An Overview of Mathematical Modeling for Pandemic Control

Harpa: I welcome you to our webinar, An Overview of Mathematical Modelling for Pandemic Control, hosted by the National Collaborating Center for Infectious Diseases. I am Harpa Isfeld-Kiely and you've joined us for the first in our series of webinars that we call the Synergies Series. In this interdisciplinary series, we invite speakers to share research evidence and consider where mathematical modelling can help answer priority public health questions. Topics begin with Covid-19, with room to grow. Today's presentation is an overview of mathematical modelling aimed to give public health a better understanding of the method, the evidence produced and potential to support policy decisions.

As I cover some housekeeping points, I invite you to answer five poll questions on the screen. If you have technical difficulties, like sound quality, please email Zeeshan Qadar. You will find his email address at the top middle of your screen. Zeeshan will do his best to help you.

I'll also point you to our chat box. That is on the right hand side and it will be used for questions to me, or to our presenter. You may ask questions at any time. However, we will generally hold questions for the speaker until the Q&A period after the presentation. Also, be aware we are recording this presentation. It will be shared with those who've missed the event and others upon request. You'll notice from the update on the screen that there was a change to our program. Dr. Amy Greer is unable to deliver the presentation that she prepared for today, but we've been very lucky to engage her trusted peer and an expert in her own right, Dr. Ashleigh Tuite. And before I introduce Dr. Tuite, let's take a look at the results of our poll.

I've broadcasted the results now, so we have: 40% follow math modelers on social media and 60% of you do not; we have about an event split on the question of whether you follow public health on social media; and there's a wide variety of platforms that appear to be utilized, although Twitter shows a somewhat clear lead at nearly 70%. I also see that over 50% of you never visit social media. So we're happy to provide this event as a bit of a stop-gap where you can engage on a webinar instead. Now, looking at the fifth poll question - which online platform do you visit the most? I see there is again a preference for Twitter at 70%. So we hope to engage with you further on Twitter.

Thanks for doing our poll. We want to understand where you find valuable modelling evidence, where you connect across disciplines, where you have those opportunities for dialogue. And we do offer one platform, Mod4PH or Modelling for Public Health, and that's a discussion form on LinkedIn. You are welcome to join the group and can learn more on our website, at nccid.ca.

Now about today's presentation. It has been prepared by Dr. Amy Greer. She is the current Canada Research Chair in Population Disease Modelling and

Associate Professor in the Department of Population Medicine at the University of Guelph. She has held positions in the Center for Communicable Disease and Infection Control at the Public Health Agency of Canada and the Dalla Lana School of Public Health at the University of Toronto.

Now I'm very pleased to introduce Dr. Ashleigh Tuite to deliver the presentation. I expect Dr. Tuite is known to many of you. She is an infectious disease epidemiologist, mathematical modeller and assistant professor at the University of Toronto's Dalla Lana School of Public Health. Welcome, Ashleigh.

Ashleigh: Thank you so much for having me and thank you everyone for tuning in despite the fact that I'm not Dr. Greer. I will do my best to give her presentation justice and anything that I say that is incorrect is entirely my own misinterpretation of what she meant to say. I will say for those of you who are on Twitter and aren't following mathematical modelers, I would very much recommend that you check out Amy Greer's Twitter feed and also, I guess, two of my favourite mathematical modelers on Twitter, Adam Kucharski from the London School of Hygiene and Tropical Medicine and Marc Lipstich from Harvard School of Public Health. So just a little bit of a plug there if you're looking to learn. I certainly learn a lot from those people on Twitter.

[Slide 1] The purpose of today's seminar is really to talk about how mathematical modelling is used for pandemic control and thinking about the synergies between people who reside more in the academics sphere and those who are working in applied public health. I think Covid-19 has demonstrated how important and useful communicable disease modelling can be. It's been an important part of the Canadian as well as the global Covid-19 pandemic response. I mean, it's been used in a number of different ways in order to guide and support policy making during the pandemic. In terms of the way that models have been used thus far, they've been used to try to predict disease burden in terms of number of infections and number of deaths; to try to understand what sorts of mitigation strategies we can use and what their impact might be; to think about the cost-effectiveness of different interventions. And we're starting to also think about how we can use models to think about vaccine prioritization, if and when a vaccine becomes available.

So although modelling has been, I think, pretty prominent during the Covid-19 pandemic so far, it's also revealed some challenges, particularly the challenges with trying to generate knowledge in real time and trying to respond to a lot of demands at once. Modelling is a tool that can be very effective for helping make decisions and helping to provide decision makers with some clear recommendations, but they do require work and they do require input from people who are on the ground and people who actually understand the systems that we're trying to model. And so, creating that synergy between modelers and public health professionals is something that, from my perspective, has always been really, really important. But it's become increasingly clear how important that is over the past several months.

[Slide 2] So why are we talking about infectious disease models? Communicable diseases are a bit of a tricky thing to model and the reason that they're tricky is because these diseases are *communicable*. So a *case* is also a risk factor. If I'm infected, I'm a risk factor to those who are around me and in the case of Covid, one of the things that's been really important is, as you know, we're not finding all cases--either because we're not testing enough, or because we have pre-symptomatic transmission ,as well as some people who have very mild symptoms. And so, in these sorts of models, in the communicable disease models that we like to use, this communicability manifests as a positive feedback. So the more cases you have, the more cases you get. And you really need to incorporate that dynamic nature into models in order to get valid outputs.

And again, this idea of communicability means that it's not just individual actions and individual risk factors that matter, because all of those individual actions impact what happens at the population level. So we need to think about how those connections work and how they manifest.

[Slide 3] Before we get too deep into this, I just wanted to make a quick clarification or an important distinction between statistical models and mathematical models. So when we talk about models, there is sometimes confusion about what exactly we're talking about. At their core, all models are simplified representations of reality. Often in the public health sphere, if we're trained as epidemiologists, or in biostats, we're most familiar with epidemiological models that describe associations between variables. For example, regression models and these types of models are an important component of the public health toolkit, but they're different from mathematical models. They're highly complementary, but I would say that mathematical models are different because of what I just talked about in terms of those dynamic feedbacks and really trying to describe the mechanisms that link exposures, interventions and infection or disease. And they are both used to understand how systems work and to make projections and predictions.

[Slide 4] Many of you may be familiar with the Meltzer model. This is a model that is used in pandemic preparedness planning and it's basically a spreadsheet model. It starts off with an assumption around the number of symptomatic cases that exist in a population and it uses effectively multipliers to try to estimate how many people would end up needing medical attention, and being a lab confirmed case, a hospitalized case, or dying. The advantage of these types of models is that they're intuitive. You can look at that on a spreadsheet and you understand what's going on. The disadvantage of this model is that because it's so simplistic and it has this sort of linear relationship--if you have 15% of the population that is infected, you multiply that by 50% symptomatic to get the number of people that are medically attended. But it's not incorporating the feedbacks. So if you implement an intervention in this type of model, it's not going to feed back into the proportion of people that are symptomatic and it's not going to capture all of those downstream effects. So this is an example of a

model that, in terms of best practices for communicable diseases epi, we wouldn't necessarily want to use this type of model. But it is useful from a resource planning perspective. You can basically email that to somebody and they can input their own parameters.

[Slide 5] So the next thing I wanted to talk about is how do you actually go about building a mathematical model? And I think that my task here is easier because we've all been exposed to a lot of these ideas over the past several months. Really, the most fundamental part of any infectious disease model is the basic reproductive number. That's the number of secondary infections that are caused by a single infectious case when they're introduced into a completely susceptible population in the absence of any sort of interventions.

And I remember in 2011, the movie Contagion came out and I went to see it with my epidemiologist friends. In the movie, Kate Winslet is the epidemiologist and she's explaining the R0 to her colleagues. I remember us laughing, thinking how weird and funny it was that they would think that the public would be interested in the basic reproductive number. And now fast forward to 2020 and people are actively monitoring the reproductive number and what they're monitoring is something that's called the effective reproductive number, which is the number of secondary infections produced by each of these original infectious individuals in the presence of interventions and once the disease has been circulating in the population. So there is the potential for acceptability.

And the reason that people are really interested in monitoring this effective reproductive number is because it tells us whether or not we're going to experience exponential growth and basically see an epidemic. If that number is greater than one, we have exponential growth. When it's less than one, we don't have exponential growth and eventually the disease will go away. When it is exactly equal to one, each old case is making exactly one new case and the disease is endemic. So it basically is in the population, but we're not going to see an epidemic.

[Slide 6] So this is an example of how the effective reproduction number works. So again, I think this is probably something that we don't need to spend a lot of time on because we're all probably fairly familiar with this. But effectively, if you have a disease where the effective reproductive number is four, that initial case is going to make four cases and then each of those make four cases and each of those make cases and you very, very quickly have an out of control epidemic. If you're able to reduce that reproductive number by either having immunity in the population or introducing interventions such that when an infectious case is in contact with a susceptible individual that can't transmit, that number will be reduced and ideally we want that number to be one or less for the disease to go away.

[Slide 7] This is an example of estimates of R0. In a completely susceptible population in

the case of SARS-CoV-2, the virus that causes Covid, we have initial estimates of the R0 that are around two to three. You can compare that to other diseases and it's relatively low compared to something like measles or tuberculosis, and that is reflected by the fact that given things (interventions) implemented at the population level, we have been fairly effectively at reducing transmission and basically reducing the effective reproductive number to less than one or around one in a lot of communities in Canada.

[Slide 8]

One thing that I think is really important to know is that although we talk about the reproductive number as though it's a fixed thing, it's actually variable. So we're talking about, on average, how many new cases are caused by each old case, but the reality is that there is heterogeneity. So individuals will have different reproductive numbers. Some people may infect only one person and some of those initial index cases may go on to infect 10 people.

This is an example of the distribution of the R0 for SARS, and you can see that the average again was around two to three, but you had this very long-tailed distribution. So some cases were infecting up to 10 people.

[Slide 9] This is an example from the Covid pandemic. This is looking at cases in Singapore, looking at basically chains of transmission that happened amongst cases that were introduced from Wuhan and what you can see is that you have these examples where a lot of cases didn't infect anyone else and then you have a few events where one of those initial cases led to large numbers of second generation cases. And a lot of those events, in this particular example, were associated with gatherings. So here we're looking at a family gathering as well as people attending church services.

That's something that's become really important, understanding this heterogeneity, or what we call an over-dispersion in the reproductive number, because that accounts for some of the strange epidemiology that we're seeing with Covid.

[Slide 10] As I said, if you understand R0, you can really start to build a model. When we talk about R, we can calculate it as basically the number of contacts that an individual has. The probability for each of those contacts that, if they do come into contact with somebody, with a probability that they transmit infection to that contact, and then how long that initial case is infectious for.

So if you have two diseases, but one where the person is infectious for twice as long as the other, the R0 will be twice as large. And those are really the key components that go into the reproduction number.

[Slide 11] Just to take a step back in terms of what are mathematical models, I think we've covered this already a little bit, but basically they are ways to represent our understanding of reality. They're conceptual tools that explain how an

object or a system behaves and they come in a variety of forms. They can be really, really complex and they can be very, very simple. And it's your choice. What type of model to use really depends on what question you're trying to answer, how precise you need your answer to be, and what data you have available. Do you have the data available to do something that's really complicated and how quickly do you want the results?

So more complicated models are going to require more work, but they're also going to require more data, which is often a limiting factor. And even the most complicated models are going to have to make simplifying assumptions. The whole point of using a model is that we're not able to look at a real world system and so there's always going to be those simplifying assumptions there.

But you want to try to capture the most essential features of the system that you're trying to explain.

[Slide 12] So if you wanted to build a model, what would the steps be that you'd have to take? The very first step is you have to define your host population of interest. So you might be thinking about a town, a province, a country. You might be specifically interested only in school aged children. You might be interested in the sexually active population. You might be interested in modelling a hospital or a daycare. And then the next step that you have to consider is how you define people amongst the different groups in your model. So the type of people who'll be in the model compartments.

Basically, you have to say, how do you divide the population and the most sort of classic model that you'll see is what's called an SIR model. You will divide the population into those who are susceptible, infectious and recovered. You can also add more complexity. You could, for example, include a vaccinated compartment. You could separate by age. You could have different groups for different ages of people. You can separate by sex. But these are really the building blocks of a model and you can model things fairly well using something as simple as an SIR type of model.

[Slide 13] The next thing you have to define is - how do you transition into these states? Let's say we start with a model where we have a population of school aged children and we put them all in a susceptible box. We have to decide how do they get out of that box? We start off with everyone susceptible. What is the process by which they enter into the infectious box? That will depend on the context between the susceptible and the infectious people, as well as the infectiousness of the disease. So if an infected person comes into contact with a susceptible person, what's the probability that they will infect them? And similarly, you have to think about the transition out of the infectious box. At what rate do people recover? And so that's something that we can get from epidemiologic studies where we can look at how long a person is infectious for.

[Slide 14 skipped]

[Slide 15] Now we have to add in the math. So we have this understanding of what the population looks like, how it's divided, and now we have to think about how we get people to move between the different boxes and this is where the math comes in. I think this is the only math I'm going to show you, so hopefully it won't be too painful. Basically, what's happening is we're saying the dS by dt (dS/dt) it's a calculus term, it's basically saying the rate at which people who are susceptible are leaving the susceptible box and entering into the infectious box depends on the number of susceptible people in the population, the number of infectious people in the population. And this term called Beta which is basically the number of contacts that happened between the susceptible and infectious people and the probability of transmission when those contacts happen. And so, those people move out of the susceptible box and then Beta SI term appears in the infectious box. So basically we're saying take those people from one box and move them to the other and similarly we're taking the infectious people and moving them out of the infectious box and into the recovered box at a rate that depends on the number of infectious people in the population and how long they are infectious for.

And because we want to add a bit more complexity, we'll also include the mortality. So basically people who get infected can die and that's represented by that final term there.

[Slide 16] So if you have a model like that and you put some parameters in there. .. if you know what the beta term looks like, if you know what the duration of infectiousness looks like, what you'll end up with is a model. And this is the output of that model. So the red is showing the number of infectious people over time and that's basically your epidemic curve. That's sort of a model. You've built your first mathematical model, if you haven't done that before.

[Slide 17] So what can mathematical models do for us? The reality is that models are very useful tools for combining data with questions, so you know, when we don't have time to conduct an experiment or do a randomized control trial, we want to understand what will happen in a population if we do something. If we do a specific intervention, what's going to happen? Modelling can basically provide a toolkit that can help to address needs and I think the really important thing here is that it needs to be used wisely. The assumptions that are built into this model need to be understood and you really need to work with policy makers in order to make sure that the questions that you're asking and the model that you're using makes sense for the question that policy makers are trying to answer.

[Slide 18] In terms of this process, the way that it really works, I think, is if you have this verbal description of a model (and that can happen collaboratively with people in diverse fields) you can translate that into a mathematical formulation. Then once you have your model, you can use that to get outputs and then just use those outputs to try and describe your answer to that particular question. And really, it allows you to examine a wide range of what-if scenarios and provide that information back to people who can actually use that in order to make

decisions and often to fuel discussion about what we may or may not think about doing in terms of whatever that particular question is that you're considering.

[Slide 19] I'm going to skip over this, in the interest of time. But basically, I wanted to say that early on, a lot of modelling really focuses on estimating Ro because it's such a critical component of models. Understanding that can be really, really useful for answering initial questions around what does this disease look like, how big do we expect the epidemic to be, how quickly do we expect it to spread in the population. And so, a lot of the really early models for H1N1 and for SARS-CoV-2 were focused on estimating Ro and also estimating some of the other epidemiologically important parameters, like how long someone is infectious for or how long the incubation period is.

[Slide 20 skipped]

[Slide 21] This is an example of a model of SARS-CoV-2. It is a model that Amy Greer, myself and David Fisman developed early on, in February/March of this year. This is how we developed our compartmental model of how SARS-CoV looks and sort of the process by which people move through the different stages of infection. And I think something that we can maybe talk about once the presentation is over is how even the model structure is something that changes a lot. So our understanding of the virus and the important stages of infection have change. So our schematics of what that model looks like is different today from what it was back in March.

[Slide 22] I think when we're working with knowledge users and stakeholders, it's really important to be able to discuss and justify the scientific rationale for the modelling decisions that were made at each point in the process in a way that is accessible to the knowledge user. One of the big issues with really complex models is that it can be hard to explain those models to others. And I think there's a desire to make models fairly complicated, because you want to capture reality. But the question is, if you're thinking about reproducing something that happens in clinical practice, you can come up with a whole bunch of outcomes that happen, but they happen fairly rarely. So the question is, how important is it to include that particular process in the model and is the complexity that we're adding and are the parameters that we're adding justified by what that adds to the model?

[Slide 23] Again, I think it's really important that when you're building models and when you're disseminating models--throughout the process really-- have a clear understanding of what's included and what was left out and why certain things were left out. Because there are always going to be simplifications that have to be made, but if you have a model that you present to stakeholders and they don't believe or have construct validity, then the outcomes are also going to be suspect. So you really need to have those conversations throughout the mode-building process.

[Slide 24] When you're looking at a model, if you're a knowledge user and you're presented with a model and you want to know should I trust this model, should I believe its outputs? To be a savvy model user, I think the really important things to consider are first of all, the parameter values. Look at them. There's usually a large table of parameter values. They're not always that exciting to look at, but they're important to look at, because if you don't trust or believe the parameters that have gone into that model, the outputs are not going to be useful to you. Also, you need to think about the assumptions. What simplifying assumptions have been made and how realistic are they?

[Slide 25] So look at the model. Can it reproduce the observed data? A lot of times we're trying to fit models to data where we don't have a lot of data points, and so, it's possible that you can have different parameters that will describe the data equally well. And so, it's important to quantify this uncertainty and to make sure that people do sensitivity analyses and are really upfront about the assumptions that went into that, the uncertainty that feeds into the model and also how that affects the intervention effectiveness.

[Slide 26] So some important considerations: The real world will never be fully captured by a series of equations. That's just a limitation of models and it's a good limitation of models. It makes the real world a little simpler and a little more tractable. They don't have the ability to identify the likelihood that a given scenario will or will not occur. It can basically present a series of "what-if" scenarios and give you a sense of the relative likelihoods of certain things happening. And they're meant to compliment public health experience, expertise and common sense. So a model alone isn't going to tell you what to do. You need to interpret that as another piece of evidence and incorporate that with your existing knowledge and expertise.

[Slide 27 skipped]

I think I'll wrap up here and just say that decision-making in times of public health crisis is really, really challenging. We all want to have the perfect data available and we all want to have really scientific evidence. The reality is that as we're experiencing this the data are constantly changing. Our understanding is constantly changing and models really are just another tool for describing the current state of knowledge, synthesizing that information in a way that really lays out our assumptions, really lays out our current understanding of a process or a system and can help guide us.

Sometimes a model will tell you that we just don't have enough information to really distinguish between different potential interventions or different potential approaches and that can actually be useful, because that can help guide you in directions of where we need more research or where we need more information or what particular interventions are we thinking about right now that we can leave off the table because they just don't seem to have any effect in a model, for example.

I think it's really important to continue a dialogue between modelers and non-modelers. As somebody who does a lot of modelling, I think modelers have a really, really important role for making sure that they are explaining what they're doing clearly and documenting what they're doing, making sure that the inputs that they're using are valid. And really try to communicate what they're doing and be transparent about what they're doing. And be upfront when things are uncertain.

And I think the role for non-modelers is don't be scared of models. I think they're a tool and I think that modelers really, really do appreciate working with non-modelers because you can point out the flaws. I'm not a clinical expert, so having someone point out to me that something is wrong or an assumption doesn't make sense, is incredibly useful. And I think modelers want our tools to be useful to others and really, really appreciate the engagement and the dialogue. I will wrap up there, and thank you very much.

Harpa: Thank you, Ashleigh. That was a wonderful overview. I recognize it's a challenge to deliver other's material, so you've just done wonderfully.

I'm going to move now to the Q&A session. We do have several minutes for some questions and I can see there's one in our chat box. Please do take some time to type into our chat box. Ashleigh, I know you'll draw from your own knowledge of modelling and public health and policy development in responding to questions. In the evaluation, participants will have a chance to pose questions that are specifically for Amy Greer.

So let's take our first question.

[Q1] Would you please explain what is the implication of population heterogeneity and age dependant effects on the model's results, specifically in the context of control measures and the herd immunity topic?

Ashleigh: Sure. So I mean, including heterogeneity is really important, particularly when you're thinking about interventions that may affect different population groups differently. And so, I think the simplest form of heterogeneity to include is age dependent effects. So, understanding that specifically for Covid-19, the disease presentation and manifestation in a child is going to be very, very different from an adult, and that's going to have very different implications in terms of health resource use as well as when we're thinking about interventions that are specifically applied to children versus those that are applied to adults. You know, school closures, what-not. So including those sorts of effects is really important.

I think another really important source of heterogeneity is geographic heterogeneity. Most of the models that we've done so far are really focused on the entire province of Ontario. And you know, that's not right, in the sense that across the province and across the country, we've seen really, really different

effects in terms of how many cases we've seen. And some of that is related to the urban versus rural divide. Some of that is just related to control measures that are in place or how quickly those initial imported cases were found. But including those sources of heterogeneity are important. When it comes to herd immunity--so basically this idea that we need to achieve a certain level of infection in the population in order to effectively shut down transmission--I think that's going to relate a little bit more to geographic heterogeneity than necessarily age effects. We're starting to see that in the United States, where there are certain states and certain regions within states that are starting to experience relatively high numbers of infections. And the rate at which case transmission is slowing, is faster than you would anticipate from simply looking at the interventions that are in place. And so, the thought in those particular regions is that the number of infections may be enough, that that population immunity is also acting to slow down the reproductive number. So we were talking about the effective reproductive number, which is the number of new cases that each old case makes, and that incorporates the proportion of the population that is susceptible as well as the presence of interventions. And so, in the case of locations where they have started to see relatively high infection rates, that immunity... we don't know at this point how long lasting it is, but that may actually be contributing to the slowing down of the effective reproductive number or the decrease in the reproductive number.

Harpa: Thank you. That was an excellent question and response.

[Q2] We have another question. How could public health benefit from modelling in planning surveillance programs and data gathering? Do you have a comment?

Ashleigh: Sure. I guess in terms of surveillance programs – I'm just trying to understand if that's related to surveillance testing or just – why don't I interpreted it as data, because that's a conversation that we have a lot. Modelers are saying "Well, we don't have enough data" and then people who work in public health will say "Well, what data do you actually want and what data is actually helpful?" And I think some of the data that will be really useful to modelers relate to understanding change in transmission and I think these are the sort of data that would come from contact tracing.

So for example, in terms of data that we have access to right now, we know a number of cases that are being identified by testing, but we don't always know the connections between cases. We don't know within a household, for example, what was the index case and how many cases did they go on to infect. And the reason that those initial cases go on to infect other cases. Where are they infecting those other cases?

And the reason that that's of so much interest right now is because we're really starting to think and starting to understand the importance of super spreading events, and this idea that most cases are not transmitting a lot – are not generating a lot of new cases. But then there are events where initial cases are

causing large numbers of downstream infections. And so, trying to understand where those events are happening and what are the factors that are contributing to that is something that's of great interest. I think it is a piece of data that is being collected, probably by local public health units, but not something that modelers are necessarily using or having access to. But I think that would be very important for helping to guide decisions around what do we reopen and what are sort of riskier environments and what sorts of activities can we resume more safely?

Harpa: OK. I see we're near our end, but if you can stay for a couple more questions, Ashleigh. I see a couple of participants have typed in additional questions.

Ashleigh: Yeah.

Harpa:

[Q3] Could you please explain the difference between the reproductive numbers again?

Ashleigh: The basic reproduction number is the average number of new cases that an index case generates. So if I'm infected, and if the entire population is susceptible. So when we have a disease that nobody's ever seen before and we have no interventions in place at all, how many people do I infect, on average? And in the case of Covid, we think it's between two to three people, on average. The effective reproductive number is the number of new infections that each old case generates at any given point in time. That means we're no longer saying that the entire population needs to be susceptible and we're not saying that there need to be no interventions in place. So if I were to go out today and if I were infected with SARS-CoV-2, I would probably infect fewer than two people, because – well, first of all, I'm not really going out, but if I was going out people are wearing masks, people are physically distancing. So, on average, each old case may only be making one new case. Basically, the basic reproductive number is what the disease would do if we let it transmit without any sort of interventions in place and without any sort of population immunity. And the effective reproductive number is what we're really looking at right now, which is at this given point in time, how many on average, how many new cases is each old case making?

Harpa: We'll close with an answer to the next question.

[Q4] Going back to your previous response, the impact on RE from the reduced susceptible proportion, it isn't unexpected though, is it?

Ashleigh: So, yeah, it's not unexpected. It's basically a component of the effective reproductive number. I think the unexpected part is maybe how quickly it's happening in certain states. So basically the idea that in Ontario, for example, the seroprevalence estimates that I've seen have been around 1%. So only about 1% of the population has been infected, so far, with SARS-CoV-2. And

you really need to have a relatively high proportion of the population affected before you start seeing a notable impact on transmission, if you were only relying on immunity. In this case, we have both immunity acting as well as intervention. So the two in tandem are working to reduce the effective reproductive number to a level that is lower than you would get if you only had interventions in place or if you were only relying on population immunity to drive the reproductive number down.

Harpa: OK. This is has been very educative and there's certainly more to say.

I will have to close our event now. But I want to make you aware of upcoming webinars in our Synergies Series. We have another event on the epidemiology of COVID on August 26 with Benjamin Cowling-- registration has opened-- and another event on September 11 on vaccine, the outlook and opportunities for modelling, with Joanne Langley.

I want to close this event with great thanks to Ashleigh and all of you for participating today and hanging on for a few additional minutes. We were happy to see some questions and engagement here. We will have further discussion on the Mod4PH forum. I invite you there online. You're free to join and participate on Mod4PH. There's information on our website about that discussion forum.

Now we'll turn your attention to our evaluation. It's very important that we get your feedback on these events to continue to improve them and to bring you other useful events in the series.

Ashleigh, again, thank you so much for stepping in at the 11th hour to share Dr Greer's material and your considerable expertise. Thank you very much.

Ashleigh: Thank you very much and thanks everyone for your patience and great questions.

Harpa: Production of this webinar has been made possible through a financial contribution from the Public Health Agency of Canada. The views expressed do not necessarily represent the views of the Agency.

Thank you all for your attendance. Be safe. Be well. Thanks and goodbye.