附：报告摘要与专家介绍

Modeling of dynamics and control of infectious diseases: latency and interactions

Jacques Bélair (Université de Montréal, Canada)

In investigating the dynamics of a disease such as COVID-19, its mathematical representation can be constructed at many levels of details, guided by the questions the model tries to help answer. Mathematical sophistication may have to yield to a more pragmatic approach closer to the ability to make predictions that inform public health policies. With that in mind, I will present circumstances in which benefit can be gained from the explicit incorporation of latent period, for both short- and long-term predictions.

Jacques Bélair is Full Professor in the department of mathematics and statistics at Université de Montréal, which he joined in 1983 as an Assistant Research Professor. He had previously obtained a PhD in applied mathematics from Cornell University (supervisor: Philip J Holmes) and worked as an NSERC postdoctoral fellow in the Department of Physiology at McGill University (supervisor: Leon Glass). He has served as associate director of the Centre de recherches mathématiques (CRM) and was also vice-dean of the Faculty of Graduate and Postdoctoral Studies; he was President of the Canadian Applied and Industrial Mathematics Society (CAIMS) from 2009 to 2011, and co-chaired the Organizing Committee of the Annual Meeting of the Society for Mathematical Biology (SMB) in 2019.

His research concerns mathematical modeling of dynamic regulatory processes in biology. In the past, he has been interested in various aspects of cardiac arrhythmias and motor control; currently, he is studying the control of blood cell production (hematopoiesis) and associated pharmaceutical interventions, and the propagation of infectious diseases in general, and COVID-19 in particular. He is affiliated with the Centre for Disease Modeling (CDM) based at York University and the Centre for Applied Mathematics in Bioscience and Medicine (CAMBAM) of McGill University.

(www.dms.umontreal.ca/~belair)

Analysis of transmissibility of COVID-19 and regional differences in disease control

Wendi Wang (Southwest University, China)

Based on the data on the first 425 confirmed cases in Wuhan from December 10, 2019 to January 4, 2020, we use the Maximum Likelihood Estimate method to obtain the basic reproduction number of COVID-19 outbreaks, which is 2.42, and the mean serial interval, which is 8.85 days. In order to characterize the regional differences in the transient transmission capacity of the disease, the daily report data of cities in Hubei province and the other provinces and cities in China were used to obtain an estimated daily basic reproduction number of each region in February 2020 on the basis of the statistical model. Further, we define a new epidemic control effectiveness formula based on the instantaneous reproduction number, and qualitatively evaluates the influence of the control strategies adopted in each region on the real-time transmission capacity of COVID-19. The results indicate that the risk of recurrence of the domestic epidemic is still high due to the imported cases at this stage, and there are obvious regional differences in the spread of COVID-19, but the factors that cause the differences deserve further follow-up.

王稳地，西南大学数学与统计学院教授，博士生导师，中国生物数学学会副理事长，2005年获得重庆市名师称号，2018年获得重庆市最美教师称号；从事生物数学的研究，在种群动力学和传染病动力学建模和分析方面发表论文100多篇，五次入选 Elsevier 数学类高引用论文作者，已经主持国家自然科学基金课题6项、教育部项目2项，目前担任两个国际刊物编委。

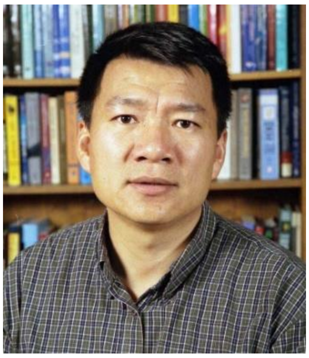
Challenges in real-world modeling: nonindentiability issues and model selection

Michael Li (University of Alberta, Canada)   myli@ualberta.ca

The disease modeling communities around the world have been actively participated in model projections for COVID-19 epidemics. Some of the lessons we have learned during this process are common to other modeling exercises of real-world diseases that use public health data: models are used to interpret the data and make short-term predictions that aim to inform public health policy. Traditional training in theoretical mathematical epidemiology focuses on long-term behaviours using tools of stability and bifurcation analysis. The approach is often to incorporate more epidemiological complexities into models and look for more interesting dynamics.

The goal of theoretical modeling is to categorizes the entire parameter space into different regions of qualitatively distinct dynamics. Real-world disease modeling such as modeling the COVID-19 epidemics has a very different nature: (1) the problem is more quantitative and finite time, so the stability concept and analysis are often not applicable; (2) we are looking for a set or a range of parameter values for which the model best describes the observed data with noises, so that bifurcation analysis is often not the goal; (3) The same model with different parameter values can give very different projections, so a model should be judged together with its specific set of parameter values rather than only by its model structure; and (4) the best model may not be the most realistic, so it is important to select the best model among a collection with a varying degree of complexity.

In this talk, I focus on two fundamental challenges to real-world modeling of infectious diseases. The first one is why should we and how do we select the best-performing model among a collection of nested models with different complexity. The second is the nonidentifiablity problem in which infinitely many sets of parameter values can produce the same representation of the observed data while giving very different future predictions. These challenges need to be rigorously addressed by the modeling community for disease models to be a reliable tool for public health research.



Michael Li is a Professor of Mathematics at the University of Alberta, Canada. His research interests expertise are in the theory and applications mathematical modeling of infectious diseases in general, and of HIV, influenza and Tuberculosis in particular, viral dynamics and immune responses dynamics to viral infections including HIV-1 and HTLV-1. Professor Li obtained his PhD in Applied Mathematics at the University of Alberta and did his postdoctoral training at the University of Montreal and Georgia Institute of Technology. He has been a faculty member at the University of Alberta since 2000, where he actively collaborate with research groups in the faculty of medicine and at the Alberta Ministry of Health on modeling research in health and public health sciences.

区域的两种演化及病毒的扩散特征
Two kinds of regional evolution and the spreading characteristics of viruses

Zhigui Lin (Yangzhou University, China)

区域的演化分为两种：已知的和未知的. 前者通常是环境引起，后者是种群自身发展的要求. 首先考虑周期演化区域上的 Logistic 种群扩散问题，给出基本再生数，得到演化率对种群扩散的影响；再研究自由变化区域上的 Logistic 种群扩散问题，给出扩张-灭绝二择一结果和扩张时的渐近速度；然后介绍自由变化区域上的 SIS 传染病模型，给出时空风险指标；最后给出一些与新冠病毒空间扩散有关的思考.

林支桂，扬州大学二级教授、博士生导师、中国数学会生物数学专业委员会副主任、《生物数学学报》和《Int. J. Biomath.》杂志编委。曾赴丹麦科技大学留学一年，在韩国浦项科技大学作博士后研究。多次应邀到丹麦科技大学、 Roskilde 大学、新加坡国立大学、韩国浦项科技大学、高丽大学、澳大利亚 New England 大学、加拿大 York 大学等作短期学术访问。从事应用数学方面的研究，已出版专著一部，发表论文100余篇。主持国家自然科学基金8项、省部级项目6项。