

# **Modeling of COVID-19 Pandemic in Canada: Projection and Interventions**

## **1 Relevance and Expected Outcomes**

- Outline the goals of the partnership and explain the potential outcomes and impacts.
- Outline efforts the partner organizations will invest following the projects completion to advance the results in Canada.

Complexities of COVID-19 etiology and quality of data used to characterize disease processes pose important challenges to authorities who need to monitor and respond to emergence of this disease. Statistical methods can have crucial roles for investigating disease-host systems and informing appropriate population management strategies. By addressing the objectives proposed in this application, we will provide new statistical techniques that solve prevalent problems due to the COVID-19 pandemic. Our partner organizations (Public Health Agency of Canada and Manitoba Health) have shown a great interest in this research proposal; they will actively contribute to the research project and also facilitate knowledge translation support for governmental stakeholders. An immediate outcome of this research is helping our partner organizations to implement novel modeling products that will improve current technologies that are used to inform population health. As the vaccine of the COVID-19 will not likely be available within a year or two, the results of this research proposal will be timely, allowing policymakers to optimize intervention strategies to improve the health of Canadians, and also decrease the current pressure on the Canadian healthcare system. Our proposed models will allow a better understanding of the true COVID-19 dynamics and account for data imperfections, and therefore decision-makers will have better tools for drawing appropriate conclusions regarding disease etiology and devising effective disease management strategies.

## **2 Partnership**

- List all partner organizations expected to play a key role in the activities.
- Describe the core activity of the partner organizations and how the topic is relevant and aligned with the partner organizations' activities.
- Explain how each partner organization will be actively involved. Describe the value added through in-kind contributions and how these are important to realizing the projects intended outcomes.

The National Microbiology Lab (NML) is Canada's principal infectious disease public health laboratory with responsibility for reference microbiology and quality assurance, laboratory surveillance for infectious diseases, identification of vulnerable populations, emergency outbreak preparedness and response,

training, research, and development. The NML is a key partner in this research project. Dr. Nicholas Ogen is the Director of Public Health Risk Sciences Division of the NML, Public Health Agency of Canada (PHAC), and he will actively contribute to the research project and facilitate knowledge translation support for governmental stakeholders.

Manitoba Health is also a critical partner in this research project. The Epidemiology and Surveillance Unit is part of the Information Management & Analytics Branch in the Department of Health, Seniors and Active Living (MHSAL). The role of the Unit is to support the public health system by monitoring, analyzing and reporting on the occurrence, spread, and severity of communicable and non-communicable diseases and conditions in Manitoba. The Surveillance Unit at MHSAL systematically receives and manages reportable communicable disease data as prescribed by The Public Health Act. The Unit is involved in notifying public health offices across Manitoba of cases of communicable disease, and managing the flow of information to and from these offices in support of regional public health investigations. Dr. Carla Loeppky (Director and epidemiologist) and Dr. Luiz Guidolin (senior epidemiologist) at the Epidemiology and Surveillance Unit who will bring important policy and a population-level approach to the study and also knowledge translation support for governmental stakeholders.

Both partner organizations mentioned above have indicated that the results of this research proposal will be very crucial and timely to implement into the Canadian healthcare system.

### 3 Proposal

- Outline the research objectives. Detail the resources and activities needed to achieve the anticipated results.
- Indicate approximate timelines for the activities to lead to milestones and deliverables using a Gant chart, table or diagram.

Two popular methods for forecasting infectious disease impact are the susceptible-exposed-infectious-recovered (SEIR) model and agent-based models (ABMs). Typically in such models, an underlying assumption is made that the infection rate will stay constant during the epidemic which may not be true. In particular, in the case of COVID-19, infection rates may change over time and may also depend on the characteristics of infected people. **At the time of writing this research proposal, some reported provincial COVID-19 projections across Canada (e.g., Ontario) are far from reality mainly because of the less precision arising from exclusively using the conventional SEIR model for projections.** To address these issues, our research goals include the projection of coronavirus accurately, the identification of vulnerable populations disproportionately affected by the virus, and the detection of spatial patterns of

coronavirus provincially and nationally. We will achieve these goals by expanding the SEIR model and using our new SEIR to inform our ABM.

**3.1 Project research objectives in the area-level statistical models (ALMs):** SEIR models are limited in the fact that they cannot account for control measure implementation, dynamic changes of factors that may influence transmission (e.g., spontaneous physical distancing), and changes in surveillance and reporting approaches. Our choice of modeling approach may also lead to unreliability in the precision of our estimated model parameters (King et al. 2015). As we will use “raw” counts of cases to fit the model, the point estimates would be biased (King et al. 2015). In the SEIR model, it is also assumed that the infection rate will stay constant over time. **Objective 1:** We propose an ALM to accurately predict the infection rate at each time by incorporating the corresponding covariates and characteristics of infected people. We will then incorporate the infection rates at each given time into the SEIR model to accurately predict the outbreak over time that may inform the public and policymakers about possible intervention strategies. To address both the incorporation of heterogeneous populations and the modeling of spatial spread of an infectious disease, we use the idea of temporal models for infectious disease which are often built around infective behavior and related changes to the susceptible population. These models offer fundamental frameworks for developing spatial models in the context of infectious diseases. Here, the disease outcome, case event or count, becomes the infectious status or count of infections, respectively. In this case, we need to consider at any given time, the number of susceptible, the number of exposed, the number of infections, and the number removed from the population, corresponding to SEIR models. Assuming  $T$  discrete time periods and  $m$  number of small areas within a study region, we can define the *true* count of new infections within time period  $t$  ( $= 1, \dots, T$ ) and small area  $i$  ( $= 1, \dots, m$ ) as  $I_{it}$  and the reported count as  $y_{it}$  by assuming that  $y_{it} \sim \text{Bin}(I_{it}, p_{it})$ , which allows for under-ascertainment via the probability of infection  $p_{it}$ . We also define  $S_{it}$  as the susceptible population at small area  $i$  and time  $t$ ,  $E_{it}$  as the count of exposed cases during the time period  $t$  at small area  $i$ , and  $R_{it}$  as the count of removed cases during the time period  $t$  at small area  $i$ . Hence, the transmission, exposed, susceptible, and removal equations would take the form:  $I_{it+1} \sim \text{Pois}(E_{it}\lambda_{it})$ ,  $E_{it} \sim \text{Pois}(\sigma S_{it})$ ,  $S_{i,t+1} \sim \text{Pois}(\mu_{i,t+1})$ ,  $\mu_{i,t+1} = S_{it} - E_{it} - I_{it} - R_{it}$ ,  $R_{it} \sim \text{Pois}(\delta I_{it})$ , where  $\lambda_{it}$  takes different forms which depends on the structure of the data. For instance, if we believe that neighborhoods play a role in transmission then we could assume a spatial structure through  $\lambda_{it}$  as

$$\lambda_{it} = I_{i,t-1} \exp(\mathbf{x}_{it}^\top \boldsymbol{\beta} + u_i + v_t), \quad (1)$$

where  $\mathbf{x}_{it}^\top$  is the vector of covariates (risk factors) with the corresponding regression coefficients  $\boldsymbol{\beta}$ ;  $u_i$

is a spatial random effect which may be modeled as for example a proper conditional auto-regressive (CAR) model (Stern and Cressie, 1999; Torabi and Rosychuk, 2010) with parameters  $(\tau, \sigma_u^2)$ ; and  $v_t$  is the temporal random effect which may be modeled as for example a random walk model with parameter  $\sigma_v^2$  (Torabi, 2012). One can also define alternative forms for modeling  $\lambda_{it}$  and in particular for spatial and temporal random effects. We will use our parameterized transmission model above to accurately predict the infection rate at any given time and update the SEIR model to be able to predict the COVID-19 outbreak in Canada. Using the model (1), we will also identify vulnerable populations (e.g., people with low socio-economic status, Indigenous people), and also obtain geographical variation of infected people to identify those health regions and communities which are most at risk. The results will help public and policymakers for intervention strategies. **Objective 2:** In order to study the ABM properly for COVID-19, different types of data are used including population statistics, geographic information system (GIS) data, school and workplace locations data. To simulate the transmission dynamics of coronavirus in the model, we use a compartmental SEIR type model (Sterling and Taveter, 2009). In particular, we will use the improved version of the SEIR model where we can accurately predict the infectivity rate at each given time as explained in objective 1. We will use many model evaluation approaches to analyze the course of simulated outbreaks with providing different scenarios in terms of interventions (e.g., self isolate if the agent is sick; closure of schools and workplaces; stay-at-home policy; physical distancing). Indeed, in the proposed ABM, we will combine the risk factors of the infected people at the area-level (health region) model for accurately predicting the probability of infection at each given time with possible intervention scenarios designed as part of the ABM. This combination will cover all possible risk factors which influence the projection of COVID-19 outbreak at the national level. Using the proposed ABM, we can look at where infections took place in the model to identify vulnerable populations and geographical variation of COVID-19 in Canada. *Our COVID-19 dataset, for the proposed ALMs in objectives 1 and 2, consist of sex, age group, date of diagnostic, hospitalization, ICU, province, and health regions. The COVID-19 dataset are available through the Canadian Government website, 2016 Canadian Census dataset through the Statistics Canada website, and provincial datasets for schools and workplaces through the provincial websites.*

**3.2 Timeline:** The proposed study activities will take one year to complete. During the first ten months of this research project, we will develop and apply our ALMs for objectives 1 and 2. The last two months of this research project will be devoted for knowledge translation and delivering the results to our partner organizations in various formats including meetings and seminars.

## 4 Team

- List the applicant, any co-applicants and key staff of the partner organizations.
- Explain how the knowledge, experience and achievements of these individuals provide the expertise needed to accomplish the project objectives. Discuss the role of each individual and how their contributions, including those of staff from the partner organizations, will be integrated into the project.

Our strong and uniquely qualified research team are all bio/statisticians and epidemiologists with extensive experience developing statistical and mathematical models on infectious diseases. Dr. Mahmoud Torabi (Applicant) is a biostatistician at the University of Manitoba with substantial knowledge in spatio-temporal models, GIS, small area analysis and has experience working with the communicable disease datasets. Dr. Rob Deardon (Co-Applicant) is a statistician, at the University of Calgary, who has been working in the area of infectious disease modeling and surveillance for over 15 years. Dr. Deardon is also member of PHAC Modelling Advisory Group in advising PHAC on the development and application of mathematical and statistical models for the spread of COVID-19 in Canada.

Drs. Charmaine Dean (University of Waterloo), Rhonda Rosychuk (University of Alberta), and Cindy Feng (University of Ottawa) are biostatisticians with extensive research experience on modeling of infectious diseases and act as collaborators in this research project. Dr. Dean is also a member of the PHAC Expert Advisory Panel for COVID modeling. Dr. Erin Rees (collaborator) is an epidemiological modeler, at the University of Montreal and PHAC, with extensive research experience in spatial modeling of infectious diseases. Collaborators from our partner organizations are Dr. Nicholas Ogden (Director of Public Health Risk Sciences at the PHAC), Dr. Carla Loeppky (Director and epidemiologist) and Dr. Luiz Guidolin (senior epidemiologist) at Epidemiology and Surveillance Unit at the MHSAL. See Section 2 for the roles and contributions of our partner organizations in this research project.

The all team members have actively been collaborating with each other in another program of research funded by the Canadian Statistical Sciences Institute- Collaborative Research Team (CANSSI-CRT) to study spatial patterns of infectious diseases such as influenza and TB and look at its impacts on the health of Canadians. Drs. Torabi, Deardon, and a trainee (post-doc) will participate in the development of techniques and apply to the COVID-19 dataset. Drs. Dean, Rosychuk, Feng, Rees, Ogden, Loeppky, and Guidolin have substantial statistical/epidemiological/knowledge translation experience and will provide the statistical and epidemiological insight required to postulate explanations and interpretations of the findings. We will have bi-weekly group meetings to discuss any issues related to the project, and will prepare the results for use for the provincial and national government agencies including PHAC and MHSAL.