Mathematical biology
Biomathématiques
(Org: **Claire Guerrier** (Université Côte d'Azur) and/et **Anmar Khadra** (McGill))

JACQUES BÉLAIR, Université de Montréal
Waning immunity in a two-strain disease model

Motivated by the interactions between two strains of the virus causing Dengue Fever, we consider a model essentially taking the form of two mutually coupled SIRS models, with general density function for the duration of stay in each of the compartments, leading to a system of nonlinear functional-differential equations. We consider the stability of equilibria, detect Hopf bifurcations and investigate the influence of the distribution of the density function on these stability properties.

IGOR BELYKH, Georgia State University
When repulsive coupling promotes synchronization of bursting neurons

Synchrony has been broadly observed in pathological brain states, especially during epilepsy and Parkinson's tremors. The neuronal mechanisms that generate such abnormal synchronous states are far from being fully understood. In this talk, we discuss the emergence of synchronization in networks of bursting neurons as highly non-trivial, synergistic effects when (i) the addition of pairwise repulsive inhibition to excitatory networks can promote in-phase synchronization and (ii) combined electrical and inhibitory coupling can induce synchronization even though each coupling alone promotes an antiphase rhythm. In particular, we reveal the underlying mechanism, which uses a balance between hidden properties of electrical and inhibitory coupling to act together to synchronize neuronal bursting. We show that this balance is controlled by the duty cycle of the self-coupled system which governs the synchronized bursting rhythm. Our studies of neuronal synchronization form a basis for understanding the counterintuitive dynamics of bursting networks, which may yield meaningful insight into the phenomenon of pathological synchrony in epileptic networks. Our results suggest that promoting normally repulsive inhibition in an attempt to prevent seizures can have an unintended effect of inducing pathological synchrony.

KHANH DAO DUC, University of British Columbia
A study of stochastic dynamics of mRNA translation and their impact across biological scales

The translation of mRNA into protein is a fundamental cellular process, mediated by the flow of ribosomes. As these dynamics can be locally regulated by many molecular mechanisms, analytical tools are needed to find the determinants of translation speed. I will present analytical and computational methods that we recently developed to study translation across different scales, using a wide array of structural, sequencing, and imaging data. These methods importantly rely on a stochastic interacting particle model that generalizes the totally asymmetric simple exclusion process (TASEP). We analytically studied this process to determine its phase diagram and find the key parameters that govern translation efficiency. In the context of recent advances in deep sequencing, we also used the model to infer translation rates for a large set of genes in yeast, and analyzed the contribution of traffic jams, codon specificity, and other biophysical parameters. These results more recently guided our studies of the molecular structure of the ribosome (obtained from cryoEM) and translation kinetics observed in vitro using lysate systems. Overall, these completing approaches emphasize the major role played by the ribosome in gene expression, at both molecular and population levels.

BARD ERMENTROUT, University of Pittsburgh
A model for the the inflammatory response to SARS-CoV-2 in the upper- and lower-respiratory tracts.

We create a two-compartment model of the upper and lower respiratory tract in order to model the progression of a viral disease such as SARS-CoV-2. The model includes viral replication, tissue damage, tissue healing, and an immune component. The

immune component includes markers for inflammation as well as pro- and anti-inflammatory cytokines. We fit the parameters of the model to recent data on rhesus monkeys. We then characterize the dynamics of the model in cases where the outcomes are (i) clearance and return to health, (ii) inability to clear the virus, (iii) clearance, but high damage incurred by the inflammatory response. In the latter two cases, we examine how the timing of anti-viral or anti-inflammatory drugs impacts the outcomes. This work is joint with Ericka Mochan (Carlow University), TJ Sego (Indiana), Emmaline Rial and Lauren Gaona.

SAEED FARJAMI, University of Surrey
Non-sequential Spike Adding in Cerebellar Stellate Cells

Cerebellar Stellate Cells are spontaneously spiking. Recently, our colleagues have recorded bursting activities in these cells by applying pharmacological agents known for blocking certain ion currents. Such activities are usually modelled in the form of systems with different time scales. When the slow variables are treated as parameters, the fast subsystem can provide good insights into the dynamics of the full model. Using slow-fast analysis, we explain the underlying mechanisms responsible for generating types of bursting emerging in the model. Also, a bifurcation analysis of the full model reveals the effect of different doses of the pharmacological agents on the system dynamics. Moreover, our investigations show that the number of spikes in an active phase of bursting changes when parameters of the system fluctuate. However, in contrast to former studies, adding new spikes does not happen sequentially. In this talk, we will discuss such phenomena and try to shed light on their underlying dynamics.

This is joint work with Ryan Alexander, Derek Bowie and Anmar Khadra.

ERIC FOXALL, UBC Okanagan
Bifurcation theory of well-mixed stochastic population models

The bifurcation theory of ordinary differential equations (ODEs), and its application to deterministic population models, are by now well established. In this article, we begin to develop a complementary theory for well-mixed stochastic population models, with the goal of understanding the scale, in both time and population density, of fluctuations near bifurcation points of the underlying deterministic system. To do so we study the ODE and SDE limits that arise in the vicinity of bifurcation points and discover that they can be neatly classified in a bifurcation diagram that complements and enhances the deterministic theory. We focus on one-dimensional bifurcations, although the general approach is extensible to higher dimensions.

PAUL FRANCOIS, McGill University
Information in cytokine dynamics : robotic mapping and machine learning

An immune response is by essence a collective computation. Starting with the initial activations of few T cells, a complex dance of immune actors self-organize over long time scales. Understanding how and why immune cells communicate with one another to perform this response could be key to a better understanding of personalized medecine and immunotherapy. In collaboration with Gregoire Altan-Bonnet (NIH), we have developped a pipeline to study, decode and model cytokine communications between T cells. I will show how simple machine learning allows to project the complex immune response into a 2D latent space, where immune parameters can be simple deconvolved. Remarkably, this suggests a simple model of collective communication and computation, highly reproducible and universal. I will show how our approach can be used to predict quality of unknown antigen, and how it can potentially help to better estimate success of immunotherapy.

SIMON GIREL, Université Côte-d'Azur
Mathematical modeling of the CD8 T-cells immune response

Infection of an organism by a pathogen triggers the activation of the CD8 T-cells and the initiation of the immune response. The result is a complex program of proliferation and differentiation of the CD8 T-cells, controlled by the evolution of their molecular content. I will introduce two mathematical models of the CD8 T-cell response. The first one is presented as an impulsive differential equation by which we study the effect of unequal molecular partitioning at cell division on the regulation of

molecular heterogeneity. The second one is an agent-based-model that couples the description of a discrete population of CD8 T-cells and that of their molecular content. This model can reproduce the different typical phases of the CD8 T-cell response at both the cellular and the molecular scales. These two studies support the hypothesis that the cell dynamics observed *in vivo* is a consequence of the molecular heterogeneity structuring the CD8 T-cell population.

THOMAS HILLEN, University of Alberta
Non-local Models for Cellular Adhesion

Cellular adhesion is one of the most important interaction forces between cells and other tissue components. In 2006, Armstrong, Painter and Sherratt introduced a non-local PDE model for cellular adhesion, which was able to describe known experimental results on cell sorting and cancer growth. Since then, this model has been the focus of applications and analysis. The analysis becomes challenging through non-local cell-cell interaction and interactions with boundaries. In this talk I will present theoretical results of the adhesion model, such as a random walk derivation, biologically realistic boundary conditions, pattern formation and results on local and global existence of solutions. (joint work with A. Buttenschoen).

DAVID HOLCMAN, Institut de Biologie École Normale Supérieure

NATHANAEL HOZÉ, Institut Pasteur
Assessing virus circulation levels in the context of high serological cross-reactivity: the case of Mayaro and Chikungunya virus

Mayaro virus (MAYV) is often cited as a likely candidate for the next major arbovirus emergence and quantifying its circulation in human populations in the Americas is therefore important to inform risk assessments. However, this task is difficult because MAYV symptoms are mostly unspecific and serology is challenging to interpret because of the large chikungunya virus (CHIKV) outbreak that occurred in 2014-2015 and high cross-reactivity between MAYV and CHIKV. This problem of cross-reactivity hampers serological studies across many different pathogens.

Here we demonstrate that by jointly analyzing serological results alongside data on the age and location of participants, we can simultaneously reconstruct the history of circulation of the viruses and the extent of cross-reactivity. We applied our approach to serological results of 2,697 individuals from across French Guiana obtained with a multiplexed immunoassay that returned a relative fluorescence intensity (RFI) for each pathogen.

We quantify the impact of cross-reactivity on the RFI for the infecting and non-infecting virus. We find evidence of regular MAYV spillovers, with male adults particularly affected and seroprevalence in forested regions as high as 10

SAM JAMALEDDINE, McGill University
Investigating the effects of T cell avidity distributions on acute vs. chronic viral infection dynamics

The generation of lymphocyte receptor diversity is a key feature of adaptive immunity. In addition to somatic recombination, diversification of the T cell repertoire is significantly enhanced by terminal deoxynucleotidyl transferase, or TdT. However, TdT-knockout studies have shown that lack of TdT does not abrogate T cell immunity in response to acute stimulation by bacterial or viral antigen, and so the specific advantage that this added TdT-dependent variability brings forth remains unclear. We propose that TdT may alter properties of the binding-avidity distribution of protective T cells, and that lack of TdT can impair the immune response against a chronic viral pathogen. In this work, we study the response of a population of T cells that together confer a continuum of T-cell avidities. By constructing and analyzing a system of integro-differential equations, we can not only consider the temporal evolution of key population sizes (namely effector T-cell levels and viral loads), but also track the evolution and infer the role of the distribution of T cell avidities over time. We observe that TdT could offer an advantage over TdT-deficient T cells in a chronic viral context, by either decreasing the average binding avidity, or broadening the range of observable T cells avidities.

ANMAR KHADRA, McGill University
Excitable media in fish keratocytes model: Canard explosion, traveling waves and beyond

A partial differential equation (PDE) model of a self-organizing lamellipodium in crawling keratocytes has been previously developed to understand the three spatiotemporal patterns of activity observed in such cells, namely, stalling, waving and smooth motility. The model consisted of three key variables: the density of barbed actin filaments, newly formed FAs called nascent adhesions (NAs) and VASP, an anti-capping protein that gets sequestered by NAs during maturation. Using parameter sweeping, the distinct regimes of behaviour associated with the three activity patterns were identified. By converted the PDE model into an ODE model, we successfully examined the excitability properties of this system and determined all of its patterns of activity. Our results revealed that there are two additional regimes not previously identified: bistability and type IV excitability (generated by three steady states and their manifolds). We found that these regimes are also present in the PDE model. Applying slow-fast analysis on the ODE model showed that it exhibits a canard explosion through a folded-saddle and that rough motility seen in keratocytes is likely due to noise-dependent motility governed by dynamics near the interface of bistability and type IV excitability. The two parameter bifurcation suggested that the increase in the proportion of rough motion is due to a shift in activity towards the bistable and type IV excitable regimes induced by a decrease in NA maturation rate. In this talk, I will provide a summary of these findings.

GRANT LYTHE, University of Leeds
How many TCR clonotypes does a body maintain?

There are approximately 400000000000 naive CD4 T cells in your body, about the same as the number of stars in our galaxy. On the other hand, the number of cells of one TCR clonotype is a small integer that increases or decreases by one cell at a time, when cells divide or die. New clonotypes are released from the thymus and compete with other clonotypes in the periphery for specific and non-specific resources. Mean clonal sizes can therefore be calculated from mean clonal lifetimes. For example, if the ratio of thymic production to peripheral division is four percent, then the number of distinct T-cell clonotypes in the human body is about nine percent of the total number of (naive CD4) T cells. In mice, most TCR clonotypes may consist of just one or two T cells.

LAURENT MACKAY, McGill University
Feedback onto cellular polarization from paxillin, implications for migrating cells.

Cellular polarization plays a critical during cellular differentiation, development, and cellular migration through the establishment of a long-lived cell-front and cell-rear. Although mechanisms of polarization vary across cells types, some common biochemical players have emerged, namely the RhoGTPases Rac and Rho. The low diffusion coefficient of the active form of these molecules combined with their mutual inhibitory interaction dynamics have led to a prototypical pattern formation system that can polarizes cell through a non-Turing pattern formation mechanism termed wave-pinning. We investigate the effects of paxillin, a master regulator of adhesion dynamics, on the Rac-Rho system through a serine phosphorylation-dependent positive feedback loop that amplifies Rac activation. We find that paxillin feedback onto the Rac-Rho system produces cells that (i) self-polarize in the absence of any input signal (i.e., paxllin feedback causes a Turing instability) and (ii) become arrested due to the development of multiple protrusive regions. The former effect is a positive finding, while the latter outcome is likely an artefact of the model. In order to minimize the effects of this artefact to produce cells that can both self-polarize and migrate for extended periods of time, we revisit some of model's parameter values and use lessons from previous models of polarization. After some simple modifcations to the model, our simulations behave very much like these previous models while being significantly simpler yet biochemically detailed. Thus this work yields insights into the biochemical acitivties of paxillin as well as general feedback patterns necessary for effective cellular migration.

BRIAN MERCHANT, University of British Columbia
Using a Rho GTPase based model of cell polarization to explain group advantage in chemotaxis

We model a migrating cell as a 2D elastic polygon, with Rho GTPase biochemistry simulated on the vertices. This biochemistry enables a model cell to polarize and migrate. Intercellular interactions between cells can emerge by allowing them to modulate each others' polarization. In particular, we recapitulate two intercellular interactions observed in neural crest cells (NCCs): 1) contact inhibition of locomotion (CIL), whereby upon making contact, cells re-polarize in order to break contact and disperse, and 2) co-attraction (COA), whereby cells attract each other at a distance. We had previously confirmed a hypothesis that model NCC clusters enjoy enhanced directional motility, compared to a single cell, due to suppression of random protrusions through CIL and COA interactions between cluster cells. Now, we investigate whether this same increase in a cluster's directional motility could also explain the ability of a cluster of NCCs to respond to a chemoattractant gradient too weak for a single cell to interpret.

LAWRENCE OPREA, McGill University
Simulation and analysis of white matter in a variably hypomyelinated transgenic mouse model

Demyelination, which causes severe reductions in the quality of action potential transmission, is important in the study of diseases such as multiple sclerosis. Recently, a series of transgenic mouse lines were developed with variable levels of myelin basic protein (mbp) mRNA. Applying semi-automated image segmentation to electron micrographs from these mice, we were able to extract information on myelin thickness, g ratio, myelin volume fraction, and geometric properties from tens of thousands of cells. Additionally, we built an axon packing algorithm to produce simulated 2D and 3D renderings of tracts with varying myelination. Results show clear nonlinear relationships between mbp levels and myelination of axons. These additionally vary across spinal cord regions and age. Compensatory mechanisms that mitigate the effects of low myelination, such as increased cell size and number, appear to occur once a demyelination threshold is reached. These data naturally lead to models investigating the energetics and electrophysiological effects of demyelination in development and maturation.

FERNANDO PERUANI, CY Cergy Paris Université
A mathematical approach to bacterial infections: models for bacterial exploration and infection

Gastrointestinal infections occur by both, motile and non-motile pathogenic bacteria. Whether there exists a correlation between bacterial motility and bacterial virulence remains a key open question. Combining mathematical models and in vitro bacterial experiments, we will analyze how pathogenic bacteria explore the bottom surface of a cell chamber and infect the human colonic epithelial cells sitting on it. The study quantifies and explains the role of bacterial motility in the infection process.

References: Perez-Ipiña et al., Nature Physics 15, 610-615 (2019), and Otte et al., to appear (2020)

CHARLES S. PESKIN, New York University
Interaction of Facilitation and Depression in Synaptic Transmission

We use experimental data to construct a simple model of stochastic vesicle release that includes facilitation, and we apply that model to study the interaction of facilitation and depression in synaptic transmission. Depending on parameters and on the rate of arrival of action potentials, we find that the model synapse can process signals in a variety of ways, and these will be discussed both from a linear, frequency-analysis viewpoint that requires consideration of small-amplitude modulation of a regular spike train, and also from a nonlinear perspective in which large-amplitude steplike changes in the rate of arrival of action potentials are considered. (Joint work with Calvin Zhang-Molina, University of Arizona.)

KHOREN PONSIN, McGill University
Mathematical Modeling of Cellular Phagocytosis During Embryogenesis of the Urogenital System

During embryonic development of the urogenital system in mice, apoptosis plays a crucial role in removing a temporal structure called the Common Nephric Duct (CND), a necessary step to connect the ureter to the bladder epithelium. Experimental data suggest that apoptotic cell removal generates pulling forces necessary for tissue rearrangement. Efferocytosis by epithelial

cells was observed during CND elimination. In this process, epithelial cells programmed to die are engulfed and subsequently phagocytosed by neighboring cells. This entire process involves a stationary distribution within the five different stages of phagocytosis and an apoptotic gradient along the CND. In this study, we used mathematical modeling approaches to analyze the spatiotemporal dynamics of this system and quantified not only the dwell time in each stage but also the flux of cells along the CND. We developed a Markov model of cellular engulfment and efferocytosis and coupled it to the transport equation to quantify dwell times and the flux of cells. The model was then solved and analyzed analytically. It revealed that cell death and processing increase along the CND towards the bladder. Model outcomes also matched biological observations and allowed us to quantify the temporal changes in the number of cells in each apoptotic stage. This apoptotic cell clearance machinery described in the model is probably the first example known so far in which its role was found to be absolutely necessary for tissue morphogenesis during normal development. This work thus provides important insights into spatiotemporal dynamics of cellular rearrangement in the CND.

STEPHANIE PORTET, University of Manitoba
Intracellular transport driven by antagonistic motor proteins

Intermediate filaments are long elastic fibers that are transported in cells along microtubules by antagonistic motor proteins. How elastic fibers are efficiently transported by antagonistic motors is not well understood and is difficult to measure with current experimental techniques. Adapting the tug-of-war paradigm for vesicle-like cargos, a mathematical model is developed to describe the motion of an elastic fiber punctually bound to antagonistic motors [1]. Combining dynamical simulations and qualitative analysis, the asymptotic behavior of the model, which defines the mode of transport of fibers, is studied; the effects of initial conditions, reflecting the intracellular context, and model parameters and functionals, describing motors and fiber properties are characterized.

Work in collaboration with J. Dallon (BYU, Provo, Utah, USA), C. Leduc and S. Etienne-Manneville (Institut Pasteur, Paris, France)

[1] Portet, S., Leduc, C., Etienne-Manneville, S., Dallon, J. Deciphering the transport of elastic filaments by antagonistic motor proteins. Phys. Rev. E. 99: 042414 (2019).

JÜRGEN REINGRUBER, Ecole Normale Superieure
Monitoring and predicting the Covid-19 epidemic and its implications for hospitals

The world and France are strongly impacted by the SARS-COV-2 epidemic. Finding appropriate measures that effectively contain the epidemic without putting severe pressure on social and economic life is a major challenge for predictive approaches. We developed an modeling framework to monitor and predict the spread of the epidemic together with its impact on the health care system. The current implementation accounts for interactions between five age-stratified population groups, and predicts disease progression and hospitalization status using eight different categories such as infected, hospitalized, occupancy of intensive care units, deceased, recovered from hospitalization and more. We use a variety of public health care data for France to calibrate the model and to predict the implications for hospitals.

LISANNE RENS, Delft University of Technology
Computational models for feedback between cell shape, cell signaling and extracellular matrix

Cell shape changes and cell migration in mammalian cells are regulated by many signaling proteins. Cells also interact with a meshwork of protein fibers, called the extracellular matrix (ECM), that affects signaling proteins that regulate cell motility, Rac and Rho. The feedback between Rac-Rho-ECM affeects invasiveness of melanoma cancer cells. In our models, we expand on a previous 2-compartment model that describes Rac-Rho mutual inhibition, self-activation, the effect of each protein on the amount of contact with the ECM, and ECM activation of Rho. We study the full spatial dynamics in 1D and in static 2D domains, demonstrating oscillations and static/dynamic waves. These results give insight into how distinct types of cell migration emerge. By simulating the set of PDEs in a fully deformable 2D cell using a Cellular Potts model, we predict how spatially distributed signaling is coupled to cell motility. Predicted cell shapes and behavior resemble experimental observations.

This full 2D model reveals how ECM anisotropy, cell stiffness, and other cell parameters affect cell migration, leading to experimentally testable predictions. Our computational models suggests insights into how the invasiveness of melanoma cells is regulated.

JOHN RINZEL, New York University
A neuronal model for learning to keep a rhythmic beat.

When listening to music, we typically lock onto and move to a beat. Behavioral studies on such synchronization (Repp 2005) abound, yet the neural mechanisms remain poorly understood. Beat perception and generation involves time estimation and plasticity for a neural circuit that can adapt and learn a rhythm. In the case of music, the range of beat frequency includes 1-6 Hz. Some models of beat perception hypothesize that the brain contains an array of self-sustaining entrainable oscillators, which resonate when forced with periodic stimuli, i.e. musical rhythms (Large et al. 2010). In contrast, our approach, in the simplest case, assumes a single beat generator neuron (BG) which can change its intrinsic frequency and phase to match that of an external rhythm, say a metronome. Our model implements an error correction scheme and includes counting of naturally occurring gamma frequency cycles to estimate time intervals. The model quickly learns new rhythms, within a few cycles as found in human behavior. When the stimulus is removed the BG continues to produce the learned rhythm in accordance with a synchronization continuation task.

MARC ROUSSEL, University of Lethbridge
Dynamics-preserving model reduction using bipartite-graph representations of biochemical systems

At a fundamental level, biochemical systems can be represented as sets of elementary reactions. These mechanistic descriptions can in turn be represented as bipartite graphs, with one vertex type representing chemical species, and the other chemical reactions. Specially constructed subsets of the bipartite graph known as fragments have a one-to-one correspondence with terms in the characteristic equation arising in stability analysis, whether for ODEs representing a well-mixed system, or for reaction-diffusion PDEs. Accordingly, there is a connection between the structure of the bipartite graph and stability. Specifically, critical fragments, those corresponding to terms in the characteristic equation with negative coefficients, are necessary to allow for Andronov-Hopf, saddle-node, or Turing bifurcations. Because biochemical networks are typically very large, it is often desirable to simplify the corresponding models. This talk will explore an idea for using the bipartite-graph representation of a biochemical network to reduce a biochemical model while preserving its dynamics, by carrying out graph transformations that preserve critical fragments.

ARTHUR SHERMAN, National Institutes of Health
Clinical Insights from a Diabetes Progression Model

Insulin is the chief hormone that regulates glucose homeostasis, preserving glucose for use by the brain in fasting conditions but sharing glucose with other tissues, such as muscle, after meals. This orderly cycle of fuel usage is disrupted in obesity, which renders tissues resistant to the effects of insulin and leads to chronic hyperglycemia, a condition known as type 2 diabetes. A salient characteristic of diabetes is its relentless progressive nature, which is almost impossible to reverse once the disease is established and difficult to reverse in the pre-diabetes stage when glucose is elevated but below the diagnostic threshold. A puzzling feature is that people with pre-diabetes or in the early stages of T2D have abnormally high plasma insulin concentrations, and insulin rises before glucose does. We show that these characteristics of diabetes are explained by a mathematical model in which the onset of T2D is represented by the crossing of a threshold. From a clinical point of view, the near irreversibility of diabetes once the threshold is crossed highlights the need for identifying people at risk early. We will present examples of how the model has provided insights for improving diabetes screening and treatment.

JOHANNES TEXTOR, Radboud University Medical Center
A tipping point in cancer-immune dynamics leads to divergent immunotherapy responses and hampers biomarker discovery

Predicting the effects of immunotherapy treatments on cancer patients remains a challenge. Efforts to overcome these challenges focus mainly on the discovery of new biomarkers. Owing to the complexity of cancers and their tumor microenvironment, only a limited number of candidate biomarkers eventually enters clinical practice, despite advances in cellular and molecular approaches. We used an ordinary differential equation model to simulate the fundamental mechanisms that dictate tumor-immune dynamics and investigated its implications on responses to immune checkpoint inhibition (ICI) and patient survival. By simulation of biomarker discovery trials, we extracted fundamental principles underlying the success rates of biomarker discovery programs. Our model predicts a tipping point – a sharp state transition between immune control and immune evasion – that induces a strongly non-linear relationship between patient survival and both immunological and tumor-related parameters. In patients close to the tipping point, ICI therapy may lead to long-lasting survival benefits, whereas patients far from the tipping point may fail to benefit from these potent treatments. Our findings imply that (1) the apparent conundrum that ICI induces substantial benefits in some patients yet completely fails in others could be, to a large extent, explained by the presence of a tipping point; (2) predictive biomarkers for immunotherapy should ideally combine both immunological and tumor-related markers, as the distance of a patient's status from the tipping point cannot be reliably determined from solely one of these. The notion of a tipping point in cancer-immune dynamics could help to optimize strategies in biomarker discovery.

JUSTIN TZOU, Macquarie University

Localized patterns and narrow escape problems in more general geometries

The main focus of this talk will be on a method for analyzing localized spot patterns on general surfaces. Past analytic frameworks have been restricted to analyses on flat and spherical surfaces; we discuss a new addition to the analytic framework that allows us to obtain results on more general (and perhaps more realistic) surfaces. We also discuss briefly recent results obtained for the narrow escape problem inside an arbitrary bounded three-dimensional domain with a small target on the boundary. Methods used for these problems may provide a way forward for understanding how cell geometry impacts processes such as cell polarization.

ROMAIN VELTZ, INRIA

Mean field study of stochastic spiking neural networks

In this work, we study the dynamics of a network of stochastic spiking neurons akin to the "generalized linear model". This network is a generalization of the one introduced in [DeMasi et al. 2014]. It allows to capture most intrinsic neuronal spiking, like bursting for example, while being quite easy to investigate compared to the Hodgkin-Huxley model. Two sets of results will be provided. On the theory side, the mean field will be derived and the stability of its invariant measure(s) will be investigated. On the numerical side, simulations of the PDE and of the finite network (on GPU) will be compared close to the bifurcations of the system. More precisely, I will present some recent results concerning the quasi-synchronisation of the neurons as function of the different parameters of the network (adaptation variable, synaptic strength...).