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UNITED STATES DISTRICT COURT
FOR THE NORTHERN DISTRICT OF CALIFORNIA
(San José Division)

RITESH TANDON, et al.,

Plaintiffs,

v.

GAVIN NEWSOM, et al.,

Defendants.

No. 20CV07108LHK

DECLARATION OF DR. MARC LIPSITCH IN SUPPORT OF DEFENDANTS JEFFREY V. SMITH AND SARA H. CODY'S OPPOSITION TO PLAINTIFFS' MOTION FOR A PRELIMINARY INJUNCTION

Date:	Dec. 3, 2020
Time:	1:30 p.m.
Crtrm.:	8, 4th Floor San Jose District Courthouse 280 S. 1St Street San Jose, California
Judge:	Hon. Lucy H. Koh

I, DR. MARC LIPSITCH, declare as follows:

1. I am the founding Director of the Center for Communicable Disease Dynamics (CCDD) at the Harvard School of Public Health, where I am also a Professor in the Department of Epidemiology and the Department of Immunology and Infectious Diseases. I have a B.A. in Philosophy from Yale University and a DPhil (the Oxford equivalent of a PhD) in Zoology from the University of Oxford, which I attended as a Rhodes Scholar. After receiving my DPhil, I completed a postdoctoral research fellowship in Biology at Emory University working on the population biology of infectious diseases. A copy of my C.V. is attached to this declaration as Exhibit A. I

have been elected as a Fellow of the American Academy of Microbiology and a member of the National Institute of Medicine for the United States.

2. CCDD is a research center committed to advancing our understanding of infectious disease and training the next generation of scientists. It was founded as a Center of Excellence in the Models of Infectious Disease Agent Study funded by the National Institute of General Medical Sciences of the U.S. National Institutes of Health (NIH). CCDD has been at the leading edge of epidemiology, pioneering new approaches and methodologies for investigating both recurring and emerging problems. The goal of our work at CCDD is to understand why and how infectious disease persists and changes and use that knowledge to lessen its burden on people.

3. CCDD is closely monitoring the progress of COVID-19. CCDD faculty—including me—are conducting research on the novel coronavirus SARS-CoV-2 and COVID-19, the disease it causes. CCDD faculty have published over 50 peer-reviewed articles about SARS-CoV-2 and COVID-19. I am the lead or a contributing author on more than 20 of those articles. CCDD faculty regularly host and contribute to online events about COVID-19, appear in national and international media, including print and broadcast news, and participate in scientific conferences, consortia, discussions, debates, and podcasts, as well as advising local, state, and federal officials and leaders of countries around the world.

4. My own work on COVID-19 has included epidemiology, mathematical modeling, and exploration of ethical issues related to vaccine trials and school reopenings. My research has helped identify countries with undetected cases before they were reported; modeled the effects of various social distancing and quarantine strategies; and contributed to some of the earliest estimates of case-fatality rates. My research has also addressed new methodologies on how to study immunity to COVID-19; and I am a co-lead on a large collaborative effort, led by experts at the University of Chicago and involving multiple European universities, to establish best practices for estimating the contagiousness of the virus. My work has also addressed the ethical aspects of COVID-19 vaccine trial design, including the first published proposal for human challenge studies, which received support from the World Health Organization (WHO) and the NIH, and which was implemented in the U.K.

5. I have advised the WHO, the International Monetary Fund, the Prime Minister of Israel, and senior government officials in the U.S., Canada, India, Germany, Austria, and Luxembourg on COVID-19, as well as the U.S. National Governors' Association and numerous state and local health officials. I am a member of the Massachusetts Governor's Medical Advisory Committee and the Massachusetts COVID-19 Vaccine Working Group. I am also an ad hoc expert to the COVID-19 Vaccine Working Group, which is part of the WHO Strategic Advisory Group of Experts. Health departments on several continents use software that I helped develop to update their estimates of trends in COVID-19 cases.

6. Over the course of the COVID-19 pandemic, I have been asked to provide and have provided interviews and analysis to national and international media outlets, including CNN, BBC, the *Guardian* and the *Wall Street Journal*; and I have published articles explaining aspects of the COVID-19 pandemic in national and international media outlets, including the *New York Times* and *Washington Post*. My public science communication efforts also include a Twitter account with an active following. Earlier this year, physicist Jonathan Oppenheim reported that I was the second-most-followed expert by other experts on the COVID-19 pandemic; and I was named by Forbes as one of the "most essential people on Twitter to follow during the COVID-19 outbreak."

7. More generally, my research has focused on biological and mathematical approaches to infectious disease questions—mainly understanding how our immune systems and medical interventions such as antibiotics and vaccines exert natural selection on pathogens, and how the resulting changes in pathogen populations affect human disease. My more recent work has focused on antimicrobial resistance, epidemiological methods, mathematical modeling of infectious disease transmission, pathogen population genomics, immunoepidemiology of *Streptococcus pneumonia*, transmission-dynamic simulations, and ethical questions surrounding vaccine trials for infectious disease.

8. My work has addressed a number of issues relevant to modern pandemic responses. My research provided modern evidence of the moderate contagiousness of the 1918 "Spanish flu." During the first SARS outbreak in 2003, I led a team that provided one of the first estimates of the virus' reproduction number. During the 2009 H1N1 pandemic, my research produced the first

reliable estimate of H1N1 flu severity. During the yellow fever outbreak in Angola and Democratic Republic of Congo in 2016, my modeling work helped support fractional dosing vaccination strategies, which helped extend vaccine availability in a shortage situation. I have written extensively on data-driven decision making in public health.

9. I have worked extensively with governments and intergovernmental bodies like WHO to address public health issues including pandemic response and preparedness. For example, in 2003 and 2004, I served on the Defense Science Board Task Force on the SARS Quarantine for the U.S. Department of Defense. In 2009, I was a member of the H1N1 Working Group of the U.S. President's Council of Advisors on Science and Technology; and in 2009 and 2010, I was a member of the Team B Advisory Body to the CDC on the Novel H1N1 Influenza. From 2017 through today, I have been a member of the Biological Agents Containment Working Group of the Board of Scientific Counselors to the Office of Public Health Preparedness and Response at the CDC.

10. I have also worked extensively on the design and analysis of vaccine trials during public health emergencies. In 2015, I served on a scientific advisory board for a major Ebola vaccine trial, and as I mentioned above, I am currently advising Massachusetts and WHO on COVID-19 vaccine issues.

11. I have published more than 330 peer-reviewed articles and a large number of other publications, including book chapters, non peer-reviewed journal articles, and popular articles in the national press. I have also contributed to a number of reports, including the President's Council of Advisors on Science and Technology (PCAST) H1N1 Working Group's 2010 Report to the President on US Preparations for 2009-H1N1 Influenza; three reports from the Center for Infectious Disease Research and Policy (CIDRAP) regarding the development of a vaccine for the ebola virus; and most recently an April 2020 CIDRAP report on COVID-19.[1] CIDRAP is based out of the University of Minnesota and is a global leader in addressing public health preparedness and emerging infectious disease response.

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[1] Moore, K., et al., *COVID-19: The CIDRAP Viewpoint*, April 30, 2020, available at https://www.cidrap.umn.edu/sites/default/files/public/downloads/cidrap-covid19-viewpoint-part1_0.pdf.

12. I continue to teach and mentor undergraduate and graduate students at Harvard, as well as supervising graduate work for doctoral candidates.

13. The County defendants in this case contacted me about providing an expert opinion regarding the declarations of Dr. Jay Bhattacharya and Dr. Rajiv Bhatia submitted by the plaintiffs in this lawsuit. I agreed to provide a declaration setting forth my professional opinions on the issues raised in those declarations. In reaching those opinions, I have relied on my knowledge, experience, and the kinds of data regularly relied on by experts in my field. If called as a witness, I could and would testify competently to the matters set forth herein. I am working pro bono and not being compensated for my time.

14. I have read the declarations of Dr. Jay Bhattacharya and Dr. Rajiv Bhatia submitted by the plaintiffs in this lawsuit. My opinions regarding those declarations are based on the available science regarding COVID-19 and my training and experience in infectious disease response.

15. Dr. Bhatia argues that public health authorities in California should employ a "targeted strategy" and focus their efforts on vulnerable populations. Dr. Bhattacharya's declaration is less clear about what he proposes for California, but he is on record as embracing a similar approach that is commonly referred to as "herd immunity with focused protection." This approach was laid out in the so-called "Great Barrington Declaration," a document published in October at a ceremony at a libertarian think tank by three scientists, including Dr. Bhattacharya. In this approach, the virus would be allowed to spread among young, healthy people with little attempt to slow it down, while officials try to keep older, more vulnerable Americans from contracting it. This strategy diverges sharply from the views of most infectious-disease epidemiologists and has been rejected by the National Institute of Allergy and Infectious Diseases Director Dr. Anthony Fauci,[2]

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[2] Mandavilli A., et al., *A Viral Theory Cited by Health Officials Draws Fire From Scientists*, New York Times, Oct. 19, 2020, available at https://www.nytimes.com/2020/10/19/health/coronavirus-great-barrington.html (visited Nov. 16, 2020).

WHO Director-General Tedros Adhanom Ghebreyesus,[3] and more than 6,900 scientists, researchers, and healthcare professionals who have signed a formal response called the John Snow Memorandum.[4] Without a vaccine, this strategy also risks the deaths of a million or more Americans.

COVID-19 Is Not Harmless For Younger Populations

16. The assumption underlying the herd immunity approach—that COVID-19 is harmless to most people and risky only for defined groups—is false.

17. The impact of a pandemic on health depends not only on the infection-fatality rate, but also on other measures of severity such as the risk of hospitalization or ICU admission among those infected. Crucially, it also depends on the number of people who become infected, because a small risk of death, ICU or hospitalization multiplied by a large number of people infected can result in large numbers of deaths and high burdens on health care resources. Indeed, the extraordinarily high peak demand for intensive care in Wuhan, China[5] and in Northern Italy[6] were two of the earliest warnings that uncontrolled SARS-CoV-2 spread could result in horrific burdens on the health care system. The intense stress on even very high-quality health systems is being felt across Europe and in many parts of the U.S. as of November 2020, with overloaded intensive care units in multiple locations due to COVID-19 surges. The U.S. has hit its highest number to date of hospitalizations, with almost 70,000 COVID-19 patients in hospital as of November 14, 2020.[7] In this context, academic debates about the risk of severe outcomes per individual, while relevant, are

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[3] *WHO chief says herd immunity approach to pandemic 'unethical'*, The Guardian, Oct. 12, 2020, available at https://www.theguardian.com/world/2020/oct/12/who-chief-says-herd-immunity-approach-to-pandemic-unethical (visited Nov. 16, 2020).

[4] Available at https://www.johnsnowmemo.com/.

[5] Li, R., et al., *Beds for Patients With COVID-19 Based on Comparisons With Wuhan and Guangzhou, China*, May 6, 2020, JAMA Netw. Open. 2020;3(5): e208297, available at https://jamanetwork.com/journals/jamanetworkopen/fullarticle/2765575.

[6] Grasselli, G., et al., *Critical Care Utilization for the COVID-19 Outbreak in Lombardy, Italy: Early Experience and Forecast During an Emergency Response*, March 13, 2020, JAMA. 2020;323(16):1545-1546, available at https://jamanetwork.com/journals/jama/fullarticle/2763188.

[7] The COVID Tracking Project, The Atlantic, available at https://covidtracking.com/data/charts/us-currently-hospitalized.

better understood in the context of the total burden created: individual risk times number of individuals infected.

18. COVID-19 is unquestionably worse for someone who is male, older, sicker, or lacks access to health care. Younger, healthier demographics do better than older demographics.[8] These facts do not mean, however, that COVID-19 is harmless for younger cohorts. To date, more than 45,000 Americans under 65 have died from the disease[9]—more than four times as many as typically die in that age group from seasonal flu in an entire year[10]—and we have only had about ten months of intense COVID-19 activity, so that number will continue to grow.

19. Dr. Bhattacharya's declaration, by focusing only on those at lowest risk, significantly underestimates the SARS-CoV-2 infection-fatality rate. The best estimate to date of the overall infection-fatality rate for SARS-CoV-2 infection is by Dr. Gideon Meyerowitz-Katz and colleagues, and is approximately 0.7%,[11] although this group's other work, approvingly cited by Dr. Bhattacharya's declaration (Para. 34), notes correctly that the risk is age specific. Importantly, while the infection-fatality rate increases sharply with age, there is no cutoff at age 70; rather, the risk of dying if infected with this virus "increases progressively to 0.4% at age 55, 1.4% at age 65, 4.6% at age 75, and 15% at age 85."[12] It is misleading to call the infection-fatality rate below age 70 "vanishingly small" given these estimates and given that over 83% of the U.S. population or nearly

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[8] CDC, *COVID-19 Hospitalization and Death by Age*, https://www.cdc.gov/coronavirus/2019-ncov/covid-data/investigations-discovery/hospitalization-death-by-age.html.

[9] CDC, *Weekly Updates by Select Demographic and Geographic Characteristics*, available at https://www.cdc.gov/nchs/nvss/vsrr/covid_weekly/index.htm (accessed Nov. 10, 2020)

[10] Quandelacy, T., et al., *Age- and Sex-related Risk Factors for Influenza-associated Mortality in the United States Between 1997–2007*, Am. J. Epidemiol. 2014 Jan. 15; 179(2): 156–167, doi: 10.1093/aje/kwt235, available at https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3873104/.

[11] Meyerowitz-Katz, G., *A systematic review and meta-analysis of published research data on COVID-19 infection fatality rates*, International Journal of Infectious Diseases, Vol. 101, P138-148, December 01, 2020, available at https://www.ijidonline.com/article/S1201-9712(20)32180-9/fulltext.

[12] Levin, A., *Assessing the Age Specificity of Infection Fatality Rates for COVID-19: Systematic Review, Meta-Analysis, and Public Policy Implications* medRxiv 2020.07.23.20160895; doi: https://doi.org/10.1101/2020.07.23.2016089, available at https://www.medrxiv.org/content/10.1101/2020.07.23.20160895v7.

274 million people are under 65 (2019 census estimate). Dr. Bhattacharya relies on a meta-analysis by Dr. John P.A. Ionnidis that estimates a lower infection-fatality rate (Para. 34), but Dr. Meyerowitz-Katz's meta-analysis is distinguished by more rigorous criteria for including studies than that by Dr. Ioannidis. While the former excludes studies expected to be heavily biased by a nonrepresentative sample, the latter does no such quality checks. On this basis, I judge the conclusions of Dr. Meyerowitz-Katz's meta-analysis more reliable.

20. If COVID-19 were judged on the criteria established for evaluating the severity of an influenza pandemic, it would land at the top—the most severe end—of the scale. The CDC in 2017 defined influenza pandemics along a scale of transmissibility (from 1-5) and clinical severity (from 1-7). Based on the reproduction number and approximately half of infections being symptomatic, COVID-19 would exceed the specifications for the highest transmissibility category (R0 > 1.8) (for COVID-19 R0 is thought to be at least 2[13] and up to 6 in some places[14]). It would also likely exceed the specification for the highest clinical severity category, which is a case-fatality ratio of 1% or more.[15] (Given the underascertainment of infections relative to cases, this criterion would be satisfied by an observed infection-fatality ratio of well under 1%, consistent with even the downwardly biased estimates of Dr. Ioannidis.) In short, the COVID-19 pandemic is at the upper end, and arguably at the very top, of the severity scale for influenza pandemics. It was for those pandemics that community mitigation strategies based on nonpharmaceutical interventions have been planned at the federal[16] and state[17] levels. A decade or more of pandemic planning envisioned

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[13] CDC, *COVID-19 Pandemic Planning Scenarios*, available at https://www.cdc.gov/coronavirus/2019-ncov/hcp/planning-scenarios.html.

[14] Sanche, S., et al., *High Contagiousness and Rapid Spread of Severe Acute Respiratory Syndrome Coronavirus 2*, Emerg Infect Dis. 2020;26(7):1470-1477, available at https://wwwnc.cdc.gov/eid/article/26/7/20-0282_article.

[15] Qualls, N., et al., *Community Mitigation Guidelines to Prevent Pandemic Influenza — United States, 2017*, Recommendations and Reports / April 21, 2017 / 66(1);1–34 (Table 6), available at https://www.cdc.gov/mmwr/volumes/66/rr/rr6601a1.htm.

[16] Qualls (2017), *supra*.

[17] California Governor's Office of Emergency Services, *Statewide Concept of Operations for Pandemic Influenza*, available at https://www.caloes.ca.gov/PlanningPreparednessSite/Documents/StatewideConOpsforPandemicInfuenza%202009.pdf.

exactly the kinds of measures being challenged by the plaintiffs in response to a pandemic of a similar viral infection, even with lower severity than COVID-19.

21. In every pandemic, decisions about control must be made before comprehensive evidence is available on the characteristics of the infection in affected populations.[18] Evidence-gathering and mitigation efforts must proceed in parallel.[19] Waiting for definitive evidence on severity, transmissibility, and other characteristics of the pathogen and the population before adopting control measures is not a viable option, because exponential or near-exponential spread of infection in new pandemics in highly susceptible populations can rapidly transform a small public threat into a large one, and the impact of control measures is often delayed. Thus it is rational to take action to avert possible negative outcomes before there is certainty about the likelihood and timing of these outcomes. There is room for legitimate disagreement about the strength of evidence and the justification for particular control measures. Yet in the face of a growing pandemic with clear ability to cause severe illnesses, to kill, and to cause health care disruption, it would be irresponsible public health policy to await definitive evidence before taking control measures that are expected to blunt the impact of the pandemic. This was the very clear situation in March 2020 in the United States, as we watched the impact of the pandemic in other countries that had been struck earlier.[20] Indeed, there is a compelling argument in my view that many state authorities were too slow, not too fast, to impose restrictions to slow the spread of SARS-CoV-2 during the early months

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[18] Lipsitch, M., et al., *Managing and Reducing Uncertainty in an Emerging Influenza Pandemic*, N. Engl. J. Med. 2009; 361:112-115, doi: 10.1056/NEJMp0904380, available at https://www.nejm.org/doi/full/10.1056/nejmp0904380.

[19] Lipsitch, M., et al., for the 2009 H1N1 Surveillance Group. *Improving the Evidence Base for Decision Making During a Pandemic: The Example of 2009 Influenza A/H1N1*, 2011, Biosecurity and Bioterrorism: Biodefense Strategy, Practice, and ScienceVol. 9, No. 2, available at https://www.liebertpub.com/doi/full/10.1089/bsp.2011.0007.

[20] Lipsitch, M., *We know enough now to act decisively against Covid-19. Social distancing is a good place to start*, March 18, 2020, STAT, available at https://www.statnews.com/2020/03/18/we-know-enough-now-to-act-decisively-against-covid-19/.

of 2020. On this view, California is a model, while other states deserve criticism for slower reactions.[21]

22. While Drs. Bhattacharya and Bhatia focus on hospitalization rates as a theoretically preferrable criterion for public action, to my knowledge, no comprehensive analyses of age-specific infection-hospitalization rates (the ratio of hospitalizations to infections within each age group) exist that could be comparable to the detailed age-specific infection-fatality rate analyses described in Paragraph 19 above. Here again, total burden, rather than per-individual risk, is of more direct public health concern.

23. The size of the vulnerable population in the United States is large. Not only are there significant numbers of American over 65—according to the U.S. Census Bureau, about 16.5% of the population was 65 or over in 2019[22]—but the CDC estimates that nearly 50 percent of Americans live with underlying conditions that predispose them to serious outcomes from COVID-19.

24. Letting the virus spread unchecked in younger populations—which include Americans with underlying conditions—will result in more serious illness and deaths, in addition to increasing the risk of transmission to older populations.

There Is No Proven Means To Protect The Vulnerable Without Restraining Transmission In The General Population

25. No one has yet devised an effective approach to protecting vulnerable populations when there is widespread community transmission. Vulnerable individuals—including older Americans and those with pre-existing conditions—live and work with, and receive care from, members of the larger community. Many of the vulnerable live in a multigenerational home, are cared for by others in nursing and long-term care facilities, and/or are essential workers with comorbidities; and these individuals cannot be completely isolated from the larger community.

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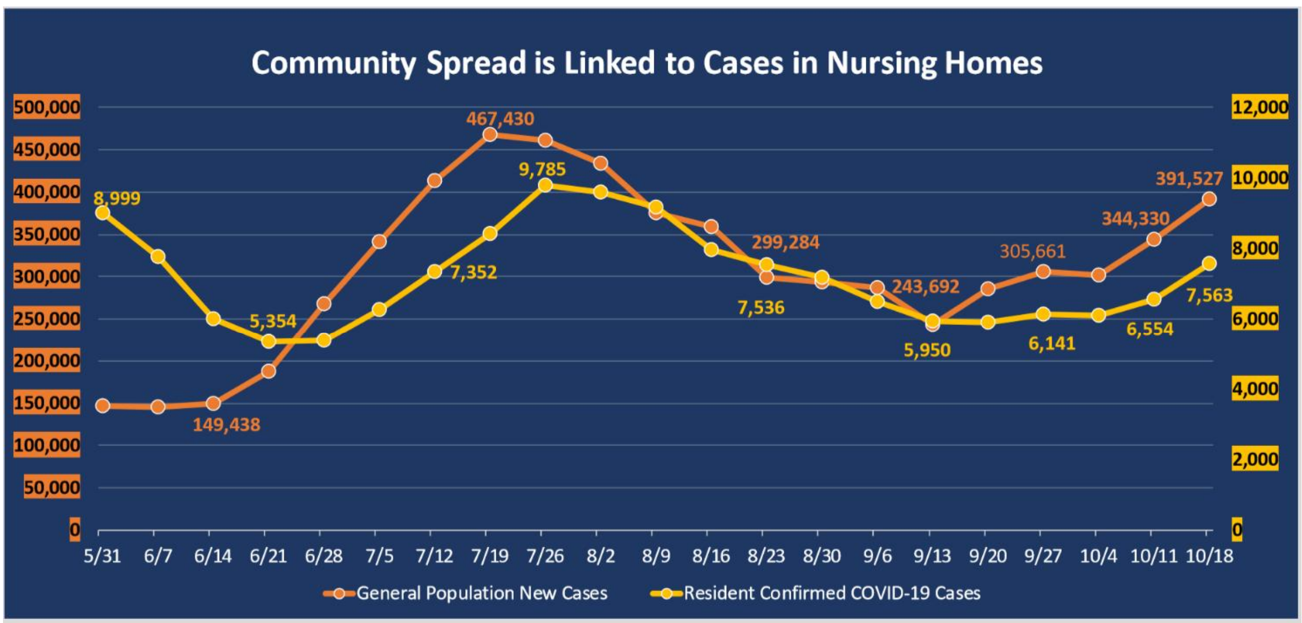
[21] Sexton, J., et al., *Two Coasts. One Virus. How New York Suffered Nearly 10 Times the Number of Deaths as California*, May 16, 2020, ProPublica, available at https://www.propublica.org/article/two-coasts-one-virus-how-new-york-suffered-nearly-10-times-the-number-of-deaths-as-california.

[22] U.S. Census Bureau, https://www.census.gov/data/tables/time-series/demo/popest/2010s-national-detail.html (visited Nov. 9, 2020).

Nonetheless, scientists, clinicians, and policy makers have been working hard to protect these groups, with little or modest success, for most of the year, while also attempting to minimize the threat that community transmission poses to them and to all of us. This "belt-and-suspenders" approach is the current consensus approach among infectious-disease epidemiologists.

26. Reducing or eliminating community transmission is critical to protecting vulnerable populations, including those in long-term care facilities. The American Health Care Association (AHCA) and the National Center for Assisted Living (NCAL) recently released a report stating that COVID-19 cases in U.S. nursing homes have risen with the community spread of COVID-19 since mid-September.[23] That report explicitly links cases in nursing homes to community spread of the virus:



Sources: Centers for Medicare & Medicaid Services (CMS), May 31 – October 18 on Nursing Home COVID Cases and Johns Hopkins on COVID Cases in General Population

27. Without reducing community transmission, strategies focused on protecting vulnerable populations are unlikely to succeed. Sweden, the best-known exemplar of the "age-targeted" approach, was unable to protect people in nursing homes. Ostensibly the goal in Sweden

[23] AHCA and NCAL, *Report: COVID-19 Cases In U.S. Nursing Homes*, updated Nov. 2, 2020, available at https://www.ahcancal.org/News-and-Communications/Fact-Sheets/FactSheets/Report-Nursing-Homes-Cases-Nov2-2020.pdf (visited Nov. 10, 2020).

was to protect the elderly and other high-risk groups while slowing viral spread enough to avoid hospitals being overwhelmed; although it has been widely reported that the goal was in fact to develop herd immunity.[24] The strategy failed to meet its goal of protecting the elderly: the virus ran rampant in nursing homes, and Stockholm's nursing homes lost 7% of their residents. Sweden's polices are now falling back in line with its European neighbors.[25] Vulnerable individuals living in multigenerational households present a distinct challenge to "focused protection" in the absence of community control, particularly given that transmission of SARS-CoV-2 in households is common,[26] and households are the single greatest known source of transmission in many locales.[27]

28. The elderly, and nursing home residents in particular, are only a fraction of the truly vulnerable population. As noted earlier, over 45,000 deaths have occurred in those under 65 in the US, about 20% of the total death toll. Some comorbidities that predispose to severe outcomes, such as hypertension, diabetes, and certain cancers, may be invisible to those who are charged with protecting the vulnerable. Nonwhite race/ethnicity,[28] low socioeconomic status,[29] and other variables are also associated with high vulnerability to severe outcomes, making the logistics of "shielding the vulnerable" even more challenging.

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[24] Vogel, G., *'It's been so, so surreal.' Critics of Sweden's lax pandemic policies face fierce backlash*, Science, Oct. 6, 2020, available at https://www.sciencemag.org/news/2020/10/it-s-been-so-so-surreal-critics-sweden-s-lax-pandemic-policies-face-fierce-backlash; Bjorklund, K., *The Swedish COVID-19 Response Is a Disaster. It Shouldn't Be a Model for the Rest of the World*, Time, Oct. 14, 2020.

[25] Vogel 2020, *supra*.

[26] Grijalva, C., *Transmission of SARS-COV-2 Infections in Households — Tennessee and Wisconsin, April–September 2020*, Nov. 6, 2020, MMWR, 69(44);1631–1634.

[27] Bebinger, M., *Mass. Takes Close Look At Cluster Origins To Stop Coronavirus Spread*, WBUR, Oct. 20, 2020, https://www.wbur.org/commonhealth/2020/10/30/massachusetts-covid-cluster-data; *Infektionsumfeld von COVID-19-Ausbrüchen in Deutschland*, Epidemiologisches Bulletin, 38 2020, Sept. 17, 2020, https://www.rki.de/DE/Content/Infekt/EpidBull/Archiv/2020/Ausgaben/38_20.pdf;jsessionid=B8D1D66F6ECEC4B21EFDF40B78C8FB74.internet071?__blob=publicationFile.

[28] APM Research Lab, *The color of coronavirus: COVID-19 deaths by race and ethnicity in the U.S.*, Oct. 15, 2020, available at https://www.apmresearchlab.org/covid/deaths-by-race.

[29] Finch, W., et al., *Poverty and Covid-19: Rates of Incidence and Deaths in the United States During the First 10 Weeks of the Pandemic*, Front. Sociol., June 15, 2020, available at https://www.frontiersin.org/articles/10.3389/fsoc.2020.00047/full.

29. Until we have a proven means to protect those most at risk and put those safeguards in place, it would be reckless to remove the protections against unmitigated community transmission and plunge ahead in pursuit of herd immunity via massive infection rates. Reducing community transmission remains one of the best ways to protect vulnerable populations.

Any Herd Immunity May Be Short-Lived And Partial

30. In the modern era, herd immunity is best achieved by vaccination—that is, when enough people acquire immunity to an infection through a shot in the arm to protect the whole community. That is our public health goal every flu season; and it is the reason we vaccinate infants against many childhood diseases.

31. The "herd immunity with focused protection" approach that plaintiffs' experts champion is to allow the spread of COVID-19 in younger populations in order to create immunity against later infection—the theory being that previously infected individuals will carry COVID-19 antibodies that will prevent reinfection. If carrying COVID-19 antibodies confers immunity, then half[30] or more[31] of the population must be seropositive—*i.e.*, COVID-19 antibody carriers—before we can control the virus without special measures, such as face coverings, social distancing, surveillance, and contact tracing.

32. It is possible that letting the virus spread uncontrolled in the younger population will build up some level of herd immunity and reduce further spread—for some period of time and with the significant cost of serious illness and death discussed above. However, the process of building up heard immunity could take a significant amount of time. The length of the pandemic could be 18 to 24 months or more, as herd immunity gradually develops in the human population.[32] The serosurveillance data available to date suggests that a relatively small fraction of the population has been infected and infection rates likely vary substantially by geographic area. In late September

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[30] Britton, T., et al., *A mathematical model reveals the influence of population heterogeneity on herd immunity to SARS-CoV-2*, Science 14 Aug 2020; 846-849.

[31] Sanche S, et al.. *High Contagiousness and Rapid Spread of Severe Acute Respiratory Syndrome Coronavirus 2*. Emerg Infect Dis. 2020;26(7):1470-1477. https://dx.doi.org/10.3201/eid2607.200282.

[32] Moore 2020, *supra*.

2020, CDC Director Robert Redfield told Congress that over 90 percent of the U.S. population remains susceptible to this coronavirus,[33] citing published data.[34] Given the transmissibility of SARS-CoV-2, half to two-thirds of the population may need to be immune to reach a critical threshold of herd immunity to halt the pandemic.[35]

33. Unfortunately, however, coronavirus immunity is notoriously short-lived and partial. Other coronaviruses are called "seasonal" because, like the flu, they circulate every year. Based on seasonal coronaviruses, we can anticipate that even if immunity declines after exposure, there may still be some protection against disease severity and reduced contagiousness, but this remains to be assessed for SARS-CoV-2.[36] As a result, widespread infection in the general population is unlikely to eliminate the disease, but will more likely result in a persistent problem until an effective vaccine is available and widely adopted.

RT-PCR Testing Provides Important Data For Clinical Use, Public Health, And Policy Decision-Making

34. There is no dispute in the epidemiological community that using RT-PCR[37] (or PCR) test data to confirm COVID-19 cases and positivity rates is an appropriate and helpful tool in managing the disease. Rapid and accurate diagnosis of the disease among suspected cases is vital to limit its spread. PCR-based assays performed on respiratory specimens are currently the gold standard for COVID-19 diagnostics.[38]

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[33] C-SPAN, *CDC Director Redfield Says 90% U.S. Population Susceptible to Coronavirus Infection, Sept. 23, 2020*, https://www.c-span.org/video/?c4909117/cdc-director-redfield-90-us-population-susceptible-coronavirus-infection.

[34] Anand, S., et al., *Prevalence of SARS-CoV-2 antibodies in a large nationwide sample of patients on dialysis in the USA: a cross-sectional study*, The Lancet, Vol. 396, Issue 10259, pp. 1335-1344, October 24, 2020, DOI: https://doi.org/10.1016/S0140-6736(20)32009-2.

[35] Britton 2020, *supra*; Sanche 2020; *supra*.

[36] Moore 2020, *supra*.

[37] Reverse transcription polymerase chain reaction, or RT-PCR, is a laboratory technique combining reverse transcription (RT) of RNA into DNA and amplification of specific DNA targets using polymerase chain reaction (PCR). This laboratory technique allows the identification of viral RNA in research and clinical settings.

[38] Younes, N., et al., *Challenges in Laboratory Diagnosis of the Novel Coronavirus SARS-CoV-2, Viruses*. 2020 May 26;12(6):582. DOI: 10.3390/v12060582.

35. There is also no dispute that PCR data must be interpreted appropriately. For example, as Dr. Bhattacharya points out, individuals that test positive may not be currently infectious; and limits on testing availability may mean that those tested are not wholly representative of the target population, although this concern has been mitigated since the beginning of the pandemic as testing has greatly expanded in Santa Clara County[39] and across California.[40] These and other potential limitations of PCR data are well known to epidemiologists and public health professionals. I am not aware of any evidence that the public health officials working for the State of California or the County of Santa Clara ignored these basic considerations when formulating and issuing their respective public health orders.

36. The PCR test amplifies genetic matter from the SARS-CoV-2 in cycles of polymerase chain reactions. Typically, the fewer amplification cycles required, the greater the amount of virus, or viral load, in the sample. The greater the viral load, the more likely the patient is to be infectious. This number of amplification cycles needed to find the virus, called the cycle threshold or Ct value, is often not included in the test results sent to doctors and coronavirus patients. While data regarding Ct values could provide helpful information for clinical diagnostics, public health, and policy decision-making, the absence of that data in test results does not render the use of PCR data scientifically unjustified, as Dr. Bhattacharya asserts.

37. In fact, Dr. Bhattacharya's rejection of PCR data as a basis for public health and policy decision-making runs counter to best practices in infectious disease response. It is a characteristic of infectious disease outbreaks that information available at the early stages is incomplete, uncertain, and often biased in the sense that observations are initially made on unrepresentative samples of the population that are easily observed (for example, those reporting to

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[39] Santa Clara County Department of Public Health, *COVID-19 Testing Dashboards*, available at https://www.sccgov.org/sites/covid19/Pages/dashboard-testing.aspx (vitisted Nov. 15, 2020).

[40] Johns Hopkins Coronavirus Resource Center, *Daily State-by-State Testing Trends*, available at https://coronavirus.jhu.edu/testing/individual-states/california (visited Nov. 15, 2020).

hospitals), and only later on more representative populations.[41] Knowledgeable public health professionals have a wealth of heuristics for filtering and integrating data to form early assessments of key quantities that are inputs to decisions—for example, current incidence and prevalence; forecasts of incidence and prevalence; geographic and demographic extent; and severity measures.

38. There is no dispute that PCR testing—like all other available measures—is an incomplete measure of disease prevalence or incidence or infectivity. Like other approaches for testing, PCR testing can be applied in ways that provide biased estimates of these quantities. Nonetheless, PCR surveillance has provided helpful data for initial and ongoing estimates of disease severity and the size and geographic extent of the COVID-19 pandemic—two critical parameters to assess in making decisions about the appropriate scale of and countermeasures deployed in the public health response to the pandemic.[42]

39. It is appropriate for California and the County of Santa Clara to use PCR test data to help guide their public health response. California's Blueprint for a Safer Economy uses case rates (adjusted for the number of tests conducted) and positivity rates to assess COVID-19 prevalence and assign counties to an appropriate tier that lays out the measures that need to be taken for the county.[43] The European Union tracks the same "common criteria" across its member states: the testing rate, the test positivity rate, and the number of new cases.[44]

40. PCR testing is of course not the only surveillance method that we should use to

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[41] Lipsitch M, et al. (2009) *Managing and reducing uncertainty in an emerging influenza pandemic* [Internet], New Engl. J. Med. 112–115, available at https://doi.org/10.1056/nejmp0904380Lipsitch; Lipsitch M., et al., 2009 H1n1 Surveillance Group (2011), *Improving the evidence base for decision making during a pandemic: the example of 2009 influenza A/H1N1*, Biosecur Bioterror 9(2):89–115.

[42] Lipsitch, M., et al., *Enhancing Situational Awareness to Prevent Infectious Disease Outbreaks from Becoming Catastrophic* (2019), Current Topics in Microbiology and Immunology, available at https://doi.org/10.1007/82_2019_172.

[43] California Department of Public Health, *Blueprint for a Safer Economy*, available at https://www.cdph.ca.gov/Programs/CID/DCDC/Pages/COVID-19/COVID19CountyMonitoringOverview.aspx (visited Nov. 15, 2020).

[44] European Centre for Disease Prevention and Control, *Maps in support of the Council Recommendation on a coordinated approach to the restriction of free movement in response to the COVID-19 pandemic in the EU/EEA and the UK*, available at https://www.ecdc.europa.eu/en/covid-19/situation-updates/weekly-maps-coordinated-restriction-free-movement (visited Nov. 15, 2020).

control this pandemic. New rapid antigen- and CRISPR-based tests will help us make better decisions if available and used properly. These tests are cheap, can be mass produced, and could be performed at home. They can capture most infections while people are still infections whereas PCR tests continue to identify people after the infectious period has passed. Rapid antigen tests have recently become available, and CRISPR-based tests appear to be on the horizon. Surveillance testing regimes including these tests should complement, not replace, the current clinical PCR diagnostic testing.[45]

41. Widespread tests to determine whether people are "seropositive"—*i.e.*, carrying antibodies indicating that they have been infected with the novel coronavirus—are also essential to understanding where we are in the pandemic. These tests, called serologic or seroprevalence surveys, can provide important information about the virus and our immunity to it.[46] Serologic surveys represent snapshots of the population rather than real-time measures of incidence; additional surveillance, including viral testing by PCR or other means, is needed to quantify the incidence of mild and severe infection in nearly real time.[47] Again, seroprevalence studies should complement, not replace, the clinical PCR diagnostic testing.

42. The quality of the seroprevalence studies conducted to date has varied widely, as have their results. The widely varying results of early seroprevalence studies emphasized the very local nature of the pandemic. For example, in a study that received extensive criticism for its sampling methods, statistics, and biased interpretation of the data obtained,[48] Dr. Bhattacharya and his co-authors found that 1.5 percent of Santa Clara County's population sampled tested positive for

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[45] Mina, M., et al., *Rethinking Covid-19 Test Sensitivity—A Strategy for Containment*, The New England Journal of Medicine, Sept. 30, 2020, DOI: 10.1056/NEJMp2025631.

[46] Lipsitch, M., *'Serology' is the new coronavirus buzzword. Here's why it matters*, The Washington Post, May 4, 3030, available at https://www.washingtonpost.com/opinions/2020/05/04/serology-is-new-coronavirus-buzzword-heres-why-it-matters/.

[47] Lipsich, M., et al., *Managing and Reducing Uncertainty in an Emerging Influenza Pandemic*, N. Engl. J. Med. 361;2, July 9, 2009.

[48] Vogel, G., *Antibody surveys suggesting vast undercount of coronavirus infections may be unreliable*. Science, Apr. 21, 2020, https://www.sciencemag.org/news/2020/04/antibody-surveys-suggesting-vast-undercount-coronavirus-infections-may-be-unreliable.

antibodies in the spring of 2020.[49] Other locales—in studies reflecting different kinds of imperfections in sampling—have shown much more widespread evidence of past infection, including 21 percent of those tested in New York City[50] and nearly a third in Chelsea, Massachusetts in April 2020.[51]

43. More recent national studies have continued to show regional variation in seroprevalence. The CDC conducted a commercial laboratory seroprevalence survey using blood samples collected from 10 U.S. sites from March to July 2020. The surveys estimated seroprevalence of 0.7% (San Francisco Bay Area) to as high as 23.2% (New York City Metro Area).[52] A recently published seroprevalence study of dialysis patients estimated that during the first wave of the COVID-19 pandemic, fewer than 10% of the U.S. adult population formed antibodies against SARS-CoV-2, with large regional variances.[53] In California, the study estimated seroprevalence of 3.8%.[54] The low seroprevalence estimates in California and the Bay Area suggest both that those regions have been successful in limiting community transmission and that any measure of herd immunity is a distant prospect.

44. Drs. Bhattacharya and Bhatia focus on hospitalization rates as a theoretically preferrable criterion for public action compared to PCR test data. Like any measure of disease severity, prevalence, and burden, hospitalization rates have their utility and their limitations, although they certainly complement other surveillance methods. However, because hospitalization

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[49] Bendavid, E., et al., *COVID-19 Antibody Seroprevalence in Santa Clara County, California*, medRXiv, doi: https://doi.org/10.1101/2020.04.14.20062463.

[50] Goodman, J., et al., *1 in 5 New Yorkers May Have Had Covid-19, Antibody Tests Suggest*, https://www.nytimes.com/2020/04/23/nyregion/coronavirus-antibodies-test-ny.html.

[51] Saltzman, J., *Nearly a third of 200 blood samples taken in Chelsea show exposure*, Boston Globe, Apr. 17, 2020, https://www.bostonglobe.com/2020/04/17/business/nearly-third-200-blood-samples-taken-chelsea-show-exposure-coronavirus/.

[52] CDC, *Commercial Laboratory Seroprevalence Surveys*, https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/commercial-lab-surveys.html#surveymap

[53] Anand 2020, *supra*.

[54] *Id*.

rates are lagging indicators—hospitalization follows the onset of COVID-19 by about 9-12 days[55]—they are less helpful than PCR test data, and much less helpful than rapid-test data, in heading off increases in community transmission. Moreover, we have seen in the COVID-19 epidemic that hospitalization rates can be temporarily low compared to new cases, especially when the new cases are primarily concentrated in the younger age groups. However, this situation is very often temporary, as cases spread from the younger to the older age groups and to more vulnerable people, leading to the intense stresses on the health care system that are evident in mid-November 2020 in many parts of the country. Additionally, in the U.S., where there are structural barriers to health care utilization, emergency room visits may undercount cases of serious illness.

Policy Implications For Schools

45. Both Drs. Bhattacharya and Bhatia lament the closure of schools in response to the COVID-19 pandemic, although it is my understanding that none of the individual plaintiffs in this lawsuit is complaining about school access. It is also my understanding that many schools in Santa Clara County are already open, others are planning to open, and some are providing in-classroom instruction for populations of students for whom distance learning is particularly difficult.

46. In my judgment, safely reopening schools full-time for all elementary school children should be a top national priority. However, the safest way to open schools fully is not to do as Drs. Bhattacharya and Bhatia suggest and throw open the floodgates to widespread infection among younger populations; but instead to reduce or eliminate community transmission while ramping up testing and surveillance. Additional mitigation measures would also be necessary: adults would need to maintain social distance from each other and engage in other measures to reduce adult-to-adult transmission, including wearing personal protective equipment (PPE) in some circumstances,

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[55] CDC, *Interim Clinical Guidance for Management of Patients with Confirmed Coronavirus Disease (COVID-19)*, available at https://www.cdc.gov/coronavirus/2019-ncov/hcp/clinical-guidance-management-patients.html (visited No. 13, 2020).

closing school buildings to all non-staff adults, and holding digital faculty meetings. These precautions are especially important insofar as 17.5% of teachers are 55 or older.[56]

47. Any region experiencing moderate, high, or increasing levels of community transmission should do everything possible to lower transmission. The path to low transmission in other countries has included adherence to stringent community control measures—including closure of nonessential indoor work and recreational spaces.[57] Such measures along with universal mask wearing (with specific exceptions[58]) are essential to bring case numbers down to safe levels for elementary schools to reopen.[59]

48. Districts and states that refuse to implement these essential public health measures, on the other hand, face a profound social and moral dilemma: namely, how to weigh the known risks to children, families, and society of closing school buildings or operating at reduced capacity against the unknown risks (especially to school personnel and to educators' and children's household members) of opening schools when the virus is still circulating at moderate or high levels.[60]

49. Ironically the consensus public health measures that plaintiffs dispute—including limits on nonessential indoor work and recreation spaces—are exactly the measures that will lower

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[56] Taie S, Goldring R. *Characteristics of public and private elementary and secondary school teachers in the United States: results from the 2017–18 National Teacher and Principal Survey first look* (NCES 2020-142). Washington, DC: National Center for Education Statistics, April 2020, available at https://nces.ed.gov/pubsearch/pubsinfo.asp?pubid=2020142.

[57] Couzin-Frankel J, Vogel G, Weiland M., *School openings across globe suggest ways to keep coronavirus at bay, despite outbreaks*, American Association for the Advancement of Science. July 7, 2020, available at https://www.sciencemag.org/news/2020/07/school-openings-across-globe-suggest-ways-keep-coronavirus-bay-despite-outbreaks.

[58] CDC, *Coronavirus Disease 2019 (COVID-19), Frequently Asked Questions*, available at https://www.cdc.gov/coronavirus/2019-ncov/faq.html?CDC_AA_refVal=https%3A%2F%2Fwww.cdc.gov%2Fcoronavirus%2F2019-ncov%2Fneed-extra-precautions%2Fpeople-with-seasonal-allergies-faqs.html#People-with-Seasonal-Allergies.

[59] Levinson, M., *Reopening Primary Schools during the Pandemic* (2020) N. Engl. J. Med. 2020; 383:981-985, DOI: 10.1056/NEJMms2024920.

[60] Stanton Z. *'That's crazy': reopening schools is possible, but we're doing it wrong*. Politico. July 9, 2020, available at https://www.politico.com/news/magazine/2020/07/09/reopening-schools-coronavirus-pandemic-expert-analysis-politics-2020-355466; Faden R., et al., *The ethics of K-12 school reopening: identifying and addressing the values at stake*, Baltimore: Johns Hopkins University, June 2020, available at https://equityschoolplus.jhu.edu/ethics-of-reopening/.

levels of community transmission and allow schools to open without necessitating a trade-off between risks to educators and harms to students.

I declare under penalty of perjury under the laws of the United States of America that the foregoing is true and correct. Executed at Jamaica Plain, Massachusetts on November 17, 2020.

/S/ *Marc Lipsitch*
MARC LIPSITCH

2309537

EXHIBIT A

CURRICULUM VITAE

DATE:	October 9, 2020
NAME:	Marc Lipsitch
ADDRESS:	Department of Epidemiology Harvard T.H. Chan School of Public Health 677 Huntington Avenue Boston, MA 02115
DATE & PLACE OF BIRTH:	November 15, 1969, New Haven, CT, USA

EDUCATION:

Date	*Discipline*	*Degree*	*Institution*
1991	Philosophy	B.A. *summa cum laude*	Yale University
1995	Zoology	D.Phil.	University of Oxford

POSTDOCTORAL TRAINING:

1995-1999	Biology	Postdoc with Dr. Bruce Levin	Emory University

ACADEMIC APPOINTMENTS:

1997-1999	Visiting Scientist, Respiratory Diseases Immunology Section, Centers for Disease Control and Prevention
1999-2004	Assistant Professor, Department of Epidemiology, Harvard School of Public Health
2004-2006	Associate Professor, Department of Epidemiology and Department of Immunology and Infectious Diseases, Harvard School of Public Health
2006-present	Professor, Department of Epidemiology and Department of Immunology and Infectious Diseases, Harvard School of Public Health
2009-present	Director, Center for Communicable Disease Dynamics, Harvard School of Public Health
2009-present	Associate Member, Broad Institute, Cambridge, MA
2012-2018	External Faculty Member, Santa Fe Institute, Santa Fe, NM

HONORS AND DISTINCTIONS:

1991	Phi Beta Kappa, Yale College
1992-1995	Rhodes Scholar, University of Oxford, England
2002	Ellison Medical Foundation New Scholar in Global Infectious Disease
2002	PhRMA Foundation Research Starter Award in Health Outcomes
2002	ICAAC Young Investigator Award, American Academy of Microbiology
2006	Mentoring Award, Harvard School of Public Health
2009	Thompson Science Hall of Fame, Westminster Schools, Atlanta, GA
2011	Kenneth Rothman Award, Best Paper in *Epidemiology* in 2010
2012	Junior Faculty Mentoring Award, Harvard School of Public Health
2013	Reviewer of the Year in *Epidemiology* in 2012
2014	Member, winning team (PI Shaman), <u>CDC Predict the Influenza Season Challenge</u>
2015	Elected Fellow, American Academy of Microbiology
2016	Robert Austrian Lecturer, International Symposium on Pneumococci and Pneumococcal Diseases
2018	2017 Article of the Year, American Journal of Epidemiology
2019	23rd Annual Robert M. Fekety, Jr., MD Lecturer, University of Michigan
2020	Elected Member, National Academy of Medicine

PROFESSIONAL SERVICE:

1999	Temporary Advisor, WHO. Priorities for Pneumococcal and Hib Vaccine Development and Introduction. Geneva, Switzerland
2000, 2002	National Institutes of Health, National Center for Research Resources, Special Emphasis Panel, Centers of Biomedical Research Excellence
2001-2003	Consultant and invited speaker for three public meetings, FDA Center for Veterinary Medicine. Topic: regulation of antimicrobial drugs in veterinary medicine
2002	Member, WHO Pneumococcal Vaccine Trials Nasopharyngeal Carriage Study Group
2003	Member, WHO Working Group on SARS Epidemiology and Modeling
2003-2004	US Department of Defense, Defense Science Board Task Force on SARS Quarantine
2005	Consultant, Ministry of Foreign Affairs, Canada – Pandemic Influenza
2005	Consultant, Congressional Budget Office – Pandemic Influenza
2006, 2007	National Institutes of Health Study Section on Genetic Variation and Evolution
2007, 2008, 2012	National Institutes of Health Special Emphasis Panels, various
2007-2011	Report reviewer, National Research Council, NEIDL Risk Assessments
2008	Food and Drug Administration, Antiviral Advisory Committee, guest member
2008-2009	Member, World Economic Forum Global Agenda Council on Pandemics
2009	Consultant, Mexico Ministry of Health, Pneumococcal Conjugate Vaccine
2009	US President's Council of Advisors on Science and Technology (PCAST)--H1N1 Working Group
2009	Massachusetts Department of Public Health H1N1 Advisory Group
2009-2010	Team B Advisory Body to CDC on Novel H1N1 Influenza

2010-2013	Member, Informal Advisory Group on 2009 Pandemic Influenza Mortality, WHO
2010-	Member, Pneumococcal Serotype Replacement Technical Advisory Group, WHO
2011-	Member, Scientific Advisory Board, Pneumococcal Global Sequencing Project (Gates Foundation, Keith Klugman, PI)
2014-2016	Member, CIDRAP/Wellcome Trust Team B on Ebola Vaccines
2015	Member, Scientific Advisory Group, Norwegian Institute of Public Health/WHO/MSF Ebola Virus Vaccine Trial
2015	Member, Scientific Review Committee, Wellcome Trust Sanger Institute 5-Year Review (4-day evaluation visit)
2017-	Member, Biological Agents Containment Working Group, Board of Scientific Counselors, Office of Public Health Preparedness and Response, CDC
2018-	Member, Advisory Board, Vaccines and Immunotherapies, CARB-X
2018-	Member, Technical Advisory Group, Pneumococcal Serotype Replacement and Distribution Project (PSERENADE), International Vaccine Action Center
2019-	Co-chair, WHO Working Group on Vaccines and Antimicrobial Resistance (VAC-AMR)
2019	Member, Steering Committee, Scorecard on Progress on Recommendations of the Review of Antimicrobial Resistance, Chatham House
2020	Member, Massachusetts Governor's Medical Advisory Committee
2020	Member, Massachusetts COVID-19 Vaccine Working Group
2020	Ad hoc expert, WHO Strategic Advisory Group of Experts, COVID-19 Vaccine Working Group

EDITORIAL BOARDS:

2002-2012	Associate Editor, *American Journal of Epidemiology*
2004-2008	Associate Faculty Editor, *Emerging Themes in Epidemiology*
2009-2010	Member, Faculty of 1000 Biology
2006-2016	Editorial Board, *PLoS Medicine*
2008-2011	Associate Editor, *Epidemics*
2008-2011	Editorial Board, *Emerging Health Threats*
2009-2010	Board of Editorial Advisors, *Journal of Infectious Diseases*
2009-present	Editorial Board, *Epidemiology*
2015-present	Board of Reviewing Editors, *eLife*

PROFESSIONAL SOCIETIES:

Society for Epidemiologic Research
American Society for Microbiology
National Center for Science Education
Union of Concerned Scientists

PUBLIC HEALTH ORGANIZATIONS:

Founder, Cambridge Working Group, 2014
Founder, Society for Safe Science, 2014

SCIENTIFIC COMMITTEES AND CONFERENCE ORGANIZING:

Scientific Committee: 4th International Symposium on Pneumococci and Pneumococcal Diseases, Helsinki, Finland, May 2004
Scientific Committee: 5th International Symposium on Pneumococci and Pneumococcal Diseases, Alice Springs, Australia, May 2006
Scientific Committee: 6th International Symposium on Pneumococci and Pneumococcal Diseases, Reykjavik, Iceland, June 2008
Scientific Committee: 7th International Symposium on Pneumococci and Pneumococcal Diseases, Tel Aviv, Israel, March 2010
Scientific Committee: 9th International Symposium on Pneumococci and Pneumococcal Diseases, Hyderabad, India, March 2014
Conference Chair: First Annual Center for Communicable Disease Dynamics Symposium: Surveillance for Decision Making in Emerging Diseases: Lessons from the 2009 H1N1 Pandemic Influenza. Boston, June 2010
Organizing Committee: Epistemology of Modeling and Simulation. University of Pittsburgh, April 2011.
Conference Chair: Second Annual Center for Communicable Disease Dynamics Symposium: Antimicrobial Resistance: Biology, Population Dynamics and Policy Options. Boston, October 2011
Conference Chair: Epidemics^3, Boston, November 2011
Scientific Committee: Epidemics^4, Amsterdam, November 2013
Conference organizer: Workshop on Modeling and Simulation for Infectious Disease Trial Design, Seattle, August 2016 (with Betz Halloran)
Workshop organizer: Ethical Design of Vaccine Trials in Emerging Infections, ETHOX, Oxford, UK, July 2017 (with Rebecca Kahn, Nir Eyal, Annette Rid)
Scientific Committee: 12th International Symposium on Pneumococci and Pneumococcal Diseases, Toronto, 2020
Advisory group on COVID-19, Science Philanthropy Alliance, August 2020

GRANT REVIEWER SINCE 2003:

Research Fund for the Control of Infectious Disease (RFCID), Hong Kong Semi-Autonomous Region, China
UK Medical Research Council
Wellcome Trust (UK)
Department of Veterans Affairs, USA
Alliance for the Prudent Use of Antibiotics
Swiss National Science Foundation
RIVM (National Institute of Health and Environment), Netherlands
Innovational Research Incentives Scheme, Royal Netherlands Academy of Sciences
National Institutes of Health, ad hoc member, GVE study section (4x), IRAP study section (1x), several telephone special review groups
Health Research Council of New Zealand

AXA Foundation Fellowships
Canadian Institutes of Health Research
Royal Society of New Zealand
French National Research Agency (ANR)
Royal Society (UK)
NIH Special Emphasis Panels (2013/01 ZRG1 IDM-A (02) S; 2014/08 ZRG1 RPHB-W (53) R - RFA-RM-13-009: NIH Director's Early Independence Awards Review)
Dutch Research Council NOW (2011, 2017)
NIH Special Emphasis Panel (2014/10 ZRG1 IDM-S (02) M)
Chair of NIH Infectious Diseases and Microbiology Integrated Review Group, ZRG1 IDM S02 10/2014 council
NIH CRFS Study section, ad hoc member, 2015
UK Medical Research Council (2016)

INVITED TALKS (SINCE 2015):

01/2015	Otto Wolff Lecture, Institute of Child Health, University College London
01/2015	London School of Hygiene and Tropical Medicine, invited lecture
01/2015	Centre for the Study of Existential Risk, Cambridge University, UK, invited lecture
02/2015	Public Health England, Colindale, London UK, invited lecture
03/2015	London School of Hygiene and Tropical Medicine, Health Protection Research Unit Annual Conference, Invited Lecture
04/2015	University of Bristol Department of Social Medicine
04/2015	University of Pittsburgh Marcella L. Finegold Memorial Public Debate Series
05/2015	Applied Bioinformatics and Public Health Conference, Wellcome Trust Sanger Institute, Keynote Lecture
06/2015	Médecins sans Frontières Science Day, Panel Discussion, Paris, France
06/2015	Eijkman Lecture, UMC Utrecht, Netherlands
07/2015	ETH Zurich Latsis Symposium, plenary talk
07/2015	Jenner Lecture, Jenner Vaccine Institute, Oxford University, UK
09/2015	[popular presentation] HubWeek *Four Global Health Threats, Four Global Health Opportunities,* Harvard University
01/2016	National Science Advisory Board on Biosecurity
02/2016	WHO Technical Expert Consultation: Alternate Dosing Schedules of Pneumococcal Conjugate Vaccines, Geneva (by videolink)
02/2016	PATH Scientific Advisory Board, PATHwSP Vaccine Trial, Geneva (by videolink)
05/2016	Department of Microbiology and Immunology, Emory University, Atlanta
05/2016	Causal Inference in the Presence of Interference, Department of Biostatistics, Harvard T.H. Chan School of Public Health, Boston, MA
06/2016	Robert Austrian Award Lecture, International Symposium on Pneumococci and Pneumococcal Diseases-10
07/2016	Glaxo SmithKline Vaccines, Rockville, MD
07/2016	White House Pandemic Prediction and Forecasting Science and Technology Working Group (PPFST WG)

09/2016	Keynote Address, Project Prometheus Workshop on Multi-Strain Modeling, RIVM (National Institute of Public Health and the Environment), Bilthoven, Netherlands
01/2017	Postdocs in Complexity Conference, Santa Fe Institute, NM (not delivered due to travel delays)
02/2017	Department of Epidemiology of Microbial Diseases, Yale School of Public Health, New Haven, CT
03/2017	Department of Mathematics, University of Utah
03/2017	The Value of Vaccines in the Avoidance of Antimicrobial Resistance, Chatham House, London
03/2017	WHO Workshop on Vaccines and Antimicrobial Resistance, London, UK
04/2017	National Math Festival, Washington, DC (two talks)
05/2017	Memorial Symposium for Ellis McKenzie, Fogarty International Center, NIH, Bethesda, MD
06/2017	EA Global, Society for Effective Altruism, Cambridge, MA
06/2017	Panelist, Surveillance workshop, Simons Foundation, New York, NY
09/2017	Emerging Leaders in Biosecurity meeting, Johns Hopkins Center for Health Security (held Cambridge, MA)
12/2017	Risk in Complex Systems: Models, Applications, Perceptions, and Policy Implications, Centre de Recherches Mathematiques, University of Montreal
3/2018	Department of Ecology and Evolutionary Biology, Princeton University
3/2018	17th Annual Symposium, Institute for Systems Biology, Seattle
4/2018	Gates Vaccine Impact Modeling Consortium, Keynote Address, annual meeting in Cambridge, MA
5/2018	”Antibiotic resistance: Evolutionary concepts versus clinical realities,” Wenner-Gren Center, Stockholm
6/2018	London School of Hygiene and Tropical Medicine
6/2018	Institut Pasteur, Paris
6/2018	Big Data Institute, University of Oxford
8/2018	PRISM (Policy relevant infectious disease simulation and mathematical modelling) Annual Meeting, Palm Cove, Australia
8/2018	David Danks Seminar, Murdoch Children’s Research Institute, Melbourne, Australia
11/2018	Berkman-Klein Center, Harvard Law School, Data and Health Seminar
6/2019	Chan-Zuckerberg Biohub, San Francisco
6/2019	Stanford Medical School, Stanford, CA
6/2019	Proctor Foundation, UC San Francisco, CA
7/2019	Wellcome Meeting on the Global Burden of Disease from Antimicrobial Resistance, London
10/2019	23rd Annual Robert M. Fekety, MD Lecture, Department of Medicine, Division of Infectious Diseases, University of Michigan
10/2019	Microbiology and Infectious Diseases Seminar, University of Geneva, Switzerland
3/2020	National Academy of Medicine/American Public Health Association First Webinar on COVID-19, Washington DC (via Zoom)
3/2020	Harvard Kennedy School Growth Lab, Cambridge, MA (via Zoom)
3/2020	White House Modeling Consortium, Washington DC (via Zoom)
4/2020	European Central Bank (via Zoom)
4/2020	*USA Today* Editorial Board (via Zoom)
4/2020	*New York Times* Editorial Board (via Zoom)

4/2020	Harvard Medical School Department of Medicine Grand Rounds (one of many short talks, via Zoom)
5/2020	Massachusetts Coalition for Pathogen Research (one of many short talks, via Zoom)
5/2020	Covid symposium, National Institute of Statistical Science/American Statistical Association
5/2020	Private briefing, Deputy Prime Minister Chrystia Freeman, Ottawa, Canada
5/2020	Briefing, New Democrat Coalition, by Zoom
5/2020	Isaac Newton Institute, Cambridge University, UK, by Zoom
5/2020	Futureproofing Public Health, University of Stellenbosch, by Zoom
5/2020	Private briefing, Rahul Gandhi, Leader, Congress Party, India
5/2020	Harvard Club of Boston, by Zoom
5/2020	Tsinghua University / AAAS Symposium, Beijing, by Zoom
5/2020	Institute for Genome Sciences, University of Maryland, by Zoom
5/2020	National Academy of Sciences, Section 43, by Zoom
5/2020	Medical Grand Rounds, Boston Children's Hospital, by Zoom
5/2020	Vaccine Research Center, Beth Israel Deaconess Medical Center, by Zoom
5/2020	COVID-19 and the Role of Modeling, American Statistical Association and the National Institute of Statistical Sciences (via Zoom)
6/2020	International Monetary Fund, by Zoom
6/2020	Webinarium: Role of a Medical University in a Pandemic, Karolinska Institutet, Stockholm, by Zoom
7/2020	Bipartisan Commission on Biosecurity, by Zoom
7/2020	National Bureau of Economic Research, by Zoom
7/2020	SAGE Working Group on COVID-19 Vaccines, by Zoom (panelist)
7/2020	Congressional Briefing on Human Challenge Trials, organized by 1DaySooner and Rep. Bill Foster, by Zoom
7/2020	International Symposium on Novel Ideas in Science and Ethics of Vaccines against COVID-19 Pandemic, India Council of Medical Research, by Zoom
7/2020	Private and Public Science, Advisory, and Consumer Food Policy Group (PAPSAC), Harvard Kennedy School, by Zoom
8/2020	National Academies (NASEM) Committee on Equitable Allocation of Vaccine for the Novel Coronavirus (panel), by Zoom
8/2020	Mathematical Sciences Research Institute, University of California, Berkeley, by Zoom
8/2020	Coronavirus Conversations, Science and Society, Duke University (panel), by Zoom
8/2020	Giving Pledge Meeting – Q&A with Scott Dowell, Bill and Melinda Gates Foundation, by Zoom
8/2020	Janelia Farm, Howard Hughes Medical Institute, via Zoom
9/2020	COVID-19, Public Health Ethics, and Policy for Pandemics, Harvard Medical School Center for Bioethics, Cambridge MA (via Zoom)
9/2020	From testing to distribution: the importance of, and challenges to, estimating the protective effects of vaccines, National Institute of Statistical Sciences, Research Triangle, NC (via Zoom)
9/2020	Epidemiology of COVID-19: Implications for Control, American Physical Society, College Park, MD (via Zoom)

10/2020	COVID-19 and Vaccines: Clinical Trials, Immunity and Immunization, American Lung Association, Chicago, IL (via Zoom)
10/2020	Board of Directors, Blue Cross-Blue Shield of Massachusetts

RESEARCH SUPPORT:

Past Funding

1997-1999	NIH postdoctoral fellowship 1 F32 GM019182 Population Genetics of Bacterial Infection and Treatment. Role: PI
1997-1999	SmithKlineBeecham unrestricted educational grant. Effects of Antiviral Usage on Resistance in Herpes Simplex Virus, Type 1. Bruce R. Levin, PI. Role: Co-PI
2001-2005	NIH research grant R01 AI051929. Drug Resistance in Tuberculosis: Genetics and Dynamics. Eric Rubin, PI. Role: Co-PI
2001-2006	NIH research grant R01 AI48935. Vaccination and the Evolutionary Dynamics of Pneumococci. Role: PI
2001-2011	NIH research grant R01 AI048935 Mechanisms of Capsular Diversity in *Streptococcus pneumoniae*. Role: PI
2002	PhRMA Foundation Research Starter Grant. Planning and Assessing Antimicrobial Cycling and Other Interventions to Control Resistance in Hospitals. Role: PI
2002-2006	Ellison Foundation New Scientist in Global Infectious Diseases Award. Antibiotic Resistance in *Streptococcus pneumoniae*: Transmission Dynamics and Consequences for Public Health. Role: PI
2003-2006	NIH research grant 5 R21 AI055825. Epidemiologic Methods: Resistant Nosocomial Infections. Role: PI
2004-2013	NIH/NIAID R01 AI058736 (Freedberg). Optimizing HIV care in less developed countries. Role: Consortium Co-Investigator
2006	Taplin Foundation Equipment Grant, Harvard School of Public Health.
2006	NIAID/TIGR Pathogen Functional Genomics Resource Center grant of access to free microarrays. Effects of Host Immunity on Pneumococcal Gene Expression. Role: PI
2006-2009	NIH cooperative agreement U01 GM076497. Methodological Approaches to Planning and Analysis of New Infectious Diseases. Role: PI. Replaced by U54 GM088558.

2006-2016	NIH/NIAID R01 AI066304 (Finkelstein). Conjugate Vaccine Impact of Pneumococcal Carriage, Disease, and Population (SPARC2). Role: Consortium PI
2010-2014	NIH/NIMH R01 MH087328 (Seage). Modeling the Impact of HIV Prevention Interventions (CEPAC Dynamic). Role: Co-PI
2011-2016	NIH/NIGMS R01 GM100467 (Shaman). Influenza Outbreak Prediction: Applying Data Assimilation Methodologies to Make Skillful Forecasts of an Inherently Chaotic, Nonlinear System. Role: Consortium PI
2012-2018	NIH/NIAID R01 AI048935-15 NCE. Mechanisms and Population Genomics of Pneumococcal Antigenic Diversity. Role: PI
2013-2019	NIH/NIGMS R01 AI106786-05 NCE (PI: Hanage). Ecological and Genetic Contributions to the Spread of Resistance in Pnumococcus. Role: Co-PI
2014-2018	Pfizer Inc. (No number). Modeling serotype replacement with Prevnar13 using an agent-based model (Phase 2). Role: PI
2014-2018	NIH/NIGMS R01 GM116525-03 (Seage). Calibration and Simulation of the Botswana Combination Prevention Project. Role: Co-PI
2014-2018	Program for Appropriate Technology in Health. 1773-00460733-COL. Modeling pneumococcal population dynamics under serotype-nonspecific vaccination. Role: PI
2015-2018	NIH/NIAID R21 AI112991-02 NCE (Huttenhower). Staphylococcus Aureus Carriage and the Nasal Microbiome. Role: Co-PI
2015-2020	NIH/NIGMS R01 GM113233 (Wargo). The impacts of host vaccination and selective breeding for disease resistance on pathogen transmission and ecology in freshwater aquaculture. Role: Consortium PI
2017-2019	Pfizer Inc. CP147216 (Lipsitch/Lewnard). Quantifying pneumococcal conjugate vaccine impact against otitis media. Role: Co-PI
2017-2020	CDC 1 U01 CK000538-01 (Samore). Modeling and simulation to support antibiotic stewardship and epidemiological decision-making in healthcare settings. Role: Consortium PI

Current Funding

2014-2021	NIH/NIGMS U54 GM088558-10 NCE. MIDAS Center for Communicable Disease Dynamics. Role: PI
2018-2022	NIH/NIAID 5 R01 AI128344-01 (Hanage). Deep sequencing of pathogens to precisely define transmission networks using rare variants. Role: Co-PI

2018-2021	National Institute for Health Research. PR-OD-1017-20006 (PI: Cooper / University of Oxford). Leveraging Pathogen Sequence Data and Adaptive Designs to Improve Vaccine Trials in Emerging Epidemics in LMICs. Role: Consortium PI
2018-2020	Pfizer Inc. A34479 (Lewnard). Changes in antimicrobial prescribing for otitis media in the era of pneumococcal conjugate vaccination. Role: Co-PI
2019-2024	CDC U01 IP001121-02 (PI: Rosenfeld / Carnegie Mellon University). Delphi Influenza Forecasting Center of Excellence. Role: Consortium PI
2020-2022	Wellcome Trust. 219759/Z/19/Z. Vaccine-avertable antimicrobial prescribing from influenza and RSV: a mixed-methods observational study. Role: PI
2020-2022	Wellcome Trust. 219812/Z/19/Z (Grad). Reducing antibiotic prescribing through a prioritized vaccination strategy. Role: Co-PI
2020-2023	Open Philanthropy Project / Silicon Valley Community Foundation. 2020-211809. Research and Policy Activities on Biosafety and Biosecurity. Role: PI
2020-2022	NIH/NCI U01 CA261277-01. Causal, Statistical and Mathematical Modeling with Serologic Data
2020-2025	CDC U01 CK000585-01 (Samore). Modeling and Simulation to support Epidemiological decision-making in Healthcare settings. Role: Consortium PI
2020-2022	Morris-Singer Foundation. Morris-Singer Fund for the Center for Communicable Disease Dynamics. Role: PI

TEACHING EXPERIENCE:

Full Courses

Biostatistics 516: Inferential Methods for Infectious Diseases. Co-developer and co-instructor of course.
Taught 2011 (Spring 2)

Epidemiology 260: Mathematical Models of Infectious Diseases: Developed course, sole instructor.
Taught 2001, 2002, 2003, 2005, 2007, 2009, 2011, 2014, 2016, 2018, 2020 always d period (Spring 2).

Interdepartmental 267-268: Seminar in Infectious Disease Epidemiology: Developed and taught course jointly with Dr. Megan Murray in 2000; sole instructor in 2001 and 2002.
Taught 2000-2001 as full year; taught 2001 and 2002 as fall only (ID267ab).

Interdepartmental 298: Inference in Infectious Disease Epidemiology. Developed course, sole instructor.
Taught 2005, 2007 winter session.

Epidemiology 502: Biology and Epidemiology of Antibiotic Resistance. Co-developed and co-taught course with Dr. Gili Regev-Yochay.
Taught 2008, 2010, 2012, 2014, 2016, 2018, 2020 winter session.

Participation

Epidemiology 201: Introduction to Epidemiology. One week each year (2 2-hr. lectures).
Taught 2000-2007; coinstructor 2005-7.

Epidemiology 200: Principles of Epidemiology. One lecture per year.
Taught 2000-2005; coinstructor 2005-7.

Epidemiology 289: two lectures on Infectious Disease Epidemiology, 2010

Interdepartmental 229: Epidemiology of Infectious Diseases of Importance in Developing Countries (and predecessors). One lecture per year.
Taught 2000-2006.

DBS205: Biological Sciences Seminars. One presentation of research per year.
Taught 2002, 2005, 2015.

RDS281 (now 285): Decision Analysis Methods in Public Health and Medicine. One lecture on infectious diseases and dynamic modeling.
Taught 2002-2007, 2010.

IMI225 Design and Development of a vaccine. One lecture per year.
Taught 2007.

IMI227 Genetics of Infectious Disease. One lecture per year.
Taught 2007-8.

Epidemiology 205: Practice of Epidemiology. Supervised one student.
Participated 2000.

Epidemiology 294: Screening. Two lectures on introductory Infectious Disease Epidemiology
2011, (Spring 2)

ID517 Public Health Response to Mass Emergencies. One lecture.
Taught 2008.

Life Sciences 120 (Harvard College): Global Health Threats.
One to three lectures, 2011, 2012, 2016

Probabilistic Risk Analysis (HSPH Continuing Education). One lecture per year.
Taught 2002-2004.

Health Science & Technology Microbiology (HMS). One lecture per year.
Taught 2002, 2003, 2005, 2007, 2008, 2009.

Modern Medical Microbe Hunters (HMS). One lecture per year.
Taught 2000, 2001, 2002, 2004.

Epidemiology 513: Issues in the Reporting of Clinical Trials. *Guest lecture 2011.*

Epidemiology 203. Four, 2-hour lectures per year on infectious disease epidemiology 2012, 2014, 2016, 2017, 2018,2019

ID250 Ethical Basis of Public Health Practice. One lecture per year
Guest lecture 2015

GHP539 Control of Infectious Diseases in Low/Mid Income Countries: Social, Political and Economic dimensions
Guest lecture 2017

MPH100
Guest lecture 2019, 2020 (Spring and Fall)

Harvard College Gen Ed 1098 Natural Disasters
Guest lecture 2020

Short Courses Outside Harvard

Harvard-Karolinska Summer School on Modern Methods in Biostatistics and Epidemiology, Treviso, Italy. Infectious Disease Epidemiology. Developed a 1-week intensive introductory course with exercises and was sole instructor. *Taught 2005.*

Hong Kong Centre for Health Protection Short Course in Mathematical Modelling of Infectious Diseases. Participated in course development and taught three lectures. *Taught 2006.*

Infection and Immunity in Children, Department of Paediatrics, Oxford University, UK. Delivered 1 lecture by videolink. *Taught June 2010.*

Winter Forum – Pandemic 2011. Duke Global Health Institute and Office for Undergraduate Education, Durham, NC. Delivered one lecture by videolink. *Taught January 2011.*

Practical Short Course in Infectious Disease Modeling. National Center for Immunization and Respiratory Diseases, US Centers for Disease Control & Prevention (CDC). Course director (collaboratively with Hong Kong University and Imperial College London) and instructor. *Taught June 2011.*

Erasmus Summer Program, Erasmus University, Rotterdam, Netherlands. Master Class taught by videolink. *Taught August 2011.*

Short Course in Infectious Disease Modeling: Hong Kong University and HSPH CCDD:
Kuala Lumpur 2014, Bangkok 2012

Course organizer and faculty: Short Course in Infectious Disease Modeling: HSPH CCDD, Imperial College London, Hong Kong University
Centers for Disease Control and Prevention 2011, 2014

Faculty Guest Lecturer: ICARe (International course on Antibiotic Resistance), Pasteur Institute, at Fondation Merieux, Les Pensieres, France.
2018, 2019

Online Modules

Herd Immunity in: Vaccines 101, Harvard School of Public Health online course
Recorded Summer 2014

Heterogeneity in: Epidemics, University of Hong Kong HKUx EdX course
Recorded Summer 2014

Guest Teaching Outside Harvard

Georgetown University Department of Microbiology and Immunology: guest lecture in Science Diplomacy and World Health, Tomoko Steen instructor (2014, 2016)

Princeton University Woodrow Wilson School: guest lecture in Topics in Development: Global Challenges of Infection, Burden and Control, Adel Mahmoud and Bryan Grenfell instructors (2016, 2018)

Supervision

Research Scientist supervisor:

2005-2008	Krzysztof Trzcinski, D.V.M., Ph.D., Research Scientist
2008-2009	Krzysztof Trzcinski, D.V.M., Ph.D., Senior Research Scientist (now Assistant Professor, University of Utrecht, Netherlands)
2008-2010	Edward Goldstein, Ph.D., Research Scientist
2010-2018	Edward Goldstein, Ph.D., Senior Research Scientist
2019-present	Rene Niehus, Ph.D, Research Associate

Postdoctoral supervisor:

2001-2005	Krzysztof Trzcinski, D.V.M., Ph.D. Assistant Professor, University of Utrecht, Netherlands.
2001-2002	Noman Siddiqi, Ph.D. (Co-supervisor with Eric Rubin). Currently BL3 Manager, Harvard School of Public Health
2001-2002	Susan Huang, M.D., M.P.H. (Secondary advisor) (currently Professor of Infectious Disease, University of California, Irvine).

2002-2003	Ben Cooper, Ph.D. Professor, Nuffield Department of Medicine, Mahidol-Oxford Tropical Research Unit, Bangkok, Thailand
2003-2005	Michael Palmer, Ph.D. Currently working in the IT Industry
2004-2008	Gili Regev-Yochay, M.D. Currently Assistant Professor, Tel Aviv University and Head of Infectious Diseases Epidemiology Unit, Gertner Institute, Tel Aviv, Israel.
2006-2008	Debby Bogaert, M.D., Ph.D. Professor of Pediatric Infectious Diseases, University of Edinburgh
2008	Edward Goldstein, Ph.D. Senior Research Scientist, HSPH
2010	Daniel Weinberger, Ph.D. Assistant Professor, Yale School of Public Health
2009-2011	Joel Miller, Ph.D. Currently Senior Research Scientist, Institute for Disease Modeling, Seattle
2010-2013	Sarah Cobey, Ph.D. Associate Professor of Ecology and Evolution, University of Chicago
2010-2014	Yuan Li, Ph.D. Epidemiologist, CDC
2010-2014	Yonatan Grad, M.D., Ph.D. Assistant Professor, Harvard TH Chan School of Public Health
2011-2013	Nicholas Croucher, Ph.D. (co-advisor with W. Hanage). Senior Lecturer and Henry Dale Fellow, Imperial College
2013-2016	Colin Worby, Ph.D. (co-advisor with W. Hanage) Staff Scientist, Broad Institute.
2013-2019	Hsiao-Han Chang, Ph.D. (co-advisor with C. Buckee). Starting 2019: Assistant Professor, National Tsing Hua University, Taiwan
2014-2016	Nadia Abuelezam, Sc.D. (secondary advisor with George Seage). Currently Assistant Professor, Boston College School of Nursing.
2014	Ben Althouse, Ph.D. (external faculty advisor for his Santa Fe Institute Postdoc)
2015-2017	Kate Langwig, Ph.D. Assistant Professor of Ecology, Virginia Tech
2015-2018	Taj Azarian, Ph.D. Assistant Professor of Medicine, Burnett School of Biomedical Sciences, Department of Molecular Microbiology, University of Central Florida College of Medicine
2015-2018	Brian Arnold, Ph.D. Bioinformatics Scientist, Faculty of Arts and Sciences, Harvard University
2015-2018	Maria Georgieva, Ph.D. Postdoctoral Fellow, Department of Physiology, University of Lausanne
2016-present	Samantha Palace, Ph.D. (co-supervisor with Y. Grad)
2017-2018	Lucy Li, Ph.D. Bioinformatics Scientist I, Chan Zuckerberg Biohub
2017-2018	Joseph Lewnard, Ph.D. Assistant Professor, Department of Epidemiology, UC Berkeley
2017-2019	Ayesha Mahmud, Ph.D. (Co-advisor with C. Buckee). Assistant Professor, Department of Demography, UC Berkeley
2018-present	Pamela Martinez, Ph.D. (Co-advisor with C. Buckee)
2019-present	Xueting Qiu, Ph.D. (Co-advisor with W. Hanage)
2019-present	Lerato Magosi, D.Phil.
2020	Lee Kennedy-Shaffer, Ph.D., Assistant Professor, Vassar College
2020-present	Rebecca Kahn, Ph.D.

Doctoral student supervisor:

2000-2001	Ivo Foppa (Epi). Currently Epidemiologist, Influenza Division, CDC
2000-2005	Hailay Teklehaimenot (Epi). Currently at Ministry of Health, Addis Ababa, Ethiopia
2000-2001	Robert Suruki (Epi): completed doctoral studies with another advisor; currently at GlaxoSmithKline.
2001-2006	Christina Mills (Epi). Currently Attending Physician, Boston Children's Hospital Boston
2002-2005	Alethea McCormick (Epi). Currently Research Associate, Harvard School of Public Health
2002-2011	Sibel Ascioglu (Epi). Currently at Glaxo SmithKline
2003-2008	Virginia Pitzer (Epi). Currently Assistant Professor, Yale School of Public Health
2004-2012	Jessica Hartman Jacobs (Epi)
2006-2012	Justin O'Hagan (Epi). Currently Head of Outcomes Research, Dengue, Merck.
2006-2010	Daniel Weinberger (BPH). Currently Assistant Professor, Yale School of Public Health
2007-2008	Chris Ford (BPH). Currently Postdoc, Broad Institute.
2007-2008	Karell Pelle (BPH)
2014-2018	Matthew Hitchings (Epi). Currently postdoctoral fellow, Emerging Pathogens Institute, University of Florida
2016-present	Christine Tedijanto (Population Health Sciences/Epi)
2016-present	Emma Accorsi (Population Health Sciences/Epi)
2018-2020	Rebecca Kahn (Population Health Sciences/Epi)
2019-present	Keya Joshi (Population Health Sciences/Epi)

Master's student supervisor:

2000-2002	Alison Han (MPH)
2000-2008	Catherine Laine (Epi MSc). Currently Founder and Deputy Director, Appropriate Infrastructure Development Group.
2001-2002	Benjamin Ip, MD (MPH)
2001-2002	Rajneesh Hazarika, MD (MPH)
2002-2004	Hoa Nguyen, MD (MS)
2003-2005	Dereje Dengela (MS)
2004-2005	Heather Green (MS)
2004-2005	Wei-yen Lim, MD (MPH)
2004-2005	Phil James, MD (MPH)
2005-2006	Jeffrey Cloud, MD (MPH)
2005-2006	Yen-Tsung Huang, MD (MPH)
2005-2006	Minghua Chen, MD (MPH)
2006-2007	Chou-Cheng Lai, MD (MS)
2006-2007	Jennifer Shuford, MD (MPH)
2006-2007	Chih-Hao Chen, MD (MS)
2006-2007	Mark Brady (MPH)
2007-2008	Indrajit Hazarika, MD (MPH)
2007-2008	Hyun Joon Shin, MD (MPH)
2007-2008	Amit Vora (MPH)
2005-2006	Christie Jeon (MS)

2004-2007	Gili Regev-Yochay, MD (MS)
2009-2011	Weixiong Ke
2010-2012	Karen Aanensen
2011-2013	Talia Quandelacy
2011-2013	Patrick Mitchell
2013-2014	Fausto Bustos
2016-2017	Say Tat Ooi, MD (MPH)
2016-2018	Michael Martin (MS)
2016-2018	Inga Holmdahl (MS)
2016-2018	Rebecca Kahn (MS)
2017-2019	Sarah Lapidus (MS)
2018-2020	Nancy Li (MS)
2019-2020	Eva Rumpler (MS)
2019-present	Rafia Bosan (MS)

Undergraduate supervisor:

Summer 2001	Eneida Villanueva (Summer Minority Intern)
Fall 2001	Jonathan Burton-MacLeod (Bio 91r supervised reading, FAS)
2016-2018	Alan Yang (Supervised research)
Summer 2018	Tara E. Gallagher, Dartmouth College (Summer intern)

Thesis committees:

2000-2001	Megan Murray (Dr. P.H., completed 2000-1)
2004-2007	Eben Kenah (Epidemiology)
2004-2005	Y. Claire Wang (Health Policy and Management)
2005	Seema Thakore Meloni (Ph.D., Biological Sciences in Public Health)
2005-2007	Mary Farrow (Ph.D., Biological Sciences in Public Health)
2007-2010	Kevin Chan (Population & International Health)
2008-2011	Amy Bei (Ph.D., Biological Sciences in Public Health)
2010-2013	Chris Ford (Ph.D., Biological Sciences in Public Health)
2010-2013	Regina Joice (Ph.D., Biological Sciences in Public Health)
2011	Rachel Daniels (Ph.D., Biological Sciences in Public Health)
2011-2017	Freeman Suber MD (Ph.D., Biological Sciences in Public Health)
2011-2012	Tami Lieberman (Ph.D., Systems Biology)
2011-2013	Wei Wu (Epidemiology)
2013	Opponent, PhD of Rolf Ypma, University of Utrecht
2014	Clare Louise Kinnear, PhD, The University of Melbourne (external examiner)
2015-2017	Corey Peak (SD, Epidemiology)
2015-2016	Patrick Mitchell (SD, Epidemiology)
2016	Hattie Chung (PhD, Systems Biology, Harvard GSAS), examination committee
2016	Nicole Espy (PhD, BPH, defense committee)
2015-2017	Quizhi Chang (SD, Epidemiology)
2017-2019	Eric Mooring (SD, Epidemiology)
2017-present	Rebecca Mandt (PhD, BPH)

2017-2020	Sarah McGough (PhD, Population Health Sciences)
2018-2020	Lee Kennedy-Shaffer (Biostatistics)

Oral exam committees:

2001	Yemane Yihdego (IID)
2001	Chris Mores (IID)
2002	Pride Chigwedere, MD (IID)
2004	Beth Ann Griffin (Biostatistics)
2004	Eben Kenah (Epidemiology)
2004	Laura Forsberg (Biostatistics)
2007	Kevin Chan (Population & International Health)
2008	Hsien-Ho Lin (Epidemiology)
2009	Regina Joice (BPH)
2009	Celene Chang (BPH)
2009	Kathleen Wirth (Epi)
2011	Freeman Suber (BPH)
2011	Wei Wu (Epi)
2012	Nicanor Rodriguez, DVM (IID)
2016	Corey Peak (Epi)
2016	Qiuzhi Chang (Epi)

Laboratory rotations supervised:

2000	Chun Chao (MS student, Immunology & Infectious Diseases)
2004	Adam MacNeil (PhD, Biological Sciences in Public Health)
2006	Daniel Weinberger (PhD, Biological Sciences in Public Health)
2006	Amy Bei (PhD, Biological Sciences in Public Health)
2008	Chris Ford (PhD, Biological Sciences in Public Health)
2009	Richa Gawande (PhD, Biological Sciences in Public Health)
2010	Sri Kalyanamaran (PhD, Biological Sciences in Public Health)
2011	Wen Xie (PhD, Biological Sciences in Public Health)
2016	Rebecca Mandt (PhD, Biological Sciences in Public Health)

SCHOOL AND DEPARTMENTAL SERVICE

Interdisciplinary Program in the Epidemiology of Infectious Disease
- Steering committee, 2000-present
- Seminar Coordinator, 2000-present
- Associate Director, 2004-present

Biological Sciences in Public Health Program
- Admissions interviewer, 2001-present
- Curriculum Committee, 2006-2012

Department of Epidemiology
- Co-leader, department retreat, 2001

- Admissions committee, 2001-2014

HSPH Epidemiology and Biostatistics Planning Committee: member, 2003-2004

HSPH Allston Planning Committee: member, 2003-2004

HSPH Information Technology Advisory Committee: member, 2004-2005

HSPH Committee on Educational Policy: member, 2005-2008

HSPH Standing Committee on Appointments, Reappointments, and Promotions: member, 2008-present, vice-chair 2010-2012, chair 2012-2013

University Pandemic Response Planning Committee: member, 2005-present

Bioinformatics Junior Faculty Search Committee: member, 2007-2008

Epidemiology Methods Junior Faculty Search Committee: member, 2008

Epidemiology Infectious Diseases Junior Faculty Search Committee: chair, 2008

HSPH Committee on the Concerns of Women Faculty: member, 2010-2012

HMS Subcommittee on Admissions for the MD/PhD: member, 2010-2012, 2014-present

Harvard University Office of Scholarly Communication Advisory Committee, member, 2013-present

Harvard T.H. Chan School of Public Health Dean Search Advisory Committee, member, 2015

Harvard T.H. Chan School of Public Health Faculty Judge, Postdoctoral Association Travel Awards, member, 2016

Epidemiology Junior Faculty Search Committee, 2017-2018

BIBLIOGRAPHY

Peer-Reviewed Articles

1. Petrie M, Lipsitch M. Avian polygyny is most likely in populations with high variability in heritable male fitness. Proc R Soc Lond B. 1994 June 22;256(1347):275-80. doi: 10.1098/rspb.1994.0081.
2. Lipsitch M, Nowak MA. The evolution of virulence in sexually transmitted HIV/AIDS. J Theor Biol. 1995 Jun 21;174(4):427-40. doi: 10.1006/jtbi.1995.0109. PMID: 7666673.
3. Lipsitch M, Nowak MA, Ebert D, May RM. The population dynamics of vertically and horizontally transmitted parasites. Proc Biol Sci. 1995 Jun 22;260(1359):321-7. doi: 10.1098/rspb.1995.0099. PMID: 7630898.
4. Lipsitch M, Herre EA, Nowak MA. Host Population Structure and the Evolution of Virulence: A "Law Of Diminishing Returns". Evolution. 1995 Aug;49(4):743-748. doi: 10.1111/j.1558-5646.1995.tb02310.x. PMID: 28565133.
5. Mangin KL, Lipsitch M, Ebert D. Virulence and transmission modes of two microsporidia in *Daphnia magna*. Parasitology. 1995;111(2):133-142. doi: 10.1017/S0031182000064878.
6. Lipsitch M, Siller S, Nowak MA. The Evolution of Virulence in Pathogens With Vertical and Horizontal Transmission. Evolution. 1996 Oct;50(5):1729-1741. doi: 10.1111/j.1558-5646.1996.tb03560.x. PMID: 28565576.
7. Lipsitch M, Moxon ER. Virulence and transmissibility of pathogens: what is the relationship? Trends Microbiol. 1997 Jan;5(1):31-7. doi: 10.1016/S0966-842X(97)81772-6. PMID: 9025233.
8. Antia R, Lipsitch M. Mathematical models of parasite responses to host immune defences. Parasitology. 1997;115 Suppl:S155-67. doi: 10.1017/s003118209700200x. PMID: 9571700.
9. Levin BR, Lipsitch M, Perrot V, Schrag S, Antia R, Simonsen L, Walker NM, Stewart FM. The population genetics of antibiotic resistance. Clin Infect Dis. 1997 Jan;24 Suppl 1:S9-16. doi: 10.1093/clinids/24.supplement_1.s9. PMID: 8994776.
10. Lipsitch M, Levin BR. The within-host population dynamics of antibacterial chemotherapy: conditions for the evolution of resistance. Ciba Found Symp. 1997;207:112-27; discussion 127-30. doi: 10.1002/9780470515358.ch8. PMID: 9189638.
11. Lipsitch M, Levin BR. The population dynamics of antimicrobial chemotherapy. Antimicrob Agents Chemother. 1997 Feb;41(2):363-73. doi: 10.1128/AAC.41.2.363. PMID: 9021193; PMCID: PMC163715.
12. Lipsitch M. Vaccination against colonizing bacteria with multiple serotypes. Proc Natl Acad Sci U S A. 1997 Jun 10;94(12):6571-6. doi: 10.1073/pnas.94.12.6571. PMID: 9177259; PMCID: PMC21091.
13. Lipsitch M. Evolution in health and disease. Trends Microbiol. 1997 Aug;5(8):303-5. doi: 10.1016/S0966-842X(97)01087-1. PMID: 9263405.
14. Datta A, Hendrix M, Lipsitch M, Jinks-Robertson S. Dual roles for DNA sequence identity and the mismatch repair system in the regulation of mitotic crossing-over in yeast. Proc Natl Acad Sci U S A. 1997 Sep 2;94(18):9757-62. doi: 10.1073/pnas.94.18.9757. PMID: 9275197; PMCID: PMC23263.
15. Bonhoeffer S, Lipsitch M, Levin BR. Evaluating treatment protocols to prevent antibiotic resistance. Proc Natl Acad Sci U S A. 1997 Oct 28;94(22):12106-11. doi: 10.1073/pnas.94.22.12106. PMID: 9342370; PMCID: PMC23718.

16. Lipsitch M. Transmission Rates and HIV Virulence: Comments to Massad. Evolution. 1997 Feb;51(1):319-320. doi: 10.1111/j.1558-5646.1997.tb02416.x. PMID: 28568797.
17. Levin BR, Antia R, Berliner E, Bloland P, Bonhoeffer S, Cohen M, DeRouin T, Fields PI, Jafari H, Jernigan D, Lipsitch M, McGowan JE Jr, Mead P, Nowak M, Porco T, Sykora P, Simonsen L, Spitznagel J, Tauxe R, Tenover F. Resistance to antimicrobial chemotherapy: a prescription for research and action. Am J Med Sci. 1998 Feb;315(2):87-94. doi: 10.1097/00000441-199802000-00004. PMID: 9472907.
18. Lipsitch M, Levin BR. Population dynamics of tuberculosis treatment: mathematical models of the roles of non-compliance and bacterial heterogeneity in the evolution of drug resistance. Int J Tuberc Lung Dis. 1998 Mar;2(3):187-99. PMID: 9526190.
19. Stewart FM, Antia R, Levin BR, Lipsitch M, Mittler JE. The population genetics of antibiotic resistance. II: Analytic theory for sustained populations of bacteria in a community of hosts. Theor Popul Biol. 1998 Apr;53(2):152-65. doi: 10.1006/tpbi.1997.1352. PMID: 9615474.
20. Levin BR, Lipsitch M, Bonhoeffer S. Population biology, evolution, and infectious disease: convergence and synthesis. Science. 1999 Feb 5;283(5403):806-9. doi: 10.1126/science.283.5403.806. PMID: 9933155.
21. Lipsitch M. Bacterial vaccines and serotype replacement: lessons from Haemophilus influenzae and prospects for Streptococcus pneumoniae. Emerg Infect Dis. 1999 May-Jun;5(3):336-45. doi: 10.3201/eid0503.990304. Erratum in: Emerg Infect Dis 1999 Sep-Oct;5(5):734. PMID: 10341170; PMCID: PMC2640786.
22. Lipsitch M, Bergstrom CT, Levin BR. The epidemiology of antibiotic resistance in hospitals: paradoxes and prescriptions. Proc Natl Acad Sci U S A. 2000 Feb 15;97(4):1938-43. doi: 10.1073/pnas.97.4.1938. PMID: 10677558; PMCID: PMC26540.
23. Lipsitch M, Dykes JK, Johnson SE, Ades EW, King J, Briles DE, Carlone GM. Competition among Streptococcus pneumoniae for intranasal colonization in a mouse model. Vaccine. 2000 Jun 15;18(25):2895-901. doi: 10.1016/s0264-410x(00)00046-3. Erratum in: Vaccine 2000 Oct 15;19(4-5):598. PMID: 10812233.
24. Bergstrom CT, Lipsitch M, Levin BR. Natural selection, infectious transfer and the existence conditions for bacterial plasmids. Genetics. 2000 Aug;155(4):1505-19. PMID: 10924453; PMCID: PMC1461221.
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– A commentary on this paper was published alongside it, to which we published a rejoinder: Goldstein E, Viboud C, Charu V, Lipsitch M. The authors respond. *Epidemiology*. 2012 Nov;23(6):829-38.

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Data Sets

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