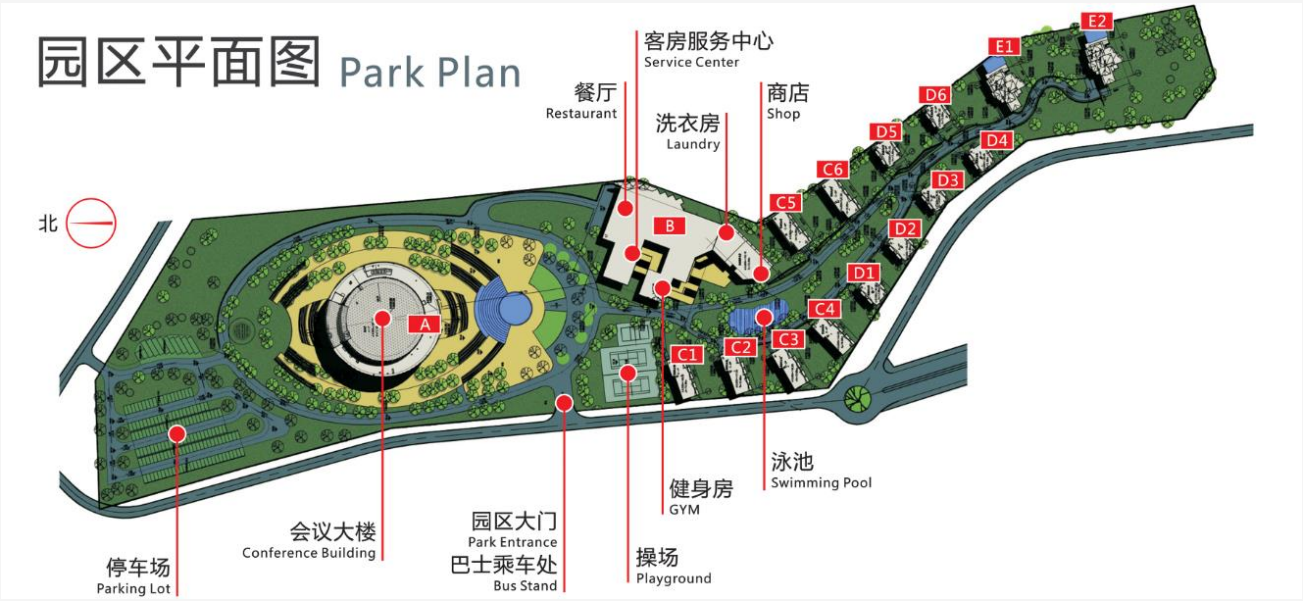
Welcome to TSIMF

The facilities of TSIMF are built on a 23-acre land surrounded by pristine environment at Phoenix Hill of Phoenix Township. The total square footage of all the facilities is over 29,000 square meter that includes state-of-the-art conference facilities (over 10,000 square meter) to hold many international workshops simultaneously, two libraries, a guest house (over 10,000 square meter) and the associated catering facilities, a large swimming pool, gym and sports court and other recreational facilities.

Mathematical Sciences Center (MSC) of Tsinghua University, assisted by TSIMF's International Advisory Committee and Scientific Committee, will take charge of the academic and administrative operation of TSIMF. The mission of TSIMF is to become a base for scientific innovations, and for nurturing of innovative human resource; through the interaction between leading mathematicians and core research groups in pure mathematics, applied mathematics, statistics, theoretical physics, applied physics, theoretical biology and other relating disciplines, TSIMF will provide a platform for exploring new directions, developing new methods, nurturing mathematical talents, and working to raise the level of mathematical research in China.

About Facilities



Registration

Conference booklets, room keys and name badges for all participants will be distributed at the Registry. Please take good care of your name badge. It is also your meal card and entrance ticket for all events.

Guest Room

Conference Center can receive about 378 people having both single and double rooms, and 42 family rooms.

All the rooms are equipped with: free Wi-Fi, TV, air conditioning and other utilities.

Family rooms are also equipped with kitchen and refrigerator.

Library

Opening Hours: 08:00am-22:00pm

TSIMF library is available during the conference and can be accessed by using your room card. There is no need to sign out books but we ask that you kindly return any borrowed books to the book cart in library before your departure.

Restaurant

All the meals are provided in the Chinese Restaurant (Building B1) according to the time schedule.

Breakfast	07:30-08:30
Lunch	12:00-13:30
Dinner	17:30-19:00

Laundry

Opening Hours: 24 hours

The self-service laundry room is located in the Building 1 (B1), next to the shop.

Convenience Store

The convenience store is located in Building 1 (B1), next to the laundry. The store sells snacks, beer, soft drinks, notepads, bathing suits and various etc.

Gym

The gym is located in the Building 1 (B1), opposite to the reception hall. The gym provides various fitness equipment, as well as pool tables, tennis tables and etc.

Playground

Playground is located on the east of the central gate. There you can play basketball, tennis and badminton. Meanwhile, you can borrow table tennis, basketball, tennis balls and badminton at the reception desk.

Swimming Pool

Please note that there are no lifeguards. We will not be responsible for any accidents or injuries. In case of any injury or any other emergency, please call the reception hall at +86-898-38882828.

Shuttle Service:

We have shuttle bus to take participants to the airport for your departure service. Please feel free to contact Ms. Li Ye (叶莉) if you have any questions about transportation arrangement. Her cell phone number is (0086)139-7679-8300. We would provide transportation at the Haipo Square （海坡广场） of Howard Johnson for the participants who will stay outside TSIMF.

Contact Information of Administration Staffs

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Schedule for Workshop on Mathematical Modeling & Computation in Medicine/Biology, December 12-16, 2016					
Time	**Mon (Dec. 12)**	**Tue (Dec. 13)**	**Wed (Dec. 14)**	**Thu (Dec. 15)**	**Fri (Dec. 16)**
7:30-8:30	*Breakfast*				
8:30-8:50	*Registration, Welcome*				
8:50-9:00	*Chair: Siv Sivaloganathan*	*Chair: Huaxiong Huang*	*Chair: Yau Shu wong*	*Chair: Liqun Cao*	*Chair: Nathan Gold*
9:00-9:40	Philip Maini	Shu Takagi	Tom Chou	Jean Clairambault	Free Discussion
9:45-10:25	Jame Drake	Guanghong Ding	Jonathan Wylie	Buyang Li	
10:25-10:55	*Tea break&Group photo*	*Tea break*			
	Chair: Philip Maini	*Chair: Shu Takagi*	*Chair: Tom Chou*	*Chair: Jean Clairambault*	
11:00-11:40	Xinzhi Liu	Maria R D' Orsogna	Graeme Fairweather	Jane Heffernan & Hanna Jankowski	Free Discussion and End of Meeting
11:45-12:25	Tzyy-Leng Horng	Xiaobo Gong	Nathan Gold	Hautieng Wu	
12:25-14:00	*Lunch*				
	Chair: Jonathan Wylie	*Chair: Jane Heffernan*	*Chair: Hanna Jankowski*		
14:00-14:40	Yanni Xiao	Xinghua Shi	Yan Yan	Free Discussion 13:30-17:00	Departure
14:45-15:25	Gibin Powathil	Naveen Vaidya	Dondong He		
15:25-15:55	*Tea break*				
	Chair: Yanni Xiao	*Chair: N. Vaidya*	*Chair: Xinzhi Liu*		
16:00-16:40	Yunqiao Liu	Fuyou Liang	Xiangsheng Wang		
17:30-19:00	*Dinner*	*Banquet 18:00-20:00*	*Dinner*		
We will arrange taking group photos on Monday, December 12, before the morning coffee break.					

Titles and Abstracts

(1) Epidemic models with switching parameters and pulse control

Xinzhi Liu, Department of Applied Mathematics, University of Waterloo, Canada

Mathematical models for infectious disease are crucial in gaining knowledge of the underlying mechanism that drives an epidemic. They are often used for implementing and evaluating control schemes in order to eradicate a disease. This talk discusses some epidemic models with switching parameters and pulse control. Hybrid control schemes are examined, and, in doing so, we hope to gain insight into the effects of a time-varying contact rate on critical control levels required for eradication. By introducing the notions of persistent limit set and persistent mode, we extend the classical LaSalle's invariance principle to epidemic models with switching parameters and pulse control. A weak invariance principle is established for such systems, under a weak dwell-time condition on the impulsive and switching signals. This weak invariance principle is then applied to establish sufficient conditions for the global asymptotic stability of the disease-free solution, which may give some insight into the effects of a time-varying contact rate on critical control levels required for eradication of a disease.

(2) Dynamics of neuroendocrine stress response: bistability, timing, and control of hypocortisolism in PTSD

Maria-Rita D'Orsogna, California State University at Northridge, Los Angeles CA (USA)

The hypothalamic-pituitary-adrenal (HPA) axis is a neuroendocrine system that regulates numerous physiological processes. Disruptions in its activity are correlated with stress-related diseases such as post-traumatic stress disorder (PTSD) and major depressive disorder. We characterize \normal" and \diseased" states of the HPA axis as basins of attraction of a dynamical system describing the inhibition of peptide hormones, corticotropin-releasing hormone (CRH) and adrenocorticotropic hormone (ACTH), by circulating glucocorticoids such as cortisol (CORT). Our model includes ultradian oscillations, CRH self-upregulation of CRH release, and distinguishes two components of negative feedback by cortisol on circulating CRH levels: a slow direct suppression of CRH synthesis and a fast indirect e_ect on CRH release. The slow regulation mechanism mediates external stress-driven transitions between the stable states in novel, intensity, duration, and timing-dependent ways. We _nd that the timing of traumatic events may be an important factor in determining if and how the hallmarks of depressive disorders will manifest. Our model also suggests a mechanism whereby exposure therapy of stress disorders may act to normalize downstream dysregulation of the HPA axis.

(3) The Mechanics of Target Drug Delivery

Xinghua Shi, National Center for Nanoscience and Technology, China

The rapid development of nanotechnology enables the successful application of target drug delivery, which provides new hope for the clinical examination and treatment. In the whole process of drug delivery, we found couple of mechanics problems existed, including the transportation of nanocarriers, the molecular level target and the cellular uptake of nanoparticles. In recent years we focused on the investigation of diffusion of drug delivery systems in mucus of gastrointestinal (GI) tract. Mucus is a viscoelastic gel layer that typically protects exposed surfaces of the GI tract, lung airways, and other mucosal tissues. Particles targeted to these tissues can be efficiently trapped and removed by mucus, thereby limiting the effectiveness of such drug delivery systems. In this study, we experimentally and theoretically demonstrated that cylindrical nanoparticles (NPs), such as mesoporous silica nanorods and calcium phosphate nanorods, have superior transport and trafficking capability in mucus compared with spheres of the same chemistry. The higher diffusivity of nanorods leads to deeper mucus penetration and a longer retention time in the GI tract than that of their spherical counterparts. Molecular simulations and stimulated emission of depletion (STED) microscopy revealed that this anomalous phenomenon can be attributed to the rotational dynamics of the NPs facilitated by the mucin fibers and the shear flow. These findings shed new light on the shape design of NP-based drug delivery systems targeted to mucosal and tumor sites that possess a fibrous structure/porous medium

(4) De-shape short time Fourier transform and several medical applications

Hau-Tieng Wu, University of Toronto, Canada

An innovative and adaptive acquisition of correct features from massive datasets with solid mathematical support is the core of modern data analysis. Such features are often nonlinear in nature. One particular interest in medicine is extracting the hidden dynamics from the observed time series. In this talk, I will discuss few progresses in the nonlinear time frequency analysis based on the cepstrum idea, particular the wave shape function analysis via de-shape short time Fourier transform, and their theoretical properties. Particularly, how to extract features from a time series composed of multiple oscillatory signals with non-sinusoidal oscillations, time varying amplitude, and time varying frequency, while contaminated with heteroscedastic noise?

The developed methods are directly applied to, for example, extract fetal ECG signal from the single lead maternal abdominal ECG signal, and extract instantaneous heart rate and instantaneous respiratory rate from the PPG signal during exercise. If time permits, its relationship with differential geometry and hence manifold learning will be discussed.

(5) Tumour growth and drug resistance: an evolutionary view with perspectives in therapeutics

Jean Clairambault, INRIA and Jacques-Louis Lions Laboratory, UPMC, Paris, France,
https://who.rocq.inria.fr/Jean.Clairambault/

I will present an evolutionary viewpoint on cancer, seen as the 2 time scales of (large-time,

billions of years) evolution in the genomes and of (short-time, a human life) evolution in the epigenetic landscape of a constituted genome. These views, based on works by Lineweaver, Davies and Vincent (cancer as anatomically located backward evolution in multicellular organisms, aka atavistic theory of cancer) and on others by Sui Huang and collaborators (revisited Waddington epigenetic landscape), respectively, may serve as guidelines to propose a global conception of cancer, including towards possible innovating therapeutic strategies.

Drug-induced drug resistance, the biological and medical question we are tackling from a theoretical point of view, may be due to biological mechanisms of different natures, mere local regulation, epigenetic modifications (reversible, nevertheless heritable) or genetic mutations (irreversible), according to the extent to which the genome of the cells in the population is affected. In this respect, the modelling framework of adaptive dynamics we will present is more likely to correspond biologically to epigenetic modifications, although eventual induction of emergent resistant cell clones due to mutations under drug pressure is never to be excluded. From the biologist's point of view, we study phenotypically heterogeneous, but in principle genetically homogeneous, cancer cell populations under stress by drugs.

The built-in targets for theoretical therapeutic control present in the phenotype-structured PDE models we advocate are not supposed to represent well-defined molecular effects of the drugs in use, but rather functional effects, i.e., related to cell death (cytotoxic drugs), or to proliferation in the sense of slowing down the cell division cycle without killing cells (cytostatic drugs). We propose that cell life-threatening drugs (cytotoxics) induce by far more resistance in the highly plastic cancer cell populations than drugs that only limit their growth (cytostatics), and that a rational combination of the two classes of drugs may be optimised to propose therapeutic control strategies to avoid the emergence of drug resistance in tumours.

Furthermore, we address this question in the context of two populations, healthy and cancer, or stromal and cancer, both endowed with phenotypes evolving with drug pressure, and either competing for space and nutrients, or on the contrary cooperating by exchanging bidirectional stimulating messages, in either case in a non-local Lotka-Volterra-like way. Our main mathematical challenge is to take into account these between-population interactions to analyse their asymptotic behaviours so as to design theoretically optimal therapeutic controls.

(6) Multi-scale modeling of the cardiovascular system with its applications to generic and patient-specific hemodynamic problems

Fuyou Liang
SJTU-CU International Cooperative Research Center, School of Naval Architecture, Ocean & Civil Engineering, Shanghai Jiao Tong University, 800 Dongchuan Road, Shanghai, China
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Hemodynamic factors have been extensively demonstrated to participate in the onset and progression of cardiovascular diseases, which has accordingly motivated numerous studies aimed to quantify hemodynamic characteristics in the context of various cardiovascular diseases[1]. Due to the inherent limitations of in vivo measurement techniques, computational modeling has been a major approach to detailed hemodynamic study. The human cardiovascular system is

highly complex and heterogeneous in terms of anatomic structure and hemodynamic behaviors. These features pose a big challenge for hemodynamic modeling, its validation and associated computational cost. In recent years, multi-scale modeling has been increasingly been adopted to provide detailed hemodynamic information in local regions of interest while accounting for systemic hemodynamics at a reasonable computational cost[2]. On the other hand, the rationality of applying general hemodynamic models to real clinical problems has been frequently questioned due to the presence of significant inter-patient differences in cardiovascular properties and pathological conditions[3]. This problem has elicited the concept of patient-specific modeling, and pronounced progresses have been achieved in this direction in the past decade. In this lecture, we will present several modeling methods that we have developed to address various hemodynamic problems and introduce some approaches to clinical data-based model personalization.

(7) Towards understanding influenza evolution

J. Heffernan & H. Jankowski (Department of Math & Stats, York U, Canada)

The greatest issue with developing a vaccine to combat influenza virus is the rapid evolution of the flu virus. We seek a better understanding of this evolution over influenza seasons. In this talk we will discuss a new method that we have developed for clustering influenza virus sequences. Application of this method to Hemagglutinin and Neurominidase glycoprotein H3N2 strain data will be shown. Using the method, we provide an investigation of past vaccines and the dominant cluster in each influenza season. An extension to an epidemiological model of influenza transmission and evolution will also be discussed.

(8) Alternating Direction Implicit Methods at Sixty – and Beyond

Graeme Fairweather, Mathematical Reviews, AMS, USA

It is now sixty years since the publication of the seminal paper by D. W. Peaceman and H. H. Rachford in which Alternating Direction Implicit (ADI) methods were first introduced, in the context of finite difference methods, for the approximate solution of parabolic and elliptic problems in two space variables. The attraction of the ADI approach is that it replaces the solution of a multidimensional problem by sequences of independent one-dimensional problems in the coordinate directions. ADI methods in conjunction with various types of spatial discretizations continue to be studied extensively today for time-stepping in methods for the numerical solution of various time-dependent problems. In this talk, we present a brief overview of the history of ADI methods, followed by a discussion of methods developed recently for solving nonlinear reaction-diffusion systems in two space variables. Emphasis is placed on the use of orthogonal spline collocation (OSC) for the spatial discretization which has several advantages over both finite difference and finite element Galerkin (FEG) methods. In particular, like FEG methods, OSC provides global approximations to the solution and its spatial derivatives on each time level. However, OSC requires no evaluation or approximation of integrals.

Moreover, it possesses certain superconvergence properties, and, in an ADI context, is applicable to more general problems than FEG methods.

(9) Mathematical models to evaluate the effects of drugs of abuse on within-host HIV dynamics

By Naveen Vaidya, U Missouri, USA

Drugs of abuse in HIV infected individuals have been associated with higher virus replication and accelerated disease progression as well as severe neuropathogenesis. In this talk, I will present mathematical models that incorporate the effects of drugs of abuse on HIV dynamics within a host. The models agree well with the experimental data from simian immunodeficiency virus infections in morphine-addicted macaques. Using our models, we quantify how morphine alters susceptibility of target cells and viral-specific antibody responses, and consequently, how these alterations affect the key components of virus dynamics. Furthermore, we incorporate pharmacodynamics properties of morphine into the models and analyze how periodic morphine intake affects the global stability properties of host-virus dynamical system.

(10) Modelling impact of interventions on control of vector-borne disease

Yanni Xiao, School of Mathematics & Statistics, Xi'an Jiaotong University

Cases of co-infection by dengue and Zika have been reported, the implication of this co-infection for an integrated intervention program for controlling both dengue and Zika must be addressed urgently. Major challenges remain when attempting to quantify and evaluate the impacts of the integrated program of control strategies on dengue infection or Zika infection. In this talk, we initially present an impulsive mathematical model to closely mimic the integrated program of impulsive vector control (every Friday afternoon since the initiation of the program) and continuous patient treatment and isolation implemented in the Guangdong Province of China during its 2014 dengue outbreak. We fitted the data of accumulated infections and used the parameterized model to carry out a retrospective analysis to estimate the basic reproduction number 1.7425 (95% CI 1.4443--2.0408), the control reproduction number 0.1709. This suggests that integrated intervention is highly effective in controlling the dengue outbreak. We also simulated outbreak outcomes under different variations of the implemented interventions. The findings indicate that quick and persistent impulsive implementation of vector control result in an effective reduction in the control reproduction number and hence lead to significant decline of new infections. Secondly, we investigate the implication of vaccination against dengue for Zika outbreak. Our analysis determines specific conditions under which vaccination against dengue can significantly increase the Zika outbreak peak, and speed up the Zika outbreak peak timing. Our results call for further study about the co-infection to direct an integrated control to balance the benefits for dengue control and the damages of Zika outbreak.

(11) Multiscale Modelling of Cancer Progression and Treatment Responses

Gibin Powathil, Swansea University, UK

Each individual cancer cell within a cancer cell mass is unique, with its own internal cellular pathways and biochemical interactions. These interactions contribute to the functional changes at the cellular and tissue scale, creating a heterogeneous cancer cell population. Multiscale mathematical models incorporating such complex interactions can help in studying cancer progression and serve as an *in silico* test base for comparing and optimising various multi-modality anticancer treatment protocols such as chemotherapy and radiation therapy.
In this talk, I will present a validated hybrid individual cell-based mathematical and computational model, incorporating single-cell based intracellular dynamics, the cell microenvironment and cell-cell interactions to study the growth and progression of cancer cell mass. The model will then be used to study the effects of radiotherapy and chemotherapy. In particular, we will model the direct and indirect responses (bystander effects) of radiation therapy and further, analyse the role of cell-cycle-based tumour heterogeneity in inducing chemotherapeutic drug resistance.

(12) Modelling Collective Cell Motion in Biology

Philip Maini, Oxford University, UK

Collective cell motion is very common in biology. Here, I will review some of the work we have been doing in two application areas:

(i) cranial neural crest cell migration,
(ii) cell sheet movement.

The mathematical models will be of discrete cell type with signalling cues modelled by partial differential equations and the results will be compared with experimental observations.

(13) Numerical simulation of the dynamic Ginzburg-Landau superconductivity equations.

Buyang Li, Hong-Kong Baptist Poly

The time-dependent Ginzburg-Landau equations (TDGL) has been widely used for numerical simulations of superconductivity phenomenon. However, the solution of the equations often exhibit singularity and unboundedness in a nonsmooth domain. In this case, we show that the standard finite element solutions of the equations are instable and will converge to incorrect solutions. To solve the equations correctly by numerical methods, we reformulate the TDGL into a new system of equations by using the Hodge decomposition. The new system is theoretically equivalent to the original TDGL, but can be solved correctly by standard finite element methods. Numerical examples are provided to support our analysis and show the efficiency of the proposed method.

(14) Optimizing outcomes for pediatric craniofacial reconstruction using mathematical modelling.

James Drake, Hospital for Sick Children, Toronto

Congenital craniofacial abnormalities are common, and frequently result from premature closure of one or more of the skull sutures. The resulting deformities are complex and involve large segments of the skull vault and base. Correcting these deformities typicall involves removing large segments of the skull and eye sockets, and reshaping them subjectively. We have developed a scalable normalized head shape for children < 1 year of age, to serve as a model for craniofacial reconstruction. We have designed titanium templates to assist with normalizing forhead shape, as well as virtual templates to evaluate final head shape outcome. With our colleagues at the Univeristy of Waterloo, we have optimized the number and position of bone cuts in the forehead for the best shape with least cost in terms of weakening the bone and fixating it. Our next phase is to optimize the cuts for the 3D shape of the front half of the skull. Mathematical modelling of skull shape and reconstruction has the potential to significantly improve clinical outcomes with decreased morbidity and costs.

(15) Multiscale Modeling for an Initial Stage of Thrombosis with Massively Parallel Computing.

Shu Takagi, Departments of Mech Eng and Dept Bioeng, University of Tokyo

A numerical method for fluid-structure interaction problems was developed for massively parallel computing and the method was applied to solve the blood flow containing a large number of red blood cells and platelets. As an initial stage of thrombosis, platelet adhesion process to the vessel wall was analyzed by multiscale modeling of coupling continuum scale finite difference method with the molecular scale Monte Carlo method. The adhesion of platelets to the injured vessel wall is triggered by the protein-protein interaction (GP1ba on the platelet – vWF on the wall.). This protein-protein binding force is evaluated by Monte Carlo simulation, solving the stochastic process of each biding. A platelet also feels the fluid mechanical force from blood flow and this force is affected by the presence of red blood cells, which causes the drastic change to the adhesion process. This phenomenon is discussed with the simulated results.

(16) Graph-theoretical methods for de novo peptide sequencing via tandem mass spectrometry

Yan Yan, Mathematics Department, University of Sakatchewan

Tandem mass spectrometry (MS/MS) has emerged as a major technology for peptide sequencing. Typically, there are two kinds of methods for the peptide sequencing: database searching, and de novo sequencing. De novo sequencing has drawn increasing attention because of its independence from existing protein database and potential for identifying proteins not including in current database. With the improvements in the accuracy of MS/MS and development of alternative fragmentation modes of MS/MS, many new de novo sequencing methods have been formulated. This talk will introduce basic background of this research topic, several newly

developed computational methods based on graph model using various MS/MS spectra, and finally, some potential future work topics.

(17) Action Potential Propagation along a Myelinated Axon

Tzyy-Leng Horng (洪子倫), Feng Chia University, Taiwan

Myelin sheath can offer insulation of a neuron's axon that avoids the electric interference from near-by neurons. Besides, it makes the action potential (AP) travel faster along a myelinated axon than an unmyelinated one. Experiments observed AP transportation speed along a myelinated axon is proportional to the radius of axon with fixed aspect ratio, while the speed is only proportional to the square root of radius of axon along an unmyelinated one. To study why so mathematically, there are two governing equations involved for the model of AP transportation along a myelinated axon. One is passive cable equation for myelin sheath part, where no ion channel is distributed. The other is reaction-diffusion equation for nodes of Ranvier, where ion channels are distributed. Usually the length ratio of myelin sheath to Ranvier node is around 1000 observed biologically. This means conduction of AP is jumping and firing along a myelinated axon, which is called saltatory conduction. Through our numerical experiments, myelin sheath too long or too short, by fixing the radius of axon, would cause conduction failure. There exists a region of aspect ratio, which is the ratio between length and diameter of myelin sheath, for successful conduction. We also found AP transportation speed is indeed proportional to axon radius with fixed aspect ratio as observed in experiments. By adjusting a few parameters, our model and computation can match experiments on the measurements of axon AP transportation speed with satisfactory agreement for several species. This is joint work with Min-Jhe Lu (呂旻哲)[2] , Tai-Chia Lin (林太家)[2].

(18) Asymptotic solutions for time-dependent Poisson-Nernst-Planck systems

Jonathan Wylie, City U, Hong Kong

Biological cells are subjected to fluxes of ions through their cell walls as a result of active pumps and passive ion channels. A detailed understanding how the ion concentrations dynamically respond to such ion fluxes ions is clearly a fundamental question in biology. In order to understand the key mechanisms underlying this process, we consider the time-dependent response of a Poisson-Nernst-Planck system with an arbitrary number of ion species with arbitrary diffusion coefficients when arbitrary fluxes are injected from the boundaries.We assume that the Debye length is small relative to the domain size and that the initial concentrations are electro-neutral away from the Debye layers. We derive an asymptotic formula for the dynamic solution by matching the outer solution and the Debye layer solutions and show that additional intermediate diffusion layers are required for consistent matching. These additional layers are asymptotically wider than the Debye layer, but small compared with the size of the domain. Such boundary layers do not occur in steady-state problems that have been the focus of most previous studies. In the case of two ionic species, we show that the problem can be reduced to the solution of a single ordinary differential equation. Remarkably, in

the symmetric case, we find an explicit solution for the full time-dependent problem. This is joint work with Xiang-Sheng Wang and Huaxiong Huang.

(19) Mathematical Modelling of Fetal Cardiovascular and Metabolic Response to Acidemia During Labour

Nathan Gold, York University, Canada

Acidemia (blood pH < 7.00) resulting from umbilical cord occlusions caused by uterine contractions poses one of the most significant risks to fetal well-being during labour. Acidosis is associated with long lasting neurological deficits such as cerebral palsy, and even death in some cases. Presently, there exists no accurate way of detecting and diagnosing acidemia with existing clinical monitoring technology, due to a lack of knowledge about which features of available data best represent acidosis. In recent work, we develop a dynamical systems model of fetal cardiovascular and metabolic response to umbilical cord occlusions in fetal sheep experiments simulating human labour. By modelling the effects of occlusions on the autonomic nervous system and fetal metabolism, our model is able to match salient features of fetal heart rate and metabolite recording from experiments. We also present sensitivity analysis of model parameters to identify the most important features related to acidosis, and use the model to investigate different features of the fetal heart rate that may be used for clinical monitoring. Finally, we present some model simplifications, and their effect on the model accuracy.

(20) Computation of dynamic thresholds for bird migration models

Xiang-Sheng Wang, University of Louisiana at Lafayette, USA

In this talk, I will introduce some new ideas to the computation of dynamic thresholds for bird migration models. First, I will study a periodic system of delay differential equations which was commonly used in modeling the seasonal activities of migratory birds. It has been shown in previous studies that this ecological system exhibits threshold dynamics: either all solutions converge to the trivial solution, or the system has a positive and globally attractive periodic solution. Computation of the dynamic threshold, however, was left as a challenging problem. I will address this issue by developing an innovative dimension reduction method. As one of the main results, I will derive a formula which expresses the dynamic threshold in terms of the model parameters explicitly. In the second part of the talk, I will study the spread of avian influenza among migratory birds. An epidemiological model coupling the bird migration with the disease transmission will be investigated. To characterize the nonlinear dynamics of the full system, more thresholds will be computed using the dimension reduction technique.

(21) Interaction of two encapsulated bubbles in an ultrasound field

Yunqiao Liu[1], Kazuyasu Sugiyama[2], Shu Takagi[3]

[1]Department of Engineering Mechanics, Shanghai Jiao Tong University, Shanghai, China
[2]Department of Mechanical Science and Bioengineering, Graduate School of Engineering Science, Osaka University, Osaka, Japan
[3]Department of Mechanical Engineering, School of Engineering, The University of Tokyo, Tokyo, Japan

Encapsulated bubbles are used widely in the application of ultrasound contrast-enhanced agents and drug-carrier capsules. Interaction with surrounding bubbles affects their behavior, leading to phenomena such as erratic drift, bubble grapes, acoustic streaming, and multibubble sonoluminescence. The study on the interaction of two bubbles may shed light on the dynamics of bubble groups, which is the motivation of this work.

We establish a theoretical model for the radial oscillations, translational motions and deformations of two interacting encapsulated bubbles. The flow field outside the bubbles is approximated by a potential flow with a viscous correction. The in-plane stresses and bending moments of the viscoelastic membranes are balanced with the hydrodynamic tractions at the interfaces of the bubbles. Since the material points move along the membranes accompanied with their movements in radial direction when the encapsulated bubbles undergo deformations, stress balance in both the tangential and normal directions and the no-velocity-jump condition at the bubble surface are applied. The derived expression for the viscous drag includes the quasisteady drag force and the history force, which is validated by the solution of the unsteady Stokes equation. With a proper choice of the interface parameters, the present model is suitable for bubbles with free-slip, viscoelastic or no-slip interfaces. The viscous correction and the potential part of our solution are validated respectively by comparing with previous experimental observations. The encapsulated bubble shows more stability in resisting shape oscillation. The attractive or repulsive movements of the two bubbles subjected to a driving frequency are consistent with the prediction by Bjerknes' theory. For gas bubbles, the drag is mainly from the quasisteady component of the flow. For encapsulated bubbles, the no-velocity-jump condition enhances viscous dissipation and thus contributes significantly to the history force in the viscous drag, generating more damping in the translational motion.

(22) The Activation of the Degranulation of Mast Cells Induced by Mechanical Signal

Ding Guanghong, Fudan University

Rotation or lift-thrusting manipulation of the acupuncture needle employed in the area under the local skin of the acupoint can deform and twist collagen fibers and other connective tissues which form an area with high stress that causes the activation and degranulation of mast cells. We applied the patch clamp to the mast cells in vitro under different osmotic stresses and observed the open-state of ion channels on the mast cell membrane. The results show that the TRPV-2 on cell membrane seemed to be the main mechanism of the activation of mast cells. The application of molecular dynamic model and numerical simulation helps to better understand the open-state of ion channels on cell membrane during the deformation caused by stress. We demonstrated that ion channels on the membrane can open in the stress leading by the

acupuncture. We found that the increase of the intracellular $[Ca^{2+}]^i$ of the mast cell under the stress, results in the activation of mast cells from the experiment of parallel plate flow chamber. These results prove that the effects of the stress in the local area plays an important role in the acupoint activation of the acupuncture effect.(This research was supported by the National Science Foundation of China: No.81574053, No.81303027, No. 81590953).

(23) Lineage tracking in hematopoiesis: the role of stem cell self-renewal and progenitor cell aging in clonal fluctuations, extinction, and resurrection.

Tom Chou, UCLA, USA

In recent experiments, virally tagged hematopoietic stem cells (HSCs) were autologously transplanted into rhesus macaques and peripheral blood cells were sampled over fourteen years. Peripheral blood samples were sequenced and the abundances of cells with different tags were quantified. Analysis of these clone sizes using a rescaled neutral growth model indicated rapid equilibration of clone size distributions after transplantation. Besides a heterogeneous clone size distribution, the data revealed that individual clones experienced temporal fluctuations that included occasional extinctions and resurrections. Through mathematical modeling and statistical analysis of the data, we find that random HSC self-renewal events in the bone marrow is consistent with the observed clonal size heterogeneity in the sampled peripheral blood. The dynamic variability in the sizes of individual clones, including the occasional extinctions and resurrections of certain clones, is naturally explained by a proliferation model that incorporates clonal aging by imposing a maximum number of divisions on progenitor cells. Our analysis quantifies the multi-stage stochastic dynamics of HSCs, progenitor cells, and peripheral blood, and shows that they can arise from an initial HSC self-renewal stage followed by generation-limited progenitor cell bursting. Within this mechanistic picture, we use the data to infer estimates for the total HSC differentiation rate and a consistent maximum number of progenitor cell divisions.

(24) Stretching of a highly viscous thread with temperature-dependent viscosity and surface tension

Dongdong He, Tongji University, China

In this talk, I will show our recent results for the extension of the highly viscous threads arising from the glass and polymer industrial processing. We consider the evolution of a long and thin vertically-aligned axisymmetric viscous thread, which is attached to a solid wall at its upper end, experiences gravity and is pulled at its lower end by a fixed force. The thread experiences either heating or cooling by its environment. Both the viscosity and surface tension are assumed to be functions of temperature. A set of one-dimensional model is derived through the formal slender body asymptotic analysis. When inertia is completely neglected and the temperature of the environment is spatially uniform, we obtain analytic solutions for an arbitrary initial shape and temperature profile. In addition, we determine the criteria for whether the cross-section of a given fluid element will ever become zero and hence determine the minimum stretching force

that is required for pinching. For non-zero Reynolds numbers, we show that the dynamics is subtly influenced by inertia and the pinching location is selected by a competition between three distinct mechanisms. In particular, for a thread with initially uniform radius and a spatially uniform environment but with a non-uniform initial temperature profile, pinching can occur either at the hottest point, at the points near large thermal gradients or at the pulled end, depending on the Reynolds number.

(25) A Numerical Method for the Oxygen Transfer Efficiency in Microcirculatory System at Cellular Scale

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In biomedical applications, understanding the effect of mechanical properties of the erythrocytes on oxygen delivery is important for identifying the biophysical origins of several diseases related to metabolic activities at the cellular level. In order to improve drug delivery efficiency, we also need to understand the effects of the physical and geometric properties of the liposome on the mass transfer rate. Our main objective in this paper is to extend the immersed boundary method for fluid flow problems with mass transfer across permeable moving interfaces.

In the present work, we present an immersed boundary method for mass transfer across permeable deformable moving interfaces interacting with the surrounding fluids based on Huang et al's recent work[1]. One of the key features of our method is the introduction of the mass flux as an independent variable, governed by a non-standard vector transport equation. The flux equation, coupled with the mass transport and the fluid flow equations, allows for a natural implementation of an immersed boundary algorithm when the flux across the interfaces is proportional to the jump in concentration [2]. As an example, the oxygen transfer from red blood cells in a capillary vessel is used to illustrate the applicability of the proposed method. We show that our method is capable of handling multi-physics problems involving fluid-structure interaction with multiple deformable moving interfaces and (interfacial) mass transfer simultaneously.

(This is joint work with Zhaoxin Gong, Shanghai Jiao Tong University and Huaxiong Huang, Fields Institute & York University, Canada)