

[Evaluating primary and booster vaccination prioritization strategies for COVID-19 by age and high-contact employment status using data from contact surveys](#)

Roubenoff, Feehan, and Mahmud, *Epidemics*

The debate around vaccine prioritization for COVID-19 has revolved around balancing the benefits from: (1) the direct protection conferred by the vaccine amongst those at highest risk of severe disease outcomes, and (2) the indirect protection through vaccinating those that are at highest risk of being infected and of transmitting the virus. While adults aged 65+ are at highest risk for severe disease and death from COVID-19, essential service and other in-person workers with greater rates of contact may be at higher risk of acquiring and transmitting SARS-CoV-2. Unfortunately, there have been relatively little data available to understand heterogeneity in contact rates and risk across these demographic groups. Here, we retrospectively analyze and evaluate vaccination prioritization strategies by age and worker status. We use a mathematical model of SARS-CoV-2 transmission and uniquely detailed contact data collected as part of the Berkeley Interpersonal Contact Survey to evaluate five vaccination prioritization strategies: (1) prioritizing only adults over age 65, (2) prioritizing only high-contact workers, (3) splitting prioritization between adults 65+ and high-contact workers, (4) tiered prioritization of adults over age 65 followed by high-contact workers, and (5) tiered prioritization of high-contact workers followed by adults 65+. We find that for the primary two-dose vaccination schedule, assuming 70% uptake, a tiered roll-out that first prioritizes adults 65+ averts the most deaths (31% fewer deaths compared to a no-vaccination scenario) while a tiered roll-out that prioritizes high contact workers averts the most number of clinical infections (14% fewer clinical infections compared to a no-vaccination scenario). We also consider prioritization strategies for booster doses during a subsequent outbreak of a hypothetical new SARS-CoV-2 variant. We find that a tiered roll-out that prioritizes adults 65+ for booster doses consistently averts the most deaths, and it may also avert the most number of clinical cases depending on the epidemiology of the SARS-CoV-2 variant and the vaccine efficacy.

[Projecting the risk of mosquito-borne diseases in a warmer and more populated world: a multi-model, multi-scenario intercomparison modelling study](#)

Colon-Gonzalez et al., The Lancet Planetary Health

## **Background**

Mosquito-borne diseases are expanding their range, and re-emerging in areas where they had subsided for decades. The extent to which climate change influences the transmission suitability and population at risk of mosquito-borne diseases across different altitudes and population densities has not been investigated. The aim of this study was to quantify the extent to which climate change will influence the length of the transmission season and estimate the population at risk of mosquito-borne diseases in the future, given different population densities across an altitudinal gradient.

## **Methods**

Using a multi-model multi-scenario framework, we estimated changes in the length of the transmission season and global population at risk of malaria and dengue for different altitudes and population densities for the period 1951–99. We generated projections from six mosquito-borne disease models, driven by four global circulation models, using four representative concentration pathways, and three shared socioeconomic pathways.

## **Findings**

We show that malaria suitability will increase by 1·6 additional months (mean 0·5, SE 0·03) in tropical highlands in the African region, the Eastern Mediterranean region, and the region of the Americas. Dengue suitability will increase in lowlands in the Western Pacific region and the Eastern Mediterranean region by 4·0 additional months (mean 1·7, SE 0·2). Increases in the climatic suitability of both diseases will be greater in rural areas than in urban areas. The epidemic belt for both diseases will expand towards temperate areas. The population at risk of both diseases might increase by up to 4·7 additional billion people by 2070 relative to 1970–99, particularly in lowlands and urban areas.

## **Interpretation**

Rising global mean temperature will increase the climatic suitability of both diseases particularly in already endemic areas. The predicted expansion towards higher altitudes and temperate regions suggests that outbreaks can occur in areas where people might be immunologically naive and public health systems unprepared. The population at risk of malaria and dengue will be higher in densely populated urban areas in the WHO African region, South-East Asia region, and the region of the Americas, although we did not account for urban-heat island effects, which can further alter the risk of disease transmission.

## [Modelling the spread of serotype-2 vaccine derived-poliovirus outbreak in Pakistan and Afghanistan to inform outbreak control strategies in the context of the COVID-19 pandemic](#)

Molodecky et al., Vaccine

### **Background**

Since July 2019, Pakistan and Afghanistan have been facing an outbreak of serotype-2 circulating vaccine derived [poliovirus](#) (cVDPV2) in addition to continued transmission of serotype-1 wild poliovirus (WPV1) and SARS-CoV-2 in 2020. Understanding the risks of cVDPV2 transmission due to pause of global vaccination efforts and the impact of potential vaccination response strategies in the current context of COVID-19 mitigation measures is critical.

### **Methods**

We developed a stochastic, geographically structured mathematical model of cVDPV2 transmission which captures both mucosal and humoral immunity separately and allows for reversion of serotype-2 [oral polio vaccine](#) (OPV2) [virus](#) to cVDPV2 following vaccine administration. The model includes geographic heterogeneities in [vaccination coverage](#), population immunity and population movement. The model was fitted to historic cVDPV2 cases in Pakistan and Afghanistan between January 2010-April 2016 and July 2019-March 2020 using iterated particle filtering. The model was used to simulate spread of cVDPV2 infection from July 2019 to explore impact of various proposed vaccination responses on stopping transmission and risk of spread of reverted Sabin-2 under varying assumptions of impacts from COVID-19 lockdown measures on movement patterns as well as declines in vaccination coverage.

### **Results**

Simulated monthly incidence of cVDPV2 from the best-fit model demonstrated general spatio-temporal alignment with observed cVDPV2 cases. The model predicted substantial spread of cVDPV2 infection, with widespread transmission through 2020 in the absence of any vaccination activities. Vaccination responses were predicted to substantially reduce transmission and case burden, with a greater impact from earlier responses and those with larger geographic scope. While the greatest risk of seeding reverted Sabin-2 was predicted in areas targeted with OPV2, subsequent spread was greatest in areas with no or delayed response. The proposed vaccination strategy demonstrated ability to stop the cVDPV2 outbreak (with low risk of reverted Sabin-2 spread) by February 2021.

### **Conclusion**

Outbreak response vaccination campaigns against cVDPV2 will be challenging throughout the COVID-19 pandemic but must be implemented urgently when feasible to stop transmission of cVDPV2.

## The role of regular asymptomatic testing in reducing the impact of a COVID-19 wave

Silva et al., Epidemics

Testing for infection with SARS-CoV-2 is an important intervention in reducing onwards transmission of COVID-19, particularly when combined with the isolation and contact-tracing of positive cases. Many countries with the capacity to do so have made use of lab-processed Polymerase Chain Reaction (PCR) testing targeted at individuals with symptoms and the contacts of confirmed cases. Alternatively, Lateral Flow Tests (LFTs) are able to deliver a result quickly, without lab-processing and at a relatively low cost. Their adoption can support regular mass asymptomatic testing, allowing earlier detection of infection and isolation of infectious individuals. In this paper we extend and apply the agent-based epidemic modelling framework *Covasim* to explore the impact of regular asymptomatic testing on the peak and total number of infections in an emerging COVID-19 wave. We explore testing with LFTs at different frequency levels within a population with high levels of immunity and with background symptomatic PCR testing, case isolation and contact tracing for testing. The effectiveness of regular asymptomatic testing was compared with 'lockdown' interventions seeking to reduce the number of non-household contacts across the whole population through measures such as mandating working from home and restrictions on gatherings. Since regular asymptomatic testing requires only those with a positive result to reduce contact, while lockdown measures require the whole population to reduce contact, any policy decision that seeks to trade off harms from infection against other harms will not automatically favour one over the other. Our results demonstrate that, where such a trade off is being made, at moderate rates of early exponential growth regular asymptomatic testing has the potential to achieve significant infection control without the wider harms associated with additional lockdown measures.

## [Unraveling the drivers of MERS-CoV transmission](#)

Cauchemez et al., PNAS

With more than 1,700 laboratory-confirmed infections, Middle East respiratory syndrome coronavirus (MERS-CoV) remains a significant threat for public health. However, the lack of detailed data on modes of transmission from the animal reservoir and between humans means that the drivers of MERS-CoV epidemics remain poorly characterized. Here, we develop a statistical framework to provide a comprehensive analysis of the transmission patterns underlying the 681 MERS-CoV cases detected in the Kingdom of Saudi Arabia (KSA) between January 2013 and July 2014. We assess how infections from the animal reservoir, the different levels of mixing, and heterogeneities in transmission have contributed to the buildup of MERS-CoV epidemics in KSA. We estimate that 12% [95% credible interval (CI): 9%, 15%] of cases were infected from the reservoir, the rest via human-to-human transmission in clusters (60%; CI: 57%, 63%), within (23%; CI: 20%, 27%), or between (5%; CI: 2%, 8%) regions. The reproduction number at the start of a cluster was 0.45 (CI: 0.33, 0.58) on average, but with large SD (0.53; CI: 0.35, 0.78). It was  $>1$  in 12% (CI: 6%, 18%) of clusters but fell by approximately one-half (47% CI: 34%, 63%) its original value after 10 cases on average. The ongoing exposure of humans to MERS-CoV from the reservoir is of major concern, given the continued risk of substantial outbreaks in health care systems. The approach we present allows the study of infectious disease transmission when data linking cases to each other remain limited and uncertain.