ICMA-VIII International Conference on Mathematical Modeling and Analysis of Populations in Biological Systems October 28-30, 2022

University of Louisiana at Lafayette Lafayette, Louisiana, USA

Contents
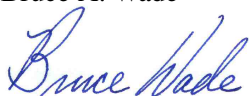
Welcome to the Eighth ICMA Meeting

On behalf of the Organizing Committee, I would like to personally welcome each of you to the Eighth International Conference on Mathematical Modeling and Analysis of Populations in Biological Systems, at Lafayette, Louisiana. It's an exciting time for research in Biomathematics, as we continue to develop new ideas, motivated and in response to the needs of modern society.

The broad, general theme of the conference is the formulation, validation, analysis and simulation of mathematical models for the spatio-temporal dynamics of biological populations. A special emphasis at this eighth conference will be placed on multiple scale dynamics in ecology, epidemiology, and systems biology; many biological systems operate on multiple spatial and temporal scales and the incorporation of these may be essential for capturing system dynamics.

ICMA-VIII aims to accomplish at least three broad tasks: scientific progress, scientific collaboration, and the training of a future generation of mathematical biologists. The conference will thus have a significant impact, both nationally and internationally, on future research in biomathematics and mathematical biology. The collaborative opportunities provided to researchers at all points of the career path from undergraduate and graduate students, to early-career faculty, to established senior researchers will establish new directions and avenues for the national and international research community.

We thank each of the local organizing committee members for bringing their energy and expertise to our meeting. We owe members of the Scientific Committee our gratitude for founding and fostering the ICMA conference series. We are grateful for signficiant support from the National Science Foundation and the University of Louisiana at Lafayette Department of Mathematics as well as Ray P. Authement College of Sciences.

Sincerely,
Bruce A. Wade

Professor & Head
Department of Mathematics, University of Louisiana at Lafayette

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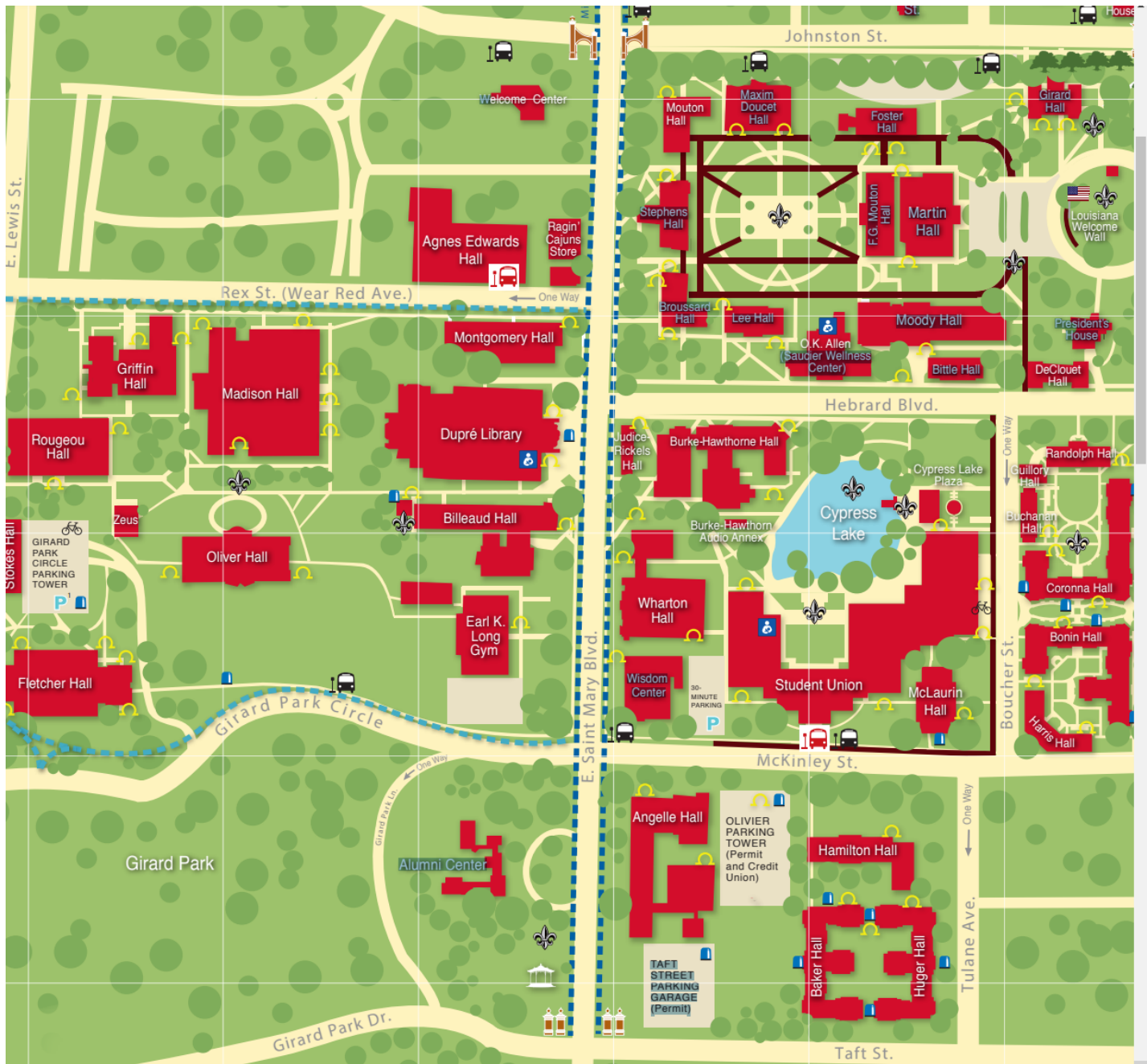
ICMA-VIII 2022 Meeting Timetable

Student Union & Oliver Hall, University of Louisiana at Lafayette

Friday, October 28, 2022

	Student Union: Helma Constantine Forum AB (Room 209)		
08:30-12:00	**Registration, Student Union**		
09:00-09:15	**Opening Remarks: Dr. Jaimie Hebert, Provost and Vice President for Academic Affairs**		
09:15-10:15	**Plenary Talk: Mark Lewis** *Target reproduction numbers in ecology and epidemiology* Chair: Amy Veprauskas		

	Student Union (Rm. 207)	**Room 209**	**Room 210**
	Session 1 Chair: Cameron Browne	**Session 2** Chair: Amy Veprauskas	**Session 3** Chair: Bruce A. Wade
10:30-11:00	Chadi M. Saad-Roy *Modeling SARS-CoV-2 immuno-epidemiological dynamics*	Saber Elaydi *Mixed Monotone Maps: Application to evolutionary Models*	Ashrafur Rahman *Mathematical modeling of L. monocytogenes under simulated human gastric conditions in the presence of milk products*
11:00-11:30	Yuganthi Liyanage *A Novel Within-Host Model of HIV and Nutrition*	Jing Li *Honey bee (Apis mellifera) hive placement is more influential than orchard layout on the fruit set of a dioecious crop*	Emmanuel Asante-Asamani *Actin-Myosin Dynamics During Bleb Stablization*
11:30-12:00	Daniela Andrea Florez Pineda *Modeling sustained transmission of Wolbachia among Anopheles mosquitoes: Implications for Malaria control in Haiti*	Cole Butler *Rethinking mosquito control: Gene drives and the consequences of over-suppression*	Naghmeh Akhavan *Affect of extracellular geometry on cluster cell migration in fruit fly egg chamber*
12:00-1:45	Lunch (on your own)		

	Oliver Hall (Rm. 112)		

	Oliver Hall (Rm. 112)	**Room 101**	**Room 117**
	Session 4 Chair: Paul Salceanu	**Session 5** Chair: Azmy S. Ackleh	**Session 6** Chair: Ross Chiquet
1:45-2:15	Cameron Browne *Prey-predator eco-evolutionary dynamics of HIV immune escape*	Jim Michael Cushing *A Darwinian SI Model*	Mohammad Mihrab Uddin Chowdhury *Coupling discrete and continuous time scales to investigate the impact of an emerging fungal pathogen in amphibian populations*
2:15-2:45	Shasha Gao *Human papillomvirus vaccination strategy: modeling and implications*	Zhijun Wu *Why multilingual, and how to keep it – An evolutionary dynamics perspective*	Tung D. Nguyen *Population Persistence in Stream Networks: Growth Rate and Biomass*
2:45:3:15	Sarafa Adewale Iyaniwura *Understanding the efficacy of capsid protein allosteric modulators using a multiscale model of hepatitis B virus*	Jordy Cevallos Chavez *Hierarchy Establishment from Nonlinear Social Interactions and Metabolic Costs: An Application to Harpegnathos saltator*	Yixiang Wu *Global dynamics of Lotka-Volterra competition patch models*
3:30-4:30	**Plenary Talk: Sheryl Chang** *Modelling infectious disease dynamics and intervention methods: COVID-19 and beyond* Chair: Elena Braverman		
	Session 7 Chair: Hayriye Gulbudak	**Session 8** Chair: Paul Salceanu	**Session 9** Chair: Jim M. Cushing
4:45-5:15	Ephraim Agyingi *Modeling immune response and disease severity in COVID-19*	Keng Deng *On a nonlinear nonlocal model for a population with separate dispersal and sedentary stages*	Amy Veprauskas *Pathogen dynamics in a tick-host system*
5:15-5:45	Yang Li *Assessing the epidemiological and economic impact of alternative vaccination strategies: a modeling study*	Jun Chen *How does seasonality and parasitism impact Honeybee population dynamics*	Azmy S. Ackleh *A Discrete-Time Spatially-Explicit Model for the Dynamics of Ticks*
5:45-6:15	Tin Phan *Modeling the viral resistance to monoclonal antibody treatment for SARS-CoV-2*	Eddy Kwessi *Hierarchical Model for Species Under an Allee Effect with Immigration and a Hollins-Type II Functional Response*	Tingting Tang *Comparing and Examining Different Methods of Determining Structural and Practical Identifiability of a Vector-Host Model*

Updated October 25, 2022

	Saturday, October 29, 2022

	Oliver Hall (Rm. 112)		
09:00-10:00	**Plenary Talk: Stanca Ciupe** *Multi-scale dynamics of SARS-CoV-2 infection* Chair: Azmy S. Ackleh		
	Oliver Hall (Rm. 112)	**Room 101**	**Room 117**
	Session 10 Chair: Hayriye Gulbudak	**Session 11** Chair: Amy Veprauskas	**Session 12** Chair: Xiang-Sheng Wang
10:15-10:45	Zhuolin Qu *Multistage spatial model for informing release of Wolbachia-infected mosquitoes as disease control*	Elena Braverman *Delayed harvesting models: sustainability challenges*	Necibe Tuncer *Structural and practical identifiability analysis of a multiscale immuno-epidemiological model*
10:45-11:15	Md Rafiul Islam *Evaluation of the United States COVID-19 Vaccine Allocation Strategy*	Ursula Trigos-Raczkowski *Coexistence due to life history variation revisited in models with explicit patch aging*	Maya Bocanegra *Mathematical Modeling of Waning and Boosting of COVID-19 Immunity through Infection and Vaccination to Predict Seroprevalence in*
11:15-11:45	Nazia Afrin *Bistability in models of Hepatitis B virus dynamics*	Jacob Duncan *Separation of Scales in an Integrodifference Equation Model of Metapopulations Predicts Climate Change Impacts on Equilibria*	Denis Patterson *Modeling immunity to malaria with an age-structured PDE framework*
11:45-1:30	Lunch (on your own)		
1:30-2:30	**Plenary Talk: Kelsey Marcinko** *A Mathematical Analysis of Host–Parasitoid Dynamics* Chair: Xiang-Sheng Wang		
2:30-3:00	**Coffee Break and Poster Session**		
	Session 13 Chair: Saber Elaydi	**Session 14** Chair: Azmy S. Ackleh	**Session 15** Chair: Xiang-Sheng Wang
3:00-3:30	Hayriye Gulbaduk *Two-Strain Multi-Scale Dengue Vaccination Model Structured by Dynamic Host Antibody Level*	Amanda Laubmeier *Intraguild predation in a two-species competition model with seasonal birth*	Adriana Maria De Mendoza Velasquez *Generalized model to predict the outcome of sequential thermoradiotherapy*
3:30-4:00	Seoyun Choe *Impact of residence time on the spread of infectious diseases in a heterogeneous environment*	Sankar Sikder *A Discrete-Time Predator-Prey Model with Selection and Mutation in the Prey*	Jacquelyn Shelton *Probabilistic machine learning for uncertainty representation and applications to neural encoding in biological sensory systems*
4:00-4:30	Xueying Wang *A reaction-advection-diffusion model of cholera epidemics with seasonality and human behavior change*	Srijana Ghimire *Supercritical Hopf Bifurcation of Cooperative Predation*	Thomas G. Stojsavljevic Jr *Adaptive deep brain stimulation in a biophysical network model of Parkinson's disease*
4:45-5:45	**Plenary Talk: Heiko Enderling** *Quantitative Personalized Radiation Oncology* Chair: Jim Cushing		
6:00-8:30	**Dinner at the Alumni Center**		

	Sunday, October 30, 2022		
	Oliver Hall (Rm. 112)		
09:00-10:00	**Plenary Talk: Carrie Manore** *Continental-Scale Model for Climate-Driven Mosquito-borne Diseases* Chair: Saber Elaydi		
	Oliver Hall (Rm. 112)	**Room 101**	**Room 117**
	Session 16 Chair: Cameron Browne	**Session 17** Chair: Saber Elaydi	**Session 18** Chair: Jim M. Cushing
10:15-10:45	Zhijun Wu *Social distancing is a social dilemma game played by every individual against his/her population*	Naghmeh Akhavan *Extinction of multiple populations and a team of Lyapunov functions*	Andjela Rodic *Using mathematical modeling and feature selection techniques to infer the predictors of the SARS-CoV-2 transmissibility*
10:45-11:15	Lale Asik *Nutrient-mediated pathogen infectivity and host immunity in primary producers*	Paul Salceanu *Dispersal-driven coexistence in a multiple-patch competition model for zebra and quagga mussels*	Yusuf Afolabi *Quantifying the efficiency of contact tracing in mitigating the spread of COVID-19*
11:15-11:45	Leah LeJeune *Effect of cross-immunity in a mult-strain cholera model*	Oluwatosin Babasola *Mathematical analysis of the delay differential equation model for the farm level cocoa yield*	Xinyue Zhao *Bifurcation Analysis of Critical Values for Wound Closure Outcomes in Wound Healing Experiments*

1 Plenary Abstracts

1.1 Chang

Modelling infectious disease dynamics and intervention methods: COVID-19 and beyond

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Abstract

Epidemics cause major disruptions in society and the rapid spread, such as the COVID-19 crisis, calls for swift intervention responses. There has been a long tradition of using computational and mathematical models to deepen the understanding of the interdependent epidemic and intervention dynamics [1], and many epidemic models demonstrated their values in the COVID-19 pandemic to help shaping more effective public health policy. Here, we present our ongoing modelling effort [2,3,4] of an agent-based modelling framework, AmTraC-19 (Agent-based Model of Transmission and Control of the COVID-19 pandemic in Australia), to study the complex dynamics between pandemics and interventions in Australia. This fine-grained model accounts for mobility and population profile derived from Australian census data and has been calibrated to reproduce key epidemiological characteristics of several COVID-19 variants. Various interventions strategies have also been implemented to determine critical transition of intervention compliance in the highly heterogeneous Australian population, including: (i) non-pharmaceutical interventions (travel restriction, case isolation, home quarantine, school closure, and social distancing), and (ii) pharmaceutical interventions (pre-pandemic vaccination phase, and progressive vaccination rollout). Our modelling effort has been successfully validated for several epidemic scenarios in Australia and will seek for further development fusing genomic surveillance data.

References

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[2]   S. L. Chang, N. Harding, C. Zachreson, O. M. Cliff, M. Prokopenko, *Modelling transmission and control of the COVID-19 pandemic in Australia*, Nature Communications, 11, 5710, 2020.

[3]   C. Zachreson, S. L. Chang, O. M. Cliff, M. Prokopenko, *How will mass-vaccination change COVID-19 lockdown requirements in Australia?*, The Lancet Regional Health – Western Pacific, 14:100224, 2021.

[4]   S. L. Chang, O. M. Cliff, C. Zachreson, M. Prokopenko, *Simulating transmission scenarios of the Delta variant of SARS-CoV-2 in Australia*, Frontiers in public health, 10, 823043, 2022.

1.2 Ciupe

Multi-scale dynamics of SARS-CoV-2 infection

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Abstract

Designing control strategies for the COVID-19 epidemic requires multi-scale understanding of individual infections, the probability of transmission through aerosol exposure, and the roles of vaccination and testing in limiting an outbreak at the population level. In the first part of this talk, I will present several studies investigating within-host and aeosol dynamics in animals and humans infected with SARS-CoV-2. They will focus on the tradeoff between viral infectiousness and viral positivity, as well as the biases induced by the scarcity of data early in the individual's infection. In the second part, I will connect the virus profile of infected individuals with transmission, testing strategies, and vaccination at the population level through multi-scale immuno-epidemiological models. Using the multi-scale models, we will predict the best testing-vaccination combinations for limiting an outbreak with variants of increased transmissibility. Our findings can improve interventions.

References

[1] N Heitzman-Breen, SM Ciupe *Modeling within-host and aerosol dynamics of SARS-CoV-2: The relationship with infectiousness*, PLoS computational biology 18 (8), e1009997, 2022.

[2] SM Ciupe, N Tuncer *Identifability of parameters in mathematical models of SARS-CoV-2 infections in humans*, Scientific reports, 12:14637, 2022.

[3] JE Forde, SM Ciupe, *Modeling the influence of vaccine administration on COVID-19 testing strategies*, Viruses 13 (12), 2546, 2021.

[4] JE Forde, SM Ciupe, *Quantification of the tradeoff between test sensitivity and test frequency in a COVID-19 epidemic—a multi-scale modeling approach*, Viruses 13 (3), 457, 2021

1.3 Engerling

Quantitative Personalized Radiation Oncology

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Abstract

Incremental improvements in cancer radiotherapy with each iteration of clinical trials have continued because they have produced reasonable outcomes. Mathematical modeling may provide the necessary tools to provide a mechanistic understanding of cancer biology and treatment response individualize therapy. Calibrated and validated mathematical models can be used to simulate previously untested treatment protocols. We develop a simple mathematical model of tumor growth and radiation response, and show that this model can accurately predict head and neck cancer patient responses to radiation. This model can then be used to predict optimal radiation fractionation and total dose for tumor control. We then extend the model to account for radiation-induced stimulation of anti-tumor immune responses. We validate the model in 10,469 patients by demonstrating clinically-detected tumors have pro-tumor immune environments. We develop an individual Radiation Immune Sensitivity (iRIS) and show that iRIS distribution across 31 tumor types is consistent with the clinical effectiveness of radiotherapy and predicts for local control and survival in a separate cohort of 59 lung cancer patients. This is the first clinically and biologically-validated model to represent the perturbation of the tumor-immune ecosystem by radiotherapy.

References

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Target reproduction numbers in ecology and epidemiology

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Abstract

Some of the most central quantities in theoretical biology are threshold parameters determining population persistence or disease invasibility. These provide biological insights regarding population protection and disease control. Reproduction numbers (e.g., R_0) are threshold parameters that have been widely used, especially in ecology and epidemiology. The purpose of this talk is to introduce the idea of a target reproduction number as a generalized reproduction number targeted at specific population control strategies. I will illustrate the theory with the ecological example of controlling an invasive weed, scentless chamomile, and will also show how target reproduction numbers can be applied in epidemiology.

1.5 Manore

Continental-Scale Model for Climate-Driven Mosquito-borne Diseases

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Abstract

Understanding the non-linear impacts of climate change on climate-driven diseases such a mosquito-borne disease is an ongoing open question. Recent research has shown that temperature will change species and virus distributions. To further understand how temperature, along with changes in hydrology, precipitation, and human populations, will change the dynamics and ranges of West Nile virus and dengue, we developed a suite of coupled models to simulate disease spread across the Americas. This includes a global climate and earth systems model, mosquito population dynamics model, and disease transmission model with host species (e.g. humans and birds) driven by the climate model output. I will present the mosquito and disease transmission models along with our new tiling method for spatial partitioning along with validation results and challenges.

1.6 Marcinko

A comparative analysis of host–parasitoid models with density dependence preceding parasitism

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Abstract

The interactions between insect parasitoids and their hosts are of great interest to ecologists. Roughly 8.5% of insect species are parasitoids, and they play a significant ecological role in regulating their hosts, often with agricultural consequences. Mathematical models of these host–parasitoid systems are notable because of the simple and specific modeling assumptions that result from the direct connection between parasitized hosts and parasitoid offspring. We present a systematic comparison and analysis of a suite of nonspatial, discrete-time, host–parasitoid models. These models were selected to compare different combinations of standard functional forms for density-dependent growth of the host species and for parasitism. Additionally, we explicitly account for the timing of the density dependence and parasitism in the host life-cycle. These models combine simple and well-understood individual components, but these particular combinations yield some unexpected dynamics and rich mathematical behavior.

2 Abstracts

2.1 Ackleh

A Discrete-Time Spatially-Explicit Model for the Dynamics of Ticks

A. S. Ackleh[*], S. Sikder, A. Veprauskas and A. Zhang

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Abstract

We develop a discrete-time spatially-explicit model that describes tick population dynamics. We analyze the behavior of the model under a nonlinear fecundity term that exhibits an Allee effect. We show that the system exhibits rich dynamics including monostable and bistable dynamics. We then incorporate demographic stochasticity into the model and use numerical simulations to understand spatial invasion patterns of ticks as they relate to different dispersal mechanisms.

2.2 Afolabi

Quantifying the efficiency of contact tracing in mitigating the spread of COVID-19

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Abstract

Contact Tracing (CT) is one of the measures taken by the government and health officials to mitigate the spread of the novel coronavirus. In this talk, we investigate its efficiency by developing a time-fractional compartmental model for assessing its impact on mitigating the spread of the virus.

References

[1] Toheeb A. Biala and Abdul Q. Khaliq, *A fractional-order compartmental model for predicting the spread of the COVID-19 pandemic*, Communications in Nonlinear Science & Numerical Simulation, 98, 105764, 2021.

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[3] Cameron Browne and Hayriye Gulbudak and Glenn Webb, *Modeling contact tracing in outbreaks with application to Ebola*, Journal of Theoretical Biology, 384, 33 - 49, 2015.

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Bistability in models of Hepatitis B virus dynamics

Nazia Afrin [1], Jessica M. Conway [2], Stanca M. Ciupe [3] and Hayriye Gulbudak[1]

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Abstract

HBV is a major global health concern with 1.5 million newly infected cases each year. It's an infection of the liver caused by the Hepatitis B virus. In this preliminary study, we formulate and analyze a within-host model that describes the progression of acute HBV in liver cells (hepatocytes). We derive the basic reproduction number R_0 and investigate the stability of the equilibria via threshold analysis. Analytical and numerical results show that the model exhibits complex bifurcation dynamics such as backward bifurcation. Finally, we discuss the epidemiological implications of bistable dynamics.

References

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[2] Ciupe, Stanca M and Ribeiro, Ruy M and Nelson, Patrick W and Dusheiko, Geoffrey and Perelson, Alan S, *The role of cells refractory to productive infection in acute hepatitis B viral dynamics*, Proceedings of the National Academy of Sciences , 104:12, 5050–5055, 2007.

[3] Ciupe, Stanca M and Ribeiro, Ruy M and Perelson, Alan S, *Antibody responses during hepatitis B viral infection*, PLoS computational biology , 10:7, e1003730, 2014.

Modeling immune response and disease severity in COVID-19

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Abstract

Infection with COVID-19 has resulted in a wide spectrum of disease severity ranging from asymptomatic illness to fatality in some patients. The role of the immune response given the different outcomes is still not fully understood. In order to understand the reason behind the different outcomes, aspects of the immune response such as cytokine storm have been implicated in some studies [1]. Other studies have associated disease severity with preexisting conditions [2]. Genetic predisposition has also been proposed as a possible culprit. No study has yielded a definite explanation thus far [3]. This paper hopes to shed more light on the interaction between COVID-19 and the immune response through mathematical modeling. A simple model reported in [4] that captures the viral load together with the collective immune response using a system of differential equations is presented. Analysis of the equilibriums points of the model for different chosen sets of parameter values produce different bifurcations, leading to states that are associated with clinical diseases. In some instances the analysis does not support the suggestion that genetic predisposition is responsible for disease severity. Numerical simulations of the model are compared to experimental data from murine studies involving rhesus macaque monkeys. When the model is updated to study the impact generated by vaccination on the viral load, it is evident that though they may not effectively stop an infection as has been observed, vaccination has a huge effect on disease severity.

References

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      application to Leishmaniasis, Mathematical Biosciences and Engineering 17: 1253-1271, 2020.

Extinction of multiple populations and a team of Lyapunov functions

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Abstract

We investigate the d-dimensional model,

$$x_i' = \frac{d}{dt} x_i = x_i \cdot \left(c_i + \sum_{j=1}^{d'} s_{ij} z_j \right), \quad \text{where } i = 1, \ldots, d.$$

where each $z_j(t)$ is a time-fluctuating resource that can depend on $x_1, \ldots, x_d$ and even on the weather or stock market. This "nonautonomous" model is a generalization of an autonomous Lotka-Volterra d-dimensional model. It is nonautonomous and it is not specified how the $z_j(t)$ are determined. Write S^T for the transpose of $S = (s_{ij})$. When the kernel of S^T has dimension k and $k > 0$, we show that for any bounded solution $X(t) = (x_1, \ldots, x_d)(t)$, at least k coordinates (or species) will die out and will do so exponentially fast. For the proof, we invent a family of "die-out" Lyapunov functions, a "team" of Lyapunov functions that work together to show that k species must die. Each die-out Lyapunov function implies one species must die out and provides constraints as to which species must die out. Together they provide a picture of which are likely to die out. We present a "trophic" condition for Lotka-Volterra systems that guarantees that there is a trapping region that is globally attracting.

References

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      1970.

2.6   Akhavan-2

Affect of extracellular geometry on cluster cell migration in fruit fly egg chamber

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Abstract

Cell migration is an essential process in animal development, immune response, and wound healing. Errors in this process can lead to birth defects and problems in immunity. Also, aberrant acquisition of cell migration is the basis for cancer metastasis. To explore these issues, we have studied and developed models for the migration of border cells in the ovary of Drosophila melanogaster, the fruit fly. we develop a new model for border cell migration and compare it to behaviors in vivo. In our model, using an extracellular geometry, and insert into chemoattractant distribution, which results in small irregularities in the chemical gradient within the migratory domain.

References

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[2]   David P Stonko, Lathiena Manning, Michelle Starz-Gaiano, and Bradford E Peercy. *A mathematical model of collective cell migration in a three-dimensional, heterogeneous environment*. PloS one, 10(4):e0122799, 2015.

2.7 Asante-Asamani

Actin-Myosin Dynamics During Bleb Stabilization

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Abstract

The actin cortex is very dynamic during cell migration. When cells move using pressure
driven leading-edge protrusions of their membrane (blebbing), they reform the cortex within
a new bleb and completely disassemble the cortex in the region devoid of the cell membrane
(actin scar). The regulation of this process, referred to as bleb stabilization, is not fully un-
derstood. Our present work investigates the role of Myosin motor proteins, which have been
shown to be necessary for blebbing, on actin dynamics during stabilization. Analysis of mi-
croscopy data from protein localization experiments in *Dictyostelium discoideum* cells reveals
a local accumulation of myosin in the actin scar prior to a significant dissasembly of the cor-
tex. A mathematical model of actin-myosin dynamics developed to explain our experimental
observations shows that the accumulation of myosin in the actin scar is a robust mechanism
driven by a significant increase in the binding rate of myosin relative to the rate of cortex dis-
assembly. Together, our experiments and theory suggest that myosin mediates the onset and
duration of cortex degradation during bleb stabilization through locally regulated accumula-
tion, which we postulate is triggered by the separation of the membrane from the cortex. A
mathematical model of a signaling pathway that regulates myosin recruitment to the cortex
during membrane separations is subsequently developed to test our hypothesis.

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Nutrient-mediated pathogen infectivity and host immunity in primary producers

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Abstract

Hosts rely on the availability of nutrients for growth,   as well as for their defense against pathogens. At the same time, changes in primary producer nutrition can alter the dynamics of pathogens that rely on their host for reproduction. Enhanced nutrient loads may thus promote faster pathogen transmission through increased pathogen reproduction and higher host biomass

that stimulates density-dependent transmission. However, this effect may be reduced if hosts allocate growth-limiting nutrients to pathogen defense. In traditional, however, mathematical models of disease, transmission is rarely a function of nutrient availability. Here, we explored the implications of nutrient-mediated pathogen infectivity and host immunity on infection outcomes using a nutrient-mediated transmission model that explicitly integrates the contrasting dependencies of pathogen infectivity and host immunity on nitrogen (N). Our findings reveal dynamic shifts in host biomass build-up, pathogen prevalence, and force of infection, along N supply gradients with N-dependent host infectivity and immunity, compared to a fixed transmission model. We show contrasting responses in pathogen performance with increasing N supply between N-dependent infectivity and N-dependent immunity, revealing an optimum for pathogen transmission at intermediate N supply. This is caused by N limitation of the pathogen at low N supply and by pathogen suppression via enhanced host immunity at high N supply. By integrating both nutrient-mediated pathogen infectivity and host immunity, we provide a theoretical framework that is a first step in reconciling the contrasting role nutrients can have on host-pathogen dynamics.

Mathematical Modeling of Waning and Boosting of COVID-19 Immunity through Infection and Vaccination to Predict Seroprevalence in Hungary

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Abstract

The emergence of Covid-19 has had enormous impacts on global health. In the past two years, we have successfully extended our previous work [1], which addressed problems related to estimating the impact of COVID-19 vaccination strategies in the study of the outbreak in Canada [2, 3] and France [4], by formulating an age-structured model based on an SEIV compartmental modeling framework to study the waning and boosting of COVID-19 through infection and vaccination in Hungary. Our model directly takes into account non-pharmaceutical mitigation strategies that impact activity and contact rates. We identify one important parameter which measures factors including compliance to non-pharmaceutical interventions (masks, social distancing), weather conditions (seasonality), shifts in testing and contact rates, and effects of different strains. We identify this parameter value by fitting our model solution to hospitalization data from Hungary using a genetic algorithm. We also use vaccination data to inform the vaccination rate. The model results enable us to calculate the attack rate and

immunity seroprevalence of SARS-CoV-2. Our predictions can provide useful information for
future disease surges and can be valuable in guiding public health policies.

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2.10 Braverman

Delayed harvesting models: sustainability challenges

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Abstract

For non-delayed models, the relation between the intrinsic growth rate and the harvesting effort completely describes the outcome. The situation changes when resource exploitation is based on the outdated information leading to delay in harvesting. We consider two types of harvesting: continuous (corresponding to permanent reduction) and impulsive (assuming that the duration of the harvesting event is negligible compared to the process time). We explore the influence of delay on sustainability. Note that extinction can be observed in the case when a positive equilibrium solution is locally stable. In line with this, optimality of a solution is not delay-dependent and is aligned with [1], see also [2].

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Prey-predator eco-evolutionary dynamics of HIV immune escape

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Abstract

Population dynamics and evolutionary genetics underly the structure of ecosystems. We
analyze a resource-prey-predator differential equation network model to characterize the emer-
gence of distinct stable equilibria and persistence of different diverse collections of virus and
immune populations. Using binary sequences to code viral strain resistance to immune re-
sponses, we prove that bifurcations are determined and simplified by a certain evolutionary
genetics measure of nonlinearity in the map from viral sequences to fitness landscape. The
results generalize to decipher stability, structure and invasion of ecological networks based on
an algebra of prey binary sequences encoding predation and fitness trade-offs.

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Rethinking mosquito control: Gene drives and the consequences of over-suppression

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Abstract

Suppression gene drives (SGDs) spread a deleterious genetic cargo through a population by biasing their own inheritance. This technology offers a promising solution to the burden posed by crop pests and vectors of important human diseases. Presently, theoretical and experimental studies favor SGD constructs that rapidly eradicate a population. If drive killing occurs faster than drive spreading, however, the target species can be locally eradicated before it is able to spread the SGD to the rest of the target population. This phenomenon, in which drive killing hinders overall gene drive performance, is referred to as over-suppression. The consequences of over-suppression can be dire, especially if the target organism is a vector of human disease, such as mosquitoes. How might we balance SGD lethality with spreading potential? To help answer this question, we develop a patch model to simulate the spread of a SGD in a wild-type mosquito population. The model captures drive spread at both local (migration) and global (immigration) scales. Using various gene drive examples from the literature, numerical experiments are performed to establish under what conditions over-suppression occurs, as well as when the gene drive fails to spread at all.

Hierarchy Establishment from Nonlinear Social Interactions and Metabolic Costs: An Application to Harpegnathos saltator

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Abstract

Social hierarchies are ubiquitous in social groups such as human societies and social insect colonies; however, the factors that maintain these hierarchies are less clear. Motivated by the shared reproductive hierarchy of the ant species Harpegnathos saltator, we have developed simple compartmental nonlinear differential equations to explore how key life-history and metabolic rate parameters may impact and determine its colony size and the length of its shared hierarchy. Our modeling approach incorporates nonlinear social interactions and metabolic theory. The results from the proposed model, which were linked with limited data, show that: (1) the proportion of reproductive individuals decreases over colony growth; (2) an increase in mortality rates can diminish colony size but may also increase the proportion of reproductive individuals; and (3) the metabolic rates have a major impact in the colony size and structure of a shared hierarchy.

Keywords: social insects; nonlinear (shared) hierarchy; nonlinear social interactions; metabolic costs; Harpegnathos saltator

Impact of residence time on the spread of infectious diseases in a heterogeneous environment

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Abstract

In the ongoing COVID-19 pandemic around the world, governments might pose various travel restriction policies internationally as well as domestically. There are several modellings about the impact of varying residence times or travel restrictions such as lockdown on the infectious disease dynamics in a heterogeneous environment. We derived the basic reproduction number and proved that it is monotonically decreasing with respect to the travel restriction factor. Also, we derived the final size relation by using the weighted geometric mean. Numerical simulations illustrate that the final size of the outbreak depends on the travel restriction measure as well as the transmissibility. Moreover, we investigate patch-specific optimal treatment strategies. (*Joint work with Zhisheng Shuai*)

2.15 Chowdhury

Coupling discrete and continuous time scales to investigate the impact of an emerging fungal pathogen in amphibian populations

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Abstract

Infectious disease dynamics in amphibians with multiple routes of transmission are a complicated interwoven system because of the unique metamorphosis over their whole life cycle. The new infectious chytrid fungal pathogen (Batrachochytrium Salamandrivorans, Bsal) has caused dramatic declines in amphibian populations across Europe. Because Bsal has yet to make an appearance in the United States, current research has focused on empirical and theoretical approaches to predicting future outbreaks and identifying control strategies to prevent or mitigate the pandemic if it happens. In this study, we develop a mathematical model of Bsal-infected Eastern Newts by taking into account the population level and age stages (larvae, juveniles, and adults). This is a hybrid modeling approach that integrates disease with amphibian life history dynamics by coupling a system of continuous Ordinary Differential Equations (intra season disease dynamics) with a discrete system of difference equations (annual population demography). In order to incorporate annual breeding seasons, we use a birth pulse for the recruitment of larvae into the model. We aim to compare model performance between purely continuous, annual discrete, and our hybrid approach.

How does seasonality and parasitism impact Honeybee population dynamics

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Abstract

Honey bees are essential pollinators worth \$15 and \$20 billion in the U.S. But climate change affects the flowering season and parasitism timing. These changes lead to a rapid decline in bee populations, which has become a global problem. This paper proposes a honeybee-parasites model that incorporates the seasonality equation into the egg-laying rate. We provide analytical and numerical analysis for our model to understand the climate effects of the honey bee population and the synergistic effects of parasitism and climate change. Exciting findings from our work include 1) climate change has positive and negative influences on the colony; 2) in the bee-only model, the length of seasonality negatively impacts the colony; 3) Parasites can destabilize or coexist with honey bees but reduce the number of bees compared to a healthy colony. Therefore, climate change can help the colonies survive to a certain extent and even help the parasitic colonies. But when the climatic pressure exceeded the colony's ability to withstand it, the colonies that had survived collapsed instead. Our findings partially uncover the intrinsic effects of climate change on bees and parasites and provide essential insights into how best to control parasites.

2.17 Cushing

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A Darwinian SI Model

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We setup a straightforward SI epidemic model in which a treatment is available that controls the pathogen (i.e. that stabilizes the disease-free equilibrium) provided the fraction τ of infected individuals who receive treatment exceeds a certain threshold. We derive a Darwinian version of the model in which the pathogen has a continuous phenotypic trait the promotes resistance to the treatment and that is subject to evolution by Darwinian principles. We analyze the equilibria and their stability properties with an eye towards answering the following question: will treatment level τ still work or will the pathogen manage to evolve resistance and stay endemic? The analysis will reveal one of three outcomes are possible:

- the treatment level τ still succeeds despite the pathogen's adaptation;

- the treatment level τ can succeed but might have to exceed a higher threshold in order to defeat the pathogen's adaptation;

- there are no conditions at all under which any treatment level τ will succeed and the pathogen will always evolutionarily adapt and be endemic.

We give conditions on the evolutionary characteristics of model parameters under which each of these possibilities occurs.

On a nonlinear nonlocal model for a population with separate dispersal and sedentary stages

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Abstract

The life cycles of many species include separate dispersal and sedentary stages. To understand the population dynamics of such species, we study a hybrid model consisting of a reaction-diffusion equation that governs the random movement and settlement of dispersal individuals and an age-structured hyperbolic equation that describes the growth of sedentary individuals. We establish the existence and uniqueness of the solution of the model using the monotone method based on a comparison principle. We then study the population persistence and extirpation by means of three measures.

Separation of Scales in an Integrodifference Equation Model of Metapopulations Predicts Climate Change Effects on Equilibria and Range Case Study: The Mexican Free-Tailed Bat

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Abstract

We develop a novel integrodifference equation (IDE) model of a metapopulation in a system of point-patch habitats wherein life-cycle dynamics within a patch are governed by a growth function (e.g., logistic equation) and movement across the landscape (and between patches) is characterized by a two-stage dispersal process transpiring at discrete time steps (e.g., diurnally). In the first stage, individuals disperse out of their current patch onto the landscape (for foraging and/or mate finding, for example) according to a dispersal kernel. In the second stage, individuals use chemotaxis (via olfactory cues or pheromone concentration gradients) to find new patches for the next time-step. The model is appropriate for a variety of organisms whose habitats may be considered isolated points on a landscape such as bat caves, bee hives, or ant colonies. Equipped with climate-sensitive demographic and dispersal parameters, e.g., birth rate and mean dispersal distance, the model captures the effects of warming temperatures and drought conditions on species persistence and range. Since organism dispersal and odor cue diffusion processes typically occur on spatial scales that differ by several orders of magnitude, we employ a separation of scales method to enable the derivation of analytic predictions of equilibrium populations, cross-roost dispersal, and range expansion/contraction in terms of climate-dependent parameters – hence elucidating the connection between climate change and spatiotemporal dynamics of metapopulations in point-patch habitats.

2.20 Elaydi

Mixed Monotone Maps: Application to evolutionary Models

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Abstract

Based on the evolutionary game theory and Darwinian evolution, we study discrete-time evolutionary population models of a single or multi-species with a single or multiple traits. We introduce the notion of mixed monotone maps and show that, under certain assumptions, these evolutionary models are indeed mixed monotone. This allows us to investigate the global stability of the survival equilibrium. the study is then generalized to evolutionary competitive multi-species with evolution. The study is then extended to periodic systems modeling species with fluctuation habitats.

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Modeling sustained transmission of *Wolbachia* among *Anopheles* mosquitoes: Implications for Malaria control in Haiti

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Abstract

Anopheles albimanus mosquitoes infected with the *wAlbB* strain of *Wolbachia* bacterium are less capable of spreading malaria. We develop and analyze an ordinary differential equation model to evaluate the effectiveness of different vector control strategies in establishing a sustained *Wolbachia* infection among wild *Anopheles* mosquitoes in Haiti. The model involves male and female mosquitoes at egg, larvae, and adult life stages. It also accounts for critical biological effects, including maternal transmission of *Wolbachia* and cytoplasmic incompatibility, which sterilizes uninfected females when they mate with *Wolbachia*-infected males. We derived and interpreted relevant dimensionless numbers, including the basic reproductive number. We then showed that the system presents backward bifurcation, characterized by the disease-free, a complete-infection, and a threshold endemic equilibrium, which corresponds to the minimal infection that needs to be achieved. We ran a sensitivity analysis to rank the relative importance of the epidemiological parameters in Haiti during the rainy season. Lastly, we simulated the integration of traditional vector controls to reduce the wild adult mosquitoes before releasing the *Wolbachia*-infected mosquitoes. Specifically, we assessed the efficacy of two vector controls targeting the larvae stage (larviciding) and adult mosquitoes (thermal fogging) by measuring the speed of establishment of *Wolbachia* among the mosquito population.

Human papillomvirus vaccination strategy: modeling and implications

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Abstract

Human papillomavirus (HPV) infection can spread between regions. What is the impact of disassortative geographical mixing on the dynamics of HPV transmission? How to allocate HPV vaccines between genders within each region and between regions to reduce the total infection? We develop a two-patch two-sex model to address these questions. The control reproduction number R_0 under vaccination is obtained and shown to provide a critical threshold for disease elimination. Both analytical and numerical results reveal that disassortative geographical mixing does not affect R_0 and only has a minor impact on the disease prevalence in the total population given the vaccine uptake proportional to the population size for each gender in the two patches. When the vaccine uptake is not proportional to the population size, sexual mixing between the two patches can reduce R_0 and mitigate the consequence of disproportionate vaccine coverage. Using parameters calibrated from the data of a case study, we find that if the two patches have the same or similar sex ratios, allocating vaccines proportionally according to the new recruits in two patches and giving priority to the gender with a smaller recruit rate within each patch will bring the maximum benefit in reducing the total prevalence.

Supercritical Hopf Bifurcation of Cooperative Predation

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Abstract

A rigorous analysis on the dynamics of a predator-prey model with cooperative predation
is conducted. From the root classification of an algebraic equation, an existence criteria of
the positive equilibria is derived. Critical conditions under which the positive equilibria are
locally asymptotically stable or unstable are found by Jacobian matrix and central manifold
theory. Using a careful computation, a concise and explicit formula for the first Lyapunov
coefficient is obtained. Especially, it is proved that the Hopf bifurcation induced by the coop-
erative predation is always supercritical, which means that the sustained oscillations near the
Hopf bifurcation points are locally asymptotically stable.

Two-Strain Multi-Scale Dengue Vaccination Model Structured by Dynamic Host Antibody Level

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Abstract

Infection by distinct Dengue virus serotypes and host immunity are intricately linked. In particular, certain levels of cross-reactive antibodies in the host may actually enhance infection severity leading to Dengue hemorrhagic fever (DHF). The coupled immunological and epidemiological dynamics of Dengue calls for a multi-scale modeling approach. In this work, we model vaccination by extending a prior model, linking a within-host model which mechanistically recapitulates characteristics of antibody dependent enhancement in Dengue infection. The within-host scale is then linked to epidemiological spread by a vector–host partial differential equation vaccination model structured by host antibody level. The coupling allows for dynamic population-wide antibody levels to be tracked through primary and secondary infections by distinct Dengue strains and vaccination, along with waning of cross-protective immunity after primary infection and vaccination. Analysis of both the within-host and between-host systems are conducted. Stability results in the epidemic model are formulated via basic, control, and invasion reproduction numbers as a function of immunological variables. Additionally, we develop numerical methods in order to simulate the multi-scale model and assess the influence of parameters on disease spread and DHF prevalence in the population.

Evaluation of the United States COVID-19 Vaccine Allocation Strategy

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Abstract

Anticipating an initial shortage of vaccines for COVID-19, the Centers for Disease Control (CDC) in the United States developed priority vaccine allocations for specific demographic groups in the population. In this talk, I present our recent study [1] that evaluates the performance of the CDC vaccine allocation strategy with respect to multiple potentially competing vaccination goals (minimizing mortality, cases, infections, and years of life lost (YLL)), under the same framework as the CDC allocation: four priority vaccination groups and population demographics stratified by age, comorbidities, occupation and living condition (congested or non-congested). We developed a compartmental disease model that incorporates key elements of the current pandemic including age-varying susceptibility to infection, age-varying clinical fraction, an active case-count dependent social distancing level, and time-varying infectivity (accounting for the emergence of more infectious virus strains). The CDC allocation strategy is compared to all other possibly optimal allocations that stagger vaccine roll-out in up to four phases (17.5 million strategies). The CDC allocation strategy performed well in all vaccination goals but never optimally. The developed global optimization approach can be used for future mass vaccination campaigns, and can be adapted for use by other countries seeking to evaluate and optimize their current prioritization strategies.

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Understanding the effiacy of capsid protein allosteric modulators using a multiscale model of hepatitis B virus

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Abstract

As the search for a cure for Hepatitis B virus (HBV) continues, pharmaceutical companies have continued to develop drugs that target different stages of the intracellular life cycle of the virus. The earlier developed drugs, the nucleoside reverse transcriptase inhibitors (NRTIs) analogues, have shown to be effective in suppressing HBV viral load (VL) in patients with chronic infection. However, these drugs need to be taken for a lifetime to maintain VL suppression, creating the risk of adverse effects and the emergence of drug-resistant strains of the virus. The development of a new class of drugs, the capsid protein allosteric modulators (CpAMs), has created a renewed hope for finding a functional cure for HBV. These drugs inhibit the encapsidation of polymerase-pregenomic RNA (pgRNA) in infected cells. We developed a multiscale age-structured model of HBV. Our model incorporates the intracellular and extracellular dynamics of HBV RNA and DNA and keeps track of the age of infection of infected hepatocytes. We derived a mean-field ODE system for our multiscale model and fitted the reduced model to the viral loads of chronic HBV patients treated with CpAMs and NTRIs, to understand the efficacies of the drugs.

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Hierarchical Model for Species Under an Allee Effect with Immigration and a Hollins-Type II Functional Response

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Abstract

In this presentation, we discuss a hierarchical model, based on the Ricker competition model. The species considered are competing for resources and may be subject to an Allee effect due to mate limitation, anti-predator vigilance or aggression, cooperative predation or resource defense, or social thermoregulation. The species may be classify as a dominant species with one or more less dominant or "wimpy" species. The model under consideration also has components taking into account immigration in the species involved and Hollins type II functional response. Stability analysis is discussed and simulations are provided. We also consider demographic stochasticity due to environmental fluctuations in the form of Wiener process and we show that there are conditions under which persistence of the species is possible.

Intraguild predation in a two-species competition model with seasonal birth

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Abstract

In many ecosystems, birth events occur in seasonal pulses. Seasonal birth pulses are sudden and spaced out, so they are well-studied by discrete-time population models. However, many important population processes occur between birth pulses. For example, competition for resources, which directly impacts the success of a birth pulse, develops occurs quickly throughout the year. This type of process is well-studied by continuous-time population models. In this work, we pair continuous- and discrete- models to describe resource competition between two consumers with seasonal birth. We assume intraguild predation, in which one consumer may eat the other as an alternative food source. We additionally assume that the intraguild predator cannot persist with only the shared food source. We determine conditions under which a fixed point for the population cannot exist, and we also conduct numerical experiments across the parameter space to characterize long-term behavior. This work builds on prior efforts to characterize the effect of seasonal birth on continuous population interactions and provides insight into how ecosystems with many interacting species may be affected by seasonal birth pulses.

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Effect of cross-immunity in a multi-strain cholera model

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Abstract

Observed in recent cholera outbreaks is the presence of two serotypes, strains of the cholera
bacteria that mainly differ in their induced host immunity. Each serotype induces both self-
immunity and a degree of cross-immunity to the other strain for some duration. We combine
and extend previously studied SIRP and multi-strain models to consider the strain diversity of
cholera. We explore various ways of incorporating host immunity into this deterministic multi-
strain model, characterizing the dynamics and long-term behavior, particularly in the case of
serotype coexistence.

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A Novel Within-Host Model of HIV and Nutrition

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Abstract

The total protein level in HIV positive individual is noticed relatively higher than the protein level of healthy individual [1, 2, 3, 4]. To understand the interaction of protein and HIV, we develop a four compartmental within-host model. We show that the model has two equilibria; namely infection free equilibrium and infection equilibrium. We also prove that both of those equilibria are unique. We calculate the basic reproduction number R_0 and show that the infection free equilibrium is locally asymptotically stable if $R_0 < 1$ and the infection equilibrium is locally asymptotically stable if $R_0 > 1$. Furthermore, we examine the structural identifiability of the model using differential algebra method. We show that the model is not structurally identifiable from CD4 cell counts and viral load but it is structurally identifiable from CD4 cell counts, viral load and total protein. Moreover, we estimate the parameters of the model using viral load, CD4 cell count and total protein obtained from HIV infected individuals [5, 6]. Next we study practical identifiability of these estimated parameters using Monte Carlo simulations. We employ Monte Carlo simulations with three different data frequencies; data collected at 10 data points each day, data collected every day and data collected more sparsely as real-life data. Monte Carlo simulations show that the clearance rate of virus by immunoglobulins, c_2, is practically unidentifiable when the data is collected at the high frequencies, namely data collected at 10 data points each day and data collected every day. For the real-life data frequency, Monte Carlo simulations show that only recruitment rate of target cells, r, and death rate of target cells, d, are practically identifiable. These results conclude that if the frequency of data collection is high then the more parameters of the model will be practically identifiable.

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Honey bee (*Apis mellifera*) hive placement is more influential than orchard layout on the fruit set of a dioecious crop

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Abstract

Managers of insect-pollinated orchards face many decisions that significantly influence crop yields, including managing pollination through use of beehives and the layout of cultivars. Because understanding the relative importance and interactions between these decisions through empirical field trials is infeasible, modelling provides valuable insights and new hypotheses. With kiwifruit (*Actinidia chinensis* var. *deliciosa* (A. Chev.) A. Chev. 'Hayward'), a dioecious fruiting vine, as an exemplar, we developed a spatially-explicit system of differential equations on a lattice to explore the effects of male and female flowering synchrony, hive placements, and orchard layout on the predicted pollination success. In our model, hive placement and orchard layout influenced the fruit set proportion more strongly than male and female flowering synchrony. Simulations with hives distributed evenly around the orchard had the most fruit set, while hives located at a single point yielded relatively low fruit set. Our model showed more impact from hive distribution on fruit production than planting regime. We used our model to obtain information that orchardists could use to optimize yields. Our model predicts that hive placement during flowering is likely to have greater influence on final orchard productivity in functionally dioecious crops than orchard planting decisions.

Assessing the epidemiological and economic impact of alternative vaccination strategies: a modeling study

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Abstract

The limited supply of the COVID-19 vaccine and its inequitable distribution pose a public health concern contributing to worsening health disparity. This study explores the public health- and economic impact of four possible vaccination strategies – fixed-dose interval (S1), prioritization of the first dose (S2), and screen-and-vaccinate those with the COVID-19 infection history with fixed-dose interval (S3) or first-dose prioritization (S4). Using mathematical modelling, we quantified the number of quarantine- and hospitalization days and deaths averted from each strategy, as well as the associated cost. The model parameters and initial conditions are based on Canada, and the simulation ran over 365 days starting from June 1st, 2021. Net monetary benefit (NMB) and incremental cost-effectiveness ratio were calculated from a societal perspective. In addition, sensitivity analysis explored how each strategy reacts to different conditions of daily vaccine supply, the initial proportion of the recovered, and the initial coverage of the first dose. The findings suggest the potential benefits of alternative vaccination strategies that can save lives and costs. Our study's framework and findings can inform policymakers to explore the optimal COVID-19 vaccination strategy under their unique settings.

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Generalized model to predict the outcome of sequential thermoradiotherapy

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Abstract

{Radiotherapy (RT) is a frequent standard-of-care treatment against cancer because it effectively eradicates malignant cells. However, curative doses may inflict severe side effects and induce secondary malignancies [1]. The efficacy of RT can be strongly enhanced by hyperthermia treatment (HT) for better therapeutic results at lower radiation doses [2]. Recent technological advances in heat application, including stimulation of metal nanoparticles, have revived HT as a promising combinatorial treatment option [3, 4]. However, the mechanisms, implications, and cause-effect relations need to be better elucidated to bring precision HT to clinical routine. In this context, mathematical modeling enlightens the behavior of biological systems under heat based on physicochemical principles, gaining insight into the underlying mechanisms and establishing meaningful quantitative relationships [4, 5]. We present a compartmental mathematical model representing stages of damage accumulation. In this model, the advance and repair rates between compartments are described by physical and biological principles. This formalism leads to treatment operators that allow predicting (i) individual or sequential treatments/fractions outcomes, (ii) the development of treatment tolerance, and (iii) the observed asymmetry in treatment order. Cell-survival predictions display excellent performance ($R^2 > 0.95$) for eight experimentally HT+RT treated cancer cell lines and many data sets from the literature derived from conventional and nanoparticles HT treatment testings.

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Population Persistence in Stream Networks:
Growth Rate and Biomass

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Abstract

We consider the logistic metapopulation model over a stream network and use the population growth rate and the total biomass (of the positive equilibrium) as measures for population persistence. Our objective is to find distributions of resources that maximize these persistence measures. We begin our study by considering stream networks consisting of three nodes and prove that the strategy to maximize the total biomass is to concentrate all the resources in the most upstream locations. In contrast, when the diffusion rates are sufficiently small, the population growth rate is maximized when all resources are concentrated in one of the most downstream locations. These two main results are generalized to stream networks with any number of patches.

Mathematical analysis of the delay differential equation model for the farm level cocoa yield

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Abstract

Cocoa is an important crop that is predominantly grown in the western part of Africa and it contributes to more than three-quarters of the total world cocoa production. However, there has been fluctuation and declining trend in production especially in West Africa and many factors have been identified to be responsible. The most significant factor is the effect of climate variations and this results in low farm-level yield. So, to assess its impact on farm productivity and to understand the contribution of climate variability on the farm level yield, a delay differential equation (DDE) model that simulates the effect of rainfall on cocoa yield was adopted. In this work, we modify and analyze the DDE model that describes the transition period from the cocoa tree flowering stage to pod formation and then harvesting. We introduce a forcing function into the model to account for the growth behavior and then conduct a sensitivity analysis to understand the effect of each model parameter. The results indicate a rapid flower growth and slow decay while the behavior of pods formed indicates a direct dependence on the flower population.

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Modeling the viral resistance to monoclonal antibody treatment for Sars-CoV-2

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Abstract

The COVID-19 pandemic has led to approximately 600 million cases and 6.5 million deaths. To mitigate the loss of lives, emergency authorization was given to several monoclonal antibody therapies for the treatments of mild-to-moderate SARS-CoV-2 patients with high risks of progressing to severe disease. Neutralizing monoclonal antibody treatments target the virus's spike proteins to block its ability to enter and infect target cells. Monoclonal antibody therapy can thus accelerate the decline in viral load, which results in a lower hospitalization rate among high-risk patients. However, viral resistance can develop and lead to the occurrence of transient viral rebound in some patients. This raises an urgent concern regarding drug resistance that could compromise the efficacy of monoclonal antibody therapy.

In this study, we develop mathematical models and fit them to data from SARS-CoV-2 patients. Our results demonstrate that a mechanism, which allows virus access to additional supply of target cells during the infection, is necessary to describe the transient viral rebound. In particular, incorporating the effect of innate and adaptive immune response in a target cell limited model with multiple viral populations paints the most accurate picture of the observed viral recrudescence.

Modeling immunity to malaria with an age-structured PDE framework

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Abstract

Individuals acquire protection from malaria through repeated exposure, and this immunity plays a crucial role in the dynamics of malaria spread. We develop and analyze an age-structured PDE model, which couples vector-host epidemiological dynamics with immunity dynamics. Our model tracks the acquisition and loss of anti-disease immunity during transmission and its corresponding nonlinear feedback onto the transmission parameters. We derive the basic reproduction number ($\mathcal{R}_0$) as the threshold condition for the stability of disease-free equilibrium and interpret $\mathcal{R}_0$ probabilistically as a weighted sum of cases generated by infected individuals at different infectious stages and ages. Numerical bifurcation analysis demonstrates the existence of an endemic equilibrium which spawns through a forward bifurcation in $\mathcal{R}_0$ (in the absence of disease induced mortality) and we study the structure of this equilibrium as a function of system parameters. Our model reproduces the heterogeneity in the age distributions of immunity profiles and infection status created by frequent exposure. Motivated by the recently approved RTS,S vaccine, we also study the impact of vaccination; our results show a reduction in severe disease among young children but a small increase in severe malaria among older children due to lower acquired immunity from delayed exposure.

Multistage spatial model for informing release of *Wolbachia*-infected mosquitoes as disease control

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Abstract

Wolbachia is a natural bacterium that can infect *Aedes* mosquitoes and block the transmission of mosquito-borne diseases, including dengue fever, Zika, and chikungunya. Field trials have been conducted worldwide to suppress local epidemics. We present a new partial differential equation model for the spread of *Wolbachia* infection in mosquitoes. The model accounts for both the complex *Wolbachia* vertical transmission cycle and detailed life stages in the mosquitoes, and it also incorporates the spatial heterogeneity created by mosquito dispersion in the two-dimensional release domain. Field trials and previous modeling studies have shown that the fraction of infection among mosquitoes must exceed a threshold level for the infection to persist. We identify a threshold condition for having a self-sustainable *Wolbachia* infection in the field. When above this threshold, we also show the model gives rise to a spatial wave of *Wolbachia* infection. We quantify how the threshold condition and invasion velocity depend on the diffusion coefficients and other model parameters, and we study different release scenarios to inform the efficient spatial design of the releases.

Mathematical modeling of L. monocytogenes under simulated human gastric conditions in the presence of milk products

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Abstract

L. monocytogenes is one of the top food pathogens that spreads through traditional foods and causes frequent outbreaks. A high number of hospitalization and casualty is associated with Listeriosis. We evaluate the survival potential of the pathogen in the initial path of human digestive tract and highlight the survival and killing factors. A human stomach simulator is used to experiment the survival factors and a mathematical model is developed to predict the pathogen dynamics in the given conditions. Key parameters are estimated. The sensitivity of the pathogen survival over the milk products and stomach acidity is important for food safety and public health.

Using mathematical modeling and feature selection techniques to infer the predictors of the SARS-CoV-2 transmissibility

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Abstract

The Basic Reproduction Number (R0) is an important epidemiological parameter measuring the inherent virus transmissibility in a population with fixed sociodemographic and environmental characteristics without any control measures. Our study aimed to identify the direct predictors of R0 for the SARS-CoV-2 virus among various, often mutually correlated factors [1]. We constructed a dynamic compartmental model to describe the COVID-19 epidemic progression in a population. From the model, we derived the dependence of R0 on the slope of the case growth curve in the initial exponential phase on a semi-logarithmic scale, which allowed us to estimate the R0 values for 118 countries. We applied the Principal Component Analysis to the meteorological and sociodemographic variable sets, and then independently used four variable selection techniques (a custom multiple regression analysis, Stepwise regression, Lasso, and Elastic net) to find the best R0 predictors among the (uncorrelated) principal components. The country's high prosperity level (probably a proxy for the extent of long-distance contacts) and unhealthy lifestyle and environment, as obtained robustly by multiple methods, might be the direct positive R0 predictors, while the low indoor crowdedness, a delayed epidemic onset, and warm summer weather could negatively influence the virus transmissibility.

Eighth International Conference on Mathematical Modeling and Analysis of Populations
in Biological Systems, Lafayette, Louisiana, October 28-30, 2022

Modeling SARS-CoV-2 immuno-epidemiological dynamics

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Abstract

The COVID-19 pandemic is a global emergency with significant morbidity and mortality. In this talk, we use mathematical models to investigate the potential future SARS-CoV-2 transmission dynamics, landscapes of immunity, and the effect of vaccination. Since there are substantial uncertainty on the strength and duration of immunity following natural infection or vaccination, we examine a range of scenarios. Through a general framework, we also explore the potential epidemiological and evolutionary considerations of various vaccine dosing regimes. We then examine the impact of vaccine nationalism on SARS-CoV-2 immuno-epidemiological dynamics and control. Finally, using a simple mathematical model, we examine the invasion dynamics of SARS-CoV-2 variants and the impacts of vaccine breakthrough infections.

Dispersal-driven coexistence in a multiple-patch competition model for zebra and quagga mussels

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Abstract

The zebra and quagga mussel are among the world notorious invasive species because of their large and widespread ecological and economic effects. Although these two species have similar life histories, share many ecological traits, they have some significant ecological differences and impacts. Understanding their long-term population dynamics is critical to determining impacts and effective management. To investigate how the population reproduction rates, intraspecific and interspecific competitions, as well as dispersal abilities affect the population persistence and spatial distributions of the two species in a spatially heterogeneous environment, we developed a dynamic model that describes the competitive interactions between zebra and quagga mussels in multiple patches. The dynamic analysis of the model yields some sufficient conditions that lead to population persistence, extirpation, as well as competitive exclusion and coexistence. By the numerical solutions of a two patch model, we examine how the interplay between the local population dynamics in each patch and the individual dispersal between patches affects the competition outcomes of the two species in a spatially variable system.

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Probabilistic machine learning for uncertainty representation and applications to neural encoding in biological sensory systems

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Abstract

Machine learning offers an immensely powerful set of methods that can analyze and automatically detect patterns in data, use these patterns to predict future data, and make decisions under uncertainty, with countless applications. Probabalistic ML employs probability theory tools to solve problems involving uncertainty, such as neural encoding. Famously, simple cells in primary visual cortex were found to respond to low-level image components (e.g. edges) [1]. Sparse coding and independent component analysis emerged as standard computational models for simple cell coding because these models linked the receptive fields to the statistics of visual stimuli [2, 3, 4, 5]. Recent psychophysical/electrophysiological studies indicate that perception encodes a posterior probability distribution over possible 'causes' of sensory stimuli (not merely the most likely interpretation) [6, 7, 8, 9, 10, 11], which is used to act close to optimally in the environment [12, 13, 14]. However, exact posteriors are generally too complex to represent directly, thus neurons will have to encode approximations of these distributions [e.g. 15, 16, 17]. In this talk I will review probabilistic ML, introduce our approach to efficient/scalable approximate inference in the context of neural encoding, present results from numerical and *in vivo* experiments, and discuss further potential biological applications.

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A Discrete-Time Predator-Prey Model
with Selection and Mutation in the Prey

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Abstract

We study a discrete-time predator-prey model with selection and mutation in the prey population, where individuals are distributed over a finite number of phenotypic traits and may reproduce individuals with same trait (selection) or with different traits (mutation). In the case of pure selection where individuals in the prey-population only reproduce individuals with the same trait, we establish conditions for competitive exclusion and demonstrate that the system converges to a boundary equilibrium that represents survival of the predator and the fittest prey trait. For the full selection mutation model, we explore coexistence by establishing the persistence of multiple traits. We conclude by conducting numerical simulations to support and supplement the theoretical results and shed light on potential model dynamics.

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Adaptive deep brain stimulation in a biophysical network model of Parkinson's disease

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Abstract

In a normal state, the thalamocortical neurons (TC) in the thalamus serve to relay excitatory inputs from the sensorimotor cortex while they are targeted by the inhibitory output from the internal segment of the globus pallidus (GPi) in the basal ganglia. In parkinsonian conditions, a TC neuron fails to respond to excitatory cortical inputs in a one-to-one fashion. The TC cell either fires multiple spikes or no spikes at all in response to a single cortical excitatory signal. In the past two decades, deep brain stimulation (DBS) - through a surgically implanted electrode to the subthalamic nucleus (STN) - has become a widely used therapeutic option for the treatment of Parkinson's disease and other neurological disorders. To overcome the limitations of continuous high frequency DBS, researchers are developing adaptive protocols where stimulation is turned on and off according a feedback signal. We incorporate two types of adaptive STN stimulation using the interspike interval as the on-off mechanism. The first protocol consists of constant pulses while the second features coordinated reset shuffling of the local field potential recorded from the STN neurons. Our computational results show both methods decrease TC relay errors. Both methods represent promising potential therapeutics for Parkinson's disease.

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Comparing and Examining Different Methods of Determining Structural and Practical Identifiability of a Vector-Host Model

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Abstract

In order to predict the spread of outbreaks of vector-host diseases such as dengue fever and malaria, researchers create compartmental models which employ ordinary differential equations. It is an expanding problem of interest to investigate the structural or a priori identifiability and the practical identifiability of compartmental models. We compare the accuracy and efficiency of multiple methods for computing structural and practical identifiability of an SIS (Susceptible-Infected-Susceptible) vector-host model. We performed structural identifiability analysis of the model via a differential algebra approach, an approximation of the differential algebra approach using truncated power series and modulo arithmetic, and a combination of the differential algebra approach and the Taylor series approach. We also performed practical identifiability analysis of the model via the Monte Carlo and Profile Likelihood methods. We found that there were instances where the approximation of the differential algebra approach differed from the results of the combination of the differential algebra approach and Taylor series approach, and computed the structural identifiability of models with certain fixed parameters and initial conditions. For the Monte Carlo method, we found that the choices of both the error model and the initial guess of parameters have a large impact on practical identifiability results. For profile likelihood, we derive formula for computing profile likelihood for relative normal noise distribution, and we explore how data and different noise distributions can impact parameter estimation, confidence intervals, and identifiability

2.47　Trigos

Coexistence due to life history variation revisited in models with explicit patch aging

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Abstract

How competing species coexist remains a major challenge for theoretical and mathematical ecology. Disturbance, and the subsequent progression of competitive dynamics, or 'aging' of patches, have been posited as creating opportunities for coexistence. However, prior work studying this possibility has limitations—importantly it has not delineated coexistence opportunities arising from the process of patch aging. We study a simple PDE model which accounts for patch aging while remaining analytically tractable in many cases. We consider two possible types of density-dependence under disturbance: 1) on reproduction and 2) on recruitment. We present conditions for feasible coexistence (both species have positive populations) and 'stable' coexistence in the sense of mutual positive long-term invasion. We confirm our results using a 2nd order flux limiter numerical method. Under density-dependent recruitment, our model does not permit coexistence. However, under density-dependent reproduction, variation between two species along either a reproduction-survival trade-off or a trade-off between robustness of reproduction to shading and survival allow for coexistence. Intermediate values of disturbance lead to a wider coexistence region. These trade-offs differ from the classic competition-colonization trade-off which prior models that ignore patch aging have highlighted as coexistence enabling.

Structural and practical identifiability analysis of a multiscale immuno-epidemiological model

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Abstract

We perform the identifiability analysis of a multiscale model of seasonal influenza with multiscale data. We show that the well studied target cell limited within-host model is not structurally identifiable. So, we reformulate the model and work with a scaled within-host model which is structurally identifiable. We find that the scaled within-host model is practically identifiable with respect to two distinct viremia data sets while fitting with weighted or unweighted least squares. We introduce a methodology on how to study the structural identifiability of multiscale epidemic models specifically nested immuno-epidemiological models. All parameters of the multiscale model are practically identifiable. Furthermore, we find that the practical identifiability of the multiscale model is significantly better when fitted to viremia and incidence data as opposed to when fitted to viremia and cumulative incidence data. Comparing first and second order numerical methods for solving the partial differential equations suggests that using a higher order numerical method does not affect the identifiability of the parameters. Further simulations suggest that the choice of the linking functions has some impact on identifiability when viremia and incidences are fitted but no impact when viremia and cumulative incidences are fitted.

Pathogen dynamics in a tick-host system

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Abstract

We develop a discrete-time tick-host-pathogen model for a hard-bodied tick population to
study the invasion and establishment of a tick-borne pathogen. This model includes the de-
velopmental stages for a tick, the dependence of the tick lifecycle and disease transmission
on host availability, and three sources of pathogen transmission. We first establish the global
dynamics of the disease-free system. We then apply the model to two pathogens, *Borellia
burgdorferi* and *Anaplasma phagocytophila*, using *Ixodes ricinus* as the tick species to study
properties of the invasion and establishment of a disease numerically. We consider three dis-
ease metrics, namely the basic reproduction number, the disease prevalence and time to disease
establishment.

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A reaction-advection-diffusion model of cholera epidemics with seasonality and human behavior change

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Abstract

Cholera is a water- and food-borne infectious disease caused by *V. cholerae*. To investigate multiple effects of human behavior change, seasonality and spatial heterogeneity on cholera spread, we propose a reaction-diffusion-advection model that incorporates human hosts and aquatic reservoir of *V. cholerae*. We derive the basic reproduction number $\mathcal{R}_0$ for this system and then establish a threshold type result on whether the cholera spreads in terms of $\mathcal{R}_0$. Further, we show that the relative rate of bacterial loss at the downstream end of the river due to water flux can reduce the disease risk, and describe the asymptotic behavior of the basic reproduction number $\mathcal{R}_0$ with small and large diffusion. We also study the transmission dynamics at the early stage of cholera outbreak numerically, and find that human behavior change may lower the infection level and delay the disease peak. Moreover, the relative rate of bacterial loss, together with convection rate, plays an important role on identifying the severe infected areas. Meanwhile spatial heterogeneity may dilute or amplify cholera infection, which increases the complexity of disease spread.

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Global dynamics of Lotka-Volterra competition patch models

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Abstract

The global dynamics of the two-species Lotka-Volterra competition patch model with asymmetric dispersal is classified under the assumptions of weak competition and the weighted digraph of the connection matrix is strongly connected and cycle-balanced. It is shown that in the long time, either the competition exclusion holds that one species becomes extinct, or the two species reach a coexistence equilibrium, and the outcome of the competition is determined by the strength of the inter-specific competition and the dispersal rates.

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Why multilingual, and how to keep it – An evolutionary dynamics perspective

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Abstract

We consider a mixed population of multilingual speakers and in particular, bilingual speakers, with multilingual defined broadly as zero, limited, or full uses of multiple languages or dialects, and propose an evolutionary dynamic model for its development and evolution. The model consists of two different parts, formulated as two different evolutionary games, respectively. The first part accounts for the selection of languages based on the competition for popularity and social or economic advantages. The second part relates to circumstances when the selection of languages is altered, for better or worse, by forces other than competition such as public policies, education, or family influences. By combining competition with intervention, we show how multilingualism may evolve under these two different sources of influences. We show that by choosing appropriate interventional strategies, the stable co-existence of languages, especially in multilingual forms, is possible, and extinction can be prevented. This is in contrast with major predictions from previous studies that the co-existence of languages is unstable in general, and one language will eventually dominate while all others will become extinct.

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Social distancing is a social dilemma game played by every individual against his/her population

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Abstract

In a severe pandemic, every individual engages in social distancing and needs to decide how to reduce social contacts while maintaining minimal social activities. A theoretical framework for the understanding of the nature of social distancing is discussed, with social distancing being considered as a social dilemma game played by every individual against his/her population. As the players of the game, an individual's decision depends on the population's action and vice versa, and the game reaches equilibrium when an optimal strategy is found for all the individuals. The optimal strategies are derived for populations with either closely related or completely separated social activities and with either single or multiple social groups. The collective behaviors of social distancing are simulated by following the individuals' actions as the distancing game is played out among them. The simulation results for populations of varying sizes and complexities are presented, which not only justify the theoretically predicted strategies, but also demonstrate the convergence of the individual actions to an optimal distancing strategy if every individual makes rational distancing decisions.

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Bifurcation Analysis of Critical Values for Wound Closure Outcomes in Wound Healing Experiments

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Abstract

A nonlinear partial differential equation containing a nonlocal advection term and a diffusion term is analyzed. The model is applicable to wound healing experiments, which are widely used in testing the efficacy of therapeutic drugs . The key issue in these experiments is the distinction of healing and non-healing . The model provides understanding of this issue in terms of critical values based on bifurcation of parameter values in the model.

3 Poster Abstracts

3.1 Chindal

Estimating R_0 For Dengue Emergence In Central Argentina Using Statistical Models

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Abstract

Dengue is a mosquito-borne disease and is prominent in tropical and subtropical regions of the world, but has recently been emerging in temperate areas. In Córdoba, a city in temperate central Argentina, there have been several dengue outbreaks in the last decade. Prior to 2009, dengue cases had not been reported in Córdoba. However, major outbreaks occurred in 2009, 2013, 2015, 2016, and 2020. The basic reproductive number, R_0, is one measure to determine the severity of new outbreaks. In this project, we make use of various statistical methods and apply them to estimate R_0 for dengue in Córdoba. Some of the statistical methods we utilized were Exponential Growth, White and Pagano Maximum Likelihood, EpiEstim Sequential Bayesian, and Wallinga and Tenunis Time-Dependent methods. We estimated R_0 for the four major outbreaks between 2009 and 2016. All the statistical methods produced similar R_0 predictions, which were comparable to estimates from other regions around the world. These estimates of R_0 can be useful for planning mosquito control and other mitigation strategies in the future.

3.2 Chukwu

Assessing the impact of co-dynamics Listeriosis-Meningitis in human population

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Abstract

The co-infection of Listeriosis and Meningitis in humans is a public health burden globally with its endemicity mostly felt in the tropical and sub-tropical countries. In this study, we develop a novel deterministic model describing the Listeriosis-Meningitis co-infection dynamics. Two sub-models, namely the Listeriosis-only and Meningitis-only sub-models are presented and analysed. Mathematical analysis of each sub-model is carried out, as well as that of the co-infection model. We use Latin-hypercube sampling to determine the parameters affecting the severity of the infection co-dynamics. Results from the numerical simulations suggest that reduction in the Listeria pathogens in the environment and an increase in the Meningitis recovery rate decreases the rate of Listeriosis-Meningitis co-infections

3.3 Keya

The influence of density in population dynamics with Allee effect

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Abstract

In this paper, we consider a reaction–diffusion model in population dynamics and study the impact of different types of Allee effects with logistic growth in the heterogeneous closed region. For strong Allee effects, usually, species unconditionally die out and an extinction-survival situation occurs when the effect is weak according to the resource and sparse functions. In particular, we study the impact of the multiplicative Allee effect in classical diffusion when the sparsity is either positive or negative. Negative sparsity implies a weak Allee effect, and the population survives in some domain and diverges otherwise. Positive sparsity gives a strong Allee effect, and the population extinct without any condition. The influence of Allee effects on the existence and persistence of positive steady states as well as global bifurcation diagrams is presented. The method of sub-super solutions is used for analyzing equations. The stability conditions and the region of positive solutions (multiple solutions may exist) are presented. When the diffusion is absent, we consider the model with and without harvesting, which are initial value problems (IVPs) and study the local stability analysis and present bifurcation analysis. We present a number of numerical examples to verify analytical results.

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A simple SEIR-V model to estimate COVID-19 prevalence and predict SARS-CoV-2 transmission using wastewater-based surveillance data

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Abstract

Wastewater-based surveillance (WBS) has been widely used as a public health tool to monitor SARS-CoV-2 transmission. However, epidemiological inference from WBS data remains understudied and limits its application. In this study, we have established a quantitative framework to estimate COVID-19 prevalence and predict SARS-CoV-2 transmission through integrating WBS data into an SEIR-V model. We conceptually divide the individual-level viral shedding course into exposed, infectious, and recovery phases as an analogy to the compartments in a population-level SEIR model. We demonstrated that the effect of temperature on viral losses in the sewer can be straightforwardly incorporated in our framework. Using WBS data from the second wave of the pandemic (Oct 02, 2020 – Jan 25, 2021) in the Greater Boston area, we showed that the SEIR-V model successfully recapitulates the temporal dynamics of viral load in wastewater and predicts the true number of cases peaked earlier and higher than the number of reported cases by 6 – 16 days and 8.3 – 10.2 folds (R = 0.93). This work showcases a simple yet effective method to bridge WBS and quantitative epidemiological modeling

Eighth International Conference on Mathematical Modeling and Analysis of Populations
in Biological Systems, Lafayette, Louisiana, October 28-30, 2022

Dynamical Models of Plant-Pollinator Interactions with Application to Honeybee

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Abstract

The interaction between plants and pollinators is one of the most important in all ecosystems on the planet. Most plants need a pollinator for a success reproduction. Balance in this relationship is vital for the maintenance of ecosystems and life as we know it today. Effective plant reproduction results in seeds and fruits that we consume and use on a daily basis. Studying and understanding mutualistic interactions between plants and their pollinators is essential to our ecosystems and our human society. In this project, we develop a modeling framework to explore how may plants and/or pollinator being faculative versus obligate to each other impact their population dynamics. We also applied the framework to honeybee to understand how may cooperative efforts in pollinator affect the population dynamics

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Temperature variations can affect the biocontrol of agricultural pests by generalist predators

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Abstract

Agricultural pests can be controlled in part by using pesticides, but natural populations of generalist predators also play a significant role. Pest control in agricultural fields depends on the potential interaction of species in the natural predator community. Predation by natural communities of beetles and spiders is influenced by intraguild interactions, species traits, and environmental factors. Temperature plays a crucial role in this context because changes in species traits occur in accordance with temperature fluctuations. Due to global warming, it's more important than ever to understand how predator-prey interactions change with temperature. In our model, we have incorporated the effect of temperature on the foraging activity of predators. Using simulations, we show how temperature-dependent behaviors may alter the expected efficacy of the generalist predators seen in agricultural fields. To find the most effective combination of predator communities for pest management, we then use an optimization technique. Finally, we investigate how the most effective predator compositions might change with increasing average daily temperature and temperature variability under climate change. This study emphasizes the significance of understanding how climate change influences natural predator communities and how to create pest management strategies that are appropriate for future biological control under various climate scenarios.

A Framework for Stochastic, Size-structured Neutral Model for Community

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Abstract

Neutral Biodiversity Theory (NBT) describes communities where competitors coexist due to their similar performance in the environment, in which case stochastic birth, death, and dispersal events are the predominant influence on community-level characteristics. Deviations in observations of these characteristics from NBT's predictions could indicate when mechanisms other than chance are important, such as classical niche differences instead enabling a stable coexistence of competing species. The original NBT ignored potential variation within species in birth and death rates. More recently, a size-structured NBT was developed to improve NBT by considering size-based variation in demographic rates. However, this size-structured NBT approximated speciation to be like immigration and ignored size variation in birth rates. In this work, we are improving upon this prior work to develop an accurate and complete size-structured NBT. We have derived an equation for the generating function of our improved size-structured NBT and found its solution. Work in progress is to use it to derive the Species Abundance Distribution (SAD) and Species Biomass Distribution (SBD), i.e. the distributions describing how many rare vs common species there are when abundance is measured on the basis of the number of individuals and total biomass across individuals respectively.