



北京国际数学研究中心
BEIJING INTERNATIONAL CENTER FOR
MATHEMATICAL RESEARCH

Mini-Workshop on Mathematical Biology

Dates:

June 28: Registration;
June 29: Round-table discussion;
June 30: Workshop

Venue:

June 29: Room 82J13, Jiayibing Building, Jingchunyuan 82, BICMR
June 30: 77201, JingChunYuan No. 78, BICMR, Peking University

Organizers:

Lei Zhang (Peking University)
Qing Nie (Peking University & UC Irvine)

Workshop Program(6.29)

Morning Session	
Time	Activities
9:00-12:00	Round-table discussion
12:00-14:00	Lunch
Afternoon Session	
Time	Activities
14:00-17:00	Free discussion
18:00	Dinner





Workshop Program(6.30)

Morning Session		
Chair: Qing Nie		
Time	People	Titles /Activities
8:50-9:00	Opening remarks	
9:00-9:40	Xinfeng Liu (U. of South Carolina)	Computational studies for Her2 signaling during cancer tumor growth
9:40-10:20	Jinzhi Lei (Tsinghua University.)	TBA
10:20-10:40	Coffee Break	
Chair: Lei Zhang		
10:40-11:20	John Glasser (Centers for Disease Control)	Realistic mixing functions for meta-population modeling to support public health policymaking
11:20-12:00	Zhilan Feng (Purdue University)	Using the partial derivatives of effective reproduction numbers to guide public health policy
12:00-14:00	Lunch	
Afternoon Session		
14:00-17:00	Free discussion	
18:00	Dinner	





Abstract

- **Computational studies for Her2 signaling during cancer tumor growth**

Xinfeng Liu (University of South Carolina)

Abstract: Solid tumors are heterogeneous in composition. Cancer stem cells (CSCs) are a highly tumorigenic cell type found in developmentally diverse tumors that are believed to be resistant to standard chemotherapeutic drugs and responsible for tumor recurrence. Thus understanding the tumor growth kinetics is critical for development of novel strategies for cancer treatment. For this talk, I shall introduce mathematical modeling to study Her2 signaling for the dynamical interaction between cancer stem cells (CSCs) and non-stem cancer cells, and our findings reveal that two negative feedback loops are critical in controlling the balance between the population of CSCs and that of non-stem cancer cells. Furthermore, the model with negative feedback suggests that over-expression of the oncogene HER2 leads to an increase of CSCs by regulating the division mode or proliferation rate of CSCs.

- **Realistic mixing functions for meta-population modeling to support public health policymaking**

Zhilan Feng (Purdue University, West Lafayette, Indiana), Andrew N. Hill, Aaron T. Curns and John W. Glasser[†] (Centers for Disease Control and Prevention, Atlanta, Georgia)

When model populations are stratified, contacts among their respective sub-populations must be described. Using a simple meta-population model, we showed that mixing among sub-populations, as well as heterogeneity in characteristics affecting their reproduction numbers, must be considered when evaluating interventions to prevent or control infectious disease outbreaks. We employed the convex combination of preferential within- and proportional among-group contacts first described by Nold and subsequently generalized by Jacquez and colleagues. As the utility of meta-population modeling in support of public policymaking depends on more realistic mixing functions, we included preferential contacts between parents and children and among co-workers as well as contemporaries. Here we add preferential contacts between grandparents and grandchildren, but omit workplace contacts. We also describe a general multi-level mixing scheme and provide several two-level examples. We describe age- and gender-specific patterns in face-to-face conversations, proxies for contacts by which respiratory pathogens might be transmitted. And we discuss how meta-population models with multi-generational mixing could be employed to reevaluate prolonged school-closures, a proposed pandemic mitigation measure.





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- **Using the partial derivatives of effective reproduction numbers to guide public health policy**

Zhilan Feng[†] (Purdue University, West Lafayette, Indiana), Andrew N. Hill, Aaron T. Curns and John W. Glasser (Centers for Disease Control and Prevention, Atlanta, Georgia)

Because the average number of secondary infections per infectious primary, called the effective reproduction number and denoted \mathfrak{R} , must exceed one for an outbreak, public health authorities endeavor to reduce $\mathfrak{R} \leq 1$. Depending on one's model, it may be possible to derive an explicit expression for \mathfrak{R} via the next-generation matrix approach of van den Driessche and Watmough (Math Biosci 2002; 180:29-48). If so, one can take its partial derivatives with respect to control parameters (Feng et al. J Theor Biol 2009; 259:165-171). But if not, one can determine their respective effects numerically. These expressions describe not only the alternative routes by which policymaking goals might be attained, but magnitudes of their respective effects and potential for effect modification. In meta-population models, the corresponding multivariate partial derivative is the gradient, a vector-valued function that Feng et al. (J Theor Biol 2015; 386:177-87) proposed as a new tool for devising optimal vaccination strategies. Using an SEIR model of pandemic influenza with 7 age groups, 51 spatial strata (states plus the District of Columbia) and a suitable two-level mixing function, we used the gradient to compare optimal and actual vaccination during the 2009-10 influenza pandemic in the United States (Feng et al. Math Biosci 2017; 287:93-104). We also showed that vaccination efforts could have been adjusted month-to-month during the fall of 2009 to ensure maximum impact. Together with colleagues at the China CDC, we are using this model to identify the optimal strategies for eliminating measles and controlling rubella in China.

[†]presenter

