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EVIDENCE SEARCH REPORT

RESEARCH QUESTION: What frequency of repeat population screening will be required? (rate of infection over time)	UNIQUE IDENTIFIER: LAB042202-01 ESR
REQUESTED RESOURCES: • medRxiv • CDC website/database • Google • Google Scholar • UpToDate • Medline • Embase • CINAHL • PubMed • WHO Global Research on COVID-19 • PHAC COVID-19 • LitCOVID	
LIMITS/EXCLUSIONS/INCLUSIONS: English	
DATE: APRIL 23, 2020	
LIBRARIAN: Brianna Howell-Spooner	REQUESTOR: Dr. Bruce Reeder
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CITE AS: Howell-Spooner, B. What frequency of repeat population screening will be required? 2020 Apr 23; Document no.: LAB042202-01 ESR. In: COVID-19 Rapid Evidence Reviews [Internet]. SK: SK COVID Evidence Support Team, c2020. 40 p. (CEST evidence search report)	

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SEARCH RESULTS

To obtain full-text articles email library@saskhealthauthority.ca.

SUMMARIES, GUIDELINES & OTHER RESOURCES

Clinical Protocols

World Health Organization

- Population-Based Age-Stratified Seroepidemiological Investigation Protocol for COVID-19 Virus Infection [2020, March 17] https://www.who.int/docs/default-source/inaugural-who-partners-forum/covid-19-seroepidemiological-investigation-protocol-v3.pdf?sfvrsn=ef4acdf9_1&download=true
- WHO Guidance for Surveillance During and Influenza Pandemic [2017] https://www.who.int/influenza/preparedness/pandemic/WHO_Guidance_for_surveillance_during_an_influenza_pandemic_082017.pdf

Grey Literature

SciELO

Trends in the prevalence of COVID-19 infection in Rio Grande do Sul, Brazil: repeated serological surveys [2020, April 16] https://preprints.scielo.org/index.php/scielo/preprint/view/41/version/74

Librarian's Notes: Abstract is in English but the article is in Brazilian Portuguese.

ARTICLES FROM LIBRARY DATABASES

Note: References are sorted by year (newest to oldest)

Pre-printed articles

1. Bendavid E, Mulaney B, Sood N, et al. COVID-19 Antibody Seroprevalence in Santa Clara County, California. medRxiv. 2020:2020.04.14.20062463. DOI: 10.1101/2020.04.14.20062463

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.Competing Interest StatementThe authors have declared no competing interest.Funding StatementWe acknowledge many individual donors who generously supported this project with gift awards. The funders had no role in the design and conduct of the study, nor in the decision to prepare and submit the manuscript for publication. Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesThe data is not available for sharing at this time.
URL: http://medrxiv.org/content/early/2020/04/17/2020.04.14.20062463.abstract
DOI: 10.1101/2020.04.14.20062463

2. Betensky RA, Feng Y. Accounting for incomplete testing in the estimation of epidemic parameters. medRxiv. 2020:2020.04.08.20058313. DOI: 10.1101/2020.04.08.20058313
ABSTRACT: As the COVID-19 pandemic evolves across the world and the United States, it is important to understand its evolution in real time and at regional levels. The field of infectious diseases epidemiology has highly developed modeling and estimation strategies that yield relevant estimates. These include the doubling time of the epidemic, i.e., the number of days until the number of cases doubles, and various representations of the number of cases over time, including the epidemic curve and associated cumulative incidence curve. While these quantities are immediately estimable given current data, they suffer from dependence on the underlying testing strategies within communities. Specifically, they are inextricably tied to the likelihood that an infected individual is tested and identified as a case. We clarify the functional relationship between testing and the epidemic parameters of interest, and thereby demonstrate simply sensitivity analyses that explore the range of possible truths under various testing scenarios. We demonstrate that crude estimates that assume stable testing or complete testing can be overly-optimistic.Competing Interest StatementThe authors have declared no competing interest.Funding StatementNo external funding was received.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesData are available at covidtracking.comhttps://covidtracking.com/data
URL: http://medrxiv.org/content/early/2020/04/11/2020.04.08.20058313.abstract
DOI: 10.1101/2020.04.08.20058313

3. Britton T. Basic prediction methodology for covid-19: estimation and sensitivity considerations. medRxiv. 2020:2020.03.27.20045575. DOI: 10.1101/2020.03.27.20045575
ABSTRACT: The purpose of the present paper is to present simple estimation and prediction methods for basic quantities in an emerging epidemic like the ongoing covid-10 pandemic. The simple methods have the advantage that relations between basic quantities become more transparent, thus shedding light to which

quantities have biggest impact on predictions, with the additional conclusion that uncertainties in these quantities carry over to high uncertainty also in predictions. A simple non-parametric prediction method for future cumulative case fatalities, as well as future cumulative incidence of infections (assuming a given infection fatality risk f), is presented. The method uses cumulative reported case fatalities up to present time as input data. It is also described how the introduction of preventive measures of a given magnitude ρ will affect the two incidence predictions, using basic theory of epidemic models. This methodology is then reversed, thus enabling estimation of the preventive magnitude ρ, and of the resulting effective reproduction number RE. However, the effects of preventive measures only start affecting case fatalities some 3-4 weeks later, so estimates are only available after this time has elapsed. The methodology is applicable in the early stage of an outbreak, before, say, 10% of the community have been infected. Beside giving simple estimation and prediction tools for an ongoing epidemic, another important conclusion lies in the observation that the two quantities f (infection fatality risk) and ρ (the magnitude of preventive measures) have very big impact on predictions. Further, both of these quantities currently have very high uncertainty: current estimates of f lie in the range 0.2% up to 2% (9], 7]), and the overall effect of several combined preventive measures is clearly very uncertain. The two main findings from the paper are hence that, a) any prediction containing f, and/or some preventive measures, contain a large amount of uncertainty (which is usually not acknowledged well enough), and b) obtaining more accurate estimates of in particular f, should be highly prioritized. Seroprevalence testing of random samples in a community where the epidemic has ended are urgently needed.Competing Interest StatementThe authors have declared no competing interest.Funding StatementStockholm University and the Swedish Research CouncilAuthor DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesNo data is used
URL: http://medrxiv.org/content/early/2020/03/30/2020.03.27.20045575.abstract
DOI: 10.1101/2020.03.27.20045575

4. Chen S, Li Q, Gao S, et al. Mitigating COVID-19 outbreak via high testing capacity and strong transmission-intervention in the United States. medRxiv. 2020:2020.04.03.20052720. DOI: 10.1101/2020.04.03.20052720
ABSTRACT: Most models of the COVID-19 pandemic in the United States do not consider geographic variation, and their relevance to public policies is not straightforward. We developed a mathematical model that characterizes infections by state and incorporates inflows and outflows of interstate travelers. Modeling reveals that curbing interstate travel when the disease is already widespread will make little difference. Meanwhile, increased testing capacity (facilitating early identification of infected people and quick isolation) and strict social-distancing and self-quarantine rules are effective in abating the outbreak. The modeling has also produced state-specific information. For example, for New York and Michigan, isolation of persons exposed to the virus needs to be imposed within 2 days to prevent a broad outbreak, whereas for other states this period can be 3.6 days. This model could be used to determine resources needed before safely lifting state policies on social distancing.Competing Interest StatementThe authors have declared no competing interest.Funding StatementS.G. and Q.L. acknowledge the funding support provided by the National Science Foundation (Award No. BCS-2027375). Q.L. and S.C. acknowledge the Data Science Initiative of UW-Madison. X.S. acknowledges the Scholarly Innovation and Advancement Awards of Dartmouth College. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.Author DeclarationsAll relevant ethical guidelines have been followed; any

necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesThe infection data from an open source project: Novel Coronavirus (COVID-19) Cases, developed by the Center For Systems Science and Engineering at the Johns Hopkins University. In addition, we collected over 3.6 million points of interest (POIs) with travel patterns in the United States from the SafeGraph business venue database. https://github.com/CSSEGISandData/COVID-19/blob/master/csse_covid_19_data/csse_covid_19_time_series/time_series_covid19_confirmed_global.csv
URL: http://medrxiv.org/content/early/2020/04/07/2020.04.03.20052720.abstract
DOI: 10.1101/2020.04.03.20052720

5. Chowell G, Dhillon R, Srikrishna D. Getting to zero quickly in the 2019-nCov epidemic with vaccines or rapid testing. medRxiv. 2020:2020.02.03.20020271. DOI: 10.1101/2020.02.03.20020271
ABSTRACT: Any plan for stopping the ongoing 2019-nCov epidemic must be based on a quantitative understanding of the proportion of the at-risk population that needs to be protected by effective control measures in order for transmission to decline sufficiently and quickly enough for the epidemic to end. Using an SEIR-type transmission model, we contrasted two alternate strategies by modeling the proportion of the population that needs to be protected from infection by one-time vaccination (assuming 100% effectiveness) or by testing with isolation and treatment of individuals within six, 24, or 48 hours of symptom onset. If R is currently 2.2, vaccination at the herd immunity coverage of 55% would drive R just below 1, but transmission could persist for years. Over 80% of coverage is required to end the epidemic in 6 months with population-wide vaccination. The epidemic could be ended in just under a year if testing with isolation and treatment reached 80% of symptomatically infected patients within 24 hours of symptom onset (assuming 10% asymptomatic transmission). The epidemic could be ended in six months if testing with isolation and treatment reached 90% of symptomatic patients. If 90% of symptomatic patients could be tested within six hours of symptoms appearing, the epidemic could be ended in under four months.Competing Interest StatementThe authors have declared no competing interest.Funding StatementGC acknowledges support from NSF grant 1414374 as part of the joint NSF-NIH-USDA Ecology and Evolution of Infectious Diseases program.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesAll data is publicly available
URL: http://medrxiv.org/content/early/2020/02/05/2020.02.03.20020271.abstract
DOI: 10.1101/2020.02.03.20020271

6. Di Domenico L, Pullano G, Sabbatini CE, et al. Expected impact of lockdown in Île-de-France and possible exit strategies. medRxiv. 2020:2020.04.13.20063933. DOI: 10.1101/2020.04.13.20063933
ABSTRACT: More than half of the global population is currently under strict forms of social distancing, with more than 90 countries in lockdown, including France. Estimating the expected impact of the lockdown, and the

potential effectiveness of different exit strategies is critical to inform decision makers on the management of the COVID-19 health crisis. We use a stochastic age-structured transmission model integrating data on age profile and social contacts in the Île-de-France region to (i) assess the current epidemic situation, (ii) evaluate the expected impact of the lockdown implemented in France on March 17, 2020, and (iii) estimate the effectiveness of possible exit strategies. The model is calibrated on hospital admission data of the region before lockdown and validated on syndromic and virological surveillance data. Different types and durations of social distancing interventions are simulated, including a progressive lifting of the lockdown targeted on specific classes of individuals (e.g. allowing a larger proportion of the population to go to work, while protecting the elderly), and large-scale testing. We estimate the basic reproductive number at 3.0 [2.8, 3.2] (95% confidence interval) prior to lockdown and the population infected by COVID-19 as of April 5 to be in the range 1% to 6%. The average number of contacts is predicted to be reduced by 80% during lockdown, leading to a substantial reduction of the reproductive number (RLD = 0.68 [0.62-0.73]). Under these conditions, the epidemic curve reaches ICU system capacity and slowly decreases during lockdown. Lifting the lockdown with no exit strategy would lead to a second wave largely overwhelming the healthcare system. Extensive case-finding, testing and isolation are required to envision social distancing strategies that gradually relax current constraints (larger fraction of individuals going back to work, progressive reopening of activities), while keeping schools closed and seniors isolated. As France faces the first wave of COVID-19 pandemic in lockdown, intensive forms of social distancing are required in the upcoming months due to the currently low population immunity. Extensive case-finding and isolation would allow the partial release of the socio-economic pressure caused by extreme measures, while avoiding healthcare demand exceeding capacity. Response planning needs to urgently prioritize the logistics and capacity for these interventions.Competing Interest StatementThe authors have declared no competing interest.Funding StatementThis study is partially funded by: ANR project DATAREDUX (ANR-19-CE46-0008-03); EU H2020 grant MOOD (H2020-874850); REACTing COVID-19 modeling grant; EU H2020 grant RECOVER (H2020-101003589).Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesAll data are available at the references cited.
URL: https://www.medrxiv.org/content/medrxiv/early/2020/04/17/2020.04.13.20063933.full.pdf
DOI: 10.1101/2020.04.13.20063933

7. Eberhardt JN, Breuckmann NP, Eberhardt CS. Multi-Stage Group Testing Optimizes COVID-19 Mass Population Testing. medRxiv. 2020:2020.04.10.20061176. DOI: 10.1101/2020.04.10.20061176
ABSTRACT: SARS-CoV-2 test kits are in critical shortage in many countries. This limits large-scale population testing and hinders the effort to identify and isolate infected individuals. Herein, we developed and evaluated multi-stage group testing schemes that test samples in groups of various pool sizes in multiple stages. Through this approach, groups of negative samples can be eliminated with a single test, avoiding the need for individual testing and achieving considerable savings of resources. We used computer simulations to assess and compare their efficiency for various prevalence rates. We found that three-stage testing schemes with pool sizes of maximum 16 samples can test up to three and seven times as many people with the same number of test kits for prevalence rates of around 5% and 1%, respectively. We propose an adaptive approach, where the optimal testing scheme is selected based on the expected prevalence rate. These group testing schemes could lead to a major reduction in the number of testing kits required and help improve large-scale population testing in general and in the context of the current COVID-19 pandemic.Competing Interest StatementThe authors have

declared no competing interest.Funding StatementNo external funding was received.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesThe authors confirm that the data supporting the findings of this study are available within the article and its supplementary materials.
URL: http://medrxiv.org/content/early/2020/04/14/2020.04.10.20061176.abstract
DOI: 10.1101/2020.04.10.20061176

8. Foddai A, Lubroth J, Ellis-Iversen J. Base protocol for real time active random surveillance of coronavirus disease (COVID-19) - Adapting veterinary methodology to public health. One health (Amsterdam, Netherlands). 2020:100129. DOI: 10.1016/j.onehlt.2020.100129
ABSTRACT: The pandemic of new coronavirus disease COVID-19 is threatening our health, economy and life style. Collaborations across countries and sectors as a One Health World could be a milestone. We propose a general protocol, for setting timely active random surveillance of COVID-19, at the human community level, with systematic repeated detection efforts. Strengths and limitations are discussed. If considered applicable by public health, the protocol could evaluate the status of COVID-19 epidemics consistently and objectively.
URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7102574/
DOI: 10.1016/j.onehlt.2020.100129

9. Gray N, Calleja D, Wimbush A, et al. "No test is better than a bad test": Impact of diagnostic uncertainty in mass testing on the spread of Covid-19. medRxiv. 2020:2020.04.16.20067884. DOI: 10.1101/2020.04.16.20067884
ABSTRACT: Background: The cessation of lock-down measures will require an effective testing strategy. Much focus at the beginning of the UK's Covid-19 epidemic was directed to deficiencies in the national testing capacity. The quantity of tests may seem an important focus, but other characteristics are likely more germane. False positive tests are more probable than positive tests when the overall population has a low prevalence of the disease, even with highly accurate tests. Methods: We modify an SIR model to include quarantines states and test performance using publicly accessible estimates for the current situation. Three scenarios for cessation of lock-down measures are explored: (1) immediate end of lock-down measures, (2) continued lock-down with antibody testing based immunity passports, and (3) incremental relaxation of lock-down measures with active viral testing. Sensitivity, specifcity, prevalence and test capacity are modified for both active viral and antibody testing to determine their population level effect on the continuing epidemic. Findings: Diagnostic uncertainty can have a large effect on the epidemic dynamics of Covid-19 within the UK. The dynamics of the epidemic are more sensitive to test performance and targeting than test capacity. The quantity of tests is not a substitute for an effective strategy. Poorly targeted testing has the propensity to exacerbate the peak in infections. Interpretation: The assessment that 'no test is better than a bad test' is broadly supported by the present analysis. Antibody testing is unlikely to be a solution to the lock-down, regardless of test quality or capacity. A well designed active viral testing strategy combined with incremental relaxation of the lock-down measures is shown to be a potential strategy to restore some social activity whilst continuing to keep infections low.Competing Interest StatementThe authors have declared no competing interest.Funding StatementThis work has been partially funded by the EPSRC IAA exploration award with grant number EP/R511729/1, EPSRC programme grant "Digital twins for improved dynamic design", EP/R006768/1, and the EPSRC and ESRC Centre

for Doctoral Training in Quantification and Management of Risk and Uncertainty in Complex Systems and Environments, EP/L015927/1 .Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesAll data can be made available
URL: https://www.medrxiv.org/content/medrxiv/early/2020/04/22/2020.04.16.20067884.full.pdf
DOI: 10.1101/2020.04.16.20067884

10. Hsiao SH, Chen TC, Chien HC, et al. Body Temperature Measurement to Prevent Pandemic COVID-19 in Hospitals in Taiwan: Repeated Measurement is Necessary. J Hosp Infect. 2020. DOI: 10.1016/j.jhin.2020.04.004
DOI: 10.1016/j.jhin.2020.04.004

11. Kamikubo Y, Takahashi A. Epidemiological Tools that Predict Partial Herd Immunity to SARS Coronavirus 2. medRxiv. 2020:2020.03.25.20043679. DOI: 10.1101/2020.03.25.20043679
ABSTRACT: The outbreak of SARS coronavirus 2 (SARS-CoV-2), which occurred in Wuhan, China in December 2019, has caused a worldwide pandemic of coronavirus disease 2019 (COVID-19). However, there is a lack of epidemiological tools to guide effective public policy development. Here we present epidemiological evidence that SARS-CoV-2 S type exited Wuhan or other epicenters in China earlier than L type and conferred partial resistance to the virus on infected populations. Analysis of regional disparities in incidence has revealed that a sharp decline in influenza epidemics is a useful surrogate indicator for the undocumented spread of SARS-CoV-2. The biggest concern in the world is knowing when herd immunity has been achieved and scheduling a time to regain the living activities of each country. This study provides a useful tool to guide the development of local policies to contain the virus.Competing Interest StatementThe authors have declared no competing interest.Funding StatementThis work was supported by Grant-in-Aid for Scientific Research (KAKENHI; 17H03597 and 16K14632) from the Japan Society for the Promotion of Science.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesData are available on request.
URL: http://medrxiv.org/content/early/2020/03/27/2020.03.25.20043679.abstract
DOI: 10.1101/2020.03.25.20043679

12. Kissler SM, Tedijanto C, Goldstein E, et al. Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. Science. 2020. DOI: 10.1126/science.abb5793
ABSTRACT: It is urgent to understand the future of severe acute respiratory syndrome-coronavirus 2 (SARS-CoV-2) transmission. We used estimates of seasonality, immunity, and cross-immunity for betacoronaviruses OC43 and HKU1 from time series data from the USA to inform a model of SARS-CoV-2 transmission. We projected that

recurrent wintertime outbreaks of SARS-CoV-2 will probably occur after the initial, most severe pandemic wave. Absent other interventions, a key metric for the success of social distancing is whether critical care capacities are exceeded. To avoid this, prolonged or intermittent social distancing may be necessary into 2022. Additional interventions, including expanded critical care capacity and an effective therapeutic, would improve the success of intermittent distancing and hasten the acquisition of herd immunity. Longitudinal serological studies are urgently needed to determine the extent and duration of immunity to SARS-CoV-2. Even in the event of apparent elimination, SARS-CoV-2 surveillance should be maintained since a resurgence in contagion could be possible as late as 2024.
URL: https://science.sciencemag.org/content/early/2020/04/14/science.abb5793
DOI: 10.1126/science.abb5793

13. Mueller M, Derlet P, Mudry C, et al. Using random testing to manage a safe exit from the COVID-19 lockdown. medRxiv. 2020:2020.04.09.20059360. DOI: 10.1101/2020.04.09.20059360
ABSTRACT: We argue that random testing (i.e., polling the fraction of infected people in the population) is central to managing the COVID-19 pandemic because it both measures the key variable controlled by restrictive measures, and anticipates the load on the healthcare system via the progression of the disease. Knowledge of random testing outcomes will therefore (i) significantly improve the predictability of the course of the pandemic, (ii) allow informed and optimized decisions on how to modify restrictive measures, with much shorter delay times than the present ones, and (iii) enable the real-time assessment of the efficiency of new means to reduce transmission rates (such as new tracing strategies based on the mobile telephone network, wearing face masks, etc.). Frequent random testing for COVID-19 infections has the essential benefit of providing more reliable and refined data than currently available, in both time and space. This is crucial to accompany and monitor the safe release of restrictive measures. Here we show that independent of the total size of population with frequent interactions among its members, about 15000 tests with randomly selected people per day suffice to obtain valuable data about the current number of infections and their evolution in time. In contrast to testing confined to particular subpopulations such as those displaying symptoms, this will allow close to real-time assessment of the quantitative effect of restrictive measures. With yet higher testing capacity, random testing further allows detection of geographical differences in spreading rates and thus the formulation of optimal strategies for a safe reboot of the economy. Most importantly, with daily random testing in place, a reboot could be attempted while the fraction of infected people is still an order of magnitude higher than the level required for a reboot without such polling.Competing Interest StatementThe authors have declared no competing interest.Funding StatementGA acknowledges the support through the ERC HERO project under grant No. 810451.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesThe data generated by the numerical simulations can be provided upon request to the authors.
URL: http://medrxiv.org/content/early/2020/04/14/2020.04.09.20059360.abstract
DOI: 10.1101/2020.04.09.20059360

14. Perez-Reche F, Strachan N. Importance of untested infectious individuals for the suppression of COVID-19 epidemics. medRxiv. 2020:2020.04.13.20064022. DOI: 10.1101/2020.04.13.20064022
ABSTRACT: A mathematical model which accounts for tested and untested infectious individuals is calibrated during the early stages of COVID-19 outbreaks in Germany, the Hubei province, Italy, Spain and the UK. The

predicted percentage of untested infected individuals depends on the specific outbreak but we found that they typically represent 50% to 80% of the infected individuals. Even when unreported cases are taken into account, we estimate that less than 8% of the population would have been exposed to SARS-CoV-2 by 09/04/2020 in the analysed outbreaks. These levels are far from the 70-85% needed to ensure herd immunity and we predict a resurgence of infection if ongoing lockdowns in the analysed outbreaks are fully lifted. We propose that partially lifted lockdowns together with fast and thorough testing allowing for quick isolation of both symptomatic and asymptomatic cases could lead to suppression of secondary waves of COVID-19 epidemics.Competing Interest StatementThe authors have declared no competing interest. Funding StatementN/AAuthor DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesDetails on data availability are given in the manuscript.
URL: http://medrxiv.org/content/early/2020/04/17/2020.04.13.20064022.abstract
DOI: 10.1101/2020.04.13.20064022

15. Richterich P. Severe underestimation of COVID-19 case numbers: effect of epidemic growth rate and test restrictions. medRxiv. 2020:2020.04.13.20064220. DOI: 10.1101/2020.04.13.20064220
ABSTRACT: To understand the scope and development of the COVID-19 pandemic, knowledge of the number of infected persons is essential. Often, the number of "confirmed cases", which is based on positive RT-PCR test results, is regarded as a reasonable indicator. However, limited COVID-19 test capacities in many countries are restricting the amount of testing that can be done. This can lead to the implementation of testing policies that restrict access to COVID-19 tests, and to testing backlogs and delays. As a result, confirmed case numbers can be significantly lower than the actual number of infections, especially during rapid growth phases of the epidemic. This study examines the quantitative relation between infections and reported confirmed case numbers for two different testing strategies, "limited" and "inclusive" testing, in relation to the growth rate of the epidemic. The results indicate that confirmed case numbers understate the actual number of infections substantially; during rapid growth phases where the daily growth rate can reach or exceed 30%, as has been seen in many countries, the confirmed case numbers under-report actual infections by up to 50 to 100-fold.Competing Interest StatementThe authors have declared no competing interest.Funding StatementNo external funding was received for this study.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesData used for this study were downloaded from the public repository at https://github.com/CSSEGISandData/COVID-19/
URL: http://medrxiv.org/content/early/2020/04/17/2020.04.13.20064220.abstract
DOI: 10.1101/2020.04.13.20064220

16. Rodriguez PF. Predicting Whom to Test is More Important Than More Tests - Modeling the Impact of Testing on the Spread of COVID-19 Virus By True Positive Rate Estimation. medRxiv. 2020:2020.04.01.20050393. DOI: 10.1101/2020.04.01.20050393

ABSTRACT: I estimate plausible true positive (TP) rates for the number of COVID-19 tests per day, most relevant when the number of test is on the same order of magnitude as number of infected persons. I then modify a standard SEIR model to model current growth patterns and detection rates in South Korea and New York state. Although reducing transmission rates have the largest impact, increasing TP rates by ~10% in New York can have an impact equal to adding tens of thousands of new tests per day. Increasing both TP rates and tests per day together can have significant impacts and likely be more easily sustained than social distancing restrictions. Systematic and standardized data collection, even beyond contact tracking, should be ongoing and quickly made available for research teams to maximize the efficacy of testing.Competing Interest StatementThe authors have declared no competing interest.Funding StatementNo external funding was received.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesData in the manuscript is publicly available at the URLs given in the references.

URL: http://medrxiv.org/content/early/2020/04/06/2020.04.01.20050393.abstract
DOI: 10.1101/2020.04.01.20050393

17. Silverman JD, Washburne AD. Using ILI surveillance to estimate state-specific case detection rates and forecast SARS-CoV-2 spread in the United States. medRxiv. 2020:2020.04.01.20050542. DOI: 10.1101/2020.04.01.20050542

ABSTRACT: Detection of SARS-CoV-2 infections to date has relied on RT-PCR testing. However, a failure to identify early cases imported to a country, bottlenecks in RT-PCR testing, and the existence of infections which are asymptomatic, sub-clinical, or with an alternative presentation than the standard cough and fever have resulted in an under-counting of the true prevalence of SARS-CoV-2. Here, we show how publicly available CDC influenza-like illness (ILI) outpatient surveillance data can be repurposed to estimate the detection rate of symptomatic SARS-CoV-2 infections. We find a surge of non-influenza ILI above the seasonal average and show that this surge is correlated with COVID case counts across states. By quantifying the number of excess ILI patients in March relative to previous years and comparing excess ILI to confirmed COVID case counts, we estimate the symptomatic case detection rate of SARS-CoV-2 in the US to be 1/100 to 1/1000. This corresponds to approximately 10 million presumed symptomatic SARS-CoV-2 patients across the US during the week starting on March 15, 2020. Combining excess ILI counts with the date of onset of community transmission in the US, we also show that the early epidemic in the US was unlikely to be doubling slower than every three days. Together these results suggest a conceptual model for the COVID epidemic in the US in which rapid spread across the US are combined with a large population of infected patients with presumably mild-to-moderate clinical symptoms. We emphasize the importance of testing these findings with seroprevalence data, and discuss the broader potential to repurpose outpatient time series for early detection and understanding of emerging infectious diseases.Competing Interest StatementThe authors have declared no competing interest.Funding StatementNo external funding was receivedAuthor DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective

interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesAll simulation and analysis files will be made available upon request
URL: http://medrxiv.org/content/early/2020/04/03/2020.04.01.20050542.abstract
DOI: 10.1101/2020.04.01.20050542

18. Sousa-Pinto B, Fonseca JA, Costa-Pereira A, et al. Is scaling-up COVID-19 testing cost-saving? medRxiv. 2020:2020.03.22.20041137. DOI: 10.1101/2020.03.22.20041137
ABSTRACT: The World Health Organization currently recommends that governments scale up testing for COVID-19 infection. We performed health economic analyses projecting whether the additional costs from screening would be offset by the avoided costs with hospitalizations. We analysed Portuguese COVID-19 data up until the 22nd March 2020, and estimated the additional number of cases that would be detected if different testing rates and frequencies of positive results would have been observed. We projected that, in most scenarios, the costs with scaling up COVID-19 tests would be lower than savings with hospitalization costs, rendering large scale testing cost-saving.Competing Interest StatementThe authors have declared no competing interest.Funding StatementNo external funding was received.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesData used to build the economic models can be provided on request.
URL: http://medrxiv.org/content/early/2020/03/27/2020.03.22.20041137.abstract
DOI: 10.1101/2020.03.22.20041137

19. Stock JH, Aspelund KM, Droste M, et al. Estimates of the Undetected Rate among the SARS-CoV-2 Infected using Testing Data from Iceland. medRxiv. 2020:2020.04.06.20055582. DOI: 10.1101/2020.04.06.20055582
ABSTRACT: Testing for SARS-CoV-2 in the United States is currently targeted to individuals whose symptoms and/or jobs place them at a high presumed risk of infection. An open question is, what is the share of infections that are undetected under current testing guidelines? To answer this question, we turn to COVID-19 testing data from Iceland. The criteria for testing within the Icelandic medical system, processed by the National University Hospital of Iceland (NUHI), have also been targeted at high-risk individuals, but additionally most Icelanders qualify for voluntary testing through the biopharmaceutical company deCODE genetics. We use results from Iceland's two testing programs to estimate the share of infections that are undetected under standard (NUHI) testing guidelines. Because of complications in the deCODE testing regime, it is not possible to estimate a single value for this this undetected rate; however, a range can be estimated. Our primary estimates for the fraction of infections that are undetected range from 88.7% to 93.6%.Competing Interest StatementThe authors have declared no competing interest.Funding StatementAt the moment we have no external support for this project (which is in process). This material is based upon work supported by the National Science Foundation Graduate Research Fellowship under Grant No. 1122374.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the

IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesAll data are publicly available. We use counts of tests and confirmed COVID-19 infections from the Icelandic Health Directorate's COVID-19 information website. We also use counts of cases reporting flu-like symptoms from the influenza website of the country's Health Directorate. We use quarantine numbers from the Department of Civil Defense's announcement
URL: http://medrxiv.org/content/early/2020/04/11/2020.04.06.20055582.abstract
DOI: 10.1101/2020.04.06.20055582

20. Victor AO. Estimation of the probability of reinfection with COVID-19 coronavirus by the SEIRUS model. medRxiv. 2020:2020.04.02.20050930. DOI: 10.1101/2020.04.02.20050930
ABSTRACT: With sensitivity of the Polymerase Chain Reaction (PCR) test used to detect the presence of the virus in the human host, the global health community has been able to record a great number of recovered population. Therefore, in a bid to answer a burning question of reinfection in the recovered class, the model equations which exhibits the disease-free equilibrium (E_0) state for COVID-19 coronavirus was developed in this study and was discovered to both exist as well as satisfy the criteria for a locally or globally asymptotic stability with a basic reproductive number R_0=0 for and endemic situation. Hence, there is a chance of no secondary reinfections from the recovered population as the rate of incidence of the recovered population vanishes, that is, B=0. Furthermore, numerical simulations were carried to complement the analytical results in investigating the effect of the implementation of quarantine and observatory procedures has on the projection of the further spread of the virus globally. Result shows that the proportion of infected population in the absence of curative vaccination will continue to grow globally meanwhile the recovery rate will continue slowly which therefore means that the ratio of infection to recovery rate will determine the death rate that is recorded globally and most significant for this study is the rate of reinfection by the recovered population which will decline to zero over time as the virus is cleared clinically from the system of the recovered class.Competing Interest StatementThe authors have declared no competing interest.Funding StatementThis study part of a series of disease control research self-sponsored by the author without any external sponsorship or grants. However, access to funds can improve the quality of the series.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesData available for this study were estimated by the author and others were retrieved from the WPR (2020), WHO (2020) and JHU (2020) which were publicly available data.
URL: http://medrxiv.org/content/early/2020/04/06/2020.04.02.20050930.abstract
DOI: 10.1101/2020.04.02.20050930

21. Weitz JS, Beckett SJ, Coenen AR, et al. Intervention Serology and Interaction Substitution: Modeling the Role of 'Shield Immunity' in Reducing COVID-19 Epidemic Spread. medRxiv. 2020:2020.04.01.20049767. DOI: 10.1101/2020.04.01.20049767

ABSTRACT: The COVID-19 pandemic has precipitated a global crisis, with more than 690,000 confirmed cases and more than 33,000 confirmed deaths globally as of March 30, 2020 1-4]. At present two central public health control strategies have emerged: mitigation and suppression (e.g, 5]). Both strategies focus on reducing new infections by reducing interactions (and both raise questions of sustainability and long-term tactics). Complementary to those approaches, here we develop and analyze an epidemiological intervention model that leverages serological tests 6, 7] to identify and deploy recovered individuals as focal points for sustaining safer interactions via interaction substitution, i.e., to develop what we term 'shield immunity' at the population scale. Recovered individuals, in the present context, represent those who have developed protective, antibodies to SARS-CoV-2 and are no longer shedding virus 8]. The objective of a shield immunity strategy is to help sustain the interactions necessary for the functioning of essential goods and services (including but not limited to tending to the elderly 9], hospital care, schools, and food supply) while decreasing the probability of transmission during such essential interactions. We show that a shield immunity approach may significantly reduce the length and reduce the overall burden of an outbreak, and can work synergistically with social distancing. The present model highlights the value of serological testing as part of intervention strategies, in addition to its well recognized roles in estimating prevalence 10, 11] and in the potential development of plasma-based therapies 12-15].Competing Interest StatementThe authors have declared no competing interest.Funding StatementResearch effort by JSW and co-authors at the Georgia Institute of Technology was enabled by support from grants from the Simons Foundation (SCOPE Award ID 329108), the Army Research Office (W911NF1910384), National Institutes of Health (1R01AI46592-01), and National Science Foundation (1806606 and 1829636). JD was supported in part by grants from the Canadian Institutes of Health Research and the Natural Sciences and Engineering Research Council of CanadaAuthor DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.Yes All simulation and codes used in the development of this manuscript are available at https://github.com/WeitzGroup/covid_shield_immunity.

URL: http://medrxiv.org/content/early/2020/04/03/2020.04.01.20049767.abstract

DOI: 10.1101/2020.04.01.20049767

22. Yadlowsky S, Shah N, Steinhardt J. Estimation of SARS-CoV-2 Infection Prevalence in Santa Clara County. medRxiv. 2020:2020.03.24.20043067. DOI: 10.1101/2020.03.24.20043067

ABSTRACT: To reliably estimate the demand on regional health systems and perform public health planning, it is necessary to have a good estimate of the prevalence of infection with SARS-CoV-2 (the virus that causes COVID-19) in the population. In the absence of wide-spread testing, we provide one approach to infer prevalence based on the assumption that the fraction of true infections needing hospitalization is fixed and that all hospitalized cases of COVID-19 in Santa Clara are identified. Our goal is to estimate the prevalence of SARS-CoV-2 infections, i.e. the true number of people currently infected with the virus, divided by the total population size. Our analysis suggests that as of March 17, 2020, there are 6,500 infections (0.34% of the population) of SARS-CoV-2 in Santa Clara County. Based on adjusting the parameters of our model to be optimistic (respectively pessimistic), the number of infections would be 1,400 (resp. 26,000), corresponding to a prevalence of 0.08% (resp. 1.36%). If the shelter-in-place led to R0 < 1, we would expect the number of infections to remain about constant for the next

few weeks. However, even if this were true, we expect to continue to see an increase in hospitalized cases of COVID-19 in the short term due to the fact that infection of SARS-CoV-2 on March 17th can lead to hospitalizations up to 14 days later.Competing Interest StatementThe authors have declared no competing interest.Funding StatementSY acknowledges support from NIH grant R01HL144555-01. NHS acknowledges salary support from the Stanford Medicine Program for AI in Healthcare. JS acknowledges support from the Open Philanthropy Project.Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesAll publicly available data included in results.
URL: http://medrxiv.org/content/early/2020/03/27/2020.03.24.20043067.abstract
DOI: 10.1101/2020.03.24.20043067

23. Zhang Z. Prevent the resurgence of infectious disease with asymptomatic carriers. medRxiv. 2020:2020.04.16.20067652. DOI: 10.1101/2020.04.16.20067652
ABSTRACT: As many countries reached the peak of the COVID-19 outbreak, there is debate on how to reopen the economy without causing a significant resurgence. Here we show, using a microsimulation model, that how to reopen safely depends on what percentage of COVID-19 cases can be detected by testing. The higher the detection rate, the less restrictive the reopen plan needs to be. If 70% of cases can be detected, schools and businesses can reopen if 2-layer quarantine is imposed on each confirmed case. Our results suggest that increasing the detection rate is essential to prevent the resurgence of COVID-19.Competing Interest StatementThe authors have declared no competing interest.Funding StatementN/AAuthor DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript.YesAll necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesAvailable upon request
URL: http://medrxiv.org/content/early/2020/04/19/2020.04.16.20067652.abstract
DOI: 10.1101/2020.04.16.20067652

24. Zwald ML, Wen L, Cooksey GLS, et al. Rapid Sentinel Surveillance for COVID-19 - Santa Clara County, California, March 2020. MMWR Morb Mortal Wkly Rep. 2020;69(14):419-21. DOI: 10.15585/mmwr.mm6914e3
ABSTRACT: On February 27, 2020, the Santa Clara County Public Health Department (SCCPHD) identified its first case of coronavirus disease 2019 (COVID-19) associated with probable community transmission (i.e., infection among persons without a known exposure by travel or close contact with a patient with confirmed COVID-19). At the time the investigation began, testing guidance recommended focusing on persons with clinical findings of lower respiratory illness and travel to an affected area or an epidemiologic link to a laboratory-confirmed COVID-19 case, or on persons hospitalized for severe respiratory disease and no alternative diagnosis (1). To

rapidly understand the extent of COVID-19 in the community, SCCPHD, the California Department of Public Health (CDPH), and CDC began sentinel surveillance in Santa Clara County. During March 5-14, 2020, four urgent care centers in Santa Clara County participated as sentinel sites. For this investigation, county residents evaluated for respiratory symptoms (e.g., fever, cough, or shortness of breath) who had no known risk for COVID-19 were identified at participating urgent care centers. A convenience sample of specimens that tested negative for influenza virus was tested for SARS-CoV-2 RNA. Among 226 patients who met the inclusion criteria, 23% had positive test results for influenza. Among patients who had negative test results for influenza, 79 specimens were tested for SARS-CoV-2, and 11% had evidence of infection. This sentinel surveillance system helped confirm community transmission of SARS-CoV-2 in Santa Clara County. As a result of these data and an increasing number of cases with no known source of transmission, the county initiated a series of community mitigation strategies. Detection of community transmission is critical for informing response activities, including testing criteria, quarantine guidance, investigation protocols, and community mitigation measures (2). Sentinel surveillance in outpatient settings and emergency departments, implemented together with hospital-based surveillance, mortality surveillance, and serologic surveys, can provide a robust approach to monitor the epidemiology of COVID-19.
URL:
http://shal.idm.oclc.org/login?url=https://search.ebscohost.com/login.aspx?direct=true&AuthType=ip,url,uid&db=rzh&AN=142714682&site=ehost-live&scope=site
DOI: 10.15585/mmwr.mm6914e3

Journal articles

1. Gorman S. How can we improve global infectious disease surveillance and prevent the next outbreak? Scand J Infect Dis. 2013;45(12):944-7. DOI: 10.3109/00365548.2013.826877
ABSTRACT: Despite a significant amount of progress in the past decade, global infectious disease surveillance still often falters, as in the case of the emerging novel coronavirus that has killed at least 17 people in Saudi Arabia. This article argues that we must continuously re-evaluate global infectious disease surveillance systems. It takes stock of problems in various countries' infectious disease surveillance systems and offers recommendations for how to improve surveillance and ensure more rapid reporting. Chief among the recommendations are strategies for reducing fragmentation in global surveillance systems and methods for making these systems less disease-specific. Suggestions are also offered for ways to improve infectious disease surveillance strategies in resource-limited settings.
URL: https://www.tandfonline.com/doi/full/10.3109/00365548.2013.826877
DOI: 10.3109/00365548.2013.826877

2. Galanti M, Birger R, Ud-Dean M, et al. Longitudinal active sampling for respiratory viral infections across age groups. Influenza Other Respi Viruses. 2019;13(3):226-32.
ABSTRACT: Background: Respiratory viral infections are a major cause of morbidity and mortality worldwide. However, their characterization is incomplete because prevalence estimates are based on syndromic surveillance data. Here, we address this shortcoming through the analysis of infection rates among individuals tested regularly for respiratory viral infections, irrespective of their symptoms. Method(s): We carried out longitudinal sampling and analysis among 214 individuals enrolled at multiple New York City locations from fall 2016 to spring 2018. We combined personal information with weekly nasal swab collection to investigate the prevalence of 18 respiratory viruses among different age groups and to assess risk factors associated with infection susceptibility. Result(s): 17.5% of samples were positive for respiratory viruses. Some viruses circulated predominantly during winter, whereas others were found year round. Rhinovirus and coronavirus were most frequently detected. Children registered the highest positivity rates, and adults with daily contacts with children experienced significantly more infections than their counterparts without children. Conclusion(s): Respiratory

viral infections are widespread among the general population with the majority of individuals presenting multiple infections per year. The observations identify children as the principal source of respiratory infections. These findings motivate further active surveillance and analysis of differences in pathogenicity among respiratory viruses. Copyright © 2018 The Authors. Influenza and Other Respiratory Viruses Published by John Wiley & Sons Ltd.
URL: https://onlinelibrary.wiley.com/doi/full/10.1111/irv.12629

3. Bai Z, Gong Y, Tian X, et al. The Rapid Assessment and Early Warning Models for COVID-19. Virologica Sinica. 2020.
ABSTRACT: Human beings have experienced a serious public health event as the new pneumonia (COVID-19), caused by the severe acute respiratory syndrome coronavirus has killed more than 3000 people in China, most of them elderly or people with underlying chronic diseases or immunosuppressed states. Rapid assessment and early warning are essential for outbreak analysis in response to serious public health events. This paper reviews the current model analysis methods and conclusions from both micro and macro perspectives. The establishment of a comprehensive assessment model, and the use of model analysis prediction, is very efficient for the early warning of infectious diseases. This would significantly improve global surveillance capacity, particularly in developing regions, and improve basic training in infectious diseases and molecular epidemiology. Copyright © 2020, Wuhan Institute of Virology, CAS.
URL: https://link.springer.com /content/pdf/10.1007/s12250-020-00219-0.pdf

4. Balilla J. Assessment of COVID-19 Mass Testing: The Case of South Korea SSRN- Lancet prepublication. 2020.
ABSTRACT: South Korea's knowledge and experience of the 2015 Middle East Respiratory Syndrome (MERS) allowed them to quickly react to the 2019 Novel Corona Virus or COVID-19. One of the lapses they have identified during the MERS outbreak was mass testing which resulted to a death toll of 38. This papers shows how South Korea's mass testing allowed them to control the further increase in the number of new infections. Furthermore, it also allowed the early detection of outbreak in the city of Daegu after a period of 33 days from the start of testing.
URL: (March 18, 2020). Available at SSRN: https://ssrn.com/abstract=3556346 or http://dx.doi.org/10.2139/ssrn.3556346

5. Biswas A, Bhattacharjee U, Chakrabarti AK, et al. Emergence of Novel Coronavirus and COVID-19: whether to stay or die out? Crit Rev Microbiol. 2020:1-12. DOI: 10.1080/1040841X.2020.1739001
ABSTRACT: AbstractThe last century has witnessed several assaults from RNA viruses, resulting in millions of death throughout the world. The 21st century appears no longer an exception, with the trend continued with escalated fear of SARS coronavirus in 2002 and further concern of influenza H5N1 in 2003. A novel influenza virus created the first pandemic of the 21st century, the pandemic flu in 2009 preceded with the emergence of another deadly virus, MERS-CoV in 2012. A novel coronavirus ?SARS-CoV-2? (and the disease COVID-19) emerged suddenly, causing a rapid outbreak with a moderate case fatality rate. This virus is continuing to cause health care providers grave concern due to the lack of any existing immunity in the human population, indicating their novelty and lack of previous exposure. The big question is whether this novel virus will be establishing itself in an endemic form or will it eventually die out? Endemic viruses during circulation may acquire mutations to infect naïve, as well as individual with pre-existing immunity. Continuous monitoring is strongly advisable, not only to the newly infected individuals, but also to those recovered individuals who were infected by SARS-CoV-2 as re-infection may lead to the selection of escape mutants and subsequent dissemination to the population.
URL: https://doi.org/10.1080/1040841X.2020.1739001
DOI: 10.1080/1040841X.2020.1739001

6. Black JRM, Bailey C, Swanton C. COVID-19: the case for health-care worker screening to prevent hospital transmission. Lancet. 2020. DOI: 10.1016/S0140-6736(20)30917-X

URL: https://doi.org/10.1016/S0140-6736(20)30917-X
DOI: 10.1016/S0140-6736(20)30917-X

7. Cohen J. Unprecedented nationwide blood studies seek to track U.S. coronavirus spread. Science. 2020. DOI: 10.1126/science.abc1319
ABSTRACT: We still don't know how many people have been infected with the novel coronavirus, SARS-CoV-2. Not only have countries struggled to roll out wide-scale testing for the virus, those efforts inevitably will miss people who have recovered from an infection. The best way to figure out how far and wide the virus has spread in a population is to look at blood. Antibodies, blood proteins that the immune system produces to attack pathogens, are viral fingerprints that remain long after infections are cleared. Sensitive tests can detect them even in people who never felt a single symptom of COVID-19. The World Health Organization has announced an ambitious global effort, called Solidarity II, of so-called serosurveys, studies that look for antibodies to SARS-CoV-2 in the population.
URL: https://www.sciencemag.org/news/2020/04/unprecedented-nationwide-blood-studies-seek-track-us-coronavirus-spread
DOI: 10.1126/science.abc1319

8. Daughton C. The international imperative to rapidly and inexpensively monitor community-wide Covid-19 infection status and trends. Sci Total Environ. 2020:138149-. DOI: 10.1016/j.scitotenv.2020.138149
ABSTRACT: Given the continuing concerns surrounding the lack of adequate diagnostic testing for Covid-19 (caused by SARS-CoV-2), even less attention is being paid to what could become an even more urgent need - - the ability to quickly determine the status and trends of Covid-19 within and across communities nationwide. The existing Covid-19 clinical diagnostic tests will prove woefully inadequate for rapidly monitoring (at comparatively low cost) the incidence of Covid-19 community-wide. It is simply not feasible to do repeated individual testing at very large scales. Rapid community-wide monitoring could prove of immense international importance in quickly determining trends in whether the spread of Covid-19 (as well as future viral epidemics) in individual communities is increasing or decreasing. This ability is critical for better informing containment and mitigation strategies as well as for better-targeting followup diagnostic testing of individuals. This would prove even more important if SARS-CoV-2 reinfections and episodic outbreaks begin to widely occur. Fortunately, the relatively new field of sewage epidemiology (also called wastewater-based epidemiology: WBE) has been advancing steadily over the last 15 years (for example, see Choi et al, 2018; Daughton 2018), with research efforts largely concentrated in Europe. Originally geared toward determining the population-wide use of illicit drugs, this monitoring concept has since evolved to include a broad array of other types of substances in wastewater, including virus particles. So the time required for developing and implementing a wastewater monitoring approach specifically designed for SARS-CoV-2 (and Covid-19) might be greatly reduced. It is critical that governments worldwide be made aware of the important role that sewage epidemiology could play in controlling the spread of Covid-19. National agencies should encourage the development of sewage monitoring capabilities. This can be done partly by soliciting and funding grant proposals; one such example is a call for research proposals dealing with many aspects of coronavirus by the Swiss National Science Foundation (http://www.snf.ch/en/funding/programmes/coronavirus/Pages/default.aspx). Future calls for proposals focused solely on WBE might be more productive. One problem is the very uneven worldwide distribution of not just R&D on WBE, but also the uneven adoption of WBE for existing purposes such as community-wide illicit drug monitoring. Some countries, such as the U.S., have little experience with the implementation of WBE. For this reason, it will be important to encourage international research collaborations. This would be the best way to ensure adoption of WBE worldwide for monitoring pandemics. Development of a rapid and economical WBE tool for monitoring status and trends of Covid-19 mass infection will encounter a number of challenges, many of which are often shared by existing WBE methods for other targets of analysis (such as chemical micropollutants). Challenges include statistically representative sampling of sewage, Journal Pre-proof Journal Pre-proofwhich is heterogeneous. With respect to its occurrence in sewage, viable SARS-CoV-2 probably enters

mainly via shedding in the stool. Non-viable virus (and associate viral debris such as RNA fragments, mRNA, or capsid subunits) could enter sewage via stool and urine. Virus particle loadings in sewage can be quantified by targeting virus functional or structural motifs. Since the half-life of viable SARS-CoV-2 in wastewater seems to be very short, any detection method should account for both viable and non-viable particles. Degradation products (such as RNA fragments) from the virus could also be selected as targets. Detection approaches could include RT-PCR (or allied approaches) and ELISA, coupled with the Most Probable Number (MPN) method for quantifying sewage loadings of combined viable and non-viable virus particles. For each individual sewage treatment plant (STP), the virus loading levels would then be directly used to establish status and t me trends. The levels could also be normalized against the populations served by each STP plant in order to rank communities with respect to their community-wide infection rates. This would facilitate rapid identification of hot spots for better-informed intervention measures and prevention of emerging clusters.
URL: https://linkinghub.elsevier.com/retrieve/pii/S0048969720316624
DOI: 10.1016/j.scitotenv.2020.138149

9. de Lusignan S, Lopez Bernal J, Zambon M, et al. Emergence of a Novel Coronavirus (COVID-19): Protocol for Extending Surveillance Used by the Royal College of General Practitioners Research and Surveillance Centre and Public Health England. JMIR Public Health and Surveillance. 2020;6(2):e18606.
ABSTRACT: BACKGROUND: The Royal College of General Practitioners (RCGP) Research and Surveillance Centre (RSC) and Public Health England (PHE) have successfully worked together on the surveillance of influenza and other infectious diseases for over 50 years, including three previous pandemics. With the emergence of the international outbreak of the coronavirus infection (COVID-19), a UK national approach to containment has been established to test people suspected of exposure to COVID-19. At the same time and separately, the RCGP RSC's surveillance has been extended to monitor the temporal and geographical distribution of COVID-19 infection in the community as well as assess the effectiveness of the containment strategy.
OBJECTIVES: The aims of this study are to surveil COVID-19 in both asymptomatic populations and ambulatory cases with respiratory infections, ascertain both the rate and pattern of COVID-19 spread, and assess the effectiveness of the containment policy.
METHODS: The RCGP RSC, a network of over 500 general practices in England, extract pseudonymized data weekly. This extended surveillance comprises of five components: (1) Recording in medical records of anyone suspected to have or who has been exposed to COVID-19. Computerized medical records suppliers have within a week of request created new codes to support this. (2) Extension of current virological surveillance and testing people with influenza-like illness or lower respiratory tract infections (LRTI)-with the caveat that people suspected to have or who have been exposed to COVID-19 should be referred to the national containment pathway and not seen in primary care. (3) Serology sample collection across all age groups. This will be an extra blood sample taken from people who are attending their general practice for a scheduled blood test. The 100 general practices currently undertaking annual influenza virology surveillance will be involved in the extended virological and serological surveillance. (4) Collecting convalescent serum samples. (5) Data curation. We have the opportunity to escalate the data extraction to twice weekly if needed. Swabs and sera will be analyzed in PHE reference laboratories.
RESULTS: General practice clinical system providers have introduced an emergency new set of clinical codes to support COVID-19 surveillance. Additionally, practices participating in current virology surveillance are now taking samples for COVID-19 surveillance from low-risk patients presenting with LRTIs. Within the first 2 weeks of setup of this surveillance, we have identified 3 cases: 1 through the new coding system, the other 2 through the extended virology sampling.
CONCLUSIONS: We have rapidly converted the established national RCGP RSC influenza surveillance system into one that can test the effectiveness of the COVID-19 containment policy. The extended surveillance has already seen the use of new codes with 3 cases reported. Rapid sharing of this protocol should enable scientific critique and shared learning.
International registered report identifier (irrid): Derr1-10.2196/18606.

URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7124955/

10. Edmond JSFCfE. Roadmap to Pandemic Resilience: Massive Scale Testing, Tracing, and Supported Isolation (TTSI) as the Path to Pandemic Resilience for a Free Society. EDMOND J SAFRA CENTER FOR ETHICS AT HARVARD UNIVERSITY. 2020.
ABSTRACT: From the Executive Summary: "We need to deliver 5 million tests per day by early June to deliver a safe social reopening. This number will need to increase over time (ideally by late July) to 20 million a day to fully remobilize the economy. We acknowledge that even this number may not be high enough to protect public health. In that considerably less likely eventuality, we will need to scale-up testing much further. By the time we know if we need to do that, we should be in a better position to know how to do it. In any situation, achieving these numbers depends on testing innovation. [...] This policy roadmap lays out how massive testing plus contact tracing plus social isolation with strong social supports, or TTSI, can rebuild trust in our personal safety and the safety of those we love. This will in turn support a renewal of mobility and mobilization of the economy. This paper is designed to educate the American public about what is emerging as a consensus national strategy."
URL: https://www.hsdl.org/?abstract&did=836787

11. Foddai A, Lindberg A, Lubroth J, et al. Surveillance to improve evidence for community control decisions during the COVID-19 pandemic – Opening the animal epidemic toolbox for public health. One health (Amsterdam, Netherlands). 2020:100130-. DOI: https://doi.org/10.1016/j.onehlt.2020.100130
ABSTRACT: During the first few months of 2020, the COVID-19 pandemic has reached Europe. Health systems all over the world are trying to control the outbreak in the shortest possible time. Exotic disease outbreaks are not uncommon in animal health and randomised surveillance is frequently used as support for decision-making. This editorial discusses the possibilities of practicing One Health, by using methods from animal health to enhance surveillance for COVID-19 to provide an evidence base fort decision-making in communities and countries.
URL: http://www.sciencedirect.com/science/article/pii/S235277142030046X
DOI: https://doi.org/10.1016/j.onehlt.2020.100130

12. Garg S, Bhatnagar N, Gangadharan N. A Case for Participatory Disease Surveillance of the COVID-19 Pandemic in India. JMIR Public Health and Surveillance. 2020;6(2):e18795.
ABSTRACT: The coronavirus disease pandemic requires the deployment of novel surveillance strategies to curtail further spread of the disease in the community. Participatory disease surveillance mechanisms have already been adopted in countries for the current pandemic. India, with scarce resources, good telecom support, and a not-so-robust heath care system, makes a strong case for introducing participatory disease surveillance for the prevention and control of the pandemic. India has just launched Aarogya Setu, which is a first-of-its-kind participatory disease surveillance initiative in India. This will supplement the existing Integrated Disease Surveillance Programme in India by finding missing cases and having faster aggregation, analysis of data, and prompt response measures. This newly created platform empowers communities with the right information and guidance, enabling protection from infection and reducing unnecessary contact with the overburdened health care system. However, caution needs to be exercised to address participation from digitally isolated populations, ensure the reliability of data, and consider ethical concerns such as maintaining individual privacy.
URL: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7164788/

13. Gudbjartsson DF, Helgason A, Jonsson H, et al. Spread of SARS-CoV-2 in the Icelandic Population. N Engl J Med. 2020;14:14.
ABSTRACT: BACKGROUND: During the current worldwide pandemic, coronavirus disease 2019 (Covid-19) was first diagnosed in Iceland at the end of February. However, data are limited on how SARS-CoV-2, the virus that causes Covid-19, enters and spreads in a population.
METHODS: We targeted testing to persons living in Iceland who were at high risk for infection (mainly those who were symptomatic, had recently traveled to high-risk countries, or had contact with infected persons). We also

carried out population screening using two strategies: issuing an open invitation to 10,797 persons and sending random invitations to 2283 persons. We sequenced SARS-CoV-2 from 643 samples.
RESULTS: As of April 4, a total of 1221 of 9199 persons (13.3%) who were recruited for targeted testing had positive results for infection with SARS-CoV-2. Of those tested in the general population, 87 (0.8%) in the open-invitation screening and 13 (0.6%) in the random-population screening tested positive for the virus. In total, 6% of the population was screened. Most persons in the targeted-testing group who received positive tests early in the study had recently traveled internationally, in contrast to those who tested positive later in the study. Children under 10 years of age were less likely to receive a positive result than were persons 10 years of age or older, with percentages of 6.7% and 13.7%, respectively, for targeted testing; in the population screening, no child under 10 years of age had a positive result, as compared with 0.8% of those 10 years of age or older. Fewer females than males received positive results both in targeted testing (11.0% vs. 16.7%) and in population screening (0.6% vs. 0.9%). The haplotypes of the sequenced SARS-CoV-2 viruses were diverse and changed over time. The percentage of infected participants that was determined through population screening remained stable for the 20-day duration of screening.
CONCLUSIONS: In a population-based study in Iceland, children under 10 years of age and females had a lower incidence of SARS-CoV-2 infection than adolescents or adults and males. The proportion of infected persons identified through population screening did not change substantially during the screening period, which was consistent with a beneficial effect of containment efforts. (Funded by deCODE Genetics-Amgen.).
URL: https://www.nejm.org/doi/full/10.1056/NEJMoa2006100

14. Hu ZB, Ci C. Screening and management of asymptomatic infection of corona virus disease 2019 (COVID-19). [Chinese]. Zhonghua yu fang yi xue za zhi [Chinese journal of preventive medicine]. 2020;54:E025.
ABSTRACT: To date, the controlling of outbreak of corona virus disease 2019 (COVID-19) has entered into a critical period in China. Recently, work resumption and public place is planning to open outside of Hubei, suggesting an uncertain and complex development of the epidemic in the next stage. Few days ago, we conducted a study on the epidemiological and clinical characteristics of asymptomatic infections of COVID-19, and found them might be the infection source. We believe that the findings are critical for developing public health intervention strategies for controlling COVID-19 infection in the future. Screening among the high-risk population and improving the sensitivity of measurement may contribute to the detection and management of asymptomatic infection.
URL: https://www.ncbi.nlm.nih.gov/pubmed/32145719

15. Koh D, Cunningham AC. Counting Coronavirus Disease 2019 (COVID-19) Cases: Case Definitions, Screened Populations and Testing Techniques Matter. Ann Acad Med Singapore. 2020;49(3):161-5.
ABSTRACT: While counting cases of disease appears straightforward, there are issues to consider when enumerating disease counts during an epidemic. For example, for Coronavirus Disease-2019 (COVID-19), how is a case defined? Hubei province in China changed its case definition twice in a fortnight-from laboratory-confirmed cases to clinically-confirmed cases without laboratory tests, and back to laboratory-confirmed cases. This caused confusion in the reported number of cases. If a confirmed case requires laboratory testing, what is the population who are laboratory-tested? Due to limited laboratory testing capacity in the early phase of an emerging epidemic, only "suspected cases" are laboratory-tested in most countries. This will result in underdiagnosis of confirmed cases and also raises the question: how is a "suspect case" defined? With the passage of time and increased capability to perform laboratory tests, more people can be screened and the number of confirmed cases will increase. What are the technical considerations of laboratory testing? This includes specimen collection (variable collection methods), samples collected (upper or lower respiratory tract biospecimens), time of collection in relation to course of disease, different laboratory test methods and kits (not all of which may be standardised or approved by authorities such as the Food and Drug Administration). Are approved laboratory facilities and trained manpower available, and how are test results interpreted and false-

negatives excluded? These issues will affect the accuracy of disease counts, which in turn will have implications on how we mount an appropriate response to the outbreak.
URL: http://www.annals.edu.sg/pdf/49VolNo3Mar2020/V49N3p161.pdf

16. Mallapaty S. How sewage could reveal true scale of coronavirus outbreak. Nature. 2020. DOI: 10.1038/d41586-020-00973-x
ABSTRACT: Wastewater testing could also be used as an early-warning sign if the virus returns. More than a dozen research groups worldwide have started analysing wastewater for the new coronavirus as a way to estimate the total number of infections in a community, given that most people will not be tested. The method could also be used to detect the coronavirus if it returns to communities, say scientists. So far, researchers have found traces of the virus in the Netherlands, the United States and Sweden.
URL: https://www.nature.com/articles/d41586-020-00973-x
DOI: 10.1038/d41586-020-00973-x

17. Marissa LZ, Wen L, Gail LSC, et al. Rapid Sentinel Surveillance for COVID-19 — Santa Clara County, California, March 2020. Morbidity and Mortality Weekly Report (MMWR). 2020. DOI: http://dx.doi.org/10.15585/mmwr.mm6914e3
ABSTRACT: What is already known about this topic? On February 27, 2020, Santa Clara County, California, identified its first case of coronavirus disease 2019 (COVID-19) associated with probable community transmission. What is added by this report? During March 5–14, among patients with respiratory symptoms evaluated at one of four Santa Clara County urgent care centers serving as sentinel surveillance sites, 23% had positive test results for influenza. Among a subset of patients with negative test results for influenza, 11% had positive test results for COVID-19. What are the implications for public health practice? COVID-19 cases identified through this sentinel surveillance system helped confirm community transmission in the county. Local health departments can use sentinel surveillance to understand the level of community transmission of COVID-19 and to better guide the selection and implementation of community mitigation measures.
DOI: http://dx.doi.org/10.15585/mmwr.mm6914e3

18. Omori R, Mizumoto K, Chowell G. Changes in testing rates could mask the novel coronavirus disease (COVID-19) growth rate. Int J Infect Dis. 2020. DOI: https://doi.org/10.1016/j.ijid.2020.04.021
ABSTRACT: Since the novel coronavirus disease (COVID-19) emerged in December 2019 in China, it has rapidly propagated to around the world, leading to one of the most significant pandemic events of recent history. Deriving reliable estimates of the COVID-19 epidemic growth rate is quite important to guide the timing and intensity of intervention strategies. Indeed, many studies have quantified the epidemic growth rate using time-series of reported cases during the early phase of the outbreak to estimate the basic reproduction number, R0. Using daily time series of COVID-19 incidence, we illustrate how epidemic curves of reported cases may not always reflect the true epidemic growth rate due to changes in testing rates, which could be influenced by limited diagnostic testing capacity during the early epidemic phase.
URL: http://www.sciencedirect.com/science/article/pii/S1201971220302368
DOI: https://doi.org/10.1016/j.ijid.2020.04.021

19. Peto J. Covid-19 mass testing facilities could end the epidemic rapidly. BMJ. 2020;368:m1163. DOI: 10.1136/bmj.m1163
In Editor's Choice of 19 March Godlee mentions the urgent need for increased capacity to test frontline healthcare workers serologically to verify their immunity to the covid-19 virus.[1] Even more urgent is capacity for weekly viral detection in the whole UK population. This, together with intensive contact tracing, could enable the country to resume normal life immediately. The virus could only survive in those who are untested, and contact tracing would often lead to them. Within the tested population anyone infected would be detected within about a week (0 to 7 days plus sample transport and testing) of becoming infectious.

Centrally organised facilities with the capacity to test the entire UK population weekly (in 6 days at 10 million tests per day) can be made available much more quickly and cheaply than a vaccine, probably within weeks. This heroic but straightforward national effort would involve a crash programme to enlist all existing PCR (polymerase chain reaction) facilities, acquire or manufacture the PCR reagents, and agree protocols including a laptop program for barcode reading in smaller laboratories. The US Food and Drug Administration (FDA) has just authorised a test kit for detecting the covid-19 virus that can be run on machines used in the NHS for HPV screening. Only laboratories that do PCR routinely would participate, subject to central quality control and at cost price. The Wellcome Sanger Institute, UK Biocentre, and smaller academic laboratories, together with all commercial facilities, should have enough machines or can get more immediately from the manufacturers. The 24-hour extra staffing to run their machines continuously would be bioscience students, graduates, and postgraduates familiar with PCR who already work in or near the laboratory. Processing capacity equivalent to 4000 Roche COBAS 8800 systems is needed, and the UK may already have both the machines and the trained staff in post or immediately available.
URL: https://www.bmj.com/content/368/bmj.m1163
DOI: 10.1136/bmj.m1163

20. Peto J, Alwan NA, Godfrey KM, et al. Universal weekly testing as the UK COVID-19 lockdown exit strategy. Lancet. 2020. DOI: 10.1016/S0140-6736(20)30936-3
The British public have been offered alternating periods of lockdown and relaxation of restrictions as part of the coronavirus disease 2019 (COVID-19) lockdown exit strategy.
Extended periods of lockdown will increase economic and social damage, and each relaxation will almost certainly trigger a further epidemic wave of deaths. These cycles will kill tens of thousands, perhaps hundreds of thousands, of people before a vaccine becomes available, with the most disadvantaged groups experiencing the greatest suffering.
There is an alternative strategy: universal repeated testing.
We recommend evaluation of weekly severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) antigen testing of the whole population in an entire city as a demonstration site (preferably several towns and cities, if possible), with strict household quarantine after a positive test. Quarantine would end when all residents of the household test negative at the same time; everyone else in the city can resume normal life, if they choose to. This testing programme should be assessed for feasibility in one or more cities with 200 000–300 000 people. Such a feasibility study should begin as soon as possible and continue after the current lockdown ends, when the infection rate will be fairly low but rising. The rate at which the number of infections then rises or falls, compared with the rest of the UK, will be apparent within a few weeks. A decision to proceed with national roll-out can then be made, beginning in high-risk areas and limited only by reagent supplies. If the epidemic is controlled, hundreds of thousands of lives could be saved, intensive care units will no longer be overloaded, and the adverse effects of lockdown on mental ill health and unemployment will end.
URL: https://doi.org/10.1016/S0140-6736(20)30936-3
DOI: 10.1016/S0140-6736(20)30936-3

21. Rogers C, Haueter A, Kiker J, et al. Observational Study of Drive Through Mass Testing and Timely Detection of COVID-19 in Alabama. SSRN- Lancet prepublication. 2020.
ABSTRACT: Background: Innovative testing strategies are urgently needed in response to the COVID-19 pandemic in the US. Objective: Present concept and impact of a mass testing strategy during critical testing capacity shortage nationwide. Design: Observational study of a Drive Through Test Site (DTTS) for collection nasopharyngeal swabs and COVID-19 PCR screening. Setting: Large parking lot of a congregational Church in Birmingham, Alabama. Patients: Consecutive children and adults self-reporting symptoms suggestive of COVID-19 infection presenting for testing. Measurements: Screening yield, overall and in patient subgroups, geographic reach. Results: From March 17 to 21, 2020, a total of 2216 patients were tested. The majority of patients were Jefferson and Shelby Counties residents (89%) and the remainder from other 23 counties statewide. The mean

age was 39 years (range 6 months to 85 years), 56% were female and 5% were ≥ 65 years. In this program, 70 patients tested positive (3% overall screening yield), an estimated 33% of the 213 statewide cases reported from March 17 to 24, 2020, and 13% of those were out of state residents. Yield was highest on March 21 (8%), significantly higher than the average yield in the previous 4 days (OR 2.95, p = 0.0005). COVID-19 positive screening yield was statistically similar in all age groups. No cases of direct patient exposure or contamination of a DTTS worker were reported. Limitations: Observational, retrospective analysis, single center experience. Conclusion: DTTS in Birmingham, AL, efficiently tested hundreds of patients per day during critical testing shortage nationally. Uniform infection rate in all age groups provided timely evidence of community spread, giving timely rationale for ongoing State and County social distancing orders.
URL: https://ssrn.com/abstract=3564819

22. Salathe M, Althaus CL, Neher R, et al. COVID-19 epidemic in Switzerland: on the importance of testing, contact tracing and isolation. Swiss Med Wkly. 2020;150:w20225.
ABSTRACT: Switzerland is among the countries with the highest number of coronavirus disease-2019 (COVID-19) cases per capita in the world. There are likely many people with undetected SARS-CoV-2 infection because testing efforts are currently not detecting all infected people, including some with clinical disease compatible with COVID-19. Testing on its own will not stop the spread of SARS-CoV-2. Testing is part of a strategy. The World Health Organization recommends a combination of measures: rapid diagnosis and immediate isolation of cases, rigorous tracking and precautionary self-isolation of close contacts. In this article, we explain why the testing strategy in Switzerland should be strengthened urgently, as a core component of a combination approach to control COVID-19.
URL: https://smw.ch/article/doi/smw.2020.20225

23. Thompson RN. Novel Coronavirus Outbreak in Wuhan, China, 2020: Intense Surveillance Is Vital for Preventing Sustained Transmission in New Locations. Journal of Clinical Medicine. 2020;9(2):11.
ABSTRACT: The outbreak of pneumonia originating in Wuhan, China, has generated 24,500 confirmed cases, including 492 deaths, as of 5 February 2020. The virus (2019-nCoV) has spread elsewhere in China and to 24 countries, including South Korea, Thailand, Japan and USA. Fortunately, there has only been limited human-to-human transmission outside of China. Here, we assess the risk of sustained transmission whenever the coronavirus arrives in other countries. Data describing the times from symptom onset to hospitalisation for 47 patients infected early in the current outbreak are used to generate an estimate for the probability that an imported case is followed by sustained human-to-human transmission. Under the assumptions that the imported case is representative of the patients in China, and that the 2019-nCoV is similarly transmissible to the SARS coronavirus, the probability that an imported case is followed by sustained human-to-human transmission is 0.41 (credible interval [0.27, 0.55]). However, if the mean time from symptom onset to hospitalisation can be halved by intense surveillance, then the probability that an imported case leads to sustained transmission is only 0.012 (credible interval [0, 0.099]). This emphasises the importance of current surveillance efforts in countries around the world, to ensure that the ongoing outbreak will not become a global pandemic.
URL: https://www.mdpi.com/2077-0383/9/2/498

24. Vogel G. 'These are answers we need.' WHO plans global study to discover true extent of coronavirus infections. Science. 2020. DOI: 10.1126/science.abc0458
ABSTRACT: In an effort to understand how many people have been infected with the new coronavirus, the World Health Organization (WHO) is planning a coordinated study to test blood samples for the presence of antibodies to the virus. Called Solidarity II, the program, which will involve more than half a dozen countries around the globe, will launch in the coming days, says Maria Van Kerkhove, who is helping coordinate WHO's COVID-19 response. Knowing the true number of cases—including mild ones—will help pin down the prevalence and mortality rate of COVID-19 in different age groups. It will also help policymakers decide how long shutdowns

and quarantines should last. “These are answers we need, and we need the right answers to drive policy,” WHO’s executive director for health emergencies, Michael Ryan, told a press briefing on 27 March.
URL: https://www.sciencemag.org/news/2020/04/these-are-answers-we-need-who-plans-global-study-discover-true-extent-coronavirus
DOI: 10.1126/science.abc0458

25. Wynants L, Van Calster B, Bonten MMJ, et al. Prediction models for diagnosis and prognosis of covid-19 infection: systematic review and critical appraisal. BMJ. 2020;369:m1328. DOI: 10.1136/bmj.m1328
ABSTRACT: Objective To review and critically appraise published and preprint reports of prediction models for diagnosing coronavirus disease 2019 (covid-19) in patients with suspected infection, for prognosis of patients with covid-19, and for detecting people in the general population at risk of being admitted to hospital for covid-19 pneumonia.Design Rapid systematic review and critical appraisal.Data sources PubMed and Embase through Ovid, Arxiv, medRxiv, and bioRxiv up to 24 March 2020.Study selection Studies that developed or validated a multivariable covid-19 related prediction model.Data extraction At least two authors independently extracted data using the CHARMS (critical appraisal and data extraction for systematic reviews of prediction modelling studies) checklist; risk of bias was assessed using PROBAST (prediction model risk of bias assessment tool).Results 2696 titles were screened, and 27 studies describing 31 prediction models were included. Three models were identified for predicting hospital admission from pneumonia and other events (as proxy outcomes for covid-19 pneumonia) in the general population; 18 diagnostic models for detecting covid-19 infection (13 were machine learning based on computed tomography scans); and 10 prognostic models for predicting mortality risk, progression to severe disease, or length of hospital stay. Only one study used patient data from outside of China. The most reported predictors of presence of covid-19 in patients with suspected disease included age, body temperature, and signs and symptoms. The most reported predictors of severe prognosis in patients with covid-19 included age, sex, features derived from computed tomography scans, C reactive protein, lactic dehydrogenase, and lymphocyte count. C index estimates ranged from 0.73 to 0.81 in prediction models for the general population (reported for all three models), from 0.81 to more than 0.99 in diagnostic models (reported for 13 of the 18 models), and from 0.85 to 0.98 in prognostic models (reported for six of the 10 models). All studies were rated at high risk of bias, mostly because of non-representative selection of control patients, exclusion of patients who had not experienced the event of interest by the end of the study, and high risk of model overfitting. Reporting quality varied substantially between studies. Most reports did not include a description of the study population or intended use of the models, and calibration of predictions was rarely assessed.Conclusion Prediction models for covid-19 are quickly entering the academic literature to support medical decision making at a time when they are urgently needed. This review indicates that proposed models are poorly reported, at high risk of bias, and their reported performance is probably optimistic. Immediate sharing of well documented individual participant data from covid-19 studies is needed for collaborative efforts to develop more rigorous prediction models and validate existing ones. The predictors identified in included studies could be considered as candidate predictors for new models. Methodological guidance should be followed because unreliable predictions could cause more harm than benefit in guiding clinical decisions. Finally, studies should adhere to the TRIPOD (transparent reporting of a multivariable prediction model for individual prognosis or diagnosis) reporting guideline.Systematic review registration Protocol https://osf.io/ehc47/, registration https://osf.io/wy245.
URL: https://www.bmj.com/content/bmj/369/bmj.m1328.full.pdf
DOI: 10.1136/bmj.m1328

26. Yongchen Z, Shen H, Wang X, et al. Different longitudinal patterns of nucleic acid and serology testing results based on disease severity of COVID-19 patients. Emerging Microbes & Infections. 2020:1-14.
ABSTRACT: Effective strategy to mitigate the ongoing pandemic of 2019 novel coronavirus (COVID-19) require a comprehensive understanding of humoral responses against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the emerging virus causing COVID-19. The dynamic profile of viral replication and shedding along

with viral antigen specific antibody responses among COVID-19 patients started to be reported but there is no consensus on their patterns. Here, we conducted a serial investigation on 21 individuals infected with SARS-CoV-2 in two medical centers from Jiangsu Province, including 11 non-severe COVID-19 patients, and 5 severe COVID-19 patients and 5 asymptomatic carriers based on nucleic acid test and clinical symptoms. The longitudinal swab samples and sera were collected from these people for viral RNA testing and antibody responses, respectively. Our data revealed different pattern of seroconversion among these groups. All 11 non-severe COVID-19 patients and 5 severe COVID-19 patients were seroconverted during hospitalization or follow-up period, suggesting that serological testing is a complementary assay to nucleic acid test for those symptomatic COVID-19 patients. Of note, immediate antibody responses were identified among severe cases, compared to non-severe cases. On the other hand, only one were seroconverted for asymptomatic carriers. The SARS-CoV-2 specific antibody responses were well-maintained during the observation period. Such information is of immediate relevance and would assist COVID-19 clinical diagnosis, prognosis and vaccine design.
URL: https://www.tandfonline.com/doi/full/10.1080/22221751.2020.1756699

SEARCH STRATEGIES

Medline – April 21, 2020, 10:37am

#	Searches	Results
1	exp population/	124773
2	(population? or people or citizen?).tw,kf,mp.	2215830
3	1 or 2	2215830
4	coronavirus/ or exp betacoronavirus/ or coronavirus infections/	10916
5	(coronavirus* or corona virus* or coronovirus* or coronaviral or (wuhan adj1 virus) or (wuhan adj1 viral) or cov or covid or WN-CoV or ncov or 2019ncov or ncov2019 or ncovid or ncovid2019 or 2019ncovid or covid-19 or covid19 or covid 19 or corvid 19 or HCov-19 or HCov-2019 or hcov19 or hcov2019 or severe acute respiratory syndrome coronavirus 2 or severe acute respiratory syndrome corona virus 2 or SARS Coronavirus 2 or SARS Corona virus 2 or SARS-COV-2 or SARSCOV2 or SARSCOV 2 or SARS2 or SARS-2 or coronavirus disease 2019 or corona virus disease 2019 or 2019 novel coronavirus infection* or 2019 novel coronavirus disease or 2019-nCoV infection* or coronavirus disease-19 or new coronavirus or novel corona virus).mp,kf,hw,rn,in.	20903
6	4 or 5	22357
7	(repeat or repetition or regular* or recurrence or interval*).tw,kf,mp.	2485568
8	(testing or screening or surveillance).tw,kf,mp.	1372554
9	3 and 6 and 7 and 8	42
10	limit 9 to yr="2019 -Current"	13
11	3 and 6 and 8	432

12	limit 11 to yr="2019 -Current"	149
13	12 not 10	136
14	3 and 6 and 7	185
15	limit 14 to yr="2019 -Current"	63
16	15 not 13	63
17	16 not 10	50

Medline Search 2 – April 21, 2020, 11:44am

#	Searches	Results
1	exp population/	124773
2	(population? or people or citizen?).tw,kf,mp.	2215830
3	1 or 2	2215830
4	coronavirus/ or exp betacoronavirus/ or coronavirus infections/	10916
5	(coronavirus* or corona virus* or coronovirus* or coronaviral or (wuhan adj1 virus) or (wuhan adj1 viral) or cov or covid or WN-CoV or ncov or 2019ncov or ncov2019 or ncovid or ncovid2019 or 2019ncovid or covid-19 or covid19 or covid 19 or corvid 19 or HCov-19 or HCov-2019 or hcov19 or hcov2019 or severe acute respiratory syndrome coronavirus 2 or severe acute respiratory syndrome corona virus 2 or SARS Coronavirus 2 or SARS Corona virus 2 or SARS-COV-2 or SARSCOV2 or SARSCOV 2 or SARS2 or SARS-2 or coronavirus disease 2019 or corona virus disease 2019 or 2019 novel coronavirus infection* or 2019 novel coronavirus disease or 2019-nCoV infection* or coronavirus disease-19 or new coronavirus or novel corona virus).mp,kf,hw,rn,in.	20903
6	4 or 5	22357
7	exp population surveillance/ or exp mass screening/	191562
8	(repeat or repetition or regular* or recurrence or interval*).tw,kf,mp.	1616713
9	7 or 8	1787416
10	(testing or screening or surveillance).tw,kf,mp.	1372554
11	3 and 6 and 9 and 10	179
12	limit 11 to yr="2019 -Current"	48

Medline Search 3 – April 22, 2020, 12:39pm

#	Searches	Results

1	exp population/	124817
2	(population? or people or citizen?).tw,kf,mp.	2217046
3	1 or 2	2217046
4	coronavirus/ or exp betacoronavirus/ or coronavirus infections/	10978
5	(coronavirus* or corona virus* or coronovirus* or coronaviral or (wuhan adj1 virus) or (wuhan adj1 viral) or cov or covid or WN-CoV or ncov or 2019ncov or ncov2019 or ncovid or ncovid2019 or 2019ncovid or covid-19 or covid19 or covid 19 or corvid 19 or HCov-19 or HCov-2019 or hcov19 or hcov2019 or severe acute respiratory syndrome coronavirus 2 or severe acute respiratory syndrome corona virus 2 or SARS Coronavirus 2 or SARS Corona virus 2 or SARS-COV-2 or SARSCOV2 or SARSCOV 2 or SARS2 or SARS-2 or coronavirus disease 2019 or corona virus disease 2019 or 2019 novel coronavirus infection* or 2019 novel coronavirus disease or 2019-nCoV infection* or coronavirus disease-19 or new coronavirus or novel corona virus).mp,kf,hw,rn,in.	21301
6	4 or 5	22755
7	models, theoretical/ or models, biological/ or exp forecasting/	560497
8	(model? or projection? or forecasting or forecast? or prediction?).tw,kf,mp.	3968863
9	7 or 8	3968863
10	molecular epidemiology/ or exp population surveillance/ or prevalence/ or epidemiological monitoring/ or seroepidemiologic studies/ or seroconversion/	376691
11	(prevalence or proportion or epidemiological monitoring or epidemiologic monitoring or epidemiological surveillance? or epidemiologic surveillance? or surveillance or biosurveillance or seroprevalence? or seroepidemiologic studies or seroepidemiologic study or seroepidemiological study or seroepidemiological studies or seroconversion? or seroconverted).tw,kf,mp.	1253383
12	10 or 11	1261538
13	exp mass screening/	126452
14	(repeat or repeated or repetition or regular* or recurrence or reoccurrence or interval?).tw,kf,mp.	1853381
15	13 or 14	1966725
16	(testing or screening or surveillance).tw,kf,mp.	1373254
17	antibodies/ or antibodies, viral/ or exp immunoglobulin g/ or polymerase chain reaction/ or immunity/ or immunity, herd/ or immunologic memory/	573881

18	(antibody or antibodies or antibody specificit* or IgG or "immunoglobulin g" or immune or immunity or immunologic memory or polymerase chain reaction? or PCR).tw,kf,mp.	2537528
19	17 or 18	2545653
20	3 and 6 and 9 and 12 and 15 and 16 and 19	1
21	3 and 6 and 9 and 12 and 15 and 16	5
22	3 and 6 and 9 and 12 and 15	9
23	3 and 6 and 12 and 15 and 16	29
24	3 and 6 and 12 and 16 and 19	123
25	3 and 6 and 12 and 15 and 19	14
26	6 and 12 and 15 and 19	76
27	6 and 9 and 12 and 15	25
28	6 and 15 and 16 and 19	59
29	20 or 21 or 22 or 23 or 24 or 25 or 26 or 27 or 28	267
30	limit 29 to yr="2019 -Current"	62

EMBASE – April 21, 2020, 10:51am

#	Searches	Results
1	exp population/	587732
2	(population? or people or citizen?).tw,hw,mp.	3048505
3	1 or 2	3048505
4	coronavirus/ or exp betacoronavirus/ or coronavirus infections/	14599
5	(coronavirus* or corona virus* or coronovirus* or coronaviral or (wuhan adj1 virus) or (wuhan adj1 viral) or cov or covid or WN-CoV or ncov or 2019ncov or ncov2019 or ncovid or ncovid2019 or 2019ncovid or covid-19 or covid19 or covid 19 or corvid 19 or HCov-19 or HCov-2019 or hcov19 or hcov2019 or severe acute respiratory syndrome coronavirus 2 or severe acute respiratory syndrome corona virus 2 or SARS Coronavirus 2 or SARS Corona virus 2 or SARS-COV-2 or SARSCOV2 or SARSCOV 2 or SARS2 or SARS-2 or coronavirus disease 2019 or corona virus disease 2019 or 2019 novel coronavirus infection* or 2019 novel coronavirus disease or 2019-nCoV infection* or coronavirus disease-19 or new coronavirus or novel corona virus).mp,hw,rn,in.	24151
6	4 or 5	24277

7	(frequency or timing or repeat or repetition or regular* or recurrence or interval*).tw,hw,mp.	3271197
8	(testing or screening or surveillance).tw,hw,mp.	2032151
9	3 and 6 and 7 and 8	63
10	limit 9 to yr="2019 -Current"	16
11	3 and 6 and 8	434
12	limit 11 to yr="2019 -Current"	117
13	12 not 10	101
14	3 and 6 and 7	254
15	limit 14 to yr="2019 -Current"	62
16	15 not 13	62
17	16 not 10	46

EMBASE Search 2 – April 21, 2020, 11:46am

#	Searches	Results
1	exp population/	587732
2	(population? or people or citizen?).tw,hw,mp.	3048505
3	1 or 2	3048505
4	coronavirus/ or exp betacoronavirus/ or coronavirus infections/	14599
5	(coronavirus* or corona virus* or coronovirus* or coronaviral or (wuhan adj1 virus) or (wuhan adj1 viral) or cov or covid or WN-CoV or ncov or 2019ncov or ncov2019 or ncovid or ncovid2019 or 2019ncovid or covid-19 or covid19 or covid 19 or corvid 19 or HCov-19 or HCov-2019 or hcov19 or hcov2019 or severe acute respiratory syndrome coronavirus 2 or severe acute respiratory syndrome corona virus 2 or SARS Coronavirus 2 or SARS Corona virus 2 or SARS-COV-2 or SARSCOV2 or SARSCOV 2 or SARS2 or SARS-2 or coronavirus disease 2019 or corona virus disease 2019 or 2019 novel coronavirus infection* or 2019 novel coronavirus disease or 2019-nCoV infection* or coronavirus disease-19 or new coronavirus or novel corona virus).mp,hw,rn,in.	24151
6	4 or 5	24277
7	exp population surveillance/ or exp mass screening/	452867
8	(repeat or repetition or regular* or recurrence or interval*).tw,hw,mp.	2107380
9	7 or 8	2509067

10	(testing or screening or surveillance).tw,hw,mp.	2032151
11	3 and 6 and 9 and 10	68
12	limit 11 to yr="2019 -Current"	15

Embase Search 3 – April 22, 2020, 12:50pm

#	Searches	Results
1	exp population/	587763
2	(population? or people or citizen?).tw,hw,mp.	3049105
3	1 or 2	3049105
4	coronavirus/ or exp betacoronavirus/ or coronavirus infections/	14758
5	(coronavirus* or corona virus* or coronovirus* or coronaviral or (wuhan adj1 virus) or (wuhan adj1 viral) or cov or covid or WN-CoV or ncov or 2019ncov or ncov2019 or ncovid or ncovid2019 or 2019ncovid or covid-19 or covid19 or covid 19 or corvid 19 or HCov-19 or HCov-2019 or hcov19 or hcov2019 or severe acute respiratory syndrome coronavirus 2 or severe acute respiratory syndrome corona virus 2 or SARS Coronavirus 2 or SARS Corona virus 2 or SARS-COV-2 or SARSCOV2 or SARSCOV 2 or SARS2 or SARS-2 or coronavirus disease 2019 or corona virus disease 2019 or 2019 novel coronavirus infection* or 2019 novel coronavirus disease or 2019-nCoV infection* or coronavirus disease-19 or new coronavirus or novel corona virus).mp,hw,rn,in.	24444
6	4 or 5	24571
7	models, theoretical/ or models, biological/ or exp forecasting/	265782
8	(model? or projection? or forecasting or forecast? or prediction?).tw,hw,mp.	5125026
9	7 or 8	5125026
10	molecular epidemiology/ or exp population surveillance/ or prevalence/ or epidemiological monitoring/ or seroepidemiologic studies/ or seroconversion/	918408
11	(prevalence or proportion or epidemiological monitoring or epidemiologic monitoring or epidemiological surveillance? or epidemiologic surveillance? or surveillance or biosurveillance or seroprevalence? or seroepidemiologic studies or seroepidemiologic study or seroepidemiological study or seroepidemiological studies or seroconversion? or seroconverted).tw,hw,mp.	1794170
12	10 or 11	1948220
13	exp mass screening/	238750
14	(repeat or repeated or repetition or regular* or recurrence or reoccurrence or interval?).tw,hw,mp.	2432194

15	13 or 14	2641709
16	(testing or screening or surveillance).tw,hw,mp.	2032491
17	antibodies/ or antibodies, viral/ or exp immunoglobulin g/ or polymerase chain reaction/ or immunity/ or immunity, herd/ or immunologic memory/	803641
18	(antibody or antibodies or antibody specificit* or IgG or "immunoglobulin g" or immune or immunity or immunologic memory or polymerase chain reaction? or PCR).tw,hw,mp.	3439158
19	17 or 18	3440029
20	3 and 6 and 9 and 12 and 15 and 16 and 19	3
21	3 and 6 and 9 and 12 and 15 and 16	7
22	3 and 6 and 9 and 12 and 15	13
23	3 and 6 and 12 and 15 and 16	35
24	3 and 6 and 12 and 16 and 19	142
25	3 and 6 and 12 and 15 and 19	29
26	6 and 12 and 15 and 19	131
27	6 and 9 and 12 and 15	41
28	6 and 15 and 16 and 19	126
29	20 or 21 or 22 or 23 or 24 or 25 or 26 or 27 or 28	371
30	limit 29 to yr="2019 -Current"	79

CINAHL – April 21, 2020, 11:06am

#	Query	Results
S1	(MH "Coronavirus") OR (MH "Coronavirus Infections+")	3,271
S2	TX (coronavirus* or corona virus* or coronovirus* or coronaviral or (wuhan w1 virus) or (wuhan w1 viral) or cov or covid or WN-CoV or ncov or 2019ncov or ncov2019 or ncovid or ncovid2019 or 2019ncovid or covid-19 or covid19 or covid 19 or corvid 19 or HCov-19 or HCov-2019 or hcov19 or hcov2019 or severe acute respiratory syndrome coronavirus 2 or severe acute respiratory syndrome corona virus 2 or SARS Coronavirus 2 or SARS Corona virus 2 or SARS-COV-2 or SARSCOV2 or SARSCOV 2 or SARS2 or SARS-2 or coronavirus disease 2019 or corona virus disease 2019 or 2019 novel coronavirus infection* or 2019 novel coronavirus disease or 2019-nCoV infection* or coronavirus disease-19 or new coronavirus or novel corona virus)	8,250
S3	TX testing or screening or surveillance	516,773
S4	TX frequency or timing or repeat or repetition or regular* or recurrence or interval*	849,632

S5	(MH "Population+") OR (MH "Population Surveillance+")	343,517
S6	TX (population# or people or citizen#)	1,289,314
S7	S1 OR S2	10,014
S8	S5 OR S6	1,492,934
S9	S3 AND S4 AND S7 AND S8	590
S10	S3 AND S4 AND S7 AND S8 [limit to 2019-2020]	20
S11	S4 AND S7 AND S8	1,218
S12	S4 AND S7 AND S8 [limit to 2019-2020]	43
S13	S12 NOT S10	23
S14	S3 AND S7 AND S8	1,515
S15	S3 AND S7 AND S8 [limit to 2019-2020]	113
S16	S15 NOT S13	113
S17	S15 NOT S10	93

CINAHL Search 2 – April 22, 2020, 1:23pm

#	Query	Results
S1	(MH "Population+")	335,208
S2	TX (population# or people or citizen#)	1,289,690
S3	S1 OR S2	1,493,281
S4	(MH "Coronavirus") OR (MH "Coronavirus Infections")	1,152
S5	TX (coronavirus* or corona virus* or coronovirus* or coronaviral or (wuhan w1 virus) or (wuhan w1 viral) or cov or covid or WN-CoV or ncov or 2019ncov or ncov2019 or ncovid or ncovid2019 or 2019ncovid or covid-19 or covid19 or covid 19 or corvid 19 or HCov-19 or HCov-2019 or hcov19 or hcov2019 or severe acute respiratory syndrome coronavirus 2 or severe acute respiratory syndrome corona virus 2 or SARS Coronavirus 2 or SARS Corona virus 2 or SARS-COV-2 or SARSCOV2 or SARSCOV 2 or SARS2 or SARS-2 or coronavirus disease 2019 or corona virus disease 2019 or 2019 novel coronavirus infection* or 2019 novel coronavirus disease or 2019-nCoV infection* or coronavirus disease-19 or new coronavirus or novel corona virus)	8,311
S6	S4 OR S5	8,311
S7	(MH "Models, Biological") OR (MH "Models, Theoretical")	115,807
S8	(MH "Forecasting")	15,840
S9	TX model# or projection# or forecasting or forecast# or prediction#	953,608

S10	(MH "Epidemiology, Molecular") OR (MH "Epidemiological Research") OR (MH "Population Surveillance+")	42,411
S11	(MH "Prevalence")	95,979
S12	(MH "Seroprevalence Studies")	814
S13	(MH "Seroconversion")	693
S14	TX prevalence or proportion or epidemiological monitoring or epidemiologic monitoring or epidemiological surveillance# or epidemiologic surveillance# or surveillance or biosurveillance or seroprevalence# or seroepidemiologic studies or seroepidemiologic study or seroepidemiological study or seroepidemiological studies or seroconversion# or seroconverted	585,644
S15	S7 OR S8 OR S9	953,608
S16	S10 OR S11 OR S12 OR S13 OR S14	603,498
S17	(MH "Rescreening")	207
S18	TX repeat or repeated or repetition or regular* or recurrence or reoccurrence or interval#	968,905
S19	S17 OR S18	969,003
S20	TX testing or screening or surveillance	616,006
S21	(MH "Antibodies") OR (MH "Antibodies, Viral") OR (MH "Immunoglobulins")	31,694
S22	(MH "Polymerase Chain Reaction")	36,566
S23	(MH "Immunity")	15,190
S24	TX antibody or antibodies or antibody specificit* or IgG or "immunoglobulin g" or immune or immunity or immunologic memory or polymerase chain reaction# or PCR	293,405
S25	S21 OR S22 OR S23 OR S24	300,573
S26	S3 AND S6 AND S15 AND S16 AND S19 AND S20 AND S25	175
S27	S3 AND S6 AND S15 AND S16 AND S19 AND S20	522
S28	S3 AND S6 AND S15 AND S16 AND S19	745
S29	S3 AND S6 AND S16 AND S19 AND S20	768
S30	S3 AND S6 AND S16 AND S20 AND S25	422
S31	S6 AND S16 AND S19 AND S25	343
S32	S6 AND S15 AND S16 AND S19	810
S33	S6 AND S19 AND S20 AND S25	375
S34	S26 OR S27 OR S28 OR S29 OR S30 OR S31 OR S32 OR S33	1,341
S35	S26 OR S27 OR S28 OR S29 OR S30 OR S31 OR S32 OR S33 [limit to 2019-2020]	58

Pubmed Search 1 – April 21, 2020, 11:16am

(((wuhan[tw] AND (coronavirus[tw] OR corona virus[tw])) OR coronavirus*[ti] OR COVID*[tw] OR nCov[tw] OR 2019 ncov[tw] OR novel coronavirus[tw] OR novel corona virus[tw] OR covid-19[tw] OR SARS-COV-2[tw] OR Severe Acute Respiratory Syndrome Coronavirus 2[tw] OR coronavirus disease 2019[tw] OR corona virus disease 2019[tw] OR new coronavirus[tw] OR new corona virus[tw] OR new coronaviruses[all] OR novel coronaviruses[all] OR Severe Acute Respiratory Syndrome Coronavirus 2[nm] OR 2019 ncov[tw] OR nCov 2019[tw] OR SARS Coronavirus 2[all])) AND ((epidemiolog*[all] OR Incidence*[all] OR occurrence*[tw] OR prevalen*[tw] OR distribut*[tw] OR deliver*[tw] OR transport*[tw] OR transmission*[tw] OR transmit*[tw] OR transfer*[tw] OR spread*[tw] OR pass[tw] OR passing[tw] OR control*[tw] OR contain*[tw] OR prevent*[tw]) AND (rate*[tw] OR number*[tw] OR frequency[tw] OR growth[tw] OR time[tw] OR length[tw] OR duration[tw]) AND (screen*[tw] OR test*[tw] OR diagnos*[tw] OR temperature scan*[tw])) AND (2019/12[dp]:2020[dp])

Pubmed Search 2 – April 21, 2020, 12:00pm

(((((population OR people OR populations OR citizen OR citizens)) OR (population[Title/Abstract] OR populations[Title/Abstract] OR people[Title/Abstract] OR citizen[Title/Abstract] OR citizens[Title/Abstract]))) AND (((testing OR screening OR surveillance OR temperature or assessment)) OR (testing[Title/Abstract] OR screening[Title/Abstract] OR surveillance[Title/Abstract] OR temperature[Title/Abstract] OR assessment[Title/Abstract]))) AND ((((wuhan[tw] AND (coronavirus[tw] OR corona virus[tw])) OR coronavirus*[ti] OR COVID*[tw] OR nCov[tw] OR 2019 ncov[tw] OR novel coronavirus[tw] OR novel corona virus[tw] OR covid-19[tw] OR SARS-COV-2[tw] OR Severe Acute Respiratory Syndrome Coronavirus 2[tw] OR coronavirus disease 2019[tw] OR corona virus disease 2019[tw] OR new coronavirus[tw] OR new corona virus[tw] OR new coronaviruses[all] OR novel coronaviruses[all] OR "Severe Acute Respiratory Syndrome Coronavirus 2"[nm] OR 2019 ncov[tw] OR nCov 2019[tw] OR SARS Coronavirus 2[all])))

Pubmed Search 3 – April 21, 2020, 1:26pm

(((((repeat OR repeated OR regular OR recurrence OR reoccurrence OR interval OR intervals OR repetition)) OR (repeat[Title/Abstract] OR repeated[Title/Abstract] OR regular[Title/Abstract] OR recurrence[Title/Abstract] OR reoccurence[Title/Abstract] OR interval[Title/Abstract] OR intervals[Title/Abstract] OR repetition[Title/Abstract]))) AND (((testing OR screening OR surveillance OR temperature OR assessment OR monitoring)) OR (testing[Title/Abstract] OR screening[Title/Abstract] OR surveillance[Title/Abstract] OR temperature[Title/Abstract] OR assessment[Title/Abstract] OR monitoring[Title/Abstract]))) AND ((((wuhan[tw] AND (coronavirus[tw] OR corona virus[tw])) OR coronavirus*[ti] OR COVID*[tw] OR nCov[tw] OR 2019 ncov[tw] OR novel coronavirus[tw] OR novel corona virus[tw] OR covid-19[tw] OR SARS-COV-2[tw] OR Severe Acute Respiratory Syndrome Coronavirus 2[tw] OR coronavirus disease 2019[tw] OR corona virus disease 2019[tw] OR new coronavirus[tw] OR new corona virus[tw] OR new coronaviruses[all] OR novel coronaviruses[all] OR "Severe Acute Respiratory Syndrome Coronavirus 2"[nm] OR 2019 ncov[tw] OR nCov 2019[tw] OR SARS Coronavirus 2[all])))

Pubmed Search 4 – April 22, 2020, 1:37pm

(((((repeat OR repeated OR regular OR recurrence OR reoccurrence OR interval OR intervals OR repetition)) OR (repeat[Title/Abstract] OR repeated[Title/Abstract] OR regular[Title/Abstract] OR recurrence[Title/Abstract] OR reoccurence[Title/Abstract] OR interval[Title/Abstract] OR intervals[Title/Abstract] OR repetition[Title/Abstract]))) AND (((testing OR screening OR surveillance OR temperature OR assessment OR monitoring)) OR (testing[Title/Abstract] OR screening[Title/Abstract] OR surveillance[Title/Abstract] OR temperature[Title/Abstract] OR assessment[Title/Abstract] OR monitoring[Title/Abstract]))) AND (((models OR model OR forecasting OR forecast OR projection OR projections OR prediction OR predictions OR immunity OR proportion OR proportions OR prevalence OR seroepidemiology)) OR (models[Title/Abstract] OR

model[Title/Abstract] OR forecasting[Title/Abstract] OR forecast[Title/Abstract] OR projection[Title/Abstract] OR projections[Title/Abstract] OR prediction[Title/Abstract] OR predictions[Title/Abstract] OR immunity[Title/Abstract] OR proportion[Title/Abstract] OR proportions[Title/Abstract] OR prevalence[Title/Abstract] OR seroepidemiology[Title/Abstract])))) AND ((((wuhan[tw] AND (coronavirus[tw] OR corona virus[tw])) OR coronavirus*[ti] OR COVID*[tw] OR nCov[tw] OR 2019 ncov[tw] OR novel coronavirus[tw] OR novel corona virus[tw] OR covid-19[tw] OR SARS-COV-2[tw] OR Severe Acute Respiratory Syndrome Coronavirus 2[tw] OR coronavirus disease 2019[tw] OR corona virus disease 2019[tw] OR new coronavirus[tw] OR new corona virus[tw] OR new coronaviruses[all] OR novel coronaviruses[all] OR "Severe Acute Respiratory Syndrome Coronavirus 2"[nm] OR 2019 ncov[tw] OR nCov 2019[tw] OR SARS Coronavirus 2[all])))

Google Scholar – April 22, 2020, 2:58pm
("covid-19" OR "coronavirus") AND (repeat OR repeated OR repetition OR regular OR recurrence OR interval OR intervals) AND (testing OR screening|surveillance|biosurveillance) AND (prevalence|proportion OR "epidemiological monitoring" OR biosurveillance)

Google – April 23, 2020,
covid-19 rate of change in population testing frequency
covid-19 population testing frequency
covid-19 population testing cohorts
covid-19 population infection surveillance cohorts
covid-19 population infection surveillance plans

ARTICLES WITHOUT ABSTRACTS

Pre-printed articles

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2. Betensky RA, Feng Y. Accounting for incomplete testing in the estimation of epidemic parameters. medRxiv. 2020:2020.04.08.20058313. DOI: 10.1101/2020.04.08.20058313 URL: http://medrxiv.org/content/early/2020/04/11/2020.04.08.20058313.abstract

3. Britton T. Basic prediction methodology for covid-19: estimation and sensitivity considerations. medRxiv. 2020:2020.03.27.20045575. DOI: 10.1101/2020.03.27.20045575 URL: http://medrxiv.org/content/early/2020/03/30/2020.03.27.20045575.abstract

4. Chen S, Li Q, Gao S, et al. Mitigating COVID-19 outbreak via high testing capacity and strong transmission-intervention in the United States. medRxiv. 2020:2020.04.03.20052720. DOI: 10.1101/2020.04.03.20052720 URL: http://medrxiv.org/content/early/2020/04/07/2020.04.03.20052720.abstract

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