

Special Session 85: New Trends in The Mathematical Modeling of Epidemiology and Immunology

Unraveling Dengue Dynamics with Data Calibration from Palu and Jakarta: Optimizing Active Surveillance and Fogging Interventions

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Abstract:

In this talk, we examine the role of active case finding and mosquito population reduction through fogging in dengue control using a mathematical model approach. Active case finding aims to identify undetected dengue cases, both asymptomatic and symptomatic, which can help prevent further transmission and reduce the likelihood of severe symptoms by enabling earlier treatment. The model was developed using a system of nine-dimensional nonlinear ordinary differential equations. We conducted a mathematical analysis of the equilibria and their stability based on the basic reproduction number (\mathcal{R}_0). Our analysis shows that the disease-free equilibrium is locally asymptotically stable when $\mathcal{R}_0 < 1$.

The effect of model structure and data availability on virus dynamics at three biological scales

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Abstract:

Understanding the epidemiology of emerging vector-borne pathogens in avian populations requires systems investigation at each scale involved in the host, virus transmission cycle, from individual bird infections, to bird-to-vector transmissions, and to viral incidence in bird and vector populations. For new pathogens field data are sparse, and predictions can be aided by the use of laboratory-type inoculation and transmission experiments combined with dynamical mathematical modelling. In this talk, I will present the differences in the dynamics of two strains of such a pathogen - the Usutu virus. I will construct mathematical models for the within-host scale, bird-to-vector transmission scale and vector-borne epidemiological scale and use individual within-host infectious virus data and per cent mosquito infection data to predict virus incidence in birds and mosquitoes. I will address the dependence of predictions on model structure, data uncertainty and experimental design.

Modelling of the spread of diseases with time-change processes

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Abstract:

The stochastic version of the SIRV (susceptible-infected-recovered-vaccinated) model in the population of non-constant size and finite period of immunity is considered. Among many parameters, the most important is the contact rate, i.e. the average number of adequate contacts of an infective person. It is expected that this parameter exhibits time-space clusters which reflects in interchanging periods of low and steady transmission and periods of high and volatile transmission of the disease. The stochastics in the SIRV model considered here comes from the noise represented as the sum of the conditional Brownian motion and Poisson random field, closely related to the corresponding time-changed Brownian motion and the time-changed Poisson random measure. From a modeling perspective, incorporating time-charged noise is an effective method for capturing temporal dependencies in noise, such as clustering and stretching periods.. The existence and uniqueness of positive global solution of the stochastic SIRV process is proven by classical techniques. Furthermore, persistence and extinction of infection in population in long-run scenario are analyzed.

On Differential Equation Models for Shared Resource Competition

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Abstract:

We analyze a differential equation model for the population dynamics of multiple species in a competitive environment. The model incorporates key ecological factors, including the conversion of available resources into per capita growth, the intrinsic harvest rate per unit area, and a uniform mortality rate. These factors influence interspecies competition and survival strategies, leading to the emergence and stability of three types of equilibrium states: extinction, competitive exclusion, and coexistence. Additionally, through a quasilinear reaction-diffusion system that models habitat selection strategies and ideal directed movement, we investigate the pattern of populations approaching coexistence equilibrium through traveling wave solutions.

Threshold dynamics in a periodic epidemic model with imperfect quarantine, isolation and vaccination

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Abstract:

In this talk, I will present a non-autonomous mathematical model that explore the complex dynamics of disease spread over time, incorporating a time-periodic transmission parameter and imperfections in quarantine, isolation and vaccination strategies. Through a detailed examination of threshold dynamics, it is revealed that the global dynamics of disease transmission are influenced by the basic reproduction number (\mathcal{R}_0), a critical threshold that determines extinction, persistence, and the presence of periodic solutions. It is shown that the disease-free equilibrium is globally asymptotically stable if $\mathcal{R}_0 < 1$. To support and validate our analytical results, the basic reproduction number and the

dynamics of the disease are estimated by fitting monthly data from two Asian countries, namely Saudi Arabia and Pakistan. Furthermore, a sensitivity analysis of the time-averaged reproduction number ($\langle \mathcal{R}_0 \rangle$) of the associated time-varying model showed a significant sensitivity to key parameters such as infection rates, quarantine rate, vaccine coverage rate, and recovery rates, supported by numerical simulations. These simulations validate theoretical findings and explore the impact of seasonal contact rate, imperfect quarantine, isolation, imperfect vaccination, and other parameters on the dynamics of measles transmission. The results show that increasing the rate of immunization, improving vaccine management, and raising public awareness can reduce the incidence of the epidemic. The study highlights the importance of understanding these patterns to prevent future periodic epidemics.

Delay induced periodic solutions in a dendritic cell therapy model

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Abstract:

We formulate a tumor-immune interaction model with a constant delay (time needed for a dendritic cell to become an effector cell) to capture the behavior following application of a dendritic cell therapy. The model is validated using experimental data from melanoma-induced mice. Through theoretical and numerical analyses, the model is shown to produce rich dynamics, such as a Hopf bifurcation and bistability. We provide thresholds for tumor existence and, in a special case, tumor elimination. Our work indicates a sensitivity in model outcomes to the immune response time. We provide a stability analysis for the high tumor equilibrium. For small delays in response, the tumor and immune system coexist at a low level. Large delays give rise to fatally high tumor levels. Our computational and theoretical work reveals that there exists an intermediate region of delay that generates complex oscillatory, even chaotic, behavior. The model then reflects uncertainty in treatment outcomes for varying initial tumor burdens, as well as tumor dormancy followed by uncontrolled growth to a lethal size, a phenomenon seen in vivo. Theoretical and computational analyses suggest efficacious treatments to use in conjunction with the dendritic cell vaccine. Analysis of a highly aggressive tumor confirms the importance of representation with a time delay, as periodic solutions are generated when a delay is present.

Analysis of Malaria Model Using Deep Learning

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Abstract:

Malaria is one of the deadliest diseases in the world, every year millions of people become victims of this disease and out of these millions thousands of people become victims of this disease. In this work, the dynamics of malaria is analyzed using deep learning by implementing the SIR-SI compartment model. The main factor that controls disease transmission is the transmission rate and two of the most important

factors that influence the transmission rate are temperature and altitude, thus in this work the transmission rate is analyzed with respect to temperature and altitude. We have performed the stability analysis of steady state solutions. After the mathematical analysis, Artificial neural network (ANN) was applied to the formulated model to predict the trajectory of all of the five compartments. As mentioned earlier the dynamics of disease are controlled by the parameters associated with the disease transmission and thus in this work three different neural network architectures namely Artificial neural network (ANN), convolution neural network (CNN), and Recurrent neural network (RNN) have been built to estimate these parameters from the trajectory of the data.

Mathematical modelling of the Allee Effect in viral infection in within-host pathogen interactions

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Abstract:

Understanding the dynamics of infectious diseases requires careful consideration of population structure and behavior, particularly in animal populations where demographic factors significantly influence transmission dynamics. Traditional deterministic models often assume a critical mass of individuals is necessary for disease spread; however, this assumption may not hold in all contexts, especially when examining the Allee effect. The Allee effect is a crucial ecological phenomenon that suggests a minimum population threshold is essential to prevent extinction, thereby complicating our understanding of pathogen dynamics. This paper presents a novel within-host model that incorporates the Allee effect to investigate its impact on viral and pathogen populations. We rigorously analyze the model's fundamental mathematical properties, including positivity, boundedness, and the existence of multiple equilibria. The local asymptotic stability of equilibrium points is explored through linear stability analysis, which provides insights into the local dynamics near the equilibria. To fully characterize the global dynamics, we conduct a bifurcation analysis that reveals the existence of two transcritical bifurcations and one Hopf bifurcation, indicating significant shifts in population behavior as parameters are varied. To illustrate our theoretical findings, we conduct numerical simulations that confirm the model's predictions and elucidate the role of the Allee parameter in shaping pathogen dynamics.

Stability switches induced by immune system boosting in an SIRS model with delays

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Abstract:

We consider an epidemiological model that includes waning and boosting of immunity. Assuming that repeated exposure to the pathogen fully restores immunity, we derive an SIRS-type model with discrete and

distributed delays. First we prove usual results, namely that if the basic reproduction number, \mathcal{R}_0 , is less or equal than 1, then the disease free equilibrium is globally asymptotically stable, whereas for $\mathcal{R}_0 > 1$ the disease persists in the population. The interesting features of boosting appear with respect to the endemic equilibrium, which can go through multiple stability switches by changing the key model parameters. We construct two-parameter stability charts, showing that increasing the delay can stabilize the positive equilibrium. Increasing \mathcal{R}_0 , the endemic equilibrium can cross two distinct regions of instability, separated by Hopf bifurcations. Our results show that the dynamics of infectious diseases with boosting of immunity can be more complex than most epidemiological models and calls for careful mathematical analysis.

Mathematical Modeling of addiction with frequency of contact incidence term

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Abstract:

This work proposes a novel approach for examining a SATR model using epidemiological modeling. Using a convex incidence function, which is a measure of the frequency of interaction between an addict and a non-addict, we want to explore the dynamics of addiction transmission within a community. We establish the well-posedness of the model, which ensures the existence, uniqueness, and positivity of the solution. We also determine the next-generation operator, which allows us to calculate \mathcal{R}_0 , the fundamental reproduction number. We examine in detail how \mathcal{R}_0 serves as a threshold quantity to regulate the behavior of the addiction. Specifically, we show that when $\mathcal{R}_0 < 1$, the addiction-free steady state is globally asymptotically stable for all values of q . Conversely, we establish the uniform persistence of the associated equilibrium when $\mathcal{R}_0 > 1$ and construct a steady state of addiction that is globally asymptotically stable for all values of q . We also analyze the asymptotic profile of the addiction stable state, considering the effects of small and high addiction rates on the state dynamics. To validate our theoretical findings, we provide numerical simulations that both confirm our findings and provide additional insights into the dynamics of the addiction.

Mathematical analysis of a generalized nonlocal dispersion epidemic model

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Co-Author(s):

Abstract:

This work investigates a generalized nonlocal dispersion epidemic model subject to the Neumann boundary conditions and spatial heterogeneity. We use a convolution operator to describe the nonlocal spatial movements of individuals. Our primary goal is to investigate this model, focusing on a generalized incidence function, which presents an additional challenge in the model analysis. We also investigate the existence and uniqueness of an endemic steady state and study the significant effects of dispersal rates on the asymptotic profiles of the steady endemic state. Finally, we discussed the global asymptotic

behavior of the solution for different dispersal coefficients.

Traveling Wave Speed and Profile of Rabies Model: Insights from the Go or Grow Hypothesis

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Abstract:

Rabies is a viral infection that affects the central nervous system, primarily transmitted through direct contact with infected animals. The disease exhibits a characteristic traveling wave pattern of spread, which can be effectively captured through mathematical modeling. In this work, we propose a two-population reaction-diffusion model for the red fox based on the Go or Grow hypothesis, which incorporates the movement and interaction between susceptible and infectious populations. Using approximation methods, we analyze various traveling wave solutions and provide new insights into the progression of the infection, offering a more accurate representation of rabies spread.

Understanding Seasonal Variations of Dengue in Brazil

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Abstract:

The timing of peak dengue cases in Brazil remains inconsistent from year to year. Our analysis of surveillance data from 2000 to 2014 reveals this variability both over time and across states. We hypothesize that several factors, including climate variability, the circulation of different dengue serotypes, and the introduction of new serotypes may be driving the shifting. To better understand these dynamics, we employed temperature-driven multi-strain dengue transmission models. Preliminary findings suggest that the timing of introducing a new serotype can cause the timing of outbreaks to vary across locations, likely as a result of variations in environmental conditions, particularly temperature, across Brazil.