Abstracts

Large scale asymptotics of velocity-jump processes and non-local Hamilton-Jacobi equations

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ABSTRACT

We investigate a simple velocity jump process in the regime of large deviation asymptotics. New velocities are taken randomly at a constant, large rate from a Gaussian distribution with vanishing variance. The Kolmogorov forward equation associated with this process is the linear BGK kinetic transport equation. We derive a new type of Hamilton- Jacobi equation which is nonlocal with respect to the velocity variable. We introduce a suitable notion of viscosity solution, and we prove well-posedness in the viscosity sense. We also prove convergence of the logarithmic transformation towards this limit problem. Furthermore, we identify the variational formulation of the solution by means of an action functional supported on piecewise linear curves. As an application of this theory, we compute the exact rate of acceleration in a kinetic version of the celebrated Fisher-KPP equation in the one-dimensional case.

Estimating the division in unicellular organisms: the incremental model

Marie Doumic

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ABSTRACT

The field of structured population equations knows a long-lasting interest for more than sixty years, leading to much progress in their mathematical understanding. They have been developed to describe a population dynamics in terms of well-chosen traits, assumed to characterize well the individual behaviour. More recently, thanks to the huge progress in experimental measurements, the question of estimating the parameters from population measurements also attracts a growing interest, since it finally allows to compare model and data, and thus to validate - or invalidate - ““the structuring”” character of the variable.

However, the so-called structuring variable may be quite abstract (““maturity””, ““satiety””...), and/or not directly measurable, whereas the quantities effectively measured may be linked to the structuring one in an unknown or intricate manner. We can thus formulate a general question: is it possible to estimate the dependence of a population on a given variable, which is not experimentally measurable, by taking advantage of the measurement of the dependence of the population on another - experimentally quantified - variable?

In this talk, we give first hints to answer this question, addressing it first in a specific setting, namely the growth and division of bacteria and yeast, and focus on a specific recently introduced model, the so-called ““increment of size””-structured equation, where the division depends on the increment of size between birth and division.

This is a common work with Adélaïde Olivier and Lydia Robert.

Macroscopic description of nonlocal movement of biological systems in R^n and in networks

Gissell Estrada-Rodriguez

Sorbonne Université, France

ABSTRACT

In the presence of sparse attractants, the movement of both cells and large organisms has been shown to be governed by long distance runs, according to an approximate Levy distribution. In this talk we clarify the form of biologically relevant PDE descriptions for such movements. Motivated by experiments we consider a microscopic velocity-jump model in which the motion of the individuals is characterized by long runs and long waiting times, according to a heavy-tailed distribution. From the kinetic equations obtained from the microscopic movement we derived nonlocal Patlak-Keller-Segel equations and fractional diffusion equations in the appropriate limit. We shed light on the extent to which Levy flight behaviour impacts on the average time taken for cells to locate the sparsely distributed infected targets. Furthermore, this nonlocal movement of individuals has been observed in more complex geometries, e.g., the brain. We propose to study the (nonlocal) diffusion using a network of subdomains, corresponding to the nodes of a graph. I will introduce metaplex networks which are networks with internal structure, and we will extend our analysis to two real world examples: a brain and a landscape network.

Rigorous derivation of the nonlocal reaction-diffusion FitzHugh-Nagumo system

Francis Filbet

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ABSTRACT

We introduce a spatially extended transport kinetic FitzHugh-Nagumo model with forced local interactions and prove that its hydrodynamic limit converges towards the classical nonlocal reaction-diffusion FitzHugh-Nagumo system. Our approach is based on a relative entropy method, where the macroscopic quantities of the kinetic model are compared with the solution to the nonlocal reaction-diffusion system. This approach allows to make the rigorous link between kinetic and reaction-diffusion models.

Multiscale modelling of particles in membranes

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ABSTRACT

We discuss the mathematical modelling of biological membranes with embedded membrane-shaping particles by hybrid approaches. The resulting models combine continuum membrane descriptions with discrete particle descriptions. The talk will give an overview of recent results on modelling, analysis, and numerical treatment of coupled membrane-particle systems and on current work combining such models with concepts from statistical mechanics and molecular dynamics.

Mathematical models of phase separation in binary liquids

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ABSTRACT

Phase separation in a binary liquid (e.g. oil and vinegar) is a phenomenon which can be described as a competition between an entropy mixing effect and a demixing effect due to the internal energy (i.e. the attraction of molecules of the same liquid), provided that, for instance, the temperature is low enough.

Liquid-liquid phase separation has recently become a sort of new paradigm in Cell Biology (see, for instance, [1, 3, 4, 5] and their references). Quoting from [2]: “Not only is phase separation intuitive, but it seems to be everywhere. Droplets of proteins and RNAs are turning up in bacteria, fungi, plants and animals. Phase separation at the wrong place or time could create clogs or aggregate of molecules linked to neuro degenerative diseases, and poorly formed droplets could contribute to cancers and might help explain the ageing process.

Typical mathematical models for phase separation are given by the so-called Cahn-Hilliard equation or by the conserved Allen-Cahn equation. However, in the case of liquids, such equations must be suitably coupled with the Navier-Stokes system for the averaged velocity of the binary mixture. I intend to present some recent results obtained for these models, focusing on incompressible conserved Allen-Cahn fluids. This is a joint research with A. Giorgini (Indiana University, Bloomington, USA) and H. Wu (Fudan University, Shanghai, PRC).

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Modeling morphogenesis in plant stem cell niches

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ABSTRACT

The shoot keeps dividing stem cells throughout the life of the plant providing material to new organs for the above ground tissue. Since cell migration is prohibited and cells are surrounded by a mechanically rigid cell wall, genes and hormones needs to act via changing the properties of the walls and grow into the shapes produced. Using Computational Morphodynamics, combining live imaging and modelling, we aim to understand the interactions between molecular and mechanical regulation that drives plant morphogenesis and differentiation.

Revertible velocity jump process and heterogeneous diffusion

YONG JUNG KIM

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ABSTRACT

Diffusivity alone is not enough to decide the diffusion phenomenon in a heterogeneous environment. In this paper, we show that the turning frequency is also needed and derive a diffusion law. To do that, a revertible kinetic equation of Stratonovich type is introduced. The new diffusion law turns into Wereide's diffusion law when the turning frequency is constant. A thought experiment is introduced to test the validity of diffusion laws.

As a biological application of the diffusion law we investigate biological invasion with the new diffusion law. Shigesada *et al.* proposed a reaction-diffusion equation in a periodic environment to model the biological invasion in heterogeneous environments. However, the model shows a counter intuitive conclusion that a species should decrease its diffusivity in undesirable patches to increase the chance of invasion. We show that Fick's diffusion law is the reason for the contradictory phenomenon and that our new diffusion law can fix it.

On the problem of spreading in Lotka-Volterra competition models

King-Yeung Lam, Adrian

Ohio State University, USA

ABSTRACT

I will report on a Hamilton-Jacobi approach to determine spreading speed in reaction-diffusion systems involving more than one species. The main idea consists in obtaining large-deviation type estimates in certain moving coordinates y = x – ct, which is inspired by the Hamilton-Jacobi approach due to Freidlin, Evans and Souganidis. This approach enables a decoupling of the problem, and allows the determination of multiple spreading speeds in certain non-cooperative systems. This is joint work with Shuang Liu and Qian Liu (Renmin and Ohio State).

Modeling and nonlinear simulation of solid tumor growth with chemotaxis

Shuwang Li

Illinois Institute of Technology, USA

ABSTRACT

The ability of tumors to metastasize is manifested by morphological instabilities such as chains or fingers that invade the host environment. In this talk, we develop a computational method for simulating the nonlinear dynamics of a tumor-host interface within the sharp interface framework. We are interested in solid tumor growth with chemotaxis and cell-to-cell adhesion, together with the effect of the tumor microenvironment by the variability in spatial diffusion gradients, the uptake rate of nutrients inside/outside the tumor and the heterogeneous distribution of vasculature modeled using complex far-field geometries. We solve the nutrient field (modified Helmholtz equation) and the Stokes/Darcy flow field using a spectrally accurate boundary integral method, and update the interface using a nonstiff semi-implicit approach. Numerical results highlight the complexity of the problem, e.g. development of spreading branching-patterns and encapsulated morphologies in a long period of time.

scRNA-seq data analysis: issues and some recent results

Tiejun Li

Peking University, China

ABSTRACT

scRNA-seq data analysis is one of the most exciting topics in computational biology and it is currently in the fast developing stage. In this talk I will introduce the main issues in this area and some recent methods developed by our group. The covered topics include the stemness identification, lineage inference, cell clustering and batch removal.

A mathematical dissection of the adaptation of cell populations to fluctuating oxygen levels

Tommaso Lorenzi

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ABSTRACT

The disordered network of blood vessels that arises from tumour angiogenesis results in variations in blood flow which generate fluctuations in the delivery of oxygen into the tumour tissue. This brings about regions of chronic hypoxia (i.e. sustained low oxygen levels) and cycling hypoxia (i.e. alternating phases of low and relatively higher oxygen levels) within vascularised tumours, and makes it necessary for cancer cells to adapt to fluctuating environmental conditions. We use a phenotype-structured model that comprises a system of non-local partial differential equations in order to dissect the adaptation of cell populations to fluctuating oxygen levels. Exploiting the analytical tractability of the model, we study the long-time behaviour of the solutions to obtain a detailed mathematical depiction of evolutionary dynamics. Our analytical results formalise the idea that when oxygen levels experience small and slow oscillations, and thus environmental conditions are relatively stable, it is evolutionarily more efficient to rarely undergo spontaneous phenotypic variations. Conversely, under relatively large and fast oscillations in the oxygen levels, higher rates of spontaneous phenotypic variation can confer a competitive advantage, as they may allow for a quicker adaptation to changeable environmental conditions. In the latter case, our results indicate that higher levels of phenotypic heterogeneity are to be expected compared to those observed under slowly fluctuating oxygen levels. Finally, our results suggest that bet-hedging evolutionary strategies, whereby cancer cells switch between antithetical phenotypic states, can naturally emerge in the presence of relatively large and fast oxygen fluctuations leading to drastic environmental changes.

Mathematical modeling and analysis to compare different mechanisms of developmental pattern formation

ANNA MARCINIAK-CZOCHRA

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ABSTRACT

Mechanisms of self-organized pattern formation in developmental biology have been the focus of experimental and theoretical research for several decades. A number of different morphologies have been subject to mathematical modeling. All these models, under different biological hypotheses, have common mathematical features and are mostly based on a limited range of mathematical mechanisms of pattern generation. The classical Turing approach relies on the concept of a chemical prepattern created by hypothetical chemicals. Nonlinear interactions facilitated by different diffusivities may yield a bifurcation leading to destabilization of constant equilibria (diffusion-driven instability) and development of spatially heterogeneous patterns. So far, identification of such Turing-type molecules active in morphological events is still rare. Recent experiments indicate that mechanical cues play an active role in tissue patterning. To investigate patterning potential of mechanochemical coupling, we proposed new mathematical models linking dynamics of diffusing molecular signals with a model of tissue deformation. Our models show that biomechanical forces may yield formation of stable spatial patterns without chemical pre-patterns and provide an alternative to the Turing-type models. In this talk, we compare both mechanisms using tools of multiscale analysis and numerical simulation.

Spontaneous recovery of loop structure in multi-state network systems

Yasumasa Nishiura

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ABSTRACT

We propose a class of directed network systems that spontaneously initiates and completes loop searching against the removal and attachment of connection links. Network nodes are either the Morris-Lecar model, FitzHugh-Nagumo model, or group oscillator model. The self-recovery process emerges out of only local interactions between the nodes without introducing a feedback function representing the global state of the system. A sudden external perturbation like removal or attachment of links in general breaks a loop structure, but at the same time it causes unleashing of inhibition of neighboring nodes and the resulting new firing (post-inhibitory rebound) becomes an onset of searching a new loop. This shows an automatic attractor switching triggered by external perturbation. The searching time depends on the topology of network, for instance, scale-free networks have shorter searching time than random networks. The concept of the model construction is applicable to a wider class of nonlinear systems including chemical reactions and neural networks. This is a joint work with K.I. Ueda (Toyama University).

PDEs for neural assemblies; models, analysis and behavior

Benoît Perthame

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ABSTRACT

Neurons exchange information via discharges propagated by membrane potential which trigger firing of the many connected neurons. How to describe large assemblies of such neurons? How can such a network generate a collective activity?

Such questions can be tackled using nonlinear partial-integro-differential equations which are classically used to describe neuronal assemblies. Among them, the Wilson-Cowan equations are the best known and describe globally brain spiking rates. Another classical model is the integrate-and-fire equation based on Fokker-Planck equations. The spike times distribution, which encodes more directly the neuronal information, can also be described directly thanks to structured population.

We will compare and analyze these models. A striking observation is that solutions to the I&F can blow-up in finite time, a form of synchronization that can be regularized with a refractory stage. We can also show that for small or large connectivities the 'elapsed time model' leads to desynchronization. For intermediate regimes, sustained periodic activity occurs compatible with observations. A common tool is the use of the relative entropy method.

A new model for the emergence of vascular networks

DIANE PEURICHARD

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ABSTRACT

The generation of vascular networks is a long standing problem which has been the subject of intense research in the past decades, because of its wide range of applications (tissue regeneration, wound healing, cancer treatments etc). The mechanisms involved in the formations of vascular networks are complex and despite the vast amount of research devoted to it there are still many mechanisms involved which are poorly understood. Our aim is to bring insight into the study of vascular networks by defining heuristic rules, as simple as possible, and to simulate them numerically to test their relevance in the vascularization process. We introduce a hybrid agent-based/continuum model coupling blood flow, oxygen flow, capillary network dynamics and tissues dynamics. We provide two different, biologically relevant geometrical settings and numerically analyze the influence of each of the capillary creation mechanism in detail. All mechanisms seem to concur towards a harmonious network but the most important ones are those involving oxygen gradient and sheer stress.

A structured population model for sexual populations

Gaël Raoul

École polytechnique, France

ABSTRACT

We will consider a population structured by a phenotypic trait and a space variable. Individuals disperse in space and are submitted to a selection term that may depend on both trait and space. We will focus our analysis on sexual populations: the reproduction then implies a mixing of traits. We will show that Wasserstein distances provide a natural framework to consider the reproduction operator (based on the infinitesimal model from population's genetics), and that these estimates can be used in combination with other quantities to study the qualitative dynamics of solutions.

A first result of this method is to relate the structured population model we introduce to existing macroscopic models (Kirkpatrick and Barton model). A second result, still in development, is to study the asymptotic stability of equilibrium for the model without a space structure. The combination of these method could lead to possible refinements of the Kirkpatrick-Barton model that would take into account the dynamics of the variance of the phenotypic diversity of the population. This perspective is appealing for evolutionary ecology applications since the variance of the phenotypic diversity plays a crucial role in the ability of a population to evolve (in particular in the context of climate change).

An asymptotic preserving scheme for capturing concentrations in age-structured models arising in adaptive dynamics

Xinran Ruan

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ABSTRACT

We propose an asymptotic preserving (A-P) scheme for a population model structured by age and a phenotypical trait with or without mutation. As shown in a paper by S. Nordmann, B. Perthame, and C. Taing, Dirac concentrations on particular phenotypical traits appear in the case without mutation, which makes the numerical resolution of the problem challenging. Inspired by its asymptotic behaviour, we apply a proper WKB representation of the solution to derive an A-P scheme, with which we can accurately capture the concentrations on a coarse, parameter-independent mesh. Important properties, including the A-P property, are rigorously proved. The scheme can be generalized to the case with mutation, where a nonlinear Hamilton-Jacobi equation will be involved in the limiting model. It can be formally shown that the generalized scheme is A-P as well.

Mathematical modeling and analysis of fractional diffusion induced by intracellular noise

Min Tang

Shanghai Jiao Tong University, China

ABSTRACT

In this talk, we use an individual-based model and its associated kinetic equation to study the generation of long jumps in the motion of E. coli. These models relate the run-and-tumble process to the intracellular reaction where the intrinsic noise plays a central role.

Mathematical modeling of propagation of Wolbachia to control dengue spread

NICOLAS VAUCHELET

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ABSTRACT

Aedes mosquitos are the main vectors of several diseases like dengue, chikungnya, zika. New strategies of control consist in acting on the mosquitos population. For example, it has ben observed that when a mosquito is infected by the bacteria Wolbachia it cannot transmit such diseases. Moreover, Wolbachia is transmitted from mother to offspring and is characterized by a cytoplasmic incompatibility.

Then a strategy of fight against arboviruses consists in releasing Wolbachia infected mosquitoes. After presenting the mathematical modeling of the spatial spread of this bacteria thanks to reaction- diffusion equations, we investigate the success of the spatial invasion thanks to local releases and the influence of spatial heterogeneities. Then we will focus on the way to optimize the releases.

Bulk-surface coupling: derivation of two models

XUEFENG WANG

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ABSTRACT

It is well-known that cell polarization and cell division are caused by protein reaction-diffusion in the cytoplasm and on the cell membrane, which are coupled due to protein cycling between them. To model these cellular phenomena, numerous bulk-surface models have been proposed, which, in the simplest form, consist of one diffusion equation for inactive protein the cytoplasm and another one for active protein on the thickless membrane, with a flux boundary condition coupling the proteins in the bulk and on the surface. A rigorous derivation of such models seems lacking, which motivates this work. We assume that the membrane has positive but small thickness δ and that the phospholipid molecules in the membrane are optimally aligned and we start with two full models each of which contains reaction-diffusion equations in the bulk and the membrane, respectively, with reasonable transmission conditions linking the two. Then in the limit of $\delta \to 0$, we obtain two effective models, with one having the same form as the simplest bulk-surface model mentioned above, the other being a single diffusion equation in the cytoplasm with a dynamical boundary condition. Our models satisfy mass conservation property, which has been a yardstick for the existing bulk-surface models. Our investigation reveals that the optimal alignment of phospholipid molecules and the tangential diffusion in the cell membrane result in the surface diffusion in bulk-surface models, and that a single diffusion equation with a dynamical boundary condition may serve as a simpler alternative model for bulk-surface coupling. This is a joint work with Jingyu Li and Linlin Su.

A unified and exactly solvable model for dimeric nanomotors

Zhisong Wang

National University of Singapore, Singapore

ABSTRACT

Experimental development of artificial translational nanomotors recently undergoes a paradigm shift from bridge-burning monomers to Cooper-pair-like symmetric dimers capable of truly sustainable motion. The Cooper-pair-like construction has potential for high-efficiency motors as friction, inevitable though for a single moving object in a viscous environment, may vanish for Cooper pairs. But how to create high-performing nanomotors remains an open question even from fundamental physics perspective. Here we introduce a unified physical model covering virtually all dimeric translational nanomotors invented to date, which span a wide variety of molecular constructions, energy sources and operational methods. This model is exactly solvable for a tri-harmonic representation of motor-track systems, revealing a wealth of emergent behaviours beyond previous independent-particle theories for molecular motors. An analytical mechanical-kinetic solution captures key features of real motors and exposes novel high-performing regimes with a sign of superlubricity. The model thus lays a physical foundation for future development of advanced nanomotors. Indeed, the model can host increasingly sophisticated motor-track representations, but exact solutions will be more challenging from mathematic perspective.

Can primitive chemotaxis generate spatial structures?

Michael Winkler

Universität Paderborn, Germany

ABSTRACT

Parabolic models for the collective behavior in populations of single-cell species are considered. A predominant emphasis will be on cases in which individuals are particularly primitive in the sense that beyond a partially oriented movement toward increasing concentrations of a nutrient, further activity can essentially be neglected. Recent developments in the analysis of such nutrient taxis systems are to be described, with a special focus set on mathematical challenges related to the fundamental question how far models of this type are capable of adequately reflecting aspects of colorful dynamics known from experimental observations.

Existence and stability of nontrivial steady states for the SKT competition model with cross-diffusion

Yaping Wu

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ABSTRACT

This talk is focused on the following quasilinear reaction diffusion model with cross-diffusion, which was first proposed by Shigesada-Kawasaki-Teramoto to describe the segregation of two competing species under the intra- and the inter specific population pressure,

$$\begin{cases} u_t = \Delta[(d_1 + \rho_{11}u + \rho_{12}v)u] + u(a_1 - b_1u - c_1v), & x \in \Omega, t > 0, \\ v_t = \Delta[(d_2 + \rho_{21}u + \rho_{22}v)v] + v(a_2 - b_2u - c_2v), & x \in \Omega, t > 0. \end{cases} \tag{1}$$

Here $u(x,t)$ and $v(x,t)$ represent the densities of two competing species at location x and time t. We always assume d_i, a_i, b_i, c_i are positive constants. The coefficients ρ_{11} and ρ_{22} denote the self-diffusion rates which represent intra-specific population pressures, ρ_{12} and ρ_{21} denote the cross diffusion coefficients which measure the population pressure from the competing species.

I shall talk about our recent work on the existence, detailed asymptotic structure and stability/instability of several types of nontrivial positive steady states for three types of limiting system of SKT model when one of the cross diffusion parameter tends to infinity and the original SKT model when one of cross diffusion parameter is large enough. The talk is based on the joint work with Qing Li, Xuefeng Wang, Kousuke Kuto and Yanxia Wu.

The responses of protein structures and protein-protein complexes to mechanical perturbations

Jie Yan

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ABSTRACT

The task of mechanosensing of cells involves dynamic assembly of various supramolecular force-transmission linkages, which allow the cells to properly sense and respond to the level of mechanical force in the linkages. A force-transmission linkage typically consists of a few non-covalently linked proteins, in which the domains and protein-protein interfaces are subject to dynamic fluctuation of intracellular forces. This results in highly complex force-dependent conformations of the domains, the interactions of these domains with numerous signaling proteins, and the connectivity of the force-transmission supramolecular linkages. Despite their crucial roles in enabling mechanosensing of cells, a systematic physical understanding of the biomolecular responses to mechanical perturbation over physiological level of forces is still lacking. In this talk, I will introduce our recent theoretical works aiming to provide a systematic understanding of the biomolecular responses to mechanical perturbation, and how such theories may provide new insights into the molecular mechanisms underlying mechanosensing of cells.

Network design principle for dual function of adaptation and noise attenuation

Lei Zhang

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ABSTRACT

Many signaling systems execute adaptation under noisy circumstances. While the adaptation or noise attenuation has been studied separately, how to achieve these two competing functions simultaneously remains elusive. To explore such dual function, we first explore three-node enzymatic regulation networks, and identify an intrinsic trade-off existing between good sensitivity and noise attenuation in the three-node networks. Although fine-tuning timescales in three-node adaptive networks can partially mediate such trade-off, it introduces prolonged adaptation time and unrealistic parameter constraints. This trade-off can be minimized in four-node networks, in which the adaptation module and the noise attenuation module can be effectively decoupled to achieve dual function. There exist constraints on assembling the two modules in order to allow high performance of dual function. Maintaining the system sensitivity is a bottleneck and the time scales of the two modules need to be well coordinated. By scrutinizing seven biological systems, we find that adaptive networks are often associated with a noise attenuation module. The obtained design principles are then studied using two examples: Dictyostelium discoideum chemotaxis and p53 signaling network. Our approach may be applicable to finding network design principles for other dual and multiple functions.

A brain-spired spiking neural model for artificial intelligence

Douglas Zhou

Shanghai Jiao Tong University, China

ABSTRACT

Spiking neural networks are widely applied to simulate cortical dynamics in the brain, and are regarded as the next generation of machine learning. Therefore, as a first step, it is important to model single-neuron dynamics quantitatively. However, the existing point neuron models fail to capture dendritic effects, which are crucial for neuronal information processing. We derive an effective point neuron model, which incorporates an additional synaptic integration current arising from the nonlinear interaction between synaptic currents across spatial dendrites. Our model captures the somatic voltage response of a realistic neuron with complex dendrites and provides some insight into the construction of basic unit in artificial neural networks.

Fokker-Planck equations of neuron networks: rigorous justification and numerical simulation

ZHENNAN ZHOU

Peking University, China

ABSTRACT

In this talk, we are concerned with the Fokker-Planck equations associated with the Nonlinear Noisy Leaky Integrate-and-Fire model for neuron networks. Due to the jump mechanism at the microscopic level, such Fokker-Planck equations are endowed with an unconventional structure: transporting the boundary flux to a specific interior point. In the first part of the talk, we present an alternative way to derive such Fokker-Planck equations from the microscopic model based on a novel iterative expansion. With this formulation, we prove that the probability density function of the "leaky integrate-and-fire" type stochastic process is a classical solution to the Fokker-Planck equation. Secondly, we propose a conservative and positivity preserving scheme for these Fokker-Planck equations, and we show that in the linear case, the semi-discrete scheme satisfies the discrete relative entropy estimate, which essentially matches the only known long time asymptotic solution property. We also provide extensive numerical tests to verify the scheme properties, and carry out several sets of numerical experiments, including finite-time blowup, convergence to equilibrium and capturing time-period solutions of the variant models.