ICMA VII: The Seventh International Conference on Mathematical Modeling and Analysis of Populations in Biological Systems

October 12 -14, 2019

Wexler Hall, Arizona State University, Tempe, Arizona, USA

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The National Science Foundation, Program in Mathematical Biology

BRIEF SCHEDULE FOR ICMA 2019

Plenary lectures will be held in Wexler Hall (WXLR) Room A21
Parallel sessions will be held in WXLR A21 (r1), WXLR A104 (r2), WXLR A107 (r3), WXLR A 113 (r4)
By default, the chair of each session is the third speaker of that session
Registration is open 8 AM to 5 PM on October 12, 2019 in WXLR 118

Schedule for Saturday, October 12, 2019

8:15 AM -8:30 AM: **Welcoming Remarks** (Wexler Hall A21)

8.30 AM- 8:45 AM: Group Photograph (Old Main Building)

8:45 AM -9:45 AM: **Plenary Lecture** (Wexler Hall A21) – Sebastian Schreiber (Chair: Abba Gumel)

9:45 AM -10:00 AM: Coffee Break

10:00 AM -12:00 PM: Parallel Sessions
Session 01 (r1): Edward Allen, Suzanne Robertson, Linda J S Allen, Nhu Nguyen.
Session 02 (r2): Peter Hinow, Craig Thalhauser, Susan Massey, Megan Sawyer.
Session 03 (r3): Adam Lampert, Daniel Cooney, Jim Cushing, Alex Farrell.
Session 04 (r4): Jun Chen, M. Gabriela Navas-Zuluoga, Oyita Udiani, Tao Feng.

12:00 PM -1:30 PM: Lunch Break (Sandwiches will be provided, or on your own)

1:30 PM -3:00 PM: Parallel Sessions
Session 05 (r1): Jack Pringle, Denis Patterson, Horst Thieme.
Session 06 (r2): Kaniz Fatema Nipa, Srijana Ghimire, Junping Shi.
Session 07 (r3): Brittany Boribong, Jay Newby, Saber Elaydi.
Session 08 (r4): Deena Schmidt, Rafiul Islam, Zhisheng Shuai.

3:00 PM-3:15 PM: Coffee Break

3:15 PM -4:15 PM: Plenary Lecture (Wexler Hall A21) – Qing Nie (Chair: Yang Kuang)

4:15 PM-4:30 PM: Coffee Break

4:30 PM-6:00 PM: Parallel Sessions
Session 09 (r1): Dilini Fonseka**,** Paul J. Hurtado, Kelly Reagan.
Session 10 (r2): Patrick De Leenheer, Ahuod Alsheri, Pauline van den Driessche.
Session 11 (r3): Jaime Lopez, Kelsey Marcinko, Glenn Ledder.
Session 12 (r4): Lihong Zhao, Matthew Beauregard, Lale Asik

6:15 PM -7:15 PM: Poster Session

Schedule for Sunday, October 13, 2019

8:45 AM -9:45 AM: Plenary Lecture (Wexler Hall A21) – Natalia Komarova (Chair: Jim Cushing)

9:45 AM -10:00 AM: Coffee Break

10:00 AM-12:00 PM: Parallel Sessions
Session 13 (r1): Ardak Kashkynbayev, Feng Fu, Evan Milliken, Harsh Jain.
Session 14 (r2): Md. Masud Rana, Md. Nazmul Hassan, Jemal Mohammed-Awel, Yixiang Wu.
Session 15 (r3): Enahoro Iboi, Michael A. Robert, Xingfu Zou, Wandi Ding.
Session 16 (r4): Ephraim Agyingi, Hitoshi Koyano, Hayriye Gulbudak, Nasser Sweilam.

12:00 PM -1:30 PM: Lunch Break (Pizza will be provided, or on your own)

1:30 PM-3:00 PM: Parallel Sessions
Session 17 (r1): Dongming Wei, Tin Phan, Lifeng Han.

Session 18 (r2): Amanda Laubmeier, Md. Kamrujjaman, Angela Peace.
Session 19 (r3): Angelica Bloomquist, Paul Salceanu, Tufail Malik.
Session 20 (r4): Nora Gilbertson, Peter Uhl, Naveen Vaidya.

3:00-3:15 PM: Coffee Break

3:15 PM-4:15 PM: Plenary Lecture (Wexler A21) –Hao Wang (Chair: Hal Smith)

4:15 PM-4:30 PM: Coffee Break

4:30 PM -6:00 PM: Parallel Sessions
Session 21 (r1): Richard Rebarber, Sabina Altus, Katherine Owens.
Session 22 (r2): Congbo Xie, Feng-Bin Wang, Morteza Rouhani.
Session 23 (r3): Khanh Dao Duc, William Fagan, Andres Baeza-Castro.
Session 24 (r4): Chadi Saad-Roy, Yufang Wang, Haiyan Wang.

Schedule for Monday, October 14, 2019

8:45 AM-9:45 AM: Featured Talk (Wexler Hall A21) –Brian Yurk and Christina Cobbold
(chair: Saber N. Elaydi)

9:45 AM -10:00 AM: Coffee Break

10:00 AM-12:00 PM: Parallel Sessions
Session 25 (r1): Christopher Heggerud, Xiao Wang, Changhan He, Xiaojun Tian.
Session 26 (r2): Benjamin Liu, Zhuolin Qu, Jean Lubuma, Daniel Collister.
Session 27 (r3): Hai-Dang Nguyen, Mughda Thakur, Yun Kang.
Session 28 (r4): Awino Maureiq Edith Ojwang, Brandon Hollingsworth.

PROGRAM SCHEDULE FOR ICMA 2019

Plenary lectures will be held in Wexler Hall (WXLR) Room A21
Parallel sessions will be held in WXLR A21 (r1), WXLR A104 (r2), WXLR A107 (r3), WXLR A 113 (r4)
By default, the chair of each session is the third speaker of that session
Registration is open 8 AM to 5 PM on October 12, 2019 in WXLR 118

SATURDAY MORNING (October 12)

8:45 AM-9:45 AM: **Plenary Talk** (WXLR A21) –Stochastically induced extinction, coexistence, and alternative stable states
Sebastian Schreiber, University of California, Davis

10:00 AM -12:00 PM: Parallel Sessions

Session 01 (r1)

10:00 -10:30 AM: Environmental variability in SDE population models
Edward Allen, Texas Tech University
10:30 -11:00 AM: The role of the avian nesting curve in structuring enzootic *West Nile virus* transmission
Suzanne Robertson, Virginia Commonwealth University, Richmond
11:00 -11:30 AM: The role of Allee effects on the evolution of semelparity and iteroparity
Linda Allen, Texas Tech University
11:30 AM-12:00PM: How the shape of the fertility-survival curve impacts expected life history strategies
Nhu Nguyen, Wayne State University

Session 02 (r2)

10:00 -10:30AM: Machine learning for automatic segmentation of multielectrode array recordings for electrophysiological analysis
Peter Hinow, University of Wisconsin, Milwaukee
10:30 -11:00 AM: Using a suite of quantitative systems pharmacology models to support clinical development of a novel therapy in autoimmune diseases
Craig Thalhauser, Bristol-Myers Squibb
11:00 -11:30 AM: Quantifying drug distribution and response dynamics in experimental glioblastoma
Susan Massey, Mayo Clinic, Phoenix
11:30 AM -12:00 PM: Exploration of global sensitivity analysis methods for physiologically-based pharmacokinetic (PBPK) models
Megan Sawyer, Southern New Hampshire University

Session 03 (r3)

10:00 -10:30 AM: How should multiple agents allocate their contributions to eradicate a common harmful species?
Adam Lampert, Arizona State University
10:30 -11:00 AM: PDE models for multilevel selection: The ghost of lower-level selection and transitions in biological complexity
Daniel Cooney, Princeton University
11:00 -11:30 AM: The role of Allee effects on the evolution of semelparity and iteroparity
Jim Cushing, University of Arizona
11:30 AM -12:00 PM: How the shape of the fertility-survival curve impacts expected life history strategies
Alex Farrell, University of Arizona

Session 04 (r4)

10:00 -10:30 AM: A honeybee population model with stage structure and seasonality
Jun Chen, Arizona State University
10:30-11:00 AM: To run or not to run? A Markov–chain model for behavioral switch during nest selection in Temnothorax
M. Gabriela Navas-Zuluoga, Arizona State University
11:00-11:30 AM: Disease, demography and the evolution of social organization
Oyita Udiani, University of Tennessee
11:30 AM-12:00 PM: Dynamics of task allocation of social insect colonies
Tao Feng, Arizona State University and Nanjing University of Science and Technology

SATURDAY AFTERNOON (October 12)

1:30 PM -3:00 PM: Parallel Sessions

Session 05 (r1)

1:30 -2:00 PM: A mathematical examination of wolf reintroduction in Yellowstone National Park: Capturing the mechanisms of predator dependent birth rates of prey
Jack Pringle, Arizona State University
2:00 -2:30 PM: Deriving a spatially extended model of savanna dynamics
Denis Patterson, Brandeis University
2:30-3:00 PM: Rabies spreading speeds, territorial and diffusing rabid foxes, and arbitrarily distributed latency
Horst Thieme, Arizona State University

Session 06 (r2)

1:30 -2:00 PM: Demographic variability, environmental variability, and periodic fluctuations in stochastic epidemic models with multiple patches
Kaniz Fatema Nipa, Texas Tech University
2:00 -2:30 PM: Traveling wave solution of a diffusive viral infection model with time delay
Srijana Ghimire, University of Louisiana at Lafayette
2:30 -3:00 PM: Effect of spatial average on the spatial-temporal pattern formation of reaction-diffusion systems
Junping Shi, College of William and Mary, Williamsburg

Session 07 (r3)

1:30 -2:00 PM: Quantifying effects of neutrophil memory on migration patterns using microfluidic platforms and ODE modeling of the mechanistic molecular pathways
Brittany Boribong, Virginia Polytechnic Institute and State University, Blacksburg
2:00 PM -2:30 PM: Weaker is better: how weak transient molecular interactions give rise to robust, dynamic immune
Jay Newby, University of Alberta, Edmonton, Alberta, Canada
2:30 -3:00 PM: A Continuous and Discrete Mathematical Models for the Aggregation of beta-Amyloid
Saber Elaydi, Trinity University, San Antonio

Session 08 (r4)

1:30 -2:00 PM: Contagion dynamics on adaptive networks: Norovirus as a case study
Deena Schmidt, University of Nevada Reno, Reno
2:00 -2:30 PM: Mathematical modeling of Batrachochytrium salamandrivorans on the Eastern Newt with multiple transmission pathways
Rafiul Islam, Texas Tech University, Lubbock
2:30 -3:00 PM: Dispersal Induced Dichotomy in Population Dynamics

Zhisheng Shuai, University of Central Florida, Orlando

3:15 -4:15 PM: **Plenary Talk** (WXLR A21) – Multiscale cell fate through lens of single cells
Qing Nie, University of California, Irvine

SATURDAY AFTERNOON (October 12)

4:30 PM - 6:00 PM: Parallel Sessions

Session 09 (r1)

4:30 -5:00 PM: Dynamics of stoichiometric plant-pollinator-herbivore models
Dilini Fonseka, Texas Tech University, Lubbock
5:00 -5:30 PM: A general 'linear chain trick' for building ODE models with flexible Dwell time assumptions
Paul J. Hurtado, University of Nevada Reno, Reno
5:30 -6:00 PM: Saving lives, limbs and healthcare costs: Quantifying the impact of CHG bathing and effective leadership on the reduction of hospital-acquired infections
Kelly Reagan, Virginia Commonwealth University, Richmond

Session 10 (r2)

4:30 -5:00 PM: Stability of diffusively coupled linear systems with an invariant cone
Patrick De Leenheer, Oregon State University, Corvallis
5:00 -5:30 PM: Spatial spread of Chagas disease
Ahuod Alsheri, University of Bisha, Animas, Saudi Arabia
5:30 -6:00 PM: Juvenile-adult discrete time infectious disease models
Pauline van den Driessche, University of Victoria, B.C., Canada

Session 11 (r3)

4:30 -5:00 PM: Nutrient levels and trade-offs control diversity in a model seasonal ecosystem
Jaime Lopez, Princeton University, Princeton
5:00-5:30 PM: A comparative analysis of host–parasitoid models in which density-dependence precedes parasitism
Kelsey Marcinko, University of Washington, Seattle
5:30 -6:00 PM: Competition between consumers in a mixed discrete-continuous model
Glenn Ledder, University of Nebraska-Lincoln, Lincoln, Nebraska

Session 12 (r4)

4:30 -5:00 PM: Resource mediated interactions and species dynamics in microbial communities
Lihong Zhao, University of Idaho, Moscow
5:00 -5:30 PM: Large and small data blow-up solutions in the Trojan Y chromosome model
Matthew Beauregard, Stephen F. Austin State University, Nacogdoches
5:30 -6:00 PM: Environmental seasonality on predator–prey systems under nutrient and toxicant constraints
Lale Asik, Texas Tech University, Lubbock

SUNDAY MORNING (October 13)

8:45 -9:45 AM: **Plenary Talk** (WXLR A21) – Mathematics of evolution: Mutations, selection, and random environments
Natalia Komarova, University of California, Irvine

10:00 AM -12:00 PM: Parallel Sessions

Session 13 (r1)

10:00 -10:30 AM: Traveling wave solutions to Glioblastoma Multiforme growth models.
Ardak Kashkynbayev, Nazarbayev University, Nur-Sultan, Kazakhstan
10:30 -11:00 AM: Multi-type branching process theory with applications to cancer and ecology
Feng Fu, Dartmouth College, Hanover
11:00 -11:30 AM: Dynamics and bifurcations of a model of dendritic cell therapy for melanoma
Evan Milliken, Arizona State University, Tempe
11:30AM-12:00PM: Exploiting androgen deprivation-induced inflammation in prostate cancer treatment
Harsh Jain, Florida State University, Tallahassee

Session 14 (r2)

10:00 -10:30 AM: Spatially heterogeneous producer-grazer model subject to stoichiometric constraints
Md. Masud Rana, Texas Tech University, Lubbock
10:30-11:00 AM: An extension to the toxicant mediated predator-prey model under stoichiometric constraints
Md. Nazmul Hassan, Blinn College, Bryan
11:00 -11:30 AM: Mathematical assessment of the role of mosquito insecticide resistance on malaria dynamics
Jemal Mohammed-Awel, Valdosta State University, Valdosta
11:30 AM-12:00 PM: An environmental model of honey bee colony collapse due to pesticide contamination
Yixiang Wu, Middle Tennessee State University, Murfreesboro

Session 15 (r3)

10:00 -10:30 AM: Long-lasting insecticidal nets and the quest for malaria eradication: A mathematical modeling approach
Enahoro Iboi, Arizona State University
10:30 -11:00 AM: Density-dependent emergence alters the efficacy of *Wolbachia*-based mosquito control programs
Michael A. Robert, University of the Sciences in Philadelphia
11:00 -11:30 AM: Modelling the potential role of engineered symbiotic bacteria in malaria control
Xingfu Zou, University of Western Ontario, London, ON, Canada
11:30 AM -12:00 PM: Mathematical modeling and optimal control for malaria transmission using sterile mosquitoes technique and bed nets
Wandi Ding, Middle Tennessee State University, Murfreesboro

Session 16 (r4)

10:00 -10:30 AM: Simulation of *Leishmania mexicana* infection: a mathematical model of the immune response
Ephraim Agyingi, Rochester Institute of Technology, Rochester
10:30 -11:00 AM: Mathematical modeling and numerical analysis of the dynamics of microbial communities
Hitoshi Koyano, Tokyo Institute of Technology, Tokyo
11:00 -11:30 AM: Infection severity across scales in multi-strain immuno-epidemiological Dengue model structured by host antibody level
Hayriye Gulbudak, University of Louisiana at Lafayette, Lafayette
11:30 AM -12:00 PM: Optimal control for a novel fractional order malaria transmission dynamics mathematical model
Nasser Sweilam, Cairo University, Giza, Egypt

SUNDAY AFTERNOON (October 13)

1:30 PM -3:00 PM: Parallel Sessions

Session 17 (r1)

1:30 -2:00 PM: Modeling population dynamics with some generalized logistic type models
Dongming Wei, Nazarbayev University, Nur-Sultan, Kazakhstan
2:00 -2:30 PM: Review: mathematical modeling of androgen deprivation therapy for prostate cancer
Tin Phan, Arizona State University
2:30 -3:00 PM: Spatio-temporal forecasting using Gaussian processes with application to predict brain cancer invasion
Lifeng Han, Arizona State University

Session 18 (r2)

1:30 -2:00 PM: Interplay between predator traits impacts benefits to biological control from predator biodiversity
Amanda Laubmeier, University of Nebraska–Lincoln, Lincoln
2:00 -2:30 PM: Dynamics of a diffusive vaccination model with therapeutic impact and non-linear incidence in epidemiology
Md. Kamrujjaman, University of Dhaka, Dhaka 1000, Bangladesh
2:30 -3:00 PM: Compensatory foraging in stoichiometric producer-grazer models
Angela Peace, Texas Tech University, Lubbock

Session 19 (r3)

1:30 -2:00 PM: Modeling the risk of HIV infection for drug abusers
Angelica Bloomquist, San Diego State University, San Diego
2:00 -2:30 PM: Persistence of chronically infecting bacteriophage in a host system
Paul Salceanu, University of Louisiana at Lafayette, Lafayette
2:30 -3:00 PM: Mathematical assessment of the impact of vaccination on pneumococcal colonization, co-colonization and serotype replacement
Tufail Malik, Merck & Co., Inc., Kenilworth, New Jersey

Session 20 (r4)

1:30 -2:00 PM: Dynamics of a discrete-time pioneer–climax model
Nora Gilbertson, University of Washington, Seattle
2:00 -2:30 PM: Modeling the effects of drugs of abuse on HIV infections with two viral species
Peter Uhl, San Diego State University, San Diego
2:30 -3:00 PM: Modeling the coral reef microbiome and black band disease
Naveen Vaidya, San Diego State University, San Diego

3:15 -4:15 PM: **Plenary Talk** (WXLR A21) – Modeling biodegradation and methane biogenesis
Hao Wang, University of Alberta, Edmonton, Canada

SUNDAY AFTERNOON (October 13)

4:30 PM - 6:00 PM: Parallel Sessions

Session 21 (r1)

4:30 -5:00 PM: Dynamic observers for prediction of stage-structured populations
Richard Rebarber, University of Nebraska, Lincoln
5:00 -5:30 PM: Multi-structured population dynamics in cyanobacteria
Sabina Altus, University of Colorado Boulder, Boulder

5:30 -6:00 PM: Modeling CAR T-cell therapy with patient preconditioning
Katherine Owens University of Washington, Seattle

Session 22 (r2)

4:30 -5:00 PM: Dynamic model for life history of scyphozoa
Congbo Xie, Dalian Minzu University, Dalian, Liaoning, China
5:00 -5:30 PM: Dynamics of an intraguild predator-prey system with internal storage in an unstirred chemostat
Feng-Bin Wang, Chang Gung University, Guishan, Taoyuan 333, Taiwan
5:30 -6:00 PM: A stage-structured population model for activity-dependent dendritic spines
Morteza Rouhani, Arizona State University

Session 23 (r3)

4:30 -5:00 PM: Towards a multi-scale modeling and analysis of translation dynamics: From molecular to cellular level
Khanh Dao Duc, University of British Columbia, Vancouver
5:00 -5:30 PM: Improved foraging by switching between diffusion and advection: Benefits from movement that depends on spatial context
William Fagan, University of Maryland, College Park
5:30 -6:00 PM: Modeling land-use change, economic development, and malaria dynamics in frontier regions
Andres Baeza-Castro, Arizona State University

Session 24 (r4)

4:30 -5:00 PM: Underlying strain space structure and *influenza A* eco-evolutionary dynamics
Chadi Saad-Roy, Princeton University, Princeton
5:00 -5:30 PM: Regional level influenza prediction model with mechanistic PDE approach and sampling twitter data
Yufang Wang, Tianjin University of Finance and Economics, Tianjin, China
5:30 -6:00 PM: Combining network theory and partial differential equation to improve influenza prediction **Haiyan Wang**, Arizona State University, Phoenix

MONDAY MORNING (October 14)

8:45 -9:45 AM: **Featured Talk** (WXLR A21) – Edge behavior determines large scale population dynamics in strongly heterogeneous landscapes
Brian Yurk and Christina Cobbold, Hope College, Holland, MI and University of Glasgow, Glasgow, UK

10:00 AM -12:00 PM: Parallel Sessions

Session 25 (r1)

10:00 -10:30 AM: Stoichiometric modeling and multi-scale dynamics of cyanobacteria
Christopher Heggerud, University of Alberta, Edmonton, Canada
10:30 -11:00 AM: Somitogenesis by a synthetic gene circuit
Xiao Wang, Arizona State University
11:00 -11:30 AM: Reaction-diffusion based pattern formation modeling and its basic dynamical behavior
Changhan He, Arizona State University
11:30 AM -12:00 PM: Control of circuit-host interactions toward engineering robust gene circuits
Xiaojun Tian, Arizona State University

Session 26 (r2)

10:00 -10:30 AM: Accelerating invasions and the asymptotics of fat-tailed dispersal
Benjamin Liu, University of Washington, Seattle
10:30 -11:00 AM: Network modeling the impact of community-based male-screening on the Chlamydia trachomatis prevalence in women
Zhuolin Qu, Tulane University, New Orleans
11:00 -11:30 AM: Backward bifurcations in discrete dynamical systems and applications to nonstandard discretizations of epidemiological models
Jean Lubuma, University of Pretoria, South Africa
11:30 AM -12:00 PM: Using satellite imagery to predict persistence and distribution of populations
Daniel Collister, University of California, Riverside

Session 27 (r3)

10:00 -10:30 AM: Persistence and extinction of stochastic Kolmogorov systems
Hai-Dang Nguyen, University of Alabama, Tuscaloosa
10:30 -11:00 AM: Investigating differential impacts of treatment non-adherence on the dynamics of vector-borne diseases: Case study of elimination of Visceral Leishmaniasis from Bihar, India by 2020
Mughda Thakur, Arizona State University
11:00 -11:30 AM: Dynamics of task allocation of social insect colonies
Yun Kang, Arizona State University, Mesa

Session 28 (r4)

10:00 -10:30 AM: Network modeling of plant disease epidemics in space and time: The case of Cucurbit Downy Mildew (CDM) in the eastern United States
Awino Maureiq Edith Ojwang, North Carolina State University, Raleigh
10:30 -11:00 AM: Targeting heterogeneity: Yard-scale treatments to reduce citywide *Aedes* populations
Brandon Hollingsworth, North Carolina State University, Raleigh

Plenary Talks

Natalia Komarova (UC Irvine)

Title: Mathematics of Evolution: mutations, selection, and random environments

Abstract: Understanding how environmental randomness affects evolution is of fundamental importance for biology. The presence of temporal or spatial randomness significantly affects the competition dynamics in populations and gives rise to some counterintuitive observations. In this talk, I will present some recent results on the evolutionary dynamics in systems where spatial and temporal randomness affects division and/or death parameters of cells. Of particular interest are the dynamics of non-selected mutants, whose rates come from the same distribution as those of wild type cells. Temporal and spatial types of randomness possess fundamentally different properties. Under temporal randomness, depending on the exact formulation of the update rules, minority mutants can be advantageous, disadvantageous, or neutral. In contrast to this, under spatial randomness, minority mutants are always advantageous. Applications to biomedical problems, including biofilms and cancer, are discussed.

Qing Nie (UC Irvine)

Title: Multiscale cell fate through lens of single cells

Abstract: Cells make fate decisions in response to dynamic environmental and pathological stimuli as well as cell-to-cell communications. Recent technological breakthroughs have enabled to gather data in previously unthinkable quantities at single cell level, starting to suggest that cell fate decision is much more complex, dynamic, and stochastic than previously recognized. Multiscale interactions, sometimes through cell-cell communications, play a critical role in cell decision-making. Dissecting cellular dynamics emerging from molecular and genomic scale in single-cell demands novel computational tools and multiscale models. In this talk, through multiple biological examples, we will present our recent works to use single-cell RNA-seq data and spatial imaging data to uncover new insights in development, regeneration, and cancers. We will also present several new computational tools and mathematical modeling methods that are required to study the complex and dynamic cell fate process through the lens of single cells.

Sebastian Schreiber (UC Davis)

Title: Stochastically induced extinction, coexistence, and alternative stable states

Abstract: In nature, environmental factors such as temperature, precipitation, and resource availability fluctuate stochastically over time. As survival, growth, and reproduction of organisms depend on these environmental factors, stochastic environmental fluctuations lead to stochastic fluctuations in population densities and genotypic frequencies. In this talk, I will discuss recent mathematical advances in the analysis of stochastic difference equations to identify when these stochastic fluctuations drive populations extinct, mediate coexistence between competing genotypes or species, or generate alternative stable states within communities. Empirically based applications will be given.

Hao Wang (University of Alberta)

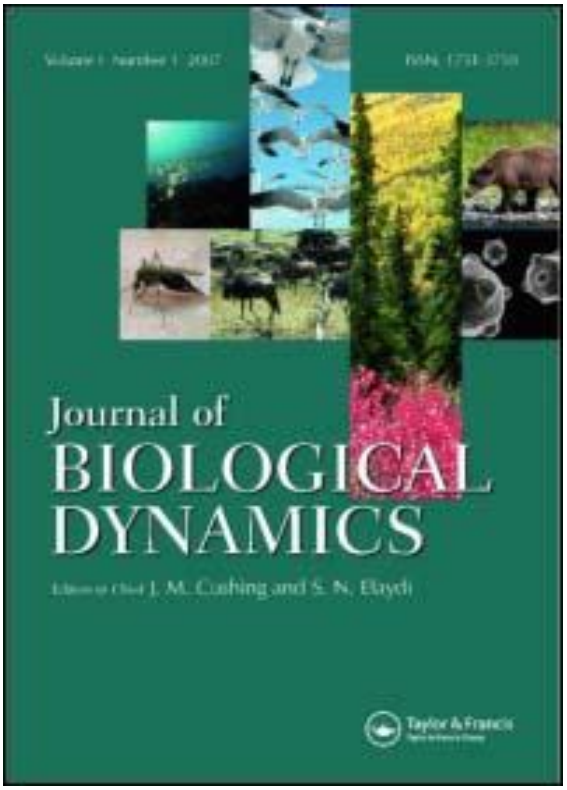
Title: Modeling Biodegradation and Methane Biogenesis

Abstract: Heterotrophic bacteria are primarily responsible for the decomposition of organic matter in many environments. In this talk, I will present multiple stoichiometric biodegradation models. As an important application, I will talk about the extension and data validation of our stoichiometric biodegradation models for predicting methane emissions from oil sands tailings in Alberta.

Microbial metabolism of fugitive hydrocarbons produces greenhouse gas (GHG) emissions from oil sands tailings ponds and end pit lakes that retain semisolid wastes from surface mining of oil sands ores. Predicting GHG production, particularly methane, would help oil sands operators mitigate tailings emissions and would assist regulators in evaluating the trajectory of reclamation scenarios.

Featured Speakers

co-Winners of the Lord Robert May Best Paper Prize
Journal of Biological Dynamics 2017-2018



Brian P. Yurk and Christina A. Cobbold
Hope College, Holland, MI and University of Glasgow, Glasgow, UK

Title: Edge behavior determines large scale population dynamics in strongly heterogeneous landscapes

Abstract: Understanding how landscape-scale patterns emerge from individual-level birth, death, and movement processes is an important problem in spatial ecology. In heterogeneous landscapes, individual animals may move through many different types of habitat during their lifetimes. Variation in habitat leads to differences in vital rates and movement behaviors with, for example, animals moving more quickly through patches with lower resource quality or higher predation risk. Many animals also respond directly to edges between different habitat patches by biasing their movement toward the more favorable patch while they are at or near an edge.

The method of homogenization is a useful technique for determining landscape-scale population patterns while accounting for the impacts of small-scale habitat variation. For certain problems in spatial ecology, the technique yields relatively simple, closed-form approximations for important quantities, such as wave speeds and invasion criteria, in terms of biologically meaningful parameters. This results in theoretical insights that are difficult to obtain using other methods. In this talk, we will discuss the application of homogenization and some of the insights it reveals for multi-scale problems in spatial ecology. We will particularly focus on the emergent effects of individual edge behavior on population-level dynamics.

Invited and contributed talks

Seventh International Conference on Mathematical Modeling and Analysis of
Populations in Biological Systems, Tempe, Arizona, October 12-14, 2019

Simulation of *Leishmania mexicana* infection: a mathematical model of the immune response

E. Agyingi[1]*, T. Wiandt[1], L. Buxbaum[2]and B. Thomas[3]

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Abstract

We present a model of the immune system response and use it to study *Leishmania mexicana* infections. *Leishmania mexicana* is an intracellular protozoan parasite that is transmitted from animals to humans by sandflies and causes the cutaneous form of leishmaniasis. The model treats the entire immune system response as a single entity and the parasite as another entity is governed by a system of differential equations. Analysis of the equilibriums points of the model for a chosen set of parameter values exhibits different bifurcations, leading to states that are associated to leishmaniasis. Using the model, we simulate different murine infections with *Leishmania mexicana*, in which specific genes are turned off. Numerical computations of the model are in close agreement with experimental results.

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Rabies spreading speeds, territorial and diffusing rabid foxes, and arbitrarily distributed latency

Dedicated to the memory of Hans F. Weinberger, 1928 - 2017

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Abstract

A mathematical model is formulated for the fox rabies epidemic that swept through large areas of Europe during parts of the last century. Differently from other models, both territorial and diffusing rabid foxes are included, which leads to a system of partial differential, functional differential and differential-integral equations. The model also includes arbitrary lengths distributions for the latent period. The system is reduced to a scalar Volterra-Hammerstein integral equation to which the theory of spreading speeds pioneered by Aronson and Weinberger is applied. The spreading speed is given by an implicit formula which involves the space-time Laplace transform of the integral kernel. This formula can be exploited to find the dependence of the spreading speed on the model ingredients, in particular on those describing the interplay between diffusing and territorial rabid foxes and on the distribution of the latent period.

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Environmental variability in SDE population models

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Abstract

In stochastic differential equation (SDE) models of populations in biological systems, environmental variability is often treated by modifying the parameters in the models [1, 2]. In the present investigation, it is shown that use of mean reverting processes is a practical and biologically realistic way to incorporate the effects of environmental variability in the parameters. In addition, mean reverting processes possess several advantages over, for example, a linear function of Gaussian white noise, such as continuity, non-negativity, possession of asymptotic distributions, and ease of fitting the parameters to environmental data. Properties of several mean-reverting processes are compared with respect to non-negativity and their asymptotic stationary behavior. The effects of different environmental variability assumptions on population size and persistence time for several population models are studied and compared.

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Populations in Biological Systems, Tempe, Arizona, October 12-14, 2019

Spatial spread of Chagas Disease

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Abstract

Diseases related to non-flying insects, such as Chagas disease, are usually considered to be regional diseases. However, although non-flying insects have extremely limited capacity for independent movement over appreciable distances, they can and do use animals as vehicles for migration into new territories. For that reason we use a reaction-diffusion system to study the spatial spread of Chagas disease, in particular, to determine the characteristics of a wave of infection into territory previously free of Chagas disease. Mathematically, a simple way in which this might happen is via a travelling wave solution that acts as a connection between the Chagas-free steady state and an endemic steady state. The diffusion terms are for the simple case of Fickian diffusion. We study the travelling wave-front solutions and their speed using linearised theory. We confirm that this analysis correctly predicts the speed of the travelling wave using numerical simulations of the initial value problem. The system is therefore linearly determinate. Results on positivity and boundedness of solutions of the reaction-diffusion system are also established.

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Backward bifurcations in discrete dynamical systems and applications to nonstandard discretizations of epidemiological models

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Abstract

The study of disease-transmission models that undergo the backward bifurcation phenomenon at the point $\mathcal{R}_0 = 1$ of the basic reproduction number $\mathcal{R}_0$ is highly relevant and has received much attention in the literature [4]. The existence of the phenomenon for dynamical systems is often established by using a reduction theorem [2]. We propose and prove a centre manifold-based theorem for the existence of backward bifurcations for discrete dynamical systems. We construct nonstandard finite difference (NSFD) schemes and prove that they preserve the backward bifurcation property of the continuous models. Our NSFD schemes add value to [1] in that the rules for their construction are suitably clarified and motivated. We make the results more specific for a relatively simple SIS model with vaccination [5] and a complex malaria model [3]. We provide numerical simulations that support the theory.

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Large and Small Data Blow-Up Solutions in the Trojan Y Chromosome Model

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Abstract

The Trojan Y Chromosome Strategy (TYC) is an extremely well investigated biological control method for controlling invasive populations with an XX-XY sex determinism. In [1, 2] various dynamical properties of the system are analyzed, including well posedness, boundedness of solutions, and conditions for extinction or recovery. These results are derived under the assumption of positive solutions. In the current manuscript, we show that if the introduction rate of trojan fish is zero, under certain large data assumptions, negative solutions are possible for the male population, which in turn can lead to finite time blow-up in the female and male populations. A comparable result is established for *any* positive initial condition if the introduction rate of trojan fish is large enough. Similar finite time blow-up results are obtained in a spatial temporal TYC model that includes diffusion. Lastly, we investigate improvements to the TYC modeling construct that may dampen the mechanisms to the blow-up phenomenon or remove the negativity of solutions. The results draw into suspect the reliability of current TYC models under certain situations.

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Modeling the risk of HIV infection for drug abusers

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Abstract

It has been well established that drugs of abuse, such as opiates, are one of the leading causes for transmission of HIV in the United States and many parts of the world. Drug abusers often face a higher risk of acquiring HIV infection because target cell (CD4+ T-cell) receptor expression differs in response to morphine, a metabolite of common opiates, exposure as shown in previous studies. In this study, we use a viral dynamics model that incorporates the T-cell expression difference to formulate the increased probability of infection among drug abusers. With a more in depth understanding of the dynamics and the increased risk for these individuals, we further evaluate how preventive therapies, including pre- and post-exposure prophylaxis, affect the infection risk in drug abusers. These results are useful to devise ideal treatment protocols to combat the several obstacles those under drugs of abuse face.

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Quantifying effects of neutrophil memory on migration patterns using microfluidic platforms and ODE modeling of the mechanistic molecular pathways

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Abstract

During sepsis, the current leading cause of death in hospitals, neutrophils migrate and accumulate in healthy organs instead of migrating toward the infection. Previous work from us described a dysfunctional phenotype, including oscillatory and spontaneous migration, in neutrophils isolated from septic burn patients [1]. We have shown that pre-conditioning neutrophils with a super-low dose of lipopolysaccharide (LPS), a pro-inflammatory stimulant, induces dysfunctional migratory phenotypes and higher migratory preference toward a pro-inflammatory signal over a pro-resolution signal. This suggests that super-low dose LPS stimulation can alter the decision-making properties of the neutrophil to migrate toward an inflammatory signal over a bacterial infection [2]. To understand the molecular mechanism of this cell memory, we developed an ODE-based dynamical framework to model the interaction of the mutually inhibitory GRK2 and GRK5 proteins and its role in neutrophil decision-making. GRK2 and GRK5 were of interest due to importance as drug targets as well as their interactions with the chemoattractant receptors and LPS. Our computational model results show a bimodal switch between high and low levels of GRK2. In the future, this platform can be used for early diagnosis of sepsis or to test the effect of pro-resolving mediators on neutrophil function.

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Multi-Structured Population Dynamics in Cyanobacteria

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Abstract

Cyanobacteria are photosynthetic microorganisms with promising applications in renewable energy and agriculture as they are able to convert light energy into more stable forms of chemical energy, such as biomass, as well as kinetic energy [1]. This process occurs within microcompartments, called carboxysomes, which are passed discretely, and persist through many cell cycles before they ultimately disintegrate [2]. Carboxysome productivity is a key factor driving cell growth, and is thought to decrease over time.

To investigate this claim, we have developed a multi-structured model for the evolution of a cyanobacteria population. The model is formulated as a partial differential equation wherein demographic parameters describing birth, death, and growth processes are all age-, size-, and carboxysome-age-dependent. Model equations are analyzed along with the associated linear operator and the strongly-continuous semigroup it is shown to generate. Comparisons between experimental data, captured through time-lapse fluorescence microscopy imaging, and the predicted age- and size-distribution of cells will be discussed along with implications for selecting appropriate models for carboxysome degradation.

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A honeybee population model with stage structure and seasonality

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Abstract

Western honeybees (*Apis Mellifera*) serve a pivotal role in our society as they pollinate 80 percent of our flowering crops, which constitute one-third of everything we eat. Unfortunately, population of honeybee population has been declining globally. In order to maintain the health of honeybee colonies, there is a need to understand what factors contribute to colony survival. In this talk, we introduce two delay differential equations of honeybees with age structure: (1) The first DDE model assumes that newborn workers come from survived eggs; and (2) The second DDE model assumes that newborn workers mature from survived brood rather than eggs. We perform analysis, simulation and data validation to explore (1) dynamical effects of various methods of incorporating age structure in the population model; (2) effects of delay; and (3) synergistic effects of both seasonality and delay. In addition, we validate our both DDE models with data to illustrate which modeling approaching is more plausible.

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Using Satellite Imagery to Predict Persistence and Distribution of Populations

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Abstract

Predicting the persistence of populations is becoming increasingly important due to the habitat deterioration caused by climate instability and pollution. Several mathematical models have been developed to represent population dynamics under a variety of conditions. In this study, we approach the problem of insect population persistence and resettlement in a river network through first principles modeling. By extracting elevation data from satellite imagery, we are able to create an energy gradient to inform a random walk agent-based model to create population dispersal kernels. By varying our model parameters, we considered several motion types for our agents, including unbiased random walk and upstream and downstream biased walks. Additional parameters were studied using the ranges established in the literature, including lifespan, reproductive rates and movement speeds. We demonstrate that there is a direct connection between the geometry of the underlying river network and the persistence locations of the species. Finally, we identified optimal values for our model parameters with respect to the population persistence and individual distance traveled, allowing to evaluate population survival and expansion in specific river basins.

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PDE Models for Multilevel Selection: The Ghost of Lower-Level Selection and Transitions in Biological Complexity

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Abstract

In this presentation, we will discuss PDE models for multilevel selection, with an emphasis on studying the evolution of cooperation when there is reproductive competition both between individuals and between groups. We focus on the derivation and analysis of the long-time behavior of the replicator dynamics for multilevel selection in the Prisoner's Dilemma, showing that how whether the individual advantage of defectors or the group advantage for groups with cooperations wins out in the long run depends on the relative selection strength at the two levels. A notable finding is the ghost of lower-level selection: if groups are best off with a mix of cooperators and defectors, then there will always be fewer cooperators than optimal at steady state, even in the limit of infinitely strong selection strength at the group level. While this ghost phenomenon can be an impediment to achieving optimal group outcomes, we discuss assortative and reciprocity-based mechanisms for game-theoretic interactions which can help overcome the ghost and potentially allow for the eventual transition to the construction of a cooperative unit capable of operating at a higher level of selection.

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The role of Allee effects on the evolution of semelparity and iteroparity

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Abstract

A classic question concerning life history strategies of biological populations involves reproductive timing and output and, specifically, the option between semelparity (one reproductive event only in an individual's life, e.g. annual plants) and iteroparity (multiple reproductive events, e.g. perennial plants). While early investigations suggested semelparity should be favored by evolution [1], subsequent studies have shown there is no simple answer to this question and that many factors can be in play, including density dependence, variable environmental conditions, and many others. Recent studies have further proposed, on the basis of an extensive review of the biological literature concerning the observed reproductive strategies of biological populations across many taxa, that reproductive parity should not be binary, but instead should be a continuous variable [2]. Darwinian dynamic (evolutionary game theoretic) modeling methodology is suitable for this approach. In this talk continue an investigation of Darwinian dynamic versions of some standard discrete time population models begun in [3] by including an Allee effect in the model. The goal is to determine circumstances under which evolution will favor one of these strategies over the other. It turns out an Allee effect can significant effect which is selected by evolution.

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Stability of diffusively coupled linear systems with an invariant cone

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Abstract

This talk concerns a question that frequently occurs in various applications: Is any diffusive coupling of stable linear systems, also stable? Although it has been known for a long time that this is not the case, we shall identify a reasonably diverse class of systems for which it is true.

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Dynamics and bifurcations of a model of dendritic cell therapy for melanoma

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Abstract

Melanoma, the deadliest form of skin cancer, is regularly treated by surgery in conjunction with a targeted therapy or immunotherapy. Dendritic cell (DC) therapy is an immunotherapy that capitalizes on the critical role dendritic cells play in shaping the immune response. Dendritic cell therapy has been modeled previously, but the complexity of these models limited the scope of mathematical analysis. In this talk, a reduced model of DC therapy is presented. This model is simple enough to allow for mathematical analysis. The model is validated using murine data. Mathematical analysis and simulation reveals rich dynamics including backward bifurcation and Hopf bifurcation, which are both likely artifacts of a Bogdenov-Takens bifurcation that occurs on the boundary of the biologically relevant parameters space. The model and bifurcation analysis are presented along simulations and discussion.

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Mathematical Modeling and Optimal Control for Malaria Transmission Using Sterile Mosquitoes Technique and Bed Nets

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Abstract

We first consider a malaria transmission model with SEIR (susceptible-exposed-infected-recovered) classes for the human population, SEI (susceptible-exposed-infected) classes for the wild mosquitoes and an additional class for sterile mosquitoes. Then, we derive a formula for the basic reproduction number of infection. Afterwards, we formulate an optimal control problem in which the goal is to minimize both the infected human populations and the cost to implement two control strategies: the release of sterile mosquitoes and the usage of bed nets to prevent the malaria transmission. Adjoint equations are derived and the characterization of the optimal controls are established. Finally, we quantify the effectiveness of the two interventions aimed at limiting the spread of Malaria. Numerical simulations are provided to illustrate the results.

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Towards a multi-scale modeling and analysis of translation dynamics: From molecular to cellular level

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Abstract

The translation of mRNA into protein is a fundamental biological process, mediated by the flow of ribosomes. As these dynamics can be locally regulated by many molecular mechanisms, analytical tools are needed to find the determinants of translation speed. I will present analytical and computational methods that we recently developed to study translation across different scales, using a wide array of structural, sequencing, and imaging data. These methods importantly rely on a stochastic interacting particle model that generalizes the totally asymmetric simple exclusion process (TASEP). We analytically studied this process to determine its phase diagram and find the key parameters that govern translation efficiency. In the context of recent advances in deep sequencing, we also used the model to infer translation rates for a large set of genes in yeast, and analyzed the contribution of traffic jams, codon specificity, and other biophysical parameters. These results more recently guided our studies of the molecular structure of the ribosome (obtained from cryoEM) and translation kinetics observed in vitro using lysate systems. Overall, these completing approaches emphasize the major role played by the ribosome in gene expression, at both molecular and population levels.

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Mathematical Modeling of the Re-emergent ZIKA Outbreak in the Endemic Region

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Abstract

Zika fever, caused by Zika virus, becomes a global threat for birth deficiency (due to the infection during pregnancy). The virus has multiple transmission routes. Other than the primary transmission mediated by Aedes mosquitoe, Zika can be transmitted sexually from men to women [1]. The Zika outbreaks reported previously, show mostly epidemic patterns, which have only one outbreak. Recently, study [2] shows the evidence of the endemic Zika in Thailand. The report [2] concludes that the persistent low level Zika in the lower level immunity population causes the outbreaks. To reveal the cause of the persistent Zika and the outbreaks, we use a simple mathematical model to reflect this endemic pattern and the outbreak cycles. Due to the special disease feature, we ignore birth induced death in our model. We model the sexual transmission routes as $\Lambda(I_h) = b_3 \frac{I_h}{K+I_h} I_h S_h$ where b_3 is the contact rate between susceptible human (S_h) and infected human (I_h) classes. This special incidence function $\Lambda(I_h)$ shows a positive effect among infected individuals during the infection. Since the sexual transmission route is secondary and more difficult, it needs several contacts for a successful transmission. Mathematical analysis shows that the model exhibits disease free equilibrium (E_0) and endemic equilibrium (E_1). We further find the analytical formula for the occurrence of the backward bifurcation when the basic reproduction number is one, $R_0 = 1$. The existence of backward bifurcation leads to the Hopf bifurcation, which serves as an oscillation source. The large periodic outbreaks follow. The amplitudes and periods of the outbreaks can vary due to the environmental stochastic influence and seasonality.

Keywords: Zika Virus, Stability, Backward Bifurcation, Hopf Bifurcation

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A Continuous and Discrete Mathematical Models for the Aggregation of β-Amyloid

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Abstract

Dementia associated with the Alzheimer's disease is thought to be correlated with the presence of the beta-amyloid (Aβ) peptides. While neuron death is coincident with formation of plaques comprising the beta-amyloid (Aβ) peptide, a direct causative link between Aβ and cell toxicity is a controversial issue. While the supporters of the amyloid hypothesis [2] believe that Aβ is the cause of Alzheimer's disease, the opponents, however, raise doubts about the validity of the amyloid hypothesis [3]

Here we study the aggregation process of Aβ from soluble monomers to aggregated oligomers and insoluble fibrils. This process consists of two stages, nucleation of monomers to oligomers, and nucleation from oligomers to fibrils. We present a continuous-time and a discrete-time mathematical model for the aggregation of Aβ from monomers to diamers, triamers, ..., into oligomers, and into fibrils or plaques. This is accomplished through using concepts from chemical kinetics and population dynamics. Conditions for the stability and instability of the equilibria of the model are established. A formula for the number of monomers that is required for producing oligomers is also given.

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Long-lasting Insecticidal Nets and the Quest for Malaria Eradication: A Mathematical Modeling Approach

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Abstract

Recent dramatic declines in global malaria burden and mortality can be largely attributed to the large-scale deployment of insecticidal-based measures, namely long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS). However, the sustainability of these gains, and the feasibility of global malaria eradication by 2040, may be affected by increasing insecticide resistance among the *Anopheles* malaria vector. We employ a new differential-equations based mathematical model, which incorporates the full, weather-dependent mosquito lifecycle, to assess the population-level impact of the large-scale use of LLINs, under different levels of *Anopheles* pyrethroid insecticide resistance, on malaria transmission dynamics and control in a community.

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Improved foraging by switching between diffusion and advection: Benefits from movement that depends on spatial context

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Abstract

Animals use different modes of movement at different times, in different locations, and on different scales. Incorporating such context-dependence in mathematical models represents an increase in complexity, but creates an opportunity to more fully integrate biological features. Here we consider the spatial dynamics of a population of foragers with two subunits. In one subunit, foragers move via diffusion (random search) whereas in the other, foragers move via advection (gradient-following search). Foragers switch between the subunits as functions of spatial context (i.e., depending on whether they are inside or outside of a patch, or depending on whether or not they can detect a gradient in resource density). We consider a one dimensional binary landscape of resource patches and non-habitat and gauge success in terms of how well the mobile foragers overlap with the distribution of resources. Actively switching between dispersal modes can sometimes greatly enhance this spatial overlap relative to the spatial overlap possible when foragers move according to a constant blend of advection and diffusion. Switching movement modes is most beneficial when an organisms gradient-following abilities are weak compared to its overall capacity for movement, but switching can actually be quite detrimental for organisms that can rapidly follow resource gradients.

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Abstract

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Applications of delay differential equation in biosciences

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Abstract

Recently, a simple population model with Darwinian evolution [1] found conditions under which semelparity (a single reproduction event at the end of an organism's life) or iteroparity (multiple reproduction events over a lifetime) evolve in the population. One assumption in this model is a linear trade-off between fertility and survival, however, previous works [2, 3], using different mathematical techniques, show that the concavity of the trade-off relationship can alter the expected life history strategies. Using a model similar to that in [1], we show how concavity of the fertility-survival curve can impact potential life history outcomes.

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[2] William M. Schaffer, *Selection for optimal life histories: the effects of age structure*, Ecology, 5:2, 291-303, 1974.

[3] William M. Schaffer and Michael L. Rosenzweig, *Selection for optimal life histories. II: Multiple equilibria and the evolution of alternative reproductive strategies*, Ecology, 58:1, 60-72, 1977.

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How the Shape of the Fertility-Survival Curve Impacts Expected Life History Strategies

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Abstract

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Dynamics of Task Allocation of Social Insect Colonies

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Abstract

Efficient and reasonable task allocation is a survival weapon for the social insect colony to continue, and it is inextricably linked with the colony size. To explore the mysterious relationship between colony size and task allocation, we present and study a general dynamical compartmental model of task allocation on the colony level. The proposed model incorporates both variation in task performance among workers and individual worker flexibility. We study the scaling effects of colony size on the resting probability as well as the task allocation. Subsequently, we apply the general modeling framework constructed above to the case on the working effort versus resting. Finally, we numerically explore the effects of stochastic noise on the task allocation of social insect colonies. Our theoretical and numerical results show that: (a) changes in colony size can regulate the probability of the colony resting and the allocation of colony task, and the direction of regulation is related to the nonlinear metabolic scaling effects of tasks; (b) an enhanced response threshold can result in the appearance of a periodic solution. In this case, we observed interesting bubble phenomena in the task allocation of social insect colonies for the first time; and (c) stochastic noise causes the probability of colony resting and the allocation of colony task to fluctuate within a range, and the amplitude of the fluctuation is positively correlated with the intensity of the noise.

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Dynamics of stoichiometric plant-pollinator-herbivore models

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Abstract

Plant-pollinator interactions play an important role in the maintenance of the balance of nature. All organisms living in the environment are composed of different ratios of chemical elements. By considering the balance of essential chemical elements in nature, we can formulate mathematical models to study their role in the dynamics of the system as well as nature. We formulate and analyze stoichiometric plant-pollinator and stoichiometric herbivore-plant-pollinator models. Our models include three dimensional and four-dimensional systems of ordinary differential equations to represent the plant, pollinator, herbivore populations, as well as the varying nutrient levels of the plant. We analyze the dynamics of the systems such as non-negativeness and boundedness of solutions, as well as the existence and stability of boundary equilbria. We perform a bifurcation analysis of the models and also a parameter sensitivity analysis of stoichiometric plant-pollinator model using Latin hypercube sampling and partial rank correlation coefficient technique. LHS show that the search rate and the carrying capacity of pollinators are most important parameters to the stoichiometric plant-pollinator model. Bifurcation analysis shows the existence of critical thresholds of number of pollinators for plants to survive and for herbivores to die.

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Multi-type Branching Process Theory with Applications to Cancer and Ecology

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Abstract

The theory of branching processes is poised to study stochastic population dynamics involving birth, death, mutation, and immigration events. It finds wide applications in the life sciences, in settings as diverse as bacterial growth, cancer treatment, and infectious epidemics. In this talk, I will first introduce two problems of historical importance: the Galton-Watson process originated from studying extinctions of English family names and the Luria-Delbrück distribution arising from the duo's famous fluctuation test of bacterial spontaneous mutations. I will then review key concepts and some recent advances in multi-type branching process theory that allow us to derive closed-form calculations in relation to cancer and ecology. After that, I will present some of my recent work on applying the theory of branching processes to model cancer dormancy and social insects, respectively. Specifically, I will focus on risk management of cancer dormancy with respect to treatment strategies that aim to reduce the risk of relapse and, if relapse is fated to happen, prolong the time to relapse. I will present methods for using branching processes for survival analysis, that is, estimating the timing of relapse regarding when the total burden of metastases reaches a threshold. As for social insects, I will quantify the risk-return trade-off of eusocial reproduction in which some individuals forgo reproduction and help others to reproduce, and demonstrate why it is so taxonomically rare, despite being hugely successful once established [1]. I will also establish the connection between the supercritical condition of the stochastic branching process for eusocial reproduction and its 'basic reproductive ratio', R_0, an important quantity that is derived from the mean behavior of the underlying branching process using the next-generation approach in mathematical epidemiology. Finally I will conclude my talk by giving an outlook for future work.

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Dynamics of a discrete-time pioneer–climax model

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Abstract

In ecological succession, newly established habitat is initially composed of pioneer plants, hardy species that do best at low population densities and are able to colonize unpopulated environments. Later in succession come the climax species which are strong competitors but poor colonizers. At low population densities, the pioneer acts as a nurse plant for the climax species, with interaction dynamics akin to predator–prey relations. As population density increases, interspecies interaction becomes more competitive. The climax species' fitness increases to a point, until crowding causes a loss of fitness[1]. As climate change alters ecosystems, we may see more successional communities. This makes an understanding of pioneer–climax dynamics critical. Here, we present a difference equation model for two linked invasive plant species whose dynamics follow pioneer–climax interactions. The long-term behaviors of the steady states of the model are analyzed in different situations, presenting scenarios of both competitive exclusion and coexistence. Neimark-Sacker and global bifurcations are found in some of these situations and examined. These results allow us to determine conditions under which each species may survive, providing valuable insight into the persistence in changing ecosystems of species that follow pioneer–climax dynamics.

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A Plausible Accelerating Function of Intermediate States in Cancer Metastasis

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Abstract

Epithelial-to-mesenchymal transition (EMT) is a fundamental cellular process and plays an essential role in development, tissue regeneration, and cancer metastasis. Interestingly, EMT is not a binary process but proceeds with multiple partial intermediate states. However, the functions of these partial states are not fully understood. Here, we will focus on a general question about how the number of partial EMT states affects cell transformation. First, by fitting a hidden Markov modelof EMT to experimental data, we proposed a statistical mechanism for EMT in which many unobservable microstates exist within one of the observable macrostates. Furthermore, we found that increasing the number of partial EMT states could accelerate EMT and that adding parallel paths or transition layers accelerates the EMT process even further. Last, a stabilized intermediate state traps a cell within its current phenotype. This work advances our understanding of the dynamics and functions of EMT plasticity during cancer metastasis.

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Numerical schemes for a chemo-attraction and consumption model in 1D domains.

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Abstract

We consider a chemo-attraction model with linear consumption in 1D domains, which is a nonlinear parabolic system for two variables; the cell density and the chemical concentration. We present a unconditionally energy-stable finite element and first order in time scheme. Moreover, we show some numerical simulations of the scheme, comparing with others classical schemes.

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Dynamic observers for prediction of stage-structured populations

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Abstract

We address the following question: How can we predict a discrete-time stage-structured population merely from knowledge of measurements of a few stages of that population, and without knowledge of the other stages at any time? As an example, we might annually census nesting turtles and the eggs they lay, but would like to obtain knowledge of the entire population structure, including pelagic life stages which spend a considerable portion of the year in oceans, where sampling is expensive, laborious, and ineffective. We propose that this ecological problem can be addressed by appealing to dynamic observers, a core component of mathematical control theory. The idea of dynamic observers is to combine partial measurements with a mathematical model to build an asymptotic estimate of the entire population distribution. We investigate the potential use of observers for density-independent models and a class of density-dependent models. In both cases, we prove, in several ecologically reasonable circumstances, that there is a natural, optimal construction of these observers. Further, we prove robustness results for these observers exhibit with respect to disturbances and uncertainty in the model and the measurements. We illustrate these concepts with several plant and animal examples.

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Infection severity across scales in multi-strain immuno-epidemiological Dengue model structured by 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 formulate a within-host model which mechanistically recapitulates characteristics of antibody dependent enhancement (ADE) in Dengue infection. The within-host scale is then linked to epidemiological spread by a vector-host partial differential equation 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, along with waning of cross-protective immunity after primary infection. Analysis of both the within-host and between-host systems are conducted. Stability results in the epidemic model are formulated via basic 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.

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Persistence of Chronically Infecting Bacteriophage in a Host System

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Abstract

We propose a delay differential equations model describing the dynamics of interactions between chronic viruses and one type microbial host. We show that when the disease-free equilibrium can be invaded the infection persists in the host population. Numerical simulations and bifurcation diagrams are also used for the study of stability of the interior equilibria.

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Spatio-temporal Forecasting Using Gaussian Processes with Application to Predict Brain Cancer Invasion

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Abstract

PDE models parameterized with MRI data are popularly used to study spatio-temporal patterns of brain cancer invasion and make predictions. In order for any model predictions to be clinically useful, they need to be confronted with data, and their uncertainty has to be quantified. However, there is no ground true models in biology and those formulations tend to under-/over-fit. We propose a nonparametric forecasting method to address these issues. In a state-space framework, we model the transition function as a Gaussian process. By exploiting the local nature of the spatio-temporal process, we can make reasonable predictions with very sparse time-series data. We test our method with synthetic data generated by a PDE model and get promising results.

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Stoichiometric modeling and multi-scale dynamics of cyanobacteria

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Abstract

Cyanobacterial blooms are becoming a global concern due to the increasing prevalence of eutrophication. The dependence of cyanobacteria dynamics on phosphorus and light inputs is modeled via a stoichiometric approach. The dynamics occur in distinct phases that allow us to make use of multiple time-scale analysis to uncover the driving mechanisms of each phase. As a result, we are able to approximate the length of time a bloom persists based on the initial level of phosphorus. This framework helps to establish the use of multi-scale methods in stoichiometric models, and provides deeper understanding of cyanobacteria dynamics.

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Persistence and Extinction of Stochastic Kolmogorov Systems

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Abstract

This talk is concerned with long-term properties of stochastic Kolmogorov systems which are used to model the dynamics of interacting populations in fluctuating environments. The environmental variation is modeled by white noise and/or coler noise. Sharp conditions for extinction and persistence are given based on analyzing invasion rates of each species when its density is rare. Examples are also given to illustrate how stochasticity can facilitate or inhibit persistence of populations.

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Targeting Heterogeneity: Yard-scale Treatments to Reduce Citywide *Aedes* Populations

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Abstract

The spatial distributions of *Aedes* populations are well known to be extremely heterogeneous across small distances, with areas of high mosquito density often confined to only a few square meters. Despite this, insecticide applications for general mosquito control, and especially for the control of mosquito-borne disease, is applied uniformly across large areas of space, often on the scale of square kilometers, using ultra-low volume (ULV) spraying from vehicle-mounted sprayers. This indiscriminate application can have implications for numerous ecological and evolutionary processes, including the evolution of insecticide resistance and off-target mortality. Here, we examine the alternative of using small-scale precision treatments and their effects on the larger-scale mosquito population. Using a field experiment conducted in the summer of 2018, we first attempt to quantify the effect of yard-scale treatments on mosquito densities both inside the treated area and in surrounding untreated areas. We use the results of this study to parameterize a model of yard-scale mosquito control..

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A General 'Linear Chain Trick' for Building ODE Models with Flexible Dwell Time Assumptions

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Abstract

ODE models are widely used and are often viewed as mean field approximation of some (often unspecified) continuous time stochastic model. Such models often implicitly assume that the time individuals spend in a given state is exponentially distributed. Altering this oversimplified assumption can often change model-derived results that are important in applications. The linear chain trick (LCT) is a well-known technique for replacing exponentially distributed dwell times with gamma distributions. However, it is not always clear how one might apply the LCT in more complex models, where easy-to-use heuristics must be replaced with the careful derivation of ODEs from integral equations models.

In this talk, I will (1) present novel extensions of the LCT to various scenarios found in applications; (2) provide formulations of the LCT and its extensions that bypass the need to derive ODEs from integral or stochastic model equations; and (3) I'll introduce a novel Generalized Linear Chain Trick (GLCT) framework that extends the LCT to a much broader family of distributions, including the flexible phase-type distributions. These results also help clarify connections between individual-level stochastic model assumptions and the structure of corresponding mean field ODE models.

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Mathematical modeling of Batrachochytrium salamandrivorans on the Eastern Newt with multiple transmission pathways

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Abstract

The recently discovered fungal pathogen, Batrachochytrium salamandrivorans (Bsal) is believed to be from Asia and was likely introduced into Europe through international trade that caused rapid die-offs of naïve salamanders in Europe and Gray et al. (2015) [1] predicts North America will soon experience similar devastation if no policy actions are taken and the pathogen emerges. Epidemic dynamics of infectious diseases with multiple routes of transmission are complex. Mathematical models can be used to determine invasion potential and identify which transmission pathway is dominant and can ultimately help identify appropriate intervention strategies. We developed compartmental host-pathogen models to examine the transmission dynamics of an emerging fungal pathogen on an amphibian population. Multiple stages of infection are incorporated into the model, allowing disease-induced mortality and zoospore shedding rates to vary as the disease progresses. Parameter sensitivity analysis shows that the recovery rate and environmental zoospore degradation rates are influential parameters. Calculation of the basic reproductive number ($\mathcal{R}_0 > 7$) highlights the virulence of this pathogen and is used to determine that direct transmission is the dominant transmission pathway for small population densities, while environmental transmission dominates in large populations.

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Exploiting androgen deprivation-induced inflammation in prostate cancer treatment

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Abstract

Biochemically failing, metastatic prostate cancer is typically treated with androgen deprivation therapy (ADT). Unfortunately, ADT eventually fails due to progression of the tumor to a castration resistant state. Recently, the FDA has approved a vaccine, Sipuleucel-t (Provenge), for the treatment of hormonally refractive prostate cancer, which as improved patient survival by $\sim$4 months. However, several open questions remain regarding the administration of this immunotherapy. For instance, optimal scheduling protocols have not yet been established. Further, ADT itself induces a strong immune response at the site of the tumor. We therefore hypothesize that combining immunotherapy with ADT will enhance the efficacy of treatment. We develop a detailed mathematical model describing the interactions of the tumor, the host immune system and ADT and vaccination therapy. The model is extensively calibrated versus available experimental data, and used to predict optimal scheduling protocols when ADT is co-administered with the vaccine. In particular, we use experimental data to generate distributions on parameters that are critical to tumor growth and immune presence within the tumor. Sampling model parameters from these distributions allows us to simulate heterogeneity, both, at the level of the tumor cells, and the individual (mouse) being treated. Treatment efficacy is measured in terms of survival times.

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Populations in Biological Systems, Tempe, Arizona, October 12-14, 2019

Machine learning for automatic segmentation of multielectrode array recordings for electrophysiological analysis

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Abstract

Microelectrode array technology is widely used to study electrogenic cellular networks of various origins. It has recently been applied to recurrent high-resolution field potential (FP) and action potential (AP) measurements from human induced pluripotent stem cell-derived cardiomyocytes (hiPSC-CM). It is of fundamental interest to investigate cardiotoxic side effects of potential pharmaceutical compounds during their testing phase. Variations of the FP or AP wave morphology from one experiment to another constitute a technical challenge. We investigate how functional modulations of hiPSC-CM populations can be linked to the FP and AP morphology using supervised machine learning methods. We present a framework for the automatic segmentation of large amounts of electrophysiological readings into regions of useful FP and AP periods. We compare classification methods such as support vector machines, neural networks and random forests. The classifiers are trained with a mixed set of synthetic and experimental data to refine the model for drug safety assessments. Future work includes modeling the effect of drug concentration on the distribution of biomarker values.

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Dynamics of a Diffusive Vaccination Model with Therapeutic Impact and Non-linear Incidence in Epidemiology

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Abstract

This study presents a spatial vaccination model with nonlinear incidence considering therapeutic impact. We discuss the well-posedness of the solution of the model. Sequentially, we study the local and global stability of the model. In the case of bounded spatial habitat $\Omega \in \mathbb{R}^n$, we investigate the global stability of the model. More precisely, it is shown that, if the threshold level $\mathcal{R}_0 \leq 1$, the disease-free equilibrium (E_0) is globally asymptotically stable while for $\mathcal{R}_0 > 1$, there exists a unique stable disease equilibrium (E^*). The uniform persistence and existence of solution of the model are studied. Finally, in a series of numerical examples, we illustrated and performed our analytic results using standard finite difference scheme. The results indicate that the global dynamics of the model are completely determined by the threshold value $\mathcal{R}_0$.

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Traveling wave solutions to Glioblastoma Multiforme growth models.

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Abstract

A brain tumor is considered as an oncology disease with the most severe health consequences. Glioblastoma Multiforme (GBM) is the most aggressive brain tumor and, as most of gliomas, it grows so fast and extensive that patients do not exhibit any symptoms and, unfortunately, have a very small chance to overcome the disease. The aim of this study to develop and analyze the dynamics of brain tumor growth and in particular glioma growth models that arise in mathematical oncology. The main research efforts will focus on the understanding complex behavior of glioblastoma growth models by means of different growth functions such as Bernoulli and von Bertalanffy. Further, by using in vitro experimental data we will compare our theoretical results with the existing results obtained in [1] and [2].

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Mathematical modeling and numerical analysis of the dynamics of microbial communities

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Abstract

From the viewpoint of mathematics, a set A^* of strings on an alphabet $A = \{a_1, \cdots, a_z\}$ is a metric space with an edit distance, such as the Levenshtein distance, and a monoid with concatenation, and consequently it forms a noncommutative topological monoid. A population of DNA sequences of a biological community in an environment can be represented as a probability function on the topological monoid A^* of strings on the alphabet $A = \{\mathtt{a}, \mathtt{c}, \mathtt{g}, \mathtt{t}\}$. In this presentation, we describe results of research in which we predicted and analyzed the time evolution of populations of 16S ribosomal RNA gene sequences of microbial communities in environments that were altered into hypersaline environments artificially, using results from our previous studies: (i) a study that constructed a statistical estimation theory for a mixture model of a parametric distribution that we introduced on A^* to describe the selection pressure exerted on a population of DNA sequences from an environment, and (ii) a study that formulated and analyzed a partial differential equation on A^* that describes the time evolution of a population of DNA sequences in an environment.

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How should multiple agents allocate their contributions to eradicate a common harmful species?

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Abstract

The management of harmful species, including invasive species, pests, parasites, and diseases, is a major, global challenge. In particular, the control of harmful species often requires cooperation among multiple agents, such as landowners, agencies, and countries. Agents may have incentives to contribute less, leaving more work for other agents, which can result in inefficient treatment. A major question is, therefore, how should the agent allocate the job? Should they work together in the same area? Or should each agent work in its own designated area? We consider a dynamic game model, in which the allocation determine the possible equilibria, which enables us to compare the efficiency of various allocations. Our results show that, if a complete eradication of the harmful species is feasible, then it is generally better if each agent works in a distinct area. However, if the cost of treatment increases as the species density declines and the control of the harmful species at some low density is needed, then it is better that the agents work together in all the areas simultaneously. This implies that the coordination among agents plays a critical role in the success of eradication and control of harmful species.

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Interplay between predator traits impacts benefits to biological control from predator biodiversity

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Abstract

Pest control by natural predators is a valuable ecosystem service and is assumed to improve with predator biodiversity. However, complex predator communities engage in a variety of predator-prey and predator-predator interactions. Depending on which interactions will dominate, we sometimes find that high biodiversity impairs pest control. In order to describe the effect of biodiversity on pest control, we require an understanding of the conditions which lead to beneficial pest control outcomes. We investigate these conditions using a trait-based differential equation model of predator-prey dynamics. Our model accounts for predator body mass, which determines activity levels and metabolic demands, as well as foraging area, which determines common spaces where species can interact. We identify the characteristics of optimal predator communities under a range of environmental conditions (temperature) in order to explore how different distributions of predator traits cause different levels of pest control. We find that foraging area is an important model mechanism, which shapes species interactions and determines the degree to which predators compete for common resources. In contrast, diversity in body mass is only beneficial in the presence of environmental variability and can impede pest control by increasing intraguild predation and interference.

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Competition between consumers in a mixed discrete-continuous model

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Abstract

Many ecological settings feature consumers that reproduce in synchronized annual birth pulses and feed on a resource that grows continuously, so that an appropriate model consists of a time-limited continuous model embedded in a discrete model. Pachepsky et al (2008) studied such a model with a single consumer species, obtaining dynamics that include stability, overcompensation cycles (such as occur in the discrete logistic map), a repetitive behavior they describe as "consumer-resource" cycles, and chaotic behavior. Here we consider a similar model with two consumer species, with competition only in resource collection. For most parameter regimes corresponding to the stable and overcompensation cases for one consumer, the two consumers cannot coexist. In these cases, we show that the successful consumer is the one whose consumer-resource equilibrium point is at a lower level of the resource. Coexistence appears to be possible for some parameter ranges corresponding to consumer-resource cycles and chaos.

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Accelerating invasions and the asymptotics of fat-tailed dispersal

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Abstract

Integrodifference equations (IDEs) are used in ecology to model the growth and spatial spread of populations. With IDEs, dispersal is specified with a probability density function called the dispersal kernel, and the shape of the kernel influences how rapidly invasions progress. Invasions with thin-tailed dispersal kernels behave qualitatively similarly to reaction-diffusion models, with traveling wave solutions and constant spreading speeds. Invasions where the dispersal kernel is fat-tailed are known to produce invasions that accelerate without bound, but analysis of these invasions has proven difficult. In this talk, we apply tail additivity, a property of regularly varying probability densities, to analyze invasions with fat-tailed (power-law decay) dispersal in one dimension. We characterize the geometric rate at which fat-tailed invasions accelerate, and also find that fat-tailed invasions have several behaviors quite different from thin-tailed models. We show that the initial condition of a fat-tailed invasion affects its asymptotic rate of invasion in a way distinct from what is possible in thin-tailed invasions. We also discuss how measures of invasion must be modified and reconsidered when invasions accelerate.

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Nutrient levels and trade-offs control diversity in a model seasonal ecosystem

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Abstract

Microbial communities feature an immense diversity of species and the extent of this diversity correlates with outcomes ranging from ecosystem stability to medical prognoses. Yet the mechanisms underlying microbial diversity are not well understood; simple resource-competition models do not allow for coexistence of a large number of species. However, it was recently shown that metabolic trade-offs can lead to unlimited diversity in a chemostat model. Do such trade-offs permit diversity under more realistic, intermittent conditions of nutrient supply? Here, we demonstrate that in serial dilution culture, metabolic trade-offs allow for high diversity. Unlike the chemostat case, diversity depends on the amount of nutrient supplied to the community. The form of this dependence varies with the precision of trade-offs and the presence of cross-feeding, immigration, or evolution. The large variation seen in this simple model suggests that real ecosystems may not obey a single universal relationship between nutrient supply and diversity. To connect to real microbial communities, we validate our model framework against previously published *Escherichia coli* batch and chemostat experiments and outline potential future experiments to test the model's multispecies predictions.

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An Environmental Model of Honey Bee Colony Collapse Due to Pesticide Contamination

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Abstract

We develop a model of honey bee colony collapse based on the contamination of forager bees in environmental regions contaminated with pesticides. An important feature of the model is the daily homing capacity each day of foragers bees. The model consists of difference equations describing the daily homing of uncontaminated and contaminated forager bees, with an increased homing failure of contaminated bees. The model quantifies colony collapse in terms of the fraction of contaminated bees subject to this increased homing failure. If the fraction is sufficiently high, then the hive falls below a viability threshold population size that leads to rapid disintegration. If the fraction is sufficiently low, then the hive can rise above the viability threshold and attain a stable population level.

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Mathematical Assessment of the Impact of Vaccination on Pneumococcal Colonization, Co-colonization and Serotype Replacement

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Abstract

A mathematical model of pneumococcal colonization, which captures transmission dynamics of streptococcus pneumoniae in the presence of a vaccine in a human population, will be presented. The model explicitly tracks the natural history of colonization, allows for the possibility of an uncolonized individual to be simultaneously colonized with a vaccine serotype and a non-vaccine serotype, accounts for temporary partial immunity following colonization, and distinguishes between three levels of vaccination, namely cohort, pre- and post-colonization vaccination. In addition to stability results for disease-free and boundary equilibria, conditions for co-colonization and serotype replacement phenomenon will also be presented.

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A Comparative Analysis of Host–Parasitoid Models in which Density-Dependence Precedes 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.

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Mathematical Assessment of the Role of Mosquito Insecticide Resistance on Malaria Dynamics

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Abstract

The widespread use of indoors residual spraying (IRS) and insecticides-treated bednets (ITNs) has led to a dramatic reduction of malaria burden in endemic areas. Unfortunately, such usage has also resulted in the challenging problem associated with the evolution of insecticide resistance in the mosquito population in those areas. Thus, it is imperative to design malaria control strategies, based on using these (IRS- and ITNs-based) interventions, that reduce malaria burden while effectively managing insecticide resistance in the mosquito population. This talk is based on using a mathematical model, which couples malaria epidemiology with mosquito population genetics, to explore control scenarios.

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Dynamics of Dengue Virus With Innate, Cellular and Humoral Responses

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Abstract

Dengue virus is a mosquito borne Flavivirus and most prevalent arbovirus in tropical and subtropical regions around the world. In recent years, the within-host dynamics of dengue infection have been increasingly characterized. The relationship between viral kinetics and immune status may help in predicting the severity of the disease and also enable rational therapeutic strategies. In this study we have developed a mathematical model which includes all the immune response systems of the body (Innate, Cellular and Humoral responses) and study the within host dynamics of the dengue virus infection. Also an time delay in production of antibodies from B cells has been incorporated. The basic Reproduction number has been computed. Mathematical and Numerical studies have been carried out for existence and stability of equilibrium points. Different methods of sensitivity analysis(Heat maps, Morris Method and Partial Rank Correlation Coefficients) were carried out to identify the parameters that contribute to the severity of the infection. The model is inline with the Clinical observations that viral load decreases within 7-14 days from the onset of primary infection.

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Probability of a Zoonotic Spillover in a Fluctuating Environment

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Abstract

Zoonotic infectious diseases are spread from animals to humans. It is estimated that over 60% of human infectious diseases are zoonotic. Many emerging or re-emerging infectious diseases are viral zoonoses, including avian influenza, rabies, Ebola, and hantaviruses. Spillover of infection from animals to humans depends primarily on the contact between animals and humans. Environmental factors, such as seasonal variations in temperature, humidity, and rainfall that affect animal or human behavior impact the spread of zoonotic diseases. A new time-nonhomogeneous stochastic process is formulated for infectious disease spread from animals to humans when transmission, recovery, and death rates are time-periodic. We assume that the disease is introduced into the animal population and apply a branching process approximation near the disease-free states. Generating functions are used to estimate the probability of the first spillover event from animals to humans. This probability is a periodic function of the time when the infection is introduced into the animal population. It is shown that the highest risk of the first spillover event generally does not coincide with the time of peak animal-to-human transmission. Applications to rabies and avian influenza are discussed.

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To run or not to run? A Markov–chain model for behavioral switch during nest selection in *Temnothorax* ants

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Abstract

Social insect colonies frequently make unanimous, decentralized decisions where no individual needs complete information about the available choices. During house–hunting, ant colonies are capable of choosing the best quality site and migrating without splitting [1]. In some species of *Temnothorax* ants, this emergent ability relies on a quorum rule: a scout assessing a nest will switch from slow recruitment (Tandem Run) to fast transportation of the majority of the colony after encountering enough nestmates in the new site [2]. The individual mechanisms for ant quorum sensing are unknown. Inspired in the classical drift–diffusion models of decision making used in cognitive psychology [3], we describe an ant's decision process as a discrete Markov chain where absorbing states represent final choices and transitions depend upon evidence accumulation (encounters). This simple, two–parameter mechanistic model reproduces accuracy and latency characteristics from real ants while also having more mathematical tractability than more complex random–walk models from psychology. The parameter values are related to the ants' cognitive complexity and their adaptive balance of speed–accuracy trade–offs for optimal decision–making. Moreover, the model's simplicity makes it amenable for implementation in applications such as engineering decision systems or swarm robotics.

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Environmental Seasonality on Predator–Prey Systems Under Nutrient and Toxicant Constraints

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Abstract

Environmental toxicants such as chemicals, heavy metals, and pesticides and environmental fluctuations are important factors influencing real aquatic ecosystems. Therefore, the investigation of the role of these factors in aquatic population dynamics is important. In this study, we extend an existing model for a toxin-dependent predator-prey model that incorporates variable food quantity as well as quality to better understand the role of seasonally varying carrying capacity on population dynamics. In the absence of seasonal effects, previous models suggest that the dynamics include Hopf bifurcation, saddle-node bifurcation, and limit cycles. However, seasonal effects can have major implications on the predicted solutions and enrich population dynamics. Bifurcation analyses demonstrate that seasonal forcing can cause periodic and quasi-periodic solutions.

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An extension to the Toxicant mediated Predator-prey model under Stoichiometric Constraints

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Abstract

Studies in ecological stoichiometry highlight that grazer dynamics are affected by insufficient food nutrient content (low phosphorus (P)/carbon (C) ratio) as well as excess food nutrient content (high P:C). Contaminant stressors affect all levels of the biological hierarchy, from cells to organs to organisms to populations to entire ecosystems. Eco-toxicological modeling under the framework of ecological stoichiometry predicts the risk of bio-accumulation of a toxicant under stoichiometric constraints. In this paper, we developed and analyzed a LotkaVolterra type predator–prey model which explicitly tracks the environmental toxicant as well as the toxicant in the populations under stoichiometric constraints. Analytic, numerical, slow-fast steady state and bifurcation theory are employed to predict the risk of toxicant bio-accumulation under varying food conditions. In some cases, our model predicts higher individual toxicity on grazer (body burden) compared to the previous model which increases the effectiveness of risk assessment protocols.

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Weaker is better: how weak transient molecular interactions give rise to robust, dynamic immune protection

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Abstract

The longstanding view in chemistry and biology is that high-affinity, tight-binding interactions are optimal for many essential functions, such as receptor-ligand interactions. Yet, an increasing number of biological systems are emerging that challenge this view, finding instead that low-affinity, rapidly unbinding dynamics can be essential for optimal function. A common mechanism has begun to emerge: rapidly diffusing third-party molecular anchors with weak, short-lived affinities play a major role for self organization of micron-scale living systems. These mechanisms have been poorly understood in the past due to the inability to directly observe such fleeting interactions and the lack of a theoretical framework to mechanistically understand how they work. In fact, it is only by tracking the motion of nanoprobes, coupled with inferences by stochastic modeling, Bayesian statistics, and bioimaging tools, that we recently begin to obtain definitive evidence of the emergent effects of these interactions. My talk will demonstrate how these ideas can answer a longstanding question: how mucosal barriers selectively arrest passive diffusion and active transport of pathogens.

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Analysis of A Spatially Inhomogeneous Stochastic Partial Differential Equation Epidemic Model

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Abstract

This work proposes and analyzes a family of spatially inhomogeneous epidemic models. This is our first effort to use stochastic partial differential equations (SPDEs) to model epidemic dynamics with spatial variations and environmental noise. After setting up the problem, existence and uniqueness of solutions of the underlying SPDEs are examined. Then definitions of permanence and extinction are given. Certain sufficient conditions are provided for the permanence and extinction. Our hope is that this paper will open up windows for investigation of epidemic models from a new angle.

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Demographic Variability, Environmental Variability, and Periodic Fluctuations in Stochastic Epidemic Models with Multiple Patches

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Abstract

Seasonality and contact patterns due to environmental fluctuations, social behavior, and physical proximity affect the dynamics of disease outbreaks. We investigate the effects of demographic, environmental and periodic variability on disease emergence and persistence in continuous-time, nonhomogeneous stochastic epidemic models, where disease is spread between several regions or patches. The continuous-time nonhomogeneous stochastic processes have either discrete or continuous random variables. A multitype branching process approximation is used to estimate the probability of a disease outbreak for various patch connectivities and periodicity assumptions in transmission and dispersal. In addition, a system of stochastic differential equations is used to investigate the effect of the three types of variability near the endemic state. The implications of these results for disease control are also discussed.

Seventh International Conference on Mathematical Modeling and Analysis of
Populations in Biological Systems, Tempe, Arizona, October 12-14, 2019

Network modeling of plant disease epidemics in space and time: The case of Cucurbit Downy Mildew (CDM) in the eastern United States

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Abstract

Over the last 20 years, systematic research has been conducted to develop and validate the prediction of cucurbit downy mildew (CDM) in space and time. These efforts have resulted in a prediction framework to guide growers and policymakers in making the relevant decision in managing the disease. The prediction framework relies on CDM reports from an extensive network of sentinel plots (disease monitoring locations that are strategically placed within specific states). The data about the current disease locations can be used to model the future spread of CDM. We developed a dynamic network model for CDM epidemics, with sentinel plots as nodes and edge weights as a function of host density, wind speed, and direction. The model incorporates a power-law function for dispersal. We used the network model and centrality measures to select the most important sentinel plots in terms of node strength, network stability, disease monitoring, and transmission. This information can be used to reduce the resources required to scout and predict CDM outbreak and invasion progress.

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Seventh International Conference on Mathematical Modeling and Analysis of
Populations in Biological Systems, Tempe, Arizona, October 12-14, 2019

Modeling CAR T-cell therapy with patient preconditioning

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Abstract

The first CAR T-cell therapies have recently been approved by the FDA for the treatment of several blood cancers, and many ongoing projects are broadening the scope of CAR T technology to address other cancer types[1]. Under standard treatment plans, patients undergo a lymphodepleting round of chemotherapy prior to CAR T infusion. Although treatment protocols exist, current understanding of the connection between preconditioning regimens and patient outcomes remains unclear. This poster presents a mathematical framework on which treatments combining chemotherapy and adoptive cellular therapy can be tested in the form of a system of differential equations. Numerical simulations of medically feasible treatment plans demonstrate scenarios in which appropriate preconditioning plans reduce the dosage of CAR T-cells required to reach a healthy outcome. Situations are also presented in which preconditioning plans using the same CAR T-cell dose and the same concentration of chemotherapy, but different delivery times lead to different patient outcomes.

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Seventh International Conference on Mathematical Modeling and Analysis of
Populations in Biological Systems, Tempe, Arizona, October 12-14, 2019

Deriving a spatially extended model of savanna dynamics

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Abstract

We introduce two interacting particle systems of vegetation dynamics (one macroscale and one mesoscale) based on the interaction rules from the mean-field Staver-Levin model of forest-savanna-grassland evolution [1,2]. Using coupling techniques for stochastic jump processes, we show the convergence of these particle systems towards McKean-Vlasov jump processes — processes solving a stochastic differential equation with self-consistent jump rates depending on the statistics of the solution. The generalized Kolmogorov equations of these processes are more amenable to analysis than the original particle systems and constitute nonlocal generalizations of the classical Staver-Levin model. Our macroscale model provides an elementary example of a jump process that does not converge to a stationary distribution but oscillates in law, while our mesoscale model can incorporate environmental heterogeneity and its solutions can exhibit waves of invasion and front pinning. Remarkably, the dynamical behavior of the particle systems finely recovers the bifurcation structure of the mean-field limit, despite almost-sure absorption for finite-size particle systems — we explain this phenomenon by computing the systems quasi-stationary distribution and deriving the absorption probability as a function of key parameters.

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Seventh International Conference on Mathematical Modeling and Analysis of
Populations in Biological Systems, Tempe, Arizona, October 12-14, 2019

Compensatory foraging in stoichiometric producer-grazer models

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Abstract

Nutritional constraints are common as food resources are rarely optimally suited for grazing species. Elemental mismatches between trophic levels can influence population growth and foraging behaviors. Grazing species, such as *Daphnia*, utilize optimal foraging techniques, such as compensatory feeding. Here we develop two stoichiometric producer-grazer models, a base model that incorporates a fixed energetic foraging cost and an optimal foraging model where energetic foraging costs depend on food nutritional content. A variable energetic foraging cost results in cell quota dependent predation behaviors. Analyzing and comparing these two models allows us to investigate the potential benefits of stoichiometric compensatory foraging behaviors on grazer populations.

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Density-dependent emergence alters the efficacy of *Wolbachia*-based mosquito control programs

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Abstract

The mosquito species *Aedes aegypti* is responsible for transmitting arboviruses such as dengue and Zika virus to humans throughout tropical and subtropical regions of the world. Populations of *Ae. aegypti* are known to be regulated by density-dependent processes that take place primarily in the juvenile aquatic stages of the mosquito's life cycle as a result of competition for limited resources. Density dependence is most often assumed to impact survival of *Ae. aegypti* larvae, and an extensive amount of empirical and modeling work has investigated the role of density-dependent survival in mosquito population regulation and its potential impact on mosquito control programs. Density dependence is, however, known to drive other aspects of mosquito life history such as development time of juvenile mosquitoes, and this too could have important consequences for mosquito control strategies. To investigate the impact of density-dependent larval development on mosquito control, we have developed an ordinary differential equations model to study *Ae. aegypti* population control by introduction of the bacterium *Wolbachia*, which impacts the lifespan and egg production of wild mosquito populations and has the potential to interfere with virus transmission. We consider various relationships between density and larval development and compare their influences on mosquito population size and the success of *Wolbachia* introductions. We find that in many cases, density-dependent emergence of *Ae. aegypti* could lead to the failure of *Wolbachia*-based control programs to reduce the population of competent vectors. The results of this study could help provide insights into appropriate control measures under different assumptions about the relationship between density and population regulation.

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Review: mathematical modeling of androgen deprivation therapy for prostate cancer

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Abstract

One of the standard treatments for advanced prostate cancer patient is the Androgen Deprivation Therapy (ADT). This accounts for the fact that the growth of tumor cell is androgen-dependent, but the development of androgen-independent tumor cells eventually takes place and renders the treatment ineffective. Due to the reduction in the male hormone during the treatment, undesirable effects can lead to loss in quality of life. Intermittent Androgen Suppression Therapy is the idea of alternating between on- and off- treatment period in accordance to the prostate specific antigen level. This has been shown to give patients better life quality; however, it remains controversial whether it is superior to the continuous-ADT in term of prolonging the life of the patient. Among other issues, there is a rising need for predicting power of cancer progress to supply patients and physicians with the necessary information to decide on the best course of action. Numerous mathematical models and computational approaches have been developed to better our understanding of prostate cancer. We review some of the major efforts in the last two decades and put forward suggestions on how to connect theoretical work to clinical application.

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A Mathematical Examination of Wolf Reintroduction in Yellowstone National Park: Capturing the Mechanisms of Predator Dependent Birth Rates of Prey

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Abstract

The reintroduction of wolves to Yellowstone National Park triggered a trophic cascade which captured the imagination of the American public with articles being published everywhere from The New York Times to Newsweek. The control of elk has lead to a myriad of benefits for other denizens of the park like beavers, bears, and aspen trees. Multiple studies have attempted to determine the Holling Type functional response of elk-wolf interactions using field measurements, but this is the first paper which fits the entire Rosenzweig-MacArthur model directly to the population count data. Our results corroborate Creel et al. (2011) [1] that the classical predator-prey models neglect the crucial impact that the presence of wolves have on elk birth rates; furthermore, we propose changes which capture this essential dynamic. We perform the perfunctory qualitative analysis of the new model. We fit a single model to two data sets with different underlying distributions simultaneously thus combining the methods of parameter estimation with multi-objective optimization in a novel way. Validity of our of the models is checked against the 2014-2019 population counts. This paper is a first step in filling a gap in the mathematical ecology literature where advanced model fitting techniques are neglected.

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Network modeling the impact of community-based male-screening on the Chlamydia trachomatis prevalence in women

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Abstract

We create and analyze a stochastic network-based model to understand the control of Chlamydia trachomatis (Ct) among young African American (AA) in New Orleans. Ct is the most commonly reported bacterial sexually transmitted infection in the United States and is a major cause of infertility, pelvic inflammatory disease, and ectopic pregnancy among women. Despite decades of screening women for Ct, the rates continue to increase among young AA compared to other groups. The community-based program "Check It" proposes that men are an important reservoir of infection for women and screening AA men could make an impact on the rates among women. To quantify the effectiveness of the male-screening strategy, we propose an agent-based network model to simulate a realistic sexual contact network for assortative mixing among the targeted population. We model both the existing intervention for women through the annual exam and the "Check It" male-screening based intervention through venue-based enrollment. The model accounts for various intervention strategies implemented in the program, including the expedited index treatment, expedited partner treatment, social network peer referral, and rescreening. We use sensitivity analysis to quantify the significance of each intervention component onto the prevalence in women.

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Spatially heterogeneous producer-grazer model subject to stoichiometric constraints

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Abstract

Known stoichiometric models of a two species producer-grazer ecosystem have either neglected spatial dynamics or failed to track free phosphorus in the media. Here we present a spatially heterogeneous model that tracks phosphorus content in the producer and free phosphorus in the media. We simulate our model numerically under various environmental conditions. Multiple equilibria, with bistability and deterministic extinction of the grazer, are possible here. In conditions that had been previously studied without tracking free phosphorus we find cases where qualitatively different behavior is observed. In particular, under certain environmental conditions, previous models predict stable equilibria where our model predicts stable limit cycles near the surface. Oscillatory dynamics can have consequences on the population densities, which may spend some time at low values throughout the cycles where they are in danger of stochastic extinction.

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Nutritional Regulation Influencing Colony Dynamics and Task Allocations in Social Insects

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Abstract

In this paper, we use an adaptive modeling framework to model and study how nutritional status may regulate population dynamics and foraging task allocation of social insect colonies. Our proposed model assumes that (1) nutritional status is measured by the protein to carbon ratio which reflects through the ratio of workers foraging protein to workers foraging carbon; (2) brood is able to survive if the protein to carbon ratio falls into a certain range; and (3) colony recruits workers to forage protein or carbon driven by maximizing the brood survival rate. In addition, our proposed model includes division of labor implicitly. Mathematical analysis shows that both investment to brood rearing and brood nutrition are important for colony survival and dynamics. When division of labor and/or nutrition are in the intermediate value range, the model undergoes a backward bifurcation and creates multiple attractors due to bistability. This bistability implies that the colony survival requires threshold initial population. When the investment on brood is large enough or nutritional requirements are less strict, the colony tends to survive, otherwise, colony faces challenges of collapsing. Our model suggests that the needs of colony survival adapt to the needs of brood survival probability which requires the good nutritional status. As a consequence, the higher nutritional status can lead to the better survival rate of larvae, and thus the larger worker population.

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Saving lives, limbs and healthcare costs: Quantifying the impact of CHG bathing and effective leadership on the reduction of hospital-acquired infections

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Abstract

Hospital-acquired infections (HAIs) impact 1 in 22 hospitalized patients and are one of the leading causes of mortality in the United States. In addition to the direct patient impact, HAIs also cost the US healthcare system about $45 billion a year. Multiple studies have shown that bathing patients with chlorhexidine gluconate (CHG) wipes reduces HAIs. We employed a Markov chain model to assess the impact of CHG bathing on yearly HAIs and associated costs. Although the cost of using CHG wipes over traditional practices is about $4 more per patient, millions of dollars still could be saved when CHG bathing compliance is improved. Furthermore, we examine the effect of active resistors and organizational constipators on the reduced number of potentially prevented HAIs and the increase in associated healthcare costs. These individuals often delay implementation of emerging best practices in infection prevention.

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The role of the avian nesting curve in structuring enzootic *West Nile virus* transmission

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Abstract

West Nile virus (WNV) was introduced into the United States in 1999 and remains a major public health concern. Birds are the primary reservoir host for WNV. While outbreaks have been widely observed to be associated with the end of the avian nesting season, the ecological mechanisms responsible for the timing and magnitude of seasonal transmission are not well understood. Vectors are known to exhibit feeding preferences for certain avian host species, and biting rates may also vary with host age. Newly hatched birds, or nestlings, have less feather coverage and fewer defense mechanisms than older birds, rendering them more vulnerable to mosquitoes. The rate at which new nestlings are produced is determined by the avian nesting curve, which varies by species and is also influenced by climate. We use a mathematical model incorporating avian stage-structure and within-species heterogeneity in the form of stage-specific mosquito biting rates to investigate the connection between properties of the avian nesting curve and enzootic WNV transmission, as well as implications for control of WNV.

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A stage-structured population model for activity-dependent dendritic spines

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Abstract

Here we present a novel application of stage-structured population modeling to explore the input-output properties of neuronal dendrites with spines. Dendritic spines are small thorn-like protusions that emanate from the dendritic shaft of several functionally important neurons in the cerebral cortex. Individually, they have a general knob-like appearance of a bulbous head and a tenuous stem. They are the postsynaptic sites of over 90% of excitatory synapses in the mammalian brain. Time lapse imaging studies have demonstrated that spines can change their structure in response to experience, such as sensory stimulation and deprivation, environmental enrichment, and various pardigms of learning [1]. Here, we formulate a stage population model of a passive dendrite with activity-dependent spines using a continuum approach. This computational study models three dynamic populations of activity-dependent spine types, corresponding to the anatomical categories of stubby, mushroom, and thin spines. In this stage-structured population model spine types are driven by calcium levels that depend on local electrical activity. In this study, we explore the influence of the changing spine population and spine types on the development of electrical propagation pathways in response to repetitive synaptic input, and which input frequencies are best for facilitating these pathways.

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Underlying strain space structure and influenza A eco-evolutionary dynamics

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Abstract

Influenza A viruses (IAVs) yearly infect a substantial fraction of the human population. These viruses are continually evading host immune pressures, aided through mutations in the immunodominant hemagglutinin (HA) surface protein. Thus, IAV evolution occurs on similar time scales as transmission dynamics, and therefore evolutionary processes must be included in transmission models. Furthermore, IAV evolution is constrained by certain biophysical properties of the HA protein. How does the underlying strain space imposed by this fundamental constraint shape eco-evolutionary dynamics? In this presentation, we formulate a mathematical model for IAV evolution and transmission dynamics that spans across scales, from molecular properties of the HA to within-host and global processes. In particular, we focus on HA protein stability, mutation, cross-immunity, and population transmission. By keeping track of infectious individuals with each strain, our formulation imposes inherent population structure through its strain space. With different underlying strain spaces, we investigate the resulting long-term dynamics. To contrast with no structure, we also compare our results to the best fit neutral model of biodiversity. Furthermore, certain sites in the HA are hidden from host

immune systems, but still impact protein stability. We investigate network dynamics that occur from "hiding" certain HA sites from immune systems, in addition to population dynamics resulting from this self-organization.

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Exploration of Global Sensitivity Analysis Methods for Physiologically-Based Pharmacokinetic (PBPK) Models

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Abstract

Confidence in mathematical models–in particular, those utilizing parameter estimation–is highly dependent on the ability to verify each component of the model. Global sensitivity analysis (GSA), the study of uncertainty in outputs of a model throughout the parameter input space, can inform researchers which parameters are relevant or redundant, and moreover, where greater care must be taken with experimental measurements. In particular, GSA can indicate the effects changing a presumed-constant parameter can have on the overall model, allowing the modeler to consider the advantages and disadvantages of including this parameter in the estimation set.

Increasingly, physiologically-based pharmacokinetic (PBPK) models are using GSA methods to aid in justification of parameter estimation. Using a published PBPK model of bromochloromethane, this talk will explore and present visualizations of several GSA methods including an adaptation of Morris' Method and the extended Fourier amplitude sensitivity testing (eFAST).

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Contagion dynamics on adaptive networks: Norovirus as a case study

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Abstract

Classical contagion models, such as SIR, and other infectious disease models typically assume a well-mixed contact process. This may be unrealistic for infectious disease spread where the contact structure changes due to individuals' responses to the infectious disease. For instance, individuals showing symptoms might isolate themselves, or individuals that are aware of an ongoing epidemic in the population might reduce or change their contacts. Here we investigate contagion dynamics in an adaptive network context, meaning that the contact network is changing over time due to individuals responding to an infectious disease in the population. We consider norovirus as a specific example and investigate questions related to disease dynamics and applications to public health.

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Populations in Biological Systems, Tempe, Arizona, October 12-14, 2019

Effect of spatial average on the spatial-temporal pattern formation of reaction-diffusion systems

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Abstract

Some quantities in the reaction-diffusion models from cellular biology or ecology depend on the spatial average of density functions instead of local density functions. We show that such nonlocal spatial average can induce instability of constant steady state, which is different from classical Turing instability. In particular, for systems of two equations containing spatial averages, spatially non-homogeneous time-periodic orbits could occur through bifurcations from the constant steady state. Examples from a nonlocal predator-prey model and a pollen tube tip model will be used to demonstrate such bifurcations.

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Dispersal Induced Dichotomy in Population Dynamics

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Abstract

Spatial heterogeneity and spatial movement play an important role in population dynamics. Such dispersal movement in a discrete heterogeneous environment can be represented by a connectivity matrix and the corresponding digraph/network, and the resulting mathematical model becomes a coupled dynamical system on network. Our studies focus on how coupling strength and topological structure of the dispersal network jointly affect the population dynamics. Specifically, our recent results, jointly with Shanshan Chen (Harbin Institute of Technology), Junping Shi (College of William & Mary) and Yixiang Wu (Middle Tennessee State University), highlight the dichotomy of population persistence vs extinction (infectious disease invasion vs eradication) with respect to the dispersal strength.

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Joining Forces: Combining Machine Learning and Mechanistic Models to Predict Tumor Cell Density

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Abstract

Glioblastoma, the most aggressive primary brain cancer, is primarily monitored via magnetic resonance imaging. However, standard clinical images are non-specific in their correlation with tumor cell density, making it difficult to define specific regions of interest to target for surgery and radiation. Previous efforts utilizing either machine learning (ML) or mechanistic modeling have shown promise for better interpreting these images, but methods to harness the strengths of both methods are sorely needed to make clinically–actionable progress. Here we present a novel, first-of-its-kind, hybrid model which brings together a graph-based semi-supervised machine learning approach with a mechanistic partial differential equation model of glioblastoma growth, known as the Proliferation-Invasion (PI) model, to generate predictive tumor cell density maps with high accuracy. We applied our ML-PI model framework to 18 patients with 82 image–localized biopsies combined. In this cohort, ML-PI was achieved higher accuracy in cell density prediction than either of the independent models (ML or PI) alone, with a mean accuracy prediction error of 0.084 vs 0.227 for PI alone and 0.220 for ML alone. We hope that with more verification, this tool can be used to guide spatially–localized therapies such as surgery and radiation, and improve image interpretation in glioblastoma.

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Optimal Control for a Novel Fractional Order Malaria Transmission Dynamics Mathematical Model

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Abstract

Recently, J. Mohammed-Awel, A. B. Gumel presented a new mathematical model [1] for assessing the impact of insecticides resistance in the mosquito population (due to widespread use of indoors residual spraying (IRS) and insecticides treated bed nets (ITNs)) on the transmission dynamics and control of malaria in a community. The model, which couples disease epidemiology with vector population genetics, incorporates several fitness costs associated with insecticide resistance.

On the other side, Atangana and Baleanu [[2]-[3]] defined a modified Caputo fractional derivative (ABC) by introducing a generalized Mittag-Leffler function with a nonlocal and a non-singular kernel [2]. This new type of derivative has been applied to model various real world problems in different fields [3]. On the other hand, the fractional optimal control (FOCP) theory is a very new topic in mathematics and has been under development. Some interesting real-life models of FOCP are presented in various real world problems [4]. In this work, we consider the model which given in [1], two control variables are presented in this model to minimize the number of the population of low-risk infectious humans and high-risk infectious humans. Necessary and sufficient conditions for the control problem are considered. The fractional derivative is defined in the ABC sense. New numerical methods for simulating a fractional order optimal system with Mittag-Leffler kernels are presented. Numerical simulations are given to validate the theoretical results.

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Seventh International Conference on Mathematical Modeling and Analysis of Populations in Biological Systems, Tempe, Arizona, October 12-14, 2019

Investigating differential impacts of treatment non-adherence on the dynamics of vector-borne diseases: Case study of elimination of Visceral Leishmaniasis from Bihar, India by 2020

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Abstract

Visceral Leishmaniasis (VL) is a neglected tropical disease with an estimated over 50,000 new cases and over 20,000 deaths annually worldwide [1]. Although elimination campaign has been effectively deployed since 2005, India alone produces more than 10,000 cases per year. Promoting treatment adherence and monitoring can play a critical role in sustaining the control of VL by different treatment regimens [2]. Self-reports highlight different causes of treatment non-adherence (like side-effects of the treatment, access to the hospital, resolution of symptoms, etc.) [3]. These, along with peoples disease literacy, reflect on different mechanisms of non-adherence. We built a vector-host model with varying functional forms that capture behavior of non-adherent population. Using this model, we investigated the differential impacts that various causes of non-adherence have on the dynamics and prevalence of VL. The major insight from this work is the redefinition of epidemiological model parameters to identify and quantify measurables such as reported prevalence and incidence. We showed that treatment adherence needs to be substantially high to facilitate elimination. Also, the average time spent in treatment before defaulting and the average time spent before reinitiating treatment have crucial impact on the potential to eliminate VL from India by 2020.

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Using a Suite of Quantitative Systems Pharmacology Models to Support Clinical Development of a Novel Therapy in Autoimmune Diseases

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Abstract

Quantitative Systems Pharmacology (QSP) is a knowledge and data driven modeling strategy that melds biology, pathology, and pharmacology into one integrated mathematical framework. A common approach to applying these models in the drug development process is by generation of a virtual patient population that captures the known mechanisms of disease and variability in processes observed in clinical trials of the disease population. Here, I will give a brief description of the process by which a virtual patient population is generated, calibrated to clinical data, and validated to be predictive of clinical outcomes. This process will be motivated by the example of application of QSP modeling to support a novel therapeutic strategy in the autoimmune disease space, in which learnings from one disease are used to improve predictions in subsequent diseases.

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Control of Circuit-Host Interactions Toward Engineering Robust Gene Circuits

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Abstract

Circuit-host interactions add an additional hidden layer to synthetic gene circuits and perturb the circuit behaviors. Growth feedback between synthetic gene circuits and host organisms leads to various emerged behaviors, including growth bistability and increased ultrasensitivity. However, the impacts of growth feedback on gene circuits remains unexplored. Here, we found that the effects of growth feedback on the functional perturbations of gene circuits depend on the network topology. Specifically, the memory of a self-activation circuit is lost due to the fast growth of host cells. Decoupling of growth feedback reveals its hysteresis property in a broad range. Interestingly, the toggle switch circuit is more refractory to the growth feedback. The underlying principle is demonstrated by systematic simulation with mathematical modeling of the interplay between microbial growth and gene circuits. Our results reveal a topology-dependent mechanism underlying the functional perturbation of gene circuits by growth-mediated feedback. Furthermore, we developed quantitative control strategies targeting on other circuit-host interactions toward engineering predictable and controllable gene circuits from different perspectives.

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Disease, demography and the evolution of social organization

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Abstract

Infectious diseases pose a threat to the stability and functioning of social groups, and the fitness costs of infections may constrain the evolution of complex social organization in group-living species. We present a mathematical model to explore the potential impact of disease on the evolutionary fitness of different organizational strategies for populations of social species whose survival depends on collaborative efficiency, especially under stochastic environmental conditions. We show that infectious diseases select for a specific regulatory feature in the organization of collaborative tasks: demographic robustness, and that this feature is more costly to maintain in environments where infection risks are absent. To illustrate and test our findings, we consider colonies of eusocial insects, which provide an unparalleled model system for these purposes; across their diversity of taxa they exhibit distinct organizational types, face a variety of infection risks, and are clearly under selective pressure for collaborative efficiency. Our study provides evidence for an often-stated (but rarely supported) claim that pathogens have been a significant force shaping the organization of insect societies and establishes a general theoretical approach for assessing evolutionary constraints on social organization from disease risk in cooperative, group-living species.

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Modeling the Effects of Drugs of Abuse on HIV Infections with Two Viral Species

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Abstract

Injection drug use is one of the greatest risk factors associated with contracting human immunodeficiency virus (HIV), and drug users infected with HIV suffer from a higher viral load and rapid parthenogenesis. Replication of HIV may result in mutant viruses that can escape recognition of the host's immune response. Experimental results have shown that morphine can decrease the viral mutation rate and cellular immune responses. We present a mathematical model to determine if the decrease in mutation and cellular immune response in the presence of morphine can account for the increased viral load. Our model shows that the morphine-altered mutation rate and cellular immune response allows the founder virus to out compete the mutant, causing a higher set-point viral load. We identify three biologically relevant equilibria of the model- infection-free, mutant only, and coexistence - and perform stability analysis on them. By controlling the fitness cost of mutation, mutant escape rate, and morphine concentration we are able to completely characterize the dynamics of our model in terms of these three equilibria. Finally, we perform numerical simulations to study the effects of morphine conditioning on viral load and selection of viral species reflect the increased viral load associated with morphine use.

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Modeling the coral reef microbiome and black band disease

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Abstract

Coral reefs are some of the most diverse and valuable ecosystems on the planet, but an estimated 20% of the world's coral reefs have been decimated due to stressors such as diseases. The microbiome associated with corals is essential to the health of coral reefs and highly affected by environmental temperature. In this talk, I will present a novel mathematical model to investigate the effects of temperature on microbiome structure. Our model can accurately predict the *P. strigosa* coral colonies data collected from reef zones of Bermuda. Using our model along with the sample data, we identified key factors shaping the coral microbiome structure in each inner and outer reef zones. Our results show that seasonal temperature variation is the primary driver to the microbiome composition, while the microbial network is a secondary driver. We further extend the microbiome model to predict black band disease dynamics and identify an environmental threshold that would shift the reef holobiont from a healthy to a disease-associated microbial community. Our results show that the environmental temperature can have significant impact on the coral reef holobiont health, and can account for susceptibility to black band disease.

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Juvenile-adult discrete time infectious disease models

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Abstract

The effect of age structure on the persistence or extinction of disease is studied with a discrete time model. When the recruitment function is of Ricker type, the population (in the absence of disease) may persist on either a fixed point or periodic k-cycles. When disease is introduced, the basic reproduction number $\mathcal{R}_0$ is calculated by an extension of the next generation matrix method. For $\mathcal{R}_0 > 1$, numerical simulations show that the juvenile-adult disease free period k-cycle dynamics drives the disease dynamics for an SIR model, but not for a model of infectious salmon anaemia virus that causes significant mortality. Joint work with A.-A. Yakubu.

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Dynamics of an intraguild predator-prey system with internal storage in an unstirred chemostat

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Abstract

In this talk, I shall present a reaction-diffusion system modeling interactions of the intraguild predator and prey in the unstirred chemostat, in which the predator can also compete with its prey for one single nutrient resource that can be stored within individuals. The existence of positive/coexistence steady state(s) is established in terms of the principal eigenvalues of associated nonlinear eigenvalue problems by means of persistence theory and the degree theory. It turns out that the introduction of predation in an ecosystem can enhance the coexistence of species.

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Combining network theory and partial differential equation to improve influenza prediction

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Abstract

The ever-increasing availability of geospatial data now opens the possibility to use spatio-temporal models to more accurately predict patterns of movement and trends in human activities, epidemic spread, environmental changes and many other natural phenomena. In this talk, we present an integrated framework for early detection of epidemic outbreaks based on geo-tagged data in Twitter. We combine network theory, data mining and partial differential equation models to describe/predict patterns of epidemic spread at a regional level. In addition, we will discuss a number of mathematical problems including free boundary value problems and bifurcation problems arising from these applications.

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Somitogenesis by a synthetic gene circuit

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Abstract

Reaction-diffusion (RD) based clock and wavefront model has long been proposed as the mechanism underlying biological pattern formation of repeated and segmented structures including somitogenesis. However, systematic molecular level understanding of the mechanism remains elusive, largely due to the lack of suitable experimental systems to probe RD quantitatively in vivo. Here we design a synthetic gene circuit that couples gene expression regulation (reaction) with quorum sensing (diffusion) to guide bacterial cells self-organizing into stripe patterns at both microscopic and colony scales. An experimentally verified mathematical model confirms that these periodic spatial structures are emerged from the integration of oscillatory gene expression as the molecular clock and the outward expanding diffusions as the propagating wavefront. Furthermore, our paired model-experiment data illustrate that the RD-based patterning is sensitive to initial conditions and can be modulated by external inducers to generate diverse patterns, including multiple-stripe pattern, target-like pattern and ring patterns with reversed fluorescence. Powered by our synthetic biology setup, we also test different topologies of gene networks and show that network motifs enabling robust oscillations are foundations of sequential stripe pattern formation. These results verified close connections between gene network topology and resulting RD driven pattern formation, offering an engineering approach to help understand biological development.

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Traveling wave solution of a diffusive viral infection model with time delay.

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Abstract

In this talk, we study the traveling waves of a diffusive viral infection model with time delay. To establish the existence result, we first consider a perturbed system and construct suitable upper and lower solutions so that Schauder fixed point theorem can be applied. Next, we use a limiting argument together with Lyapunov functional techniques to find a traveling wave solution which connects the infection-free equilibrium and the endemic equilibrium.

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Regional Level Influenza Prediction Model with Mechanistic PDE Approach and Sampling Twitter Data

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Abstract

Real-time and geo-tagged Twitter streaming data on flu epidemics provides timely data for researchers to effectively explore, model, and predict the trends of flu cases in our daily life. However, the explosive growth of big social media data calls for more novel and effective techniques such as data sampling, summarization, and sketching. In this paper, we propose a partial differential equation (PDE) model to characterize and predict temporal-spatial patterns of aggregated flu tweet volumes. Our PDE model incorporates the effects of flu spreading, people's recovering and active human interventions for reducing flu. Our experimental evaluations show that this mechanistic PDE model can almost eliminate the data reduction effects due to the sampling process: our PDE model requires fewer historical data, but achieves stronger prediction results with the relative accuracy of over 90% with the 1% sampling data. Even for the more aggressive data sampling ratios such as 0.1% and 0.01% sampling, our model is still able to achieve relative accuracies of 85% and 83%, respectively. The promising and powerful results highlight the ability of our mechanistic PDE model in predicting temporal-spatial patterns of flu trends even in the scenario of small sampling Twitter data.

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Modeling population dynamics with some generalized logistic type models

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Abstract

The three two parameter generalized logistic model $\frac{dp}{dt} = r(1-p)^{\beta}p^{\alpha}$, with two exponential parameters α, $\beta > 0$ is studied for modeling of some population data. Comparision of the classical and one exponential parameter models are presented for the data, and challenges in performing regression analysis are demonstrated. An approximation of the model is proposed which metigates the difficulties in performing regression analysis and is shown to provide satisfactory results. The model offers an alternative for population modeling and can serve a model for harzard and actuarial risk estimates.

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Reaction-diffusion based pattern formation modeling and its basic dynamical behavior.

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Abstract

Reaction-diffusion (RD) based pattern formation model has long been proposed as the mechanism underlying biological pattern formation of repeated and segmented structures including somitogenesis. However, systematic molecular level understanding of the mechanism remains elusive, largely due to the lack of neither suitable experimental systems to probe RD quantitatively in *vivo* nor reasonable mathematical models to study the mechanism. In this talk, we will present how we model the synthetic gene circuit with reaction-diffusion equation and how it can capture the experimental results constantly. Then we studied the mechanism of this gene circuit via the mathematical model and explained the cause of different experimental observations. Last but not least, we will also cover some dynamical analysis framework of our model.

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Dynamic Model for Life History of Scyphozoa

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Abstract

A two-state life history model governed by ODEs is formulated to elucidate the population dynamics of jellyfish and to illuminate the triggering mechanism of its blooms. The polyp-medusa model admits trichotomous global dynamic scenarios: extinction, polyps survival only, and both survival. The population dynamics sensitively depend on several biotic and abiotic limiting factors such as substrate, temperature, and predation. The combination of temperature increase, substrate expansion, and predator diminishment acts synergistically to create a habitat that is more favorable for jellyfishes. Reducing artificial marine constructions, aiding predator populations, and directly controlling the jellyfish population would help to manage the jellyfish blooms. The theoretical analyses and numerical experiments yield several insight into the nature underlying the model and shed some new light on the general control strategy for jellyfish.

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Resource Mediated Interactions and Species Dynamics in Microbial Communities

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Abstract

Microbes are everywhere; they form complex communities which are essential in maintaining the balance of ecosystems and hosts health. While there is an extensive literature applying the generalized Lotka-Volterra (gLV) model to estimate interactions and gain insight into the stability of microbial communities, this model has at least a few limitations in this context. In particular, we hypothesize that in many microbial communities, interactions are typically indirect and mediated by molecules in the environment (e.g., resources, toxins), rather than direct as assumed in the gLV model. We have developed a system of differential equations describing an m-resource, n-species microbial community. In the model, we allow species to transition between various metabolic states; specifically, we track the number of species of type i that are consuming resource j. To gain insight into dynamics, we have rewritten the model in terms of the proportion of microbial biomass that is a given species. Rewriting the equations in this way uncovers relationships governing the evolutionary dynamics of the system explicitly in terms of the fitness of each species relative to the mean fitness of the entire population.

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Modelling the potential role of engineered symbiotic bacteria in malaria control

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Abstract

A recent experimental study suggests that the engineered symbiotic bacteria Serratia AS1 may provide a novel, effective and sustainable biocontrol of malaria. These recombinant bacteria have been shown to be able to rapidly disseminate throughout mosquito populations and to efficiently inhibit development of malaria parasites in mosquitoes in controlled laboratory experiments. In this talk, I will report a recent work in which we develop a climate-based malaria model which involves both vertical and horizontal transmissions of the engineered Serratia AS1 bacteria in mosquito population. We show that the dynamics of the model system is totally determined by the vector reproduction ratio R_v, and the basic reproduction ratio R_0. If $R_v \leq 1$, then the mosquito-free state is globally attractive. If $R_v > 1$ and $R_0 \leq 1$, then the disease-free periodic solution is globally attractive. If $R_v > 1$ and $R_0 > 1$, then the positive periodic solution is globally attractive. Numerically, we verify the obtained analytic result and evaluate the effects of releasing the engineered Serratia AS1 bacteria in field by conducting a case study for Douala, Cameroon. We find that ideally, by using Serratia AS1 alone, it takes at least 25 years to eliminate malaria from Douala. This implies that continued long term investment is needed in the fight against malaria and confirms the necessity of integrating multiple control measures. This is joint work with Dr. Xiunan Wang.