Endnotes 1 and 11

COVID-19 MODELLING

Update

April 8, 2020

Introduction

- COVID-19 continues to spread rapidly across the globe.
- To date, Alberta has fared better than most.
- Albertans need to know what they can expect over the next 6 to 8 weeks:
    - How is COVID-19 expected to spread in Alberta?
    - What actions should Albertans take?
    - What is the Alberta plan?

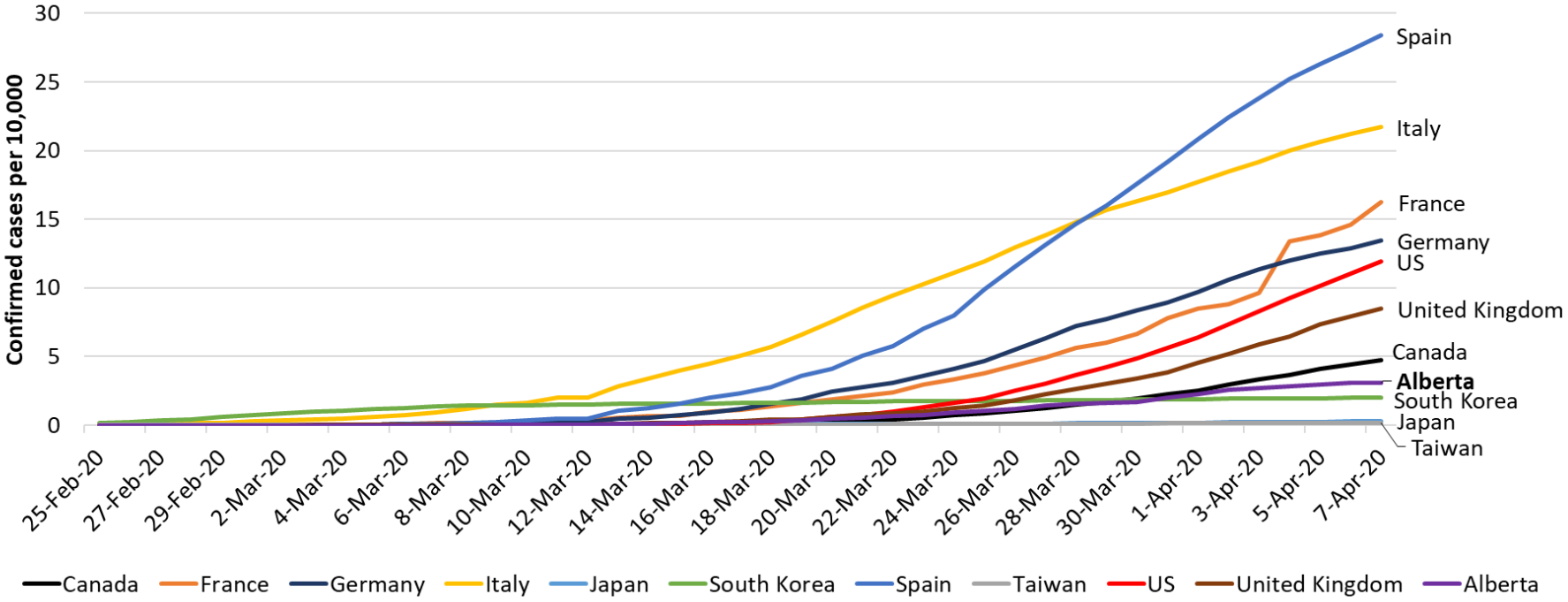
Alberta

Introduction

- Alberta continuously monitors the spread of COVID-19 – locally, across Canada and globally.
- Public health interventions that slow the spread have been developed based on what has worked elsewhere.
- Evidence gathered from other outbreaks informs the modelling of COVID scenarios in Alberta.
- The scenarios help the health system and Albertans plan for the potential impact of the pandemic and its peak.

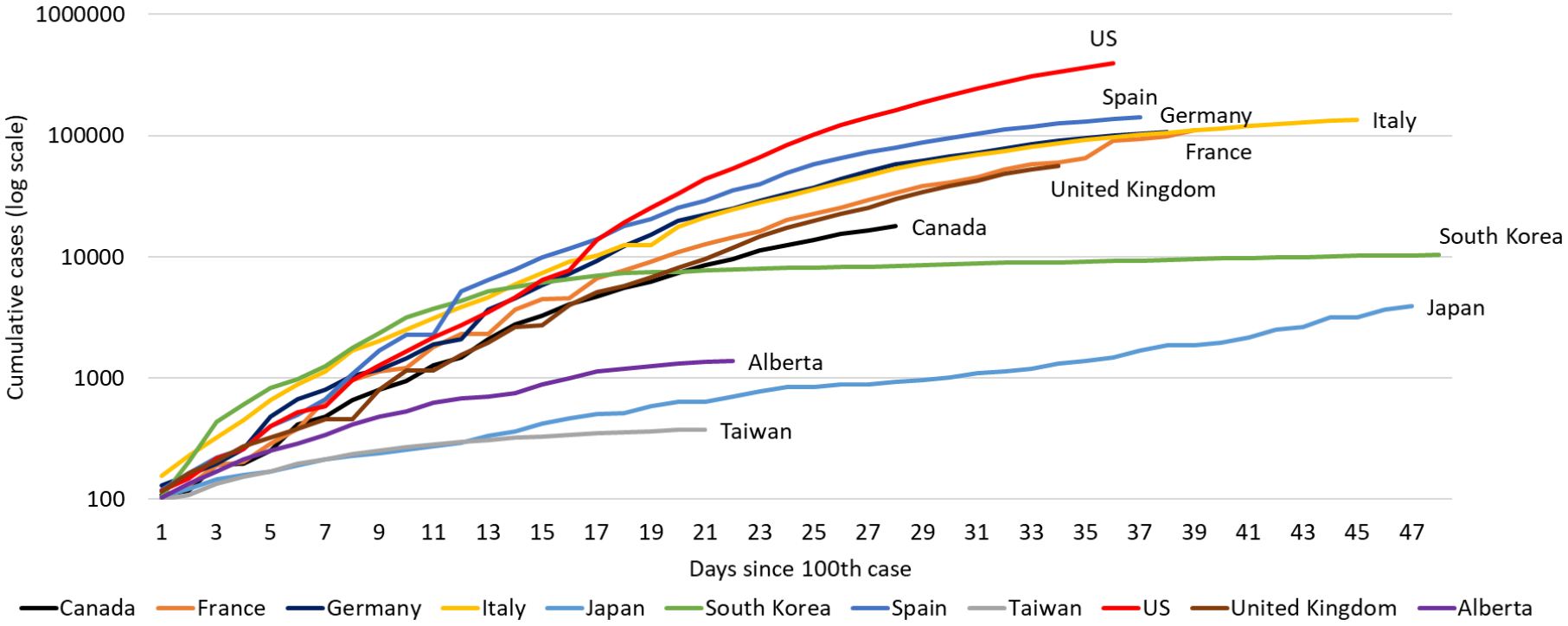
Current State

Comparison of Alberta to countries



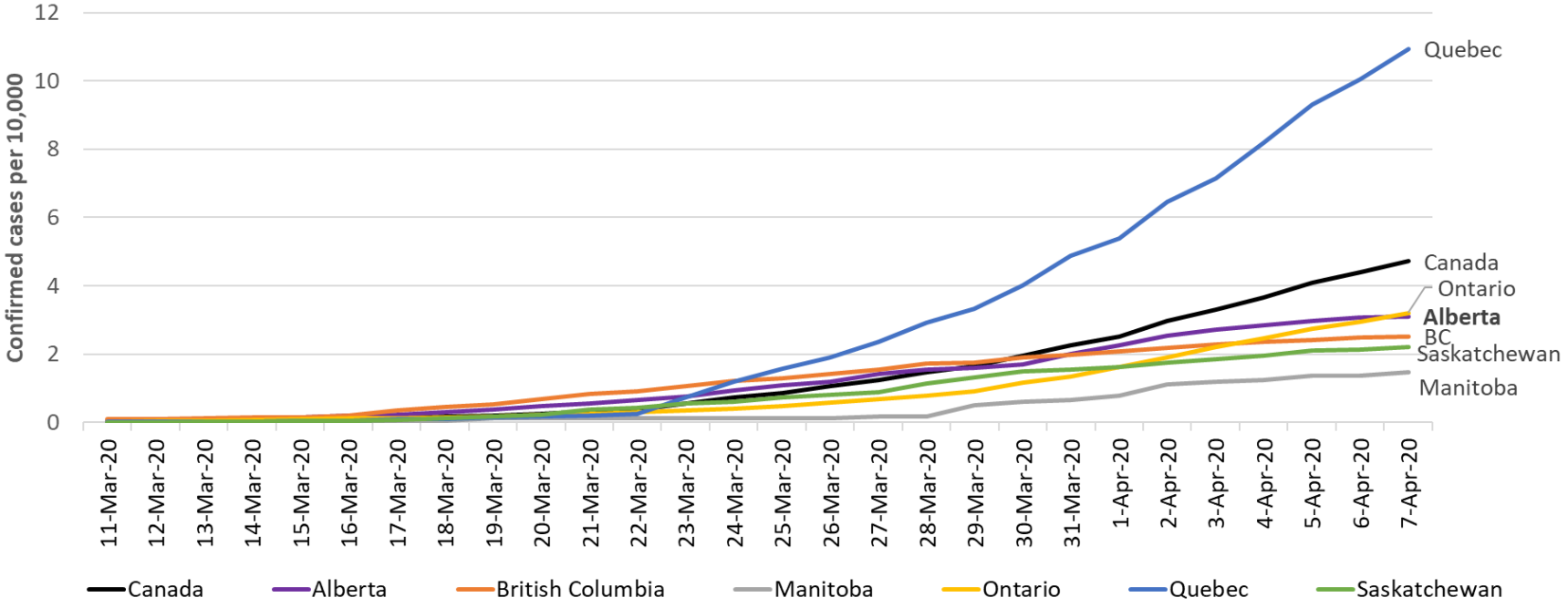
Data as of April 7, 2020, respective country websites. When not available Johns Hopkins CSSE github repository

Comparison of Alberta to countries (log scale)



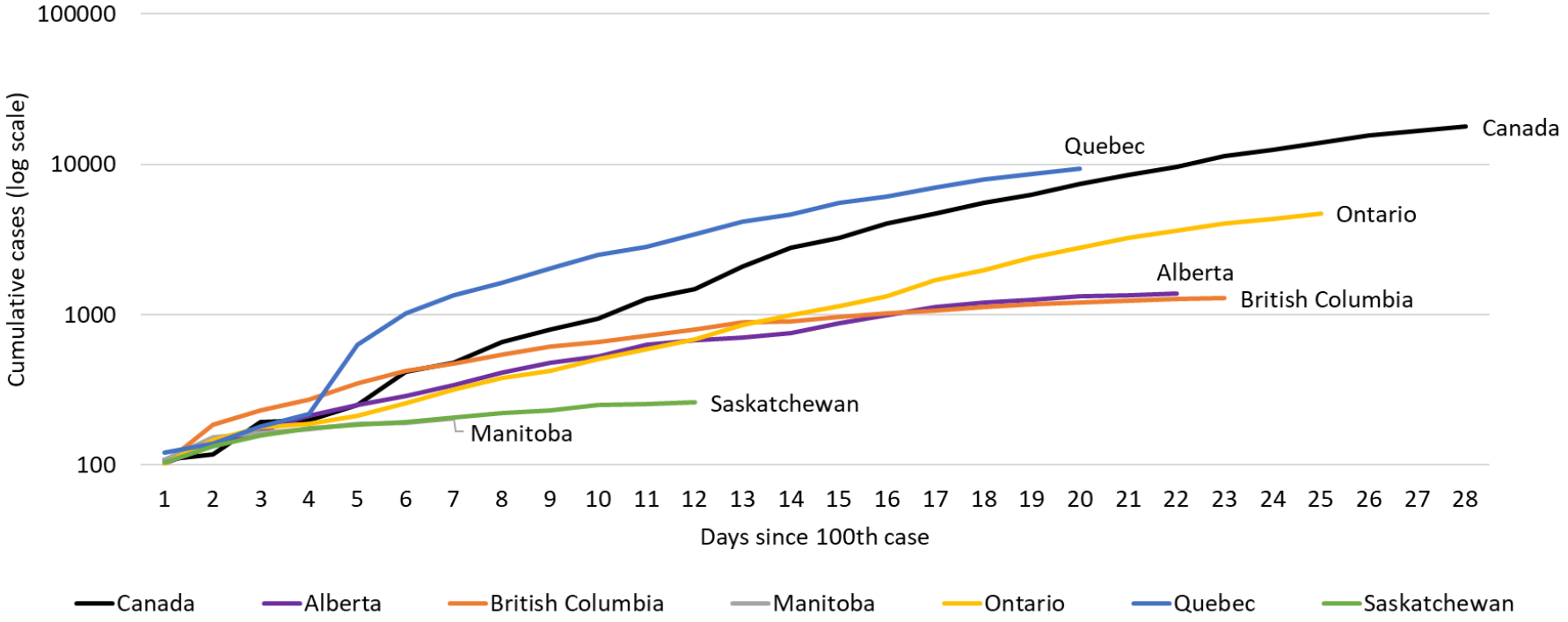
Data as of April 7, 2020, respective country websites. When not available Johns Hopkins CSSE github repository

Comparison of Alberta to other provinces



Data as of April 7, 2020, source PHAC: https://health-infobase.canada.ca/covid-19/

Comparison of Alberta to other provinces (log scale)



Data as of April 7, 2020, PHAC: source https://health-infobase.canada.ca/covid-19/

Confirmed cases, hospitalization, ICU, and deaths for Canada's 6 largest provinces

	Confirmed cases		Hospitalization		ICU		Deaths	
	# Cases	Per 10,000	# Cases	Per 10,000	# Cases	Per 10,000	# Deaths	Per 10,000
AB	1348	3.05	90	0.2	31	0.07	24	0.05
QC	9340	11.00	902	1.06	286	0.34	121	0.14
ON	4726	3.24	614	0.45	216	0.15	132	0.09
BC	1291	2.58	290	0.57	72	0.14	39	0.08
SK	260	2.21	4	0.03	2	0.02	3	0.03
MB	217	1.58	11	0.08	7	0.05	2	0.01

Data as of April 7, 2020, source PHAC :Epi summary, health-infobase.canada.ca and provincial dashboards
* Reporting of ICU, hospitalizations and deaths has a lag in Ontario, which would understate severity

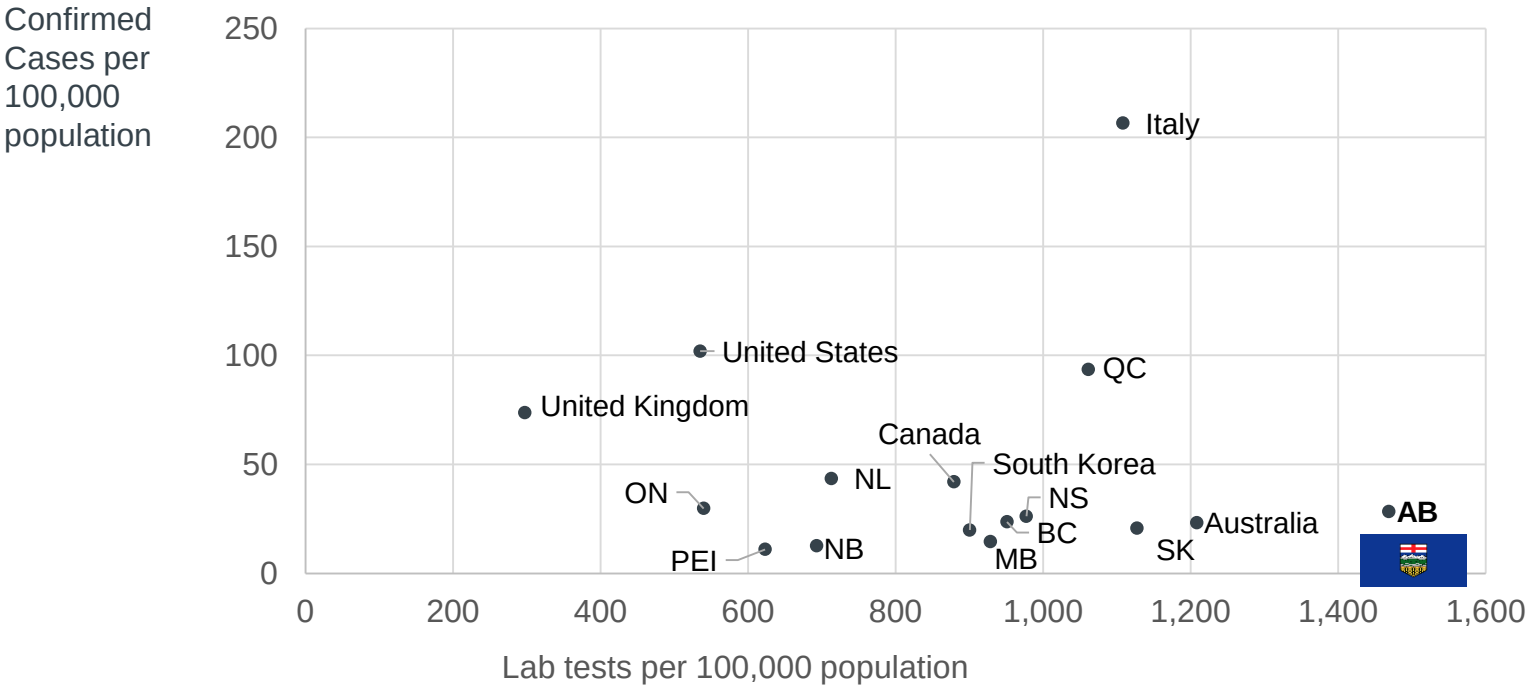
Alberta

Cases and deaths by age group in Alberta

Age Group	Cases	Death	Case Fatality Ratio
19 and under	149	0	-
20-39	446	2	0.45%
40-59	446	1	0.22%
60-79	256	4	1.56%
80+	76	19	25.0%
Total	1,373	26	1.89%

Data as of April 6, 2020, source https://www.alberta.ca/covid-19-alberta-data

Comparison of testing rates across jurisdictions



Data as of April 6, 2020, source https://ourworldindata.org/covid-testing

Modelling

Modelling

- Many jurisdictions use data from other countries, like China or Italy, to model the spread of COVID-19.
- Due to its extensive testing and surveillance program, Alberta case data is used to develop more accurate model scenarios.
- The modelling is updated as new data becomes available.
- Alberta has modelled two core scenarios – Probable and Elevated.

Scenarios

Probable Scenario

- For every case, 1-2 more people are infected.
- This scenario is comparable to the more moderate growth seen in the UK and countries that have had some success in “containing” growth.
- Given our early and aggressive interventions and contact tracing to limit spread, this is expected to be the most likely scenario for Alberta.

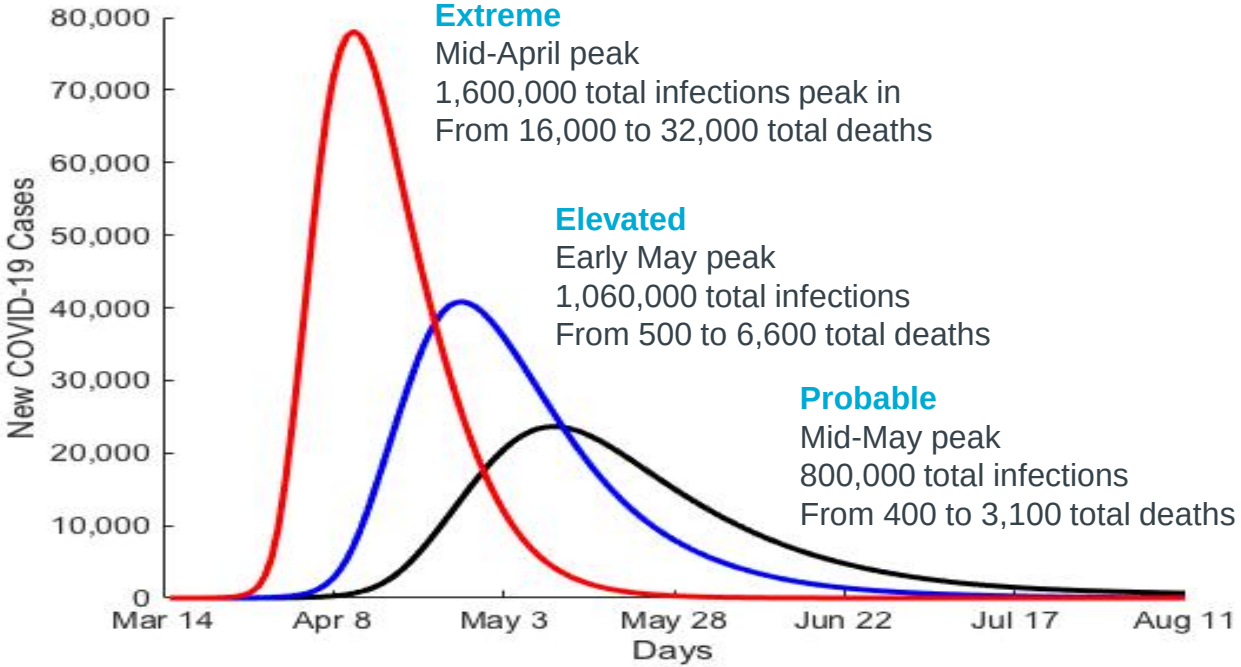
Elevated Scenario

- For every case, 2 people are infected.
- This is comparable to the more rapid growth initially seen in Hubei.
- Planning for this scenario is prudent and responsible given the catastrophic impacts should the health system become overwhelmed.

Extreme Scenario

- For every case, 3 more people are infected.
- This scenario assumes limited and late interventions so that COVID-19 rapidly spreads through the population.
- This scenario shows what would have happened if Alberta did not undertake early and aggressive interventions and contact tracing to limit spread.

Illustrative comparison of the scenarios

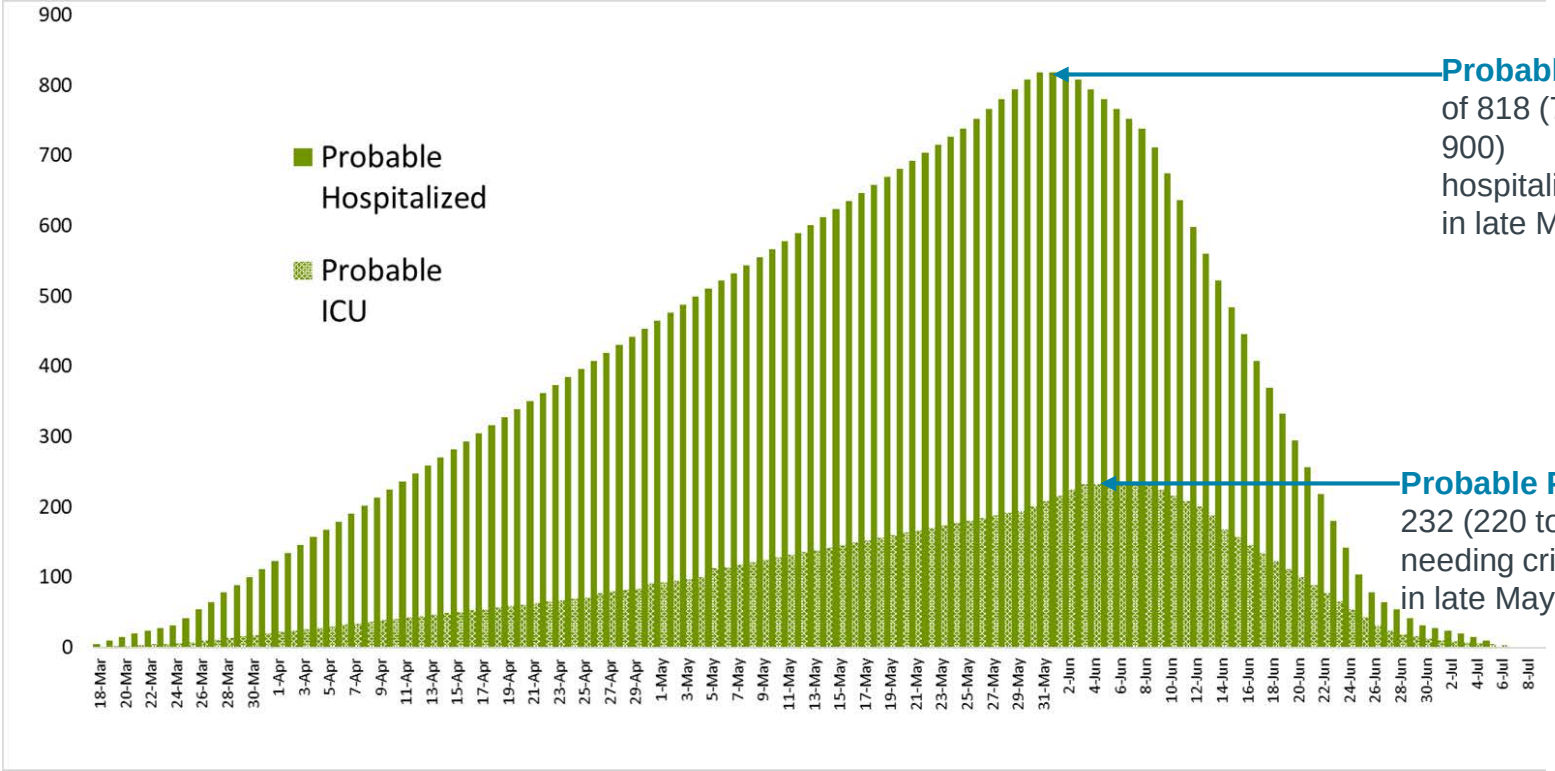


Extreme
Mid-April peak
1,600,000 total infections peak in
From 16,000 to 32,000 total deaths

Elevated
Early May peak
1,060,000 total infections
From 500 to 6,600 total deaths

Probable
Mid-May peak
800,000 total infections
From 400 to 3,100 total deaths

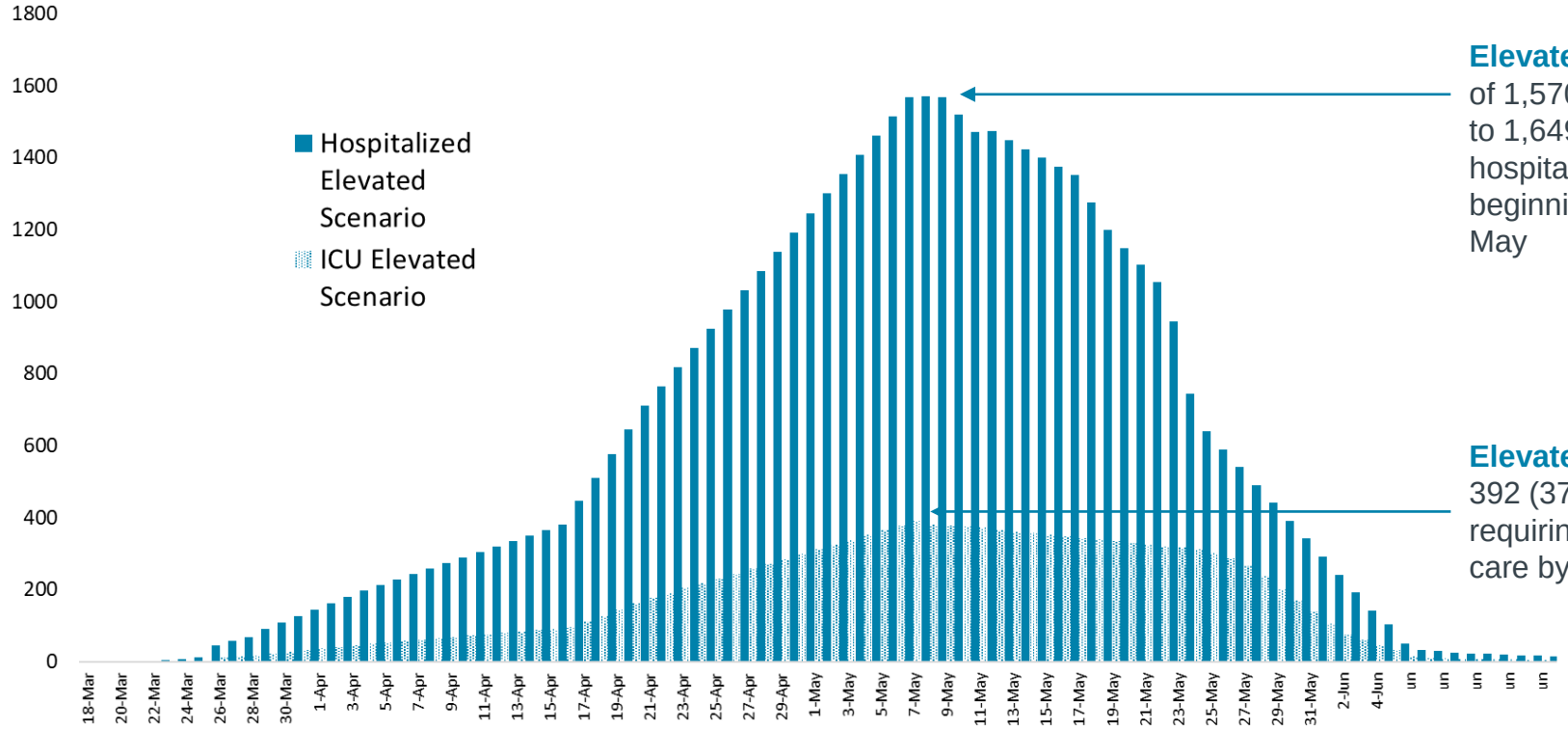
Hospitalizations and ICU - Probable



Probable Peak of 818 (736 to 900) hospitalizations in late May

Probable Peak of 232 (220 to 244) needing critical care in late May-June

Hospitalizations and ICU – Elevated Scenario



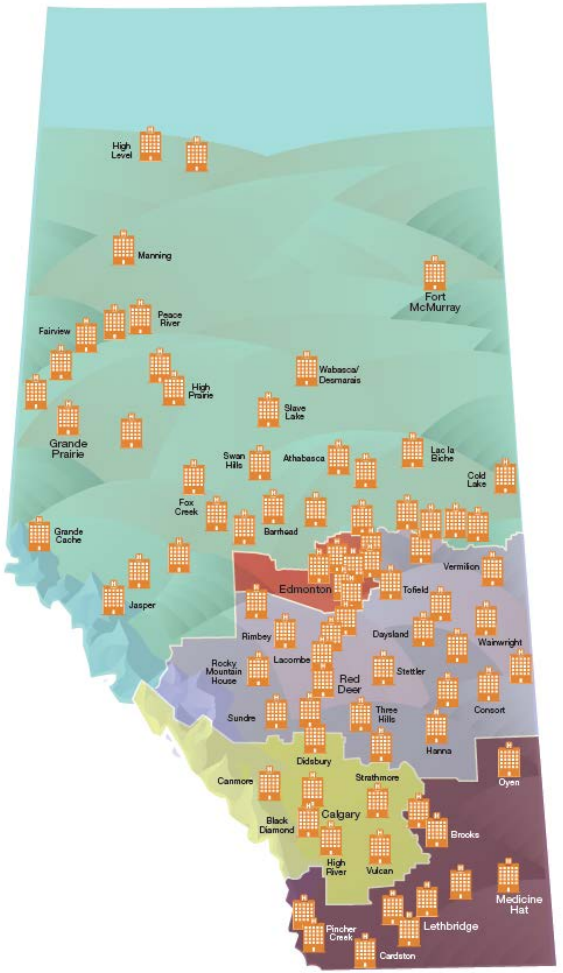
Elevated Peak of 1,570 (1,491 to 1,649) hospitalizations beginning of May

Elevated Peak of 392 (372 to 412) requiring critical care by early-May

Health System Capacity

Existing Capacity

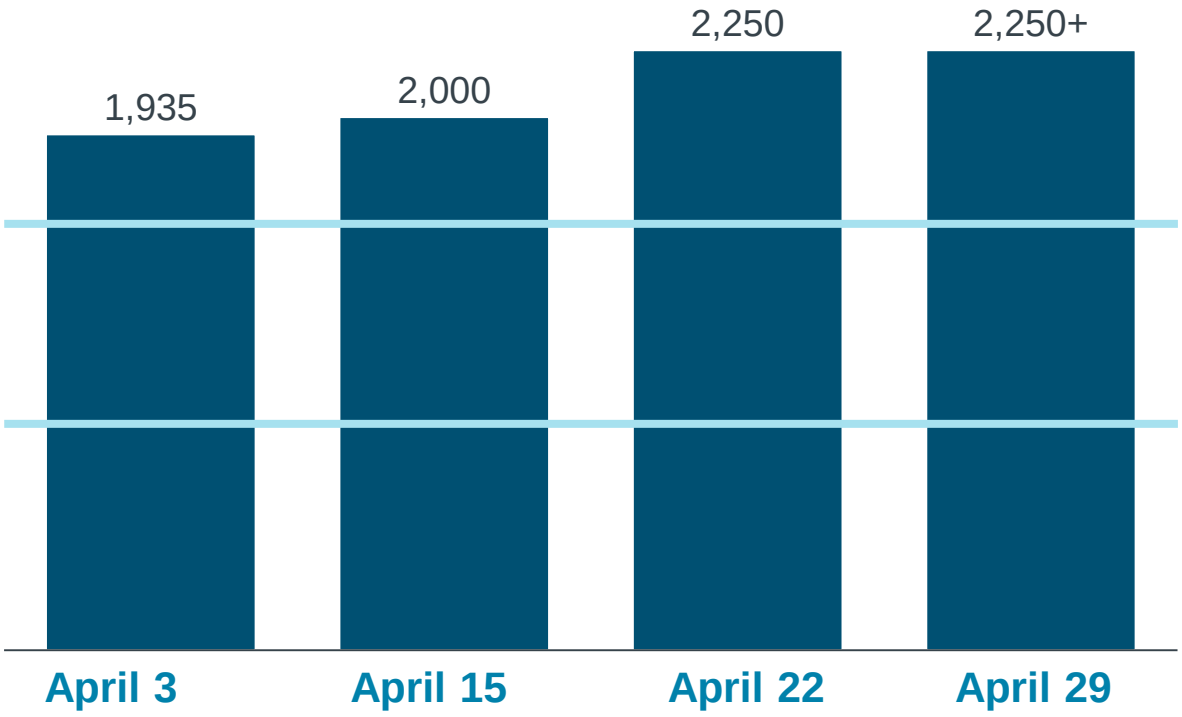
	North	Edm.	Central	Cgy.	South	Total
Hospitals	33	12	30	13	12	100
Hospital Beds	929	3,020	1,098	2,791	645	8,483
ICU beds	12	150	12	97	24	295
Ventilators	33	205	27	213	31	509



Building Acute Care Capacity

- **AHS plans to have 2,250 COVID-19 designated acute care beds by the end of April:**
  - As of April 3, 2020, 1,935 are available for COVID patients; and
  - New COVID dedicated spaces are being brought online.
- **COVID-19 acute care capacity is being achieved by:**
  - Postponing scheduled surgeries, tests and procedures while ensuring urgent, emergent and oncology surgeries continue;
  - Transferring patients who no longer require acute care to a community setting;
  - Increasing occupancy while maintaining physical distance between patients; and
  - Opening overcapacity, and new and decommissioned spaces.

Building acute care capacity



Peak of 1,570 (1,491 to 1,649) hospitalizations in **elevated** scenario, which is projected start of May

Peak of 818 (736 to 900) hospitalizations in **probable** scenario, which is projected late May

Building ICU Capacity

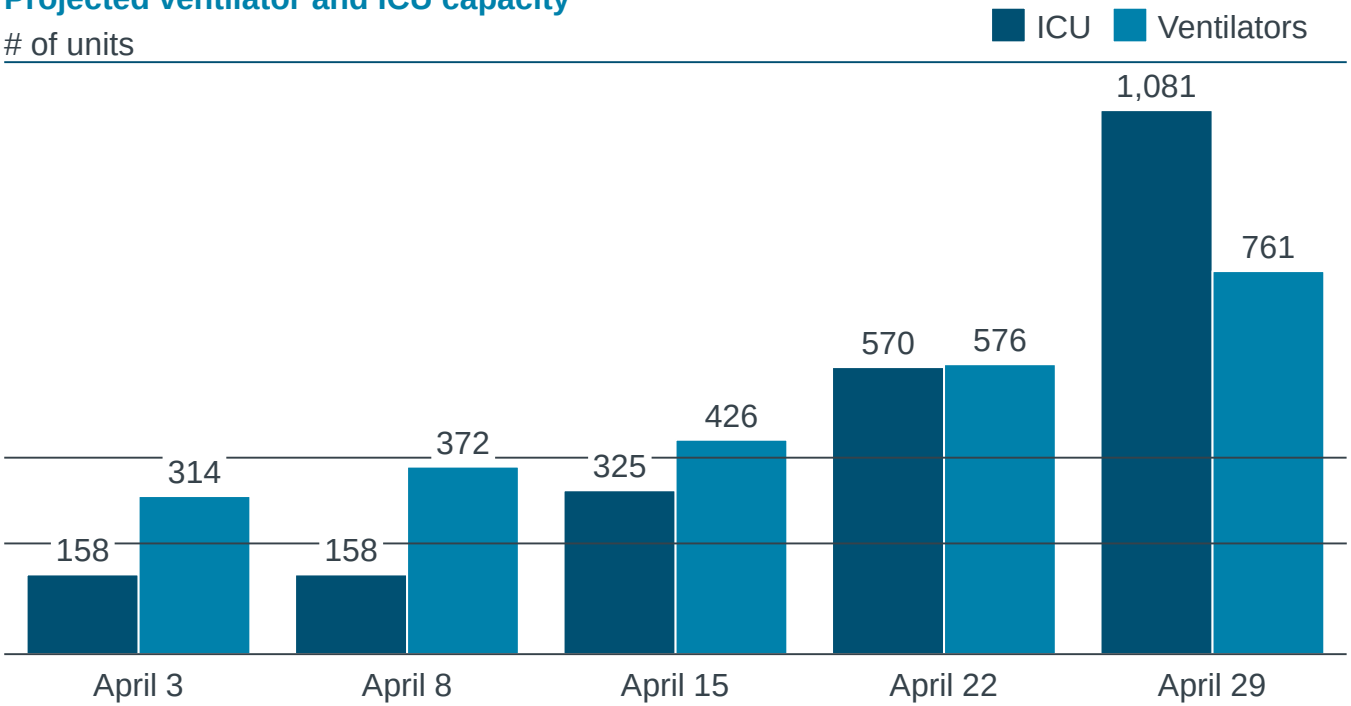
- **AHS plans to be able to increase ICU capacity by 1081 beds for COVID-19 patients by the end of April, if necessary.**
- **ICU capacity will be increased by:**
  - Adding ICU beds to existing ICU rooms;
  - Converting operating rooms and recovery rooms to ICU capacity;
  - Converting procedure and treatment rooms to ICU capacity; and
  - New models of care (e.g. more aggressive use of step down care).

Building Ventilator Capacity

- **AHS plans to have 761 ventilators available by the end of April for COVID-19 patients, if necessary, to respond to severe a scenario.**
- **314 ventilators are currently dedicated to COVID-19 patients and the capacity will be increased by:**
  - Purchased ventilators on order (35 that have arrived and another 30 in May);
  - Ventilators from NAIT and SAIT Respiratory Therapy program (40), STARS (6) and AADL Respiratory Outreach Program (25);
  - Repurposed from Chartered Surgical Facilities (30);
  - Alternative devices capable of mechanical ventilation including transport, anaesthetic and pediatric devices (305); and
  - Ventilators from Public Health Agency of Canada (6).

Building ICU & Ventilator Capacity

Projected ventilator and ICU capacity



Peak of 392 (372 to 412) needing critical care in **elevated** scenario, which is projected early May

Peak of 232 (220 to 244) needing critical care in **probable** scenario , which is projected May-June

Note: assumes that 195 of existing 295 ICU with ventilators are available to non-COVID cases

Workforce

- **Preparing for COVID-19 is about more than beds and equipment – it is about health care providers.**
- **To ensure Alberta has the highly skilled staff to respond to the pandemic the following is being developed:**
  - Accelerated training for ICU nurses;
  - New models of care to expand the reach of existing ICU nurses;
  - Working with the faculties of nursing to complete senior practicums to enable the nurses to enter the workforce;
  - Contacting former RNs with ICU experience and other recently retired staff; and
  - Redeployment of anesthesiologists, other physicians, other nurses, respiratory therapists, other allied health professionals and other staff with appropriate skills to work in a critical care environment.

Personal Protective Equipment (PPE)

	Forecast days of supplies inventory at end of April		Forecast days of supplies inventory at end of June	
Category of critical PPE	**Probable[1]**	**Elevated[2]**	**Probable[1]**	**Elevated[2]**
Face shields (single use)	12	5	-11	-13
Goggles	50	29	1	-5
Gowns/coveralls	39	19	19	7
Gloves	110	85	79	63
Procedural masks	76	51	26	15
N95 masks	32	7	-4	-12

Increasing PPE Stocks

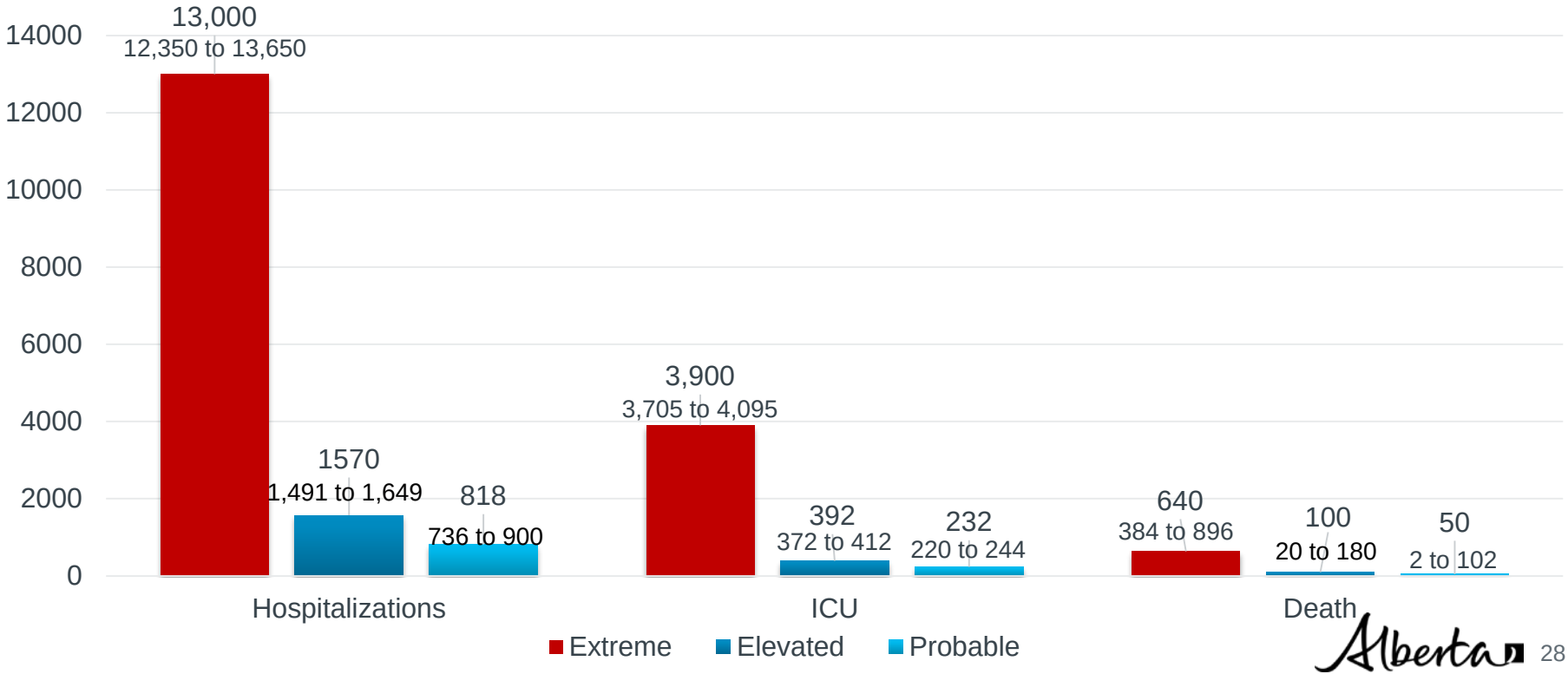
Demand levers

- Tracking PPE inventory and distribution across non-health sites
- Ensuring appropriate PPE according to recommended guidelines
- PPE reuse where safe and appropriate – e.g. sterilizing N95 masks for multiple use

Supply levers

- Increasing number of domestic and global suppliers to meet PPE demands
- Creating and working with local companies to increase production of supplies (e.g. face shields, scrubs, gowns and hand sanitizer)
- Virtual trade show April 8, 2020

Comparison of All Scenarios at the Peak



The Plan

Alberta’s Plan – the next 6 to 8 weeks

- World class testing and surveillance
- Aggressive contact tracing and containment
- Public health Interventions based on evidence of what works
- Supporting Albertans in pushing the peak down
- Supporting fellow Canadians in a time of crisis

What’s next?

- Relaunch Strategy
  - Aggressive system of mass testing, including serological testing
  - Strong tracing and tracking of contacts leveraging technology
  - Strong border screening
  - Use of masks

Endnotes 2 and 3

Apr 22, 2020

COVID-19 in Alberta

Highlights Cases Characteristics Severe outcomes Geospatial Laboratory testing Data export Data notes

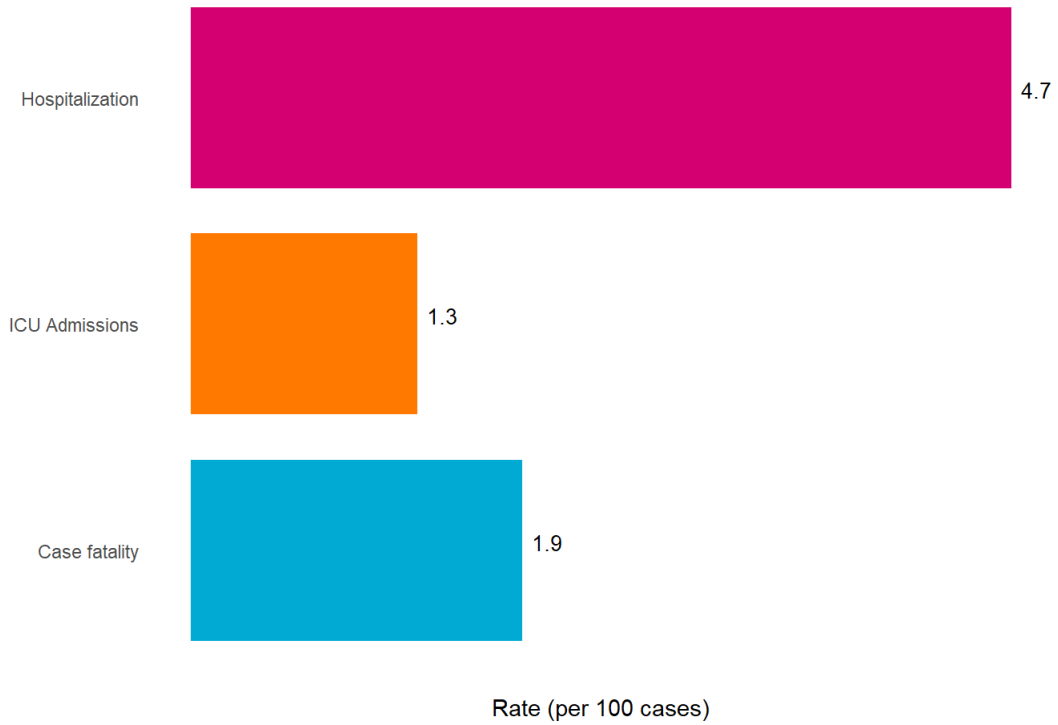


Figure 6: Rate of total hospitalizations, ICU admissions, and deaths among COVID-19 cases in Alberta

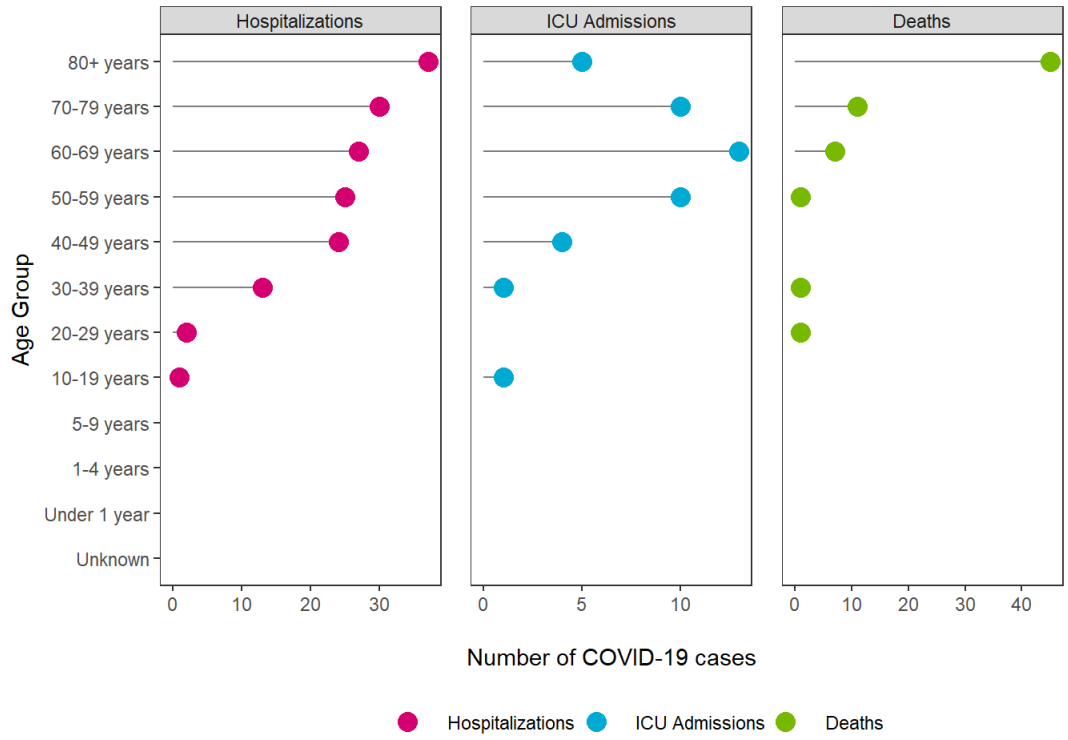


Figure 7: Total hospitalizations, ICU admissions and deaths (ever) among COVID-19 cases in Alberta by age group. Each ICU admission is also included in the total number of hospitalizations.This is based on totals rather than current hospitalizations and ICU admissions.

Table 2. Total Hospitalizations, ICU admissions and deaths (ever) among COVID-19 cases in Alberta by age group

Age Group	Cases	Hospitalized			ICU			Deaths		
	Count	Count	Case rate	Pop. rate	Count	Case rate	Pop. rate	Count	Case rate	Pop. rate
Total	3401	159	4.7	3.6	44	1.3	1.0	66	1.9	1.5
Under 1 year	11	0	0.0	0.0	0	0.0	0.0	0	0.0	0.0
1-4 years	68	0	0.0	0.0	0	0.0	0.0	0	0.0	0.0
5-9 years	61	0	0.0	0.0	0	0.0	0.0	0	0.0	0.0
10-19 years	235	1	0.4	0.2	1	0.4	0.2	0	0.0	0.0
20-29 years	442	2	0.5	0.3	0	0.0	0.0	1	0.2	0.2
30-39 years	660	13	2.0	1.8	1	0.2	0.1	1	0.2	0.1
40-49 years	794	24	3.0	4.0	4	0.5	0.7	0	0.0	0.0
50-59 years	497	25	5.0	4.5	10	2.0	1.8	1	0.2	0.2
60-69 years	308	27	8.8	5.9	13	4.2	2.8	7	2.3	1.5
70-79 years	138	30	21.7	12.2	10	7.2	4.1	11	8.0	4.5

Note:
Based on total hospitalizations and ICU admissions ever.
Row percent is out of the number of cases in each age group.
Each ICU admission is also included in the total number of hospitalization
Case rate (per 100 cases)
Population rate (per 100,000 population)

Age Group	Cases	Hospitalized			ICU			Deaths		
	Count	Count	Case rate	Pop. rate	Count	Case rate	Pop. rate	Count	Case rate	Pop. rate
80+ years	187	37	19.8	27.2	5	2.7	3.7	45	24.1	33.1

Note:
Based on total hospitalizations and ICU admissions ever.
Row percent is out of the number of cases in each age group.
Each ICU admission is also included in the total number of hospitalization
Case rate (per 100 cases)
Population rate (per 100,000 population)

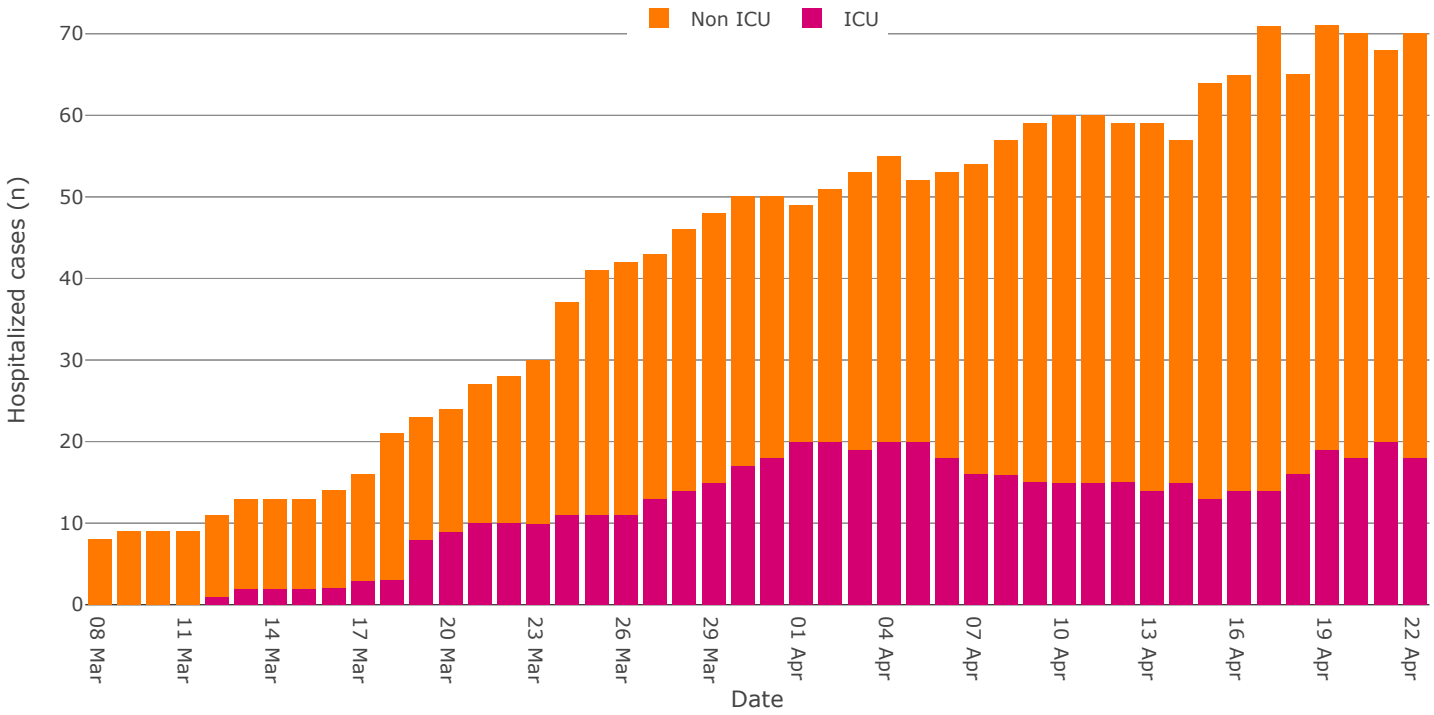
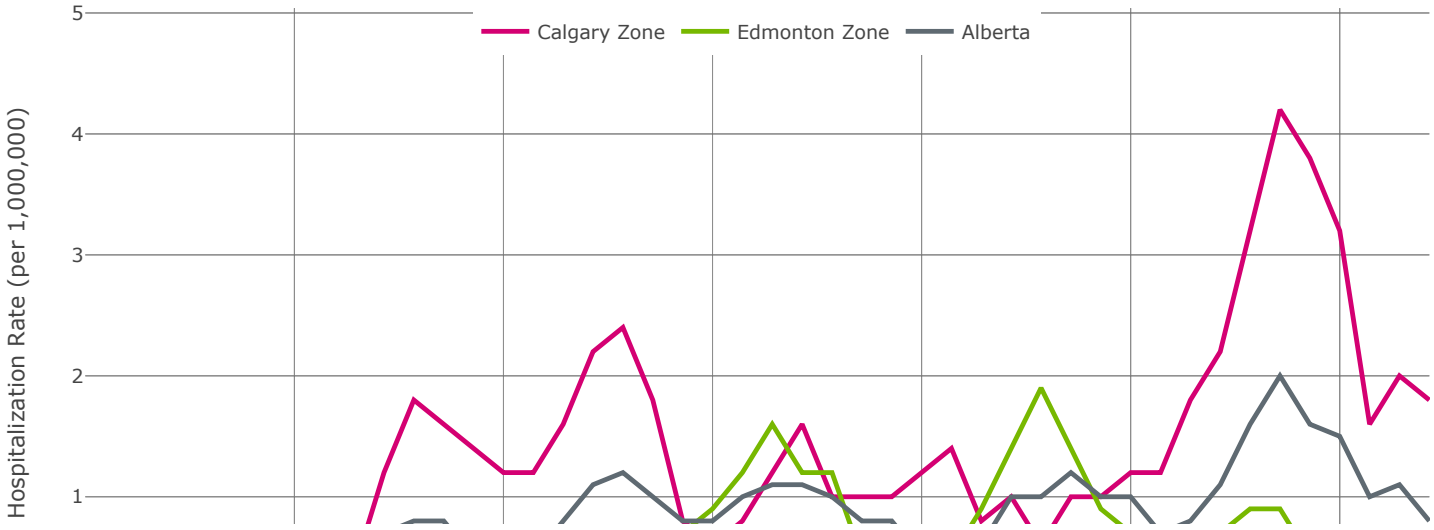


Figure 8: Number of current COVID-19 patients in hospital, ICU and non-ICU



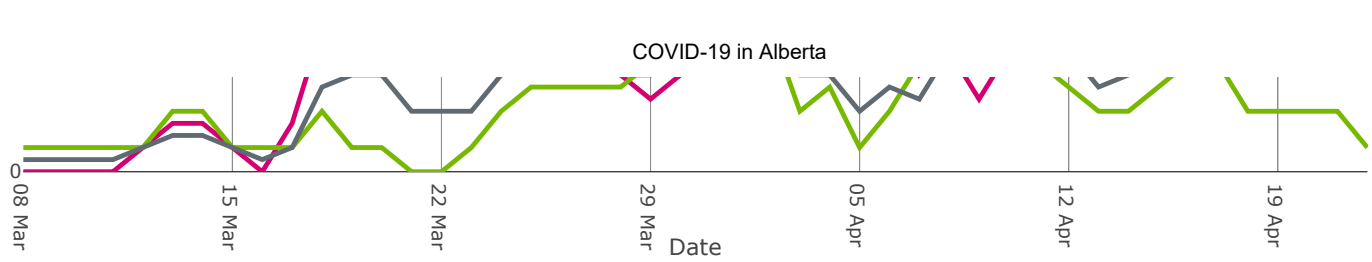


Figure 9: Rate of new hospitalizations (3-day moving average, average of current day and previous two days) by admission date, Alberta, Calgary and Edmonton Zones. Hospitalization in other Zones are still low.

Endnote 4

Fundamental principles of epidemic spread highlight the immediate need for large-scale serological surveys to assess the stage of the SARS-CoV-2 epidemic

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The spread of a novel pathogenic infectious agent eliciting protective immunity is typically characterised by three distinct phases: (I) an initial phase of slow accumulation of new infections (often undetectable), (II) a second phase of rapid growth in cases of infection, disease and death, and (III) an eventual slow down of transmission due to the depletion of susceptible individuals, typically leading to the termination of the (first) epidemic wave. Before the implementation of control measures (e.g. social distancing, travel bans, etc) and under the assumption that infection elicits protective immunity, epidemiological theory indicates that the ongoing epidemic of SARS-CoV-2 will conform to this pattern.

Here, we calibrate a susceptible-infected-recovered (SIR) model to data on cumulative reported SARS-CoV-2 associated deaths from the United Kingdom (UK) and Italy under the assumption that such deaths are well reported events that occur only in a vulnerable fraction of the population. We focus on model solutions which take into consideration previous estimates of critical epidemiological parameters such as the basic reproduction number (R_0), probability of death in the vulnerable fraction of the population, infectious period and time from infection to death, with the intention of exploring the sensitivity of the system to the actual fraction of the population vulnerable to severe disease and death.

Our simulations are in agreement with other studies that the current epidemic wave in the UK and Italy in the absence of interventions should have an approximate duration of 2-3 months, with numbers of deaths lagging behind in time relative to overall infections. Importantly, the results we present here suggest the ongoing epidemics in the UK and Italy started at least a month before the first reported death and have already led to the accumulation of significant levels of herd immunity in both countries. There is an inverse relationship between the proportion currently immune and the fraction of the population vulnerable to severe disease.

This relationship can be used to determine how many people will require hospitalisation (and possibly die) in the coming weeks if we are able to accurately determine current levels of herd immunity. There is thus an urgent need for investment in technologies such as virus (or viral pseudotype) neutralization assays and other robust assays which provide reliable read-outs of protective immunity, and for the provision of open access to valuable data sources such as blood banks and paired samples of acute and convalescent sera from confirmed cases of SARS-CoV-2 to validate these. Urgent development and assessment of such tests should be followed by rapid implementation at scale to provide real-time data. These data will be critical to the proper assessment of the effects of social distancing and other measures currently being adopted to slow down the case incidence and for informing future policy direction.

Disclaimer: (a) This material is not final and is subject to be updated any time. (b) Code used will be made available as soon as possible. (c) Contact for press enquiries: Cairbre Sugrue, cairbre@sugruecomms.com, +44 (0)7502 203 769.

Results

Our overall approach rests on the assumption that only a very small proportion of the population is at risk of hospitalisable illness. This proportion is itself only a fraction of the risk groups already well described in the literature [1–4], including the elderly and those carrying critical comorbidities (e.g. asthma). We used a susceptible-infectious-recovered framework (SIRf) to examine the effects of varying the vulnerable fraction of the population on the transmission dynamics of SARS-CoV-2, fixing other model parameters to ranges supported by previous studies **(Table 1).** We fit the model to cumulative deaths in the United Kingdom and Italy in the first 15 days following the first recorded death to avoid any potential effects of local control strategies implemented since that time.

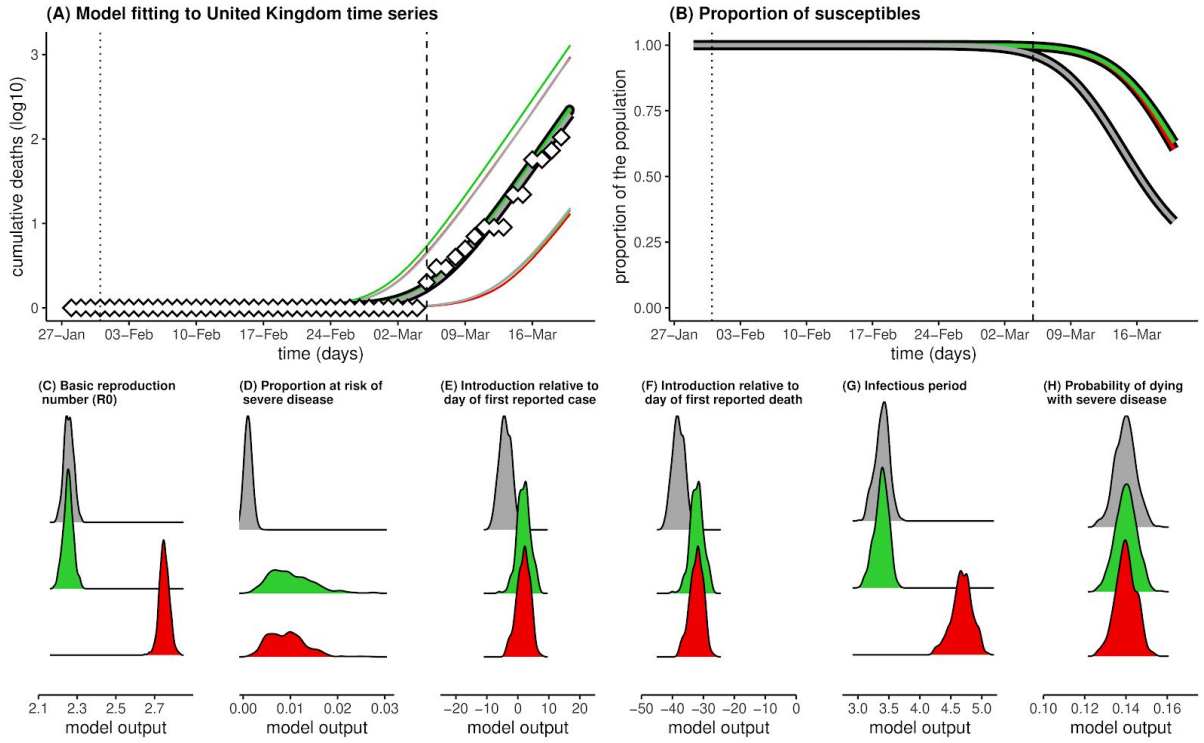


Figure 1. *Results for the United Kingdom for three scenarios:* $R_0 = 2.25$ *and* $\rho = 0.001$ *(grey),* $R_0 = 2.25$ *and* $\rho = 0.01$ *(green), and* $R_0 = 2.75$ *and* $\rho = 0.01$ *(red). MCMC ran for 1 million steps. Results presented are the posteriors (model output) using 1000 samples after a burnout of 50%* ***(A)*** *Model fits showing reported (diamonds) and model (lines) cumulative death counts. Deaths are log10 transformed for visualisation.* ***(B)*** *Mean proportion of the population still susceptible to infection (1-z, see Model).* ***(A-B)*** *Vertical lines mark the date of the first confirmed case (dotted) and date of first confirmed death (dashed).* ***(C)*** *Posteriors for* R_0*,* ***(D)*** *proportion of population at risk of severe disease (*ρ*),* ***(E)*** *Time of introduction relative to the date of the first reported case,* ***(F)*** *Time of introduction relative to the date of first reported death,* ***(G)*** *infectious period,* ***(H)*** *probability of dying with severe disease.*

Three different scenarios under which the model closely reproduces the reported death counts in the UK up to 19/03/2020 are presented in **Figure 1**. Red and green colours represent solutions attached respectively to transmission scenarios with R_0=2.75 and R_0=2.25 (reflecting variation in estimates of R_0 in literature) with the proportion of the

population at risk being distributed around 1%. The model output (posterior) for time of introduction (the start of transmission) place this event a couple of days after the first confirmed case in the country, and over a month before the first confirmed death **(Figures 1E-F)**. In both R_0 scenarios, by the time the first death was reported (05/03/2020), thousands of individuals (~0.08%) would have already been infected with the virus (as also suggested by [5]). By 19/03/2020, approximately 36% (R_0=2.25) and 40% (R_0=2.75) of the population would have already been exposed to SARS-CoV-2. Running the same model with R_0=2.25 and the proportion of the population at risk of severe disease being distributed around 0.1%, places the start of transmission at 4 days prior to first case detection and 38 days before the first confirmed death and suggests that 68% would have been infected by 19/03/2020.

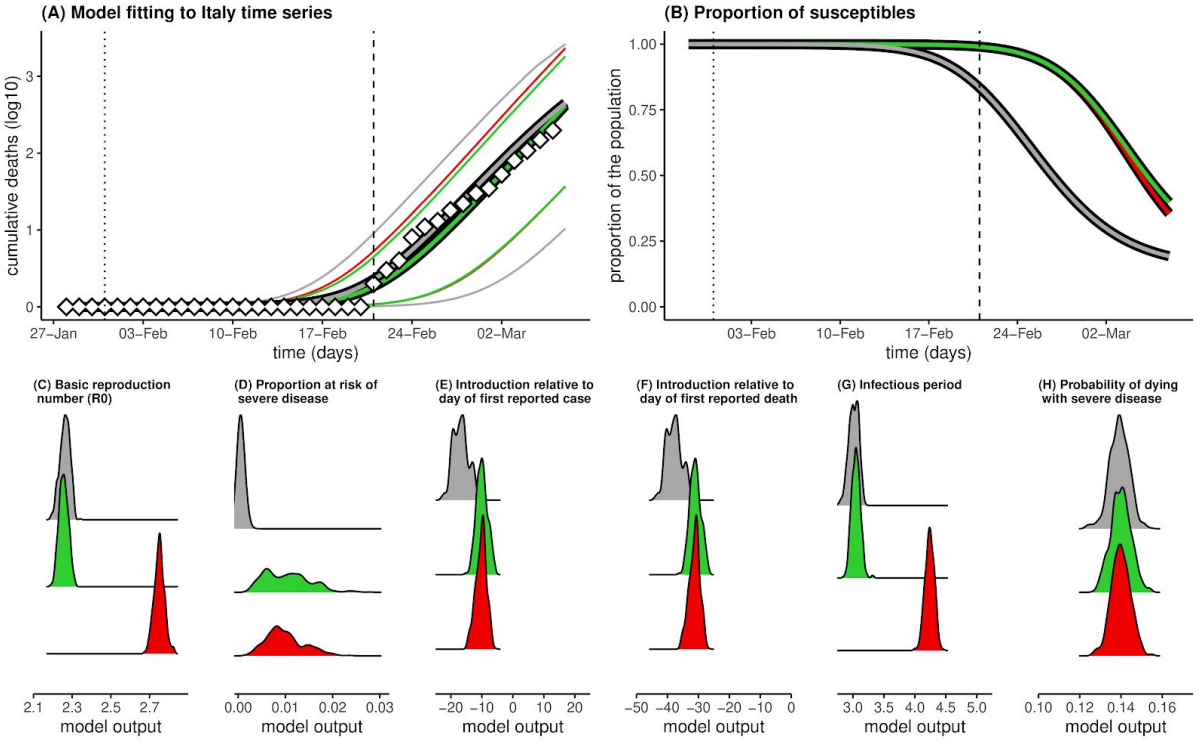


Figure 2. *Results for Italy.* ***(A-H)*** *Legend as in Figure 1.*

The results of the same exercise for Italy (**Figure 2)** place the time of introduction around 10 days before the first confirmed case, and around a month before the first confirmed death **(Figures 2E-F)** when the proportion of the population at risk of severe disease is around 1%. By 06/03/2020, approximately 45 days post introduction, the model suggests that approximately 60% (R_0 = 2.25) and 64% (R_0 = 2.75) of the population would have already been exposed to SARS-CoV-2. When the proportion of the population at risk is around 0.1%, the start of transmission is likely to have occurred 17 days prior to first case detection and 38 days before the first confirmed death with 80% already infected by 06/03/2020.

Overall, these results underscore the dependence of the inferred epidemic curve on the assumed fraction of the population vulnerable to severe disease (ρ) showing significant population level immunity accruing by mid March in the UK as ρ is decreased to plausible values (**Figure 3**). They also suggest a way of determining this fraction by measuring the proportion of the population already exposed to SARS-CoV-2.

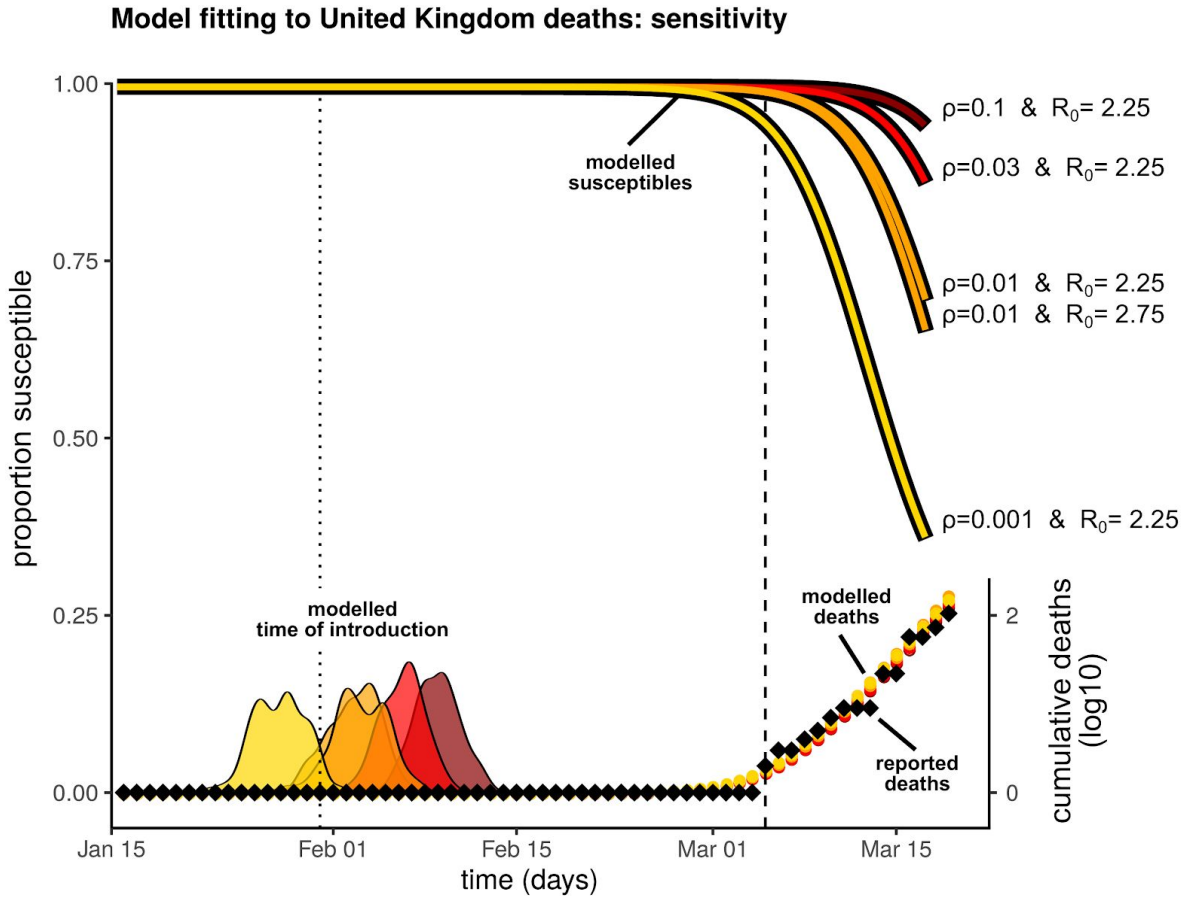


Figure 3. *Sensitivity of results to the fraction of the population vulnerable to severe disease. Four scenarios are presented:* $R_0 = 2.25$ *and* $\rho = 0.1$ *(dark red),* $R_0 = 2.25$ *and* $\rho = 0.03$ *(red),* $R_0 \in \{2.25, 2.75\}$ *and* $\rho = 0.01$ *(both orange),* $R_0 = 2.25$ *and* $\rho = 0.001$ *(yellow). MCMC ran for 1 million steps. Posteriors (model output) were obtained using 1000 samples after a burnout of 50%. Vertical lines mark the date of the first confirmed case (dotted) and date of first confirmed death (dashed).*

Model

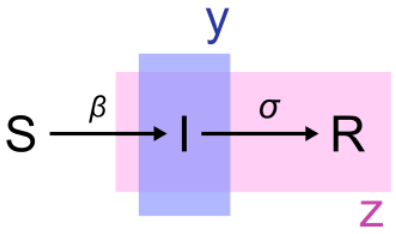
We model a susceptible-infectious-recovered framework (SIRf) [6] to simulate the spread of SARS-CoV-2. The population is separated into those currently contributing to transmission (y, **equation 1**) and those not available for infection (z, **equation 2**). Cumulative death counts (Λ, **equation 3**) are obtained by considering that mortality occurs with probability θ, on a proportion of the population that is at risk of severe disease (ρ) among those already exposed (z); we consider the delay between the time of infection and of death (ψ) as a combination of incubation period and time to death after onset of symptoms. The small proportion of the population that is at risk of severe disease (ρ) is an aggregate model parameter, taking into consideration both a potentially lower risk of infection than the rest of the population, as well as the actual risk of severe disease.

equation 1: $dy/dt = \beta y\,(1-z) - \sigma y$

equation 2: $dz/dt = \beta y\,(1-z)$

equation 3: $\Lambda_t = N\rho\theta z_{t-\psi}$

equation 4: $R_0 = \beta/\sigma$



Model output on cumulative death counts (Λ) is fitted to the reported time series of deaths (see Data) using a Bayesian MCMC approach previously implemented in other modelling studies [7–10]. Model variables are summarized in **Table 1**.

Variable / Parameter		Assumptions / Priors	Support
proportion infectious	y	equation 1	---
proportion of population no longer susceptible	z	equation 2	---
cumulative deaths	Λ	equation 3	---
time (day) of introduction	τ	Uniform distribution (-∞, +∞)	---
basic reproduction number	R_0	Gaussian distributions: G1(M=2.25, SD=0.025), G2(M=2.75, SD=0.025)	[11–13]
infectious period (days)	$1/\sigma$	Gaussian distribution G(M=4.5, SD=1)	[11,14–16]
transmission coefficient	β	$\beta = \sigma R_0$	---
time (days) between infection and death	ψ	Gaussian distribution G(M=17, SD=2)	[14]
probability of dying with severe disease	θ	Gaussian distribution G(M=0.14, SD=0.007)	[1,2,11,17]
proportion of population at risk of severe disease	ρ	Gamma distribution G1(S=5, R=5/0.01), G2(S=5, R=5/0.001)	---
population size	N	UK 66.87M, Italy 60M	---

Table 1 - Model variables and parameters. M=mean. SD=standard deviation. S=scale. R=rate.

Data: cumulative number of deaths

Italy: A time series was obtained from the Italian Department of Civil Protection GitHub repository [18] (accessed on 17/03/2020). We trimmed the data to the first 15 days of death counts above zero (21/02/2020 to 06/03/2020) to include only the initial increase free of effects from local control measures.

UK: A time series was obtained from the John Hopkins University Centre for Systems Science and Engineering COVID-19 GitHub repository [19](accessed 19/03/2020). We trimmed the data to the first 15 days of death counts above zero (05/03/2020 to 19/03/2020) to include only the initial increase free of effects from local control measures.

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Endnote 5

COVID-19 Antibody Seroprevalence in Santa Clara County, California

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April 11, 2020

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Abstract

Background
Addressing COVID-19 is a pressing health and social concern. To date, many epidemic projections and policies addressing COVID-19 have been designed without seroprevalence data to inform epidemic parameters. We measured the seroprevalence of antibodies to SARS-CoV-2 in Santa Clara County.

Methods
On 4/3-4/4, 2020, we tested county residents for antibodies to SARS-CoV-2 using a lateral flow immunoassay. Participants were recruited using Facebook ads targeting a representative sample of the county by demographic and geographic characteristics. We report the prevalence of antibodies to SARS-CoV-2 in a sample of 3,330 people, adjusting for zip code, sex, and race/ethnicity. We also adjust for test performance characteristics using 3 different estimates: (i) the test manufacturer's data, (ii) a sample of 37 positive and 30 negative controls tested at Stanford, and (iii) a combination of both.

Results
The unadjusted prevalence of antibodies to SARS-CoV-2 in Santa Clara County was 1.5% (exact binomial 95CI 1.11-1.97%), and the population-weighted prevalence was 2.81% (95CI 2.24-3.37%). Under the three scenarios for test performance characteristics, the population prevalence of COVID-19 in Santa Clara ranged from 2.49% (95CI 1.80-3.17%) to 4.16% (2.58-5.70%). These prevalence estimates represent a range between 48,000 and 81,000 people infected in Santa Clara County by early April, 50-85-fold more than the number of confirmed cases.

Conclusions
The population prevalence of SARS-CoV-2 antibodies in Santa Clara County implies that the infection is much more widespread than indicated by the number of confirmed cases. Population prevalence estimates can now be used to calibrate epidemic and mortality projections.

Introduction

The first two cases of COVID-19 in Santa Clara County, California were identified in returning travelers on January 31 and on February 1, 2020, and the third case was identified four weeks later on February 27, 2020.[1] In the following month, nearly 1,000 additional cases were identified in Santa Clara County, showing a pattern of rapid case increase reflective of community transmission as well as the scaling up of SARS-CoV-2 viral testing that was common across many communities globally. In some countries, the rapid increase in COVID-19 case counts and hospitalizations has overwhelmed health systems and led to large reductions in social and economic activities. The measures adopted to slow the spread of COVID-19 were justified by projected estimates of health care system capacity and case fatality rate. These projections suggested that, in the absence of strict measures to reduce transmission, the COVID-19 pandemic would overwhelm existing hospital bed and ICU capacity throughout the United States and lead to over 2 million deaths.[2]

Measuring fatality rates and projecting the number of deaths depend on estimates of the total number of infections. To date, in the absence of seroprevalence surveys, estimates of the fatality rate have relied on the number of confirmed cases multiplied by an estimated factor representing unknown or asymptomatic cases to arrive at the number of infections.[3–6] However, the magnitude of that factor is highly uncertain. Because the implications of infection fatality rate and projected deaths are large, the extent of COVID-19 infection under-ascertainment (the multiplier used to arrive from cases to infections) has been a topic of great interest and provided estimates of the number of infections about 1-6-fold higher than the number of cases.[7–10] The extent of infection under-ascertainment has been difficult to assess because of three biasing processes: (i) cases have been diagnosed with PCR-based tests, which do not provide information about resolved infections; (ii) the majority of cases tested early in the course of the epidemic have been acutely ill and highly symptomatic, while most asymptomatic or mildly symptomatic individuals have not been tested; and (iii) PCR-based testing rates have been highly variable across contexts and over time, leading to noisy relationships between the number of cases and infections. If, in the absence of interventions, the epidemic's early doubling time is estimated to be four days[6,11,12], then by February 27th, 2020, when the third case was identified in Santa Clara County, the county may have already had 256 infections.

At the time of this study, Santa Clara County had the largest number of confirmed cases of any county in Northern California (1,094). The county also had several of the earliest known cases of COVID-19 in the state - including one of the first presumed cases of community-acquired disease - making it an especially appropriate location to test a population-level sample for the presence of active and *past* infections.

On April 3rd and 4th, 2020 we conducted a survey of residents of Santa Clara County to measure the seroprevalence of antibodies to SARS-CoV-2 and better approximate the number of infections. Our goal is to provide new and well-measured data for informing epidemic models, projections, and public policy decisions.

Methods

We conducted serologic testing for SARS-CoV-2 antibodies in 3,330 adults and children in Santa Clara County using capillary blood draws and a lateral flow immunoassay. In this section we describe our sampling and recruitment approaches, specimen collection methods, antibody testing procedure, test kit validation, and statistical methods. Our protocol was informed by a World Health Organization protocol for population-level COVID-19 antibody testing.[13] We conducted our study with the cooperation of the

Santa Clara County Department of Public Health. The IRB at Stanford University approved the study prior to recruitment.

Study Participants and Sample Recruitment

We recruited participants by placing targeted advertisements on Facebook aimed at residents of Santa Clara County. We used Facebook to quickly reach a large number of county residents and because it allows for granular targeting by zip code and sociodemographic characteristics.[14] We used a combination of two targeting strategies: ads aimed at a representative population of the county by zip code, and specially targeted ads to balance our sample for under-represented zip codes. In addition, we capped registrations from overrepresented areas. Individuals who clicked on the advertisement were directed to a survey hosted by the Stanford REDcap platform, which provided information about the study.[15] The survey asked for six data elements: zip code of residence, age, sex, race/ethnicity, underlying co-morbidities, and prior clinical symptoms. Over 24 hours, we registered 3,285 adults, and each adult was allowed to bring one child from the same household with them (889 children registered).

Specimen Collection and Testing Methods

We established drive-through test sites in three locations spaced across Santa Clara County: two county parks in Los Gatos and San Jose, and a church in Mountain View. Only individuals with a participant ID were allowed into the testing area. Verbal informed consent was obtained to minimize participant and staff exposure. With participants in their vehicles, sample collectors in personal protective equipment drew 50-200μL of capillary blood into an EDTA-coated microtainer. Tubes were barcoded and linked with the participant ID. Samples were couriered from the collection sites to a test reading facility with steady lighting and climate conditions. Technicians drew whole blood up to a fill line on the manufacturer's pipette and placed it in the test kit well, followed by a buffer. Test kits were read 12-20 minutes after the buffer was placed. Technicians barcoded tests to match sample barcodes and documented all test results.

Test Kit Performance

The manufacturer's performance characteristics were available prior to the study (using 85 confirmed positive and 371 confirmed negative samples). We conducted additional testing to assess the kit performance using local specimens. We tested the kits using sera from 37 RT-PCR-positive patients at Stanford Hospital that were also IgG and/or IgM-positive on a locally developed ELISA assay. We also tested the kits on 30 pre-COVID samples from Stanford Hospital to derive an independent measure of specificity. Our procedure for using these data is detailed below.

Statistical Analysis

Our estimation of the population prevalence of COVID-19 proceeded in three steps. First, we reported the raw frequencies of positive tests as a proportion of the final sample size. Second, we re-weighted our sample by zip code, sex, and race/ethnicity (non-Hispanic White, Asian, Hispanic, and other). We chose these three adjustors because they contributed to the largest imbalance in our sample, and because including additional adjustors would result in small-N bins. Our weights were the zip-sex-race proportion in Santa Clara County divided by the zip-sex-race proportion in our sample, for each zip-sex-race combination in the county and in the sample.

$$weight_{zsr} = \frac{\frac{N^C_{zsr}}{N^C_{total}}}{\frac{N^S_{zsr}}{N^S_{total}}}$$

Where N^C represents county counts, N^S represents sample counts, and the subscripts zsr identifies the unique zip-sex-race groups. These weights were then applied to the entire sample. To provide a concrete example, suppose the populations of two zip codes (A and B) include 10,000 men and 10,000 women. Our sample included 250 men and 500 women from zip A, and 750 men and 1500 women from zip B. This is exemplary of the imbalance in our sample. Applying the formula above, we get a weight of 3 for men in zip A, 1.5 for women in zip A, 1 for men in zip B, and 0.5 for women in zip B.

Third, we adjusted the prevalence for test sensitivity and specificity. Because SARS-CoV-2 lateral flow assays are new, we applied three scenarios of test kit sensitivity and specificity. The first scenario uses the manufacturer's validation data (S1). The second scenario uses sensitivity and specificity from a sample of 37 known positive (RT-PCR-positive and IgG or IgM positive on a locally-developed ELISA) and 30 known pre-COVID negatives tested on the kit at Stanford (S2). The third scenario combines the two collections of samples (manufacturer and local sample) as a single pooled sample (S3). We use the delta method to estimate standard errors for the population prevalence, which accounts for sampling error and propagates the uncertainty in the sensitivity and specificity in each scenario. A more detailed version of the formulas we use in our calculations is available in the Appendix to this paper.

Results

The test kit used in this study (Premier Biotech, Minneapolis, MN) was tested in a Stanford laboratory prior to field deployment. Among 37 samples of known PCR-positive COVID-19 patients with positive IgG or IgM detected on a locally-developed ELISA test, 25 were kit-positive. A sample of 30 pre-COVID samples from hip surgery patients were also tested, and all 30 were negative. The manufacturer's test characteristics relied on samples from clinically confirmed COVID-19 patients as positive gold standard and pre-COVID sera for negative gold standard. Among 75 samples of clinically confirmed COVID-19 patients with positive IgG, 75 were kit-positive, and among 85 samples with positive IgM, 78 were kit-positive. Among 371 pre-COVID samples, 369 were negative. Our estimates of sensitivity based on the manufacturer's and locally tested data were 91.8% (using the lower estimate based on IgM, 95 CI 83.8-96.6%) and 67.6% (95 CI 50.2-82.0%), respectively. Similarly, our estimates of specificity are 99.5% (95 CI 98.1-99.9%) and 100% (95 CI 90.5-100%). A combination of both data sources provides us with a combined sensitivity of 80.3% (95 CI 72.1-87.0%) and a specificity of 99.5% (95 CI 98.3-99.9%).

Our study included 3,439 individuals that registered for the study and arrived at testing sites. We excluded observations of individuals who could not be tested (e.g. unable to obtain blood or blood clotted, N=49), whose test results could not be matched to their personal data (e.g. if an incorrect participant ID was recorded onsite, N=30) , who did not reside in Santa Clara County (N=29), and who had invalid test results (no Control band, N=1). This yielded an analytic sample of 3,330 individuals with complete records including survey registration, attendance at a test site for specimen collection, and lab results (Figure 1). The sample distribution meaningfully deviated from that of the Santa Clara County population along several dimensions: sex (63% in sample was female, 50% in county); race (8% of the sample was Hispanic, 26% in the county; 19% of the sample was Asian, 28% in the county); and zip

distribution (median participant density per 1,000 population 1.6, IQR 0.9-3.6). Table 1 includes demographic characteristics of our unadjusted sample, population-adjusted sample, and Santa Clara County.[16] Figure 2 shows the geographical zip code distribution of study participants in the county (counts and density per 1,000 population).

The total number of positive cases by either IgG or IgM in our unadjusted sample was 50, a crude prevalence rate of 1.50% (exact binomial 95% CI 1.11-1.97%). After weighting our sample to match Santa Clara County by zip, race, and sex, the prevalence was 2.81% (95% CI 2.24-3.37 without clustering the standard errors for members of the same household, and 1.45-4.16 with clustering). We further improved our estimation using the available data on test kit sensitivity and specificity, using the three scenarios noted above. The estimated prevalence was 2.49% (95CI 1.80%-3.17%) under the S1 scenario, 4.16% (95CI 2.58%-5.70%) under the S2 scenario, and 2.75% (95CI 2.01%-3.49%) under the S3 scenario. Notably, the uncertainty bounds around each of these population prevalence estimates propagates the uncertainty in each of the three component parameters: sample prevalence, test sensitivity, and test specificity.

Discussion

After adjusting for population and test performance characteristics, we estimate that the seroprevalence of antibodies to SARS-CoV-2 in Santa Clara County is between 2.49% and 4.16%, with uncertainty bounds ranging from 1.80% (lower uncertainty bound of the lowest estimate), up to 5.70% (upper uncertainty bound of the highest estimate). Test performance characteristics are the most critical driver of this range, with lower estimates associated with data suggesting the test has a high sensitivity for identifying SARS-CoV-2, and higher estimates resulting from data suggesting over 30% of positive cases are missed by the test.

These results represent the first large-scale community-based prevalence study in a major US county completed during a rapidly changing pandemic, and with newly available test kits. We consider our estimate to represent the best available current evidence, but recognize that new information, especially about the test kit performance, could result in updated estimates. For example, if new estimates indicate test specificity to be less than 97.9%, our SARS-CoV-2 prevalence estimate would change from 2.8% to less than 1%, and the lower uncertainty bound of our estimate would include zero. On the other hand, lower sensitivity, which has been raised as a concern with point-of-care test kits, would imply that the population prevalence would be even higher. New information on test kit performance and population should be incorporated as more testing is done and we plan to revise our estimates accordingly.

The most important implication of these findings is that the number of infections is much greater than the reported number of cases. Our data imply that, by April 1 (three days prior to the end of our survey) between 48,000 and 81,000 people had been infected in Santa Clara County. The reported number of confirmed positive cases in the county on April 1 was 956, 50-85-fold lower than the number of infections predicted by this study.[17] The infection to case ratio, also referred to as an under-ascertainment rate, of at least 50, is meaningfully higher than current estimates.[10,18] This ascertainment rate is a fundamental parameter of many projection and epidemiologic models, and is used as a calibration target for understanding epidemic stage and calculating fatality rates.[19,20] The under-ascertainment for COVID-19 is likely a function of reliance on PCR for case identification which misses convalescent cases, early spread in the absence of systematic testing, and asymptomatic or lightly symptomatic infections that go undetected.

The under-ascertainment of infections is central for better estimation of the fatality rate from COVID-19. Many estimates of fatality rate use a ratio of deaths to lagged cases (because of duration from case confirmation to death), with an infections-to-cases ratio in the 1-5-fold range as an estimate of under-ascertainment.[3,4,21] Our study suggests that adjustments for under-ascertainment may need to be much higher.

We can use our prevalence estimates to approximate the infection fatality rate from COVID-19 in Santa Clara County. As of April 10, 2020, 50 people have died of COVID-19 in the County, with an average increase of 6% daily in the number of deaths. If our estimates of 48,000-81,000 infections represent the cumulative total on April 1, and we project deaths to April 22 (a 3 week lag from time of infection to death[22]), we estimate about 100 deaths in the county. A hundred deaths out of 48,000-81,000 infections corresponds to an infection fatality rate of 0.12-0.2%. If antibodies take longer than 3 days to appear, if the average duration from case identification to death is less than 3 weeks, or if the epidemic wave has peaked and growth in deaths is less than 6% daily, then the infection fatality rate would be lower. These straightforward estimations of infection fatality rate fail to account for age structure and changing treatment approaches to COVID-19. Nevertheless, our prevalence estimates can be used to update existing fatality rates given the large upwards revision of under-ascertainment.

While our prevalence estimates of 2.49% to 4.16% are representative of the situation in Santa Clara County as of April 4, other areas are likely to have different seroprevalence estimates based on effective contact rates in the community, social distancing policies to date, and relative disease progression. Our prevalence estimate also suggests that, at this time, a large fraction of the population remains unexposed in Santa Clara County. Repeated serologic testing in different geographies, spaced a few weeks apart, could establish extent of infection over time.

This study had several limitations. First, our sampling strategy selected for members of Santa Clara County with access to Facebook and a car to attend drive-through testing sites. This resulted in an over-representation of white women between the ages of 19 and 64, and an under-representation of Hispanic and Asian populations, relative to our community. Those imbalances were partly addressed by weighting our sample population by zip code, race, and sex to match the county. We did not account for age imbalance in our sample, and could not ascertain representativeness of SARS-CoV-2 antibodies in homeless populations. Other biases, such as bias favoring individuals in good health capable of attending our testing sites, or bias favoring those with prior COVID-like illnesses seeking antibody confirmation are also possible. The overall effect of such biases is hard to ascertain.

The Premier Biotech serology test used in this study has not been approved by the FDA by the time of the study, and validation studies for this assay are ongoing. We used existing test performance data to establish a range of sensitivity and specificity, including reliable but small-size data sourced at Stanford. Test sensitivity varied between the manufacturer's data and the local data. It is possible that asymptomatic or mildly symptomatic individuals may generate only low-titer antibodies, and that sensitivity may be even lower if there are many such cases.[23] Additional validation of the assays used could improve our estimates and those of ongoing serosurveys.

Several teams worldwide have started testing population samples for SARS CoV-2 antibodies, with preliminary findings consistent with a large under-ascertainment of SARS CoV-2 infections. Reports from the town of Robbio, Italy, where the entire population was tested, suggest at least 10% seropositivity;[24] and data from Gangelt, a highly affected area in Germany,[25] point to 14% seropositivity.

A recent effort to test the town of Telluride, Colorado is underway, and interim results suggest a prevalence just under 2%.[26] Our data from Santa Clara county suggest higher spread of the infection than Telluride but lower than some areas in Europe.

We conclude that based on seroprevalence sampling of a large regional population, the prevalence of SARS-CoV-2 antibodies in Santa Clara County was between 2.49% and 4.16% by early April. While this prevalence may be far smaller than the theoretical final size of the epidemic,[27] it suggests that the number of infections is 50-85-fold larger than the number of cases currently detected in Santa Clara County. These new data should allow for better modeling of this pandemic and its progression under various scenarios of non-pharmaceutical interventions. While our study was limited to Santa Clara County, it demonstrates the feasibility of seroprevalence surveys of population samples now, and in the future, to inform our understanding of this pandemic's progression, project estimates of community vulnerability, and monitor infection fatality rates in different populations over time. It is also an important tool for reducing uncertainty about the state of the epidemic, which may have important public benefits.

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Figures

Figure 1

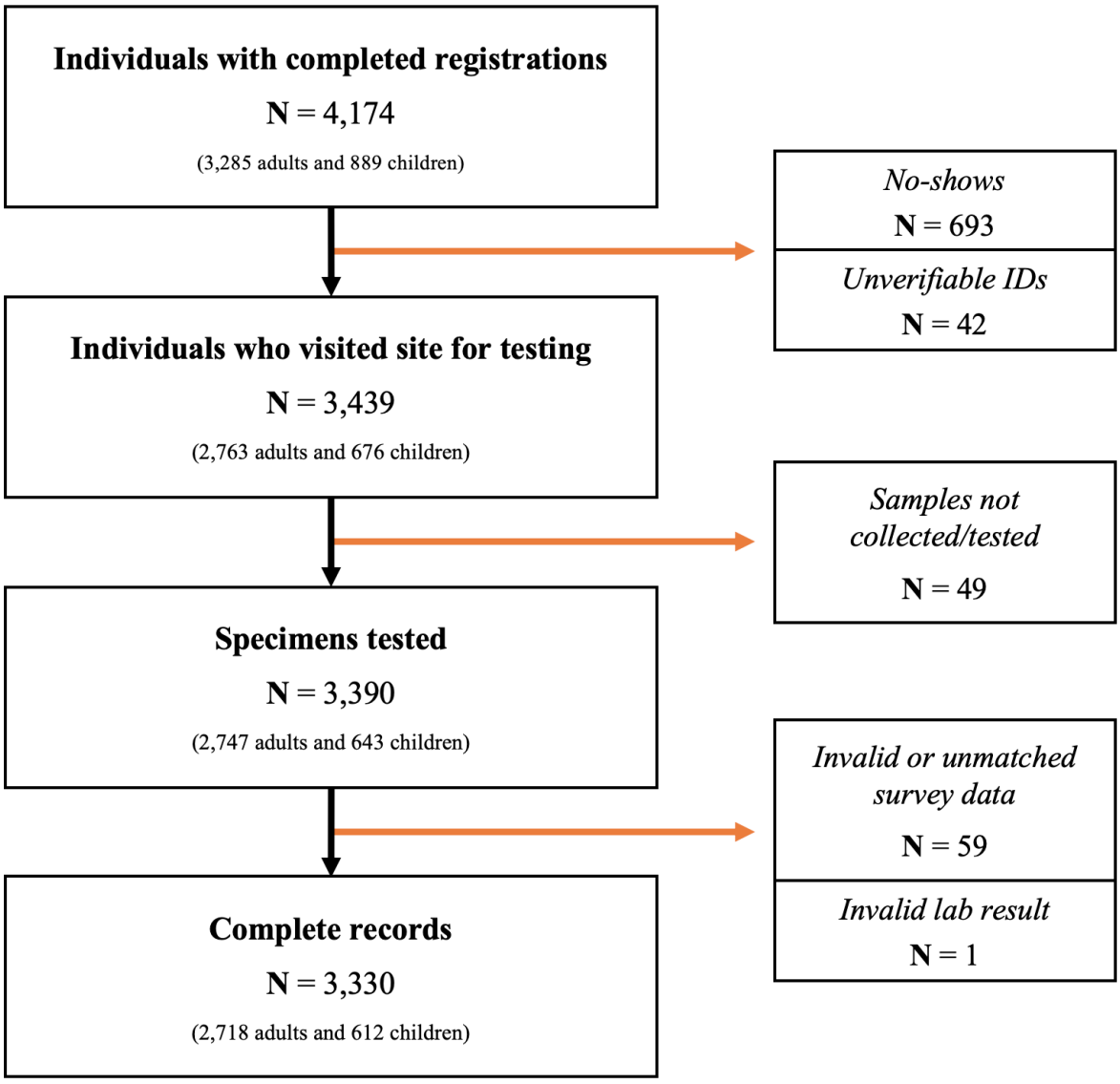
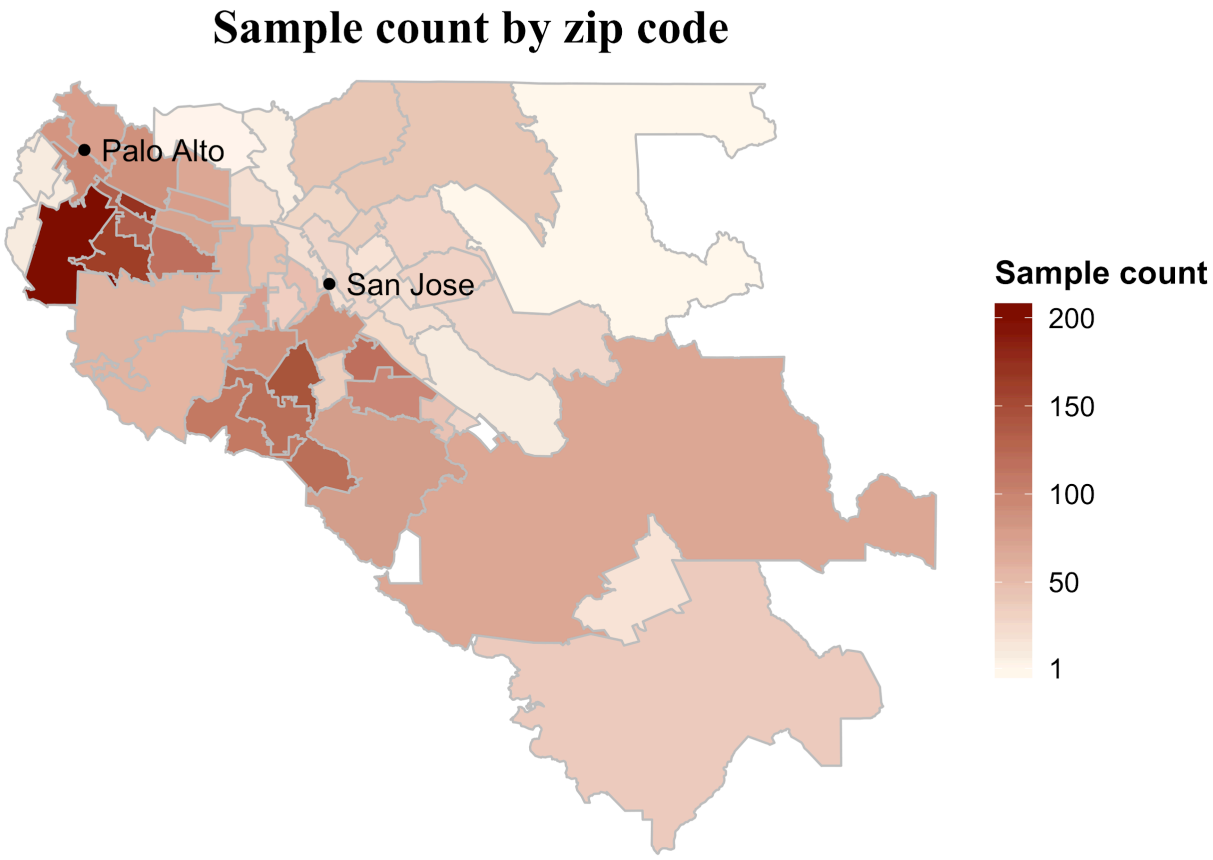


Figure 1: Of 3,439 individuals that arrived for testing, samples could not be obtained or tested (e.g. blood clotted) on 49, and an additional 60 were excluded because of invalid data (e.g. residence outside Santa Clara County), test data that could not be matched to a participant, or invalid test results. The final sample contained 3,330 records.

Figure 2



Santa Clara County

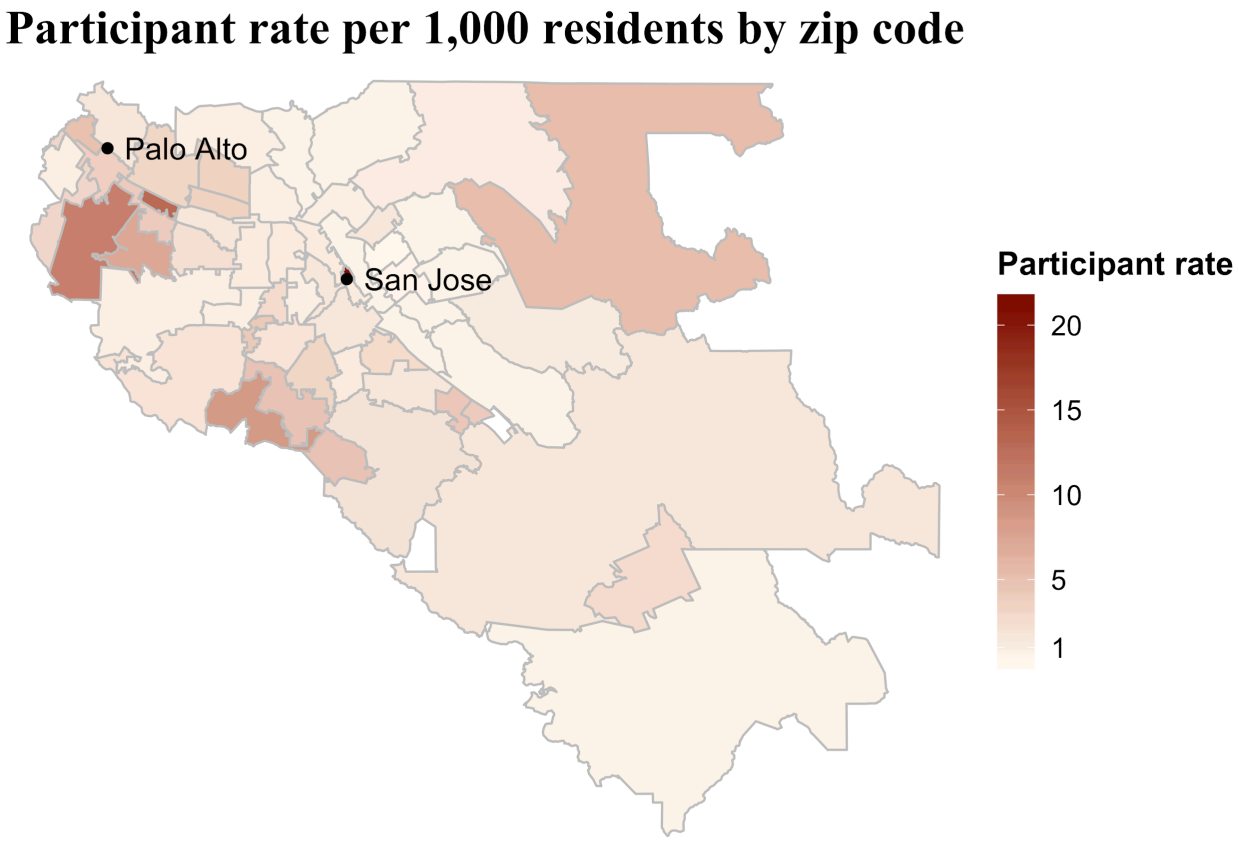


Figure 2: The number of registrations with complete records in our analytic dataset by zip code (panel A), and the participant rate per 1,000 residents in the zip code (panel B).

Tables

Table 1: Sample characteristics, relative to Santa Clara County population estimates from the 2018 American Community Survey

Characteristic		Sample - unadjusted	Sample - adjusted	County
Population (N)		3,330	3,330	1,943,411
Women (%)		63.1	49.7	49.5
Men (%)		36.9	50.3	50.5
Age (%)	0-4	2.1	2.6	6.2
	5-18	16.5	14.5	18.6
	19-64	76.3	78.4	62.3
	⩾65	5.0	4.5	12.9
Race/ethnicity (%)	Non-hispanic white	64.1	35.4	33.1
	Hispanic	8.0	24.9	26.3
	Asian	18.7	28.9	27.8
	Other	9.2	10.8	12.8

Table 2: Prevalence estimation in Santa Clara County. We report the prevalence and uncertainty bounds of estimates from unadjusted frequency counts, population-adjusted estimates, and population-adjusted + test performance-adjusted estimates. For the population-adjusted + test performance-adjusted estimates, we show estimates using the three test performance scenarios described in the Methods. For each point estimate, we present the method used to estimate the uncertainty bounds. Where noted, we clustered the standard errors for participants that brought a child with them (members of the same household).

Approach		Point estimate (%)	Uncertainty (95% CI)
Unadjusted (%)		50/3,330 = 1.50	1.11-1.97 (binomial exact) 1.07-1.93 (normal approximation, cluster adjusted)
Population-adjusted (only, %)		2.81	2.24-3.37 (normal approximation) 1.45-4.16 (normal approximation, cluster adjusted)
Population & test-performance adjustment	Manufacturer's data	2.49	1.80-3.17 (delta method)
	Local Stanford data	4.16	2.58-5.70 (delta method)
	Manufacturer's data + local data	2.75	2.01-3.49 (delta method)

Article Information

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Conflict of interest
None. Of note, test kits were purchased from Premier Biotech for this study, and none of the authors have a relationship to the test manufacturer (beyond purchasing the tests).

Funding/Support
We acknowledge many individual donors who generously supported this project with gift awards.

Role of Funders
Our funders had no role in the design and conduct of the study, nor in the decision to prepare and submit the manuscript for publication.

Endnote 6

USC-LA County Study: Early Results of Antibody Testing Suggest Number of COVID-19 Infections Far Exceeds Number of Confirmed Cases in Los Angeles County

*Watch the L.A. County Department of Public Health briefing livestream at 1 p.m. on **Facebook**.*

Contact: Leigh Hopper, USC Media Relations, **uscnews@usc.edu** or (213) 740-2215;

Carl Kemp, LA County Public Health Communications, **ckemp@ph.lacounty.gov** or (323) 365-7260

Los Angeles (April 20, 2020) – USC and the Los Angeles County Department of Public Health (Public Health) today released preliminary results from a collaborative scientific study that suggests infections from the new coronavirus are far more widespread – and the fatality rate much lower — in L.A. County than previously thought.

The results are from the first round of an ongoing study by USC researchers and Public Health officials. They will be conducting antibody testing over time on a series of representative samples of adults to determine the scope and spread of the pandemic across the county.

Based on results of the first round of testing, the research team estimates that approximately 4.1% of the county's adult population has antibody to the virus. Adjusting this estimate for statistical margin of error implies about 2.8% to 5.6% of the county's adult population has antibody to the virus—which translates to approximately 221,000 to 442,000 adults in the county who have had the infection. That estimate is 28 to 55 times higher than the 7,994 confirmed cases of COVID-19 reported to the county by the time of the study in early April. The number of COVID-related deaths in the county has now surpassed 600.

"We haven't known the true extent of COVID-19 infections in our community because we have only tested people with symptoms, and the availability of tests has been limited," said lead investigator Neeraj Sood, a USC professor of public policy at USC Price School for Public Policy and senior fellow at USC Schaeffer Center for Health Policy and Economics. "The estimates also suggest that we might have to recalibrate disease prediction models and rethink public health strategies."

The results have important implications for public health efforts to control the local epidemic.

"These results indicate that many persons may have been unknowingly infected and at risk of transmitting the virus to others," said Dr. Barbara Ferrer, director of the L.A. County Department of Public Health. "These findings underscore the importance of expanded polymerase chain reaction

(PCR) testing to diagnose those with infection so they can be isolated and quarantined, while also maintaining the broad social distancing interventions."

The antibody test is helpful for identifying past infection, but a PCR test is required to diagnose current infection.

"Though the results indicate a lower risk of death among those with infection than was previously thought, the number of COVID-related deaths each day continues to mount, highlighting the need for continued vigorous prevention and control efforts," said Dr. Paul Simon, chief science officer at L.A. County Department of Public Health and co-lead on the study.

The study's results have not yet been peer reviewed by other scientists. The researchers plan to test new groups of participants every few weeks in coming months to gauge the pandemic's trajectory in the region.

About the study
With help from medical students from the Keck School of Medicine of USC, USC researchers and Public Health officials conducted drive-through antibody testing April 10th and 11th at six sites. Participants were recruited via a proprietary database that is representative of the county population. The database is maintained by LRW Group, a market research firm.

The researchers used a rapid antibody test for the study. The FDA allows such tests for public health surveillance to gain greater clarity on actual infection rates. The test's accuracy was further assessed at a lab at Stanford University using blood samples that were positive and negative for COVID-19.

In addition to Sood and Simon, other authors and institutions contributing to the study include Peggy Ebner of the Keck School; Daniel Eichner of the Sports Medicine Research & Testing Laboratory; Jeffrey Reynolds of LRW Group; Eran Bendavid and Jay Bhattacharya of Stanford University School of Medicine.

The study was supported with funding from USC Schwarzenegger Institute, USC Lusk Center, USC President's Office, Jedel Foundation, LRW Group, Soap Box Sample, and several individual donors.

More information

- A recent Q&A with Neeraj Sood on antibody testing can be found **here**.
- See the Los Angeles County's April 16, 2020, **Health Advisory SARS-CoV2 Serology Advisory** for clarification on antibody testing.
- B-roll and photos from the April 10-11, 2020 antibody testing conducted in Los Angeles can be found **here**.

To learn more about the L.A. County Department of Public Health and the work they do, visit the following sites and pages:

- L.A. County Channel: **http://bit.ly/CountyChannel**
- Online: **http://publichealth.lacounty.gov/**
- Facebook: **https://www.facebook.com/countyofla/**
- Twitter: **https://twitter.com/LAPublicHealth**
- YouTube: **https://www.youtube.com/LAPublicHealth**

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Endnote 8

Gov. Ron DeSantis says Florida has flattened the curve

'We have flattened the curve': Gov. Ron DeSantis says Florida's efforts against COVID-19 have been successful

Gov. DeSantis said criticisms of Florida's response to the virus -- namely thos he said predicted Florida that hospitals would be overwhelmed -- proved to l false.

TALLAHASSEE, Fla. — Florida Gov. Ron DeSantis said during a news conference Tuesday afternoon th the state has flattened the curve in regards to COVID-19.

DeSantis said criticisms of Florida's response to the virus -- namely those he said predicted Florida hospitals would be overwhelmed -- proved to be false.

"Those predictions have been false," DeSantis said. "Our work is succeeding. We have flattened the cu

The governor said available hospital beds in the state have actually increased since the start of the pandemic and that newly constructed field hospitals in South Florida that were meant to take on an overflow of patients currently sit empty.

“We heard report after report saying it was just a matter of time before Florida’s hospital system was overwhelmed with COVID-19 patients,” DeSantis said.

As of 5:30 p.m. Tuesday, there are 27,869 confirmed cases of COVID-19 across Florida and a reported 4,226 hospitalizations due to the virus.

DeSantis also announced more personal protection equipment will be sent to Florida health care work in long-term health care facilities. The incoming PPE includes about 4 million masks, 200,000 face shi and 500,000 gloves.

The state is also working to increase testing for antibodies that can help fight against the virus.

RELATED: **LIVE BLOG: Some non-essential Georgia businesses allowed to reopen April 24**

RELATED: **100+ COVID-19 questions answered: Send yours and we'll work to get answers**

Endnote 9

Prognosis

Sweden Says Controversial Virus Strategy Proving Effective

By Niclas Rolander
Updated on

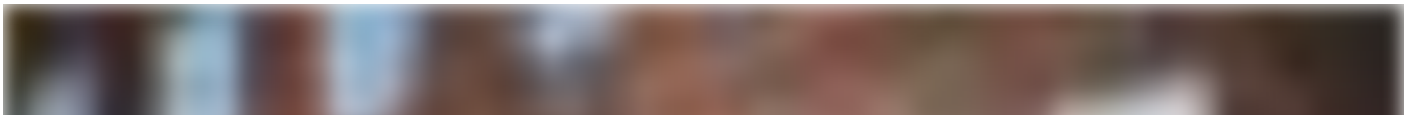
When and How Will the Coronavirus Pandemic End?

Sign up here for our daily coronavirus newsletter on what you need to know, and subscribe to our Covid-19 podcast for the latest news and analysis.

Sweden's unusual approach to fighting the coronavirus pandemic is starting to yield results, according to the country's top epidemiologist.

Anders Tegnell, the architect behind Sweden's relatively relaxed response to Covid-19, told local media the latest figures on infection rates and fatalities indicate the situation is starting to stabilize.

"We're on a sort of plateau," Tegnell told Swedish news agency TT.



Anders Tegnell *Photographer: Jonathan Nackstrand/AFP via Getty Images*

Sweden has left its schools, gyms, cafes, bars and restaurants open throughout the spread of the pandemic. Instead, the government has urged citizens to act responsibly and follow social distancing guidelines.

The spread of Covid-19 across the globe is triggering different responses across national and even state borders, as authorities struggle to contain an outbreak about which much remains unknown.

More From
Prognosis

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It’s unclear which strategy will ultimately prove most effective, and even experts in Sweden warn it’s too early to draw conclusions. But given the huge economic damage caused by strict

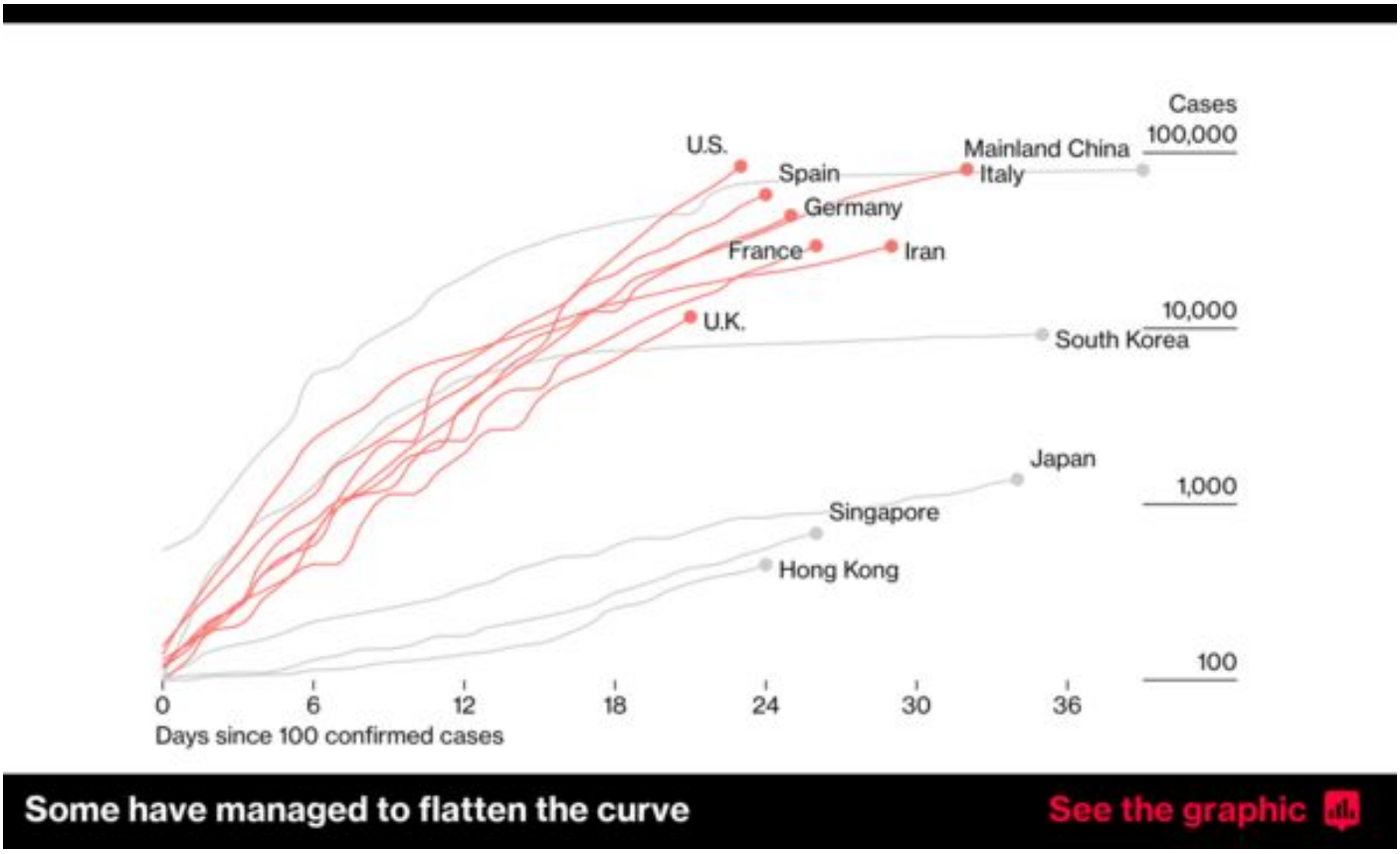
It's too early to draw conclusions. But given the huge economic damage caused by strict lockdowns, the Swedish approach has drawn considerable interest around the world.

Part of that approach relies on having access to one of the world's best-functioning health-care systems. At no stage did Sweden see a real shortage of medical equipment or hospital capacity, and tents set up as emergency care facilities around the country have mostly remained empty.

Death Rates

As of Sunday, Sweden had reported 1,540 deaths tied to Covid-19, an increase of 29 from Saturday. That's considerably more than in the rest of Scandinavia, but much less than in Italy, Spain and the U.K., both in absolute and relative terms.

Tegnell isn't the only high-level official in Sweden to claim the country may be over the worst.



Some have managed to flatten the curve See the graphic

"The trend we have seen in recent days, with a more flat curve -- where we have many new cases, but not a daily increase -- is stabilizing," Karin Tegmark Wisell, head of the microbiology department at Sweden's Public Health Authority, said on Friday. "We are seeing the same pattern for patients in intensive care."

Just two weeks ago, the picture was considerably bleaker, and Prime Minister Stefan Lofven

suggested the government may need to review its approach amid the prospect of thousands of Swedish deaths. In particular, the failure to protect people in nursing homes has stood out as a clear weakness, which has contributed to higher death rates than in neighboring countries.

"The protection for people in elderly care should have been better," Lofven said last week. "We need to look closer at what has gone wrong."

Yet overall, Lofven's strategy has won the approval of Swedes, and his personal popularity has soared.

"I have very high confidence in the Swedish authorities that manage this," Volvo Cars CEO Hakan Samuelsson said in a phone interview. "It's a hard balance to strike, but I have full confidence in the measures that Sweden has taken."

Volvo, which was forced to halt production across Europe and furlough about 20,000 Swedish employees, will resume production at its Swedish plants on Monday.

"Our measures are all based on individuals taking responsibility, and that is also an important part of the Swedish model," Samuelsson said.

The Economy

Sweden's Covid-19 strategy may ultimately result in a smaller -- albeit historically deep -- economic contraction than the rest of Europe is now facing, according to HSBC Global Research economist James Pomeroy.

"While Sweden's unwillingness to lock down the country could ultimately prove to be ill-judged, for now, if the infection curve flattens out soon, the economy could be better placed to rebound," he said.

Pomeroy pointed to some Swedish characteristics that may be helping the country deal with the current crisis. More than half of Swedish households are single-person, making social distancing easier to carry out. More people work from home than anywhere else in Europe, and everyone has access to fast Internet, which helps large chunks of the workforce stay productive away from the office.

And while many other countries have introduced strict laws, including hefty fines if people are caught breaching newly minted social-distancing laws, Swedes appear to be following such guidelines without the need for legislation. Trips from Stockholm to Gotland -- a popular

vacation destination -- dropped by 96% over the Easter weekend, according to data from the country's largest mobile operator, Telia Company. And online service Citymapper's statistics indicate an almost 75% drop in mobility in the capital.

Sweden also recently pushed back against the notion that there's little to no social distancing going on.

"We don't have a radically different view," Foreign Minister Ann Linde said in an interview with Radio Sweden. "The government has made a series of decisions that affect the whole society. It's a myth that life goes on as normal in Sweden."

(Adds reference to controversy around nursing homes)

Endnote 10

Stockholm hospitals brace for 'increasing coronavirus storm'

Healthcare workers in protective clothes at an infectious diseases clinic in Kalmar. File photo: Mikael Fritzon / TT

The Local

30 March 2020 | 11:25 CEST+02:00

The demand for health care in Stockholm is growing rapidly, health director in the Stockholm region Björn Eriksson said on Monday as the coronavirus outbreak continues to pile pressure

on hospitals. But he said that thus far, the capital has been well prepared.

"We can see right now that the storm is here and it is increasing in strength. The trend is very clear and it is that the need for care is increasing rapidly day by day," the healthcare director told reporters.

The pressure on intensive care units in Stockholm's hospitals is increasing drastically but authorities say the system has so far managed to cope.

"Thus far the health care system has been one step ahead of the virus", Eriksson told Swedish radio.

- **Coronavirus LATEST: Follow the latest updates from the outbreak in Sweden**

Over the last couple of days, Stockholm's health care system has been completely transformed to manage the rise in patients in need of medical assistance.

Hospitals have doubled their intensive care capacity within ten days, Eriksson told a press conference Monday morning. The next step is to triple capacity.

"We do not see any slowdown in the rate of increase; quite the contrary," Eriksson said. But he added: "Right now, we have available capacity at the hospitals, because we have been able to expand capacity so much. It's about hoping for the best but preparing for the worst."

A field hospital has been installed just outside Stockholm, to add 140 beds to the 450 already made available for those being treated for Covid-19. Only patients being treated for the new virus will receive care at the field hospital, and none have been treated there so far.

If needed, it will be possible to expand the field hospital to hold 600 beds, and this is expected to be complete before Easter.

A key task at the field hospital was preparing to offer oxygen treatment, which is used in the care of most patients who are hospitalised with Covid-19. Getting such a large oxygen tank in place usually takes three to four months, but in the new field hospital this was done in three days.

- **How you can help others in Sweden during the coronavirus outbreak**

According to the latest figures, the Stockholm region has had 1,657 confirmed cases and 68 fatalities as of the afternoon of March 29th.

Countrywide approximately 3,700 people have tested positive for corona, with 110 fatalities. And at least 280 people have received care at an intensive care unit.

However the real number of coronavirus cases in the country is likely far higher.

The Stockholm region has been hit hardest. "It's for real now, the virus is here and it is spreading quickly" an unnamed doctor in the capital told Dagens Nyheter last week.

"What the citizens of Stockholm can help with is to limit their social contact."

Everyone in Sweden has been asked to avoid non-essential domestic travel, particularly over the usually busy Easter period, in order to limit the spread of the virus. This is considered to be particularly important for people from Stockholm, the current epicentre of Sweden's outbreak, who typically travel to regions which have warned they do not have the healthcare capacity to care for the sudden rise in cases this could bring.

"We've got it under control, but it's extremely tough", nurse Anna Helmerson at Karolinska University Hospital told TT news. The staff at the intensive care unit is now working 12.5 hour shifts, caring for three times the usual number of patients.

Thousands of people have applied to help out in the Stockholm region's healthcare system. Around 6,500 people including doctors, nurses and students have applied, which the region's healthcare director described as a "fantastic response".

The region has now paused its recruitment of extra help, but the healthcare director said they expected to need further help soon. The website to bookmark if you're interested is here.

coronavirus