2020中国人民大学—生物数学最新进展学术研讨会

会议主题：为了推动数学与其它相关学科交叉研究的发展，交流生物数学相关领域的最新研究成果和学术发展动态，促进学术交流与合作，中国人民大学数学科学研究院将于2020年11月7-8日、11月14日以腾讯会议形式在线上举办“生物数学最新进展学术研讨会”。 本次会议将分两个主题：

I. **种群动态和传染病动态模型**（**11月7-8日**）;

II. **生物医学模型**（**11月14日**）.

本次会议将围绕生态学、生命科学、生物医学等领域的实际问题，深入探讨数学与数据在生物、生态、医学领域相关系统理论研究中的重要作用，通过问题驱动的理论与应用研究促进生物数学的发展。

学术委员会：（以姓氏拼音为序）

崔景安（北京建筑大学） 韩丽涛（中国人民大学） 靳 祯 （山西大学）
雷锦志（天津工业大学） 楼 元 （俄亥俄州立大学） 马万彪（北京科技大学）
唐三一（陕西师范大学） 肖燕妮（西安交通大学） 邹幸福（西安大略大学）

组织委员会： 韩丽涛（中国人民大学） 赖秀兰（中国人民大学）

会议形式：腾讯会议
11月07日（会议 ID：497 926 150，会议密码：1107）
11月08日（会议 ID：147 147 057，会议密码：1108）
11月14日（会议 ID：500 904 107，会议密码：1114）

主办单位：中国人民大学数学科学研究院

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主题 I．种群动态和传染病动态模型（11月7-8日）

2020年11月7日，周六		
会议 ID：497 926 150，会议密码：1107		
08:30-08:45	开幕式	
时间	**报告人**	**报告题目**
主持人：楼 元		
08:45-09:25	肖燕妮	Effect of spatial and temporal heterogeneity on disease transmission dynamics
09:25-10:05	范 猛	COVID-19动力学建模：资源有限性的影响
茶歇 10:05-10:15		
主持人：马万彪		
10:15-10:55	赵洪涌	Modeling and dynamics of Zika transmission with contaminated aquatic environments
10:55-11:35	刘胜强	On the asymptotic behaviour of traveling wave solution for a discrete diffusive
午休 11:35-14:00		
主持人：宋新宇		
14:00-14:40	刘贤宁	An age-structured mathematical model on mumps outbreaks in Jiangsu province, China
14:40-15:20	原三领	Noise-induced transitions in a nonsmooth producer–grazer model with stoichiometric constraints
茶歇 15:20-15:30		
主持人：娄 洁		
15:30-16:10	徐 瑞	Mathematical analysis and application of a cholera transmission model with waning vaccine-induced immunity
16:10-16:50	祖 建	宿主抵抗力多样性的演化动力学模型研究
16:50-17:30	王 霞	HIV low viral load persistence under treatment: Insights from a model of cell-to-cell viral transmission

主题 I．种群动态和传染病动态模型(11 月 7-8 日)

2020 年 11 月 8 日，周日		
会议 ID：147 147 057，会议密码：1108		
时间	**报告人**	**报告题目**
主持人：邹幸福		
08:30-09:10	崔景安	新发传染病传播动力学模型在新冠肺炎传播中的应用
09:10-09:50	唐三一	Modeling the impact of air pollution on respiratory infection risk in China
09:50-10:30	靳 祯	A stochastic model explains the periodicity phenomenon of influenza in network
茶歇 10:30-10:40		
主持人：张凤琴		
10:40-11:20	林支桂	周期演化区域、自由变化区域和有向图上的扩散
11:20-12:00	李学志	Coinfection dynamics of heroin transmission and HIV infection in a single population
午休 12:00-14:00		
主持人：高道舟		
14:00-14:40	黄继才	Global dynamics of a susceptible-infectious-recovered epidemic model with a generalized nonmonotone incidence rate
14:40-15:20	张天然	Traveling waves for a nonlocal viral infection dynamical model
茶歇 15:20-15:30		
主持人：赖秀兰		
15:30-16:10	黄启华	Spread rates of a juvenile-adult population in constant and temporally variable environments
16:10-16:50	高道舟	Effects of human movement on disease persistence and disease prevalence

主题 II. 生物医学模型(11 月 14 日)

2020 年 11 月 14 日，周六		
会议 ID：500 904 107，会议密码：1114		
08:20-08:30	致辞	
时间	**报告人**	**报告题目**
主持人：裴永珍		
08:30-09:10	王稳地	前列腺癌治疗动力学模型
09:10-09:50	雷锦志	From single-cell based modeling to population dynamics
09:50-10:30	邹秀芬	Quantitative integration of radiomic and genomic data improves survival prediction of low-grade glioma patients
茶歇 10:30-10:40		
主持人：韩丽涛		
10:40-11:20	何泽荣	具有个体等级差异的群落生态模型分析与控制
11:20-12:00	李建全	Dynamics of a structured predator-prey system with predator cannibalism
午休 12:00-14:00		
主持人：		
14:00-14:40	王开发	长效聚乙二醇干扰素治疗下慢性乙肝患者 HBsAg 水平动力学：一项基于医院的真实世界数据分析
14:40-15:20	李春贺	Landscape and flux quantify the stochastic transition dynamics for p53 cell fate decision
茶歇 15:20-15:30		
主持人：		
15:30-16:10	周 达	Modeling tissue hierarchical architecture
16:10-16:50	孙小强	肿瘤耐药的组学数据分析和数学建模
16:50-17:30	赖秀兰	Mathematical modeling about the scheduling of combination cancer therapy with immune checkpoint inhibitors

报告题目与摘要

（以姓氏拼音为序）

主题 I. 种群动态和传染病动态模型(11 月 7-8 日)

新发传染病传播动力学模型在新冠肺炎传播中的应用

崔景安 北京建筑大学

摘要：针对新冠肺炎等新发传染病传播动力学模型的实际应用问题，提出了与确诊病例实时数据相关联的接触数，优化了新发传染病传播动力学模型，提升了模型的实用价值。 把实时数据信息应用于模型参数估计，并将动力学模型应用于预估广州、武汉的新冠肺炎传播的峰值、最终规模、达峰时间。 这类接触数可推广应用于其他一些新发传染病，揭示其暴发过程中不同时期的传播风险。

COVID-19 动力学建模：资源有限性的影响

范猛 东北师范大学

摘要：介绍我们最近在 COVID-19 动力学建模方面的一些研究工作，着重考虑医疗资源有限性对疫情传播与防控的影响，以及在研究中的一些思考。

Effects of human movement on disease persistence and disease prevalence

高道舟 上海师范大学

Abstract: In this talk, based on an SIS patch model with standard incidence, we first show that the basic reproduction number of the model is either strictly decreasing and strictly convex with respect to the diffusion coefficient of infected subpopulation if the patch reproduction numbers of at least two patches in isolation are distinct or constant otherwise. Biologically, it means that fast diffusion of the infected people reduces the risk of infection. This completely solves and generalizes a conjecture by Allen et al. (SIAM J Appl Math, 67: 1283-1309, 2007). Then we give some general results on the local and global disease prevalence at the endemic equilibrium. For the two-patch submodel, a complete classification of the model parameter space as to when dispersal causes more or less infections than no dispersal is obtained. Particularly, fast diffusion always decreases the basic reproduction number but may increase the overall disease prevalence, highlighting the necessity of evaluating control measures with other quantities besides the basic reproduction number.

Global dynamics of a susceptible-infectious-recovered epidemic model with a generalized nonmonotone incidence rate

黄继才 华中师范大学

Abstract: A susceptible-infectious-recovered (SIRS) epidemic model with a generalized nonmonotone incidence rate is considered. It is shown that the basic reproduction number R_0 does not act as a threshold value for the disease spread anymore, and there exists a sub-threshold value R_*(<1) such that: (i) if R_0<R_*, then the disease-free equilibrium is globally asymptotically stable; (ii) if R_0=R_*, then there is a unique endemic equilibrium which is a

nilpotent cusp of codimension at most three; (iii) if R_*<R_0<1, then there are two endemic equilibria, one is a weak focus of multiplicity at least three, the other is a saddle; (iv) if R_0 ≥ 1, then there is again a unique endemic equilibrium which is a weak focus of multiplicity at least three. As parameters vary, the model undergoes saddle-node bifurcation, backward bifurcation, Bogdanov-Takens bifurcation of codimension three, Hopf bifurcation, and degenerate Hopf bifurcation of codimension three.

Spread rates of a juvenile-adult population in constant and temporally variable environments

黄启华　西南大学

Abstract: The question of how growth, dispersal, and environmental factors affect the persistence and spread of an invasive species is of great importance in spatial ecology. Motivated by the fact that in a species, different development stages may have different vital rates and dispersal characteristics, we propose and study a reaction-diffusion juvenile-adult model, which is a natural extension of the classical Fisher's equation. We investigate the spread rates of the population if persistent. By comparing our juvenile-adult model with the physically unstructured Fisher model, we find that Fisher equation can be approximated by our juvenile-adult model in several ways. Accordingly, the spreading speed for Fisher's model represents a special case of that for the juvenile-adult model. We analyze how the vital rates and different dispersal abilities between juveniles and adults influence the spreading spread of the structured population, the results indicate that the juvenile-adult model provides more insights into population spread than Fisher equation. We then study a reaction-diffusion juvenile-adult model with temporally periodic coefficients. We develop a novel numerical method to calculate the spreading speed under temporal variability. Finally, we utilize the time-periodic model to understand the spatial spread of a population with separate breeding and non-breeding seasons. In particular, we scrutinize how the seasonal variation in vital rates and dispersal rates, and the duration of the breeding season affect the spreading speed of the population. The theory developed here can provide effective strategies to control the spread of invasive species.

A stochastic model explains the periodicity phenomenon of influenza in network

靳祯　山西大学

Abstract: Influenza is an infectious disease with obvious periodic changes over time. It is of great practical significance to explore the non-environment-related factors that cause this regularity for influenza control and individual protection. In this talk, based on the randomness of population number and the heterogeneity of population contact, we have established a stochastic infectious disease model based on the degree of the network, and used the van Kampen expansion method to obtain the power spectral density function of the main equation. The relevant parameters were obtained by fitting the influenza data of Sentinel hospitals.

Coinfection dynamics of heroin transmission and HIV infection in a single population

李学志　河南师范大学

Abstract: We propose a model of a joint spread of heroin use and HIV infection. The unique disease-free equilibrium always exists and it is stable if the basic reproduction numbers of heroin use and HIV infection are both less than 1. The semi-trivial equilibrium of HIV infection (heroin use) exists if the basic reproduction number of HIV infection (heroin use) is larger than 1 and it is locally stable if and only if the invasion number of heroin use (HIV infection) is less than 1. When both semi-trivial equilibria lose their stability, a coexistence equilibrium occurs, which may not be unique. We compare the model to US data on heroin use and HIV transmission. We conclude that the two diseases in the US are in a coexistence regime. Elasticities of the invasion numbers suggest two foci for control measures: targeting the drug abuse epidemic and reducing HIV risk in drug-users.

周期演化区域、自由变化区域和有向图上的扩散

林支桂　扬州大学

摘要：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；最后介绍描述新冠病毒的有向图上的扩散.

On the asymptotic behaviour of traveling wave solution for a discrete diffusive epidemic model

刘胜强　天津工业大学

Abstract: A recent paper [Y.-Y. Chen, J.-S. Guo, F. Hamel, Traveling waves for a lattice dynamical system arising in a diffusive endemic model, Nonlinearity, 30 (2017), 2334-2359] presented a discrete diffusive Kermack-McKendrick epidemic model, and the authors proved the existence of traveling wave solutions connecting the disease-free equilibrium to the endemic equilibrium. However, the boundary asymptotic behavior of the traveling waves converge to the endemic equilibrium at infinite is still an open problem. In this talk, we investigate the above open problem and completely solve it by constructing suitable Lyapunov functional and employing Lebesgue dominated convergence theorem. This is a joint work with Dr Ran Zhang.

An age-structured mathematical model on mumps outbreaks in Jiangsu Province, China

刘贤宁　西南大学

Abstract: Measles, mumps and rubella (MMR) vaccine program was introduced in Jiangsu province of China in May 2008 and have greatly contributed to decreasing of mumps cases. However, mumps is re-emerging after year 2015. A number of studies have put forward that the resurgence of mumps is due to vaccine failure. In this report, we investigate other reasons of the re-emerging of mumps, such as the changes in seasonal transmission patterns and demographic structures using an age-structured mathematical model. We divided the history (2005.01-2019.05) of mumps epidemics of Jiangsu province into three different stages (period): no vaccine stage (2005.01-2008.12), effectively controlled stage (2009.01-2015.12) and resurgence stage (2016.01-2019.05). The features of mumps epidemics in three stages, such as seasonality and basic reproduction number R0, are compared under different demographic structures with same physical contact rate. We found that the mumps transmission rate was increasing in summer, changes in demographic structure is explained why the mumps outbreaks among 10 years of children in stage I and among 5 years of children in stage III. We have concluded that the vaccine failure, changes in seasonality and demographic structure were associated with the mumps outbreak in recent years. We gives the patterns of mumps dynamics considering age, vaccine and seasonality, which can help health program planners to implement more preventive interventions in mumps control during the period of higher risk of infection.

Modeling the impact of air pollution on respiratory infection risk in China

唐三一　陕西师范大学

Abstract: China is now experiencing major public health challenges caused by air pollution, and there are many challenges to quantify the dynamics of air pollution and its impact on the risk of respiratory infection. This talk we would like to present our recent work on this topic, and to show an integrated data analysis to quantify the association among air quality index (AQI), meteorological variables and respiratory infection risk in Shaanxi province of China in the period of November 15th, 2010 to November 14th, 2016. Our analysis illustrated a statistically significantly positive correlation between the number of influenza-like illness (ILI) cases and AQI, and the respiratory infection risk has increased progressively with increased AQI with a time lag of 0-3 days. We also developed mathematical models (deterministic and stochastic models) for the AQI trend and respiratory infection dynamics, incorporating AQI-dependent incidence and AQI-based behaviour change interventions. Our combined data, model identification and theoretical analysis estimated the basic reproduction number for the respiratory infection during the studying period to be 2.4076, higher than the basic reproduction number of the 2009 pandemic influenza in the same province. Moreover, some novel methods have been developed for the SDE model, and the switching points related to the smog seasons have been estimated. Our modelling-based simulations concluded that, in terms of respiratory infection risk reduction, the persistent control of emission in the China's blue-sky programme is much more effective than substantial social-economic interventions implemented only during the smog days. Finally, I would like to mention that the non-smooth Filippov system could also be used to model the smog season and non-smog season (switching system), and then to analyze its dynamics.

HIV low viral load persistence under treatment: Insights from a model of cell-to-cell viral transmission

王霞　信阳师范学院

Abstract: In this talk, we develop a mathematical model that includes cell-to-cell viral transmission to study HIV persistence. During cell-to-cell transmission, it is assumed that various number of virus particles are transmitted with different probabilities and antiretroviral therapy has different effectiveness in blocking their infection. We analyze the model by deriving the basic reproduction number and investigating the stability of equilibria. Sensitivity analysis and numerical simulation show that the viral load is still sensitive to the change of the treatment effectiveness in blocking cell-free virus infection. To reduce this sensitivity, we modify the model by including density-dependent infected cell death or HIV latent infection. The model results suggest that although cell-to-cell transmission may have reduced susceptibility to HIV drugs, HIV latency represents a major reason for HIV persistence in patients on suppressive treatment.

Effect of spatial and temporal heterogeneity on disease transmission dynamics

肖燕妮　西安交通大学

Abstract: There are many challenges to quantifying and evaluating the impact of spatial and temporal heterogeneity on infectious diseases transmission dynamics. In this talk, we initially proposed a delay differential model, associated with the response time for mass media to cover the current infection and for individuals' behavior changes to media coverage. With two time delays, we comprehensively investigated the local and global bifurcation by considering the summation of delays as a bifurcation parameter. Main results show that either the media described feedback cycle, from infection to the level of mass media and back to disease incidence, or time delays can induce Hopf bifurcation and result in periodic oscillations. This indicates that the delayed media impact leads to a richer dynamics that may significantly affect the disease infections. We then proposed a SEIRS-type reaction-diffusion model to examine the spatial heterogeneity and obtained the basic reproduction number (R0), which is connected with the principal eigenvalue of a linear cooperative elliptic system. Threshold-type results on the global dynamics in terms of R0 are established. The monotonicity of R0 with respect to the diffusion rates of the exposed and infected individuals is established in several cases. This is joint work with Dr Pengfei Song and Prof Yuan Lou.

Mathematical analysis and application of a cholera transmission model with waning vaccine-induced immunity

徐瑞　山西大学

Abstract: Cholera is a common infectious disease caused by Vibrio cholerae, which has different infectivity. In this work, a cholera infection model with vaccination is investigated, in which hyperinfectious and hypoinfectious vibrios, both human-to-human and environment-to-human transmission pathways, and waning vaccine-induced immunity are considered. The basic reproduction number is calculated and verified to be a threshold determining the global dynamics of the model. In addition, an application is demonstrated by investigating the cholera outbreak in Somalia, and the relevant control measures in the short term are given by elasticity and sensitivity analysis.

Noise-induced transitions in a nonsmooth producer–grazer model with stoichiometric constraints

原三领　上海理工大学

Abstract: Stoichiometric producer–grazer models are nonsmooth due to the Liebig's Law of Minimum and can generate new dynamics such as bistability for producer–grazer interactions. Environmental noises can be extremely important and change dynamical behaviors of a stoichiometric producer–grazer model. In this paper, we consider a stochastically forced producer–grazer model and study the phenomena of noise induced state switching between two stochastic attractors in the bistable zone. Namely, there is a frequent random hopping of phase trajectories between attracting basins of the attractors. In addition, by applying the stochastic sensitivity function technique, we construct the confidence ellipse and confidence band to find the configurational arrangement of equilibria and a limit cycle, respectively.

Modeling and dynamics of Zika transmission with contaminated aquatic environments

赵洪涌　南京航空航天大学

Abstract: Since the outbreak in Brazil, Zika has received the worldwide attention. Zika virus is mainly transmitted via the bites of Aedes mosquito. Recently, experimental evidence indicates that Zika virus in contaminated aquatic environments can be transmitted to aquatic mosquitoes through breeding. To study the effects of contaminated aquatic environments on Zika transmission, we propose a new Zika model by introducing a general incidence function. We calculate the basic reproduction number, analyze the stability of disease free equilibria, and give general conditions with the occurrence of backward bifurcation. Analysis results suggest that transmission force from contaminated aquatic environments to aquatic mosquitoes plays an important role in generating complex dynamics.

Traveling waves for a nonlocal viral infection dynamical model

张天然　西南大学

Abstract: In this paper, the minimal wave speed problem of a viral infection dynamical model with nonlocal diffusion operator is studied. Firstly, the existence of traveling semi-front connecting to the virus-free steady state for $c > c*$ is obtained by using Schauder's fixed point theorem and limiting arguments, where $c*$ is the minimal wave speed. In order to use Lyapunov method to show that such traveling semi-front is indeed a traveling front connecting to the positive steady state, some boundedness estimations about the wave are given by adopting rescaling methods and comparison principle. Secondly, the existence of traveling front for $c = c*$ is established via limiting arguments, and the nonexistence of traveling front is shown by Laplace transform. Finally, the relationships between minimal wave speed and asymptotic spreading speed, and the influences of diffusion mode and diffusion ability on minimal wave speed or asymptotic spreading speed are investigated via simulations.

宿主抵抗力多样性的演化动力学模型研究

祖建　西安交通大学

摘要：宿主-病原体的相互作用在自然界中普遍存在，并且宿主的抵抗力已经演化出多样化的特点．在这次报告中，我们将介绍具有密度依赖死亡率的宿主-病原体模型中，宿主抵抗力的演化动力学模型．我们假设宿主的抵抗力会适应性地演化，不同类型的宿主对病原体的抵抗力不同，但是抵抗力较高的宿主将导致较低的出生率．通过使用适应动力学和临界函数分析的方法，我们发现演化结果主要依赖于宿主抵抗力与其出生率之间的权衡关系．如果权衡曲线是全局凹的，那么可以得到演化奇异策略是一个连续稳定的策略．相反，如果权衡曲线在演化奇异策略附近是弱凸的，那么宿主抵抗力的演化分支是可能的．在宿主抵抗力发生演化分支后，我们研究了双同态宿主的演化动力学模型，发现对于一种凹-凸-凹的权衡曲线，最终的演化结果可能包含一个相对较高抵抗力的宿主和一个相对较低抵抗力的宿主,它们可以长期连续稳定共存.对于一种S形权衡曲线，在演化分支发生后，具有较高抵抗力的宿主由于其在出生率上付出的较高代价而可能会灭绝，最终演化结果只包含一种具有相对较低抵抗力的单同态宿主．最后，我们介绍宿主-病原体的共同演化动力学模型．我们假设宿主的抵抗力和病原体的毒力都可以适应性地演化，但是在它们的出生率和因病死亡率方面存在一定的代价．我们发现了三种不同的共同演化结果，包括宿主和病原体连续稳定共存、宿主抵抗力发生演化分支和周期性演化等现象．

报告题目与摘要

（以姓氏拼音为序）

主题 II. 生物医学模型(11 月 14 日)

具有个体等级差异的群落生态模型分析与控制

何泽荣　杭州电子科技大学

摘要：基于种群内部个体之间的等级差异，为两种群所构成的群落系统建立一类偏微分－积分方程组模型，其边界条件具有全局反馈形式。在合理的参数条件下，分析模型的适定性、正平衡态的存在性与稳定性、系统的近似能控性、最优控制，等问题。给出严格的理论结果，并辅之以数值实验。主要运用不动点理论、凸分析中的锥理论、算子半群等工具，研究结果对生物多样性维护、种群分布优化、可再生资源科学管理具有积极意义，也能拓展无穷维系统控制问题的研究前沿。

Mathematical modeling about the scheduling of combination cancer therapy with immune checkpoint inhibitors

赖秀兰　中国人民大学

Abstract: There has been much progress in recent years in developing checkpoint inhibitors, primarily PD-1 antibodies and PD-L1 antibodies. However, because of lack of tumor-infiltrating effector T cells, many patients in clinical trials do not respond to checkpoint inhibitor treatment. It was recently suggested that the combination of an immune checkpoint inhibitor and another anti-tumor drug, such as a chemotherapy drug or radiotherapy, may function synergistically to induce more effective antitumor immune responses. The questions in the design of cancer clinical trials with combination of two drugs includes in which proportion (dosage) and in which order to administer the drugs. In this talk, I will address the scheduling question by mathematical modeling approaches. We considered the combination therapies of cancer with a checkpoint inhibitor and a cancer vaccine (or anti-VEGF) using mathematical models. We use mathematical models to explore the efficacy (synergistic or antagonistic) of the two drugs and the appropriate dosage and timing of the combination treatment.

From single-cell based modeling to population dynamics

雷锦志　天津工业大学

Abstract: In understanding the evolution process of a multicellular system, it is challenging issue to establish the relationship that connects the microscopic state of individual cells with the macroscopic population dynamics. In this talk, I will introduce a framework of individual-cell based computational modeling and the related mathematical model. Moreover, in order to describe the dynamics of intrinsic state of individual cells, we introduce the concept of single-cell entropy (scEntropy) based on single cell RNA sequencing data, which can be used to describe the order parameter of gene expressions in a single cell. The main point of this talk is trying to establish a connection between microscopic information and macroscopic states in multicellular systems.

Landscape and flux quantify the stochastic transition dynamics for p53 cell fate decision

李春贺　复旦大学

Abstract: The p53 transcription factor is a key mediator in cellular responses to various stress signals including DNA repair, cell cycle arrest, and apoptosis. In this work, we employ landscape and flux theory to investigate underlying mechanisms of p53-regulated cell fate decisions. Based on a p53 regulatory network, we quantified the potential landscape and probabilistic flux for p53 system. The landscape topography unifies and quantifies three cell fate states, including limit cycle oscillations (representing cell cycle arrest), high p53 state (characterizing apoptosis), and low p53 state (characterizing normal proliferative state). Landscape and flux results provide a quantitative explanation for the biphasic dynamics of p53 system. In the oscillatory phase (first phase), landscape attracts the system into the ring valley and flux drives the system cyclically moving, leading to cell cycle arrest. In the fate decision-making phase (second phase), the ring valley shape of landscape provides an efficient way for cells to return to normal proliferative state once DNA damage is repaired. If the damage is unrepairable with larger flux, the system may cross the barrier between two states and switch to apoptotic state with high p53 level. By landscape-flux decomposition, we revealed a trade-off between stability (guaranteed by landscape) and function (driven by flux) in cellular systems. Cells need to keep a balance between appropriate speed to repair DNA damage and appropriate stability to survive. This is further supported by flux landscape analysis showing that flux may provide dynamical origin of phase transition in non-equilibrium system by changing landscape topography.

Dynamics of a structured predator-prey system with predator cannibalism

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Cannibalism as a behavioral trait is prevalent in some species. A structured predator-prey system with predator cannibalism is investigated, where the growth of the prey is subject to two ways, the exponential form and the logistic model, in the absence of the predator. The effects of the cannibalism attack rate and the corresponding benefit rate of cannibals on model dynamics are analyzed. Complex phenomena, including the bistability, the existences of two positive equilibria and stable/unstable periodic solution, are found. Some quantities with clear biological meanings are defined. Conditions determining the local and global dynamics of the model in terms of these quantities are established. The sufficient conditions ensuring the global stability of equilibria are found by constructing appropriate Lyapunov functions. Our results show that, when the growth of the prey is subject to the logistic model, the final states of populations would depend on not only the related model parameters but also the initial conditions of solutions for certain cases.

肿瘤耐药的组学数据分析和数学建模

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摘要：肿瘤耐药是癌症难以治愈并导致复发的最主要原因之一，但是其机理尚不甚清楚。数学建模和数据分析有助于探索肿瘤耐药的动态机理和发现相关生物标志物。在此报告中，我将介绍我们近期在肿瘤耐药的组学数据分析和数学建模方面的一些研究工作。首先，我将汇报一种基于时间序列的转录组数据的基因调控网络构建和分析方法，用于分

析肿瘤耐药的适应性机制和关键基因；接着，将介绍我们提出的一种基于单细胞测序数据的多层网络方法（scMLnet），其不仅可以推断细胞间通讯的信号网络，而且能推断微环境调控基因表达的细胞内信号网络，并将介绍此方法在癌症耐药预测和新冠病毒感染机制研究中的应用。进一步，将探讨细胞微环境的适应性演变介导肿瘤耐药的相关多尺度动力学模型，包括随机微分方程模型和 PDE-Agent 多尺度模型等。

长效聚乙二醇干扰素治疗下慢性乙肝患者 HBsAg 水平动力学：一项基于医院的真实世界数据分析

王开发　西南大学

摘要：HBsAg 的持续性清除（sustained loss）是 CHB 功能性治愈（functional cure）的重要标志，但长期干扰素治疗情形下相关感染指标（包括但不限于 HBsAg）的动力学变化规律尚不清楚。根据浙江大学医学院第四附属医院收治的 CHB 患者病例资料库，我们对此做了初步的统计分析。

Modeling tissue hierarchical architecture

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Abstract: Many fast renewing tissues are characterized by a hierarchical cellular architecture, which would minimize the risk of the accumulation of genomic damage in the long-term self-renewing stem cells. In this talk, we will review some mathematical models about the cellular hierarchy. Specifically, we are concerned about different modes of cell proliferation, cell differentiation and de-differentiation, cell competition, and their effects on the risk of cancer.

前列腺癌治疗动力学模型

王稳地　西南大学

Abstract: I first introduce the mathematical models of prostate cancer, where stochastic noises are introduced or immunotherapy using dendritic cells as antigen-presenting cells is incorporated. The threshold conditions between extinction and persistence in mean for the stochastic system are obtained where noises play an important role in persistence and extinction of tumor cells. Then I talk about the second model where immunotherapy is considered. It is shown that the model admits the complex behaviors such as a saddle-node bifurcation, Hopf bifurcation, Bogdanov-Takens bifurcation and generalized Hopf bifurcation. These suggest that the vaccines amount and T-cells killing efficiency of tumor cells have a significant effect on tumor cells, which provides new insights to improve treatment outcomes even for patient with a weak immune system.

Quantitative integration of radiomic and genomic data improves survival prediction of low-grade glioma patients

邹秀芬　武汉大学

Abstract: Brain tumors are considered to be almost the most fatal type of cancer. In this study, we combine the machine learning method and network analysis to integrate radiomic and genomic data for lower grade gliomas. Results demonstrate that the proposed method and integrated index can improve survival prediction of lower grade gliomas.