2010 Red Raider Mini-Symposium Abstracts

Jorge A. Alfaro-Murillo (Purdue University)
An Agent-Based Model With Drift and Cross-Immunity for Infuenza
An agent-based model is used to describe the dynamics of influenza drift and cross-immunity in host populations with different characteristics. Each different mutation of the virus will be represented as a point in a phylogenetic map, and a strain of the virus by a region in that map. Each individual has a history of all his previous infections, represented by a vector consisting of points in the map. At a given time each infected individual will have contact with other individuals of the population. The probability that this contact results in an infection, depends on how far the virus is to the closest point in the history of the individual to be infected (cross-immunity). If the contact is effective, the individual will be infected for the next time period. However, since the virus is going to mutate in his body, for the next time period the active mutation will be one that is not the same that got him infected, but very close in the map to it (drift). Special attention will be given to the infection of influenza in the tropics, since this area has not been well characterized by mathematical models. Patterns similar to the ones observed in the tropics are obtained in the simulations with low values of contact or infection rates.

John Alford (Sam Houston State University)
Modeling Energetic and Theoretical Costs of Thermoregulatory Strategy
Poikilothermic ectotherms are those animals whose body temperatures fluctuate with ambient environmental temperatures. Some ectotherms have evolved behaviors to maintain or thermoregulate their body temperature around a preferred temperature. Thermoregulatory behaviors may range from body positioning to optimize heat gain to shuttling among preferred microhabitats. We have modeled movement and shuttling behavior within a habitat as a biased random walk. Timber rattlesnakes (Crotalus horridus) are sit-and-wait foragers that passively thermoconform to their environment. We quantify the required movements and potential energetic cost for a timber rattlesnake to actively thermoregulate rather than thermoconform using a model parameter that forces the snake to precisely maintain its preferred temperature. In addition, we investigate the behavioral life histories of sit-and-wait versus active foraging behaviors and their associated thermoregulatory strategies by quantifying the benefits and the metabolic and locomotory costs of thermoconforming versus actively thermoregulating.

Julien Arino (University of Manitoba, Canada)
The mathematics of the Bio.Diaspora project The potential role of the global air transportation system in the fast and widespread dissemination of an infectious pathogen was emphasized by the SARS epidemic of 2003. The Bio.Diaspora Project was initiated in Toronto a few years later. Our objective is to develop a better understanding of the architecture and dynamics of the commercial air transportation network and use this knowledge to assess risk to various health entities in the case of a newly emerging or reemerging infection. In this project, we make use of several types of mathematical objects and approaches. Network theory is used to study the architecture. Metapopulation-type models formulated as continous-time Markov chains are used to simulate the spread of infection. Tesselations are used to evaluate population densities. In this talk, I will discuss the global air transportation network and present some of the tools used in our project.

Majid Bani-Yaghoub (Texas A & M University)
Environmental decontamination and control of infectious disease: An SIS model
Background: The effectiveness of environmental decontamination as a control measure is controversial. Some studies conclude that decontamination of the inanimate environment is only a minor factor; others indicate that decontamination helps control and prevent infection in a host population.
Method: The present work quantifies the effectiveness of environmental decontamination by analyzing the underlying mechanisms governing pathogen interactions with hosts and environment. The basic Susceptible-Infected-Susceptible (SIS) model is developed to account for the transmission of pathogens from the environment to susceptible hosts.
Results: Changing the parameter values in the SIS model can result in a bifurcation, where the unstable disease-free and the globally stable endemic equilibrium are switched with the stable disease-free equilibrium. This result implies that environmental decontamination can render a population

disease-free only when the duration of infection is in a certain range. When the duration of infection falls outside this range, higher levels of environmental decontamination have a diminishing return in reducing the number of infected hosts at the endemic equilibrium. To avoid this diminishing return, environmental decontamination can be combined with other control measures, such as treating infected individuals to push the duration of infection into the specified range. We provide a method to determine the efficiency of the control policies that include environmental decontamination as a control measure. Therefore, the minimal intensity of decontamination and the other measures are determined for an efficient control policy.

Souvik Bhattacharya (University of Florida)
Modeling major factors that control tuberculosis(TB) in China
This article introduces a novel model that studies the major factors jeopardizing the TB control programme in China. A previously developed two strain TB model is augmented with a class of individuals not registered under the TB control programme. The paper investigates the basic reproduction number and proves the global stability of the disease free equilibrium. The presence of three endemic equilibria is established in the model. With the help of numerical simulations a comparative study has been performed to test the validity of the model presented here to the real data available from the Ministry of Health of the People's Republic of China. Sensitivity and elasticity analysis suggest the impact of key parameters on the tuberculosis control in China.

Vrushali Bokil (Oregon State University)
A Spatiotemporal Model for the Spread of Barley and Cereal Yellow Dwarf Viruses in a Patchy Landscape
We present a model for transmission of barley and cereal yellow dwarf viruses (B/CYDV) spread by aphid vectors among non-native annual and native perrenial grass species in the western United States. We model transmission of disease within a patch framework that incorporates the movement of aphid vectors between discrete patches. Our spatiotemporal model incorporates age structure in perrenial grasses, competition between the grass species and seasonal variations in population dynamics of the host species. Using this B/CYDV system as a case study we investigate the effects of spatial distributions and relative abundances of different host species on disease dynamics. An analysis of a simplified two-patch model identifies how key parameters influence both the ability of the pathogen to invade a heterogeneous host community and the effect of the pathogen on host coexistence. Numerical simulations over a larger group of patches demonstrate that increasing connectivity between patches tends to increase prevalence at the regional scale. We find that host composition and patch structure can affect not only the ability of the pathogen to invade a system but can either facilitate or hinder invasion by non-native competitor host species.

Ummugul Bulut (Texas Tech University)
Derivation of stochastic partial differential equations for correlated random walk models
Derivation of stochastic correlated random walk models. Two well-known random walk models are studied. Specifically, the telegraph equation in one-dimension and the linear transport equation in two dimensions. These equations are useful, for instance, in animal movement. In present investigation, stochastic telegraph and linear transport are derived from basic principles. In particular, dynamical systems, with time discrete, are studied to determine the different independent random changes. As the time interval decreases, the discrete stochastic models lead to certain stochastic differential equation systems. Then Brownian sheets are appropriately substituted for Wiener processes in SDE systems. When intervals in the secondary variables go to zero, the final SPDE models are derived.

John Calhoun (Texas Tech University)
Complex Predator and Prey Population Dynamics
Predator and prey relations are well studied and import in biology but there are situations where the pattern is more complex than these two populations. This simulation models the case where two populations feed off each other but one population can absorb the other population into itself. This situation is seen in disease or insurgency spread. The preliminary results show that these two populations can't coexist and that when a population begins in domination, has the larger population,

it will stay in domination over the other population. Interactions and spread across a network are explored.

Carlos Castillo-Chavez (Arizona State University)
Cross-immunity and Influenza Epidemics
Disease dynamics are intimately connected to biological, environmental and social processes over multiple time scales and levels of social and biological organization. Despite the myriad of complexities associated with disease dynamics, macroscopic epidemic patterns emerge but finding effective ways of making use of this knowledge remain. In a highly interconnected world, epidemic outbreaks become instant potential health and/or economic global threats with increasing segments of the population playing active roles on the transmission patterns of infectious diseases like influenza but we cannot and should not ignore the role of evolutionary forces at the individual and population level. In this talk I will address the role of cross immunity on influenza epidemics after a brief summary of the 2009 A/H1N1 pandemic.

Gerardo Chowell (Arizona State University)
Adaptive vaccination strategies to mitigate pandemic influenza: Mexico as a case study
We explore vaccination strategies against pandemic influenza in Mexico using an age-structured transmission model calibrated against local epidemiological data from the Spring 2009 A(H1N1) pandemic. In the context of limited vaccine supplies, we evaluate age-targeted allocation strategies that either prioritize youngest children and persons over 65 years of age, as for seasonal influenza, or adaptively prioritize age groups based on the age patterns of hospitalization and death monitored in real-time during the early stages of the pandemic. Overall the adaptive vaccination strategy outperformed the seasonal influenza vaccination allocation strategy for a wide range of disease and vaccine coverage parameters. This modeling approach could inform policies for Mexico and other countries with similar demographic features and vaccine resources issues, with regard to the mitigation of pandemic influenza. Logistical issues associated with the implementation of adaptive vaccination strategies in the context of past and future influenza pandemics will be discussed.

Daniel J. Coffield Jr. (University of Michigan-Flint)
V. Cholerae Colonization Simulations Via Discontinuous Galerkin Methods
Vibrio cholerae is a bacterial pathogen that colonizes the upper, small intestine where it produces a toxin that causes the characteristic watery diarrhea of the disease cholera. Although a large initial infectious dose is required for infection, data suggests that only a smaller sub-population colonizes a portion of the small bowel leading to disease. Additionally, there are many barriers to colonization in the intestines including peristalsis, fluid wash-out, viscosity of the mucus layer, and PH. In order to study the largely unknown dynamics of V. cholerae colonization, we are developing a mathematical model and a corresponding numerical method for the dynamics of Vibrio cholerae colonization in the human host. The numerical method is of the Discontinuous Galerkin type and we use it to create simulations based on the model.

J. M. Cushing (University of Arizona)
Matrix models for semelparous populations: dynamics and evolution
Of long standing interest in population dynamics are questions concerning the dynamic consequences and evolutionary aspects of different life history strategies. One aspect of a life history strategy is the allocation of resources to reproduction, growth, and survival and the resulting tradeoffs among these. One basic strategy is semelparity, a life cycle in which an individual has only one reproductive event after which it dies (annual plants, many species of insects, etc.). In this talk I will focus on matrix models for the dynamics of semelparous populations — specifically, on nonlinear, semelparous Leslie matrix models. A basic issue for biological populations is, of course, extinction versus persistence. For a population dynamic model, this question concerns the stability and instability of zero equilibrium state, which generally loses stability as a parameter measuring reproductive output increases through a critical value (for example, as R_0 increases through 1). The bifurcation that occurs generally results in a persistence state for the population (for example, a positive equilibrium). This Fundamental Bifurcation Theorem has been proved for numerable kinds of population (and epidemiological) models. For semelparous Leslie models, however, it turns out that the bifurcation is non-generic and the

Fundamental Theorem does not apply (and indeed is not in general true). As a result these models have mathematical as well as biological interest. I will describe recent results that establish, for general nonlinear semelparous Leslie models, the existence of a dynamic dichotomy that results from the loss of stability of the extinction state. This dichotomy arises from two bifurcating branches of invariant sets that bifurcate from the extinction state as R_0 increases through 1. Mathematically, the dichotomy is between positive equilibrium states and synchronous cycles (and/or invariant loops of synchronous orbits) lying on the boundary of the positive cone. Biologically, the dichotomy is between equilibration with overlapping generations and synchronized oscillations with non-overlapping generations. I will also show that it the intensity of inter-class competition (relative to that of intra-class competition) that determines which of the bifurcating branches is attracting. I will also discuss this unusual bifurcation scenario in an evolutionary context by considering evolutionary game theoretic extensions of semelparous Leslie models.

Elife Dogan (Texas Tech University)
Derivation of Stochastic Partial Differential Equations for Reaction-Diffusion Processes and Population Genetics
Stochastic partial differential equations are derived for population genetics and reaction-diffusion process in one and two dimensions. Specifically, stochastic partial differential equations are derived for the random dynamics of individuals that are reacting and diffusing in a medium. In the derivation, a discrete stochastic equation is first constructed from basic principles, i.e., from the changes that occur in a small time interval. As the time interval goes to zero, the discrete stochastic model leads to a system of It stochastic differential equation. As the spatial intervals approach zero, a stochastic partial differential equation is derived for the reaction-diffusion process and infinite number of alleles. The stochastic reaction-diffusion equation can be solved computationally using numerical methods for systems of It stochastic differential equations. Comparisons between numerical solutions of stochastic reaction-diffusion equations and independently formulated Monte Carlo calculations support the accuracy of the derivations.

Abdoul Aziz Fall (Ohio State University)
Strategies for controling Hepatitis B virus spread in adult population
Hepatitis B virus (HBV) disease continues to spread among the adult population, though the disease is gradually driven towards eradication among infants and children due to vaccination. We present a deterministic model for controlling the spread of HBV among the adult population using adult catch-up vaccination and change sexual habits as control measures. Our model is simulated to examine the effects of combination of different levels of these control measures using parameter values estimated from Nigeria/Senegal demographic and HBV data. We also estimate the cost associated with the proposed control interventions. We show how the prevalence of the disease falls after a period of six years under the implementation of the proposed control intervention given a fixed budget.

Zhilan Feng (Purdue University)
Mathematical models of influenza dynamics
In this talk I will present two examples of mathematical models for the transmission dynamics of influenza. The first example is a simple SIR epidemic model with a seasonally forced infection rate. The model provided an accurate Prediction on the course of the 2009 H1N1 influenza pandemic in the United States. The second example is an endemic model with both drug sensitive and drug resistant strains of influenza. The influence of antiviral use on the prevalence of both strains are discussed, and the results are made accessible via user-friendly Mathematica notebooks.

Raju Gautam (Texas A & M University)
Modeling effect of ambient temperature on pathogen population and infection transmission for pathogens spreading by fecal oral route in dairy cattle
Purpose: To better understand the influence of seasonal variation in ambient temperature on the population dynamics of a representative pathogen and its transmission, via free-living stages in a cattle herd.

Methods: We developed and evaluated a simulation model that incorporates into the classical Susceptible-Infectious-Susceptible (SIS) model, temperature effects on population dynamics and transmission of Escherichia coli O157:H7 in a dairy herd.
Results: Model results suggest that seasonal variation in ambient temperature has considerable impact on pathogen population densities on barn surfaces and in water troughs. Contaminated drinking water emerged as the most important pathway of E. coli O157:H7 transmission. Sensitivity analysis indicated that water-mediated transmission is amplified in the warmer seasons when the amount of drinking water available to the cattle herd is increased. Specifically, the increased prevalence of E. coli O157:H7 in the herd during summer is a consequence of faster replication of the pathogen favored by elevated temperature and slower turn-over rate of water leading to greater pathogen load in drinking water.
Conclusions: The model predicts that spread of infection via indirect transmission can be effectively controlled by improved drinking-water management. This includes reducing the total amount of available drinking water per animal or other strategies to reduce growth of the pathogen in water, including lowering drinking-water temperature during the warmer seasons.

Sze-Bi Hsu (National Tsing-Hua University, Taiwan)
Single phytoplankton species growth with light and advection in a water column
We investigate a nonlocal reaction-diffusion-advection equation which models the growth of a single phytoplankton species in a water column where the species depends solely on light for its metabolism. We study the combined effect of death rate, sinking or buoyant coefficient, water column depth and vertical turbulent diffusion rate on the persistence of a single phytoplankton species. Under a general reproductive rate which is an increasing function of light intensity, we establish the existence of a critical death rate; i.e., the phytoplankton survives if and only if its death rate is less than the critical death rate. The critical death rate is a strictly monotone decreasing function of sinking or buoyant coefficient and water column depth, and it is also a strictly monotone decreasing function of turbulent diffusion rate for buoyant species. In contrast to critical death rate, critical sinking or buoyant velocity, critical water column depth and critical turbulent diffusion rate may or may not exist. For instance, it is shown that if the death rate is suitably small with respect to the water column depth, the phytoplankton can persist for any sinking or buoyant velocity; i.e., there is no critical sinking or buoyant velocity under such situation. We further show that critical water column depth, critical sinking or buoyant velocity and critical turbulent diffusion rate for buoyant species can exist for some intermediate range of phytoplankton death rates and, whenever they exist, are always unique. In strong contrast, we show that there may exist two critical turbulent diffusion rates for sinking species. The phytoplankton forms a thin layer at the surface of the water column for sufficiently large buoyant rate, and it forms a thin layer at the bottom of the water column for sufficiently large sinking rate. Precise characterizations of these thin layers are also given.

Qihua Huang (University of Louisiana at Lafayette)
Deterministic and Stochastic Juvenile-Adult Model with Application to Green Tree Frog Population
We consider an amphibian population where individuals are divided into two groups: juveniles (tadpoles) and adults (frogs). We assume that juveniles are structured by age and adults are structured by size. Since juveniles (tadpoles) live in water and adults (frogs) live on land we assume that competition occurs within stage only. This leads to a system of nonlinear and nonlocal hyperbolic equations of first order. An explicit finite difference approximation to this partial differential equation system is developed. Existence and uniqueness of the weak solution to the model are established and convergence of the finite difference approximation to this unique solution is proved. We derive several stochastic models from a deterministic population model that describes the dynamics of age-structured juveniles coupled with size-structured adults. Numerical simulation results of the stochastic models are compared with the solution of the deterministic model. These models are then used to understand the effect of demographic stochasticity on the dynamics of an urban green tree frog population.

Glenn Lahodny Jr. (Texas Tech University)
Discrete Time Lotka-Volterra Systems
Conditions for the dynamical consistency of discrete time Lotka-Volterra systems (competition, cooperative, predator-prey) are established. Consistencies include the conditions for existence and

stability of steady state solutions and monotonicity of the cooperative and competition systems. The discrete time systems are derived from a nonstandard finite difference scheme.

Namyong Lee (Minnesota State University, Mankato)
Coexistence of multipatch population model with migration and selection
Population ecology is concerned with the growth and decay of specific populations. This field has a variety of applications ranging from evolution and survival at the environmental level to the spread of infectious disease at the cellular and molecular levels. This paper is to investigate the spatial patterns in population of species (or gene frequencies in multialleic polymorphism) due to the joint action of migration and selection. We considered the conditions for the maintenance of coexistence under various migration schemes with continuous-time and discrete-space model.

Chelsea Lewis (Texas Tech University)
A stochastic model for down regulation of the CTL response due to an infection of hantavirus in mice and in humans
Viral-hemorrhagic fevers are a suite of diseases that are a threat to public health. These viruses induce an overwhelming response of cytotoxic T-cells (CTLs) which eliminate the virus by either killing or damaging infected cells. This response may lead to a loss in a critical number of functioning cells that are critical to the appropriate execution of certain processes. For hantavirus, a zoonotic disease carried by mice and rats, many of the target cells are the specialized epithelial cells that regulate solute movements, and hence are essential components of osmotic regulation and metabolic waste disposal of particular solutes in the blood. It is because of the intimate relationship these epithelial cells have with the vascular system, an infection from the hantavirus may lead to either hantavirus pulmonary syndrome (HPS) or hemorrhagic fever with renal syndrome (HFRS). A crucial loss of too many functioning cells, results in pulmonary edema, hemorrhage and even death.
Mice and rats are the natural reservoirs for hantavirus that spread the virus to humans. Mice have been exposed to this virus much longer than humans and may have co-evolved with the virus. Because of this, mice have evolved a mechanism of down regulation of their own CTL response. This means that hantavirus infection does not result in fatality in mice; this is good for the virus as well as the mice. Humans, having had limited exposure to the virus in evolutionary time, have yet to develop a means of "co-existing" with hantavirus. It is the natural response of our immune system to attack an infection via the CTL response when there is no previous exposure to, or memory for, the virus, resulting in many of the symptoms associated with HPS or HFRS.
We use a mathematical model for the virus and the immune response, including antibodies and the CTLs, to describe the cellular dynamics of a viral infection. The original model was formulated by Wodarz (2005). We extend this model to a stochastic model and examine possible dynamics of this model that apply to humans and mice. It is the aim of the model to predict the effects of the immunological mechanisms on the host both in humans and in the mice reservoirs. Understanding the mechanisms by which mice are able to successfully down regulate the immunological response to hantavirus will help us find appropriate treatments for this disease in humans.

Anna Mummert (Marshall University)
Get the News Out Loudly and Quickly: Modeling the Influence of the Media on Limiting Infectious Disease Outbreaks
During outbreaks of serious infectious diseases many individuals closely follow media reports of the outbreak and take steps, including self-isolation, to protect themselves from infection and possibly death. Self-isolation can take many forms including restricting local and long-distance travel, using face masks, and choosing to receive a vaccine.
In this poster, I will use mathematical modeling to show that public health agencies working together with the media can significantly decrease the severity of an outbreak by providing timely and accurate accounts of the numbers of new infections and deaths. This model also shows that although providing such information beginning as early as possible is best, even starting to provide it well into the course of an outbreak can significantly reduce the severity of the outbreak. I will illustrate these results with a simulated outbreak of Ebola Hemorrhagic Fever in Huntington, WV (population 50,000).

Samares Pal (University of Kalyani, India)

Role of infection in an eco-epidemiological system: a mathematical study
Mathematical ecology has its roots in population ecology, which treats the increase and fluctuations of populations. It was along these lines that Lotka (1924) and Volterra (1926) established their original works on the expression of predator-prey and competing species relations in terms of simultaneous nonlinear differential equations, making the first breakthrough in modern mathematical ecology.
The importance of transmissible disease in an ecological situation is not to be ignored. There are many references in this context (Beltrami and Caroll (1994), Chattopadhyay and Pal (2002)) in such eco-epidemiological system. The viral disease can infect bacteria and even phytoplankton in coastal water. We have dealt with the problem of a classical predator-prey dynamics in which viral infection spread on prey population and classical predator-prey system is splitted into three groups, namely susceptible prey, infected prey and predator. We have observed the dynamical behaviour of this system around each of the equilibrium and pointed out the "exchange of stability".
Force of infection in any eco-epidemiological system is of great importance. Here we have considered standard incidence as the force of infection. This system is of rich dynamics in zero equilibrium. Moreover, the co-existence of the species is of ecological importance. We find some conditions on this force of infection for which the extinction possibilities of the species may overcome. We investigate the criteria for which the system will persist. We may conclude that infection factor may act as a biological control.

Alicia Prieto (University of Texas at Arlington)
A Cellular Automat Model of Infection Control on Medical Implants
S.epidermidis infections on medically implanted devices are a common problem in modern medicine due to the abundance of the bacteria on many surfaces. Once inside the body, S. epidermidis gather in communities called biofilms and can become extremely hard to eradicate, causing the patient serious complications. We simulate the complex S. epidermidis-Neutrophils interactions in order to determine the optimum implant conditions for the immune system to be able to contain the infection and avoid implant rejection. Our cellular automata model can also be used as a tool for determining the optimal amount of antibiotics for combating biofilm formation on medical implants.

Naveen G. Ramunigari (University of Texas at El Paso)
Computational Approach to Analyze an Epidemiological Event Deep Vein Thrombosis
Our present study is to understand the complex biological functions which have gained significant importance in the development of computational biology. Epidemiological studies have shown that Deep vein thrombosis (DVT) occurs in 10 persons per 10,000 persons each year in United States, and rises exponentially from ¡5 cases per 100,000 persons ¡15 years old to 500 cases (0.5100,000 persons at age 80 years. We are trying to propose a model explaining the DVT using the theory of fluid mechanics. DVT is caused by the blood clot in veins deeply rooted in the body, resulting in loss of blood flow, pain and numbness of the body part associated with that particular vein. Coagulation is considered as a primary factor in the development of DVT. Venous thrombi undergo an evolution beginning early after their formation. This condition can get complicated and can be fatal when the blood clot travels to other parts of the body which may result in pulmonary embolism. Pulmonary embolism (PE) may have caused approximately 300,000 deaths annually in the United States alone. Valves of the deep veins are damaged as a result of DVT, with no valves to prevent deep system reflux, the hydrostatic venous pressure in the lower extremity increases dramatically. In our study we are trying to establish a model that mimics the venous blood flow that will be depicting the thrombus formation in the veins. We analyzed the flow patterns with various foreign objects in the veins using the proposed approach. This helps in predicting the areas of concentration, which might help in estimating the chance of clot formation in any specific area around the region of concentration. Our research will help to identify the affected region at a faster using the computational approach which might help in reducing the death occurrence rate which is 6% of DVT cases and 12% of PE cases within 1 month of diagnosis across united states.

L. R. Ritter (Southern Polytechnic State University)
A dynamic model of atherogenesis as an inflammatory response
Atherosclerosis is a disease of the vasculature that is characterized by chronic inflammation and the accumulation of lipids and apoptic cells in the walls of large arteries. This disease results in plaque

growth in an infected artery possibly leading to occlusion of the artery. Atherosclerosis is the leading cause of human mortality in the United States, much of Europe, and parts of Asia. We propose a dynamic model of certain biochemical aspects of atherosclerosis. In particular, we consider the interaction be- tween immune response cells in the presence of chemically modified low density lipoprotein which is known to interfere with normal immune function. The general model consists of a system of nonlinear evolution equations governing the interaction of chemical and cellular species leading to the disease initiation.

Libin Rong (Oakland University)
Hepatitis C virus drug resistance: modeling and applications
Hepatitis C virus (HCV) infection remains an important health problem worldwide. The current standard therapy leads to sustained viral elimination in only about 50% of the treated patients. New direct acting antiviral agents are in clinical trials. In a recent study, when HCV genotype 1a infected persons were given monotherapy with telaprevir, a potent HCV protease inhibitor, over 5% of virus isolated after a couple days of therapy exhibited drug resistance. Further, drug resistant virus grew so as to dominate the population during the 14 day trial. Before therapy patients were chronically-infected with HCV and had high viral loads. Thus, one could assume that most cells susceptible to infection were already infected. This then gives rise to the question of where does newly arising drug resistant variants grow so that they can appear rapidly and at high levels. I will discuss the possible replication spaces available to the virus and present a model consistent with the available data on the kinetics of resistant virus growth. I will also discuss the treatment implications for hepatitis C.

Anna Spagnuolo (Oakland University)
A mathematical model for Vibrio Cholera colonization in the human intestine
Vibrio cholera is a strict human pathogen that causes pandemic cholera. It is an old-world pathogen that has re-emerged as a new threat since the early 1990s. V. cholera colonizes the upper, small intestine where it produces a toxin that leads to the watery diarrhea, characterizing the disease. Colonization dynamics of the bacteria are largely unknown. Although a large initial infectious dose is required for infection, data suggests that only a smaller sub-population colonizes a portion of the small bowel leading to the disease. There are many barriers to colonization in the intestines. In this talk, I will elaborate on the dynamics of V. cholera infection by describing a mathematical model that governs the colonization process for the bacterial dynamics.

Horst Thieme (Arizona State University)
Global attractors and stability, persistence, and the Laplace transform
Global compact attractors, in combination with Lyapunov functions and the Laplace transform, can be used to prove the global stability of extinction and persistence equilibria. A linearized stability analysis can be bypassed. For illustration, two models are considered: one for bacteria and phages in a chemostat and one for the spread of an infection in spatially distributed population.

Jianjun Tian (College of William and Mary)
On the global stability of cholera models
We conduct global stability analysis for the endemic equilibria of several deterministic cholera models. These models, incorporating both human population and pathogen concentration, constitute three-dimensional nonlinear autonomous systems where the classical Poincaré-Bendixson theory is not applicable. We employ three different techniques, including the monotone dynamical systems, geometric approach, and Lyapunov functions, to investigate the endemic global stability for several biologically important cases. The analysis and results presented in this paper make building blocks towards a comprehensive study of the general mathematical cholera model. This is the joint work with Jin Wang.

Sherry Towers (Purdue University)
Modelling the global dynamics of influenza genetic diversity, using a deterministic seasonally forced SIR model with mutations and strain cross-competition
It has been hypothesized by Rambaut et al. ("The genomic and epidemiological dynamics of human influenza A virus", Nature (2008) Vol 435) that influenza viral genetic diversity is continuously generated in the tropics, whereupon the strains spread to the temperate regions in the northern and

southern hemispheres. These temperate regions subsequently exhibit less influenza antigenic diversity than the tropics.
In our analysis we model influenza using a deterministic seasonally forced SIR model that includes strain mutations, and also cross-competition between the resulting influenza strains. Our model includes three population enclaves- northern hemisphere, southern hemisphere, and tropics- which are allowed to interact via immigration/emigration between the populations. The northern and southern hemispheres incorporate a seasonally forced SIR model 180 degrees out of phase with one and other, while the model used in the tropical enclave assumes no seasonal forcing. We examine the genetic diversity of the influenza strains circulating during a typical flu "season" within the three enclaves.

Pauline van den Driessche (University of Victoria, Canada)
Modeling the spread of West Nile Virus
West Nile virus is a vector disease maintained in a mosquito bird cycle with humans as dead end hosts. To model the recent spatial spread of West Nile virus across North America, a reaction diffusion model is developed with cross infection between birds and mosquitoes. A simplified version of the model is analyzed, then comparison theorems used to give a biologically reasonable upper bound on the spread rate of the more complex model.

Glenn Webb (Vanderbilt University)
Analysis of a model for transfer phenomena in biological populations
P-glycoprotein (P-gp) is a protein overexpressed in cancer cells that causes multi-drug resistance to cancer therapy. Recent experimental evidence demonstrates that P-gp is transferred directly cell-to-cell in in vitro cell cultures of breast tumor cell lines. A mathematical model quantifies the transfer process of P-gp in in vitro cultures of MCF-7 human breast adenocarcinoma cells. The model supports the hypothesis that P-gp is transferred directly cell-to-cell and provides a framework for optimizing chemotherapy regimens.

Mohammed Yahdi (Ursinus College)
Vancomycin-Resistant Enterococci Colonization-Infection Model: Parameter Impacts, Outbreak Risk and Control
Vancomycin-Resistant Enterococci (VRE) infections have been linked to increased mortality and ICU costs. We developed and analyzed a new model of a VRE infested intensive care unit (ICU) based on transitions between five stages related to VRE: susceptible, colonized without special preventive care, colonized under special preventative care, infected undergoing VRE treatment and infected without that treatment. We investigated the dynamics of the corresponding system of non-linear differential equations, as well as the interplay and impacts of nineteen independent parameters involved in the transitions. The parameters include colonization rate, fitness cost, plasmid transfer, antibiotics use, preventive care, treatment schedule and infection factors. Interactive simulations were created to show the behavior of the VRE dynamics as the parameters change within given ranges to represent different ICUs. Analysis diagrams where given to measure the impacts of the parameters, and determine efficient strategies to control VRE. Disease free analysis was performed to compute the basic reproduction rate, related sensitivity analysis and to investigate good outbreak prevention strategies. Values of parameters with the most impact to reduce the outbreak risk were identified. In particular, threshold values were given for the proportion of colonized patients that need special preventative care and for the level of effectiveness of compliance with preventative measures needed to minimize the basic reproduction rate for any given set of parameters.

Pei Zhang (University of Louisiana at Lafayette)

We develop a discrete stage-structured model that describes the dynamics of two competing ecologically similar species. Motivated by plant populations such as irises, each species is assumed to reproduce both sexually and clonally. We first analyze the dynamical behavior of the single species model. We show that when the inherent net reproductive number is smaller than one then the population will go to extinction and if it is larger than one then an interior equilibrium exists and it is globally asymptotically stable. For the two-species competition model, by allowing species to have different competition efficiencies, we show that the model can obtain different dynamics including competitive

exclusion, coexistence and bistability, which is similar to the competition outcomes of the classical continuous two-dimensional Lotka-Volterra model.