

***The 3<sup>rd</sup> China-Japan Colloquium of Mathematical Biology***

**October 18<sup>th</sup> –21<sup>st</sup>, 2010, Beijing, China**

**Programme and Abstract Book**

**Organized and hosted by**



**Institute of Botany, Chinese Academy of Sciences (IB-CAS)**

**The Chinese Society for Mathematical Biology (CSMB)**

**In conjunction with**



**The Japanese Society for Mathematical Biology (JSMB)**

**Under the auspices of**



**National Natural Science Foundation of China (NSFC)**



**Japan Society for the Promotion of Science (JSPS)**



**State Key Laboratory of Vegetation and Environmental Change**

## Table of contents

<b>General information</b> .....	<b>1</b>
<b>Programme overview</b> .....	<b>3</b>
<b>Detailed Programme</b> .....	<b>4</b>
<b>Abstracts</b> .....	<b>10</b>

## Scientific committee

### Co-Chairs

Lansun Chen	Chinese Academy of Sciences
Yasuhiro Takeuchi	Shizuoka University

### Members

Jingan Cui	Beijing University of Civil Engineering & Architecture
Zhen Jin	North University of China
Zhenqing Li	Chinese Academy of Sciences
Zhengyi Lu	Shichuan Normal University
Yi Tao	Chinese Academy of Sciences
Wendi Wang	Southwest University
Dayong Zhang	Beijing Normal University
Yoh Iwasa	Kyushu University
Tsuyoshi Kajiwara	Okayama University
Masayasu Mimura	Meiji University
Toshiyuki Namba	Osaka Pref. University
Nanako Shigesada	Doshisha University
Yasuhiro Takeuchi	Shizuoka University

## Organizing Committee

### Chairman

Zhenqing Li	Institute of Botany, Chinese Academy of Sciences
-------------	--

### Members

Yasuhiro Takeuchi	Shizuoka University
Ming Dong	Institute of Botany, Chinese Academy of Sciences
Wanbiao Ma	University of Science and Technology Beijing
Xinzhu Meng	Institute of Botany, Chinese Academy of Sciences
Guohua Song	Beijing University of Civil Engineering & Architecture
Fengmei Tao	Anshan normal University
Shichang Wang	Institute of Botany, Chinese Academy of Sciences
Dongmei Xiao	Shanghai Jiaotong University
Zongqiang Xie	Institute of Botany, Chinese Academy of Sciences

## General information

### Conference rooms

**Invited Talks:**

Lecture hall、Lecture hall \ Conference room II(Oct.18, Afternoon)

**Contributed Talks:**

Lecture hall \ Conference room II(Oct.19, Afternoon) ,Lecture hall(Oct.21, Afternoon)

**Posters:** Corridors outside the Conference Hall

### Meals

**Oct. 18<sup>th</sup> to 21<sup>st</sup>, 2010**

Breakfast is included in the hotel charges.

Lunch and supper following the conference schedule.

### Oral Presentations

Please upload your PowerPoint file to the conference computer [\*prior to your talk.\*](#)

Please contact *Yanfeng Fu & Shichang Wang.*

### Posters

Posters will be displayed in the corridors of the Corridors outside the Conference Hall.

Please submit your poster to the Conference Organizing Committee after registration.

Please contact *Shichang Wang.*

### Welcome banquet

Welcome banquet will be held at [Sea North Green Garden](#) from **18:30** on Oct.18<sup>th</sup>.

### Farewell banquet

Farewell banquet will be held at [Sea North Green Garden](#) from **18:30** on Oct.21<sup>st</sup>.

### Travel information desk

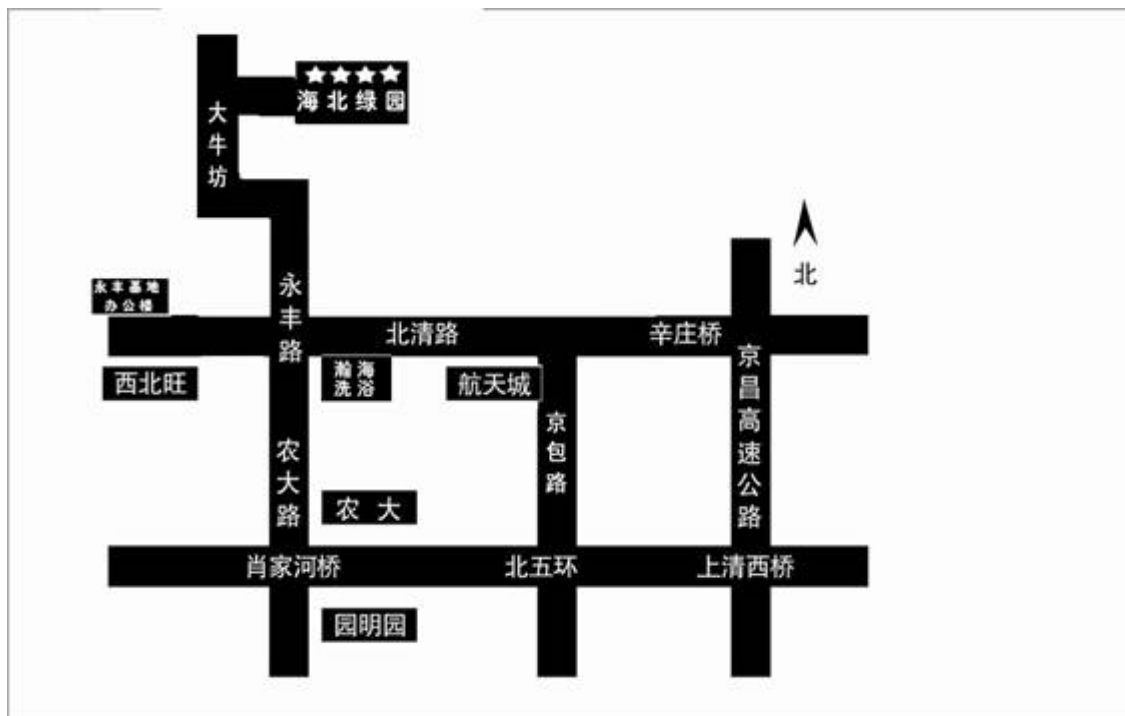
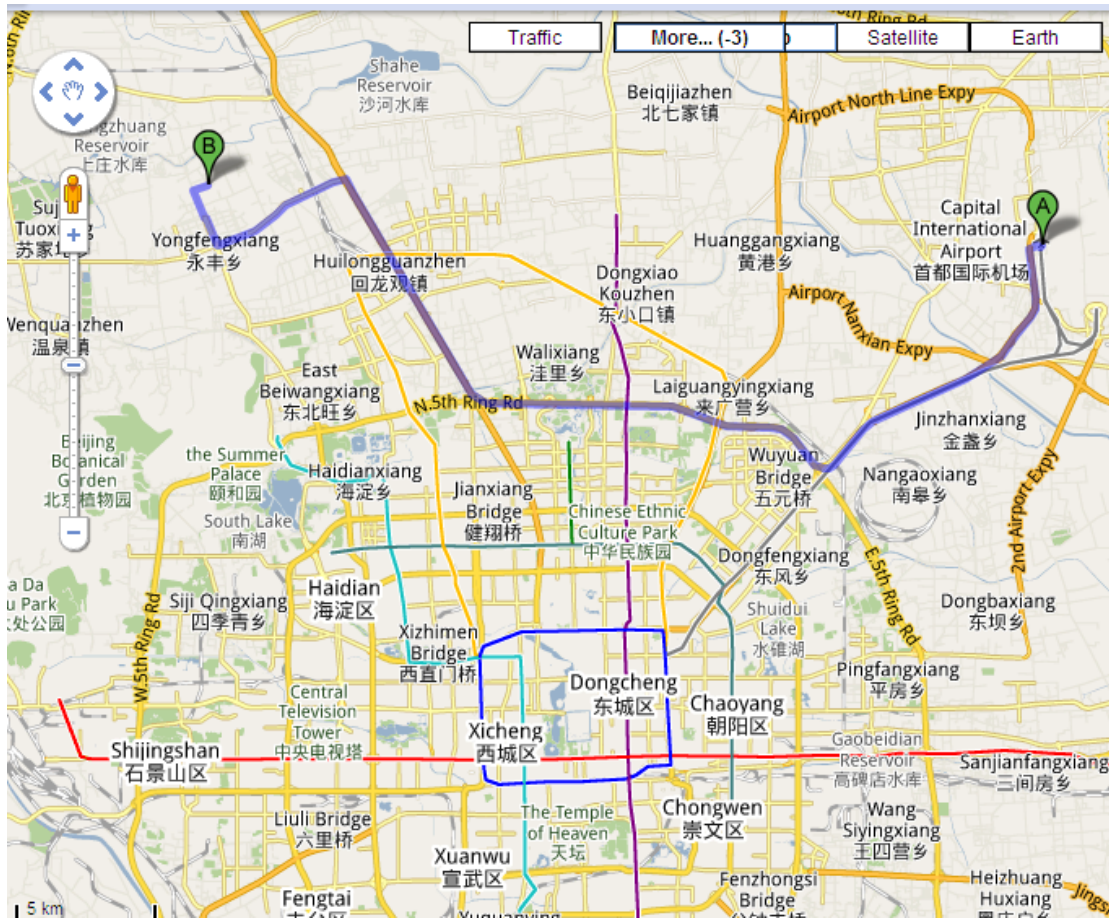
Travel information desk will be located [next the registration desk](#) to answer any inquiries related to excursions. *Please contact Yanfeng Fu & Shuqin Hou.*

### ***For questions, please contact***

<b>Zhenqing Li</b>	<b>13521935032</b>
<b>Shichang Wang</b>	<b>13466720523</b>
<b>Yanfeng Fu</b>	<b>13681570871</b>
<b>Shuqin Hou</b>	<b>13020040001</b>

## Hotel Location:

**B: Sea North Green Garden (海北绿园) Tel: 010-62494088,82479858**



## Programme overview

Date	Morning (8:30-12:00)	Afternoon (13:30-18:00)	Evening (18:30-)
<b>Oct. 17 (Sun.)</b>	<b>Registration (Housekeeping center)</b>		
<b>Oct. 18 (Mon.)</b>	<b>Invited Talks (Lecture hall)</b>	<b>Invited Talks S01:Lecture hall S02:Conference Room II</b>	<b>Welcome banquet</b>
<b>Oct. 19 (Tue.)</b>	<b>Invited Talks (Lecture hall)</b>	<b>Contributed Talks &amp; Posters SA: Lecture hall SB: Conference Room II</b>	
<b>Oct. 20 (Wed.)</b>	<b>Invited Talks (Lecture hall)</b>		
<b>Oct. 21 (Thur.)</b>	<b>Invited Talks (Lecture hall)</b>	<b>Contributed Talks (Lecture hall)</b>	<b>Farewell banquet</b>

## Detailed Programme

### Oct. 18 (Monday)

09:00-09:30	<b>Opening ceremony</b>
	<b>Prof. Jingan Cui, Vice president of CSMB</b>
	<b>Prof. Yasuhiro Takeuchi, President of JSMB</b> <i>Representative of IBCAS</i>
9:30-10:00	<b>Photo taking</b>

### Oct. 18 Invited Talks

#### Plenary Session (Lecture hall)

**Chairman:** Zhenqing Li

10:00-10:50	<b>Yoh Iwasa</b> , Kyushu University, Japan Evolution of masting -- synchronized and intermittent reproduction of trees.
10:50-11:40	<b>Dayong Zhang</b> , Beijing Normal University, China Neutral and nearly neutral models of biodiversity
12:00-13:30	<b>Lunch and break</b>

#### Concurrent Session

<b>Session 01 (Lecture hall)</b>	
<b>Co-Chairs:</b> Jingan Cui and Yasuhiro Takeuchi	
13:30-14:00	<b>Xuezhi Li</b> , Xinyang Normal University, China Modeling major factors that control tuberculosis(TB) spread in China
14:00-14:30	<b>Wanbiao Ma</b> , University of Science and Technology Beijing, China Differential equation models in theoretical prediction on nitrogen and phosphorus and algae of Guishui Lake in Beijing
14:30-15:00	<b>Tsuyoshi Kajiwara</b> , Okayama University, Japan Models of pathogen-immune interactions with absorption and time delays
15:00-15:30	<b>Toru Sasaki</b> , Okayama University, Japan Mathematical Analysis of models describing multi-strain infections
15:30-15:50	<b>Break</b>
15:50-16:20	<b>Xianning Liu</b> , Southwest University, China Disease transmission with population dispersal
16:20-16:50	<b>Rui Xu</b> , Shijiazhuang Mechanical Engineering College, China Dynamics of Infectious Disease models with Delays and Spatial diffusion
16:50-17:20	<b>Shinji Nakaoka</b> , The University of Tokyo, Japan Mathematical study on hematopoiesis
<b>Session 02 (Conference Room II)</b>	
<b>Co-Chairs:</b> Dayong Zhang and Hisashi Inaba	
13:30-14:00	<b>Hiromi Seno</b> , Hiroshima University, Japan A Mathematical Model of Population Dynamics with Predator's Behavioral Change Induced by Prey's Batesian Mimicry
14:00-14:30	<b>Weiming Wang</b> , Wenzhou University, China

## Detailed Programme

	Complex Dynamics of a Reaction-Diffusion Epidemic Model
14:30-15:00	<b>Kei-ichi Tainaka</b> , Shizuoka University Individual-based models for mutualism
15:00-15:30	<b>Meng Fan</b> , Northeast Normal University, China Mechanisms for Stable Coexistence in an Insect Community
15:30-15:50	<b>Break</b>
15:50-16:20	<b>Kei Tokita</b> , Osaka University, Japan Adaptive species interactions promote species abundance
16:20-16:50	<b>Shengqiang Liu</b> , Harbin Institute of Technology, China Competition Exclusion in Chemostat Models with Delays
16:50-17:20	<b>Ryusuke Kon</b> , University of Vienna, Japan Permanence induced by life-cycle resonances: the periodical cicada problem

### **Oct. 18 Reception Party (Free for all members who register)**

18:30—	Sea North Green Garden-Beijing
--------	--------------------------------

### **Oct. 19 (Tuesday)**

#### **Oct. 19 Invited Talks (Lecture hall)**

<b>Co-Chairs:</b> Wendi Wang and Tae-Soo Chon	
08:30-09:00	<b>Jingan Cui</b> , Beijing University of Civil Engineering & Architecture, China Models of infectious disease control with media coverage and treatment resource
09:00-09:30	<b>Yongkuk Kim</b> , Kyungpook National University, Republic of Korea The spread of pine wilt disease subject to early eradication of infected trees.
09:30-10:00	<b>Inkyung Ahn</b> , Korea University, Republic of Korea A Spatio-Temporal Model among HIV-1 and Immune Systems
10:00-10:20	<b>Break</b>
10:20-10:50	<b>Toshiyuki Namba</b> , Osaka Prefecture University, Japan Multiple unstable steady states and ungulate population dynamics
10:50-11:20	<b>Takenori Takada</b> , Hokkaido University, Japan Obtaining yearly transition of Markovian matrix in land-use models and its difficulties
11:20-11:50	<b>Jan Bogaert</b> , Université Libre de Bruxelles, Belgium A multiscalar quantitative approach to assess landscape dynamics and anthropogenic effects
12:00-13:30	<b>Lunch and break</b>

#### **Oct. 19 Poster session (13:30-14:30)**

<b>Emiko Ishiwata</b> , Tokyo University of Science Global dynamics of a discretized SIRS epidemic model with time delay and its applications
<b>Shinichiro Higa</b> , Shizuoka University A primitive model for the population dynamics of mutualism
<b>Kazunori Sato</b> , Shizuoka University Can spatial interaction with Allee effects promote dynamical complexity?
<b>Kojiro Tanaka</b> , Graduate School of Engineering, Shizuoka University Evaluation on efficiency of BCG vaccination for the prevention of tuberculosis epidemics

## Detailed Programme

<b>Byul Nim Kim</b> , Kyungpook National University Influenza Vaccine Allocation Strategies
<b>Kwang Sung Lee</b> , Pusan National University, Republic of Korea Mathematical analysis of a host-vector model with pine wilt disease
<b>Gi Phil Cho</b> , Pusan National University, Republic of Korea Mathematical model and control strategy for resource recovery of sailfin sandfish, <i>Arctoscopus japonicus</i> , in Korea East Sea.
<b>SookJung Ku</b> , National Institute for Mathematical Sciences, Republic of Korea Measuring the Time Spent for a Termite to Pass Tunnel Intersections
<b>Yeontaek Choi</b> , National Institute for Mathematical Sciences, Republic of Korea A Novel Approach to Characterize the Behavioral Shape of <i>Caenorhabditis elegans</i>
<b>Joobaek Leem</b> , National Institute for Mathematical Science, Republic of Korea Behavioral Analysis of Fish Schooling Behavior
<b>Wonju Jeon</b> , National Institute for Mathematical Science, Republic of Korea Graph-Theoretical Analysis on Foraging Strategy of Subterranean Termites
<b>Hiroki Yokoi</b> , Shizuoka University Coexistence in Prey-Predator Chemostat Model with Single Nutrient
<b>Yuma Sakai</b> , Hokkaidou university Propagation model of pathogen on clonal plants using contact process

### Oct. 19 Contributed Talks

<b>Session A (Lecture hall)</b>	
<b>Co-Chairs :</b> Tsuyoshi Kajiwara and Wanbiao Ma	
13:40-14:00	<b>Joe Wakano</b> , Meiji University Pattern formation and chaos in spatial ecological public goods games
14:00-14:20	<b>Jian Zu</b> , Meiji University, Adaptive evolution of foraging-related traits in a predator-prey community
14:20-14:40	<b>Hong Zhang</b> , Jiangsu University Population Dynamics and Strategies of Biological Pest Control
14:40-15:00	<b>Sang-Hee Lee</b> , National Institute for Mathematical Sciences The influence of branching tunnels on subterranean termites' foraging efficiency
15:00-15:20	<b>S. Seirin Lee</b> , The University of Tokyo Barrier Wall Strategy with Transgenic Technologies on Vector-born Diseases Control
15:20-15:40	<b>Gang Huang</b> , Shizuoka University Mathematical Analysis for Virus Evolution against Specific Immune
15:40-16:00	<b>Break</b>
16:00-16:20	<b>Feng Rao</b> , East China Normal University Stochastic Analysis of a Delayed Harrison-type Predator-Prey Model
16:20-16:40	<b>Jianjun Jiao</b> , Guizhou University of Finance and Economics A stage-structured predator-prey system with impulsive diffusion
16:40-17:00	<b>Shingo Iwami</b> , Japan Science and Technology Agency (JST) Quantification of viral dynamics in vitro
17:00-17:20	<b>Hiroto Shoji</b> , Kyoto Prefectural University of Medicine Three-Dimensional Aggregation Patterns in Keller-Segel Models
17:20-17:40	<b>To be arranged</b>
17:40-18:00	<b>To be arranged</b>

**Detailed Programme**

---

<b>Session B (Conference Room II)</b>	
<b>Co-Chairs:</b> Yoshihisa Morita and Rui Xu	
13:40-14:00	<b>Zhipeng Qiu</b> , Nanjing University of Science and Technology Complex dynamics of an epidemic model with targeted antiviral prophylaxis
14:00-14:20	<b>Toshikazu Kuniya</b> , The University of Tokyo Global stability of a multigroup SIR epidemic model for the geographical spread of influenza
14:20-14:40	<b>Yong Zhang</b> , Beijing Normal University Estimation of the reproduction number for pandemic influenza A (H1N1) in mainland China
14:40-15:00	<b>Schehrazad Selmane</b> , LAID3. University of sciences and technology of Algeria The Impact of Screening for Breast Cancer on the Incidence of the Disease
15:00-15:20	<b>Yoichi Enatsu</b> , Waseda University Global asymptotic stability of SIRS models with a class of nonlinear incidence rates and distributed delays
15:20-15:40	<b>Yoshiaki Muroya</b> , Waseda University Global stability of delayed multi-group SIRS epidemic models and related problems.
15:40-16:00	<b>Break</b>
16:00-16:20	<b>Yong han Kang</b> , Pusan National University Optimal control problem for Malaria in Republic of Korea
16:20-16:40	<b>Wataru Nakahashi</b> , Meiji University Evolution of learning abilities in the genus Homo
16:40-17:00	<b>Xueyong Zhou</b> , Nanjing Normal University Analysis of stability and bifurcation for an SEIV epidemic model with vaccination and nonlinear incidence rate
17:00-17:20	<b>JianHua Pang</b> , Nanjing Normal University Dynamical behavior of a hepatitis B virus transmission model with vaccination
17:20-17:40	<b>Jinliang Wang</b> , Harbin Institute of Technology SVEIR epidemiological model with varying infectivity and distributed delay
17:40-18:00	<b>To be arranged</b>

**Oct. 20 (Wednesday)**

**Oct. 20 Invited Talks (Lecture hall)**

<b>Chairman:</b> Yanni Xiao	
08:30-09:00	<b>Yasuhiro Takeuchi</b> , Shizuoka University, Japan Paradox of vaccination
09:00-09:30	<b>Xinyu Song</b> , Xinyang Normal University, China Global asymptotic stability and Hopf bifurcation for a delayed viral infection model
09:30-10:00	<b>Tae-Soo Chon</b> , Pusan National University, Republic of Korea Analysis of movement behaviors of indicator animals under stressful conditions
10:00-10:20	<b>Break</b>
10:20-10:50	<b>Il Hyo Jung</b> , Pusan National University, Republic of Korea Mathematical model for an integrated pest management in an agro-ecosystem
10:50-11:20	<b>Bing Liu</b> , Anshan Normal University, China Existence and attractiveness of order one periodic solution of a Holling II predator-prey

## Detailed Programme

	model with state feedback control
11:30-13:00	<b>Lunch and break</b>

### **Oct. 20 Afternoon: City tour (Great Wall)**

**The colloquium will supply free service from the hotel to Great Wall, and every participant who would like to go to the Great Wall needs to pay for the ticket. Please register the excursion to the travel desk.**

### **Oct. 21 (Thursday)**

#### **Oct. 21 Invited Talks (Lecture hall)**

<b>Chairman:</b> Xinyu Song	
08:30-09:00	<b>Yoshihisa Morita</b> , Ryukoku University, Japan On a reaction-diffusion system with conservation of a mass for cell polarity
09:00-09:30	<b>Hisashi Inaba</b> , University of Tokyo, Japan On the definition of the basic reproduction number for infectious diseases in heterogeneous environments
09:30-10:00	<b>Yi Tao</b> , Institute of Zoology, CAS, China Stochastic dynamics in gene expression
10:00-10:20	<b>Break</b>
10:20-10:50	<b>Yanni Xiao</b> , Xi'an Jiaotong University, China Threshold Dynamics for an HIV Model melding pharmacokinetics.
10:50-11:20	<b>Wendi Wang</b> , Southwest University, China Evolution of population dispersal between patches
11:20-11:50	<b>Zhonghua Lu</b> , Computer Network Information Center,CAS, China HPC in Bioinformatics of SCCAS
11:50-12:20	<b>Zhongzhan Zhang</b> , Beijing University of Technology Variable Selection in Double Generalized Linear Models
12:20-13:20	<b>Lunch and break</b>

#### **Oct. 21 Contributed Talks (Lecture hall)**

<b>Co-Chairs:</b> Fengqin Zhang and Fengmei Tao	
13:20-13:40	<b>Wanli Yang</b> , Academy of Armored Forces Engineering,Beijing Impulsive Synchronization for Reaction-Diffusion System
13:40-14:00	<b>Linfei Nie</b> , Xinjiang University Dynamic analysis for a class of two-species population systems with state dependent impulsive effects
14:00-14:20	<b>Cong Li</b> , Institute of Zoology, CAS Evolution of cooperation and network structure
14:20-14:40	<b>Lijiang Zeng</b> , Zunyi Normal College Equivalence on finitely generated R[G] module
14:40-15:00	<b>Ryo Oizumi</b> , Hokkaido University The optimal control of growth process under environmental stochasticity.
15:00-15:20	<b>Shu-ichi Kinoshita</b> , Meiji University The gene regulatory dynamics in complex networks

## Detailed Programme

---

15:20-15:40	<b>Break</b>
15:40-16:00	<b>Yincui Yan</b> , Southwest University Global Dynamics of CD4+ T Cells and CTL Immune Responses to HIV Infection
16:00-16:20	<b>Kaifa Wang</b> , Third Military Medical University Numerical diagnoses of superinfection in chronic hepatitis B viral
16:20-16:40	<b>Yukihiko Nakata</b> , BCAM - Basque Center for Applied Mathematics Stability analysis of multi-compartment models for cell production systems
16:40-17:00	<b>Yunxin Huang</b> , Hubei University The spatial patterns and range of competing and coevolving species
17:00-17:20	<b>Junyuan Yang</b> , Yuncheng University Intrinsic transmission global dynamics of tuberculosis with age structure
17:20-17:40	<i>To be arranged</i>
17:40-18:00	<i>To be arranged</i>
18:00-18:20	<b>Closing ceremony</b>
18:30-21:00	<b>Farewell Party</b>

## *Invited Talks*

### **A Spatio-Temporal Model among HIV-1 and Immune Systems**

**Inkyung Ahn**

*Korea University, Republic of Korea*

*ahnik@korea.ac.kr*

Recent investigations, including the CD4+T cells' homing to the lymph system in HIV-1 infection and the localized behavior of the virus, exhibits the heterogeneous nature of the immune cells and virus. In this talk, a reaction-diffusion system as a spatially non-homogeneous model, is proposed, and the qualitative properties of the dynamic system are investigated. Since the positive steady-state and Omega-limit of the PDE system are closely related to stabilizing the infection, conditions are provided for the existence of a strictly positive solution, a steady-state above certain positive levels and the existence of a positive Omega-limit. A possible role of stem cells stabilizing the disease is suggested.

**\*\*This is a joint-work with Lige Li.**

### **A multiscalar quantitative approach to assess landscape dynamics and anthropogenic effects**

**Jan Bogaert**

*Université Libre de Bruxelles, Belgium*

*jan.bogaert@ulb.ac.be*

Landscape ecology can be defined as the study of ecological patterns and processes in their spatial context. Landscape ecology is motivated by a need to understand the development and dynamics of pattern in ecological phenomena, the role of disturbance in ecosystems, and characteristic spatial and temporal scales of ecological events. In order to enable the development of appropriate landscape management plans, the causes and impacts of landscape dynamics should be fully understood. According to the pattern/process paradigm, landscape configuration and composition are directly related to landscape function, which justifies the study of landscape pattern by means of landscape metrics; the quantification of landscape pattern is an area of broad practical interest, driven by the premise that ecological processes are linked to and can be predicted from some broad-scale spatial pattern. A number of case studies, situated in West and Central Africa, are presented that illustrate the use of quantitative techniques in landscape ecology in order to understand and characterize landscape dynamics due

to anthropogenic activities. This type of approach is justified by the variability of the ecosystems and landscapes subject to anthropogenic disturbances worldwide, and by the ongoing discussion and controversy on the (ecological) consequences of these disturbances.

### **Analysis of movement behaviors of indicator animals under stressful conditions**

Tae-Soo Chon

*Pusan National University, Republic of Korea*

*tschon@pusan.ac.kr*

Response behavior of indicator animals has garnered a special attention in risk assessment in aquatic ecosystems, filling the gap between macro-scale (e.g., community structure) and micro-scale (e.g., molecular response) measurements. Behavior is an integrative expression of physiological processes at the level of the whole body. While behavioral monitoring could be conducted on the real time basis without much demanding observation efforts and facilities, behavioral data are highly variable and sensitive to noise. Computational methods applied to analysis of the movement data are outlined in revealing structural properties in the movement data, including hidden Markov model (HMM), comparison of activity levels, and artificial neural networks. The model results were evaluated with observation data of indicator species including *Daphnia magna* and *Danio rerio*, after the animals were treated with low levels of toxic chemicals.

### **Models of infectious disease control with media coverage and treatment resource**

Jingan Cui

*Beijing University of Civil Engineering & Architecture, China*

*cuija@bjceia.edu.cn*

The number of patients need to be treated may exceed the carrycapacity of local hospitals during the spreading of a severe infectious disease. We propose two epidemic models with media coverage and saturation recovery from infective individuals to understand their effect on the emergency disease control, respectively. It is shown that saturation recovery from infective individuals leads to vital dynamics, such as bistability and periodicity, when the basic reproduction number is less than unity.

## Mechanisms for Stable Coexistence in an Insect Community

Meng Fan

*Northeast Normal University, China*

*mfan@nenu.edu.cn*

In this talk, we formulate a three-species ecological community model consisting of two aphid species (*Acyrtosiphon pisum* and *Megoura viciae*) and a specialist parasitoid (*Aphidius ervi*) that attacks only one of the aphids (*A. pisum*). The model incorporates both density-mediated and trait-mediated host-parasitoid interactions. Our analysis shows that the model possesses much richer and more realistic dynamics than earlier models. Our theoretical results reveal a new mechanism for stable coexistence in a three-species community in which any two species alone do not co-exist. More specifically, it is known that, when a predator is introduced into a community of two competing species, if the predator only predaes on the strong competitor, it can allow the weak competitor to survive, but may drive the strong competitor to extinction through over-exploitation. We show that if the weak competitor interferes the predation on the strong competitor through trait-mediated indirect effects, then all three species can stably co-exist.

## On the definition of the basic reproduction number for infectious diseases in heterogeneous environments

Hisashi Inaba

*University of Tokyo, Japan*

*inaba@ms.u-tokyo.ac.jp*

During the last two decades, the definition and computing methods for the basic reproduction number  $R_0$  for infectious diseases have been widely accepted and developed to become a most important keystone of the mathematical epidemiology. However,  $R_0$  is originally defined by renewal systems with time-independent parameters describing the disease invasion process, it can not be applied to formulate the threshold principle for infectious diseases in time-heterogeneous environments, which are described by non-autonomous dynamical systems.

Recently, several authors proposed some ideas to extend the definition of  $R_0$  to the case of infectious diseases in periodic environments. In a most general abstract setting, Thieme (2009) formulated the next generation operator (NGO) for infinite-dimensional non-autonomous dynamical system based on the idea of evolutionary semigroups, and

has successfully established the threshold relation between the extended  $R_0$ , which is given as the spectral radius of the NGO, and the spectral bound of the evolutionary system describing the linear population dynamics in heterogeneous environments.

In my talk, I would like to propose another approach to the definition of  $R_0$  in heterogeneous environments. First we review existing ideas of the definition of  $R_0$  in heterogeneous (in particular, periodic) environments. Next we reconstruct the definition of  $R_0$  introduced by Wang and Zhao (2008) for the ODE model and by Bacaer and Guernaoui (2006) for the infection-age dependent model and show the threshold principle that the sign of  $R_0-1$  determines the sign of the intrinsic growth rate of infected population. Moreover we formulate  $R_0$  for the age-duration dependent SIR model with periodic coefficients. Our arguments depend on the weak ergodicity of the positive evolutionary system and the existence of exponential solution, so we can avoid heavy mathematical equipments as the evolutionary semigroups, and clear the basic idea underlying the extended  $R_0$  and the NGO. Its advantage is to be able to determine the dominant exponential solution representing the asymptotic behavior of the basic system, the price we pay is to assume the irreducibility of the evolution process.

### **Evolution of masting – synchronized and intermittent reproduction of trees**

**Yoh Iwasa**

*Kyushu University, Japan*  
*yohiwasa@kyudai.jp*

**Trees in mature forests often show intermittent reproduction (masting), synchronized over a long distance. According to the dynamics of the resource reserve of individuals, trees can show a large between-year fluctuation in the seed crop even in a constant environment. Reproduction of different trees may be synchronized if fruit production is limited by the availability of outcross pollen. We study conditions for masting to evolve. Assumptions are: the forest consists of many sites, each occupied by a single canopy tree. After a canopy tree falls, the vacant site (gap) becomes available for recruitment.**

**We first show that masting never evolves if all vacant sites are filled by individuals from seeds produced in the same year. Then we demonstrate that masting can evolve if some seedlings survive for several years, forming a seedling bank on the forest floor, where seeds produced in different years compete for gap acquisition.**

**We also study the effect of specialist seed predators. In the complete absence of seeding bank, masting never evolves even in the presence of seed predators. If seedling survivorship is positive but small, then the presence of seed predators can promote the evolution of masting.**

## **Mathematical model for an integrated pest management in an agro-ecosystem**

**Il Hyo Jung**

*Pusan National University, Republic of Korea*

*ilhjung@pusan.ac.kr*

The aim of this talk is to derive and analyze an integrated pest management model in an agro-ecosystem by mathematical modeling. Here we consider 2-control parameters; sterile males and pesticide as control measures for pest population. Using optimal control technique, we investigate the optimal amount of pesticides and sterile males to be used for best and economic crop production. Lastly numerical simulations to verify the results are given.

## **Models of pathogen-immune interactions with absorption and time delays**

**Tsuyoshi Kajiwara**

*Okayama University, Japan*

*kajiwara@ems.okayama-u.ac.jp*

Interactions between pathogens and immune system in vivo are described by ordinary differential equations with or without time delays. Stability of interior equilibria determines whether the state of disease oscillates or not in long time. When a pathogen infects an uninfected cell, the number of pathogens in blood decreases by one. We call it the effect of absorption. The authors showed that the effect of absorption can destabilize interior equilibria which are stable if the effect of absorption does not exist, in a previous paper. In this talk, we present the results of stability of models of pathogens-immune interactions with absorption effects and time delays.

## **The spread of pine wilt disease subject to early eradication of infected trees**

**Yongkuk Kim**

*Kyungpook National University, Republic of Korea*

*yongkuk@knu.ac.kr*

Pine wilt disease is currently among the most devastating pine trees plagues on earth. It is caused by the pinewood nematode *Bursaphelenchus xylophilus* in a perfect, and beautifully synchronized, mutualistic relationship with beetles of the genus *Monochamus*. The disease has a fast and efficient spread, which turns most of the

efforts to control it practically insufficient. We investigate how early eradication of infected pine trees, i.e. eradication of trees which just ceased oleoresin exudation, may affect the disease spread. In contrast to the sole eradication of killed trees, our results show that under an appropriate combination of eradication strategies:

- (1) There is a significant increase in the minimum pine density below which the disease fails to invade,
- (2) The region where reproductive Allee effects may take place are significantly enlarged,
- (3) It is possible to design optimal policies for eradication through stochastic search optimization techniques, for instance.

We conclude that disease extinction can be reached faster with appropriate combinations of eradication policies, which minimize the damage on healthy pine trees and operational costs.

### **Permanence induced by life-cycle resonances: the periodical cicada problem**

Ryusuke Kon

*University of Vienna, Japan*  
*ryusuke.kon@univie.ac.at*

Periodical cicadas (*Magicicada* spp.) are known for their unusually long life cycle for insects and their prime periodicity of either 13 or 17 years. One of the explanations for the prime periodicity is that the prime periods are selected to prevent cicadas from resonating with predators with submultiple periods (e.g., see Lloyd and Dybas, 1966). Based on this idea, Webb (2001) constructed mathematical models and gave a numerical example that periodically oscillating predators with 2- or 3-year period eliminate nonprime number periodical cicadas. However, in Webb's model, the interaction between well-timed cicada-cohorts and their predators is ignored. In our study, we construct an age-structured model for dynamically interacting predator and prey populations and consider the problem of the predator-resonance hypothesis. Our main result shows that preys are not necessarily eliminated by predators with submultiple periods since invasion of preys is always facilitated by their well-timed cohorts. It is also shown that synchronized life-cycles between predator and prey populations can produce a permanent system, in which no cohorts are missing in both populations. This contrasts with the result that systems with asynchronous life-cycles always have a stable coexistence state where perfect periodicity is maintained in both populations.

These results suggest that resonances with predators are not always deleterious to their preys.

## **Modeling major factors that control tuberculosis(TB) spread in China**

**Xuezhi Li**

*Xinyang Normal University, China*

*xzli66@126.com*

**This article introduces a novel model that studies the major factors jeopardizing the TB control programme in China. A previously developed two strain TB model is augmented with a class of individuals not registered under the TB control programme. The paper investigates the basic reproduction number and proves the global stability of the disease free equilibrium. The presence of three endemic equilibria is established in the model. With the help of numerical simulations a comparative study has been performed to test the validity of the model presented here to the real data available from the Ministry of Health of the People's Republic of China. Sensitivity and elasticity analysis suggest the impact of key parameters on the tuberculosis control in China.**

## **Competition Exclusion in Chemostat Models with Delays**

**Shengqiang Liu**

*Harbin Institute of Technology, China*

*sqliu@hit.edu.cn*

**We consider the global asymptotic behaviors of three exploitative competition models among n-species for a chemostat with general response functions and differential removal rates. Three different classes of delays in describing the conversion process of nutrient to new cells are studied separately: 1. infinite-distributed type; 2. finite-distributed type; 3. discrete type. By carefully constructing the proper Lyapunov functionals, it is shown that competitive exclusions hold for these models with a series of general growth response functions. Previous results in the literatures are significantly improved and extended.**

**\*\*Joint work with Lin Wang, Xinxin Wang and Haitao Song**

## **Disease transmission with population dispersal**

**Xianning Liu**

*Southwest University, China*

*liuxn@swu.edu.cn*

Population dispersal, as a common phenomenon in human society, may cause the spread of many diseases such as influenza and SARS, which can be easily transmitted from one region to other regions. In this report, an SIQS model is introduced to discuss the effect of transport-related infection, exit screening and entry screening. The basic reproduction number is computed and the dynamical behaviors of the model are analyzed. If the basic reproduction number is below unity, the disease free equilibrium is globally asymptotically stable. And there exists an endemic equilibrium which is stable if the reproduction number is larger than unity. It is shown that the disease is endemic in the sense of permanence if and only if the endemic equilibrium exists. Exit screening and entry screening are shown to be helpful for disease eradication since they can always have the possibility to eradicate the disease endemic led by transport-related infection and furthermore have the possibility to eradicate disease even when the isolated sites are disease endemic.

## **Existence and attractiveness of order one periodic solution of a Holling II predator-prey model with state feedback control**

**Bing Liu**

*Anshan Normal University, China*

*Liubing529@126.com*

According to biological and chemical control strategy for pest control, a Holling II functional response predator-prey system concerning impulsive state feedback control is investigated. The conditions for the existence and attractiveness of order one periodic solution are obtained by using the successor functions of semi-continuous dynamic system. Numerical simulations confirm our theoretical results.

## **HPC in Bioinformatics of SCCAS**

**Zhonghua Lu, Qiang Tu and Xianyu Lang**  
*Computer Network Information Center, CAS*  
*zhlu@sccas.cn*

**InsPecT is a software for identifying post-translational modifications (PTMs) of protein. It can search PTMs in unrestrictive mode via the MS-Alignment algorithm, even reveal unknown types of modifications. Because MS-Alignment takes more than 99% computing complexity of InsPecT, we accelerated it using GPUs and obtained at least 30X speedup after using several optimization methods of CUDA. We also parallelized InsPecT with MPI to make it running on multi-GPU environment. cuda-InsPecT is the MPI+CUDA version based on InsPecT, which will be open source. Currently, cuda-InsPecT software has been deployed for users' online computation on SCCAS bioinformatics Grid ( <http://scbg.sccas.cn>).**

**Key words: InsPecT, MS-Alignment, GPU, CUDA, MPI, SCBG**

## **Differential equation models in theoretical prediction on nitrogen and phosphorus and algae of Guishui Lake in Beijing**

**Wanbiao Ma**

*University of Science and Technology Beijing, China*  
*wanbiao\_ma@sas.ustb.edu.cn*

**In this talk, some differential equation models have been proposed to describe the interactions among nitrogen source, phosphorus source and Microsystems (MCs), based on the experimental data in the project of “the integrated control strategies on preventing eutrophication and algal blooms of Guishui Lake in Beijing”.**

## On a reaction-diffusion system with conservation of a mass for cell polarity

Yoshihisa Morita

*Ryukoku University, Japan*

*morita@rins.ryukoku.ac.jp*

We are dealing with a reaction-diffusion system proposed as a conceptual model for the cell polarity by Otsuji-Ishihara et al. This system is given by two-component reaction-diffusion equations modeling a switching dynamics for proteins in an active form in the membrane and an inactive one in the cytosol with diffusions. The model equations have some interesting mathematical properties about equilibrium solutions and the stability of them. We state those properties and show a mathematical mechanism how the system allows a stable spiky pattern through the Turing instability.

## Mathematical study on hematopoiesis

Shinji Nakaoka

*The University of Tokyo, Japan*

*snakaoka@ms.u-tokyo.ac.jp*

Hematopoietic cells such as red blood cells, granulocytes, platelets and white blood cells arise from a hematopoietic stem cell by cell differentiation. The hematopoietic system is regulated by several factors, including intrinsic/genetic factors as well as extrinsic factors, interactions at local environments and so on. Several mathematical models which describe the population dynamics of hematopoiesis have been proposed and investigated in order to obtain basic insights to the cause of dynamic hematopoietic diseases such as cyclic neutropenia. Although several qualitative aspect for the generation mechanism of such dynamics diseases have been revealed, some of recent molecular based knowledge has not been incorporated into mathematical studies yet.

In this talk, I present our recent mathematical studies on the dynamics of hematopoiesis. Our mathematical model is formulated in terms of delay equations, a coupled system of renewal equations and delay differential equations (Diekmann et al, Springer 1995; SIAM J. Math. Anal. 39:1023--1069, 2007). It is shown that a mathematical model studied by Foley et al (J. Theor. Biol., 257:27--44, 2009) can be equivalently reformulated by delay equations with some modification. The key feature of using delay equations is that three compartments representing the developmental stages of hematopoiesis of granulocytes are described by one renewal equation. I show some analytical and numerical computation results for stability and bifurcation properties of the linearized system around an equilibrium, and some numerical simulations which represent periodic oscillations of neutrophils. Several applications and use of delay equations to treat clinical data will be discussed.

## **Multiple unstable steady states and ungulate population dynamics**

**Toshiyuki Namba**

*Osaka Prefecture University, Japan*  
*tnamba@b.s.osakafu-u.ac.jp*

Ungulate populations have become overabundant and expanded their ranges in many countries in recent decades. Ungulate population dynamics often follows a rapid increase to peak abundance and a subsequent collapse to much lower abundance, a process known as irruption. Overabundant ungulate herds can extirpate palatable plant species and drive the natural plant communities into those dominated by unpalatable species. In this talk, we consider a simple three-species Lotka-Volterra model of a palatable and an unpalatable plant and an herbivore species to understand how competition between palatable and unpalatable plants affects herbivore dynamics. We will show that instability of both the palatable-dominated and the unpalatable-dominated steady states may explain violent ungulate oscillations and that the introduction of carnivores should be useful to suppress the oscillations. Finally, we will discuss what is the effective measure to control ungulate populations when the carnivore introductions is unrealistic.

## **Mathematical Analysis of models describing multi-strain infections**

**Toru Sasaki**

*Okayama University, Japan*  
*sasaki@ems.okayama-u.ac.jp*

We consider, in a mathematical point of view, several models describing multi-strain infections. These models were developed to consider the evolution of virulence. We here deal with ordinary differential equation models. Hence our target is the dynamics of well mixed population. Even in that case, it is known that superinfection can induce the evolution of virulence. We compare several models which differ in the uninfected host population dynamics

## **A Mathematical Model of Population Dynamics with Predator's Behavioral Change Induced by Prey's Batesian Mimicry**

**Hiromi Seno**

*Hiroshima University, Japan*  
*seno@math.sci.hiroshima-u.ac.jp*

In this work, we analyze a mathematical model of the population dynamics among a mimic, corresponding model, and their predator populations. The predator changes its search-and-attack probability by forming and losing its search image. We analyze a mathematical model consisting of the daily population dynamics with ordinary differential equations, the seasonal population dynamics with difference equations, and the annual population dynamics with difference equations. Each predation season is composed with the daily dynamics repeated day by day in  $\Delta t$  days. The predator population size is assumed to be kept constant, given by  $P_0$ , independently of the model and the mimic population sizes. The predator cannot distinguish the mimic from the model, so that each predator searches and attacks them with common probability. Once a predator predaes a model individual, it comes to omit both the model and the mimic species from its diet menu, and then not to search nor attack them in the same day. If a predator predaes a mimic individual, it comes to increase the search-and- attack probability for the model and the mimic. The frequency of predators with higher search-and-attack probability and that with zero search-and-attack probability decreases by a rate between the subsequent days, because of the predator's losing (i.e., forgetting) the search image. The reproductions in model, mimic, and predator populations are assumed to occur between the subsequent predation seasons. In other words, there is no reproduction of model, mimic or predator within the predation season, so that the model and the mimic populations monotonically decrease due to the predation during the predation season. Analyzing our model system, we can get the result such that the condition for the persistence of model population does not depend on the mimic population size, while the condition for the persistence of mimic population does depend on the predator's ability of the search image formation.

## **Global asymptotic stability and Hopf bifurcation for a delayed viral infection model**

**Xinyu Song**

*Xinyang Normal University, China*

*Xysong88@163.com*

**Target-cell dynamics plays a crucial role in the dynamics of viral infection in vivo.**

**Target cells are produced at a constant rate, we can obtain the complete result on the global stability of the chronic-infection equilibrium for the virus infection models with intracellular delays. The global stability result is essential for our conclusion that the delay does not produce periodic oscillations.**

**Target cells are produced at a logistic function, by stability analysis we obtain sufficient conditions on the parameters for the global stability of the infected steady state and the infection-free steady-state. We also show that periodic oscillations in the viral load and T cell populations are possible. Biologically, it implies that some of the parameter values can cause the cell and virus population to fluctuate.**

## **Individual-based models for mutualism**

**Kei-ichi Tainaka**

*Shizuoka University, Japan*

*tainaka@sys.eng.shizuoka.ac.jp*

**Much literature on population dynamics has been published, especially for predation and competition. However, for mutualism, the population dynamics is rarely studied. We introduce our studies of individual-based models. In particular, we describe recent studies for obligated mutualism.**

## **Obtaining yearly transition of Markovian matrix in land-use models and its difficulties**

**Takenori Takada**

*Hokkaido University, Japan*  
*takada@ees.hokudai.ac.jp*

Transition matrices have often been used in landscape ecology and GIS studies of land-use to quantitatively estimate the rate of change. When transition matrices for different observation periods are compared, the observation intervals often differ because satellite images or photographs of the research site taken at constant time intervals may not be available. For such calculation, several previous studies have utilized a linear algebra formula of the power root of matrices. However, three difficulties may arise when applying this formula to a practical dataset from photographs of a research site. We examined the first difficulty, namely that plural solutions could exist for a yearly transition matrix, which implies that there could be multiple scenarios for the same transition in land-use change. Using data for the Abukuma Mountains in Japan, we then looked at the second difficulty, in which we may obtain no positive Markovian matrix and only a matrix partially consisting of negative numbers. We propose a way to calibrate a matrix with some negative transition elements and to estimate the prediction error. Finally, we discuss the third difficulty that arises when a new land-use category appears at the end of the observation period and how to solve it. We developed a computer program to calculate and calibrate the yearly matrices and to estimate the prediction error.

## **Paradox of vaccination**

**Yasuhiro Takeuchi**

*Shizuoka University, Japan*  
*takeuchi@sys.eng.shizuoka.ac.jp*

We investigated, in the context of the emergence of a vaccine-resistant strain, whether a vaccination program can prevent the spread of infectious disease. We also investigated how losses from immunization by vaccination imposed by the resistant strain affect the spread of the disease. We designed and analyzed a deterministic compartment model illustrating transmission of vaccine-sensitive and vaccine-resistant strains during a vaccination program. We investigated how the loss of protection effectiveness impacts the program. Results show that a vaccination to prevent the spread of disease can instead spread the disease when the resistant strain is less virulent than the sensitive

strain. If the loss is high, the program does not prevent the spread of the resistant strain despite a large prevalence rate of the program. The epidemics final size can be larger than that before the vaccination program. We propose how to use poor vaccines, which have a large loss, to maximize program effects and describe various program risks, which can be estimated using available epidemiological data.

## Stochastic dynamics in gene expression

Yi Tao

Institute of Zoology, CAS

*yitao@ioz.ac.cn*

To investigate the effects of bidirectional regulation on the noise in protein concentration, a theoretical and simple three-gene network model is considered. The basic idea behind this model is from Paulsson's proposition (J. Paulsson, *Phys. Life Rev.* 2005, 2, 157–175), where the synthesis and degradation of a mRNA species corresponding to a target protein are regulated directly and indirectly by a certain s-factor, and a random increase in the concentration of the s-factor should increase both the synthesis and degradation rates of the mRNA species (bidirectional regulation). Using the standard O-expansion technique (linear noise approximation) and Monte Carlo simulation, our main results show clearly that for the steady-state statistics the effects of the noise of the s-factor on the stochastic fluctuation of the target protein could partially cancel out.

## Adaptive species interactions promote species abundance

Kei Tokita<sup>1,2,3</sup> and Masanori Sugiura<sup>1,2</sup>

<sup>1</sup>*Cybermedia Center, Osaka University*

<sup>2</sup>*Graduate School of Science*

<sup>3</sup>*Graduate School of Frontier Bioscience, Osaka University, Japan*

*tokita@cmc.osaka-u.ac.jp*

There have been many discussions on the relationship between adaptation and the species abundance in ecological communities. We consider a random community model with adaptive species interactions and present an equilibrium statistical mechanics analysis which supports the hypothesis that species abundance is promoted by adaptive

species interactions. We also discuss the potential applicability of the model to a real ecosystem.

## Complex Dynamics of a Reaction-Diffusion Epidemic Model

Weiming Wang<sup>1</sup>, Yongli Cai<sup>1</sup> and Huaiping Zhu<sup>2</sup>

<sup>1</sup>*College of Mathematics and Information Science, Wenzhou University, Wenzhou, 325035  
P.R. China*

<sup>2</sup>*Department of Mathematics and Statistics, York University, 4700 Keele Street, Toronto, ON,  
M3J1P3, Canada*

In this talk, we investigate the complex dynamics of a reaction-diffusion S – I model incorporating demographic and epidemiological processes with zero-flux boundary conditions. We give some qualitative properties of the solutions and the condition of the global stability of the disease free equilibrium. By analyzing the corresponding characteristic equations and the Lyapunov function, we show the local and global stability of the epidemic equilibrium. In addition, we show the conditions of Turing instability and give the Turing space in the parameters space. Furthermore, we present novel numerical evidence of typical Turing patterns, and find that the model dynamics exhibits a diffusion-controlled formation growth to stripes, stripes–spots and hot/cold spots pattern replication. Our results indicate that the diffusion has a great influence on the spread of the epidemic and extend well the finding of spatiotemporal dynamics in the epidemic model.

**Key words:** Epidemic model; Dissipation; Persistence; Turing instability; Turing pattern.

*E-mail: weimingwang2003@163.com (W. Wang)*

*caiyongli06@163.com (Y. Cai)*

*huaiping@mathstat.yorku.ca (H. Zhu)*

## **Evolution of population dispersal between patches**

**Wendi Wang**

*Southwest University, China*

*wendi\_wangswu@yahoo.com.cn*

**First, I will review recent advances in the evolution of population migrations. Then I present mathematical models that simulate the evolution population dispersals between patches, and analyze consequences of adaptations by means of analytical method and numerical simulation.**

## **Threshold dynamics for an HIV model melding pharmacokinetics**

**Yanni Xiao**

*Xi'an Jiaotong University, China*

*yxiao@mail.xjtu.edu.cn*

**We investigate an HIV model incorporating the effect of an ARV regimen. Firstly, the periodic drug efficacy, followed by periodic variation in drug concentration during dose intervals, is considered, our model is then a periodic time-dependent system. We get a threshold value between the extinction and the uniform persistence of the disease by applying the persistence theory. The threshold dynamics is in agreement with that for the system with constant coefficients, which extends the classic results for the corresponding autonomous model. Secondly, we meld pharmacokinetics with a viral dynamical model, which results in a piecewise continuous drug efficacy, to investigate how to design the optimal drug administration regimen such that the basic reproductive number for the melded model reaches minimum. We obtain a threshold parameter involving dosage and administration interval which governs the extinction or the uniform persistence of the virus by applying Floquet theory and the comparison theorem of impulsive differential equations.**

## **Dynamics of Infectious Disease models with Delays and Spatial diffusion**

**Rui Xu**

*Shijiazhuang Mechanical Engineering College, China*

*rxu88@yahoo.com.cn*

**In this talk, some recent works on the dynamics of some infectious disease models are introduced. The talk is composed of three parts. First, we study SIR and SEIRS epidemic models with saturation incidence and time delays describing the infection period and latent period, respectively. By using an iteration scheme, sufficient conditions are derived for the global stability of endemic equilibrium of the models above. Second, we study a hepatitis B infection model with saturation incidence and time delay accounting for the time between viral entry into a target cell and the production of new virus particles. By using suitable Lyapunov functionals and the LaSalle invariant principle, it is proved that if the basic reproduction ratio is greater than unity, the chronic-infection equilibrium is globally asymptotically stable. Third, we study a hepatitis B infection model with spatial diffusion of virus and time delay describing the time between viral entry into a target cell and the production of new virus particles. By comparison arguments and by successively modifying the coupled lower-upper solution pairs, the global stability of the uninfected steady state the infected steady state is established. By assuming that the incidence is bilinear, we study the existence of travelling waves to the model above. By using the cross iteration method and the Schauder's fixed point theorem, we reduce the existence of travelling waves to the existence of a pair of upper-lower solutions. By constructing a pair of upper-lower solutions, we derive the existence of a travelling wave connecting the uninfected steady state and the infected steady state.**

## *Contributed Talks*

### **Global asymptotic stability of SIRS models with a class of nonlinear incidence rates and distributed delays**

**Yoichi Enatsu**

*Waseda University, Japan*

*yenatsu@gmail.com*

**In this talk, for SIRS epidemic models with distributed time delays, we establish the global stability of an endemic equilibrium. By using an extension of Lyapunov functional in McCluskey [2], it is shown that the endemic equilibrium is globally asymptotically stable for any rate of immunity loss, if a basic reproduction number of the model is greater than unity and less than or equal to a critical value. Otherwise, there exists a maximal rate of the immunity loss which guarantees the global stability of the endemic equilibrium. This provides a partial answer to an open problem, whether the endemic equilibrium is globally stable whenever it exists.**

#### **References:**

- [1] Z. Jin, Z. Ma and M. Han, Global stability of an SIRS epidemic model with delays, *Acta. Math. Sci.* 26B (2006) 291-306.**
- [2] C.C. McCluskey, Complete global stability for an SIR epidemic model with delay-Distributed or discrete, *Nonl. Anal. RWA.* 11 (2010) 55-59.**
- [3] Y. Nakata, Y. Enatsu and Y. Muroya, Global stability of SIR epidemic models with a wide class of nonlinear incidence rates and distributed delays, accepted in *Discrete and Continuous Dynamical Systems, Series B*.**
- [4] Y. Nakata, Y. Enatsu and Y. Muroya, On the global stability of an SIRS epidemic model with distributed delays, submitted.**

## Mathematical Analysis for Virus Evolution against Specific Immune

Gang Huang

*Shizuoka University, Japan*  
*f5845034@ipc.shizuoka.ac.jp*

During the course of viral infection, evolution of virus is inescapable and relentless. We apply three models to study and compare on evolutionary dynamics of virus in host against immune response. For such general viruses as the hepatitis B virus, the hepatitis C virus, influenza and other infectious agents, the first and second models expose the conditions of competition and coexistence between different strains. In absence of all specific immune responses, only one strain with the maximum basic reproductive number can survive via competitive exclusion principle; When specific immune responses are activated, multiple viral strains can coexist under immune pressure. Accompany new viral successful invasion, the diversity of viruses and the total population of infected cells would increase slowly and continuously. In particular, for human immunodeficiency virus (HIV), since its target cells (CD4+T cells) are also helper cells which support specific immune. HIV impair immune indirectly by infecting healthy CD4+T cell. We construct the third model to describe the interaction between HIV and specific immune response as measured by levels of CD4+T cells. From analysis and simulate our third model, theoretical results purpose that HIV can escape the control of specific immune response by continuous evolution to decrease the level of helper cells. Finally the level of HIV break out and the patient enters into AIDS.

## The spatial patterns and range of competing and coevolving species

Yunxin Huang

*Hubei University, China*  
*yunxin.huang@gmail.com*

Understanding the spatial patterns and rang of interacting species and the underlying ecological and evolutionary mechanisms by which they form has been one of the important topics in theoretical population biology. Here we study the stable patterns and range of two similar species that compete for resources along environmental gradient, mediated by phenotypic evolution. When the environmental gradient is linear across space, three evolutionarily stable patterns are identified where the two species are either completely sympatric, partially allopatric or completely allopatric. When the environmental gradient is nonlinear, with rapid regional changes, two additional stable patterns are identified where the two species are partially allopatric with limited

over-lapping ranges or distributed as spatial mosaics with large overlapping ranges. The ecological and evolutionary mechanisms for these patterns are analyzed by a quantitative genetic model. Results show that nonlinear environmental gradient may promote spatial coexistence of competing species.

## **Quantification of viral dynamics in vitro**

**Shingo Iwami**

*Japan Science and Technology Agency (JST)*

*siwami@ms.u-tokyo.ac.jp*

Recently, we have established in vitro experimental system to quantify viral dynamics by using mathematical model. I am going to show how we design the experiment and estimate viral dynamics. Furthermore, I'd like to discuss possibilities of the "in vitro viral dynamics quantification system" in the future research.

## **A stage-structured predator-prey system with impulsive diffusion**

**Jianjun Jiao**

*Guizhou University of Finance and Economics, China*

*jiaojianjun05@126.com*

In this work, we propose a stage-structured predator-prey model with prey impulsively diffusing between two patches. Using the discrete dynamical system determined by the stroboscopic map, we obtain a predator-extinction periodic solution. Further, the predator-extinction periodic solution is globally attractive. By the theory on the delay and impulsive differential equation, we prove that the investigated system is permanent. Our results indicate that the discrete time delay has influence to the dynamical behaviors of the investigated system.

## Optimal control problem for Malaria in South Korea

Yong han Kang<sup>1</sup> and Kyeongah Nah<sup>2</sup>

<sup>1</sup>*Pusan National University, Republic of Korea*

<sup>2</sup>*Kyungpook National University, Republic of Korea*  
*yonghann@pusan.ac.kr*

We consider about the optimal control problem of Malaria in South Korea. We deal with each different control strategies and compare to the effects about each other control strategy. We illustrate by computer simulations each case.

## The gene regulatory dynamics in complex networks

Shu-ichi Kinoshita

*Meiji University, Japan*  
*kinop0124@gmail.com*

Long time ago, S. A. Kauffman introduced and studies the famous “Random Boolean network model (RBN)” that describes temporal development of state dynamics of a random network. This model has been successful to elucidate many important aspects of the random network dynamics. However, recent developments of gene network study have shown that the gene-gene interaction in living cells is not homogeneous like random network but heterogeneous such as scale-free network. Therefore, we need some generalizations of the RBN. So, we have generalized the RBN to incorporate the various network structures into the models. Using this generalization, I will discuss the above issues.

## **Global stability of a multigroup SIR epidemic model for the geographical spread of influenza**

**Toshikazu Kuniya**

*The University of Tokyo, Japan*

*tkuniya@ms.u-tokyo.ac.jp*

**In this talk, we shall construct a multigroup SIR epidemic model for the geographical spread of influenza and prove that the disease free equilibrium of the model is globally asymptotically stable if the basic reproduction number  $R_0$  is less than or equal to 1, and whereas the endemic equilibrium of the model is so if  $R_0 > 1$ . In particular, although the global stability of the endemic equilibrium had not been established for metapopulation SIR models such as our model, we shall succeed in obtaining the stability result not only by the classical method of Lyapunov functions and the graph theoretic approach recently developed, but also by an original idea of differential inequalities. Numerical simulations shall show the validity of main theorem and simultaneously provide some insights into the geographical spread of influenza.**

## **Barrier Wall Strategy with Transgenic Technologies on Vector-born Diseases Control**

**S. Seirin Lee**

*The University of Tokyo, Japan*

*seirin.lee@gmail.com*

**Vector-borne diseases cause a considerable burden for human health, medical treatments as well as economy. Malaria, transmitted exclusively by Anopheles mosquitoes infected with Plasmodium protozoan parasites, causes the death of more than a million people each year, and over 2 billion people are currently at risk of infection with dengue fever, transmitted by the vector, Aedes aegypti mosquitoes. In order to prevent vector-born diseases, reduction or elimination of vector populations is critically important. Recently, the novel approach for vector controls, techniques for the genetic modification of a number of vector species (ex. mosquitoes) have been developed and provide the means to manipulate the ability of vector mosquitoes transmitting disease. One representative approach for the use of transgenic technologies is the Sterile Insect Technique (SIT) or the Release of Insects carrying a Dominant Lethal (RIDL). Though these control techniques are considered to be environmentally friendly and potential methods, there are little evidence of effectiveness or measurement for control success. Moreover, they have not been widely used against insect disease vectors such as mosquitoes. Thus a theoretical study via mathematical modelling is highly required in advance.**

**In this talk, I will present the barrier wall strategy models of SIT and RIDL in order to prevent the spreading of mosquitoes serving as disease vectors, and discuss the effectiveness of the two techniques and the release efforts of transgenic species (or sterile species) on the availability of control success.**

**\*\* This work was collaborated with E.A. Gaffney (University of Oxford, UK), R.E. Baker (University of Oxford, UK) and S. White (Centre for Ecology & Hydrology, UK).**

## **The influence of branching tunnels on subterranean termites' foraging efficiency**

**Sang-Hee Lee**

*National Institute for Mathematical Sciences, Republic of Korea  
sunchaos@nims.re.kr*

**In my previous study, I constructed a lattice model of termite tunnel pattern to explore the relationship between tunnel geometry and foraging efficiency. The model was based on experimental data obtained from homogeneous soil substrates without food resource. In the present study, I adopted a more general rule in the model to determine branching tunnel lengths. The rule was described by two variables, the probability of tunnel branching,  $P_{branch}$ , and the probability for a branching tunnel to terminate,  $P_{term}$ . With the modified model, I explored the influence of the geometry of branching tunnel on foraging efficiency,  $\gamma$ , for two termite species, *Coptotermes formosanus* and *Reticulitermes flavipes* (Isoptera: Rhinotermitidae). For *C. formosanus*,  $\gamma$  map consisting of the two variables were partitioned in three regions by the level of  $\gamma$  value, while  $\gamma$  for *R. flavipes* was categorized as two regions: higher  $\gamma$  and lower  $\gamma$ . This result was discussed in termite foraging strategy.**

## Evolution of cooperation and network structure

Cong Li and Yi Tao

*Institute of Zoology, Chinese Academy of Science*

*Neill@163.com*

A simple rule for the evolution of cooperation on graphs and social networks developed by Ohtsuki et al. (2006, *Nature*, 44, 502-505) shows that for all graphs including typical cycles, spatial lattices, random regular graphs, random graphs and scale-free networks, natural selection favours cooperation if the altruistic act,  $b$ , divided by the cost,  $c$ , exceeds the average number of neighbours,  $k$ , which means  $b/c > k$ . On the other hand, Santos et al. (2008, *Nature*, 454, 213-216) investigated the emergence of cooperation in public goods game. They introduce the concept of social diversity and show that cooperation is promoted by the diversity. When social ties follow a scale-free distribution, cooperation is enhanced whenever all individuals are expected to contribute a fixed amount. In this research, we focused our attention on how the evolution of cooperation is affected by the network structure. Our main goal is to show whether the evolution of cooperation sensitively depends on the network structure. Many biological, technological and social networks lie somewhere between two extremes which are regular and random networks, respectively. Watts and Strogatz (1998, *Nature*, 393, 440-442) found these systems can be highly clustered, like regular lattices, they have small characteristic path lengths, like random graphs, and they called these networks the ‘small-world’ networks. Barabasi and Albert (1999, *Science*, 286, 509-512) also noticed that a common property of many large networks is that the vertex connectivities follow a scale-free power distribution, i.e.  $P(k) \sim k^{-\gamma}$ , where  $P(k)$  is the probability that a vertex in the network interacts with  $k$  other vertices. Here, we first consider whether the ‘small-world’ networks can promote more effectively cooperation than the regular and random networks (since we notice that the effects of regular and random networks on the evolution of cooperation seems to be same). Secondly, the effect of the scale-free network is also considered.

## **Global stability of delayed multi-group SIRS epidemic models and related problems**

**Yoshiaki Muroya**

*Waseda University, Japan*

*ymuroya@waseda.jp*

Recently, it is known some techniques (see for example, [1]) to obtain sufficient conditions of global asymptotic stability for endemic equilibrium of SIRS epidemic model.

In this talk, we show some applications of these. We first investigate permanence and global stability of a delayed multi-group SIRS epidemic model. Next, we study a multi-group SIRS model which describes the spread of a disease with latency in a heterogeneous host population that assumes an identical natural death rate for all groups and with a gamma distribution for the latency (see [2]). The related problems are also discussed.

### **References:**

- [1] Y. Nakata, Y. Enatsu and Y. Muroya, On the global stability of an SIRS epidemic model with distributed delays. (submitted).
- [2] Z. Yuan and X. Zou, Global threshold property in an epidemic model for disease with latency spreading in a heterogeneous host population. *Nonlinear Analysis: Real World Applications* (2010), doi:10.1016/j.nonrwa.2009.12.008.

## Evolution of learning abilities in the genus Homo

Wataru Nakahashi

*Meiji University, Japan*

*n\_wataru@isc.meiji.ac.jp*

Against the backdrop of human (hominid) evolution in its totality, the evolution of learning abilities is very important. As is well known, the enlargement of the brain was achieved in the genus Homo, and the improvement of learning abilities may be one of the reasons behind it. For example, more complex technologies (e.g., stone tools, bone tools, fire) emerged as the brain of Homo grew larger, and such technologies may have demanded high levels of individual and social learning for their acquisition. A higher level than other species in both individual and social learning is the reason the human (*Homo sapiens*) has cumulative culture. However, the reason high learning levels (large brain) evolved in the human is uncertain. It is sometimes argued that bipedalism caused the enlargement of the brain; however, the brain only started to grow (the genus Homo emerged) a few million years after the advent of bipedalism. As such, bipedalism cannot be cited as the necessary and sufficient condition for the brain to enlarge, although it is probably the necessary condition. What brought on the enlargement of the brain (evolution of high learning abilities) in the genus Homo? I study the effects of environmental change on the evolution of the effectiveness and accuracy of individual and social learning (individual and social learning levels) and the number of pieces of information learned individually and socially (individual and social learning capacities) by analyzing a mathematical model. I show that individual learning capacity decreases and social learning capacity increases when the environment becomes more stable; both decrease when the environment becomes milder. I also show that individual learning capacity increases when individual learning level increases or social learning level decreases, while social learning capacity increases when individual or social learning level increases. The evolution of high learning levels can be triggered when the environment becomes severe, but high social learning level can evolve only when high individual learning level can simultaneously evolve with it. Therefore, if the ancestor of the genus Homo experienced drastic environmental change, the enlargement of brain size in the genus Homo can be explained. From paleoclimatic evidence, African climate became drier about 2-3 million years ago. This climate change might have caused the improvement of learning abilities (the enlargement of the brain) in the genus Homo.

## **Stability analysis of multi-compartment models for cell production systems**

**Yukihiko Nakata**

*BCAM - Basque Center for Applied Mathematics, Spain*

*nakata@bcamath.org*

**We study two- and three-compartment models of a hierarchical cell production system with cell division regulated by the level of mature cells. We investigate the structure of equilibria with respect to parameters as well as local stability properties for the equilibria. To interpret the results we adapt the in ecology well-known concept of reproduction numbers to stem cell population dynamics, where to date it seems unused. In the two-compartment model the positive equilibrium is stable wherever it exists. In the three-compartment model we find that the intermediate stage of differentiation is responsible for the emergence of an instability region in the parameter plane. Moreover we prove that this region shrinks as the mortality rate for mature cells increases and discuss this result.**

**\*\* Joint work with Philipp Getto, Anna Marciniak-Czochra and Tomas Alarcon**

## **Dynamic analysis for a class of two-species population systems with state dependent impulsive effects**

**Linfei Nie**

*Xinjiang University, China*

*lfnie@163.com*

**The study on the dynamic behaviors of population systems with state dependent impulsive effects is the focus and difficulty problems in recent years. In this paper, according to biological and chemical control strategy for population, we construct a class of two-species population systems with state dependent impulsive effects. By using Poincaré map, the analogue of Poincaré's criterion the properties of the Lambert W function, the sufficient conditions for the existence and stability of semi-trivial solution and positive periodic solution are obtained. Numerical results are carried out to illustrate the feasibility of our main results.**

## The optimal control of growth process under environmental stochasticity

Ryo Oizumi

*Hokkaido University, Japan*

*zumi@ees.hokudai.ac.jp*

Organisms resist various risks (such as natural enemy, diseases, competition with other species, the variance of growth rate, etc) in terms of various manners of life history strategies. Above all, it is obtained with mathematical analysis (Tuljapurker, 1990) that variance of growth rate reduces fitness. In fact, it is known that sensitivity of the fitness to each parameter has negative correlation with its variance in some species, by using the transition matrix model (Pfister, 1998). However, there are a few papers that the models include the control of the variance in the life-history strategy. Therefore, we directly derived a theoretical model, which is taken into account the control of the variance in their growth process, from typical demographic models (such as the transition matrix model and integration projection model (Zuidema, et.al 2010)). Then, we present our analysis on the optimal control of variance in their growth process, based on our model.

## Dynamical behavior of a hepatitis B virus transmission model with vaccination

JianHua Pang

*Nanjing Normal University, China*

*pjh968@126.com*

Hepatitis B virus (HBV) infection is a globally health problem. In 2005, the WHO Western Pacific Regional Office set a goal of reducing chronic HBV infection rate to less than 2% among children five years of age by 2012, as an interim milestone towards the final goal of less than 1%. Many countries made some plans (such as free HBV vaccination program for all neonates in China now) to control the transmission HBV. We develop a model to explore the impact of vaccination and other controlling measures of HBV infection. The model has simple dynamical behavior which has a globally asymptotically stable disease-free equilibrium when the basic reproduction number  $R_0 \leq 1$ , and a globally asymptotically stable endemic equilibrium when  $R_0 > 1$ . Numerical simulation results show that the vaccination is a very effective measure to control the infection and they also give some useful comments on controlling the transmission of HBV.

## **Complex dynamics of an epidemic model with targeted antiviral prophylaxis**

**Zhipeng Qiu**

*Nanjing University of Science and Technology, China  
smoller\_1@163.com*

Due to the increasing risk of drug resistance and side effects with large scale antiviral use, it has been suggested to provide antiviral drugs to susceptibles who have had contacts with infectives. This antiviral distribution strategy is referred to as "targeted antiviral prophylaxis". The question of how effective this strategy is in the infection control is of great public health interest. In this paper, we formulate an ordinary differential equation model to describe the transmission dynamics of infectious disease with targeted antiviral prophylaxis, and provide the analysis of dynamical behaviors of the model. The control reproduction number  $R_c$  is derived and shown to govern the disease dynamics, and the stability analysis is carried out. Local bifurcation theory is applied to explore the variety of dynamics of the model. Our theoretical results show that the system undergoes two Hopf bifurcations due to the existence of multiple endemic equilibria and the switch of their stability. Numerical results demonstrate that the system may have more complex dynamical behaviors including multiple periodic solutions and a homoclinic orbit. The results of this study suggest that the use of targeted antiviral prophylaxis may have an important effect on the qualitative behaviors of the disease dynamics.

## **Stochastic Analysis of a Delayed Harrison-type Predator-Prey Model**

**Feng Rao**

*East China Normal University, China  
raofeng2002@163.com*

In this paper, we study a stochastic delay version of the Harrison-type predator-prey model. We firstly analyze the dynamical behaviours of the model. Considering the effect of a noisy environment, the growth rates of the prey and predator are perturbed by Gaussian white noises. Then using Fourier transforms method to calculate population fluctuation intensities of prey and predator species for stochastic delay differential equation model. At last, we give some numerical simulations to illustrate the analytical results.

## **The Impact of Screening for Breast Cancer on the Incidence of the Disease**

**Schehrazad Selmane**

*LAI3. University of sciences and technology of Al, Algerian  
schehrazad.selmane@gmail.com*

**In Algeria, breast cancer is the predominant form of cancer in females and also leading cause of death from cancer among women; accidental and late detection and the organization lack in load taking are the main causes.**

**In this work we present a population model structured by age of women, size and growth rate of the tumour and time elapsed since detection. The impact of screening on the detection of the disease is investigated, and an optimal strategy of periodic mammography is derived.**

## **Three-Dimensional Aggregation Patterns in Keller-Segel Models**

**Hiroto Shoji**

*Kyoto Prefectural University of Medicine, Japan  
shoji@koto.kpu-m.ac.jp*

**Among a number of signaling behaviors ranging from environmental adaptation to biomedical processing in brains, the directed movement of cells and organisms in response to a chemical gradient, chemotaxis, has attracted significant interest due to its critical role.**

**The theoretical and mathematical modeling of chemotaxis has been studied as examples of a movement of cells and organisms. To understand the chemotactic behavior of slime molds, Keller and Segel proposed the mathematical model of a coupled reaction-diffusion equations. In the model, molds move freely and they also move in a direction of a positive gradient of the chemical. On the other hand chemical diffuse with faster diffusion coefficient than one of molds. Besides chemical is produced by molds with a rate and degraded with a rate. We call these systems are Keller-Segel (KS) models. Although KS models have been studied numerically and analytically as simple aggregation models, almost all of the previous investigations were restricted to one or two dimensions because of technical demands and time consumptions. For**

three-dimensional applications of KS model, it is required to understand the mechanisms of pattern formation of KS models.

Here, we investigate three-dimensional aggregation patterns. We will mainly report the results of volume-filling Keller-Segel model, which adopts the population-sensing term where the chemotactic response is switched off at high cell densities by parabolic function. We solved the volume-filling Keller-Segel model numerically in three dimensions. Lamellar, hexagonal, spherical and perforated lamellar patterns are obtained as stable motionless equilibrium patterns. The relative stability of these patterns is studied numerically based on the derived free energy. We will show diversity of obtained results among other KS models.

## Pattern formation and chaos in spatial ecological public goods games

Joe Wakano

*Meiji University, Japan*

*joe@math.meiji.ac.jp*

Cooperators and defectors can coexist in ecological public goods games. When the game is played in two-dimensional continuous space, a reaction diffusion model produces highly irregular dynamics, in which cooperators and defectors survive in ever-changing configurations (Wakano et al. 2009, *Proc.Nat.Acad.Sci.*106:7910-7914). The dynamics is related to the formation of Turing patterns, but the origin of the irregular dynamics is not well understood. In this paper, we first classify the dynamics based on the dispersion relation. The irregular dynamics is discussed in detail by an analysis of the trajectories, the break-down of symmetry, the maximum Lyapunov exponent, and the excitability of the reaction-term dynamics. These results not only support that the observed irregular dynamics exhibit spatio-temporal chaos, but also that the origin of chaos can be attributed to the interplay between two linearly unstable modes. A particular type of chaotic pattern dynamics, which we call intermittent bursts, clearly demonstrates the effects of the two modes.

## Numerical diagnoses of superinfection in chronic hepatitis B viral dynamics

Kaifa Wang

*Third Military Medical University, China*

*kaifawang@yahoo.com.cn*

Fluctuation profile has been observed in chronic hepatitis B patients who are untreated or interrupt therapy. Mathematical model and its parameters could be used to diagnose the assumption of superinfection of hepatocytes and to understand the causes for the spontaneous fluctuation pattern of HBV DNA loads in chronically infected patients. **Methods:** We propose a new conceptual model in terms of chemical kinetics, which is based on the assumption that hepatocytes can be superinfected with hepatitis B virus (HBV). Minimizing the sum of squares of the deviations, we fitted the model to the HBV DNA trajectories from clinical data and obtained the model parameters. **Results:** The model with the fitted parameters can capture the tendency of HBV DNA trajectories. The mean value of the fitted number of virions that enter a single hepatocyte at the beginning stage of an invasion is  $2.10 \pm 0.18$ . The dynamics patterns may correlate with the clinical phenotypes of patients and the value of clinical parameters, such as alpha-fetoprotein (AFP), hepatitis B e-antigen (HBeAg), hepatitis B e-antibody (HBeAb), total bilirubin (TBIL) and alanine transaminase (ALT). **Conclusions:** The superinfection scenario is possible in HBV infection and it may induce HBV DNA fluctuation in the host.

## SVEIR epidemiological model with varying infectivity and distributed delay

Jinliang Wang

*Harbin Institute of Technology, China*

*jinliangwang@hit.edu.cn*

Based on an SEIR epidemic model with distributed infinite delay to account for varying infectivity, we introduce a vaccination compartment, leading to an SVEIR model. We show that the global dynamics are completely determined by the basic reproduction number  $R_0^V$ . More precisely, we prove that, if  $R_0^V \leq 1$ , then the infection-free equilibrium is globally asymptotically stable; if  $R_0^V > 1$ , then there exists a unique endemic equilibrium which is globally asymptotically stable. Our proof of global stability of the equilibria utilizes the method of Lyapunov functionals. Mathematical results suggest that vaccination is helpful for disease control by

decreasing the basic reproduction number. However, there is a necessary condition for successful elimination of disease. If the time for the vaccinees to obtain immunity or the possibility for them to be infected before acquiring immunity can be neglected, this condition will be satisfied and the disease can always be eradicated by some suitable vaccination strategies. This may lead to over-evaluating the effect of vaccination.

## **Global Dynamics of CD4+ T Cells and CTL Immune Responses to HIV Infection**

**Yincui Yan**

*Southwest University, China*  
*yincui@swu.edu.cn*

**In this article, we study a more general mathematical model to describe the dynamics of CD4+ T cells and CTL immune responses to HIV infection. The dynamics of our model is completely determined by the basic reproductive number  $R_0$ . When  $R_0 \leq 1$ , the infection-free steady state is globally asymptotically stable; when  $R_0 > 1$ , the trivial equilibrium loses stability and the infection steady state is globally asymptotically stable.**

## **Impulsive Synchronization for Reaction-Diffusion System**

**Wanli Yang**

*Academy of Armored Forces Engineering, Beijing, China*  
*ywl-math@21cn.com*

**In this paper, an impulsive reaction-diffusion system which arises in mathematical biology as a model of two competitive species which interact each other and migrate under self and cross-diffusion effects is studied. Sufficient conditions are obtained for the global existence of solution for the impulsive system. By considering the equi-attractivity property of the impulsive error system, the impulsive synchronization of the reaction-diffusion system is investigated, and the sufficient conditions leading to the equi-attractivity property are obtained, and a numerical example is given.**

## **Intrinsic transmission global dynamics of tuberculosis with age structure**

**Junyuan Yang**

*Yuncheng University*

*yangjunyuan00@126.com*

**An age-structured epidemiological model for the disease transmission dynamics of TB is studied. We show that the infection-free steady state is locally and globally asymptotically stable if the basic reproductive number is below one, and in this case, the disease always dies out. We prove that the endemic steady state exists when the productive number is above one. In addition, the endemic steady state is globally asymptotically stable if the productive number is above one and death rate due to TB is zero.**

## **Equivalence on finitely generated $R[G]$ module**

**Lijiang Zeng**

*Zunyi Normal College, China*

*zlj4383@sina.com*

**In the article,  $G$ -invariant element and other concepts were introduced, Several lemmas were proved to use these concepts, Finally, the equivalence on the subgroup  $H$  of group  $G$ , finitely generated  $R[G]$  module  $V$ , and others had been proved.**

## **Estimation of the reproduction number for pandemic influenza A (H1N1) in mainland China**

**Yong Zhang**

*Beijing Normal University, China*

*zhangyong@bnu.edu.cn*

**The influenza A H1N1 pandemic in 2009 had significant impacts on our social society and economy. In this paper, we use the data for the outbreak in mainland China to**

determine the reproduction number of the disease and the potential impact of the introduction of control policies. We adopt a susceptible-exposed-infectious-removed (SEIR) compartmental framework to describe the dynamics of influenza A (H1N1). Three methods are derived for estimating the reproduction number of influenza A. Method 1 uses the exponential growth rate  $r$  of the cumulative incidence data to calculate  $R_0$  and gives an estimate of 1.55. Method 2 derives a formula for calculating  $R_0$  based on an extended SEIR model which includes the effect of imported cases from other countries as well as containment strategies (quarantine and isolation), yielding an estimated value of 1.54. Method 3 estimates the time-dependent effective reproduction number  $R_t$  from the weekly data of the new cases. During the course of the epidemic, the value of  $R_t$  is found to fluctuate significantly, with a general decreasing trend as the effects of quarantine and vaccination become evident, such that it eventually drops below 1 towards the end of 2009. This highlights an important premise – the implementation of rapid intervention strategies is vital in preventing large-scale outbreaks of disease.

## Population Dynamics and Strategies of Biological Pest Control

Hong Zhang

*Jiangsu University, China*

*hongzhang@ujs.edu.cn*

We deal with a group of nonlinear differential systems of modeling biological pest control for soybean crops, considering both the cost of application of the control action and profit of harvesting crops, and then numerically compare the qualitative and practical aspects of different release strategies including optimal one-off control, continuous optimal closed-loop control and optimal impulsive control.

## Analysis of stability and bifurcation for an SEIV epidemic model with vaccination and nonlinear incidence rate

Xueyong Zhou

*Nanjing Normal University, China*

*xueyongzhou@126.com*

In this paper, an SEIV epidemic model with vaccination and nonlinear incidence rate is formulated. The analysis of the model is presented in terms of the basic reproduction number  $R_0$ . It is shown that the model has multiple equilibria and using the center

manifold theory, the model exhibits the phenomenon of backward bifurcation where a stable disease-free equilibrium co-exists with a stable endemic equilibrium for a certain defined range of  $R_0$ . We also discuss the global stability of the endemic equilibrium by using a generalization of the Poincare-Bendixson criterion. Numerical simulations are presented to illustrate the results.

## **Adaptive evolution of foraging-related traits in a predator-prey community**

**Jian Zu**

*Meiji University, Japan*  
*zujian122281@yahoo.com.cn*

On the population dynamical timescale, two predators with linear functional responses can coexist on two competing prey. In this talk, with the methods of adaptive dynamics and critical function analysis, we will discuss under which conditions such coexistence is also evolutionarily stable, and whether the two predator types evolve from a single ancestor via evolutionary branching. We assume that predator strategies differ in capture rates. Specialization on one prey type is assumed to go at the expense of specialization on another. First, by using the method of critical function analysis, we identify the characteristics of trade-off function that allow for evolutionary branching in predator strategy. Generally, if there is a small switching cost near the singular strategy, then this singular strategy is an evolutionary branching point, in which predator population will change from monomorphism to dimorphism. Second, we find that after branching in predator phenotype, if the trade-off curve is globally convex, then predator population will eventually branch into two extreme specialists, each completely specializing on a particular prey species. However, if the trade-off curve is concave-convex-concave, then the two predator types will evolve to an evolutionarily stable dimorphism at which they can continue to coexist. The analysis reveals that an attractive dimorphism will always be evolutionarily stable and that no further branching is possible under this model.

## **Poster Presentations**

### **Mathematical model and control strategy for resource recovery of sailfin sandfish, *Arctoscopus japonicus*, in Korea East Sea**

**Gi Phil Cho**

*Pusan National University, Republic of Korea*

*yogof@naver.com*

The biomass of *Arctoscopus japonicus* was estimated at approximately 15000mt in 1991 but since 1994 decreased to below 7000mt by 2001 in Korea East Sea. We consider that overfishing for juvenile and a spawning ground damage of climate change caused resource to decrease. We propose to mathematical model for the population dynamics of *Arctoscopus japonicus* and simulate to two control strategy, catch limitation for juvenile and construct of a spawning ground, for resource recovery.

### **A Novel Approach to Characterize the Behavioral Shape of *Caenorhabditis elegans***

**Yeontaek Choi, Won-ju Jeon, Tae-Soo Chon, and Sang-Hee Lee\***

*Division of Fusion Convergence of Mathematical Sciences,*

*National Institute for Mathematical Sciences, Republic of Korea*

*ytchoi@nims.re.kr*

In recent, the behavioral movement of *Caenorhabditis elegans* has been extensively studied in various aspects from individual to population level. Most studies necessarily required the methods for characterizing the movement patterns of the organism in order to reveal the relationship between the behavior and the neural system. In the present study, we suggested a new approach to characterize the movement patterns of the organisms based on a “branching length similarity” (BLS) entropy. This entropy is defined on a simple branching network consisting of a single node and branches. The organism’s movement shape was recorded, and 13 points with equal interval were extracted from the shape. We formed simple networks by neighbor-joining of the points, acting as nodes, and computed BLS entropy for line and angle. The results showed that our method based on BLS entropy is successful to characterize the organism’s behavioral shape. In addition, we briefly discussed the application of the method to biomonitoring system.

**Keywords:** behavioral analysis, shape pattern, BLS entropy, *C.elegans*

## **A primitive model for the population dynamics of mutualism**

**Shinichiro Higa**

*Shizuoka University, Japan*

*f0030287@ipc.shizuoka.ac.jp*

The population dynamics provides important results for various fields of life sciences. The most famous model dealing with species interactions is Lotka-Volterra equations. Although this model is useful for the relations of prey-predator and competition, it fails for mutualistic interaction. In the present paper, we present a primitive model for the population dynamics of mutualism. First, our attention is paid on "correspondence principle" between individual based models on a lattice and their mean-field theories. For example, basic lattice models for prey-predator or competition systems are called lattice Lotka-Volterra models: this is because their mean-field theories becomes equivalent to the Lotka-Volterra equations. Second, on the basis of the correspondence principle, we build a primitive mutualistic model of population dynamics. The most useful result of this model is the Allee effect for obligatory mutualisms.

## **Global dynamics of a discretized SIRS epidemic model with time delay**

**Emiko Ishiwata**

*Tokyo University of Science, Japan*

*ishiwata@rs.kagu.tus.ac.jp*

We derive a discretized SIRS epidemic model with time delay by applying a nonstandard finite difference scheme. Sufficient conditions for the global dynamics of the solution are obtained by improvements in discretization and applying proofs for continuous epidemic models. These conditions for our discretized model are the same as for the original continuous model.

**\*\*This is a joint work with Sekiguchi Masaki.**

## **Graph-Theoretical Analysis on Foraging Strategy of Subterranean Termites**

**Wonju Jeon and Sang-Hee Lee**

*Division of Fusion Convergence of Mathematical Sciences,*

*National Institute for Mathematical Sciences, Republic of Korea*

*wjeon@nims.re.kr*

For the purpose of searching and transporting food, subterranean termites excavate tunnels which result in a complex network below the ground. It is important to understand termites' tunneling strategy from the environmental aspects as well as the academic viewpoints. Previous studies have investigated the relationship between termite branch tunnel geometry and foraging efficiency using a simulation model for two termite species, *Coptotermes formosanus* and *Reticulitermes flavipes*, by changing two parameters - the probability of tunnel branching ( $P_{branch}$ ) and the probability of tunnel branch termination ( $P_{term}$ ). In the present study, the connectedness of the network is explored by using spectral graph theory. In the theory, a tunnel network is expressed by a matrix and the second smallest eigenvalue of the matrix reflects the degree of connectedness. We discuss the results in relation to foraging efficiency evaluated in the previous study. It is found that the best simulated strategy for *C. formosanus* and *R. flavipes* termites is to increase both  $P_{branch}$  and  $P_{term}$ .

## **Influenza Vaccine Allocation Strategies**

**Byul Nim Kim**

*Kyungpook National University, Republic of Korea*

*air1227@knu.ac.kr*

We develop a deterministic, age-structured compartmental model of influenza transmission and compare mortality-based strategies with morbidity-based strategies.

## Measuring the Time Spent for a Termite to Pass Tunnel Intersections

Sook Jung Ku and Sang-Hee Lee

*Division of Fusion Convergence of Mathematical Sciences,*

*National Institute for Mathematical Sciences, Republic of Korea*

*sjku0123@nims.re.kr*

Subterranean termites build complex tunnel networks below the ground for foraging. During the foraging activity, termites are more likely to encounter a lot of tunnel intersections. It is important for termites to select their direction at the intersections for their survival because depending on their selection, the path length from food resources to the nest can vary significantly. In our previous study, we revealed the relationship between tunnel width and the directional preference. In the present study, we focused our attention on the time,  $\tau$ , spent for a termite to pass the intersection in order to understand why termites have the directional preference in terms of traffic cost caused by tunnel geometry. To do so, we observed termite behavior at the right-angled tunnel intersections with the width of W1 and W2 (W1 and W2; 2, 3, or 4mm) and measured  $\tau$  for different directional selection, left, right, and straight. For the combinations of W1 and W2, (W1, W2) = (2, 2), (3, 3), (2, 3), (2, 4) and (4, 3), the passing time,  $\tau$ , was almost same regardless of directions. For (W1, W2) = (4, 4), (3, 2), and (4, 2),  $\tau$  was relatively shorter in advancing straight direction than in turning left or right. On the other hand, when (W1, W2) = (3, 4),  $\tau$  was statistically longer when termites take straight direction in comparison with other directions at the intersection. We briefly discussed the meaning of the results in terms of the traffic cost and foraging efficiency.

**Keyword:** Termite traffic cost, Tunnel intersection, Directional selection, Foraging efficiency, Termite tunnel network

## **Mathematical analysis of a host-vector model with pine wilt disease**

**Kwang Sung Lee**

*Pusan National University, Republic of Korea*

*ksl@pusan.ac.kr*

**In this talk, we propose a mathematical host-vector model of pine wilt disease which spread by vectors such as *Monochamus alternatus* and analyze it mathematically. It is shown that the stability of the equilibria in the proposed model can be controlled by the basic reproduction number for the vector-host model.**

## **Behavioral Analysis of Fish Schooling Behavior**

**Joo Baek Leem, Yeontaek Choi and Sang-Hee Lee**

*Division of Fusion Convergence of Mathematical Sciences,*

*National Institute for Mathematical Sciences, Republic of Korea*

*jbleem@nims.re.kr*

**The schooling behavior of the fish, *Oryzias latipes* (Medaka), was examined in a circular water tank with 100 cm diameter and 30 cm height for 4 hrs. The water depth was 5 cm in consideration of fish body length (~ 5 cm), which in turn confined fish movement to quasi-two dimension. The swimming behavior of individuals was recorded by digital camcorder and statistically analyzed by extracting individual location from the recorded movies. We investigated a few relevant quantities such as mean distance among individuals and mean velocity of fishes of each schooling group, which is useful for numerical modelling for fish schooling behavior.**

**Keywords: Medaka, schooling behavior, video analysis, physical variables**

## **Disease pathogen model on clonal plants using contact process**

**Yuma Sakai**

*Hokkaidou university, Japan*

*sakai@ees.hokudai.ac.jp*

**Clonal plants reproduce the same individual as old stock. by vegetative organ Therefore if some individual is infected with pathogen, populations are more likely to extinction by spread throughout population. So I use contact process that express the process of disease propagation to think the quality. In this model, each site on graph is occupied by healthy or infected host, and healthy host is infected at propagation rate in proportion to number of infected host of nearest-neighbors of a site.**

**In my research, plant populations exist on site of two-dimensional square lattice. Then we express the reproduction process of plant and propagation process of disease, and analyzing by pair approximation and computer simulation. In the result we can output the pattern of distribution of plant and survival rate of healthy host.**

## **Can spatial interaction with Allee effects promote dynamical complexity?**

**Kazunori Sato**

*Shizuoka University, Japan*

*sato@sys.eng.shizuoka.ac.jp*

**Hui & Li (2004) analysed metapopulation dynamics with Allee effects, which showed some interesting results such as chaotic dynamics or spatial distribution. Unfortunately, however, it is not clear whether the results come from Allee effects themselves or not because of their unique calculation techniques.**

**In my presentation I discuss several problems concerned with it, and show another example of well-defined spatially explicit model including Allee effects.**

## **Evaluation on efficiency of BCG vaccination for the prevention of tuberculosis epidemics**

**Kojiro Tanaka**

*Graduate School of Engineering, Shizuoka University, Japan  
f0030279@ipc.shizuoka.ac.jp*

**Tuberculosis (TB) is regarded as the most cause of death from infectious diseases. The number of tuberculosis patients increase about 9 million, and 2 million people are killed yearly. Especially the situation in Asia and Africa are critical. Besides, one third of the world's population is estimated that they are infected with Mycobacterium tuberculosis to be the pathogen of TB. As a way to prevent tuberculosis, Bacillus Calmette-Guerin (BCG) vaccination has been used in many places around the world. In this paper, we construct a mathematical model of the dynamics of tuberculosis infection, and we evaluate the effectiveness of BCG vaccination.**

## **Coexistence in Prey-Predator Chemostat Model with Single Nutrient**

**Hiroki Yokoi**

*Shizuoka University, Japan  
f5945038@ipc.shizuoka.ac.jp*

**The chemostat is a laboratory apparatus used for the continuous culture of microorganisms and has played an important role in microbiology and population biology. For the competition of simple chemostat model, coexistence of several organisms for a single nutrient cannot occur. It is also known that multiple competitors can coexist under the predation pressure in real ecosystems.**

**This presentation shows that it is possible for multiple competitors to coexist with a predator also in chemostat.**