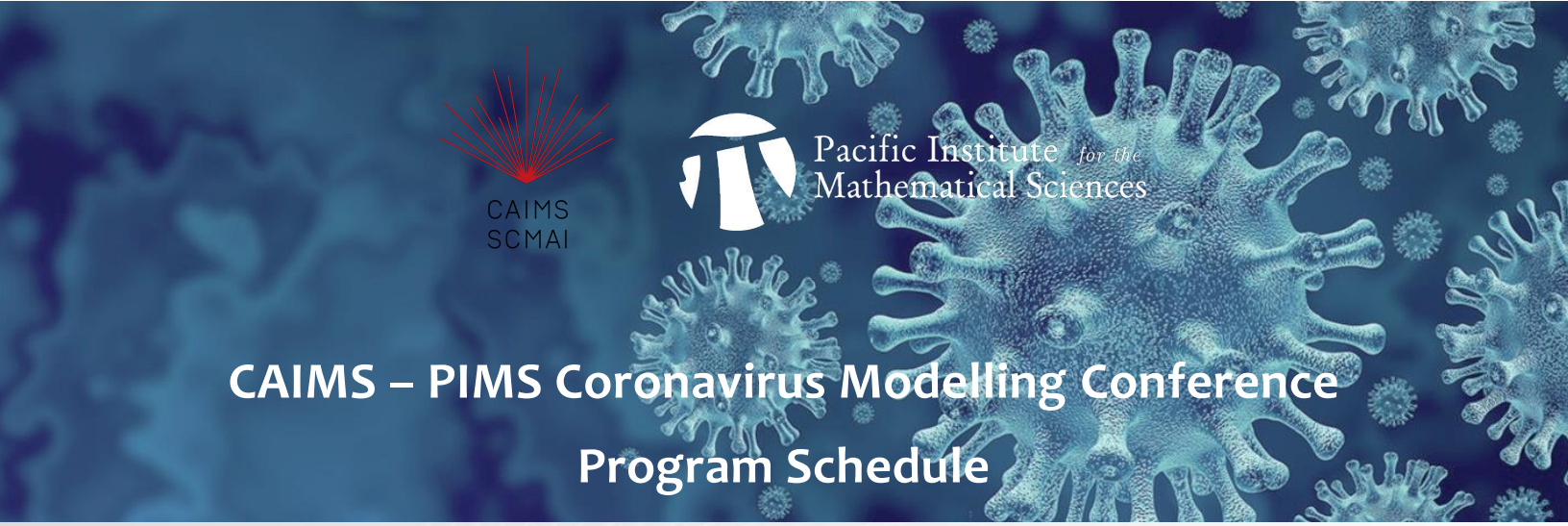


CAIMS – PIMS Coronavirus Modelling Conference

Program Schedule

Image Credit: www.paho.org

June 22 - 24, 2020

*All times indicated in Pacific Standard Time (PST)

About this Conference:

The mathematical modelling of SARS-CoV-2 infection and the spread of the disease COVID-19 is focussing on two major objectives. The first one is to understand and manage the epidemiology of the disease. To understand the transition of the epidemic through the society, to forecast the impact of social distancing and other measures, and to help manage the outbreak on the global and local scales. Secondly, modellers are interested in the within-host dynamics of the virus. How does the virus enter the body, how does it spread, how does it interact with the immune system, how does it react to medications, and how does it lead to death in critical cases? Linking the scales, there are people studying the physical transmission characteristics though aerosols, droplets or direct contact.

The modelling tools used to investigate these questions of COVID-19 epidemiology and physiology include a wide range of methods such as individual based models, stochastic models, statistical analysis and machine learning, and differential equation models. These models become more refined as more and more COVID-19 data become available. The community works closely with clinicians and experimentalists, with access to current data. Many of the research groups have made progress and some sophisticated models have been presented on preprint servers. Now is the right time to bring researchers together to exchange ideas and to learn from each other. COVID-19 models are published on a weekly basis and it is difficult to keep track. This conference will help us to paint a fuller picture of the activities, and to critically discuss alternative approaches. It will allow us to exchange data and expertise, and to connect to governments and the public.

Conference Format:

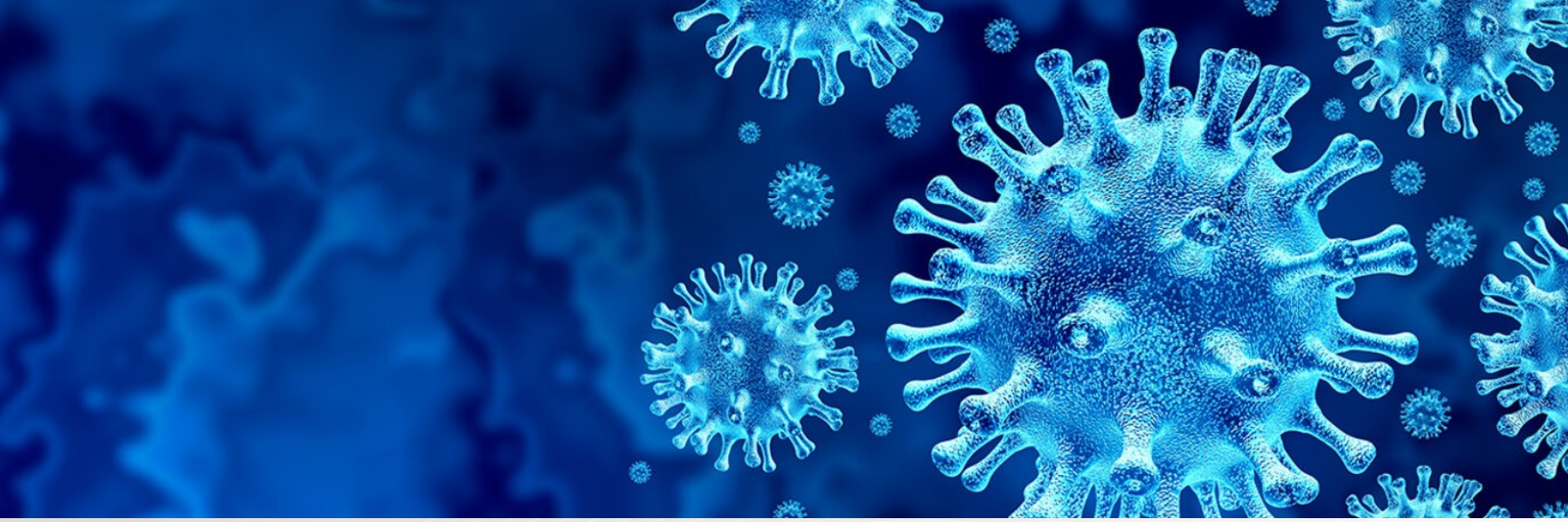
The event runs over two and half days with eight different sessions and more than 25 speakers from around the globe.

- There are three sessions per day, beginning at 8:00am; 11:00am and 2:00pm PST
- Each session is 2.5 hours long, consisting of:
  - 3-4 talks of 30 min each
  - 30 min of Q & A
- Registered participants will receive their specific meeting link and can join any session, on any day during the event.

We look forward to hosting this meeting and thank our sponsors, PIMS and CAIMS, for their support.

Dr. Thomas Hillen, University of Alberta;
Dr. Daniel Coombs, University of British Columbia;
Dr. Morgan Craig, Université de Montréal & Centre de Recherche Mathématique.

Event Webpage: https://www.pims.math.ca/scientific-event/200622-cpcmc



Monday June 22nd

0800 – 1030: Session I (Data)

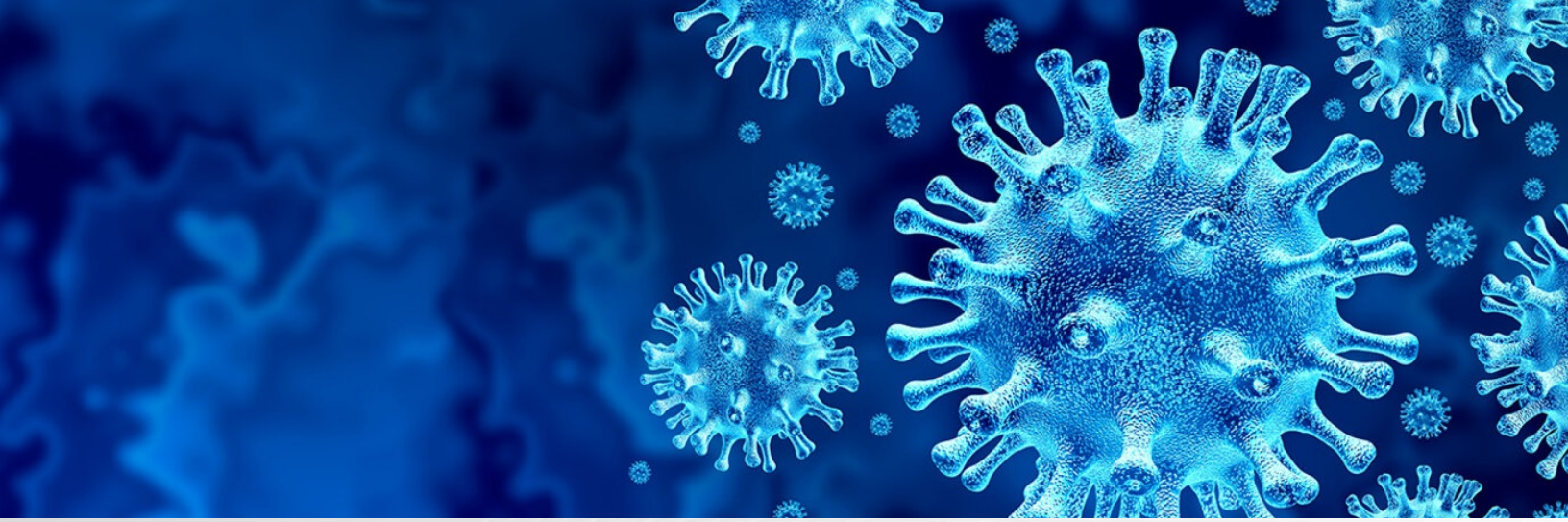
- **Dean Karlen**, University of Victoria & TRIUMF
  Characterizing the spread of COVID-19 in Canada and the USA.
- **Ruian Ke**, T-6 & Los Alamos National Laboratory
  Fast spread of SARS-CoV-2 in China, Europe and the US.
- **Ashok Krishnamurthy**, Mount Royal University
  Spatiotemporal Transmission Dynamics of COVID-19 in Spain.
- **Jody Reimer**, University of Utah
  Impacts on community transmission and disease burden of a clinical prediction tool to prioritize limited COVID testing.

1100 – 1330: Session II (Interventions I)

- **Marco Tulio Angulo**, Universedad Nacional Autónoma de México
  A simple criterion to design optimal nonpharmaceutical interventions for epidemic outbreaks.
- **Joost Joritsma**, University of Technology Eindhoven
  Not all interventions are equal for the height of the second peak.
- **Ilyssa Summer**, CarePredict Inc.
  Modeling intervention strategies for containing Covid-19 in Nursing homes with digital contact tracing.
- **Rebecca Tyson**, UBC – Okanagan
  The timing and nature of behavioural responses affect the course of an epidemic.

1400-1600 Session III (Miscellaneous)

- **Ernie Chang**, Consultant
  Epidemiology CovidSimABM: An Agent-Based Model of Contagion.
- **Mayra Nunez Lopez**, Instituto Tecnológico Autónomo de México
  Implementation of quarantine measures accounting for Covid-19 hospital saturation.
- **Mario Santa Cibrian**, Universedad Nacional Autónoma de México
  Flattening the curve and the effect of atypical events on mitigation measures.



Tuesday, June 23rd

800-1030: Session IV (Physiology I)

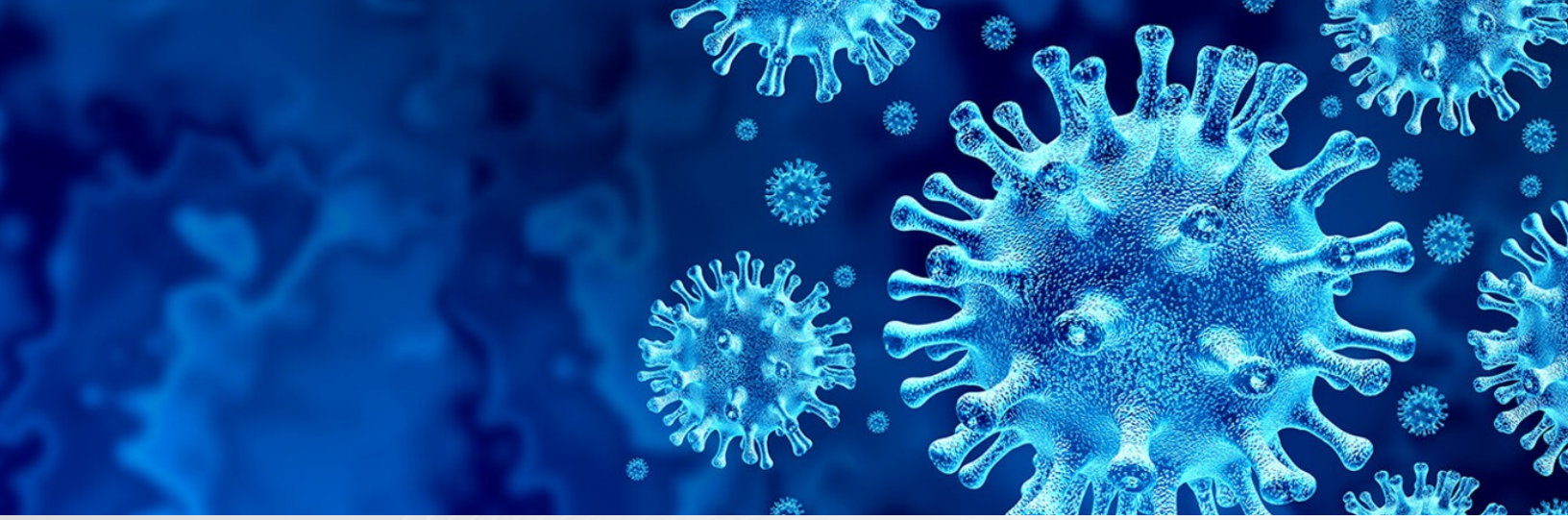
- **Mohit Kumar Jolly**, Indian Institute of Science
  Mechanistic modeling of the SARS-CoV-2 and immune system interplay unravels design principles for diverse clinicopathological outcomes.
- **Esteban A. H. Vargas**, Universedad Nacional Autónoma de México
  In-host Modelling of COVID-19 in Humans.
- **Dennis Hou**, Rutgers University–New Brunswick
  Topological Analysis for Selecting Network Models of Cytokine Dynamics.
- **Sally Otto**, UBC
  Modelling evolutionary epidemiology of COVID-19.

1100-1330: Session V (SIR I)

- **Chunyi Gai**, Dalhousie University
  Localized outbreaks in S-I-R model with diffusion.
- **Ronald Dickman**, Federal University of Minas Ferais
  A SEIR-like model with a time-dependent contagion factor describes the dynamics of the Covid-19 pandemic.
- **Cedric Chauve**, Simon Fraser University
  Modelling the impact of asymptomatic individuals.
- **Jacques Belair**, Université de Montréal
  Latent period distribution and the epidemic curve.

Session VI 1400-1600 (Interventions II)

- **Martin Barlow**, University of British Columbia
  A branching process with contact tracing.
- **Simon de Montigny**, Université de Montréal
  Modelling future biomedical interventions in the COVID-19 epidemic.
- **Mark Lowerison**, University of Calgary
  Calibration of time varying contact compartmental models of SARS-COVID-19.



Wednesday June 24th

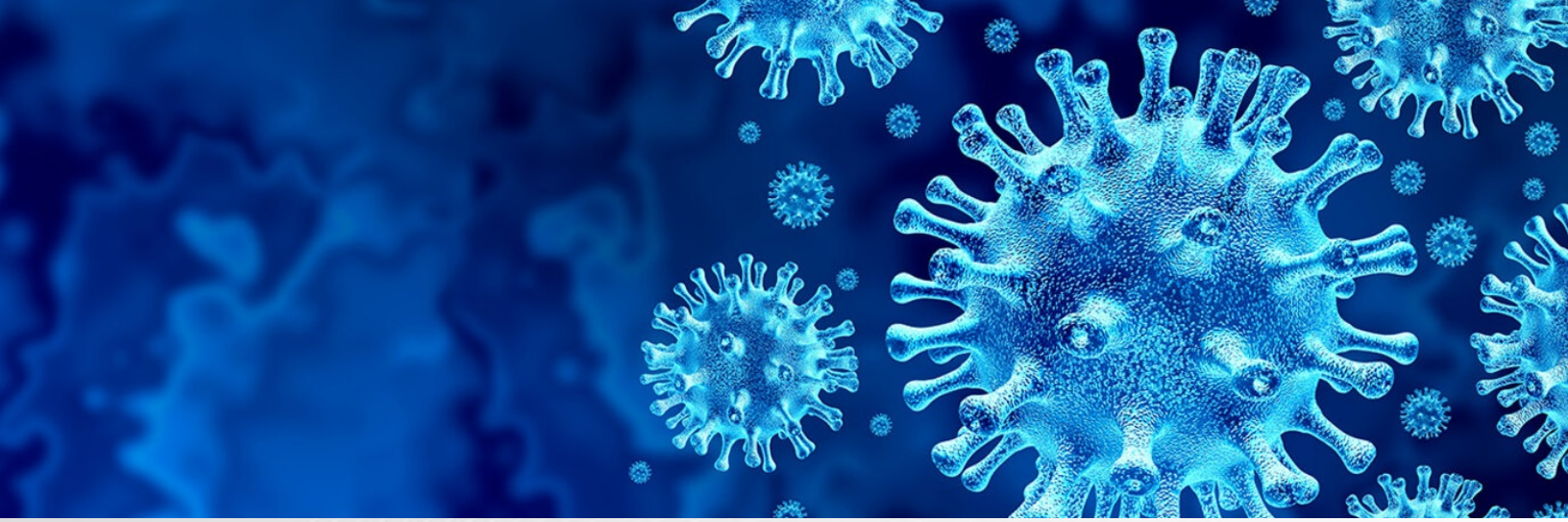
800-1030: Session VII (Physiology II)

Joint Session: Modelling interactions between infection, inflammation, and damage.

- **Penelope Morel**, University of Pittsburgh
  The immune response to SARS-CoV-2: Friend or Foe?
- **Adrianne Jenner**, Université de Montréal, CHU Sainte-Justine Research Centre
  Modelling the systemic and tissue-level immune response to SARS-CoV-2.
- **Jane Heffernan**, York University
  Models for immune system interaction and evolution.
- **Wei Dai*, Rohit Rao*, Anna Sher, CJ Musante, Richard Allen**, Pfizer Inc.
  A Quantitative Systems Pharmacology Model of the Immune Response to SARS-COV-2.

1100-1330: Session VIII (SIR II)

- **Theodore Kolokolnikov,** Dalhousie University
  Law of mass action and saturation in SIR model with applications to coronavirus.
- **Kyeongah Nah,** York University
  Scenario tree and adaptive decision making on optimal type and timing for intervention and social-economic activity changes.
- **Meir Shillor**, Oakland University
  Mathematical model, analysis and simulations of the COVID-19 pandemic with variable infection rate: Application to South Korea.



Speaker Abstracts

Marco Tulio Angulo, Universedad Nacional Autónoma de México
A simple criterion to design optimal nonpharmaceutical interventions for epidemic outbreaks.
To mitigate the COVID-19 pandemic, much emphasis exists on implementing non-pharmaceutical interventions to keep the reproduction number below one. But using that objective ignores that some of these interventions, like bans of public events or lockdowns, must be transitory and as short as possible because of their significative economic and societal costs. Here we derive a simple and mathematically rigorous criterion for designing optimal transitory non-pharmaceutical interventions. We find that reducing the reproduction number below one is sufficient but not necessary. Instead, our criterion prescribes the required reduction in the reproduction number according to the maximum health services' capacity. To explore the implications of our theoretical results, we study the non-pharmaceutical interventions implemented in 16 cities during the COVID-19 pandemic. In particular, we estimate the minimal reduction of the contact rate in each city that is necessary to control the epidemic optimally. We also compare the optimal start of the intervention with the start of the actual interventions applied in each city. Our results contribute to establishing a rigorous methodology to guide the design of non-pharmaceutical intervention policies. Preprint: https://www.medrxiv.org/content/10.1101/2020.05.19.20107268v1

Martin Barlow, University of British Columbia
A branching process with contact tracing
I will look at a simple theoretical model of a standard branching process with branchers removed by a contact tracing procedure. The talk will identify the parameter range in which the contact tracing is able to make the process sub-critical.

Jacques Bélair, Université de Montréal
Latent period distribution and the epidemic curve.
The epidemic curve is influenced by the structure of the latency period in the infected population. Oscillations can be explained by time delays in the governing equations.

Ernie Chang, Consultant
Epidemiology CovidSimABM: An Agent-Based Model of Contagion
This is the prototype of an agent based model for a closed universe of a population experiencing a contagion-based epidemic, in which risk factors, movement, time of incubation and asymptomatic infection are all parameters. The model allows the operator to intervene at any step and change parameters, thus analytically visualizing the effect of policies like more testing, contract tracing, and shelter in place. Under current development, CovidSimMV is an ABM that supports a Multiverse of different environments, in which agents move from one to another according to ticket with stops. Each universe has its own characteristic mix of residents, transients and attached staff, and persons are able to adopt different roles and characteristics in different universes. The fundamental disease characteristics of incubation, asymptomatic infection, confirmed cases will be preserved. The Multiverse model will support a rich

diversity of environments and interpersonal dynamics. These are JavaScript programs that can be run in a browser as HTML files. The code is open source, and available on github.com/ecsendmail.

Cedric Chauve, Simon Fraser University
Modelling the impact of asymptomatic individuals.
We designed a simple SEIR-like model including asymptomatic individuals and we explore a wide grid of parameters related to asymptomatic rate and infectiousness.

Wei Dai*, Rohit Rao*, Anna Sher, CJ Musante, Richard Allen, Pfizer Inc
A Quantitative Systems Pharmacology Model of the Immune Response to SARS-COV-2.
Rapid development of a QSP model to support novel COVID-19 therapies. We intend to publish this model quickly to encourage community feedback. The simulated dynamics of immune response are modeled by describing viral activation of innate and adaptive immune processes involving both pro-inflammatory mediators regulating viral clearance and cell damage (e.g. neutrophils and cytotoxic lymphocytes) as well as counter-regulatory immune suppressive mediators (e.g. Treg cells and IL-10).

Ronald Dickman, Federal University of Minas Ferais (UFMG), Brazil
A SEIR-like model with a time-dependent contagion factor describes the dynamics of the Covid-19 pandemic.
We show how a simple deterministic epidemic model without spatial structure can reproduce the evolution of confirmed Covid-19 case numbers in diverse countries and Brazilian states through use of a time-dependent contagion factor, beta(t). One expects that this function provides a link between the growth rate and mitigation policies. The model inserts a state A (presymptomatic) between states E (exposed) and I (infected) in the usual SEIR model, as well as distinguishing between confirmed and unconfirmed infected. With transition rates fixed at literature values, we vary the four free parameters in beta(t) to obtain a good description of time series of the cumulative number of confirmed cases. We then analyze the relation between changes in the contagion factor, as inferred from the time-series analysis, and mobility indexes based on cell-phone data

Chunyi Gai, Dalhousie University
Localized outbreaks in S-I-R model with diffusion.
We investigate a SIRS epidemic model with spatial diffusion and nonlinear incidence rates. We show that for small diffusion rate of the infected class D_I, the infected population tends to be highly localized at certain points inside the domain, forming K spikes. We then study three distinct destabilization mechanisms, as well as a transition from localized spikes to plateau solutions. Two of the instabilities are due to coarsening (spike death) and self-replication (spike birth), and have well-known analogues in other reaction-diffusion systems such as the Schnakenberg model. The third transition is when a single spike becomes unstable and moves to the boundary. This happens when the diffusion of the recovered class, DR becomes sufficiently small. In all cases, the stability thresholds are computed asymptotically and are verified by numerical experiments. We also show that the spike solution can transit into a plateau-type solution when the diffusion rates of recovered and susceptible class are sufficiently small. Implications for disease spread and control through quarantine are discussed.

Jane Heffernan, York University
Models for immune system interaction and evolution
We have developed mathematical models to study SARS-CoV-2 pathogen evolution probabilities, and immunization effectiveness. In this talk, I will provide an overview of our models, and will discuss some preliminary results.

Dennis Hou, Rutgers University–New Brunswick
Topological Analysis for Selecting Network Models of Cytokine Dynamics.
Moderate and severe cases of COVID-19 exhibit distinct immunological profiles, but cytokine dynamics are complex and poorly quantified, posing a challenge for their incorporation into models of immune response. To find suitable models for cytokine interaction, we begin with the expected qualitative dynamical behavior of inflammatory response and determine whether a candidate regulatory network is compatible with it. By associating it with equations with

symbolic parameters, a given network admits a combinatorial decomposition of parameter space into semi-algebraic sets that yields information about global dynamical structures without specifying the nonlinearities in advance. We first apply this approach to coarse-grained examples with a single generic pro-inflammatory cytokine, then at higher resolution with the addition of particular cytokines of interest such as IL-6. The resulting network can then be given an appropriate Lipschitz continuous parametrization as desired.

Adrianne Jenner, Université de Montréal, CHU Sainte-Justine Research Centre*****
Modelling the systemic and tissue-level immune response to SARS-CoV-2
The primary distinction between severe and mild COVID-19 infections is the immune response. Disease severity and fatality has been observed to correlate with lymphopenia (low blood lymphocyte count) and increased levels of inflammatory cytokines and IL-6 (cytokine storm), damaging dysregulated macrophage responses, and T cell exhaustion due to limited recruitment. The exact mechanism driving the dynamics that ultimately result in severe COVID-19 manifestation remain unclear. Over the past two months, we have been working on developing tissue- and systemic-level models of the immune response to SARS-CoV-2 infection with the goal of pinpointing what may be causing dysregulated immune dynamics in severe cases. At the tissue level, we been working as part of an international collaboration to build a computational framework to study SARS-CoV-2 in the tissues. This platform is based upon PhysiCell, an open-source computational cell-based software. With this model, we have been investigating how the level of pro-inflammatory cytokines influence immune cell recruitment into the infected tissue and how this correlates with tissue damage. In parallel, we have constructed a systemic, within-host delay-differential equation model that accounts for the interactions between immune cell subsets, cytokines, lung tissue, and virus to help understand differential responses in COVID-19. While this work is still ongoing, this talk will address how a variety of mathematical and computational techniques contribute to the ongoing study of SARS-CoV-2 infections, helping to increase our understanding of COVID-19 severity.
***** with Sofia Alfonso (McGill University), Rosemary Aogo (University of Tennessee Health Science Center), Courtney Davis (Pepperdine University), Amber M. Smith (University of Tennessee Health Science Center), Morgan Craig (Université de Montréal, CHU Sainte-Justine Research Centre)

Mohit Kumar Jolly, Indian Institute of Science
Mechanistic modeling of the SARS-CoV-2 and immune system interplay unravels design principles for diverse clinicopathological outcomes.
The disease caused by SARS-CoV-2 is a global pandemic that threatens to bring long-term changes worldwide. Approximately 80% of infected patients are asymptomatic or have mild symptoms such as fever or cough, while rest of the patients have varying degrees of severity of symptoms, with 3-4% mortality rate. Severe symptoms such as pneumonia and Acute Respiratory Distress Syndrome can be caused by tissue damage mostly due to aggravated and unresolved innate and adaptive immune response, often resulting from a cytokine storm. However, the mechanistic underpinnings of such responses remain elusive, with an incomplete understanding of how an intricate interplay among infected cells and cells of innate and adaptive immune system can lead to such diverse clinicopathological outcomes. Here, we use a dynamical systems approach to dissect the emergent nonlinear intra-host dynamics among virally infected cells, the immune response to it and the consequent immunopathology. By mechanistic analysis of cell-cell interactions, we have identified key parameters affecting the diverse clinical phenotypes associated with COVID-19. This minimalistic yet rigorous model can explain the various phenotypes observed across the clinical spectrum of COVID-19, various co-morbidity risk factors such as age and obesity, and the effect of antiviral drugs on different phenotypes. It also reveals how a fine-tuned balance of infected cell killing and resolution of inflammation can lead to infection clearance, while disruptions can drive different severe phenotypes. These results will help further the case of rational selection of drug combinations that can effectively balance viral clearance and minimize tissue damage.

Joost Jorritsma, University of Technology Eindhoven
Not all interventions are equal for the height of the second peak.
We present a simulation study of the spread of an epidemic like COVID-19 with temporary immunity on finite spatial and non-spatial network models. In particular, we assume that an epidemic spreads stochastically on a scale-free

network and that each infected individual in the network gains a temporary immunity after its infectious period is over. After the temporary immunity period is over, the individual becomes susceptible to the virus again. When the underlying contact network is embedded in Euclidean geometry, we model three different intervention strategies that aim to control the spread of the epidemic: social distancing, restrictions on travel, and restrictions on maximal number of social contacts per node. Our first finding is that on a finite network, a long enough average immunity period leads to extinction of the pandemic after the first peak, analogous to the concept of ``herd immunity''. For each model, there is a critical average immunity duration L_c above which this happens. Our second finding is that all three interventions manage to flatten the first peak (the travel restrictions most efficiently), as well as decrease the critical immunity duration L_c, but elongate the epidemic. However, when the average immunity duration L is shorter than L_c, the price for the flattened first peak is often a high second peak: for limiting the maximal number of contacts, the second peak can be as high as 1/3 of the first peak, and twice as high as it would be without intervention. Thirdly, interventions introduce oscillations into the system and the time to reach equilibrium is, for almost all scenarios, much longer. We conclude that network-based epidemic models can show a variety of behaviors that are not captured by the continuous compartmental models.

Dean Karlen, University of Victoria and TRIUMF
Characterizing the spread of COVID-19 in Canada and the USA.
Provincial and US state case, hospitalization, and death data can be characterized by relatively long periods of nearly constant growth/decline along with some large outbreaks. This talk will compare the spread in the different jurisdictions and how it has changed with relaxed social distancing measures.

Ruian Ke, Los Alamos National Laboratory
Fast spread of SARS-CoV-2 in China, Europe and the US.
SARS-CoV-2 is a novel pathogen causes the COVID-19 pandemic. Some of the basic epidemiological parameters, such as the exponential epidemic growth rate and R0 are debated. We collected and analyzed data from China, eight European countries and the US using a variety of inference approaches. In all countries, the early epidemic grew exponentially at rates between 0.19-0.29/day (epidemic doubling times between 2.4-3.7 days). I will discuss the appropriate serial intervals to estimate the basic reproductive number R0 and argue that existing evidence suggests a highly infectious virus with an R0 likely between 4.0 and 7.1. Further, we found that similar levels of intervention efforts are needed, no matter the goal is mitigation or containment. Early, strong and comprehensive intervention efforts to achieve greater than 74-86% reduction in transmission are necessary.

Theodore Kolokolnikov, Dalhousie University
Law of mass action and saturation in SIR model with applications to coronavirus
It is common in SIR models to assume that the infection rate is proportional to the product S*I of susceptible and infected individuals. This form is motivated by the law of mass action from chemistry. While this assumption works at the onset of the outbreak, it needs to be modified at higher rates such as seen currently in much of the world (as of June 2020). We propose a physics-based model which leads to a simple saturation formula based on first principles incorporating the spread radius and population density. We then apply this modified SIR model to coronavirus and show that it fits much better than the ``classical'' law of mass action.

Ashok Krishnamurthy, Mount Royal University
Spatiotemporal Transmission Dynamics of COVID-19 in Spain
Mathematical modelling of infectious diseases is an interdisciplinary area of increasing interest. Tracking and forecasting the full spatio-temporal evolution of an epidemic can help public health officials to plan their emergency response and health care. We present advanced methods of spatial data assimilation to epidemiology, in this case to the ebb and flow of COVID-19 across the landscape of Spain. Data assimilation is a general Bayesian technique for repeatedly and optimally updating an estimate of the current state of a dynamic model. We present a stochastic spatial Susceptible-Exposed-Infectious-Recovered-Dead (S-E-I-R-D) compartmental model to capture the transmission dynamics and the spatial spread of the ongoing COVID-19 outbreak in Spain. In this application the machinery of data

assimilation acts to integrate incoming daily incidence data into a fully spatial population model, within a Bayesian framework for the tracking process. For the current outbreak in Spain we use registered data (CCAA-wide daily counts of total COVID-19 cases, recovered, hospitalized, and confirmed dead) from the Instituto de Salud Carlos III (ISCIII) situation reports. Our simulations show good correspondences between the stochastic model and the available sparse empirical data. A comparison between daily incidence data set and our SEIRD model coupled with Bayesian data assimilation highlights the role of a realization conditioned on all prior data and newly arrived data. In general, the SEIRD model with data assimilation gives a better fit than the model without data assimilation for the same time period. Our analyses may shed light more broadly on how the disease spreads in a large geographical area with places where no empirical data is recorded or observed. The analysis presented herein can be applied to a large class of compartmental epidemic models. It is important to remember that the model type is not particularly crucial for data assimilation, the Bayesian framework is the key. Data assimilation neither requires nor presupposes that the model of the infectious disease be in the family of S-I-R compartmental models. The projected number of newly infected and death cases up to August 1, 2020 are estimated and presented.

Mayra Núñez López, Instituto Tecnológico Autónomo de México
Implementation of quarantine measures accounting for Covid-19 hospital saturation.
A SEIRS model was developed to describe the spread of COVID-19 in Mexico, assuming different quarantine scenarios as a function of the conditions of hospital shortage. The presented model takes into account the heterogeneity of the state of infection, that is, the groups of clinical variants that can occur when the disease is contracted. Finally, the model allows different policy options to be implemented in different sectors of population.

Mark Lowerison, University of Calgary
Calibration of time varying contact compartmental models of SARS-COVID-19
We present an age stratified SEIR model of COVID 19 accounting for mitigated social contacts. With this model we explore a series of relaxation and return to normal scenarios, in terms of health system burden.

Simon de Montigny, Université de Montréal
Modelling future biomedical interventions in the COVID-19 epidemic.
To date, intervention modelling in support of the COVID-19 public health response has focused on non-pharmaceutical interventions. With biomedical tools undergoing clinical trials, it is the moment to think ahead and assess how future interventions, based on these likely imperfect tools, could be used to control the COVID-19 epidemic and allow some de-escalation of current mitigation strategies. In this talk, we will discuss our preliminary work on antibody testing and vaccine interventions in a COVID-19 transmission model based on differential equations.

Penelope Morel, University of Pittsburgh
The immune response to SARS-CoV-2: Friend or Foe?
The novel SARS-CoV-2 coronavirus is responsible for worldwide pandemic that has infected over 8 million people resulting in close to 500,000 deaths. The immune response to SARS-CoV-2 involves both innate and adaptive responses and it appears that the timing and magnitude of these responses are important factors in determining the outcome of the infection. For the vast majority of those infected by SARS-CovV-2 the clinical course is mild, with a significant proportion of individuals experiencing asymptomatic infection. In mild cases, it appears that classic anti-viral immunity, manifested by early type 1 interferon production, virus-specific CD8 T cells and the generation of neutralizing antibodies, is responsible for rapid viral clearance. However, the picture is very different for the 10% of infected individuals who develop serious disease, which can lead to respiratory failure, multi-organ failure and death. This is associated with a hyperinflammatory state, with high levels of circulating cytokines, and a failure of the adaptive immune response. New data are emerging concerning the factors, both genetic and environmental, that determine the clinical outcome of disease. In this talk we will examine the host and viral factors that lead either to rapid viral clearance or to severe clinical disease. Deeper understanding of the immune response to SARS-CoV-2 will lead to the development of novel therapeutics that can be tested in a modeling framework.

Kyeongah Nah, York University*

Scenario tree and adaptive decision making on optimal type and timing for intervention and social-economic activity changes.

We assess Ontario's reopening plans, taking into account the healthcare system capacity and uncertainties in contact rates during different reopening phases. Using stochastic programming and a disease transmission model, we find the optimal timing for each reopening phase that maximizes the relaxation of social contacts under uncertainties, while not overwhelming the health system capacity by an expected arrival time of a SARS-CoV-2 vaccine/drug.

* Written with Michael Chen and LIAM De-escalation Group

Sally Otto, University of British Columbia

Modelling evolutionary epidemiology of COVID-19.

Evolutionary epidemiological models illustrate how selection might act on SARS-CoV-2. Considering the limited data, selection favors increased transmission, longer pre-symptomatic periods, fewer asymptomatic cases, and lower disease severity. Viral mutations are expected to affect combinations of these traits, however, making it challenging to predict the direction and disease impact of evolution.

Jody Reimer, University of Utah

Impacts on community transmission and disease burden of a clinical prediction tool to prioritize limited COVID testing.

Community spread of coronavirus disease 2019 (COVID-19) continues to be high in many areas, likely due, in part, to insufficient testing and contact tracing. As regional test kit shortages are likely to continue with increased transmission, it is important that available testing capacity be used effectively. To date, testing for COVID-19 has largely been restricted to persons reporting symptoms, with no additional criteria being systematically employed to select who is tested. In situations when testing capacity is limited, we propose the use of a clinical prediction rule to allow for prioritized testing of people who are most likely to test positive for COVID-19. Using data from the University of Utah Health system, we developed a robust, deployable clinical prediction rule which incorporates data on demographics and clinical characteristics to predict which patients are most likely to test positive. We then incorporated prioritized testing into a stochastic SEIR model for COVID-19 to measure changes in disease burden compared to a model with indiscriminate testing. Our best performing clinical prediction rule achieved an AUC of 0.7. When incorporated into the SEIR model, prioritized testing resulted in a delay in the timing of the infection peak, a meaningful reduction in both the total number of infected individuals and the peak height of the infection curve, and thus a reduction in the excess demand on local hospital resources. These effects were strongest for lower values of Rt and higher proportions of infected individuals seeking testing.

Mario Santana-Cibrian, Universedad Nacional Autónoma de México

Flattening the curve and the effect of atypical events on mitigation measures.

On March 23rd and March 30th, 2020, the Mexican Federal government implemented social distancing measures to mitigate the COVID-19 epidemic. In this work a mathematical model is used to explore atypical transmission events within the confinement period, triggered by the timing and strength of short time perturbations of social distancing. Is shown that social distancing measures were successful in achieving a significant reduction of the epidemic curve growth rate in the early weeks of the intervention. However, "flattening the curve" had an undesirable effect, since the epidemic peak was delayed too far, almost to the government preset day for lifting restrictions (June 1st, 2020). If the peak indeed occurs in late May or early June, then the events of children's day and Mother's Day may either generate a later peak (worst case scenario), a long plateau with relatively constant but high incidence (middle case scenario) or the same peak date as in the original baseline epidemic curve, but with a post-peak interval of slower decay.

Meir Shillor, Oakland University*

Mathematical model, analysis and simulations of the COVID-19 pandemic with variable infection rate: Application to South Korea

The talk describes a substantial extension of the Middle East Respiratory Syndrome (MERS) model constructed, analyzed and simulated in Al-Asuoad et. al. BIOMATH 5 (2016)[1], Al-Asuoad, Oakland University Dissertation (2017), and Al-Asuoad and Shillor, BIOMATH 7(1)(2018)[2] to the case of the current COVID-19 Respiratory Syndrome pandemic that is sweeping the globe. It is caused by the new SARS-CoV-2 coronavirus that has been identified in December 2019 and since then outbreaks have been reported in all parts of the world. To help predict the dynamics and possible controls of the pandemic we developed a mathematical model for the pandemic. The model has a compartmental structure similar but more complex to the SARS and MERS models. It is a coupled system of nonlinear ordinary differential equations (ODEs) and a differential inclusion for the contact rate parameter. The talk will describe the model in detail, mention some of its analysis, and describe our computer simulations of the pandemic in South Korea. The main modeling novelties are in taking into account the shelter-in-place directives, the rates at which the populations obey them and the observed changes in the infectiveness of 'contact number' of the SARS-CoV-2 virus. The model predictions are fitted to some of the data from the outbreak in South Korea. Since the DFE (in South Korea) is found to be asymptotically stable, the pandemic will eventually die out (as long as some control measures remain in place). And, indeed, the model simulations show that the COVID-19 will in the near future be contained. However, the containment time and the severity of the outbreak depend crucially on the contact coefficients and the isolation or shelter-in-place rate constant. The simulations show that when randomness is added to the model coefficients the model captures the pandemic dynamics very well. Finally, the model highlights the importance of isolation of infected individuals and may be used to assess other control measures. It is general and will be used to analyze outbreaks in other parts of the world.

*with Aycil Cesmelioglu and Anna M. Spagnuolo

[1] http://dx.doi.org /10.11145/j.biomath.2016.12.141

[2] http://dx.doi.org/10.11145/j.biomath.2018.02.277

Ilyssa Summer, CarePredict, Inc

Modeling intervention strategies for containing Covid-19 in Nursing homes with digital contact tracing.

Contact tracing is a key initiative in public health to contain Covid-19. At CarePredict, Inc., we developed a real-time digital contact tracing system that Long Term Care (LTC) facilities can use to rapidly identify and contain exposed, asymptomatic and symptomatic COVID-19 contacts. An SEIR deterministic model was developed to compare traditional and digital intervention methods for contact tracing in LTC Facilities. Data from our LTC facilities, skilled nursing homes, and nursing home data of residents affected by Covid-19, is utilized to form our parameter estimates and to inform the projections of the impact of contact tracing interventions. The model quantifies infection spread comparing across symptom tracing, manual contact tracing, PCR testing, and digital contact tracing in a nursing home setting. We computed the reproductive number per intervention type and compare parameter sensitivity to the base model to understand key components that can reduce spread.

Rebecca Tyson, University of British Columbia- Okanagan

The timing and nature of behavioral responses affect the course of an epidemic.

During an epidemic, the interplay of disease and opinion dynamics can lead to outcomes that are different from those predicted based on disease dynamics alone. Opinions and the behaviors they elicit are complex, so modeling them requires a measure of abstraction and simplification. In this talk, we develop a differential equation model that couples SIR-type disease dynamics with opinion dynamics. We assume a spectrum of opinions that change based on current levels of infection as well as interactions that to some extent amplify the opinions of like-minded individuals. Susceptibility to infection is based on the level of prophylaxis (disease avoidance) that an opinion engenders. In this setting, we observe how the severity of an epidemic is influenced by the distribution of opinions at disease introduction, the relative rates of opinion and disease dynamics, and the amount of opinion amplification. Some insight is gained by considering how the effective reproduction number is influenced by the combination of opinion and disease dynamics.

Esteban Abelardo Hernandez Vargas, Universedad Nacional Autónoma de México

In-host Modelling of COVID-19 in Humans

COVID-19 pandemic has underlined the impact of emergent pathogens as a major threat for human health. The development of quantitative approaches to advance comprehension of the current outbreak is urgently needed to tackle this severe disease. In this work, different mathematical models are proposed to represent SARS-CoV-2 dynamics in infected patients. Considering different starting times of infection, parameters sets that represent infectivity of SARS-CoV-2 are computed and compared with other viral infections that can also cause pandemics. Based on the target cell limited model, SARS-CoV-2 infecting time between susceptible cells is much slower than those reported for Ebola virus infection (about 3 times slower) and influenza infection (60 times slower). The within-host reproductive number for SARS-CoV-2 is consistent to the values of influenza infection (1.7-5.35). The best model to fit the data was including immune cell response, which suggests a slow immune response peaking between 5 to 10 days post onset of symptoms. The model with eclipse phase, time in a latent phase before becoming productively infected cells, was not supported. Interestingly, both, the target cell model and the model with immune responses, predict that SARS-CoV-2 may replicate very slowly in the first days after infection, and it could be below detection levels during the first 4 days post infection. A quantitative comprehension of SARS-CoV-2 dynamics and the estimation of standard parameters of viral infections is the key contribution of this pioneering work. This work can serve for future evaluation of the potential drugs with different methods of action to inhibit SARS-CoV-2.