeni osservati, come le oscillazioni a bassa frequenza di glicemia ed insulinemia, così come l'induzione di oscillazioni di insulina ad alta frequenza. L'idea su cui si basa questo modello è che il pancreas si comporti come una popolazione di controllori indipendenti (le unità secretorie, cioè le isole di Langerhans), che reagiscono "coralmente" allo stesso stimolo di glucosio ma con differenti risposte dovute a differenti caratteristiche intrinseche. Questo modello è stato validato su dati di esperimenti in vivo. In questo talk verrà mostrato come la stessa struttura matematica può replicare anche una serie di esperimenti in vitro, adattando tale modello alla differente struttura sperimentale. Più in dettaglio, verrà mostrato come il modello riproduca la doppia fase del rilascio di insulina durante uno stimolo glicemico prolungato: una prima fase di rilascio impulsivo di insulina (immediatamente dopo la somministrazione glicemica), seguita da una seconda fase di rilascio più graduale, dipendente dall'effetto di potenziamento delle unità secretorie..

Chiara Giverso.
Politecnico di Torino

Influence of nucleus mechanical properties on cell entry into ECM channels.

Mechanical properties of cell nucleus have been demonstrated to play an important role in cell movement across extracellular networks and channels. We focus on the mathematical description of a cell entering inside a cylindrical channel composed of extracellular matrix. An energetic approach is derived in order to obtain a criterion for which cell can enter or not inside cylindrical structures. The nucleus of the cell is treated either (i) as an elastic membrane surrounding a liquid droplet or (ii) an incompressible elastic solid with a neo-Hookean constitutive equation.

The results obtained highlight the importance of the interplay between mechanical deformability of the nucleus and the capability of the cell to establish adhesive bonds and generate active forces. TBA

Giorgio Guzzetta
Fondazione Bruno Kessler

Hope-Simpson's progressive immunity hypothesis explains Herpes Zoster incidence data Running head: Progressive immunity hypothesis explains Zoster

Varicella-zoster virus (VZV) is the causative agent of both varicella and herpes zoster (HZ). After varicella infection, the virus remains dormant in the host's dorsal ganglia and can reactivate due to waning cell-mediated immunity (CMI), causing HZ. Exposure of varicella-immune individuals to VZV may boost the host's immune response, resulting in a protective effect against HZ. In this study, mathematical models of VZV transmission and HZ development are used to test the biological hypothesis of "progressive immunity", originally proposed by Hope-Simpson, that cell-mediated protection against HZ increases after each episode of exposure to VZV. Predictions from a model incorporating such hypothesis were compared to those of other models where VZV exposure only restores the initial level of CMI after primary varicella infection. The progressive immunity model explains significantly better the age profile of HZ incidence for Finland, Italy, Spain and United Kingdom, suggesting that this mechanism is critical in shaping HZ patterns. These findings might greatly improve VZV models currently used to evaluate the impact of mass immunization programs for varicella and therefore to cope with the present decision paralysis on their introduction.

Deborah Lacitignola.
University of Cassino and Southern Lazio

Toward an environmental low-impact electroplating: mathematical and experimental study of forcing voltage effects on electrochemical growth dynamics

Electroplating is ubiquitous in surface treatment technologies and has wide-ranging applications from biomedical to energy production and conversion. Unfortunately electroplating can be regarded as one of the most polluting industries, especially because extremely poisonous and polluting additives are employed. We think this is essentially due to the poor fundamental knowledge of the physico-chemical basis of electrochemical metal growth and, in particular, of its dynamics. We address this point by considering a mathematical model - which accounts for the coupling between surface morphology and surface composition - as a means for understanding the formation of morphological patterns found in electroplating. We show how system dynamics exhibits some subtle interactions with an applied forcing frequency, giving rise to intriguing effects that are likely to offer green solutions to problems that are traditionally attacked with the use of non-sustainable chemistries.

Fabio Lamantia
Department of Economics, Statistics and Finance, University of Calabria

Evolution of competition and cooperation in fish wars

We introduce a simple punishment scheme in the 'great fish war' model with many players. An imitative process regulates how a coalition of cooperators is dynamically updated over time. An intuitive effect of adding sanctions is that they could enlarge the possible sustainable coalitions. However, the evolution toward full cooperation can be sustained by a punishment scheme provided that a critical mass of agents enforces cooperation at the beginning of the game. Moreover, we show the presence of thresholds in sanctions or in the cost for punishing such that if these thresholds are trespassed then dramatic reductions in the resource level and in the agents' welfare may occur as a consequence of free riding effects. We show by some examples that these phenomena are due to the presence of tipping points in the model.

Chiara Lelli
Politecnico di Torino

A mathematical model of mechano-physiological processes regulating in vitro tissue growth

A novel mathematical model of the mechanophysiology of engineered tissue growth at the microscale level is investigated. In the proposed formulation, the growing tissue construct is represented as a mixture of different cellular populations (proliferating, biosynthesizing and quiescent cells) and of extracellular matrix, that dynamically evolve under the external supply of a growth factor (nutrient concentration). The biomechanical interaction among the various mixture components is mathematically treated through the introduction of appropriate visco-elastic constitutive laws and the characterization, in the stress state, of the active forces exerted by the cells on the surrounding environment.

The resulting mathematical model is constituted by a coupled system of partial differential equations describing the interaction between the perfusion medium that conveys nutrient to the growing construct, and the corresponding cellular metabolic response driven by biomechanical processes. Cellular response results into a net biomass production that, in turn, determines the updated position of the fluid-biomass interface, until the growth process is terminated.

Stefano Merler
Fondazione Bruno Kessler

Determinants of the Spatiotemporal Dynamics of the 2009 H1N1 Pandemic in Europe: Implications for Real- Time Modelling

Influenza pandemics in the last century were characterized by successive waves and differences in impact and timingbetween different regions, for reasons not clearly understood. The 2009 H1N1 pandemic showed rapid global spread, but with substantial heterogeneity in timing within each hemisphere. Even within Europe substantial variation was observed, with the UK being unique in experiencing a major first wave of transmission in early summer and all other countries having a single major epidemic in the autumn/winter, with a West to East pattern of spread. Here we show that a microsimulation model, parameterised using data about H1N1pdm collected by the beginning of June 2009, explains the occurrence of two waves in UK and a single wave in the rest of Europe as a consequence of timing of H1N1pdm spread, fluxes of travels from US and Mexico, and timing of school vacations. The model provides a description of pandemic spread through Europe, depending on intra-European mobility patterns and socio-demographic structure of the European populations, which is in broad agreement with observed timing of the pandemic in different countries. Attack rates are predicted to depend on the socio-demographic structure, with age dependent attack rates broadly agreeing with available serological data. Results suggest that the observed heterogeneity can be partly explained by the between country differences in Europe: marked differences in school calendars, mobility patterns and sociodemographic structures. Moreover, higher susceptibility of children to infection played a key role in determining the epidemiology of the 2009 pandemic. Our work shows that it would have been possible to obtain a broad-brush prediction of timing of the European pandemic well before the autumn of 2009, much more difficult to achieve with simpler models or pre-pandemic parameterisation. This supports the use of models accounting for the structure of complex modern societies for giving insight to policy makers.

Eleonora Messina, A. Vecchio ,
University of Naples Federico II

Numerical stability theory for Volterra Integral Equations

An important topic in the numerical analysis of Volterra Integral Equations is the stability theory.
Although significative results are available in the linear convolution case, many important questions are still opened in the nonlinear case. Here, we review some well known results and show some recent advances which represent a further step in the construction of a global theory. This theory has mathematical significance in its own but, at least in part, attempts to generate insight into the performance of real life models.

Pamela Moschini
University of Trento

A semi-discrete model for the West Nile virus

West Nile virus is a mosquito–borne virus transmitted primarily by bite of infected mosquitoes that acquire the virus by feeding on infected birds. West Nile virus has been described in Africa, Europe, The Middle East, west and central Asia, Oceania, and most recently, in North America. The first recorded North American epidemic of West Nile virus was detected in New York state in 1999, and since then the virus has spread and become established in much of North America. Mathematical models for this disease have recently been formulated with the aim of predicting disease dynamics and evaluating possible control methods. In this work we emphasize the seasonal aspects of transmission by building a simple semi-discrete model for the transmission dynamics of West Nile virus infection. The enzootic transmission in an avian population with a single mosquito population is modeled in a SIS/SIR epidemiological framework, where mosquitoes' feeding is assumed to occur only during the summer of each year. Two types of R0 are considered: a short-term R0 and a long- term R0 to distinguish the number of infected cases produced in the next generation of infecteds and the number of infected mosquitoes produced at the beginning of next season;
Simulations are somehow reminescent of what happens in USA (1999-2012); when the short-term R0 is larger than 1, but the long-term below 1, one may have epidemic bursts lasting a few years, as apparently occurred in Italy (2008-2009); virus overwintering in the mosquito population appears to be a crucial parameter.

Thierry Nieus
Istituto Italiano Tecnologia

Investigating the interplay between intrinsic and evoked activities in cultured neuronal networks by dimensional reduction techniques

High density MEAs, providing extracellular recordings from thousand of electrodes, are a novel commercial tool (www.3brain.com) to investigate spontaneous or chemically modulated activity in cultured neuronal networks as well as ex vivo brain tissues. In this study we report both on technological and data analysis advancements to investigate the propagation of spontaneous and evoked activities in hippocampal neuronal cultures with high density MEAs. We have developed and validated the use of high density MEAs with on-chip stimulating electrodes. These devices provide 4’096 recording electrodes with a pitch of 81 um (active area of 8 mm by 8 mm) interlaced with 16 stimulating electrodes every 8 recording sites. At the mature stage neuronal cultures display a peculiar intrinsic firing regime characterized by periodic synchronized network-wide bursts. Network bursts originate from specific ignition sites of the cultured network (i.e. characterized by more excitable cells) and can propagate through the entire network. Since these propagations, i.e. neural trajectories, are informative of the underlying network connectivity, classifying these events might elucidate the network's organization and its ongoing dynamic. Previous studies have described neural trajectories by tracking their center activity trajectory (CAT). Although CATs provide a good overall description of spatio-temporal patterns, they are not suited for fine studies on these propagations. Given the limitations of the previous method, we have adopted a more rigorous approach by applying dimensional reduction techniques that take advantage of the redundancy and the sparseness of multi-unit recordings. Our results show that by a Principal Component Analysis (PCA) we can properly reconstruct the time course of neural trajectories in the different acitivity regimes of the cultured networks with a minimal set of three components (i.e. explaining ~90% of the variance of the trajectories). The PCA classification based approach showed that electrical stimulation could evoke: 1. distinctive trajectories that depended on the specific spatial-temporal properties of the stimulus 2. trajectories already present in the intrinsic 'repertoire'. We are currently investigating the interplay between intrinsic and stimulated propagations to characterize the processing capabilities of the cultured networks.

Simone Palamara
Politecnico di Milano - Mox

Patient-specific computational generation of the Purkinje fibers network driven by clinical measuraments

The main result of our work is the implementation of an algorithm for the explicit generation of a patient-specific PF network for the left ventricle. This generative procedure is divided into three consecutive stages:
1) Manually design of the main branches representing the PF network by means of anatomical knowledge;
2) Generation of a tentative PF network by using a fractal rule;
3) Adapting the tentative network to the clinical patient-specific data of the activation times on the endocardium previously acquired.
In this work we considered patient-specific clinical data related to the activation times on the endocardium, thus we decided to model the activation times just on the endocardium. Regarding the mathematical models used to compute the activation times in the PF network and on the endocardium, we considered the isotropic version of the Eikonal equation, with values of the velocities in the physiological range. The patient-specific PF network built with this approach proved the essential role of the PF in modeling the activation of the left ventricle, both in healthy and in pathological activations and the importance, when clinical measurements are available, to generate a patient-specific PF network, allowing to significantly improve the accuracy of the numerical results.

Michele Piana
Dipartimento di Matematica Università di Genova and CRN - SPIN, Genova

Estimation of the whole bone marrow asset in humans by integrated nuclear medicine and X-ray tomography data

This talk describes a new method to estimate extension and activity of bone marrow in humans by combining structural and functional maps provided by Positron Emission Tomography (PET) and X-ray Computed Tomography (CT), respectively. This approach applies computational techniques for pattern recognition in CT images to determine the intra-bone volume of all different skeleton districts and utilizes this information to extract from PET data the metabolic activity of the bone marrow. An analysis of data from leukemic patients show both a diagnostic and a prognostic power of this approach.

Piero Poletti
Univerista` Bocconi

The impact of varicella vaccination on the epidemiology of Herpes Zoster

The introduction of mass vaccination against Varicella-Zoster-Virus (VZV) is being delayed in many European countries because of, among other factors, the possibility of a large increase in Herpes Zoster (HZ) incidence in the first decades after the initiation of vaccination, due to the expected decline of the boosting of Cell Mediated Immunity caused by the reduced varicella circulation. A multi-country model of VZV transmission and reactivation, is used to evaluate the possible impact of varicella vaccination on HZ epidemiology in Italy, Finland and the UK. Despite the large uncertainty surrounding HZ and vaccine-related parameters, surprisingly robust medium-term predictions are provided, indicating that an increase in HZ incidence is likely to occur in countries where the incidence rate is lower in absence of immunization, possibly due to a higher force of boosting (e.g. Finland), whereas increases in HZ incidence might be minor where the force of boosting is milder (e.g. the UK). Moreover, a convergence of HZ post vaccination incidence levels in the examined countries is predicted despite different initial degrees of success of immunization policies. Unlike previous model-based evaluations, our investigation shows that after varicella immunization an increase of HZ incidence is not a certain fact, rather depends on the presence or absence of factors promoting a strong boosting intensity and which might or not be heavily affected by changes in varicella circulation due to mass immunization. These findings might explain the opposed empirical evidences observed about the increases of HZ in sites where mass varicella vaccination is ongoing.

Giuseppe Pontrelli
IAC-CNR

Drug delivery in biological tissues: a semi-analytical study

In many drug delivery processes the mass is transferred from a porous reservoir where it is initially loaded in polymer-encapsulated solid-phase, and then released to the biological tissue, often constituted by a sequence of layers. The drug dynamics through them is modelled by a non-homogeneous set of coupled partial differential equations that describe a local mass non-equilibrium diffusion problem.

Davide Radi, GianItalo Bischi
Università di Bergamo

Multi-species exploitation with evolutionary switching of harvesting strategies

In this paper, we propose a bioeconomic model which describes a fishery where each of two non-interacting species is harvested by a given group of fishermen during a defined time period. Then each fisherman is allowed by the fishing.

Marco Scianna
Politecnico di Torino

A measure-theoretic approach to cell migration and organization

This presentation will deal with the derivation of a measure-theoretic model for the evolution and organization of cell populations. By starting with a microscopic Lagrangian description of the physical particle system, an ensemble representation of the dynamics of cell aggregates will be obtained in term of time-evolving probability measures. In particular, such an approach will introduce the concept of level of intercellular interactions, i.e. of how each cell senses and interacts with its neighboring individuals, i.e., if in a pointwise (discrete) manner or if in a more distributed (continuous) way. Also hybrid situations will be taken into account. The proposed model will indeed provide consistency to span different levels of representation of intercellular dynamics, i.e., to be a multiscale framework. Finally, sets of test simulations will be presented in order to show specific model applications.
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Alberto Sorrentino
Dipartimento di Matematica, Università di Genova

Sequential Monte Carlo samplers for multi-dipole estimation in Magnetoencephalography

Magnetoencephalography (MEG) records non-invasively and with outstanding temporal resolution (1,000 Hertz) the magnetic fields produced by the neural currents. Localizing the generators of the measured fields is crucial to improve our understanding of the brain, as well as to investigate pathological conditions such as epilepsy. Under the dipolar approximation, the neural current can be represented as a set of point-like sources, named current dipoles.

We consider the problem of estimating the number of dipoles and the dipole parameters from a single distribution of magnetic field. To this aim, we develop a Bayesian approach and a variable-dimension model. As the data depend non-linearly on the dipole parameters, the posterior distribution is complex and cannot be treated analytically: we develop a sequential Monte Carlo (SMC) sampler (Del Moral et al. 2006, JRRS B), whereby a tempering sequence of artificial distributions is built, that smoothly transits from the prior to the posterior. We suggest this one-parameter family of distributions closely reminds the one-parameter family of functionals in classical regularization. In this sense, SMC samplers naturally explore the whole regularization path.

We describe application of this method to both synthetic and experimental MEG data..

Serena Spina
Dipartimento di Matematica, Università di Salerno

A Jump Stochastic Gompertz Model for an Intermittent Treatment in Cancer Growth

Various stochastic models based on the Gompertz curve have been proposed recently to analyze the evolution of a cancer mass subject to therapies that alter the growth rates of cells.
In the present context, we analyze the effect of a therapeutic program that provides intermittent suppression of cancer cells. In particular, we suppose that the Gompertz diffusion process is influenced by jumps that occur according to a probability distribution, producing instantaneous changes of the system state. A jump represents an application of the therapy that leads the cancer mass to a return state. To analyze the evolution of the proposed process, we study its transition distribution function, the average state of the system, representing the mean size of the cancer, and the number of therapeutic applications to be carried out in time intervals of fixed amplitude. In particular, constant and exponential distributions are considered for the time elapsing between to successive therapeutic applications. We perform several numerical analyses to understand the behaviour of the process.

Federico Vaggi
Fondazione Edmund Mach

Cell Polarity in Fission Yeast

In this talk, we describe multiple integrated computational and experimental approaches to study the polarity network in fission yeast. We carry out a large-scale analysis of the protein-protein interaction (PPI) network of fission yeast (Schizosaccharomyces pombe) and establish a method to identify 'linker' proteins that bridge diverse cellular processes - integrating Gene Ontology and PPI data with network theory measures. We test the method on a highly characterized subset of the genome consisting of proteins controlling the cell cycle, cell polarity and cytokinesis and identify proteins likely to play a key role in controlling the temporal changes in the localization of the polarity machinery. Experimental inspection of one such factor, the polarity-regulating RNB protein Sts5, confirms the prediction that it has a cell cycle dependent regulation.
We also discuss how the integration of high throughput microscopy, image analysis, and modeling can be used to study fission yeast polarity.

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