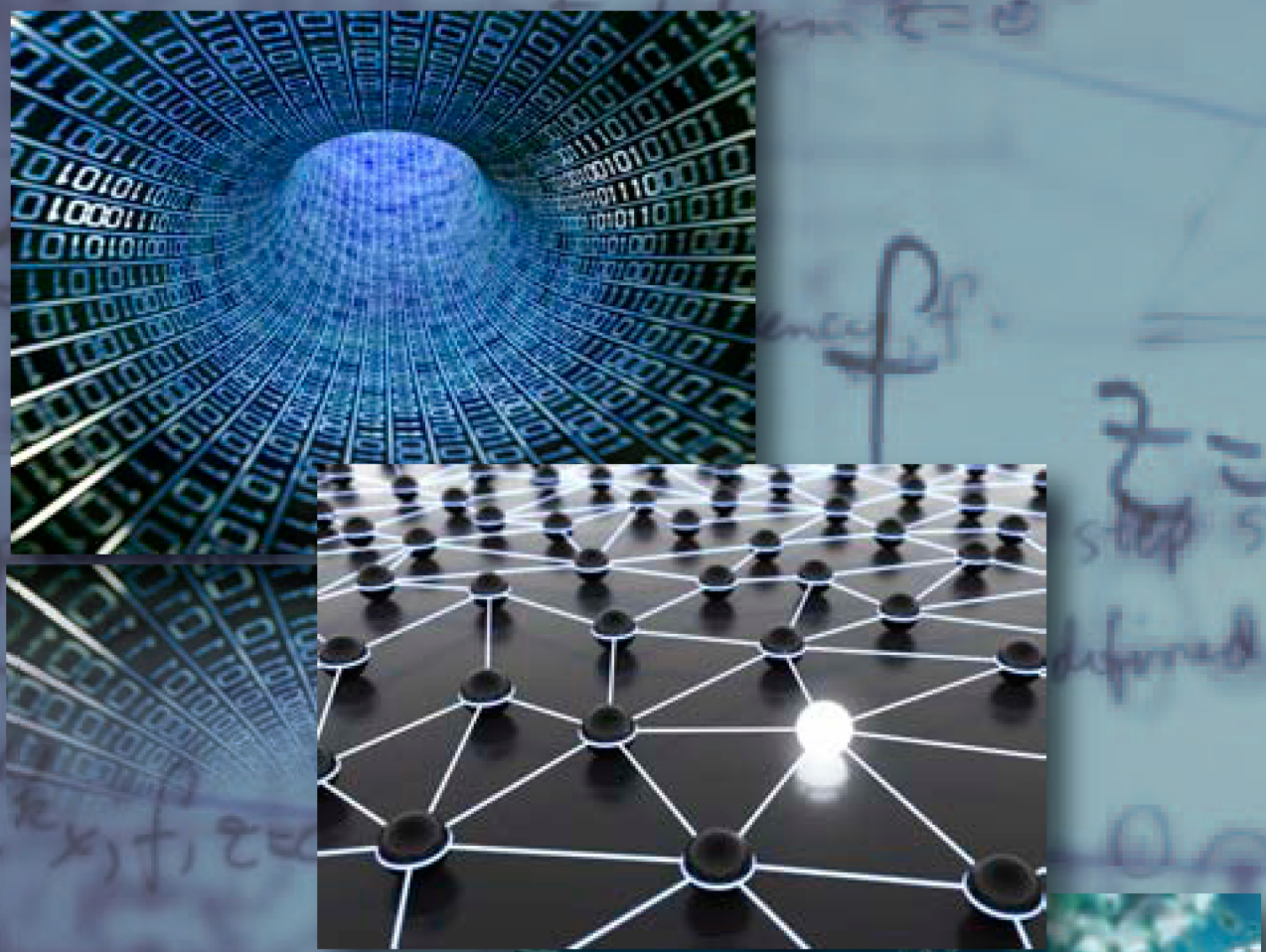
CANPAN

Canadian Consortium for Pandemic Preparedness Modeling



An Overview of Mathematical Modeling Projects Pertaining to Pandemic (H1N1) 2009 Influenza

Executive Summary

With the support of a CIHR Pandemic Team Leader (Phase 1) and a Catalyst Grant, the Canadian Consortium for Pandemic Preparedness Modeling (CanPan) was established. CanPan's overall objective is to harness Canadian expertise in mathematical modeling, surveillance and infectious diseases to create state of-the-art, real-time, quantitative risk assessment infrastructure to assist policymakers during the course of an influenza pandemic or other emerging infectious diseases (EIDs).

Shortly after CanPan's timely formation, it was called into action to address the outbreak of the novel pandemic (H1N1) 2009 influenza virus in Mexico in March of 2009. A core group of CanPan members were among the first investigators involved in modeling the pandemic influenza virus (pH1N1). This group was granted exclusive access to datasets that had not yet been made publicly available. In keeping with CanPan's objectives these investigators sought to create rapid-response modeling platforms to quickly and efficiently analyze the situation using (often incomplete) data from the "field". In order to design optimal intervention strategies to assist policymakers across Canada, and beyond, this information had to be rapidly streamlined and cross-validated. To accomplish this large undertaking, CanPan, with the support of a CIHR Team Leader Grant (Phase 2), developed an internship program to help bridge these knowledge gaps and to facilitate knowledge transfer in an efficient and timely manner.

CanPan's membership is made up of top Canadian researchers and public health officials from leading institutions across the country and is, thus, ideally situated to offer superlative mentorship – a key component of a successful internship program. More than fifteen internships were offered to carefully selected graduate students or postdoctoral researchers that were currently involved in the field. The internships were designed to address topics pivotal to the containment of the initial outbreak of pH1N1 in Mexico and later, to the containment of its global reemergence in the fall of 2009.

Within the scope of this opportunity, several novel projects were undertaken; many of the projects fell within themes, while others were broader, longer term or more cross-cutting. Some of the key internship themes included identifying or refining the basic reproduction number, enhancing or expanding a mathematical model, estimating disease prevalence or cases averted and identifying the impact of interventions. Each of these internships focused on one of several key objectives identified by CanPan members. These internships identified new and enthusiastic researchers and allowed their innovative project ideas to be cross-fertilized with other supervisory expertise across the identified CanPan hubs. This format ensured more concurrent rather than consecutive project results and allowed for increased rapid response and knowledge translation of the findings. Additionally, subsequent cohorts of interns could, in turn, build on the results of earlier cohorts and still provide timely and relevant results and recommendations, which are imperative to the pandemic response. Due to the rapid and practical response required and the specific expertise of the interns, some projects were adapted to meet the needs of decision-makers as the ambient conditions surrounding the pandemic strain evolved.

Each of the internships yielded valuable information and tools that were used to inform public health policy throughout the duration of the pandemic. As a result of this program, several publications are in progress to outline the significant contributions of this group. We have strengthened our relationships and created synergies between the three main hub sites and created opportunities for the learners of today to be the leaders of tomorrow.

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Message from the Principal Investigator & Program Manager

Babak Pourbohloul PhD
Principal Investigator

Krista English EMBA
Program Manager

As we complete our review of the past year – one that has been most eventful and productive – it is almost unbelievable that this much time has past. First and foremost, we would like to acknowledge the generous support and insight of CIHR and its partners; their timely response to research efforts prior to, and amidst the pH1N1 outbreak was remarkable.

Through this early support, the Canadian Consortium for Pandemic Preparedness Modeling (CanPan) was established to link nodes of Canadian expertise in mathematical modeling, surveillance and infectious disease. This program was launched at a time of confusion and doubt and amidst a potential global disaster. Only a few months after its inception, CanPan was called into action to address the pH1N1 outbreak that began in Mexico, in March 2009. We are humbled and grateful, however, for all the interest and participation in this collaborative effort. This was an opportunity to demonstrate a true willingness and ability to coordinate and collaborate in a strategic way during an emergency situation. Amid this uncertainty we were able to optimize our nation's mathematical modeling resources as well as provide a ripe training ground for tomorrow's modeling leaders. Our research took place across Canada and benefited greatly from the diversity and depth of our investigators' expertise.

We continue to marvel at the adaptability of our partners, collaborators and interns, who were able to respond to the call for a rapid response given so much uncertainty. This enthusiasm has yielded new partnerships among colleagues and opportunities for several new researchers to establish themselves within our research teams. Each internship was a self-contained project, which contributed to our larger objectives. These internships yielded a high output of valuable results in a very short period of time. The depth and breadth of research undertaken within the significant scope under the umbrella of a single grant opportunity demonstrates the remarkable dedication, organization and support of our colleagues for this initiative. Moreover, they provided young researchers the opportunity to gain valuable insight, experience and skills from working with host site PIs.

Upon reflection, we feel strongly that CIHR's investment in its national networks of interconnected expertise with demonstrated leadership, such as CanPan, will return dividends in Canada's ability to respond and protect the safety of Canadians in the event of a future pandemic. The cumulative results of a new cohort of young professionals working collaboratively with Canada's leading experts will demonstrate the value of this investment for years to come.

Babak Pourbohloul PhD
Principal Investigator

Krista English EMBA
Program Manager

Message from the Toronto Site Principal Investigator

David Fisman MD MPH FRCP(C)

My involvement with the CanPan group precedes the 2009 influenza pandemic. Many infectious disease epidemiologists and mathematical modelers in Canada were concerned at the under-utilization of mathematical epidemiology in support of disease control strategies during the 2003 SARS outbreak. With concern around the pandemic potential of highly-pathogenic influenza A H5N1 ("bird flu"), such conversations ultimately led to the creation of the CanPan group under the leadership of Dr. Pourbohloul; this organization has served as a "center of gravity" for many modeling activities during the 2009-2010 pandemic. My involvement with CanPan has focused recently on mentorship and supervisory activities around CanPan's internship program. I have worked with three interns (alphabetically: Dr. Venkata Duvvuri, Ashleigh Tuite, and Yanyu Xiao) on projects related (respectively) to the role of cross-reactive cell-mediated immunity in attenuating the impact of the current pandemic; optimal vaccination strategies for the pandemic; and the impact of mass antiviral treatment in controlling influenza spread in a First Nations reserve. Ms. Tuite has recently joined my group at University of Toronto as a full-time research officer, and is focusing on modeling the interactions between influenza and bacterial pathogens. This work is emblematic of CanPan's broadening focus on respiratory infectious diseases that transcend the current influenza pandemic.

Message from the Montreal Site Principal Investigator

David Buckeridge MD PhD

From its inception, I have been an active member of the CIHR-supported Canadian Consortium for Pandemic Preparedness Modeling (CanPan) and provided mentorship in CanPan's internship program. As a project and site supervisor for this program I have worked with five interns, namely, Dr. Katia Charland, Mike Delorme, Dr. Masoumeh Izadi, Carly Rozins, and Dr. Aman Verma, on a variety of projects: Estimating the true incidence of pH1N1 from the synthesis of multiple formal and informal surveillance data streams: assessing the lead-lag relationship between time series; estimating the number of H1N1 cases averted through the vaccination campaign; developing tools to estimate the potential infection rate of H1N1; determining the role of different age groups in the spread of H1N1 in Montreal and testing a variety of intervention methods; and, estimating the actual incidence of H1N1 influenza in Quebec. The information obtained and modeling tools developed by these interns has furthered CanPan's goal of investigating, addressing and controlling infectious disease outbreaks.

Project Summaries

The following summaries are a collection of the larger scale, ongoing or overarching projects conducted by our researchers and/or collaborators. These projects are part of the framework from which many of the internship projects were catalyzed. Thus far, the results have yielded some very interesting outcomes. These combined project outcomes represent exciting opportunities for further exploration to facilitate continued synergy.

CanPan's Meeting with Mexico City's Ministry of Health (Secretaría de Salud del Distrito Federal) Mexico City -- July 14-15, 2009

During the fourth week of April 2009, a novel swine-origin influenza A (H1N1) virus consisting of North American and Eurasian components was identified as the cause of sporadic but mild human illness in California and a substantial and severe outbreak in Mexico.

Mexico is a vast country of 110 million people, yet its surveillance system was able to spot the outbreak of several hundred cases and locate the victims. Working with Canadian specialists to identify the genetic makeup of the virus enabled deployment of a nationwide response. Between March 15 and April 28, the high-tech command center in Mexico City, linked a nationwide network of 11,000 disease surveillance units and learned that sporadic cases within the Federal District (D.F.) had increased erratically. Person-to-person transmission became sustained and amplified after the mass population returned to the city following the Holy Week holiday (April 5-19). A public health emergency was declared in Mexico on April 23. After laboratory confirmation of pandemic (H1N1) 2009 infection on April 23, *Dirección General de Epidemiología, Secretaría de Salud, México* (DGE) developed case definitions.

Mexico's president, Felipe Calderón, ordered all schools closed indefinitely over the weekend and forbade any public gatherings until the outbreak was brought under control. This exercise was thought to be pivotal during the rapid containment strategy put into place once cases were identified outside Mexico.

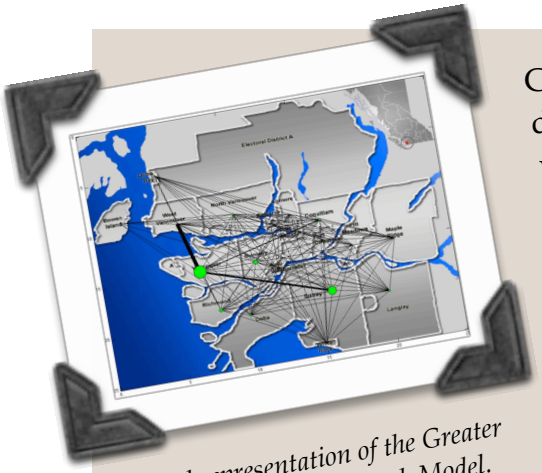
Travelers returning home from Mexico had since seeded outbreaks worldwide. On June 11, 2009, the World Health Organization declared a global pandemic due to community-level outbreaks in multiple parts of the world.

On the invitation of Mexico City public health officials, representatives of CanPan traveled to Mexico City on July 14-15, 2009 to participate in the project named, "New mathematical models to assess the impact of mitigation strategies against the spread of the pH1N1 virus" in the Mexico City Ministry of Health offices. This meeting included approximately 50 experts from the Mexico City, D.F. Ministry of Health team, Area Coordinators, Directors, and Epidemiological Staff to sign a Memorandum of Understanding and to begin a mutually beneficial collaboration to exchange knowledge, data and trainees. Using the expertise within CanPan, in combination with extensive demographic information, case notification data and experience from Mexico City, this collaboration refined the early estimate of R_0 for the epidemic area of metropolitan Mexico City.

The publication resulting from this collaboration was the following:

Pourbohloul B, Ahued A, Davoudi B, Meza R, Meyers LA, Skowronski DM, et al. Initial human transmission dynamics of the pandemic (H1N1) 2009 virus in North America. Influenza Other Respi Viruses 2009; 3: 215-22.

Building Contact Networks for Canada



Pictorial representation of the Greater Vancouver Contact Network Model. Circles represent the number of inhabitants in each of the municipalities and the lines the connectivity between them

Communicable diseases are spread throughout the population depending on individuals' contact networks. Individuals with many interactions (or contacts) may play a more significant role in the spread of infection compared to someone with fewer interactions. Accordingly, obtaining detailed information on various contact networks and patterns within a community, province or country, allows us to model how different diseases spread through these various contact networks.

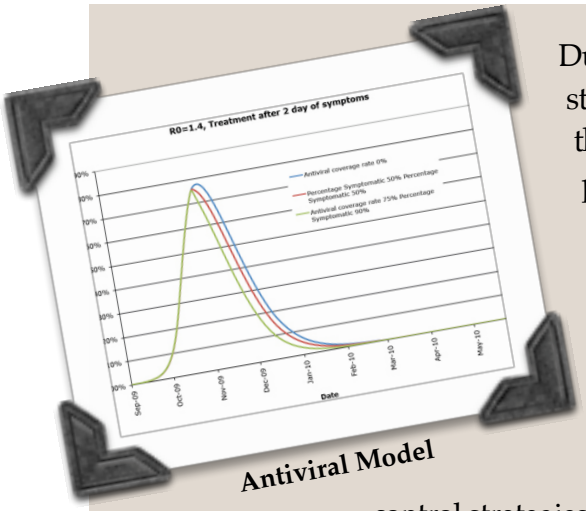
To address this information gap, our group has begun to construct and model networks within the Canadian population. The group had already built a detailed contact network for the Greater Vancouver Area and acquired data from Statistics Canada to expand this comprehensive contact network to include three major Canadian cities and ultimately the entire Canadian population.

With the most recent census data, as well as customized datasets from Statistics Canada, Dr. Jiansen Lu, a Scientific Computer Programmer with the Division of Mathematical Modeling UBCCDC, constructed or modified representative contact networks for Vancouver, Toronto and Montreal. These contact networks allow us to model the spread of infectious disease using disease specific parameters, in real-time and in each of these major cities. We have expanded on the initial major cities to demonstrate the relationship between them and their surrounding cities to create a Canada wide context. Thus, we provide an invaluable tool to be expanded upon and applied in real-time, to prevent or mitigate the spread of infectious disease.

Real-time intervention decision-making during a pandemic is more effective than the generic strategies summarized in most pandemic preparedness plans. It is also recognized that individuals' behaviors change during the course of a pandemic and this has a great impact on reducing the risk of further spread of infection. We have, therefore, developed a novel method which uses a time-dependent risk assessment model to study the impact of variations in intervention strategies for major Canadian urban areas. Together, these models will provide an essential tool kit for public health policy- and decision-makers facing the daunting task of preparing for the next pandemic.

Contact Network Building
DMM Scientific Computer Programmer:
Jiansen Lu, PhD

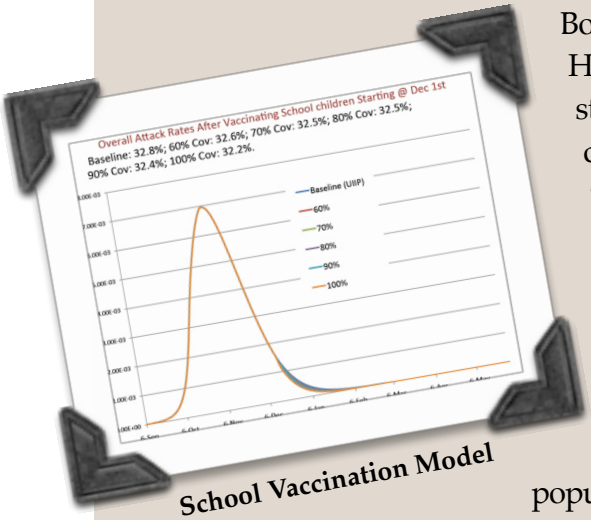
Assessing the impact of widespread antiviral use or a massive school-children vaccination campaign during the second wave of the H1N1 pandemic



Antiviral Model

During the second wave of the pandemic, different control strategies were considered to minimize the pandemic's impact on the population. Halfway through the second wave of the pandemic, strong consideration was given to the widespread use of antivirals as one potential method to prevent cases with severe symptoms and reduce the spread of the disease. Moreover, the targeted vaccination of school-children was also suggested as a potentially effective measure to contain the spread of influenza.

To assist public policy decision-makers in determining the best control strategies for the pandemic, researchers within the Division of Mathematical Modeling developed two mathematical models to investigate the second wave of the H1N1 epidemic in British Columbia. These models examined the efficacy of a variety of control strategies. The first model was based on an existing epidemiological contact network model of Vancouver, BC, while the second one was a deterministic version (using ordinary differential equations) of the first. Both models incorporated detailed information of the natural history of the H1N1 infection, the demographic and contact structure of the population of BC, and the preexisting H1N1 vaccination program in BC. Both models considered, in detail, the potential effects of antiviral use among pre-symptomatic, symptomatic and clinical cases on disease severity and transmission. The models were further used to assess the impact of a massive school-children vaccination campaign, which targeted school-aged children halfway through the pandemic. This newly proposed vaccination campaign was in addition to the general population campaign already in place.



School Vaccination Model

Both models were used to simulate BC's second wave of the H1N1 epidemic and suggested that the use of either intervention strategy examined (the use of antivirals or a massive school-children vaccination campaign) halfway through the epidemic would have had minimal impact on the total number of clinical and severe cases, and on the mortality rates due to pH1N1 infection. Extensive sensitivity analysis assured the model assumptions and the parameter values, that informed the conclusions, were robust. These analyses suggested that given the significant monetary and logistical costs associated with the implementation of these strategies in the population, they were not a cost-effective solution. Our conclusions were shared with decision-makers of BC and Canada to aid them in their public policy decision process.

DMM Researchers: Drs. Jessica M. Conway, Rafael Meza and Bahman Davoudi

Antiviral Optimization

Pictorial representation of a mathematical model for the optimization of antiviral distribution across Canada.

A spatial network model of Pandemic 2009 H1N1 transmission throughout Canada

Sebastian Goll

The early spread of the 2009 influenza pandemic was fueled by the movement of infected travelers. We built a spatially explicit network model of pH1N1 transmission within Canada that allowed us to investigate the impact of air travel on the epidemic and forecast the magnitude and timing of local outbreaks.

The model included a realistic network of the 141 largest Canadian cities (totaling 25.6 million people) and was based on detailed domestic air and ground travel data. Disease spread occurred between cities via the travel of infected individuals and within cities according to mass action models.

We used the model to create visualizations of pH1N1 spread across Canada. Using transmission rates estimated for 2009 pH1N1 flu, the model predicted that, without any intervention, the outbreak would infect approximately 16.5 million people in Canada.

We can use this model to evaluate the efficacy of various intervention strategies for ongoing and future epidemic and pandemic outbreaks of flu. For example, we used the model to evaluate various distribution policies for the national antiviral stockpile. It predicted that, under an optimal distribution schedule, aggressive use of antivirals might avert up to 75% of cases. However, under more realistic treatment rates, even the best policies will only moderately mitigate transmission.

Project Supervisor and Graduate Mentor:
Dr. Lauren Ancel Meyers
The University of Texas at Austin

Intern Project Summaries

The following are the project summaries of the work undertaken by the interns. Each profile includes the project title, the intern's name and photo, a project description, with a diagram and results where available. Project Supervisors directly oversaw the work outlined within the projects related to this grant opportunity, while Academic Supervisors are acknowledged due to their essential support for the participation of their MSc student, PhD student or Postdoctoral Researcher in this internship program.

Estimation of the true incidence of pandemic A(H1N1) from the synthesis of multiple formal and informal surveillance data streams: assessing the lead-lag relationship between time series

Katia Charland

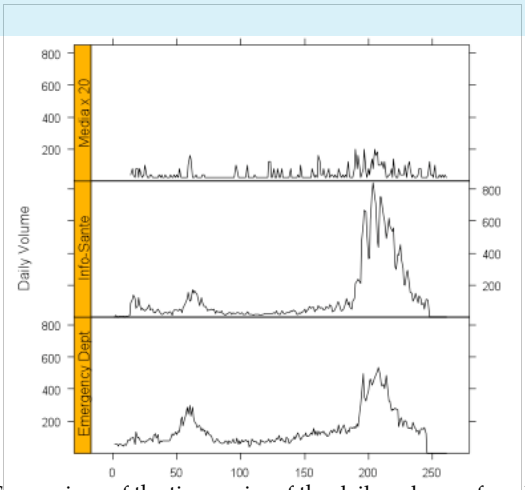
Project Description

As the true incidence of pH1N1 infection is not a directly observable quantity, we needed to estimate the true rate of infection from several data sources. By synthesizing the information from several formal and informal data sources we expected to produce a more accurate representation of the true rate of infection. The synthesis of information from various data sources was to be achieved through Dynamic Bayesian Network methodology but as a first step we needed to assess the lead-lag relationship and the extent of the correlations between the various data streams.

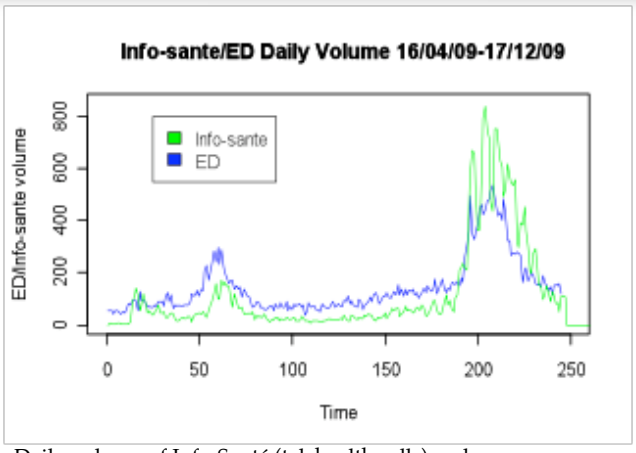
We were provided with four different data sources by the department of public health in Montreal, including the daily number of emergency department visits and Info-Santé (telehealth) calls, as well as the weekly number of pH1N1 vaccinations and lab-confirmed pH1N1 cases. We have recently extracted the daily number of media reports in Montreal that were related to pH1N1 from HealthMap. Media reports of deaths from pH1N1 were considered important because of their pronounced effect on the utilization of healthcare services (see figures below), thus media reports were filtered for content. The extent of the temporal relationship between series was estimated using wavelet coherency analyses.

Project Supervisor: Dr. David Buckeridge
McGill University

Postdoctoral Mentors: Drs. John Brownstein & David Buckeridge
Children's Hospital Boston/Harvard Medical School



Comparison of the time series of the daily volume of media, calls to Info-Santé (telehealth) and emergency department (ED)



Daily volume of Info-Santé (telehealth calls) and emergency department visits in Montreal from April 16-December 17, 2009

Results

The temporal relationships between the emergency department and Info-Santé data series remain fairly consistent in the context of seasonal influenza (e.g., Info-Santé series leads emergency department (ED) series by 2 to 4 days). However, for pH1N1, our methods suggested a varying relationship throughout the pandemic period with the most pronounced change occurring in the first week of November. Nevertheless, the wavelet coherency analyses suggested the following relationships for further analysis in the Dynamic Bayesian Networks:

-ED leading Info-Santé by 1 days

-Info-Santé leading ED by 2 days

-Media leading Info-Santé by one day and Info-Santé leading ED by 2 days

Does geographic variation in human contact patterns drive spatial heterogeneity in influenza spread and diversification?

Ben Dalziel

Project Description

Human influenza spreads and evolves at different rates in different locations. A striking example involves the surges in infection and viral diversification rates which occur each winter at temperate latitudes. Despite their predictable timing, these fluctuations show significant unexplained variability in amplitude and spatial coherence. The unknown processes that drive these patterns are implicated in significant human mortality and morbidity and thus represent an important target for public health research. What geographic differences in human populations underlie the observed heterogeneities in influenza spread and diversification?

Recently-developed mathematical models suggest that cities may have characteristic patterns of infectious contact between individuals, mediated by differences in the size and structure of social groups (i.e., households, schools, workplaces, etc.), which affect epidemic and evolutionary outcomes. Intensive monitoring during the 2009 H1N1 pandemic has generated concurrent data on contact patterns and infection levels, as well as collections of viral sequences, from across Canada. For this project we have accumulated a database of over 500 sequenced pH1N1 samples from BC and another 200 sequenced samples from across Canada. These data represent an opportunity to apply recent advances in spatial epidemiological modeling to test the relationship between human contact patterns and influenza dynamics. We are planning to link geographic variation in human contact patterns to variation in the amplitude and coherence of H1N1 infection and viral diversification rates by comparing the predictions of network epidemic models developed at the BCCDC with reconstructed weekly epidemic and evolutionary time-series for major Canadian cities during the 2009 pandemic.

Project Supervisor: Dr. Babak Pourbohloul
UBC Centre for Disease Control

PhD Advisor: Dr. Stephen Ellner
Cornell University

Estimation of the Reproductive Number of an Emergent Disease

Cindy Feng

Project Description

The emergence of infectious disease epidemics poses a significant threat to public health; thus, signifying the importance of developing statistical methods to produce more accurate estimates for key epidemiological parameters. The basic reproduction number, R_0, is a parameter used to characterize the potential transmissibility of a disease and, hence, must be taken into account when developing intervention strategies.

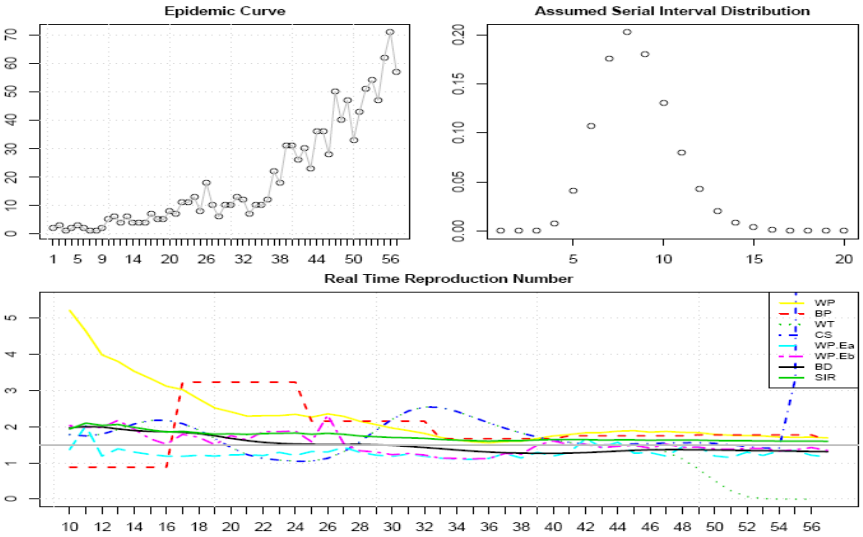
The purpose of this project was to investigate various methods of estimating R_0 and to highlight the differences between each method by way of simulation studies. Our results were used to investigate differences in pH1N1 transmission dynamics by geographic location, population size, and control strategies implemented.

Project Supervisors: Drs. Babak Pourbohloul & Rafael Meza

UBC Centre for Disease Control

PhD Advisor: Dr. Charmaine Dean

Simon Fraser University



The top left panel shows the epidemic curve; the top right panel shows the assumed serial interval distribution and the bottom panel shows the real-time R_0 estimates. The true R_0=1.5 is represented by the grey line.

Results

Our simulation results showed that the efficacy of the estimation methods depended upon the underlying process of the epidemic curves. Therefore, better understanding of the epidemic behavior is necessary before applying the methods to estimate R_0. Estimating the serial interval is challenging; however, the method proposed by White and Pagano is promising, as it is able to address the issue of simultaneously estimating R_0, the serial interval mean and variance in real time. This method requires a minimal amount of prior information, but identifiability issues may exist for smaller outbreak sizes. Most other methods assume that the serial interval distribution is known, so the results depend on how close the assumed value is to the true distribution. The method by Davoudi *et al* is also promising, because it can use the removal time distribution, which is easier to obtain in many cases from real data, instead of the serial interval distribution.

A discrete time network model for disease spread in large populations

Jennifer Lindquist

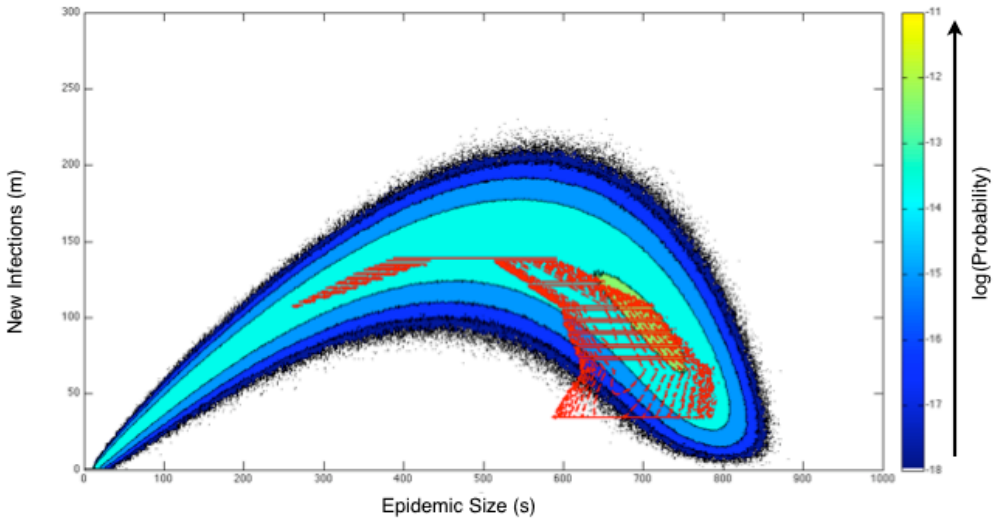
Project Description

The focus of my internship with the UBCCDC was the implementation and exploration of a hybrid simulation algorithm. This method allows us to perform very fast simulations of epidemic outbreaks within large populations; analysis of the resulting simulation data provides both insight into pandemic disease dynamics, and clues as to what public health actions will be most effective.

Large networks of individuals are inherently difficult to simulate. The huge number of calculations required to track interpersonal connections alongside disease dynamics results in high computational costs and long running times. In the onset of a real epidemic outbreak, these limits are a serious barrier to effectively comparing and understanding the effects of intervention strategies.

Hybrid modeling/simulation refers to the use of multiple methods within a single model or simulation framework. We combine stochastic and deterministic methods, which greatly reduces the time needed for simulations. The stochastic portion of the work preserves important effects of initial conditions and randomness inherent in real situations. By also incorporating a deterministic regime, our method allows practical and timely computation of large scale simulations. In the event of a new outbreak, public health officials can then quickly identify those interventions most effective for a particular population network.

Project Supervisor: Drs. Babak Pourbohloul & Bahman Davoudi
UBC Centre for Disease Control
PhD Advisor: Dr. Junling Ma
University of Victoria



Stochastic simulations (blues/greens) compared with simulation output (red) for a network of 100,000 nodes

A game theoretical approach to modeling non-vaccinator and delayer behaviours in pandemic influenza

Samit Bhattacharya

Project Description

An individual's perception of vaccine safety is one of the significant factors determining the success of vaccine coverage strategies. Vaccines for pandemic influenza are relatively new, and thus cause a relatively common behavioural pattern of delaying vaccination. The reasoning behind this delay is twofold: delay because the individual intends to rely on herd immunity for protection, or delay to wait for more information on vaccine safety to become available.

To investigate this common behavioural trend we constructed a game theoretic model that incorporated this 'wait and see' strategy. We considered two major cases: constant perceived vaccine risk and a declining vaccine risk proportional to the number of individuals vaccinated (thus increasing one's safety through herd immunity). A wide variety of possible dynamics emerged from this model.

Project Supervisor: Dr. Chris Bauch
University of Guelph

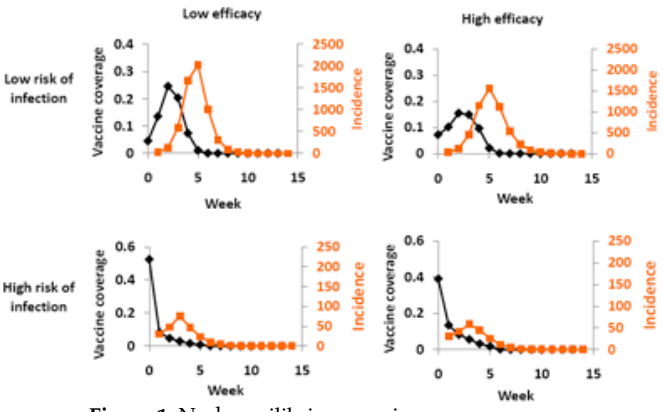


Figure 1. Nash equilibrium vaccine coverage over weeks for low (r_{inf} = 0.0004) and high (r_{inf} = 0.04) disease risk, and low (ε = 0.6) and high (ε = 0.9) efficacy of vaccine. Incidence is per 100,000 people.

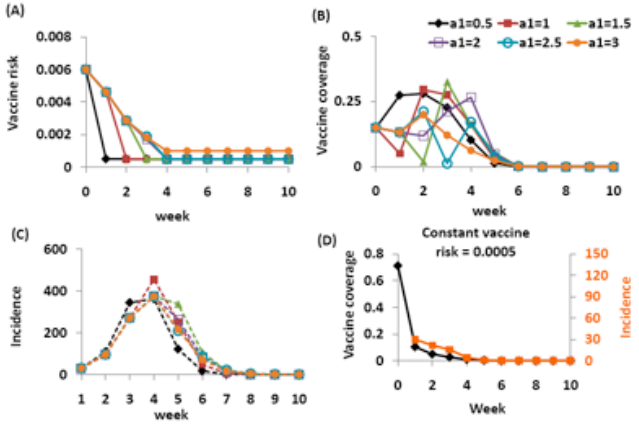


Figure 2. Nash coverage at variable perceived risk of vaccine. (A) Variable vaccine risk over weeks for different values of slope in the risk and corresponding (B) Nash equilibrium vaccine coverage and (C) disease prevalence. ε =0.75 and r_{inf} = 0.02. The incidence shown in the figure is per 10,000 people. (D) indicates vaccine coverage with the same parameter as in (B) except the vaccine risk is constant (0.0005) during the entire period of disease outbreak.

Results

The model exhibited both feed-forward and feed-back dynamics. We observed that for some parameter regimes, in both the constant and declining vaccine risk scenarios, the Nash equilibrium strategy was to delay vaccination until the outbreak was under way (Figure 1). When vaccine risk varied, we found that vaccine coverage initially declined as the outbreak proceeded, but a rebound was observed once enough individuals had been vaccinated to reassure the population of vaccine safety (Figure 2). These results highlight the importance of imparting accurate and useful vaccine safety information, especially for a novel vaccine, in a timely manner to ensure a successful vaccination campaign.

Evaluating the impact of pH1N1 vaccination in Montreal using SEIR based forecasting

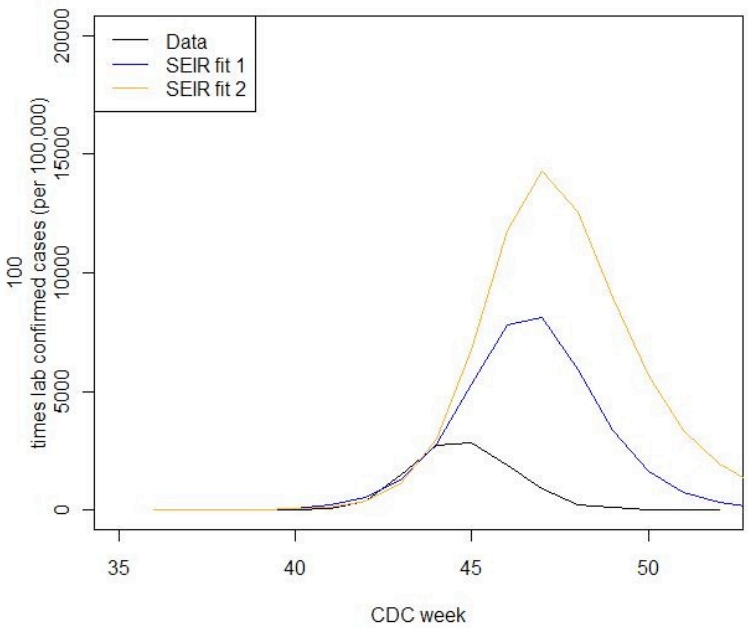
Mike Delorme

Project Description

In 2009/2010 a new strain of influenza A H1N1 posed a risk to many people in North America. One of the tools used by public health professionals to fight the epidemic was the pH1N1 vaccine. The two-fold benefits of vaccination (one, individuals protect themselves and two, individuals prevent spreading the virus) are sometimes difficult to measure using traditional studies. Previous studies have addressed vaccine effectiveness by following cohorts and estimating the extent to which vaccination reduces the risk of infection, hospitalization and death. This study uses a theoretical disease dynamic model and data on laboratory confirmed cases to make a direct estimate of the number of cases averted. This differs from other vaccine studies because the vaccine was introduced during the influenza epidemic.

Within the assumptions of the study, the estimate of the number of pH1N1 cases averted through the vaccination campaign was found. Using Montreal specific hospitalization and death rates, we predicted the number of hospitalizations and deaths averted in Montreal. Modeling the second wave of the H1N1 pandemic produced estimates of the duration of infectiousness and latent period that can be compared with other studies.

Project Supervisor: Dr. David Buckeridge
McGill University
Master's Advisor: Dr. Jonathan Dushoff
McMaster University



In this plot the weekly incidence is plotted for the course of the second wave of pH1N1 in Montreal. The blue line (SEIR fit 1) is the output of a mathematical model fit to the incidence data using an ordinary least squares fit. The orange line (SEIR fit 2) is the output of the model for the incidence data using a Poisson distribution.

Role of CD4+ T-cell receptor HA epitopes in the dynamics of infection by swine origin influenza A virus H1N1

Venkata Duvvuri

Project Description

A novel H1N1 virus (pH1N1) was identified as a potential pandemic strain by the World Health Organization on June 11, 2009, due to its rapid spread and lack of cross-reactive antibody titers in the population. However, it has been characterized as a milder strain based on the account of relatively mild clinical outcomes in the vast majority of individuals. This reduced severity could be from existing T-cell immunity due to epitope (i.e., a part of the pathogen recognized by the host's immune system) conservedness across influenza A virus strains; thus, permitting memory T-cells to contribute to protective immunity. To perform the bioinformatics analysis, hemagglutinin (HA) protein sequences for seasonal influenza A (sH1N1 and sH3N2) from 1968-2009 and pandemic (H1N1) 2009 strains were downloaded from the flu genome databank.

Project Supervisor: Dr. David Fisman
York University

Results

From the bioinformatics analyses, T-cell epitope regions were predicted based on the major histocompatiblility complex (MHC) class II, which are the proteins expressed on the surface of a cell that presents epitopes. This presentation of epitopes can further lead to the activation of cellular level immunity. Each predicted epitope was examined against all the protein sequences that correspond to sH1N1, sH3N2 and pH1N1. Maximum epitope conservedness was found between sH1N1 and pH1N1 with a significant correlation ($p < 0.05$). This correlation explains the close evolutionary relationship of sH1N1 and pH1N1 strains. To evaluate the implications of cross-immunity at the population level, we would like to simulate a stochastic continuous time Monte Carlo Markov Chain model of disease transmission (*in progress*). According to earlier studies, cross-immunity may result in prolonged incubation periods, and change epidemic dynamics via changes in the spectrum of illness observed in infected individuals. The model outcome would highlight the role of cellular cross-protection in understanding the inter-pandemic variability in severity, and would assist with future planning for emerging influenza viruses.

Fusion of Epidemiological Data Sources Using Probabilistic Graphical Models and Its Application in Real-Time Estimation of pH1N1 Incidence

Masoumeh Izadi

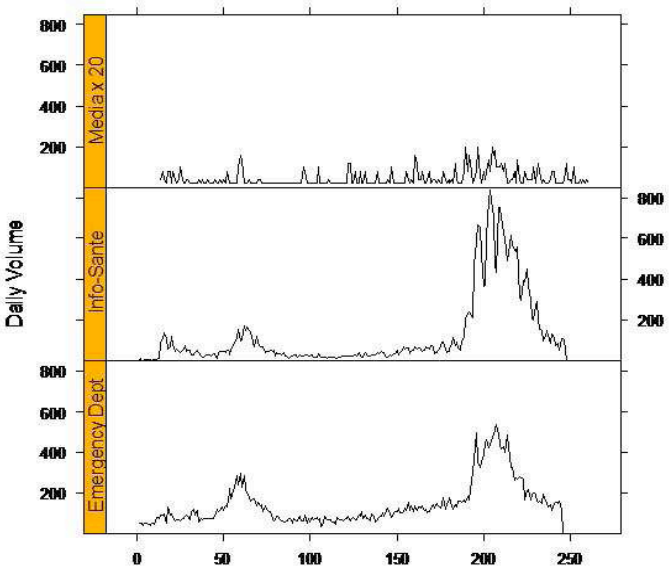
Project Description

It is generally difficult to estimate disease prevalence or true infection probabilities because they are not completely observable quantities. However, these parameters can be derived from other available data sources; there are usually observable data sources that can provide partial indications of the true incidence of infected cases or prevalence rates. Yet, a fundamental question remains: what are the most appropriate data sources and how do we combine these heterogenous data sources to achieve this objective?

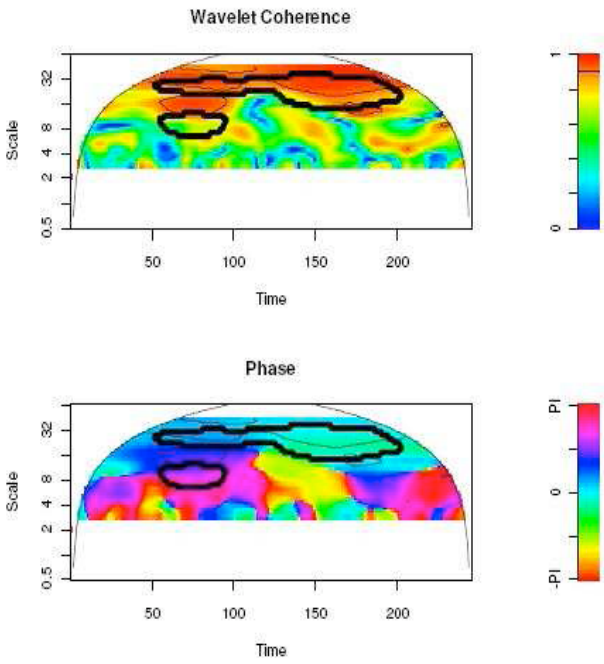
In the present H1N1 flu pandemic context, most modeling approaches used to derive the infection rate are based on observable data, which uses strong assumptions that do not reflect the dynamical characteristics of a pandemic. Consequently, these models may underrate or overrate the true infection. It is also critical to estimate the prevalence of the pH1N1 strain in a timely manner.

In this project, we present tools for identifying probabilistic relationships between data streams, which support real-time estimations of such rates using probabilistic graphical models. In particular, we use Bayesian inference in a dynamical model of data fusion to learn the probabilistic relationships between epidemiological data streams from Montreal, Quebec and to estimate the potential infection rate of pH1N1. Our results show that our dynamic Bayesian network model generalizes well.

Project Supervisor: Dr. David Buckeridge
McGill University



Three data sources of media reports, calls to Info-Santé, and emergency department visits from top to bottom.



Wavelet coherency analysis for two data sources: ED and Info-Santé.

Estimation of the basic reproduction number in the early phase of an epidemic in a population with a heterogenous contact pattern

Kin On Kwok

Project Description

Whether it is a new emerging (SARS in 2003) or reemerging infectious disease (pH1N1 in 2009) that strikes the population, policymakers are interested in the magnitude of the basic reproduction number (R_0) in the early phase of the epidemic; this parameter is used to define the best possible intervention strategies to effectively control the spread of the diseases. Previous studies have shown that R_0 can be accurately estimated, in the early phase of an outbreak, with case notification data, the potential transmission contact network and the biological characteristics of the disease; however, homogeneous contact patterns were assumed for the population in the preexisting network model (Model A).

In reality, contact patterns will vary across different age groups. For example, school-aged children have more contacts (schoolmates, teachers and their parents) and thus greater exposure, compared to individuals from other age groups. Therefore, during an infectious disease outbreak – such as the pandemic influenza in 2009 – school-aged children contribute significantly to the number of infections. In response to this situation, we incorporated contact pattern heterogeneity, across different age groups, into the preexisting model to create a new model (Model B).

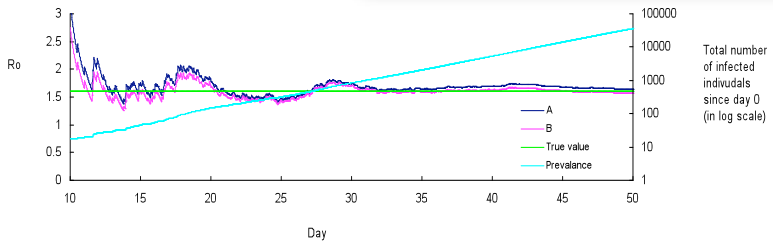
When simulating the spread of an infectious diseases in an idealized contact network with a true value of R_0 equal to 1.6, both Model A and Model B (with two heterogeneity contact age groups – adults and children) have consistent patterns in the stochastic regimes. The models converge quickly to 1.6 (the blue line and the pink line) between day 14 and day 16 with less than 100 infected individuals (figure below). In the early phase of the simulated epidemic, less fluctuation around the true value is seen in Model B when compared to Model A.

Project Supervisor: Drs. Babak Pourbohloul & Bahman Davoudi

UBC Centre for Disease Control

Postdoctoral Mentor: Dr. Steven Riley

University of Hong Kong



Results

The results suggest that incorporating information on the heterogeneity of contact patterns will provide a more accurate estimate of R_0 in the early phase of an epidemic with a small number of infected individuals. With a more accurate estimate of this parameter, policymakers can implement the best intervention strategies in the early phase of the epidemic to rapidly control the spread of the diseases, despite having only a limited amount of information. In the later phase of the epidemic, the contact patterns become less heterogeneous, as intervention strategies lead to changes in contact behavior. For example, the closure of schools during the pandemic influenza in 2009 significantly reduced the number of contacts of school-aged children. This explains why both approaches consistently converge to the true value in the exponential regime after day 32. Our approach to estimate R_0 can be further refined if information on contact network heterogeneity (such as susceptibility profiles) becomes known for other age groups.

The utility of influenza-like illness (ILI) syndromic indicators in the early detection and monitoring of influenza outbreaks

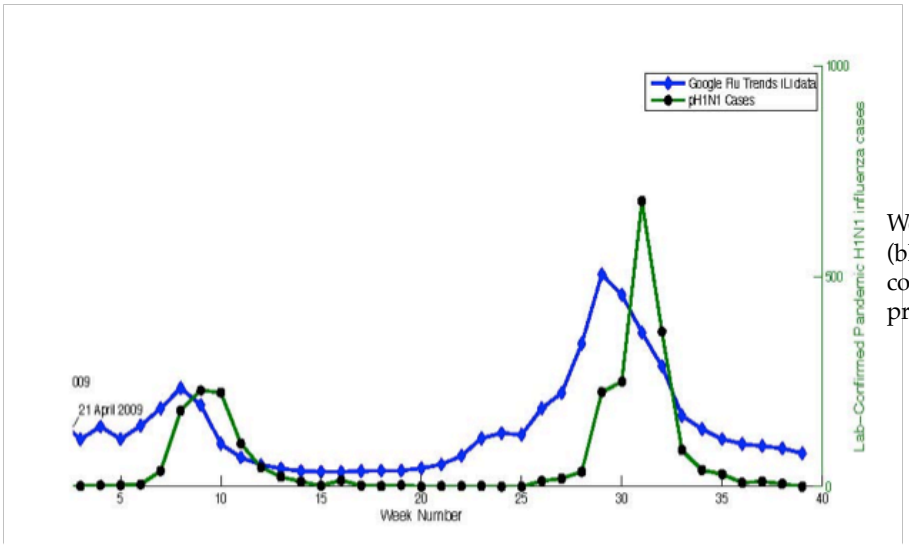
Tufail Malik

Project Description

Syndromic surveillance involves using health-related data that precede diagnosis and signals a sufficient probability of a case or an outbreak. Traditional methods of public health surveillance based on clinical or laboratory case reports are usually expensive, not sensitive enough to detect an outbreak during its early phases, and not suitable to detect outbreaks of novel pathogens. Syndromic surveillance is an emerging approach to early detection and monitoring of infectious disease outbreaks that does not rely on the collection of data from diagnosed cases. Instead, clinical syndromes and other proxies (e.g., number of emergency room visits due to ILI) are used to monitor disease activity with the aims of detecting and monitory new outbreaks.

Within this project we examined the performance of several influenza syndromic indicators with respect to early detection and monitoring of the recent pH1N1 epidemic in Manitoba. One of the data sources examined was Google Flu Trends (GFT). GFT uses Google's aggregated search query data on symptoms to estimate disease activity in near real-time. Google claims that GFT data is 'up to two weeks faster than traditional systems'.

Supervisors: Drs. Abba Gumel & Salah Mahmud
University of Manitoba



Weekly Google Flu Trends ILI Manitoba data (blue line) compared to the number of lab-confirmed pH1N1 influenza cases in the province (green line).

Results

The recent H1N1 pandemic provided a unique opportunity to examine the characteristics and uses of GFT. The GFT data were compared graphically with the actual number of the lab confirmed cases, as reported on the Manitoba Health website. The correlation coefficient computed after shifting the GFT data ahead by two weeks yielded a correlation of 0.83. The remarkable correlation between the two data sets supports Google's claim of being up to two weeks faster. In summary, the GFT data generally leads the Manitoba Health data, a fact that may be exploited to better prepare for a forthcoming challenge.

Contact Network Modeling

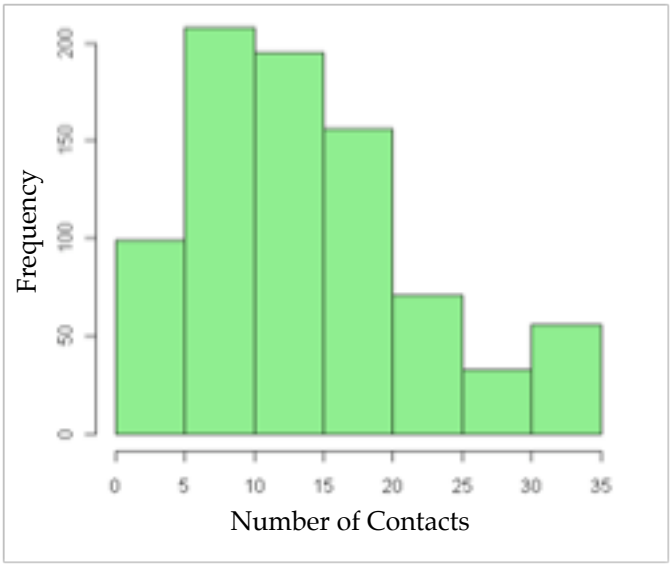
Flavia Moser

Project Description

A typical network structure consists of individuals (or "nodes") and connections (or "edges") between individuals. Depending on the type of network, connections can reflect a number of different types of contacts and are thus termed "contact networks". When modeling infectious diseases, contacts are typically defined as interactions that can lead to the transmission of disease. These parameters are based on epidemiological data for the pathogen of interest, and thus, enable the model to accurately reflect disease transmission within a specific facility or community as well as throughout a broader population.

The main goal of my internship was to develop a mathematical model for simulating contact networks, based on three types of observed data. The first type of data was the degree of an individual, i.e., the number of contacts reported by an individual. The second data type included an individual's background information, such as gender or age. The final type of data referred to structural information, such as triangles or other motives, required to be present in the network.

Project Supervisor: Dr. Babak Pourbohloul
UBC Centre for Disease Control
Postdoctoral Mentor: Dr. Charmaine Dean
Simon Fraser University



Frequency of the number of contacts, per person, within a simulated contact network

Results

The model developed was an extension of the well-known Exponential Random Graph Model (ERGM). ERGMs are probability models for networks that generalize beyond the restrictive edge independence assumption made by many other network models. My extension of the model enabled us to generate an ensemble of graphs (networks), which incorporated all three aforementioned data types by imposing constraints on each of them. The estimation of the model parameters as well as the simulations were based on a Markov Chain Monte Carlo (MCMC) approach. The simulation process used a restricted tetrad-swap, which complied with all constraints simultaneously.

Examining the effects of behavioral heterogeneity in the transmission dynamics of the H1N1 virus

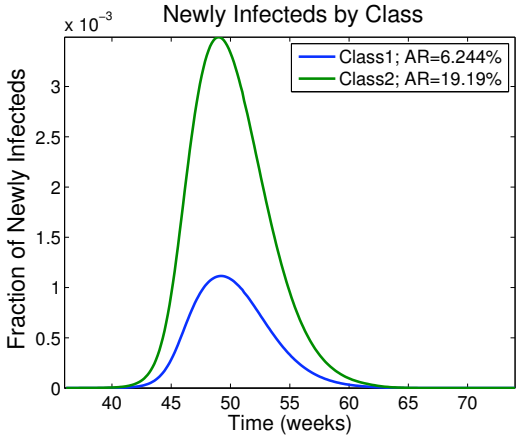
Heidi Muller

Project Description

Behavioural interventions have the potential to be an important prevention/containment strategy against emerging infectious diseases. However, in contrast to other interventions, behavioural change is difficult to quantify, while its impact on disease transmission – at the population level – is almost impossible to assess. Therefore, behavioural interventions are generally given less emphasis than other intervention strategies, such as, vaccination or antiviral use; behavioural interventions, however, have the potential to be very cost-effective.

In order to assess the impact of behaviour on pH1N1 transmission, we investigated the effects of including a behavioural component in a transmission model for pH1N1 in Vancouver. In this model, the population was split into two classes where one class had a higher perceived vulnerability than the other. This 'cautious' group (class one) had a lower susceptibility to pH1N1 infection due to behaviours like increased hand washing, for example. This group also had a lower disease transmission rate, due to more dramatic change in behaviour when ill; that is, this group was more likely to stay home from work or school while experiencing flu symptoms, when compared to the remaining population (class two).

Project Supervisor: Drs. Babak Pourbohloul & Rafael Meza
UBC Centre for Disease Control
Master's Advisor: Dr. Chris Bauch
University of Guelph



Epidemic curves for the 'cautious' group, class 1, and the average group, class 2, with baseline parameters. The proportion of the class 2 population that becomes infected is much higher than that for class 1. Class 2 is responsible for causing more infections than class 1. This indicates that behaviour plays an important role in disease transmission.

Results

Our analysis concluded that these differences in behaviour play an important role in the disease outcome. In particular, we found that changes in behavior can impact disease transmission to a similar degree as vaccination and other interventions. In terms of the model we found that the proportion of the population in class two (average individuals) that became infected (i.e. attack rate) was much higher than the infected proportion of those in class one (cautious individuals); moreover, the former class is responsible for most infections. As parameters are varied, the influence of behavioural choices affects the epidemic outcomes. Our model and findings can help inform public health decisions on choosing and promoting various preventative or intervention strategies.

Examining Potential Determinants of the Multiple Wave Structure of Influenza Pandemics Through SEIR Modeling

Carly Rozins

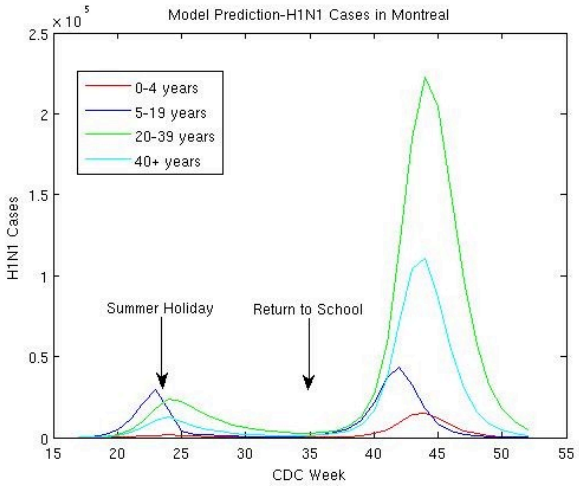
Project Description

While contemplating what type of model would be appropriate for the spread of pandemic influenza in Montreal, we realized that conventional disease models may not be the best fit for modeling a pandemic. Traditional SEIR models produce a single wave of incidence. Unlike seasonal influenza, pandemic influenza will infect the population in multiple waves.

We started thinking about possible factors that could have contributed to the sudden decline in pandemic influenza incidence in the spring and then initiated incidence weeks later in the fall. While reviewing the literature it became clear that there is a seasonal component to influenza virus survival and transmission. Moreover, it is widely recognized that school-aged children play a significant role in the spread of respiratory infections, specifically at the start of an epidemic.

Our aim was to incorporate these two factors into a traditional SEIR model to generate two waves, which would hopefully model the spread of pH1N1 in Montreal within a single model. To incorporate these factors into an already existing age-structured SEIR model, we scaled the contact matrix by an environmental factor and allowed the average number of school-aged contacts – with individuals of their own age group – to change at the start of summer holidays and again when they returned to school.

Project Supervisor: Dr. David Buckeridge
McGill University
PhD Advisor: Dr. Rebecca Tyson
University of British Columbia



Model prediction of H1N1 incidence, by age class, in Montreal

Results

By incorporating seasonality and changes in school-aged contacts into the model, we were able to model the pandemic with a single modified age-structured SEIR model. By fitting our model to Montreal specific data, we will be able to determine the role of different age groups in the spread of pH1N1 in Montreal and test a variety of intervention methods.

Impact of timing of pandemic vaccine availability on the effectiveness of vaccination as a mitigation strategy

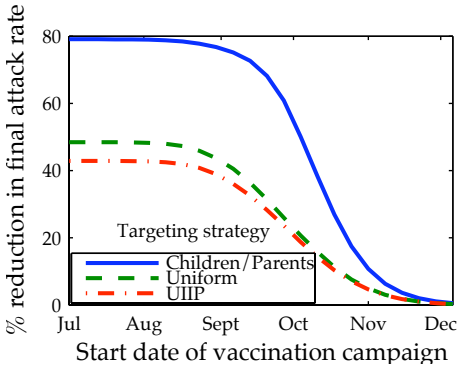
Ashleigh Tuite

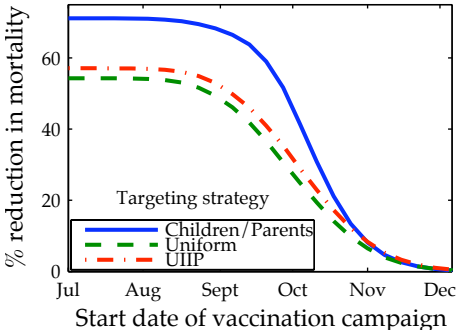
Project Description

Vaccination is an important tool for both the control of influenza transmission and the reduction of influenza-attributable morbidity and mortality. Production of the pH1N1 vaccine began soon after the pandemic potential of pH1N1 was recognized; however, the early arrival of the second wave of pH1N1, in the autumn of 2009, in many regions of the northern hemisphere resulted in the implementation of vaccination programs in populations already experiencing moderate to high levels of pH1N1 activity. This sequence of events differed from the situation with seasonal influenza, where vaccination programs are generally implemented prior to widespread circulation of influenza in the population.

We sought to evaluate the impact that timing of the availability of pH1N1 vaccine, relative to when the peak of pH1N1 epidemic occurred, would have on the ability to effectively use vaccination to mitigate a pH1N1 epidemic. We also investigated the interaction between different possible vaccine distribution schemes, such as targeted vaccination of children and parents. To do this, we used an age-structured compartmental mathematical model developed by the team at the University of British Columbia Centre for Disease Control that describes the transmission of pH1N1. This model uses demographic and behavioral data specific to Vancouver to construct a realistic pattern of contacts.

Project Supervisors: Drs. Babak Pourbohloul & Jessica Conway
UBC Centre for Disease Control
Master's Advisor: Dr. David Fisman
Dalla Lana School of Public Health at the University of Toronto





Impact of timing on the effectiveness of different vaccine prioritization strategies. Vaccination campaigns were implemented weekly, starting July 5, 2009, with the last campaign started on November 22, 2009. For a given campaign start date, the reduction in (a) final attack rates and (b) mortality relative to no vaccination was assessed. We considered three vaccinations strategies: Ontario's Universal Influenza Immunization Plan (UIIP) vaccination rates, uniform vaccination coverage across the entire population, regardless of age, or children and parents only (100% coverage in children aged 5-17 and adults aged 30-39 only). The start of the Vancouver influenza season is September 6, 2009. All simulations assumed R_0 of 1.4, latent period of 3 days, infectious period of 7 days, and an eight-week vaccination campaign length.

Results

Key among our findings, is the importance of timing of vaccine administration relative to levels of pH1N1 activity in the population. The effectiveness of vaccination during a pandemic is dependent on being able to deliver vaccine in a timely manner. In particular, although the choice of vaccination strategy can have a significant impact on the overall attack rate if vaccines are delivered before or during the initial phases of an epidemic, once influenza transmission is widespread, differences between different prioritization strategies are much less marked.

Estimating Actual Incidence of H1N1 Influenza in Quebec

Aman Verma

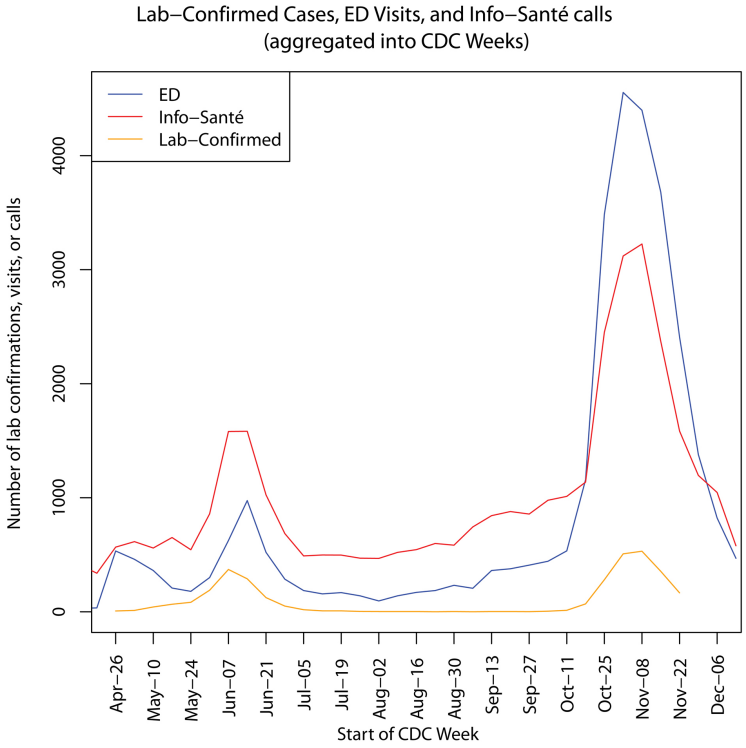
Project Description

This project focused on estimating the actual incidence of pH1N1 in Quebec. Proxy data, such as lab-reported cases, emergency department visits related to influenza, a telephone survey measuring influenza-like illness, and calls to a health hotline (Info-Santé) were used to estimated incidence rates. The influenza incidence estimates not only helped to guide policy, but also supported the development of mathematical models that accurately predict the likely spread of influenza infection.

The figure shows three examples of data sources used to approximate the actual incidence of pH1N1. The emergency department visits (ED), health hotline calls (Info-Santé calls) and laboratory confirmed cases (Lab-Confirmed) are shown as separate time-series. These three data sources serve as proxies for the desired data: the true rate of pH1N1 infection in Quebec. Interestingly, all three data sources distinctly show the two peaks of pH1N1 infection.

Additionally, all three data sources "track" each other with surprising accuracy, suggesting that they are all proxies for a similar trend.

Project Supervisor: Dr. David Buckeridge
McGill University



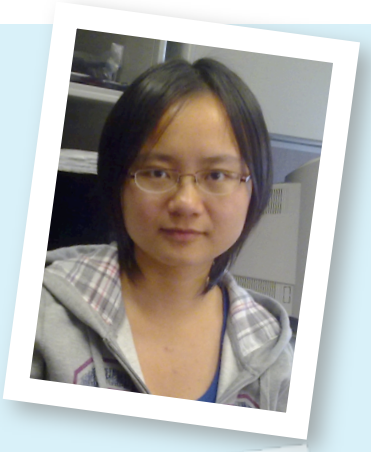
Data sources used to approximate the actual incidence of pH1N1 influenza. The emergency department visits (ED), health hotline calls (Info-Santé calls) and laboratory confirmed cases (Lab-Confirmed) are shown as separate time-series.

Results

These data suggest that routinely collected data can be used to monitor the progress of influenza epidemics. Such data can guide public health policy, and help measure the effectiveness of interventions such as vaccination campaigns.

Simple and patch models for the pH1N1 outbreak in 2009

Yanyu Xiao



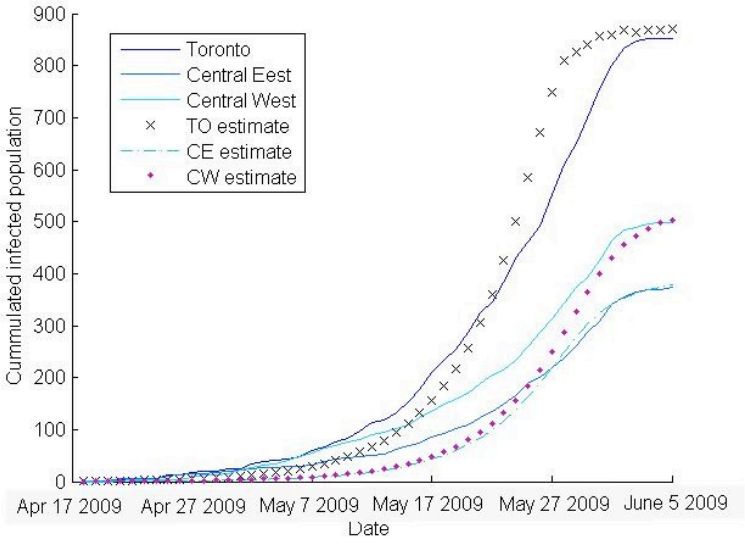
Project Description

The initial pH1N1 outbreak of 2009 occurred in Mexico but later re-emerged on an international scale. However, it was locally reported as endemic in North America from the spring to the fall of that same year. The symptoms associated with the 2009 pandemic were remarkably mild, when compared to those of earlier influenza pandemics, the impact varied across populations, geographical regions, and ethnic groups.

This project focused on a pH1N1 outbreak that spread rapidly within a community on a remote First Nations reserve in northern Ontario. This community experienced a cumulative symptomatic attack rate of 10.6%, with 244 cases of influenza-like illness reported in the community by September 2009. We sought to use the limited epidemiological data derived from this community outbreak to parameterize a simple epidemiological growth model (the Richards model). We derived estimates for the rate of growth of pH1N1 outbreaks in the context of a small, isolated First Nations reserve, and identified the possible impact of non-pharmacological interventions on disease transmission.

In Ontario, 12,000 patients were recorded to have visited healthcare facilities for flu-like symptoms, between April 9 and June 5. Among these patients, 1,819 were identified to have pH1N1. We set up a patch model incorporating the Richards model according to Ontario's public health unit division. We estimated the growth rates and the likely final sizes of pH1N1 outbreaks in three health unit areas in the Greater Toronto Area, as their infected population was large enough to analyze. We analyzed the impact of individuals' movements, between each division, on the dispersal of the disease.

Project Supervisor: Dr. David Fisman
University of Toronto
PhD Advisor: Dr. Xingfu Zou
University of Western Ontario



Epidemic curves for pH1N1 cases reported in the Toronto area, Central East and Central West areas of Ontario, between April 17 - June 6. Solid lines represent real data, while others are estimations from the patch model.

Co-Hub Site Member Biographies:

Vancouver, Montreal & Toronto

Vancouver

Babak Pourbohloul PhD

Dr. Pourbohloul's research interests center around modeling the transmission dynamics of infectious diseases and the impact of different control strategies on disease dynamics, the results of which aid in designing optimal public health and infection control policy. He received his PhD in theoretical physics (Nonlinear Dynamics, Complex Systems, and Chaos Theory) from Laval University and now applies mathematics and computer simulations to the study and control of various communicable diseases. Dr. Pourbohloul is currently serving as the Chair of the CIHR-funded Canadian Consortium for Pandemic Preparedness Modeling (CanPan), a national mathematical modeling network formed to address pressing issues related to influenza and other emerging infections preparedness. He also acts as the CIHR spokesperson on issues related to mathematical modeling and parameter estimation of pandemic (H1N1) 2009.

Dr. Pourbohloul currently leads and is actively involved in several research projects: modeling the transmission dynamics of sexually-transmitted diseases such as HIV, syphilis, and chlamydia in sexual networks; modeling the spread of blood-borne pathogens such as hepatitis C virus among injection drug users; developing and applying mathematical models to design policy to control the spread of various vaccine-preventable infections such as pertussis and human papillomavirus (HPV) infection; and modeling transmission dynamics of nosocomial infections in healthcare settings.

Montreal

David L. Buckeridge MD, PhD, FRCPC

Dr. David Buckeridge is an Assistant Professor of Epidemiology and Biostatistics at McGill University in Montreal where he holds a Canada Research Chair in Public Health Informatics. He is also a Medical Consultant to the Montreal Public Health Department and the President of the International Society for Disease Surveillance. Dr. Buckeridge has consulted on surveillance to groups such as the Institute of Medicine and the World Health Organization. He has an MD from Queen's University in Canada, an MSc in Epidemiology from the University of Toronto, and a PhD in Biomedical informatics from Stanford University. Dr. Buckeridge is also a Fellow of the Royal College of Physicians and Surgeons of Canada with specialty training in Community Medicine.

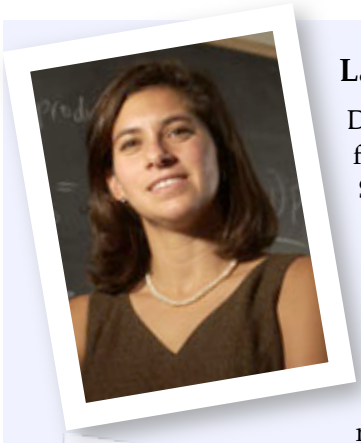
Dr. Buckeridge's research focuses on using advanced computational methods to detect and respond to disease epidemics in healthcare institutions and in the community. This research includes identifying individual cases of disease using automated health information systems, detecting epidemics in the pattern of individual cases, and providing real-time decision support to facilitate the management of epidemics. The goal of Dr. Buckeridge's research is to understand how epidemics spread in populations and how information systems can be used to help monitor and contain epidemics.

Toronto

David Fisman MD, MPH, FRCP(C)

Dr. David Fisman is an Associate Professor and holds the chair in Infectious Diseases Epidemiology at the Dalla Lana School of Public Health at the University of Toronto. He received his MD degree from the University of Western Ontario and an MPH from Harvard School of Public Health; he also completed fellowships in clinical infectious diseases and health policy within the Harvard system. He was Assistant Professor of Epidemiology at Drexel University School of Public Health in Philadelphia from 2003-2006 and in 2005-2006 he served as a Visiting Scholar and Visiting Assistant Professor at the Center for Health and Wellbeing at Princeton University. Dr. Fisman's research interests involve the application of novel epidemiologic methods to the study of infectious diseases of public health importance, including vaccine-preventable diseases, sexually transmitted infections and bacterial respiratory pathogens. He is currently a member of the CIHR supported Canadian Consortium for Pandemic Preparedness Modeling (CanPan) and Pandemic Influenza Outbreak Research Modeling Team (PanINFORM).

Member Biographies

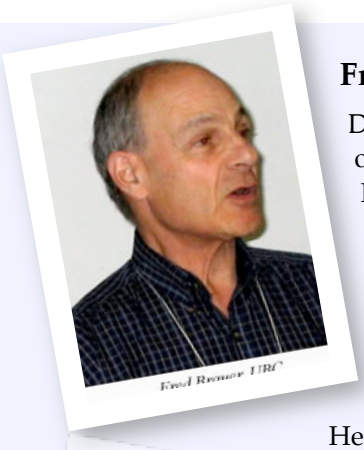


Lauren Ancel Meyers PhD

Dr. Lauren Ancel Meyers received her BA degree in Mathematics and Philosophy from Harvard University in 1996 and her PhD from the Department of Biology at Stanford University in 2000. After completing a postdoctoral fellowship supported by the National Science Foundation and the Santa Fe Institute, she joined the faculty of Integrative Biology at the University of Texas at Austin in 2003, where she is now an Associate Professor. She has also been an active member of the external faculty of the Santa Fe Institute since 2003. Dr. Ancel Meyers' research lies at the interface of evolutionary biology and epidemiology. She has developed new network-based mathematical methods to study the interplay between disease transmission dynamics, human behavior and the evolution of pathogens including those responsible for epidemic meningitis, influenza, walking pneumonia, and SARS. Her research has been funded by research grants from National Institutes of Health (MIDAS), the National Science Foundation, Canadian Institutes of Health Research and the James S. McDonnell Foundation. The Wall Street Journal, Newsweek, the BBC and other news sources have highlighted her work; and a number of government agencies have sought Dr. Ancel Meyers' expertise, including the Centers for Disease Control and Prevention (CDC), the Biomedical Advanced Research and Development Authority (BARDA), the British Columbia Centre for Disease Control (BCCDC), the US National Intelligence Council, Los Alamos National Labs, and Lawrence Livermore National Labs. In 2004, the MIT Technology Review named Dr. Ancel Meyers as one of the top 100 global innovators under age 35.

Chris Bauch PhD

Dr. Chris Bauch is an Associate Professor of Mathematics at the University of Guelph. He is a specialist in mathematical models of infectious disease transmission (dynamic models) and has experience in a broad range of modeling techniques, including differential equations, agent-based computer simulations, spatial models, stochastic models and network models. Dr. Bauch is interested in using models to assess the impacts of vaccination and other control strategies, incorporation of human behavioral elements into transmission models and economic evaluation of infectious disease interventions. He has worked extensively with epidemiologists, health economics, physicians and public health researchers from both government and industry on various interdisciplinary collaborations. He has published 36 peer-reviewed papers, serves as an Associate Editor for *BMC Infectious Diseases*, and is on the editorial board for *Computational and Mathematical Methods in Medicine*.



Fred Brauer PhD

Dr. Fred Brauer obtained his BA in Mathematics and Physics from the University of Toronto. He completed both his MSc and PhD, in Mathematics, at Massachusetts Institute of Technology. Dr. Brauer is currently a Professor Emeritus at the University of Wisconsin-Madison, an Honorary Professor at the University of British Columbia and a Research Professor at Arizona State University.

Dr. Brauer has authored and co-authored 130 research papers on differential equations, mathematical population biology, and mathematical epidemiology. He has edited one textbook and co-authored four others.

Dr. Brauer's work focuses on modeling disease dynamics, epidemiology and population biology. He formulates mathematical models and analyzes their qualitative behavior. Dr. Brauer is particularly interested in models for sexually transmitted diseases, which incorporate behavioral effects but are still reasonably tractable. Since experiments in this area are difficult to design and may be constrained by ethical considerations, models play an important role and may help to indicate strategies for disease control through treatment and/or education.

Jessica Conway PhD

Dr. Jessica Conway obtained her PhD in Applied Mathematics from Northwestern University in 2008. Dr. Conway's dissertation thesis focused on modeling complex patterns in oscillatory systems. Upon completion of her PhD, Dr. Conway began a postdoctoral fellowship, jointly supervised by Dr. Babak Pourbohloul in the Division of Mathematical Modeling at the UBCCDC, and by Dr. Daniel Coombs in the Department of Mathematics at the University of British Columbia. As part of Dr. Pourbohloul's team she worked on problems in both HIV and influenza epidemiology. In addition, while under the supervision of Dr. Coombs, she has studied problems in mathematical immunology and infectious diseases, specifically with regards to HIV.

Currently, Dr. Jessica Conway works in the Mathematical Biology group in the Department of Mathematics at the University of British Columbia under the supervision of Dr. Daniel Coombs. Her research interests center around mathematical immunology and epidemiology, infectious disease modeling and the applications of nonlinear dynamics to problems in pattern formation.

Bahman Davoudi PhD

Dr. Bahman Davoudi Dehaghi is a Research Associate with the Division of Mathematical Modeling at the University of British Columbia Centre for Disease Control (UBCCDC). Dr. Davoudi received his PhD in condensed matter physics from Sharif University and Technology in Tehran, Iran. Initially, Dr. Davoudi completed a 3-year postdoctoral fellowship at Scuola Normale Superiore in Pisa, Italy. He later went on to complete a second fellowship with the Department of Physics of Sherbrooke University in Sherbrooke, Quebec.

Dr. Davoudi's current research interests focus on the mathematical modeling of disease spread within specific subsets of the population. He is interested in modeling and developing an analytical or numerical methodology capable of examining both the dynamical and statistical aspects of disease spread. Furthermore, this methodology will provide an estimate of the speed and the configuration of disease spread, thus facilitating the development of an effective intervention plan.

Charmaine Dean PhD

Dr. Charmaine Dean is Professor and Burnaby Mountain Research Chair in the Department of Statistics and Actuarial Science at Simon Fraser University (SFU). Her research interest lies in the development of methodology for disease mapping, longitudinal studies, the design of clinical trials, and spatio-temporal analyses. Recently, Dr. Dean's focus has been the study of climate change impacts, particularly in the area of forestry.

Dr. Dean received her BSc from the University of Saskatchewan in 1980, and her MMath and PhD degrees from the University of Waterloo in 1984 and 1988. She was President of the Statistical Society of Canada, the International Biometrics Society (Western North American Region) and the Biostatistics Section of the Statistical Society of Canada. Dr. Dean has given seven years of service to the Natural Sciences and Engineering Research Council of Canada and has served in governance at SFU in many capacities in addition to playing a major role in establishing the Faculty of Health Sciences in her capacity of Associate Dean of that faculty.

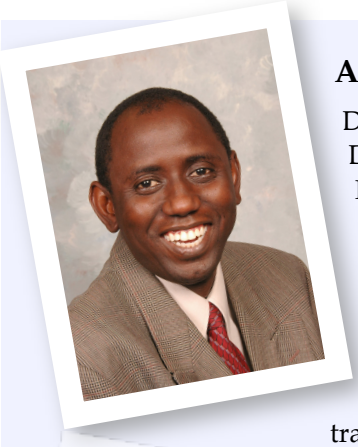
Jonathan Dushoff PhD

Dr. Jonathan Dushoff is a theoretical biologist at McMaster University in Hamilton, Ontario. He has broad interests in modeling the evolution and spread of infectious diseases, with a particular focus on applications to human public health. He uses a wide range of quantitative approaches, from epidemiological statistics, to dynamical modeling, to genomic analysis. Diseases of current interest in the Dushoff lab include influenza, HIV and rabies.

Dr. Dushoff was born and raised in Philadelphia, Pennsylvania. He has a BA in Mathematics and Environmental Studies from University of Pennsylvania, and a PhD in Ecology from Princeton University. He has also done graduate work at Cornell University and a postdoctoral fellowship at Academia Sinica in Taipei, Taiwan. He served as a volunteer for the United States Peace Corps in Swaziland from 1987-1989 and as Research Director for Ralph Nader's 2000 Green Party campaign for President of the United States.

David Earn PhD

Dr. David Earn is a Professor of Mathematics in the Department of Mathematics and Statistics at McMaster University, where he has been based since January 2000. While at McMaster, Dr. Earn has been a recipient of a CIHR New Investigator Award and an Ontario Premier's Research Excellence Award and he currently holds a J. S. McDonnell Foundation Research Award. Dr. Earn is the founder and curator of the International Infectious Disease Data Archive (IIDA), which makes a wide variety of infectious disease data easily accessible online. He combines analysis of historical data with mathematical modeling in order to learn from previous epidemics and contribute to the development of improved infectious disease control strategies for the future.



Abba Gumel PhD

Dr. Abba Gumel is a full Professor in the Department of Mathematics and the Director of the Institute of Industrial Mathematical Sciences (IIMS), University of Manitoba. Dr Gumel received BSc and PhD degrees from Bayero University in Kano, Nigeria and Brunel University in London, England, respectively. Dr. Gumel's main research interests are in mathematical biology, nonlinear dynamical systems and computational mathematics. The main objective of his research work is to use mathematical theories and methodologies to gain insights into dynamical systems arising from the mathematical modeling of phenomena in the natural and engineering sciences, with emphasis on the transmission and control dynamics of human diseases of public health interest. Dr. Gumel has supervised a number of research students (NSERC-funded summer undergraduate and graduate students) and postdoctoral fellows and has recently received several awards for research and outreach excellence.

Nathaniel Hupert MD, MPH

Dr. Nathaniel Hupert is a primary care internal medicine specialist and a researcher in public health emergency response and medical decision-making. He is an Associate Professor of Public Health and Medicine at Cornell University's Weill Medical College in New York City, and was the founding Director and current Senior Medical Advisor for the Preparedness Modeling Unit of the U.S. Centers for Disease Control and Prevention (CDC) in Atlanta, Georgia. He trained at Harvard Medical School, the University of Pittsburgh Medical Center and the Harvard School of Public Health.

His research concerns a number of topics that fall under the heading of "computational public health", the application of mathematical and simulation modeling techniques to health problems that extend beyond the bounds of traditional epidemiology. Since September 2000, he has collaborated with local, State, Federal, and international public health officials in a series of federally financed research projects on hospital and clinical preparedness for bioterrorism.

Salah Mahmud MD, PhD

Dr. Salah Mahmud received his PhD from the University of Manitoba in 2009. His thesis centered on the use of non-steroidal anti-inflammatory drugs and prostate cancer risk. Dr. Mahmud has received a number of awards for his leading research as a doctoral student; he was the recipient of the Governor General's Gold Medal from the University of Manitoba. He was also awarded a University of Manitoba Distinguished Dissertation Award. The Distinguished Dissertation Awards are given annually to recognize doctoral graduates who have made groundbreaking novel contributions to their academic discipline.

Currently, Dr. Mahmud is a Medical Officer of Health in Winnipeg and an assistant professor at the Department of Community Health Sciences, University of Manitoba. His areas of research include communicable disease epidemiology and modeling.

Rafael Meza PhD

Dr. Rafael Meza is a Research Scientist with the Division of Mathematical Modeling at the University of British Columbia Centre for Disease Control (UBCCDC). Dr. Meza received his BSc in applied mathematics from the Instituto Tecnológico Autónomo de México (ITAM) and his PhD in applied mathematics from the University of Washington (Seattle). Dr. Meza completed a 2-year postdoctoral fellowship in the Program in Biostatistics and Biomathematics at the Fred Hutchinson Cancer Research Center prior to joining the UBCCDC.

Dr. Meza's research interests lie at the interface of biomathematics, biostatistics and epidemiology. In particular, he is interested in the analysis of cancer epidemiology using mechanistic models of carcinogenesis. He is also interested in the mathematical modeling of infectious disease dynamics and its applications on public health policy design. Dr. Meza's long-term goal is to develop methodologies to evaluate the effects of infectious disease dynamics on the risk of cancers with infectious disease origins.

Steven Riley PhD

Dr. Steven Riley studies the infectious disease dynamics of human pathogens. He has worked mainly on outbreak systems using both mathematical models and data from empirical studies to investigate interesting "ecological" questions that are relevant to public health: what made SARS controllable when HIV was not? Would mass vaccination be a good response to the re-emergence of smallpox in the United Kingdom? Would it make sense to implement dose-splitting strategies for vaccines during a severe pandemic? How can you reduce the risk of emergence of antiviral resistance during a global influenza outbreak? How much was the transmission of pandemic influenza reduced during school vacations?

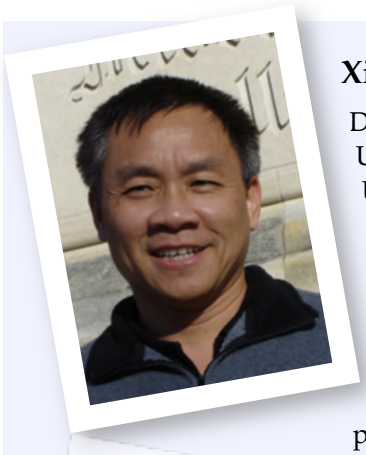
Steven received a DPhil in Zoology at Oxford University before completing a postdoctoral fellowship in the Department of Infectious Disease Epidemiology at Imperial College London. He is currently an Assistant Professor in the School of Public Health at the University of Hong Kong. Outside of work, he enjoys sailing, cycling, and basketball.

Pauline van den Driessche PhD

As an applied mathematician, Dr. Pauline van den Driessche's research in mathematical epidemiology is interdisciplinary and is done with collaborators and students. Dr. van den Driessche is a core investigator on the MITACS team "Transmission Dynamics and Spatial Spread of Infectious Diseases: Modelling, Prediction and Control" led by Jianhong Wu of York University. Some of Dr. van den Driessche's current research projects include disease transmission models that are appropriate for influenza, West Nile virus and Bluetongue virus, whereas previous models considered are appropriate for hantavirus, HIV/AIDS, SARS, gonorrhea and bovine tuberculosis. Some models include control strategies (e.g., vaccination and antiviral drugs for influenza) and aim to address questions relevant to public health. She has helped to organize workshops and graduate summer schools on disease modeling. Notes from these summer schools are collected in a Springer volume published in 2008 that is edited by Drs. Brauer, Wu and van den Driessche.

Jianhong Wu PhD

Dr. Jianhong Wu is a senior Canada Research Chair in Industrial and Applied Mathematics and the President of the Canadian Industrial and Applied Mathematics Society. He is a founding member and the Director of the MITACS Centre for Disease Modelling, and has lead Canadian and international research projects on infectious disease modeling and geo-simulations including those funded by MITACS, GEOIDE, IDRC and CRC. He has been participating in various pandemic influenza modeling projects and has been involved in the organization of a pandemic influenza modeling workshop series.



Xingfu Zou PhD

Dr. Xingfu Zou obtained a Bachelor degree in mathematics from Zhongshan University (China) in 1983, a Master degree in applied mathematics from Hunan University (China) in 1989 and his PhD from York University in 1997. Dr. Zou was an NSERC postdoctoral fellow conducting research at the University of Victoria and Georgia Institute of Technology until joining Memorial University in January 1999. In January 2004, he joined the University of Western Ontario and he is now a full professor at the Department of Applied Mathematics. Dr. Zou's research interests are centered around modeling disease dynamics, at both the population and host levels, using differential equations. He has published his results on applied dynamical systems and mathematical biology in noteworthy journals. Currently, he is a co-editor-in-chief of the journal of Differential Equations and Dynamical Systems, and associate editor of four other journals. He received a Petro-Canada Young Innovator Award in 2002, and Premier's Research Excellence Award (Ontario) in 2005.

We would also like to acknowledge the thoughtful contribution of **Junling Ma** of the University of Victoria and **Michael Wolfson** from Statistics Canada, whose biographies were not available at the time of print.

Intern Biographies

Katia Charland PhD

Katia M. Charland received her doctorate from McGill University's Department of Epidemiology, Biostatistics and Occupational Health under the co-supervision of Drs. Russell Steele and Christina Wolfson. Her PhD thesis (Biostatistics) focused on the accuracy of Bayesian spatio-temporal models in identifying high-risk areas in the context of small-area studies/disease mapping.

Her postdoctoral research at Children's Hospital Boston/ Harvard Medical School, co-supervised by Drs. John Brownstein and David Buckeridge, examined the impact of environmental factors on the spatio-temporal patterns of seasonal influenza transmission. More recently, using medical billings claims for visits to outpatient clinics and emergency departments in Montreal, she examined the relationship between social and material deprivation and healthcare utilization rates for influenza and found lower rates in the more socially deprived populations but no meaningful association between rates of utilization for influenza and material deprivation. In addition, using the same data, she examined the relative risk of influenza in an urban First Nations reserve using adjacent neighborhoods as a reference region and found elevated rates among residents of the reserve.

Ben Dalziel PhD Student

Ben Dalziel is a PhD student in the Department of Ecology and Evolutionary Biology at Cornell University, advised by Dr. Stephen Ellner. His dissertation work focuses on the emergence of conserved spatial patterns in population dynamics from individual behavior. In an effort toward a general account of this phenomenon the research considers two disparate study systems: the spread and evolution of influenza H1N1 in Canadian cities during the 2009 pandemic, and caribou migration patterns in northern Quebec. Ben obtained his BSc in ecology and mathematics at the University of Guelph, where he stayed to do a master's thesis with Dr. John Fryxell on the influence of landscape structure and spatial memory on the movement patterns of elk. Before starting his PhD he worked as a research scientist with the Ontario Ministry of Natural Resources on the ecology of boreal forest fires, examining the dialogue between forest community structure and fire behavior across space, time and scale of observation.

Cindy Feng PhD Student

Cindy Feng is currently perusing her PhD in the Department of Statistics and Actuarial Science at Simon Fraser University (SFU). She received a BSc in applied mathematics from Beijing University of Technology and an MSc in statistics from SFU.

Cindy's research interests are in the areas of developing methods for disease surveillance in spatial disease mapping and infectious disease modeling. Her research at SFU focuses on the identification of regions with high or low mortality rates and on cluster identification for functional data in disease mapping.

While at the UBCCDC her project focused on the estimation of the basic reproduction number of an emergent disease from both the dynamical and statistical perspective of disease spread, which is crucial for designing adequate intervention strategies.

Jennifer Lindquist PhD Student

Jennifer Lindquist is a PhD student in applied mathematics at the University of Victoria. She completed an undergraduate science degrees in Biology and Mathematics, and a Master of Science in mathematics. Her MSc work began with the collection and analysis of survey data regarding syringe sharing risk behaviors; her thesis culminated with a data-informed model of infectious disease transmission among persons using injection drugs in Victoria.

Jennifer believes strongly in the importance of inter- and transdisciplinary work as a foundation for maximizing the benefits of mathematics in public health research. In her case, this work includes encouraging public education and discussion, participating in academic collaboration, and frontline service provision with AIDS Vancouver Island's (AVI) Street Outreach Services as a harm reduction worker. Disparities between evidence-based recommendations and actual policy - especially as applied in the health of marginalized persons - motivate Jennifer's particular interest in striving to increase functional communication and mutual understanding between public health and the sciences.

Samit Bhattacharya PhD

Dr. Samit Bhattacharya received his PhD in 2006 from the University of Calcutta, India. During his PhD he worked on mathematically modeling pest management problems, with special emphasis on microbial control of pest populations. From 2007 to 2008, he was a DBT-postdoctoral fellow at the Centre for Cellular and Molecular Biology in India; while there he studied the role of life-history traits of insects in host-pathogen dynamics.

Currently, Samit is working as a postdoctoral fellow in Mathematics and Statistics at the University of Guelph. His main research focus is modeling infectious diseases, with special emphasis on individual vaccinating behavior, using the game theoretic approach.

His research interests cover a wide range of infectious disease modeling and use various mathematical and simulation approaches. His research interests also include the in-host modeling of pathogen dynamics, such as co-infection by multiple pathogens within a host. Additionally, Samit is interested in modeling ecological systems (for example, the evolution of predator-prey dynamics in spatial structure).

Mike Delorme MSc Student

Mike Delorme is an MSc student in the Mathematical Biology Research Group at McMaster University supervised by Drs. Jonathan Dushoff and David Earn. He went to Queen's University and in 2008 graduated with a BScH through the Mathematical Biology program. For Mike's 4th year honors thesis he developed and analyzed an evolutionary model of the adaptive coral bleaching hypothesis.

At McMaster he is a member of the Biology Graduate Society and the Mathematical Biology Research Group. Mike has participated in significant Bio-Math workshops at the University of Alberta and the University of Ottawa as well as pandemic influenza workshops. In the summer of 2009 he was a MITACS ACCELERATE Intern in the Centre for Infectious Disease Prevention and Control of PHAC under Dena Schanzer. The title of the four-month research project was "Model predictions of the effects of vaccination on the epidemic growth rate of seasonal influenza epidemics".

Venkata Duvvuri PhD

Dr. Venkata Duvvuri received his PhD in Zoology from Osmania University, Hyderabad, India in 2005. Upon completion of his PhD he received a postdoctoral fellowship in the Department of Epidemiology and Preventive Medicine at the University of Maryland, Baltimore. In July 2006, he accepted a postdoctoral fellowship (Epidemiology and Biology), with Prof. Jianhong Wu, at the Centre for Disease Modelling (MITACS-CDM) at York University in Toronto.

Dr. Duvvuri has conducted research on emerging infectious diseases, such as avian influenza (H5N1), seasonal influenza (H3N2, H1N1), swine influenza (2009 H1N1), and *Neisseria meningitidis*, as well as on vector-borne diseases. Dr. Duvvuri's particular research interests are in the areas of overlap between immunology, epidemiology, medical entomology, ecology and evolutionary biology of emerging infectious diseases and vector-borne diseases. Further, he has interest in developing the theoretical models for understanding the intervening disease mechanisms at population and cellular levels for pathogens and/or vectors and/or hosts.

Masoumeh Izadi PhD

Dr. Masoumeh Izadi completed her PhD in Computer Science, Artificial Intelligence at McGill University in 2007. Prior to commencing her PhD, Masoumeh completed an MSc in Advanced Computing at King's College University of London (UK) and a BSc in Applied Mathematics at the University of Tehran (Iran).

Since graduation Masoumeh has been working as a postdoctoral fellow within the McGill Clinical and Health Informatics research group. Her postdoctoral research, under the supervision of Dr. David Buckeridge, is mainly concerned with the development and application of methods to improve public health surveillance. Modeling the decisions faced by surveillance systems for providing warning to public health personnel is essential for the prevention and control of epidemics. Forecasting and visualizing the likely evolution of epidemics is necessary so that public health personnel can assess and organize the necessary clinical and public health resources.

Kin On Kwok PhD

Dr. Kin On Kwok obtained his PhD from the University of Hong Kong in 2008. His research interests focus on the study of infectious disease dynamics, specifically outbreak pathogens such as SARS and influenza. He uses both mathematical models and empirical data to address research questions that are relevant to public health. Some of the questions Dr. Kwok has investigated are: what are the magnitudes of different routes of transmission among patients, healthcare workers and visitors in the hospital outbreak of SARS in one acute hospital in 2003? What is the optimal way to allocate antiviral drugs at the household level (treatment versus prophylaxis) to reduce the mortality in an influenza pandemic?

Tufail Malik PhD

Tufail Malik obtained his PhD in Microbial Quiescence from Arizona State University in 2007 and an MSc in Mathematics and Computer Science from Ohio University in 2002.

From 2007 to 2009 Tufail worked as a McCain Postdoctoral Research Associate at Mount Allison University. Currently, he is working as a research associate within the Department of Mathematics at the University of Manitoba. His research focuses on building and analyzing ordinary differential equation models of photosynthetic machinery to investigate the evolution and ecology of phytoplankton with different light harvesting and resource allocation strategies aimed at acclimation to changing irradiance levels. The results of this work will be used to predict how marine primary producers (essentially microscopic plants) will respond to changing temperatures and ocean circulation. This is essential to understanding feedbacks between climate change and life on Earth.

Dr. Malik's other research interests include microbial quiescence, pandemic H1N1 influenza virus, and West Nile virus.

Flavia Moser PhD

Dr. Flavia Moser received her MSc in Computing Science from Ludwig-Maximilians-Universität in Munich. She completed her PhD in Computing Science at Simon Fraser University (SFU). Her dissertation was mainly concerned with the development of algorithms for the analysis of networks. During her time at SFU she was involved in several interdisciplinary research projects. As a research assistant for the Institute for Canadian Urban Research Studies (ICURS) she worked on the development of a crime data warehouse. Flavia also worked in collaboration with microbiologists on a research project that focused on finding modules in protein-protein interaction networks.

Dr. Moser has authored several peer-reviewed publications mainly in data mining and computational biology. During her internship at Microsoft Corporation in Redmond, WA she became co-inventor on a patent filed by Microsoft Corporation.

Following her CanPan internship, she has continued to work with UBCCDC, in the Division of Mathematical Modeling (DMM), as a Research Scientist. Within the DMM Flavia's work centers on modeling contact networks and the spread of disease within such networks.

Heidi Muller MSc

Heidi completed her undergraduate degree in Physical Science at the University of Guelph in Guelph, Ontario. She recently obtained her MSc in Applied Mathematics from the University of Guelph in December 2009. Her MSc thesis examined the significance of including sexual partnership dynamics in two transmission models for human papillomavirus (HPV). Heidi co-authored a peer-reviewed publication with her MSc advisor, Dr. Chris Bauch, based on her MSc work.

During her internship at the UBCCDC her project focused on including a human behavioral component in a transmission model for pandemic H1N1. The role of behavior may be an important factor in the model and may influence healthcare decisions.

Heidi's research interests are in the area of developing mathematical models of emerging and re-emerging infectious diseases as well as implementing preventative strategies. She is enthusiastic about using mathematical models and is curious to see where this research will lead her.

Carly Rozins PhD Student

Carly Rozins obtained an honors degree in Biological Sciences and a minor in Mathematics from the University of Guelph in Guelph, Ontario. Carly went on to do an MSc in Mathematics at Queen's University in Kingston, Ontario. Her supervisor at Queen's was Dr. Peter Taylor, and her primary research focus was on stochastic models and parameter fitting.

Currently, Carly is a PhD student at the University of British Columbia Okanagan in Kelowna, BC. She is studying mathematical biology under the supervision of Dr. Rebecca Tyson. Dr. Tyson and Carly are currently developing a bobcat-hare, predator-prey model to investigate how bobcats are able to persist in forestry-dominated landscapes that are experiencing rapid changes in depths and durations of snow-cover.

Ashleigh Tuite MSc, MPH

Ashleigh Tuite recently completed her MPH in Epidemiology at the University of Toronto. She previously obtained her MSc in Biochemistry from McGill University, where her research focused on the genetic basis of infectious diseases. She is currently a Research Officer at the Dalla Lana School of Public Health at the University of Toronto, where she has been involved in the development of mathematical models of pandemic H1N1 influenza and sexually transmitted infections.

Aman Verma PhD Student

Aman Verma's academic career began with a Bachelor's degree in Computer Science; in recent years he has become interested in health-related fields. After finishing his Bachelor's degree, he worked on an internship for the Pan-American Health Organization in Suriname, where he built the national HIV / AIDS database and developed a surveillance system for infectious disease. This experience sparked Aman's interest in applying computer techniques in health-related fields, ultimately leading to his decision to enrol in the Master of Health Informatics program at Dalhousie University.

While at Dalhousie, Aman developed a web tool for pharmacists to record health-related indicators for diabetes. Soon after, he became a research assistant in Dr. David Buckeridge's Surveillance Lab at McGill University. Aman became involved in a wide variety of projects, including using syndromic surveillance to detect anthrax attacks, developing models to predict fall-related injury from psychotropic drug use, and evaluating the utility of spatial surveillance in tuberculosis. Currently, Aman is a PhD student in Epidemiology at McGill, where he is developing an agent-based simulation of outbreaks of cryptosporidiosis in the water systems of Montreal.

Yanyu Xiao PhD Student

Yanyu Xiao is a PhD candidate in Applied Mathematics at the University of Western Ontario. Yanyu also completed her MSc. in Applied Mathematics at the University of Western Ontario (2007) and received a BSc from Hunan University in Changsha, China (2006).

Her research interests focus on the mathematical analysis of the dynamic behaviors of vector-borne diseases such as malaria and influenza. She uses various mathematical techniques, such as ODEs, DDEs, and PDEs, to derive models for the spread, outbreak and control of these diseases. Yanyu is also concerned with how disease latency and the spatial mobility of individuals, during the latent period, jointly affect disease dynamics. The purpose of this is to determine effective ways to prevent and control these diseases.

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