

Mathematics in Emerging Infectious Disease Management

Centro Internacional de Ciencias

Cuernavaca, Morelos, México

January 10-14, 2011

ABSTRACTS

What have we learned from and about pandemic influenza?

Fred Brauer

University of British Columbia, Canada

Each recent major epidemic (or threat of a major epidemic) has led to some important modeling developments. For example, the severe acute respiratory syndrome (SARS) epidemic of 2002-3 led to models incorporating isolation of diagnosed infectious individuals and quarantine of individuals suspected of having been infected.. The observation that the spread of SARS was far from what would be expected in populations with homogeneous mixing was a key to the development of contact network epidemiology in studying the spread of disease and the observation that an epidemic might move a long distance in a short time led to detailed studies of transportation networks, especially airline routes. Another product of the SARS epidemic was the recognition of the importance of nosocomial (in-hospital) infections in the spread of communicable diseases.

The threat of an avian (H5N1) influenza epidemic beginning in 2005 led to the recognition that advance planning for an epidemic with unknown model parameters would require estimates based on a range of reproduction numbers. The possibility that antiviral drug treatment could be used to stop or slow the spread of infection led to development of detailed network models. Detailed large - scale models and increased computing power made studies of such questions in real time possible. Although no avian influenza epidemic has developed (yet), the knowledge gained from these studies were very important when a new strain of H1N1 influenza developed and spread in 2009.

The H1N1 influenza pandemic of 2009 has taught us that data are unreliable because there were so many asymptomatic or mild unreported cases. New methods have been developed for rapid parameter estimation. We have learned that study of age heterogeneity is vital, and that modification of behaviour during an epidemic, both through public health initiatives and through individual actions, is important. The prediction of a second epidemic wave is a new question. Let us solve this problem before the next epidemic.

Role of cross-immunity, quarantine, isolation and other factors on the transmission dynamics of influenza

**Carlos Castillo-Chávez
Arizona State University, USA**

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Predictability in the spatiotemporal dynamics of the 2009 H1N1 pandemic in Europe

**Stefano Merler
Fondazione Bruno Kessler, Trento, Italy**

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Role of large scale computational models in forecasting spreading patterns of emerging infectious diseases: Experiences from the 2009 H1N1 influenza pandemic

**Duygu Balcan
Indiana University, USA**

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Spatiotemporal dynamics of avian influenza: roles of and impact on migratory birds and interaction of low and high pathogenic strains

**Dr. Jianhong Wu
York University, Canada**

This talk is based on some recent joint work with Lydia Bourouiba, Venkaka Duvvuri, Stephen Gourley, Rongsong Liu and Sasha Alexandra Teslya, and in collaboration with FAO (United Nation) and USGS (USA Geological Survey) Avian Influenza Program. We will show how mathematical modeling and nonlinear dynamical systems theory can be used to address a number of issues raised by the virulent outbreaks of highly pathogenic avian influenza since 2005. These issues include the roles of migratory and wild birds in the disease's transmission dynamics and spatial spread, and the co-existence and interaction of low and high pathogenic strains. We will also talk about the application-driven theoretical challenges for the theory of dynamical systems involving network structure, feedback delay, periodic environment and climate change.

Stochastic methods in the study of epidemics

**Eliane R. Rodriguez
Instituto de Matemáticas, UNAM**

We are going to present some stochastic models used to describe the behaviour of epidemics. Those models depend on some parameters that need to be estimated. There are several ways to estimate the parameters of a given model. In here, we are going to present the analysis under the Bayesian point of view using Markov chain Monte Carlo methods such as the Metropolis-Hastings algorithm.

Recombination and the evolutionary epidemiology of drug resistance

**Troy Day
Queen's University, Canada**

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Challenges of community health protection in the face of emerging infectious diseases

**Seyed Moghadas
National Research Council of Canada, Canada**

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The impact of media coverage on the transmission dynamics of human influenza

**Robert Smith?
University of Ottawa, Canada**

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A semi-empirical model to help understand therapy effect on HIV-1 infected patients

**Robersy Sánchez
Cambridge University, United Kingdom**

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Disease transmission in a layered network

James Watmough

**Department of Mathematics and Statistics, University of New Brunswick Fredericton,
NB Canada**

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Local transportation and social distancing explain the different “waves” of A-H1N1pdm cases observed in Mexico during 2009

**Marco Arieli Herrera-Valdez
Arizona State University, USA**

Influenza outbreaks have been of relatively limited historical interest in México. The 2009 influenza pandemic not only changed México’s health priorities but also brought to the forefront some of the strengths and weaknesses of México’s epidemiological surveillance and public health system. México’s data of influenza cases of 2009 shows an epidemic pattern characterized by three “waves”. This research supports the view that the three epidemic “waves” are the result of the synergistic interactions of three factors: regional movement patterns of Mexicans, the impact and effectiveness of dramatic social distancing measures imposed during the first outbreak, and the summer release of school children followed by their subsequent return to classes in the fall. The three “waves” (outbreaks) cannot be explained by the transportation patterns alone but only through the combination of transport patterns and changes in contact rates due to the use of explicit or scheduled social distancing measures.

Economic analysis of the use of facemasks during pandemic (H1N1) 2009

Samantha M. Tracht^{1,2}, Sara Y. Del Valle¹, Brian K. Edwards¹

¹Los Alamos National Laboratory, USA; ²University of Tennessee, USA

A large-scale pandemic could cause severe health, social, and economic impacts. The recent 2009 H1N1 pandemic confirmed the need for mitigation strategies that are cost-effective and easy to implement. In the early stages of a pandemic, as seen with pandemic (H1N1) 2009, vaccines and antivirals were non-existent or very limited, resulting in the need for non-pharmaceutical strategies to reduce the spread of disease and the economic impact. Several non-pharmaceutical interventions were implemented including school closures, social distancing, and facemasks. We construct and analyze a mathematical model for a population with three different age groups in which some individuals wear facemasks. We then quantify the impact facemasks have on the spread of pandemic (H1N1) 2009 and examine the cost effectiveness of using facemasks as a mitigation strategy. Our analyses show that an unmitigated pandemic could result in losses of nearly \$836 billion in the United States. Based on present value of future earnings, hospital costs, and lost income estimates due to illness, this study estimates that the use of masks by 10%, 25%, and 50% of the population could reduce economic losses by \$479, \$571, and \$573 billion, respectively. The results show that facemasks

can significantly reduce the number of influenza cases as well as the economic losses due to a pandemic.

Mathematical Models of Influenza with Imperfect Quarantine

Mustafa Erdem^{1,2}, Carlos Castillo-Chavez²

Sinop University, Turkey¹, Arizona State University, USA²

In my talk, I will address some of the challenges posed by the transmission dynamics of infectious diseases when the host population is highly heterogeneous. Emphasis has been put in discussing our motivation and result in the context of influenza. Specifically, we explain the role of quarantine/isolation on the transmission dynamics of influenza within an SIR model with varying effectiveness of isolation. Thresholds, persistence, equilibria and their stability are found for models with quarantine dependent. We found for influenza type parameters, periodic solutions arise via Hopf bifurcation as the effectiveness of quarantine varies. The Hopf bifurcation surface and stable periodic solutions are found numerically.

Stochastic system of delay-difference equations for a SEIR(S) epidemiological model

Alma V. Lara-Sagahón^{1,2} and Marco V. José^{1,3}

¹Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México; ²FES Cuautitlán, Universidad Nacional Autónoma de México; ³Centro Internacional de Ciencias, Cuernavaca, Morelos, México.

We obtain, for the first time, multifractal spectra of various childhood epidemics, such as rubella, chickenpox, and poliomyelitis. The multifractal behavior of these epidemics is a fundamental characteristic that had been unnoticed in the epidemiological literature, perhaps because it is practically impossible to reproduce it with standard compartmental epidemiological models. A deterministic SEIRS epidemiological model is here developed in terms of a system of delay-difference equations. Non-linear incidence and constant periods of latency, infectiousness and immunity are assumed. The stochastic version of this SEIRS epidemiological model is able to exhibit a wider range of dynamics than previous epidemiological models. In particular, the model is able to reproduce observed data behaviors such as: sustained oscillations, fade-outs, a great variability in epidemic sizes and, the multifractal nature of childhood epidemics. We present comparisons of the predictions of our model with actual data of rotavirus epidemics. We explore the stability of the system by determining the bifurcation diagrams of several parameters of the model. In particular, we have found bifurcations for the immunity periods which are directly related to the inter-epidemic periods.

Towards the use of mathematical modeling with surveillance data to support rapid decision-making in public health practice

**David Buckeridge
McGill University, Canada**

Mathematical modeling has demonstrated considerable promise for guiding decisions in public health, especially during crises such as the recent 2009 H1N1 influenza pandemic. In most situations, however, model results are generated 'off-line' by experts and the delay between the initiation of development and the availability of the model or results can be considerable. From a public health perspective, it would be preferable to have models developed in advance of crises and linked to existing surveillance systems, so that these models could produce insights rapidly as soon as data become available. Developing such 'in-line' models, however, requires: 1) understanding of, and adjustment for, the biases inherent in surveillance data, and 2) adaptation of models to 'fit' with public health workflows.

Aspects of homogeneous vs. heterogeneous transmission **Ping Yan** **Public Health Agency of Canada, Canada**

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Marco V. José **Modeling the geographical spread of influenza A (H1N1) in Mexico** **Instituto de Investigaciones Biomédicas, UNAM, México y Centro Internacional de Ciencias Cuernavaca, Morelos** **(Joint work with A. Lara-Sagahón, T. Govezensky, C. Varea and R. A. Barrio)**

A novel mathematical model of the geographical spread of influenza A (H1N1) is developed. First, a system of delay-difference equations for a SEIR (susceptible-exposed-infectious-recovered) epidemiological model is able to reproduce the temporal behavior of the infection in a given community. The model assumes exponential incidence of the infection and constant periods of latency, infectiousness and immunity. Second, the same model is extended to reproduce the geographical spread of the disease coupled with a network of air transportation and terrestrial mobilisation. Thus, the spatiotemporal evolution is composed by a local dynamics as determined by the deterministic SEIR model, and a spatial stochastic global dynamics. The model is able to reproduce both, the local dynamics of the epidemics and the stochastic global path of the pandemic. Actual data on the mobilisation of people and incidence of the infection in Mexico is used to test the model. The agreement of the predictions with actual data is remarkable and it accounts for the effect of social distancing implemented in Mexico during the early stages of the pandemic. Influenza pandemics are noise-driven systems showing an abrupt change of behaviour as a function of the mobility of people. The model can easily be extended to several other types of viral pandemics.

Modeling the antigenic drift and cross-immunity of influenza strains in a population

**Jorge A. Alfaro Murillo
Purdue University, USA**

Because influenza is an RNA virus, it lacks proof-reading and error-correction ability. This allows mutations to develop during viral replication which leads to the emergence of new strains of the virus. This process is known as antigenic drift, and causes reinfection with influenza viruses to occur commonly. Because new strains are constantly evolving, a mathematical model that aims to describe the dynamics of infection over a period of several years should include multiple strains and consider drift as well as partial immunity to related strains. Agent-based and deterministic models that include these characteristics are presented. Our main objective is to examine possible causes of differences between disease dynamics in temperate and tropical regions that are apparent in empirical observations, such as seasonality, incidence and viral diversity.

Internet-based monitoring of respiratory infections

**Natalia Mantilla-Beniers
Universidad Nacional Autónoma de México, México**

In recent years, a number of countries started monitoring influenza-like illnesses (ILI) through direct reporting of symptoms in internet websites. In Mexico, this kind of monitoring began in 2009, with the opening in May 7th of Reporta (<http://reporta.c3.org.mx>). Participants in Reporta register and anonymously complete two questionnaires. The first of them gathers socio-demographic information and is filled in once only. The second questionnaire is completed weekly, and asks the participant whether (s)he has presented one or several of a series of symptoms, and what kind of medical attention (s)he sought when ill.

The (weekly) frequency with which information is gathered in monitoring websites reduces the delay typical of conventional reporting systems, in which symptom onset may occur more than a week before health authorities are notified. Thus, web monitoring may aid early detection of epidemiologic changes.

I will describe the social and demographic traits of the population registered in Reporta, followed by the epidemiological information gathered in the website and the risk factors associated to ILI in our sample population. This information will be contrasted with the data available from population and health authorities in order to assess the reliability of our system. Lastly, further explorations of the collected data will be presented to support the motivations behind our latest campaigns for promoting participation.

Dynamics of two-strain influenza model with isolation and partial cross-immunity

Zhilan J. Feng

(Joint work with M. Nuno, C. Castillo-Chavez, M. Martcheva)

Purdue University, USA

The time evolution of the influenza A virus is linked to a nonfixed landscape driven by interactions between hosts and competing influenza strains. Herd-immunity, cross-immunity, and age-structure are among the factors that have been shown to support strain coexistence and/or disease oscillations. In this talk, I will present a mathematical model with two influenza strains under various levels of (interference) competition. We establish that cross-immunity and host isolation lead to periodic epidemic outbreaks (sustained oscillations) in this multistrain system. Conditions that guarantee a winning type or coexistence are established in general by computing two invasion reproduction numbers. Oscillatory coexistence is established via Hopf bifurcation theory and confirmed via numerical simulations.

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David Fisman

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Controlling the evolution of antimicrobial resistance: information is power

Rafael Peña-Miller

Imperial College, United Kingdom

The rate at which pathogenic bacteria evolve resistance to multiple antibiotics is dramatically decreasing the efficacy of current antimicrobial treatments. Different interventions have been proposed to control the emergence and spread of resistant pathogens in clinical settings, for instance by modifying drug prescription patterns. It has been proposed, for example, that cycling antibiotics would reduce the selective pressures to any one antimicrobial class, but so far clinical trials remain inconclusive and theoretical models have presented arguments in favour of the optimality of antibiotic mixing. Using tools from control and systems theory, we show that the optimal drug deployment protocol for standard epidemiological, SI models of drug deployment is, in general, a non-periodic form of drug rotation. Furthermore, we discuss different single-host and epidemiological scenarios that allow us to design practicable and effective antibiotic usage strategies and discuss how these may be tested with experimental model systems. We conclude with a general principle: the best performing drug usage policies utilise the highest quality of available information.

Assessing the potential impact of emergent infectious diseases: Lessons from the 2009 H1N1 influenza pandemic

Rafael Meza¹, Bahman Davoudi¹, Jessica M. Conway³ and Babak Pourbohloul^{1,2}

¹Division of Mathematical Modeling, University of British Columbia Centre for Disease Control, Vancouver, BC, Canada; ²School of Population & Public Health, Faculty of Medicine, University of British Columbia, Vancouver, BC, Canada; ³Department of Mathematics, University of British Columbia, Vancouver, BC; Canada

The 2009 influenza pandemic gave public health practitioners an opportunity to test several mathematical methodologies designed to assess the threat posed by an emergent disease. In this talk I will go over some of the issues and challenges experienced by the Division of Mathematical Modeling at the UBC Centre for Disease Control during the 2009 H1N1 pandemic. In particular, I will go over our estimation of the reproductive number during the early stages of the pandemic, using data from Mexico City and Canada as well as a novel methodology based on contact network theory. I will also review our assessment of the potential level of impact of various intervention strategies during the second wave.

Influenza vaccination strategies when supply is limited.

**Romarie Morales , Sunmi Lee, and Carlos Castillo-Chavez,
Arizona State University, USA**

The aim of this work is to find alternatives that mitigate the transmission of influenza via vaccination in a finite time period. To understand the dynamics of transmission we will use a more complex SIR model with data from the 1918-19 pandemic influenza [1]. Previous work has shown that the Pandemic Influenza transmission model with control [2] can be used to better understand the spread of the virus in a population that has full or limited access to vaccination. We will use optimal control techniques to explore these constraints and provide a more realistic approach that public health Policy makers can work with when trying to meet the highly difficult task that comes from having a limited vaccination supply. Given that this previous study does not include an asymptomatic class and the ramifications of this subpopulation on disease transmission, we will focus our attention on understanding the impact and how to minimize transmission when this class is added to the epidemiological model. Also previous research [3] does not fully analyze the vaccine time production and deployment after the virus has been identified. In order to make our analysis more realistic we intend to add a time delay on the supply of the vaccines and utilize optimal control theory to provide a more realistic approach that public health policy makers can work with when trying to meet the highly difficult task that comes from having a limited vaccination supply.

Transmissibility of H5N1 avian influenza in Nigeria: The 2006 epidemic
Emmanuel Morales
Arizona State University, USA

The current worldwide transmission of the highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1), which affects poultry, primarily, also represents a pandemic threat for human populations. In this study we evaluate the net effectiveness of control measures, namely, depopulation of infected premises, movement restrictions, and biosecurity measures in reducing virus transmissibility. Assuming gamma-distributed incubation and infectious periods within infected poultry farms, we apply a deterministic non-spatial multi-stage compartmental model with classes of poultry farms, and use a least-square approximation to estimate the pre and post-intervention transmission rates between premises of the HPAI H5N1 epidemic in Nigeria in 2006, where 113 premises were reported as infected. The basic reproduction number R_0 was estimated to be 2.10 (95% CI: 2.03, 2.17). We analyze numerical uncertainty on the estimates of R_0 due to various model formulations and give a bound for R_0 of [1.98,3.1]. The post-intervention reproduction number (R_p), which captured the effects of interventions on reducing transmissibility, was estimated to be 0.57 (95% CI: 0.48, 0.66). These estimates lead to an approximate percent reduction of the reproduction number (R_t) between 66.6% and 84.3%. A stochastic model was used to compute the empirical distributions of the peak epidemic size and epidemic size at week ten, with and without interventions. The approximate percent reduction of the mean of peak epidemic size and epidemic size at week ten due to interventions were: 98.4% and 98.2%, respectively. Our study confirmed the between-premise transmissibility ranges of the HPAI H5N1 previously reported for virus subtype H5N1 outbreaks in other continents and the effectiveness of the intervention strategies. Lastly, we describe potential ways that spatial information about the spread of influenza between poultry farms could be used in future investigations.

Optimal control on a discrete time influenza model

Paula A. González-Parra^{1,2}, Sunmi Lee³, Leticia Velazquez¹, Carlos Castillo-Chavez³

¹The University of Texas at Carlos Castillo-Chavez, ²El Paso, USA and Universidad Autónoma de Occidente, Cali – Colombia, ³Arizona State University, USA

A discrete time Susceptible - Asymptomatic - Infectious - Treated - Recovered (SAITR) model is introduced in the context of influenza transmission. We evaluate the potential effect of control measures such as social distancing and antiviral treatment on the dynamics of a single outbreak. Optimal control theory is applied to identify the best way of reducing morbidity and mortality at a minimal cost. The problem is solved by using a discrete version of Pontryagin's maximum principle. Numerical results show that dual strategies have stronger impact in the reduction of the final epidemic size.

Assessing the benefits and potential drawbacks of anti-viral use during the summer wave of infection of influenza pandemics

**Sherry Towers
Purdue University, USA**

The 2009 H1N1 influenza pandemic exhibited a dual wave of infection in Northern hemisphere temperate climates, similar to that observed during the 1918 pandemic. This phenomenon is believed to be due to the seasonal nature of influenza transmission in temperate climates, in combination with the high average transmissibility of pandemic influenza. After the observation of the beginning of a significant summer wave of infection in 2009, doses of vaccine were ordered by first world countries in sufficient quantities to vaccinate large fractions of their populations. Unfortunately, influenza vaccines take several months to produce, and most H1N1 vaccines were distributed after the fall wave had already peaked. Use of antivirals are thus one of the few tools at the disposal of public health officials to stem the tide of infection before vaccines can be made available. In the work presented here, we use a seasonally forced SEIR ODE model to examine the effect of anti-viral use during the first summer wave of infection of influenza epidemics. We examine the impact on the final size, and the timing and size of the fall peak.

Control theory in influenza.

**Sunmi Lee
Arizona State University, USA**

In the context of pandemic influenza, the immediate and effective implementation of control measures is of great concern for public health officials around the world. In particular, the role of influenza vaccines should be considered as part of any pandemic preparedness plan. The rapid production and efficient distribution of pandemic influenza vaccines are important factors to consider in mitigating the morbidity and mortality impact of an influenza pandemic, particularly on those individuals at highest risk of developing severe disease. In this talk, we use a mathematical model that incorporates age-structured transmission dynamics of influenza to evaluate optimal vaccination strategies in the context of the Spring 2009 A (H1N1) pandemic in Mexico. We extend previous work on age-specific vaccination strategies to time-dependent optimal vaccination policies by solving an optimal control problem with the aim of reducing the overall number of symptomatic cases over the course of a single pandemic wave. Optimal vaccination policies are computed and analyzed under different vaccination coverages and different transmissibility levels (R_0). The results suggest that optimal vaccination can be achieved by allocating most vaccines to young adults (20-39 y) followed by school age children (6-12 y) in the Mexican population. In addition, our results underscore the need of an universal influenza vaccine since this leads to the minimization of the overall number of symptomatic cases.

Adaptive vaccination strategies to mitigate pandemic influenza: Mexico as a case study

Gerardo Chowell-Puente
Arizona State University, USA

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.

Genomic landscapes of influenza virus: relevant information content and its impact on influenza pandemics

Víctor Serrano-Solís, Marco V. José
Instituto de Investigaciones Biomédicas, UNAM, México

RNA viruses are especially relevant for the study of emerging infectious diseases, owing to their rapid replication rates. Examples of RNA viruses are HIV, influenza A (H1N1), foot and mouth disease, hepatitis C and poliovirus. The high mutation rates of RNA virus generate a large pool of viral genome variants. In this work, we have analyzed whole genomes of both DNA and RNA viruses using the Mutual Information Function (MIF). An unexpected phenomenon occurs in certain segments of few RNA genome viruses, a U-pattern in which the Information values decreases at short distances, remains constant for a while and later on increases at long distances. We focused on the particular case of the influenza A virus. Strains of influenza A virus (H3N2, H1N1) of different countries over different years were analyzed. Intra-segments comparisons over each genome revealed that only in segments 7 and 8 of each viral genome this phenomenon occurs. RNA viruses do not display the typical three-base-periodicity of coding regions of cellular organisms and the majority of DNA viruses analyzed. Segments 7 and 8 of the influenza A genome codify for two non-informational proteins each. This association of information values and the polycistronic character in the influenza A genome is a novel feature previously undetected. We were able to show that this U-pattern is not due to a bias artefact associated to a short distance series. Rather, this U-pattern indicates that the MIF can detect not only statistical differences that may reflect sequence composition but it has a biological

meaning. For example, this may be due to the coexistence of two different dynamics within influenza A genome segment 7 and segment 8 and it is also associated to the secondary complementary structure of RNA.

On the role of unconfirmed cases and vaccination during an influenza pandemic

Maytee Cruz-Aponte
Arizona State University, USA

A year after the AH1N1 pandemic, México's data show an epidemic pattern characterized by three "waves". Accurate quantification of influenza cases documentation is difficult, especially during a pandemic. Among other reasons, many cases are not reported because they are mild enough to be noticed. Therefore, it is possible that a significant fraction of disease transmission comes from people that were never tested and confirmed to have influenza. The presence of a population of asymptomatic or not confirmed cases has been documented to be non-negligible. It is believed that for the past AH1N1/2009 pandemic around 80% or 90% of the infected people were asymptomatic. A more detailed analysis of aspects related to the unconfirmed population is study in this work. The role of not confirmed cases and vaccination is studied taking into account delays in access and limitations in the total and daily numbers of vaccines available. In addition, our research identifies possible vaccination schemes planned in conjunction with the school calendar. A possible enhancement of vaccination by social distancing measures is also put into consideration taking into account different factors such as limited impact of the late arrival of the vaccine.

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Susie El saadany
University of Ottawa, Canada

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Time evolution of the spread of diseases with a general infectivity profile on a complex dynamic network

Bahman Davoudi¹ and Babak Pourbohloul^{1,2}

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Within this talk we will introduce a new analytical approach to study the time evolution of disease spread on a finite-size network. Our methodology can accommodate any disease with a general infectivity profile. This new approach is able to incorporate the impact of a general intervention - at the population level - in a number of different ways. We will discuss the details of the equations involved and compare the outcomes of analytical calculation against simulation results. A discussion of possible extensions of this methodology will conclude this talk.

Innate Immunity to Pandemic Influenza: a Double-edge Sword

Beni M. Sahai

University of Winnipeg, Manitoba, Canada

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Timing of vaccination campaigns against pandemic influenza in a population dynamical model of Vancouver, Canada

Jessica M. Conway¹, Rafael Meza², Ashleigh Tuite³, Babak Pourbohloul²

¹Dept of Mathematics, University of British Columbia, Vancouver BC, Canada; ²Division of Mathematical Modeling, University of British Columbia Centre for Disease Control, Vancouver BC, Canada; ³Dalla Lana School of Public Health, University of Toronto, Toronto, ON, Canada

We present a compartmental epidemic model, extended to capture age structure and transmission network dynamics, for the Greater Vancouver Regional District (population 2 million) as a representative urban area. Using our model we evaluate the efficacy of pH1N1-influenza vaccination campaigns initiated between mid-July/late-November 2009 in terms of infections and deaths averted. We also consider three vaccine-distribution strategies differing in age-specific coverage and show that for campaigns initiated early in the epidemic, targeting strategies can make a substantial difference in outcomes. However this effect strongly wanes as the epidemic proceeds. Thus we show that having a good estimate of epidemic peak timing is critical when making policy decisions on vaccination strategies.

Network Evolution in the Presence of an Influenza-like Disease with Adaptive Behavior
Ben Morin
Arizona State University, USA

This talk is based on some preliminary work considering the effect of social distancing in the event of an Influenza-like epidemic akin to the 2009 AH1N1 pandemic. This is studied via a generalization on existing scale-free-like dynamic network construction. Dynamic network construction of this type traditionally introduces new nodes (individuals) which form edges (connections) to the existing network according to a frequency dependent probability distribution (proportionate mixing). An Influenza-like SIR disease model is either 1) introduced to a scale-free network which has been established as in the work of Pastor-Satorras and Vespignani (2001), 2) introduced to the network at some point in its formation (with no behavior change) or 3) introduced to the network during its formation but allowing an individual level response that will alter both the network's growth and its "established" structure. With the advent of an outbreak within the network, connections will now be biased on the infectious state of nodes (i.e. the proportionate mixing will now be weighted to reflect a desire to avoid infectious individuals). In addition to adjusting how nodes enter the network at large, edge removal will be introduced. This removal will again be based on the desire to avoid infectious individuals.

Optimal control applied to a discrete influenza model

Paula González-Parra¹, Leticia Velázquez², María C. Villalobos, Carlos Castillo-Chávez¹
¹Arizona State University, ²The University of Texas at El Paso

A discrete time SIR model is proposed for analyzing the influenza dynamics for a given population over a time interval. The total population is divided into susceptible (S), infected (I), and recovered (R) individuals. Assuming limited resources, the model is expanded in order to evaluate the potential effect of control measures such as treatment and social distancing. By using 1918 influenza pandemic data and optimal control with interior-point methods, our goal is to estimate the fraction of treatment and social distancing in order to minimize the number of infected individuals.

Global air transportation and the spread of infectious diseases

Julien Arino

University of Manitoba, Centre for Disease Modelling, Yorke University, National Research Council Institute for Biodiagnostics, Canada

The spread of infectious diseases has been greatly eased by the expansion of the global air transportation network. I will discuss methods used in the BioDiaspora Project (a project based at St Michael's Hospital in Toronto) to study the global spread of infections, and will present results concerning the movements out of Mexico during the 2009 H1N1 pandemic.