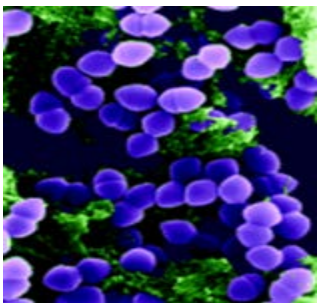
MRSA

CD



VRE

International Workshop on Antibiotic-Resistant Infections: Mathematical Modeling, Transmission Dynamics and Control

University of Miami, Coral Gables, Florida
December 9-11, 2011

Program

University Center (UC)
2nd floor, Flamingo Ballroom C & D
1306 Stanford Drive, Coral Gables, FL 33146

National Science Foundation
WHERE DISCOVERIES BEGIN

Mission. The emergence and spread of antibiotic-resistant bacteria is considered to be one of the biggest threats to human health in the 21st century. For example, a recent estimate showed that there were 18,650 deaths in patients with invasive methicillin-resistant Staphylococcus aureus (MRSA) in the United Sates in 2005, exceeding the total number of deaths due to HIV/AIDS in the same year (R. M. Klevens et al., JAMA, 2007). In the last decade, mathematical models have been increasingly used as tools to identify factors responsible for observed patterns of antimicrobial resistance, to predict the effect of various factors on the prevalence of primary and secondary antimicrobial resistance, and to help design effective control and intervention programs. The goal of the workshop is to bring together researchers in biology, epidemiology, medical clinics, and mathematics to report their current research, initiate collaborations, and stimulate progress in studying antibiotic-resistant infections. The workshop will also provide a unique opportunity for graduate students and postdoctoral fellows to interact with leading researchers from medicine and mathematics in a productive and sustained way.

Acknowledgments. The workshop is generously supported by the National Science Foundation, the Office of Research, the College of Arts and Sciences, and the Department of Mathematics at the University of Miami. The staff in the Department of Mathematics has provided professional assistance in organizing the workshop.

Internet Access. The University of Miami provides free internet access on campus. Just connect as a guest.

Breakfast. Complimentary breakfast will be provided at the workshop.

Lunch. The university cafeteria and the Faculty Club are near the workshop site.

Parking. Please make sure you park in the visitor's parking spot and purchase your parking ticket from the nearby machine.

Restaurants. There are plenty of restaurants in downtown South Miami which is a few blocks from the Holiday Inn (along US1 in the southwest direction).

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December 6th, 2011

Dear Workshop Participants:

It is with great pleasure that I extend you a warm welcome to the University of Miami campus. The College of Arts and Sciences and the Department of Mathematics are very glad to host the International Workshop on Antibiotic-Resistant Infections: Mathematical Modeling, Transmission Dynamics and Control. Antibiotic-resistant bacteria unquestionably pose a growing and serious threat to human health. Professor Ruan has prepared an excellent program, combining cutting-edge presentations by many distinguished mathematicians and life scientists. As such, this workshop represents a truly interdisciplinary effort to address an important health problem.

I wish all of you a very productive and scientifically stimulating time in Coral Gables. I hope that you will find some time to enjoy the beauty of our campus and the many attractions that South Florida offers to visitors at this balmy time of the year.

Best regards,

Angel E. Kaifer
Senior Associate Dean for
Research and Graduate Education
College of Arts and Sciences

Schedule

December 9, 2011, Friday

8:30 – 9:00 Breakfast

Session 1 (Chair, Shigui Ruan)

9:00 – 9:20 Opening
Angel Kaifer, Senior Associate Dean, College of Arts and Sciences, Univ of Miami
Gregory Galloway, Chair, Department of Mathematics, University of Miami

9:20 – 10:00 **Martin Bootsma**, Estimation of Important Parameters for Transmission Models

10:00 – 10:30 Coffee break

Session 2 (Chair, Troy Day)

10:30 – 11:10 **Cristina Lanzas**, *Clostridium difficile* Transmission Dynamics and Control at the Hospital

11:10 – 11:50 **Pierre Magal**, Modelling Antibiotic Resistance in Hospital Environment

11:50 – 14:00 Lunch

Session 3 (Chair, Sergei Pilyugin)

14:00 – 14:40 **H. T. Banks**, A Comparison of Stochastic Simulation Algorithms in Infection Models

14:40 – 15:20 **Robert Beardmore**, Antibiotic Rotation, Mixing, and what Mathematical Models Say about It

15:20 – 15:50 Coffee break

Session 4 (Chair, Ivana Gudelj)

15:50 – 16:30 **Farida Chamchod**, Modeling the Spread of Methicillin-resistant *Staphylococcus aureus* in Nursing Homes for Elderly

16:30 – 17:10 **Joanna Wares**, Efficacy of Infection Control Interventions in Reducing the Spread of Multidrug-resistant Organisms in the Hospital Setting

17:10 – 17:40 Discussion

December 10, 2011, Saturday

8:30 – 9:00 Breakfast

Session 5 (Chair, H. T. Banks)

9:00 – 9:40 **Troy Day**, Optimal Control of Drug Resistant Pathogens and the Mixing versus Cycling Controversy

9:40 – 10:20 **Mohammed Yahdi**, Parameter Analysis and Optimal Control of a VRE Model

10:20 – 10:50 Coffee break

Session 6 (Chair, Cristina Lanzas)

10:50 – 11:30 **Song Liang**, Modeling the Transmission of Antimicrobial Resistant (AMR) Bacteria from Wildlife to Livestock: A Multi-host Framework

11:30 – 12:10 **Amy Hurford**, Linking Antibiotic Prescribing to Antibiotic Resistance in the ICU: Before and After an Antibiotic Stewardship Program

12:10 – 14:00 Lunch

Session 7 (Chair, Tim Reluga)

14:00 – 14:40 **Ivana Gudelj**, Evolutionary Ecology of Fungal Pathogens

14:40 – 15:20 **Roy Malka**, From Theory to Experiments: Evidence for Bistable Bacteria Neutrophils Interactions and Its Medical Implications

15:20 – 15:50 Coffee break

Session 8 (Chair, Song Liang)

15:50 – 16:30 **Cameron Browne**, Modeling within-host Virus Dynamics with Time-periodic Combination Drug Therapy

16:30 – 17:00 Discussion

19:00 Banquet (on your own)

December 11, 2011, Sunday

8:30 – 9:00 Breakfast

Session 9 (Chair, Joanna Wares)

9:00 – 9:40 **Sergei S. Pilyugin**, A Size-structured Model of Bacterial Growth and Reproduction

9:40 – 10:20 **Lei Wang**, Modelling the Transmission Dynamics of Meticillin-resistant Staphylococcus aureus in Beijing Tongren Hospital

10:20 – 10:50 Coffee break

Session 10 (Chair, Pierre Magal)

10:50 – 11:30 **Rafael Pẽna-Miller**, The Dynamic Nature of Drug Interactions

11:30 – 12:00 Discussion

Abstracts

A Comparison of Stochastic Simulation Algorithms in Infection Models

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We consider infectious progression models for two infections: a Vancomycin Resistant Enterococcus (VRE) bacterial infection and an Human Immunodeficiency Virus (HIV). For each of these we present a stochastic small population version and its deterministic large population limit under the Kurtz limiting process. The deterministic versions are ordinary differential equations which are readily simulated while the stochastic versions are difficult to simulate (or use in inverse problems at population levels of interest. We compared one hybrid method and several alternate stochastic algorithms to determine appropriateness for use with a large (10^6 viral particles) vs. small (10^3 particles). We report on investigations and simulations of five particular algorithms. The relative efficiency of each algorithm is determined based on computational time and degree of precision required. We have found that with the larger and more complex HIV model, implementation and modification of Tau-Leaping methods are preferred.

Antibiotic Rotation, Mixing, and what Mathematical Models Say about It

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Many mathematical models used to evaluate antibiotic rotations and to decide whether, or not, it is better rotate or to "mix" drugs have been linear with respect to the deployment protocol: such models can be cast in the form

$$\frac{dy}{dx} = f(x) + u(t)\, g(x).$$

Here the state x(t) is defined for t∈[0,T] and 0≤u≤1 is the protocol. Assume the model is control dissipative, meaning there is an M such that $\sup_{\{t\geq 0\}}|x(t)| \leqslant M$, where the latter is independent of initial data and u. This condition holds for many models in the current literature. This structure yields a well-defined "performance measure" P(u) for each protocol $u \in L^{\infty}$,

$$P(u) = \int_0^T w^T x(t)\, dt,$$

where w is a weight vector, that is continuous with respect to weak-star L^{∞}topologies. Moreover, as constant functions are the weak-star limit of periodic bang-bang functions, we immediately deduce a

worst-case-best-case result when comparing mixing and cycling. This result says that the performance of mixing and cycling protocols is "intertwined": pick a mixing protocol at random, and pick a cycling protocol at random. Without further information, we cannot say which of the two has the better performance in terms of minimising P. This result is robust to small noise, where the latter is defined in terms of small, L^{∞}-perturbations in u. It is therefore incorrect to claim that current mathematical models predict random drug mixing is the optimal way of allocating antibiotics to patients in hospitals and ICUs. This is joint work with Rafael Pena-Miller.

Estimation of Important Parameters for Transmission Models

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In my talk I will discuss several methods to estimate parameters which are important in mathematical models for the spread of antibiotic-resistant bacteria. More specifically, I will use data from the "Mastering hospital antimicrobial resistance" (MOSAR)-study, a trial in 13 Intensive Care Units in 8 European countries to estimate the duration of colonization outside ICUs. I will use MOSAR data and data obtained from contact screening after detection of an index case to estimate the transmission rate of several antibiotic resistant pathogens. Knowledge of these parameters is essential to accurately predict the effect of transmission prevention programs.

Modeling within-host Virus Dynamics with Time-periodic Combination Drug Therapy

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We add periodic forcing to a classical within-host virus model in order to analyze the consequence that combination drug therapy has on the dynamics of the system. The combination drug therapy consists of two classes of drugs which are assumed to have periodic efficacy functions. Using analytical methods, it is found that when the two classes of drugs have small amplitude sinusoidal efficacy functions, the phase difference between these functions can critically affect the asymptotic behavior of the virus. Numerical simulations illustrate this effect and provide further insights. I modify the model by explicitly including the age since infection of an infected cell, in order to separate the viral production from the infected cell death rate. The basic reproduction number, R_0, of the modified model is calculated. When

R_0>1, there is a unique positive steady state and a corresponding Lyapunov function. For both models, I will discuss connections and implications for treatment of bacterial infections by phage therapy.

Modeling the Spread of Methicillin-resistant *Staphylococcus aureus* in Nursing Homes for Elderly

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Methicillin-resistant *Staphylococcus aureus* (MRSA) is endemic in many hospital settings, including nursing homes. It is an important nosocomial pathogen that causes mortality and an economic burden to patients, hospitals, and the community. The epidemiology of the bacteria in nursing homes is both hospital- and community-like. Transmission occurs via hands of health care workers (HCWs) and direct contacts among residents during social activities. In this work, mathematical modeling in both deterministic and stochastic frameworks is used to study dissemination of MRSA among residents and HCWs, persistence and prevalence of MRSA in a population, and possible means of controlling the spread of this pathogen in nursing homes. The model predicts that: (i) without strict screening and decolonization of colonized individuals at admission, MRSA may persist; (ii) decolonization of colonized residents, improving hand hygiene in both residents and HCWs, reducing the duration of contamination of HCWs, and decreasing the resident:staff ratio are possible control strategies; (iii) the mean time that a resident remains susceptible since admission may be prolonged by screening and decolonization treatment in colonized individuals; (iv) in the stochastic framework, the total number of colonized residents varies and may increase when the admission of colonized residents, the duration of colonization, the average number of contacts among residents, or the average number of contacts that each resident requires from HCWs increases; (v) an introduction of a colonized individual into an MRSA-free nursing home has a much higher probability of leading to a major outbreak taking off than an introduction of a contaminated HCW. This is a joint work with Shigui Ruan.

Optimal Control of Drug Resistant Pathogens and the Mixing versus Cycling Controversy

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The evolution of drug resistance presents a major challenge for the control of infectious diseases. Numerous recent simulation studies suggest that deploying drugs at an intermediate level in the population can sometimes minimize the total size of infectious disease outbreaks. In this talk I will revisit this issue from the standpoint of optimal control theory. I will demonstrate that the optimal drug deployment strategy is, in fact, one that uses a maximal treatment level but that times the treatment

appropriately during the outbreak. From this conclusion I will then go on to consider the optimal deployment of two drugs. Again, optimal control theory will be used to shed light on recent controversies about drug mixing versus drug cycling. I present analytical results demonstrating how some situations lead to mixing being optimal and others lead to a form of cycling being optimal. These results help to partially resolve some discrepancies among other studies.

Evolutionary Ecology of Fungal Pathogens

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Invasive fungal pathogens pose a serious threat to human health - they are the second biggest killer of hospital patients in intensive care units. The most common invasive fungal pathogens isolated in clinical practice belong to the *genus Candida*. The composition of Candida infections has dramatically changed over time. Historically, the usual suspect *C. albicans* has accounted for the majority of Candida isolates but species such as *Candida glabrata* are now increasing in prevalence. This is an alarming development as *C. glabrata* infections are often resistant to fluconazole, the most frequently used antifungal drug. Is the selection pressure exerted by the prevalent use of fluconazole in clinical practice sufficient to explain the shift from *C. albicans* to *C. glabrata* within an infection niche? We explore this question using a combined approach of mathematical modeling and experimental studies and show that ecological interactions can shed light on the emerging epidemiological trends of Candida infections.

Linking Antibiotic Prescribing to Antibiotic Resistance in the ICU: Before and After an Antibiotic Stewardship Program

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Pseudomonas aeruginosa is a commonly acquired nosocomial infection. *P. aeruginosa* is highly drug-resistant and patients infected with resistant-*P. aeruginosa* have an elevated mortality risk and treatment costs. In February 2009, an antibiotic stewardship program (ASP) was implemented at Mount Sinai Hospital (MSH; Toronto, Canada). Aspects of this program were (a) to decrease the prescribing of antibiotics to patients without a *P. aeruginosa* infection; (b) to decrease the duration of antibiotic treatment; and (c) to prescribe ciprofloxacin (the antibiotic with the highest risk of treatment failure)

less frequently for treated patients without a *P. aeruginosa* infection. We derive a mathematical model that links antibiotic prescribing to *P. aeruginosa* epidemiology. We then use data on *P. aeruginosa* colonization and antibiotic resistance from the MSH ICU between 2005 and 2011 to fit the mathematical model and to quantify how the ASP altered antibiotic prescribing to patients. Finally, we consider each of the different aspects of the ASP to determine which aspect contributed most substantially to the decrease in *P. aeruginosa* colonization and resistance observed at MSH. We find that (a) contributed most to the decrease in the number of colonized patients, while (c) contributed most to the decrease in the number of colonized patients with antibiotic-resistant first isolates. This is a joint work with Andrew Morris (Infectious Diseases and Internal Medicine, Mount Sinai Hospital), David Fisman (The Dalla Lana School of Public Health, University of Toronto), and Jianhong Wu (The Centre for Disease Modelling, York University).

Clostridium difficile Transmission Dynamics and Control at the Hospital

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Clostridium difficile is the leading cause of infectious diarrhea in hospitals, and has become one of the most common causes of health-care associated infections. In recent years, an epidemic strain, resistant to fluoroquinolones, has been associated with an increased in disease severity. Both clinically infected patients and asymptomatic carriers are sources of *C. difficile*. Current *Clostridium difficile* infection (CDI) prevention strategies focus on preventing *C. difficile* transmission only from patients with symptomatic CDI and ignore asymptomatic carriers. We developed deterministic and stochastic models to (1) evaluate the contributions of asymptomatic and symptomatic *C. difficile* carriers to new CDI cases, (2) determine the most important epidemiological factors influencing *C. difficile* transmission, and (3) evaluate the effect of screening and applying contact precautions measures to detect and control transmission from asymptomatic carriers. Patients could be in one of five transition states in the model: resistant to colonization, susceptible to colonization, asymptomatically colonized without protection against CDI, asymptomatically colonized with protection against CDI, and patients with CDI. Data from a retrospective cohort study of all patients admitted to medical wards at a large tertiary care hospital in the United States in the calendar year 2008 and published literature were used to parameterize the model. Contact precautions for asymptomatic carriers could effectively decrease the nosocomial transmission of *C. difficile* if a rapid diagnostic test with good sensitivity were available to detect asymptomatic carriers. Our study underscores the need to further evaluate the role of asymptomatically colonized patients in *C. difficile* transmission.

Modeling the Transmission of Antimicrobial Resistant (AMR) Bacteria from Wildlife to Livestock: A Multi-host Framework

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Although it is increasingly recognized that microbial ecosystems of humans, domestic animals, wildlife, and the environment are intimately intertwined in complicated ways, much remains unknown on how such interactions shape the epidemiology of many diseases caused by zoonotic pathogens. This is especially true for emerging antimicrobial resistant (AMR) strains of foodborne pathogens of zoonotic origin. A new research project has been recently initiated, aiming to understand the role of wildlife (e.g. birds) as reservoirs and vectors in the transmission of AMR bacteria throughout the food chain. Here we present a conceptual modeling framework, as part of the project, through which to explore the interactions among the wildlife, livestock, the environment, and AMR bacteria. A multi-host patch model is proposed, specifically taking into account wild birds, livestock, the soil/water environment, and their interactions with AMR bacteria. The model is explored under a scenario involving European starlings and dairy cow in multiple farms based on a previous study. A Monte Carlo simulation approach (model parameter priors are based on field/laboratory observations and extensive literature review on studies under similar settings) is employed and relative importance of model parameters/processes is subsequently assessed.

Modelling Antibiotic Resistance in Hospital Environment

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The development of drug-resistant strains of bacteria is an increasing threat to society, especially in hospital settings. Many antibiotics that were formerly effective in combating bacterial infections in hospital patients are no longer effective due to the evolution of resistant strains. The evolution of these resistant strains compromises medical care worldwide. In this talk, we formulate a two-level population model to quantify key elements in nosocomial infections. At the level of one patient, the bacteria level infecting a patient with generate both nonresistant and resistant bacteria. We start the presentation by describing some models to describe this class of problems. Then we will turn to the level of one hospital, by consider an infection age structured models, and we will describe the relationships with stochastic numerical simulation of the hospital. The objectives are to analyze the dynamic elements of non-resistant and resistant bacteria strains in epidemic populations in hospital environments and to provide understanding of measures to avoid the endemicity of resistant antibiotic strains.

From Theory to Experiments: Evidence for Bistable Bacteria Neutrophils Interactions and Its Medical Implications

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Axiomatic modeling describing pathogenic bacterial growth in the presence of phagocytes suggests that this system should exhibit bi-stability. Indeed, our experimental investigation of the in-vitro bacteria and human neutrophil interaction clearly exhibits such bistability. We find that for each neutrophil level and function, there exists an associated bacterial concentration above which an infection develops and below which the neutrophils defeat the bacteria. This finding, combined with a mathematical model, provide new organizing principles behind two distinct immunodeficiency disorders: neutropenia and CGD. With normal neutrophil levels and function, only very high bacterial loads may develop into an acute infection. Yet, under neutropenic conditions, or when there is a neutrophil dysfunction, the critical bacterial load is within the clinically relevant range. We conclude from our experimental data and the model that the maximal bearable bacterial load depends sensitively on the neutrophil levels, the bactericidal activity and the integrity of the patient barriers. Moreover, this critical load may vary by orders of magnitude between patients. These findings may lead to methods for improving the identification and treatments of populations with these immunodeficiency disorders. This is a joint work with V. Rom-Kedar, B. Wolach R. Gavrieli and E. Shochat.

The Dynamic Nature of Drug Interactions

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A common strategy to dealing with the evolution of antibiotic resistance and to increase the efficacy of antimicrobial treatments is to use multidrug combination therapies. In particular, synergistic drug combinations whereby the combined effect is greater than the predicted individual effect are highly prized. These treatments, however, are also associated with the strongest selection for resistance and hence for escape from inhibition by antibiotics. In this talk we use mathematical models to show that the nature of the interaction profile depends on the population structure and therefore is a dynamic property of the system. Using optimality theory we demonstrate that when designing optimal therapies the effects of natural selection should be accounted for, and as the bacteria we are trying to kill the best treatment strategies have to be adaptive in time. We demonstrate our theoretical predictions using an

experimental evolution approach. This is joint work with Robert Beardmore, Hinrich Schulenburg, David Lahnemann and Gunther Jansen.

A Size-structured Model of Bacterial Growth and Reproduction

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I will discuss a size-structured bacterial population model in which the rate of cell growth is both size- and time-dependent and the average per capita reproduction rate is specified as a model parameter. It is shown that the model admits classical solutions. The population-level and distribution-level behaviours of these solutions are then determined in terms of the model parameters. The distribution-level behaviour is found to be different from that found in similar models of bacterial population dynamics. Rather than convergence to a stable size distribution, the size distributions repeat in cycles. This phenomenon is observed in similar models only under special assumptions on the functional form of the size-dependent growth rate factor. The main results will be illustrated with examples. This work is joint with Sean Ellermeyer of Kennesaw State University.

Modelling the Transmission Dynamics of Meticillin-resistant *Staphylococcus aureus* in Beijing Tongren Hospital

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Semi-professional volunteers work in many tertiary care hospitals in China as healthcare assistants. Proper infection control measures are needed to reduce nosocomial transmission involving volunteers. A compartmental model was constructed to describe the transmission characteristics of meticillin-resistant *Staphylococcus aureus* (MRSA) in the emergency ward (EW) and respiratory intensive care unit (RICU) for volunteers in Beijing Tongren Hospital, Beijing, China. The model consists of components describing uncolonized and colonized patients, uncontaminated and contaminated healthcare workers (HCWs), and uncontaminated and contaminated volunteers. The basic reproduction number (R_0) was calculated, and the dependence of R_0 on various model parameters was analysed. Moreover, simulations of the model were performed for comparision with the reported data on the numbers of colonized patients in the EW and RICU from 3 March 2009 to 28 February 2010, respectively. Sensitivity analysis of R_0 showed that increasing handwashing compliance among HCWs and volunteers would reduce the risk of transmission dramatically. As volunteers care for patients on a one-to-one basis, this study showed that the number of MRSA-positive patients would increase if volunteers were replaced by

HCWs. Therefore, in addition to improving hand hygiene among HCWs, the employment of properly trained volunteers is an attractive alternative to decrease MRSA and other multi-drug resistant bacteria infections in the hospital setting. This is a joint work with X. Lu, P. Magal, S. Ruan etc.

Efficacy of Infection Control Interventions in Reducing the Spread of Multidrug-resistant Organisms in the Hospital Setting

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Multidrug-resistant organisms (MDRO) continue to spread in hospitals globally, but the population-level impact of recommended preventive strategies, and the relative benefit of individual strategies targeting all MDRO in the hospital setting, is unclear. To explore the dynamics of MDRO transmission in the hospital, we developed a model extending data from clinical, individual-level studies to quantify the impact of hand hygiene, contact precautions, reducing antimicrobial exposure and screening surveillance cultures in decreasing the prevalence of MDRO colonization and infection. This talk will discuss our finding that most recommended strategies have substantial effect in decreasing the prevalence of MDRO over time, except for screening for asymptomatic MDRO colonization among patients who are not receiving antimicrobials, which is of minimal value in reducing the spread of MDRO.

Parameter Analysis and Optimal Control of a VRE Model

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Vancomycin-Resistant Enterococci (VRE) infections have been linked to increased mortality and costs. A new model of antibiotic resistant VRE infested intensive care units (ICU) is introduced that involves transmission dynamics between VRE colonization and infection stages. The impacts of nineteen parameters on the VRE dynamics and the outbreak risk are analyzed with a focus on special preventive care. Key parameters are used to determine optimal control strategies to prevent outbreaks and limit the emergence of VRE.

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Conference Announcements

Everything Disperses to Miami: The Role of Movement and Dispersal in Spatial Ecology, Epidemiology and Environmental Science

December 14-16, 2012
The University of Miami, Coral Gables, Florida

Principal Speakers***:***
Don DeAngelis (University of Miami and the United States Geological Service)
William Fagan (University of Maryland)
Suzanne Lenhart (Univ of Tennessee and National Institute for Mathematical and Biological Synthesis)
Yuan Lou (Ohio State University and Mathematical Biosciences Institute)
Wei-Ming Ni (University of Minnesota and Center for PDE at East China Normal University)
David Smith (Johns Hopkins University)
Jianhong Wu (York University and Centre of Disease Modeling)

Organizing Committee: **Stephen Cantrell** (University of Miami), **Suzanne Lenhart** (University of Tennessee and NIMBioS), **Yuan Lou** (Ohio State University and MBI), **Shigui Ruan** (University of Miami)

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CMPD4
The 4th International Conference on Computational and Mathematical Population Dynamics

May 29 – June 2, 2013
Taiyuan, China

This is the fourth joint meeting of the Conference on Mathematical Population Dynamics (MPD) and the Conference on Deterministic and Stochastic Models for Biological Interactions (DeStoBio), with a 26-year history of international meetings. The previous conferences are: MPD1 (University of Mississippi, USA, 1986); MPD2 (Rutgers University, USA, 1989); MPD3 (University of Pau, France, 1992); MPD4 (Rice University, USA, 1995); MPD5 (Zakopane, Poland, 1998); DeStoBio1 (Sofia, Bulgaria, 1997); DeStoBio2 (West Lafayette, USA, 2000); and the past joint conferences are CMPD1 (Trento, Italy, 2004); CMPD2 (Campinas, Brazil, 2007); CMPD3 (Bordeaux, France, 2010).

Chair of the Organizing Committee:
Professor Shigui Ruan, Department of Mathematics, University of Miami, Coral Gables, FL 33124, USA.
Email: ruan@math.miami.edu
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