COMMONWEALTH OF MASSACHUSETTS
SUPREME JUDICIAL COURT

Suffolk, ss. No. SJ-2020-757

COMMITTEE FOR PUBLIC COUNSEL SERVICES and
MASSACHUSETTS ASSOCIATION OF
CRIMINAL DEFENSE LAWYERS,
Plaintiffs,

v.

BARNSTABLE COUNTY SHERIFF'S OFFICE, BERKSHIRE COUNTY SHERIFF'S OFFICE, BRISTOL COUNTY SHERIFF'S OFFICE, DUKES COUNTY SHERIFF'S OFFICE, ESSEX COUNTY SHERIFF'S OFFICE, FRANKLIN COUNTY SHERIFF'S OFFICE, HAMPDEN COUNTY SHERIFF'S OFFICE, HAMSPHIRE COUNTY SHERIFF'S OFFICE, MIDDLESEX COUNTY SHERIFF'S OFFICE, NORFOLK COUNTY SHERIFF'S OFFICE, PLYMOUTH COUNTY SHERIFF'S OFFICE, SUFFOLK COUNTY SHERIFF'S OFFICE and
WORCESTER COUNTY SHERIFF'S OFFICE
Defendants.

SUPPLEMENTAL AFFIDAVIT OF
DR. YONATAN GRAD (MD, PhD) AND DR. EMMA ACCORSI (BS)

I, Dr. Yonatan Grad, and I, Emma Accorsi, state that the following is a true and accurate statement to the best of our knowledge and belief:

Background (Yonatan Grad)

1. I, Yonatan Grad, am the Melvin J. and Geraldine L. Glimcher Associate Professor in the Department of Immunology and Infectious Diseases at the Harvard T.H. Chan School of Public Health, and associate physician in the Division of Infectious Diseases at Brigham and Women's Hospital (BWH) and Harvard Medical School. I earned my MD and PhD at Harvard Medical School, completed my internal medicine residency at BWH and clinical infectious diseases fellowship in the Massachusetts General Hospital/BWH combined program, and performed postdoctoral work in the Center for Communicable Disease Dynamics at the Harvard T.H. Chan School of Public Health.

2. My research investigates how pathogens evolve and spread through populations with the motivation of improving clinical and public health strategies to decrease the burden of disease. I use a variety of methods, including genomics, epidemiological tools, and microbiology, to define the dynamics of spread and investigate pathogen genotypic and phenotypic diversity.

3. I am the author of more than 90 peer-reviewed articles in epidemiology, infectious diseases, and other areas that have been cited over 6,500 times. Most recently, I am the author of 9 peer-reviewed papers, 5 submitted manuscripts available as pre-prints, and several op-eds covering the COVID-19 pandemic. Among these, I am co-senior author on the paper "Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period," published in *Science*, in which we built a mathematical model for SARS-CoV-2 transmission incorporating viral, environmental, and immunologic factors and evaluated the impact of social distancing efforts on curbing the COVID-19 pandemic. I am a co-author on "Model-informed COVID-19 vaccine prioritization strategies by age and serostatus," also published in *Science*, in which we describe approaches to optimizing vaccine distribution to minimize the number of cases and deaths from COVID-19. In addition, I am one of the science advisors for the National Basketball Association, and I worked with the team of advisors and members of the NBA and NBA Players Association to implement, oversee, and monitor the resumption of the 2019-20 season in the "bubble." I have also been interviewed, quoted, and featured in multiple media outlets, including CNN, MSNBC, the New York Times, the Atlantic, the Washington Post, and the Boston Globe.

4. A copy of my curriculum vitae is attached as Exhibit A.

Background (Emma Accorsi)

5. I, Emma Accorsi, am a fifth-year PhD candidate in the Department of Epidemiology at the Harvard T.H. Chan School of Public Health with a focus on infectious disease epidemiology. I defended my dissertation in March, 2021 and my degree will be conferred in May, 2021. Starting this summer, I will join the 2021 class of the CDC's competitive Epidemic Intelligence Service (EIS) fellowship. I am the author of six peer-reviewed papers, and four manuscripts currently under scientific review, and have been an instructor for one course in quantitative methods, and a teaching fellow for six courses in epidemiology. I completed my B.S. in Applied Mathematics at Emory University where I was an Emory Scholar and a Barry M. Goldwater Scholar.

6. A copy of my curriculum vitae is attached as Exhibit B.

SARS-CoV-2 (the virus that causes the disease "COVID-19") is a highly transmissible pathogen and can spread easily in crowded jails and prisons where physical distancing is not possible.

7. COVID-19 is a contagious, dangerous and sometimes deadly disease, which can damage the lungs, heart, and brain.[1]

8. The Centers for Disease Control and Prevention (CDC) stresses the necessity of physical distancing to reduce SARS-CoV-2 transmission. As the news website STAT summarized, "the closer you are to someone infectious and the longer you are in contact with them, the

[1] Andrew Joseph et al., *Seven Months Later, What We Know About Covid-19 — and the Pressing Questions that Remain*, STAT (Aug. 17, 2020), https://www.statnews.com/2020/08/17/what-we-now-know-about-covid19-and-what-questions-remain-to-be-answered.

more likely you are to contract the virus."[2] Because the virus can spread through aerosol transmission, ventilation, distancing, and masking are key elements to reducing risk of disease spread.

9. Due to these characteristics, COVID-19 transmission is especially problematic in communal living environments such as colleges and universities, nursing homes, and jails and prisons.

10. Jails and prisons in particular can act as reservoirs of infection and facilitate transmission. Without reducing the incarcerated population, it is impossible to practice physical distancing in jails and prisons. It is therefore not surprising that as of August 2020, 90 of the largest 100 cluster outbreaks in the United States had occurred in prisons and jails.[3] These outbreaks can cause infections to spill over into surrounding communities.[4]

11. As one group of Stanford researchers explains, jails are "an epicenter of COVID-19 transmission in the United States," where the virus can spread 3.6 times faster than aboard the Princess Diamond Cruise ship or over 4 times faster than it spread in Wuhan.[5]

12. Indeed, across the United States, jails and prisons have higher rates of infection and mortality compared to the general public. As of April 9, 2021, at least 392,565 incarcerated individuals have contracted COVID-19 nationwide and at least 2,516 have died from the virus.[6]

13. As of April 8, 2021, every county in Massachusetts had at least 50-99 new cases per 100,000 individuals over the course of the last week; six had 100-199 new cases, four had 200-499, and one had 500-749.[7]

14. Some of this uptick in cases may be caused by the increasing prevalence of SARS-CoV-2 variants in the Commonwealth. The CDC has identified five "variants of concern" for which "there is evidence of an increase in transmissibility, more severe disease (increased deaths), significant reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures."[8]

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[2] *Id.*

[3] Nayanah Siva, *Experts Call to Include Prisons in COVID-19 Vaccine Plans*, The Lancet (Dec. 12, 2020), https://www.thelancet.com/action/showPdf?pii=*S0140*-6736%2820%2932663-5.

[4] American Civil Liberties Union, *Flattening the Curve: Why Reducing Jail Populations is Key to Beating COVID-19*, https://www.aclu.org/report/flattening-curve-why-reducing-jail-populations-key-beating-covid-19?redirect=covidinjails;https://www.medrxiv.org/content/10.1101/2020.04.08.20058842v2.full.pdf.

[5] Edmund L. Andrews, *Stanford Researchers Find COVID-19 Spreads Faster in American Jails Than on Cruise Ships*, Stanford News (Sept. 24, 2020), https://news.stanford.edu/2020/09/24/covid-19-spread-american-prisons.

[6] The Marshall Project, A State-by-State Look at Coronavirus in Prisons, https://www.themarshallproject.org/2020/05/01/a-state-by-state-look-at-coronavirus-in-prisons (last checked April 14, 2021).

[7] White House COVID-19 Team, *COVID-19 State Profile Report – Massachusetts*, https://beta.healthdata.gov/Community/COVID-19-State-Profile-Report-Massachusetts/j75q-tgps (last visited April 14, 2021).

[8] CDC, *SARS-CoV-2 Variant Classifications and Definitions*, https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html (last visited Apr. 15, 2021).

15. These variants include (1) B.1.1.7, which first emerged in the United Kingdom and whose known attributes include an estimated "50% increased transmission" and "likely increased severity based on hospitalizations and case fatality rates"; (2) B.1.351, which first emerged in South Africa and whose known attributes include and estimated "50% increased transmission" and "moderate reduction on neutralization by convalescent and post-vaccination sera"; and (3) P.1, which first emerged in Brazil and whose known attributes include "reduction in neutralization by convalescent and post-vaccination sera."[9]

16. Massachusetts now has reported cases of each of these three variants,[10] and as of April 1, 2021, had more confirmed cases of the P.1 variant than any other state in the country.[11]

17. The CDC recently announced that the B.1.1.7 variant has become the dominant variant in the United States.[12]

18. The CDC has also identified "variants of interest," defined as variants with "specific genetic markers that have been associated with changes to receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity."

19. A variant of interest is B.1.526, which has been spreading in New York faster than B.1.1.7 and has become a substantial fraction of cases in Connecticut.[13] Given this variant's spread, it seems likely that it will spread within Massachusetts, as well.

Post-acute sequelae of SARS-CoV-2 infection (PASC)—including what is often colloquially referred to as "Long Haul COVID-19"— represent a substantial threat to the health of incarcerated individuals, including those who were not hospitalized or only had mild COVID-19 symptoms.

20. We continue to learn more about the long-term medical impacts of COVID-19, but growing anecdotal evidence shows that a significant percentage of individuals—many of whom did not experience severe symptoms at the initial onset of the disease—experience lingering symptoms including fatigue, joint pain, chest pain, shortness of breath, headache, and brain fog. The National Institute of Health has implemented a 3-year study of this "long haul"

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[9] *Id.*
[10] CDC, *US COVID-19 Cases Caused by Variants*, https://www.cdc.gov/coronavirus/2019-ncov/transmission/variant-cases.html (last visited Apr. 15, 2021).
[11] Caroline Enos, *Mass. becomes state with most cases of new COVID-19 variant after Cape Cod outbreaks, Bos. Globe* (Apr. 3, 2021), https://www.bostonglobe.com/2021/04/03/metro/mass-becomes-state-with-most-cases-new-covid-19-variant-after-cape-cod-outbreaks.
[12] Summer E. Galloway et al., Emergence of SARS-CoV-2 B.1.1.7 Lineage — United States, December 29, 2020–January 12, 2021, CDC, https://www.cdc.gov/mmwr/volumes/70/wr/mm7003e2.htm; Nicole L. Washington et al., *Emergence and Rapid Transmission of SARS-CoV-2 B.1.1.7 in the United States*, Cell (2021), https://www.cell.com/cell/pdf/S0092-8674(21)00383-4.pdf.
[13] @NathanGrubaugh, Twitter (Apr. 1, 2021, 4:16PM, https://mobile.twitter.com/NathanGrubaugh/status/1377716444536864769.

COVID-19, which experts estimate could ultimately impact tens of thousands of Americans.

21. In particular, post-acute sequelae of SARS-CoV-2 infection (PASC) includes both long term damage to specific body systems, such as the lungs or heart, due to COVID-19, as well as "long" or "long haul" COVID-19. Although it has not been formally defined, "long" COVID is characterized by an set of symptoms that develop during or after COVID-19 illness - commonly including but not limited to fatigue, post-exertional malaise, and cognitive dysfunction[14] - and continue for an extended period of time. The minimum period of time that symptoms need to last to qualify as "long" COVID is undefined, although one[15] or six[16] months have been used or proposed as thresholds. However, symptoms can extend for much longer than this period of time. A number of recent studies have reported substantial ongoing illness following SARS-CoV-2 infection in patients whose initial onset of COVID-19 illness was not severe enough to become hospitalized. We have reviewed these studies, and summarize their findings below.

22. A large study[17] of the electronic medical records of 190,077 non-hospitalized COVID-19 patients reported that in the six months following COVID-19 diagnosis, 32% of patients received a neurological or psychiatric diagnosis, with 12% receiving a new diagnosis of this type. Although the COVID-19 patients had fewer health-care visits during the six months than matched controls with influenza, they had a 47% higher rate of neurological and psychiatric diagnoses, including an 83% higher rate of first diagnoses. For example, the rate of a first diagnosis of a mood, anxiety, or psychiatric disorder or insomnia was approximately 2 times higher, while the rate of myoneural junction or muscle diagnosis was approximately 3 ½ times higher. The authors conclude there is "substantial neurological and psychiatric morbidity in the 6 months after COVID-19 infection."

23. A study of data from a mobile health application (the COVID Symptom Study app)[18] that included 4,182 members of the general population with a positive COVID-19 test found that 13.3%, 4.5%, and 2.3% of subjects reported symptoms lasting 28 days or longer, 8 weeks or longer and 12 weeks or longer, respectively. Among those with symptoms lasting

[14] Hannah E. Davis et al., *Characterizing Long COVID in an International Cohort: 7 Months of Symptoms and Their Impact*, medRxiv (Dec. 27, 2020), https://www.medrxiv.org/content/10.1101/2020.12.24.20248802v2.full.pdf
[15] *Id.*; see also Carole H. Sudre et al., *Attributes and Predictors of Long COVID*, Nature (Mar. 10, 2021), https://www.nature.com/articles/s41591-021-01292-y.
[16] Anthony Komaroff, *The Tragedy of Long Covid*, Harvard Health Blog (Oct. 15, 2020), https://www.health.harvard.edu/blog/the-tragedy-of-the-post-covid-long-haulers-2020101521173.
[17] Maxime Taquet et al., *6-month Neurological and Psychiatric Outcomes in 236 379 Survivors of COVID-19: a Retrospective Cohort Study Using Electronic Health Records*, The Lancet (Apr. 6, 2021), https://linkinghub.elsevier.com/retrieve/pii/S2215036621000845.
[18] Carole H. Sudre et al., *Attributes and Predictors of Long COVID*, Nature (Mar. 10, 2021), https://www.nature.com/articles/s41591-021-01292-y.

at least 28 days, the most commonly reported symptoms were fatigue, headache, anosmia and lower respiratory symptoms.

24. A patient-led (Body Politic) study[19] paints a picture of what this long lasting illness may look like for those affected. Of 3,762 survey respondents with illness lasting longer than 28 days, of which only approximately 8% of respondents were hospitalized, 67.5% of respondents could not work or required reduced work hours due to their ongoing symptomology. Of those experiencing symptoms at 6 months, over half experienced fatigue, post-exertional malaise, cognitive dysfunction, sensorimotor symptoms, headaches, and memory issues.

25. Patient reports[20] of "long" COVID and statements from experts, including Dr. Anthony Fauci[21], suggest that some "long" COVID patients may already have or may go on to develop myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS). It is estimated that in one year the COVID-19 pandemic has caused the number of patients with ME/CFS in the U.S. to double.[22] In fact, 3% of Body Politic survey takers had already received a diagnosis of ME/CFS, and more likely qualified based on reported symptoms[23]. The CDC describes ME/CFS as "a serious, long-term illness that affects many body systems."[24] They note that many patients develop ME/CFS after an acute infection; however, the cause of ME/CFS is unknown and there are currently no approved cures or treatments. A patient may struggle with ME/CFS for years and more than 25% of ME/CFS patients will be bed- or house-bound for extended periods.[25]

26. The full extent of sequelae of SARS-CoV-2 infection is not yet known. However, the existing evidence suggests that more than one in ten COVID-19 patients— many of whom will not experience severe symptoms at the initial onset of the disease—will experience symptoms, such as fatigue and headache, lasting beyond one month or receive a new neurological or psychiatric diagnosis within 6 months of COVID-19 diagnosis. A subset of COVID-19 patients already display the hallmarks of ME/CFS, a poorly-understood illness capable of causing severe disability.

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[19] Davis et al., *supra* n.16.
[20] *Id.*
[21] Anthony L. Komaroff and Lucinda Bateman, *Will COVID-19 Lead to Myalgic Encephalomyelitis/Chronic Fatigue Syndrome?*, Frontiers in Medicine (Jan. 18, 2021), https://www.frontiersin.org/articles/10.3389/fmed.2020.606824/full.
[22] *Id.*
[23] Davis et al., *supra* n.16.
[24] CDC, *Myalgic Encephalomyelitis/Chronic Fatigue Syndrome*, https://www.cdc.gov/me-cfs/index.html (last visited Apr. 15, 2021).
[25] *Id.*

Testing of individuals without symptoms is necessary to stem the tide of COVID-19 infections in Massachusetts jails and prisons.

27. It is well recognized that SARS-CoV-2 infected individuals are infectious before they develop symptoms and even if they never develop recognizable symptoms. These pre-symptomatic and asymptomatic infected individuals are important contributors to transmission.[26]

28. For example, after a skilled nursing facility in Washington screened all residents for COVID-19 - of positive residents, 56% did not have symptoms when tested. Researchers found that the majority of these pre-symptomatic individuals shed infectious virus one to six days before symptom development.[27]

29. Mass testing that is conducted only after a symptomatic case has been detected is too delayed to contain outbreaks in a prison setting. A Montgomery County, PA facility that tested all incarcerated individuals found that 177 of 948 were positive with 171 (97%) having no symptoms at the time of testing,[28] while a Goldsboro, NC facility found 444 of 723 total incarcerated individuals were positive, 98% of whom were asymptomatic.[29] Similar findings have been reported by facilities across the United States in Arkansas, Ohio, Virginia, Michigan, and Tennessee,[30] and an August CDC Report demonstrated "that mass testing in 16 U.S. prisons and jails found a 12-fold increase over the number of cases identified through symptoms alone."[31]

30. Pre-symptomatic and asymptomatic cases play an important role in transmission,[32] and

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[26] Seyed M. Moghadas et al., *The Implications of Silent Transmission for the Control Of COVID19 Outbreaks*, Proc. Natl. Acad. Sci. U. S. A. (July 6, 2020); Anne Kimball et al., *Asymptomatic and Presymptomatic SARS-CoV-2 Infections in Residents of a Long-Term Care Skilled Nursing Facility - King County, Washington*, 69 MMWR Morb. Mortal. Wkly. Rep. 377–81 (Apr. 3, 2020); Melissa M. Arons et al., *Presymptomatic SARS-CoV-2 Infections and Transmission in a Skilled Nursing Facility*, N. Engl. J. Med. (Apr. 24, 2020); W.E. Wei et al., *Presymptomatic Transmission of SARS-CoV-2 - Singapore, January 23-March 16, 2020*, 69 MMWR Morb. Mortal. Wkly. Rep. 411–15 (June 27, 2020); Zhanwei Du et al., *Serial Interval of COVID-19 among Publicly Reported Confirmed Cases*, 26 Emerging Infectious Disease 1341–43 (Mar. 19, 2020); Xi He et al. *Temporal Dynamics in Viral Shedding and Transmissibility of COVID-19*, Nature Medicine (Apr. 15, 2020).

[27] Melissa M. Arons et al., *Presymptomatic SARS-CoV-2 Infections and Transmission in a Skilled Nursing Facility*, N. Engl. J. Med. (Apr. 24, 2020).

[28] Jeremy Roebuck and Allison Steele, *Montgomery County's Jail Tested Every Inmate for COVID-19 — and Found 30 Times More Cases than Previously Known*, Philadelphia Inquirer (Apr. 28, 2020).

[29] Linda So and Grant Smith, *In Four U.S. State Prisons, Nearly 3,300 Inmates Test Positive for Coronavirus -- 96% Without Symptoms*, Reuters (Apr. 25, 2020).

[30] *Id.*

[31] Cid Standifer and Frances Stead Sellers, *Prisons and Jails Have Become a 'Public Health Threat' During the Pandemic, Advocates Say*, Washington Post (Nov. 11, 2020), https://www.washingtonpost.com/national/coronavirus-outbreaks-prisons/2020/11/11/b8c3a90c-d8d6-11ea-930e-d88518c57dcc_story.html.

[32] Seyed M. Moghadas et al., *The Implications of Silent Transmission for the Control Of COVID19 Outbreaks*, Proc. Natl. Acad. Sci. U. S. A. (July 6, 2020); Anne Kimball et al., *Asymptomatic and Presymptomatic SARS-CoV-2 Infections in Residents of a Long-Term Care Skilled Nursing Facility - King County, Washington*, 69 MMWR Morb. Mortal. Wkly. Rep. 377–81 (Apr. 3, 2020); Melissa M. Arons et al., *Presymptomatic SARS-CoV-2 Infections and Transmission in a Skilled Nursing Facility*, N. Engl. J. Med. (Apr. 24, 2020); W.E. Wei et al., *Presymptomatic*

research suggests that outbreaks occur even with the immediate isolation of all symptomatic cases.[33]

31. Thus, public health and infectious diseases researchers and officials recognize that, particularly in vulnerable communal living environments, the frequent testing of individuals without symptoms is necessary to contain the pandemic.[34]

32. Testing is all the more important given the growing prevalence of the B.1.1.7 and P.1 variants in the Commonwealth and the expectation that B.1.526 will spread here as well. Because these variants are estimated to be 50% more transmissible, even more testing of non-symptomatic individuals is necessary to prevent an outbreak.

33. Recent research from Larremore, *et al*. compared different testing strategies in simulated populations, including varying testing frequency, test sensitivity, and the amount of time from sample collection to result return.[35] They assumed that 35% of infected individuals would self-isolate due to symptoms around the time of their peak viral load without testing, while 65% would not be detected without testing. The authors found that total infectiousness was reduced by 62-66% for weekly testing, and 45-57% under biweekly testing, although some of this reduction was due to self-isolation (**Fig. 2**). The authors determined that symptom-based screening alone was insufficient to control case numbers and that surveillance testing should emphasize frequency and the time from obtaining the sample to receiving results. In simulations of a large university setting, the authors conclude "direct examination of simulations showed that … screening weekly with either [test] effectively attenuated surges of infections".

34. A similar study used modeling to compare testing strategies in a college population and found that symptom-based screening alone did not control dormitory outbreaks under any of the considered scenarios.[36]

Transmission of SARS-CoV-2 - Singapore, January 23-March 16, 2020, 69 MMWR Morb. Mortal. Wkly. Rep. 411–15 (June 27, 2020); Zhanwei Du et al., *Serial Interval of COVID-19 among Publicly Reported Confirmed Cases*, 26 Emerging Infectious Disease 1341–43 (Mar. 19, 2020); Xi He et al. *Temporal Dynamics in Viral Shedding and Transmissibility of COVID-19*, Nature Medicine (Apr. 15, 2020).

[33] Seyed M. Moghadas et al., *The Implications of Silent Transmission for the Control Of COVID19 Outbreaks*, Proc. Natl. Acad. Sci. U. S. A. (July 6, 2020).

[34] Daniel B. Larremore, et *al*, *Test Sensitivity Is Secondary to Frequency and Turnaround Time for COVID-19 Screening*, Science Advances (Nov. 20, 2020).

[35] *Id*.

[36] A. David Paltiel et al., *Assessment of SARS-Cov-2 Screening Strategies to Permit the Safe Reopening of College Campuses in The United States*, 3 JAMA Open Network (July 31, 2020).

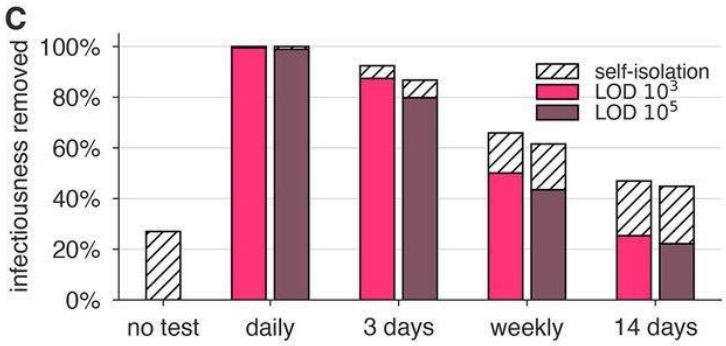

Figure 2: Figure 1c from Larremore, et al.[37] shows that the total infectiousness of 10,000 simulated individuals was reduced by 62-66% and 45-57% for weekly and biweekly testing, respectively, although some of the reduction occurred due to self-isolation after symptom development (shown by the cross-hatch pattern). More frequent testing resulted in additional dramatic decreases in total infectiousness. The pink and maroon colors represent two different SARS-CoV-2 tests with different limits of detection (LOD) for the virus, and the cross-hatch pattern represents reductions in total infectiousness from self-isolation due to symptom development.

35. Slovakia performed mass testing of their population (combined with isolation of identified cases with their family members). A study of Slovakia's mass testing strategy found that in counties with two rounds of weekly mass testing, the prevalence of detected infections dropped approximately 60% between rounds.[38]

36. For prisons, failing to conduct regular testing of asymptomatic individuals decreases the likelihood of identifying cases, preventing outbreaks, and limiting the number of individuals who develop symptomatic disease, including those that manifest in severe disease and death. Simulations of a university setting showed that weekly testing with prompt return of results effectively controlled case numbers,[39] while symptom-based screening only did not prevent outbreaks.[40] To the extent that testing frequency decreases and test results are delayed, testing will be less effective for controlling outbreaks because infected individuals cannot be identified and isolated. Testing non-symptomatic individuals only at intake, or only once every few months, is not an effective strategy to prevent disease transmission. Because individuals can be infected once they are incarcerated, such infrequent testing will not identify non-symptomatic cases before the virus can spread broadly amongst incarcerated individuals and staff.

37. Testing that only targets symptomatic individuals is useful for diagnosis and identifying the cause of death, but testing must be frequent and target asymptomatics as well if it is to prevent disease transmission. Testing non-symptomatic individuals only after a

[37] Larremore, *supra* n.24.
[38] Martin Pavelka et al., *The Effectiveness of Population-Wide, Rapid Antigen Test Based Screening in Reducing SARS-Cov-2 Infection Prevalence in Slovakia*, medRxiv (Dec. 4, 2020).
[39] Larremore, *supra* n.24.
[40] Larremore, *supra* n.24; Paltiel, A. D., Zheng, A. & Walensky, R. P. Assessment of SARS-CoV-2 Screening Strategies to Permit the Safe Reopening of College Campuses in the United States. *JAMA Netw Open* **3**, e2016818 (2020).

symptomatic case is discovered similarly will not prevent the virus from spreading broadly amongst incarcerated individuals and staff.

38. In situations in which the prevalence of infection is anticipated to be low, it is possible to pool samples to monitor a facility for cases. In such "batch testing," further individual testing is required only in the event of a positive result.[41]

39. Testing protocols at congregate facilities in Massachusetts and throughout the country reflect the reality that regular testing of pre-symptomatic and asymptomatic people is central to public health.

40. For example, ICE protocols now recognize that "expanded testing strategies are a critical tool in the prevention and management of COVID-19 infections," and mandates that "all new admissions to ICE detention facilities require COVID-19 testing within 12 hours of arrival."[42] The speed with which testing should be done underscores as well the importance of the speed of returning the results, so that appropriate measures can be taken if the results return positive.

41. At the same time, the Executive Office of Health and Human Safety requires all skilled nursing facilities, rest homes and assisted living residences to conduct weekly testing of all non-vaccinated staff, and bi-weekly testing of fully-vaccinated staff.[43]

42. Similarly, more than 100 New England colleges have tested all of their students once or twice a week.[44] According to Stacey Gabriel at the Broad Institute, "schools that have done frequent testing of asymptomatic students have kept their rates at well below 1% positivity, whereas schools that use another approach of only testing symptomatic or only contacts of positives, have a rate at least tenfold higher."[45]

43. Routine and large-scale testing was a core element of the safe resumption of the 2019-20 and 2020-21 NBA seasons, demonstrating the utility of testing to promote an environment in which individuals engage safely in high-risk activities, such as playing basketball while unmasked.

44. Regular testing in jails and prisons for individuals who are not symptomatic is similarly an important factor to interrupt transmission chains in these facilities, thereby preventing outbreaks and helping our state to contain the pandemic.

45. An editorial in the New England Journal of Medicine called for regular testing of

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[41] Centers for Disease Control and Prevention, *Interim Guidance for Use of Pooling Procedures in SARS-CoV-2 Diagnostic, Screening, and Surveillance Testing* (2020), https://www.cdc.gov/coronavirus/2019-ncov/lab/pooling-procedures.html.
[42] U.S. Immigration and Customs Enforcement, Enforcement and Removal Operations, *COVID-19 Pandemic Response Requirements*, 33 (Oct. 27, 2020), https://www.ice.gov/doclib/coronavirus/eroCOVID19responseReqsCleanFacilities.pdf.
[43] March 12, 2021 Updates
[44] Carey Goldberg, *Initial Results from a Massive Experiment: Over 3 Million Coronavirus Tests at New England Colleges*, WBUR (Nov. 25, 2020), https://www.wbur.org/commonhealth/2020/11/25/on-campus-testing-colleges-broad.
[45] *Id.*

asymptomatic individuals in correctional facilities, writing "this recommendation for SARS-CoV-2 testing of asymptomatic persons...should most likely be expanded to other congregate living situations, such as prisons and jails."[46]

46. Most notably, in its March 17, 2021 updated guidance for testing in correctional and detention facilities, the CDC explains that screening testing—which is "viral testing of asymptomatic staff or incarcerated/detained persons without known or suspected exposure to SARS-CoV-2," otherwise known as surveillance testing—"is a key component of a layered approach to prevent SARS-CoV-2 transmission" in carceral settings.[47]

47. The CDC's March 17, 2021 guidance instructs that "screening testing for staff should be considered in all facilities" including "testing of all staff before entering the facility every 3-7 days."[48]

48. The CDC also instructs that "facilities should consider implementing serial screening testing among additional incarcerated/detained persons" who are not symptomatic and have no known contact with an infected individual every 3-7 days.[49]

49. The CDC emphasizes that "testing any less frequently than once a week is unlikely to be effective in identifying recently infected asymptomatic persons who need to be isolated" and that "outbreak control depends largely on the frequency of testing and the speed of returning results."[50]This matches the findings of the studies we discussed above.

50. It is our understanding that the CDC does not have the authority to require jails and prisons to implement any particular testing policy. However, it is our expert opinion, based on our experience reviewing CDC guidelines in other contexts, that the CDC's March 17 updated guidance for testing in correctional and detention facilities is the agency's strong recommendation that jails and prisons implement routine, comprehensive testing of non-symptomatic incarcerated people and staff in jails and prisons where there are no asserted resource constraints.

51. Based on our expert opinion, and as reflected in the policies and protocols described above, routine testing of pre-symptomatic and asymptomatic individuals in jails and prisons is the medical standard of care to protect the public health of prisoners, staff and the surrounding community.

The failure of the Houses of Correction to conduct routine, comprehensive testing of asymptomatic and pre-symptomatic prisoners and staff means that they cannot take effective action to protect the incarcerated population from COVID-19.

52. The fact that many cases are initially pre-symptomatic or asymptomatic but can still be infectious means that the vast majority of cases among incarcerated individuals cannot be

[46] Monica Gandhi et al., *Asymptomatic Transmission, the Achilles' Heel of Current Strategies to Control Covid-19*, N. Engl. J. Med. (May 28, 2020).
[47] https://www.cdc.gov/coronavirus/2019-ncov/community/correction-detention/testing.html
[48] *Id.*
[49] *Id.*
[50] *Id.*

identified in time if there is no regular testing of prisoners without symptoms. If infections are not identified due to a lack of testing, the facility cannot take effective action to protect the rest of its incarcerated population from exposure and infection.

53. It is our understanding that the Houses of Correction are not conducting routine, comprehensive testing of non-symptomatic prisoners and staff. It is our expert opinion that the Houses of Correction are not conducting the level of testing necessary to identify infected prisoners and staff and that the Houses of Correction therefore lack the information necessary to take steps to protect uninfected people in the facilities.

54. The positive impact of quarantining, masking, distancing and hygiene is severely limited if the facilities do not first identify infectious individuals through routine testing. Sufficient testing of the incarcerated individuals and staff is a fundamental and necessary predicate to preventing the spread of COVID-19 in a communal living facility. Because asymptomatic and pre-symptomatic individual can be infectious, relying only on symptom screening is insufficient to prevent introductions of COVID-19 and to keep prisoners and staff safe.

55. There is no medical or scientific reason to avoid conducting more tests of prisoners and staff. If the discovery of more cases through sufficient testing leads to a logistical burden on the Houses of Correction, the proper medical answer is not to stop looking for cases, but rather to make other changes —such as decarceration—to ease the logistical burden of properly addressing any positive cases.

56. The failure of the Houses of Correction to regularly test individuals without symptoms means that their reported number of confirmed positive cases are not meaningful indicators of how many people are actually infected with COVID-19 at each facility, given the incidence of asymptomatic and pre-symptomatic infections.

57. The medical need for the Houses of Correction to regularly test individuals without symptoms continues to exist despite the fact that they are now offering the vaccine to incarcerated people and staff.

58. First, it is our understanding that there is a high turnover of incarcerated people in the Houses of Correction. Given that it takes weeks for the vaccines to confer full effectiveness, routine testing of non-symptomatic people is critical to preventing outbreaks amongst the constantly changing population.

59. Second, studies have already shown that the Johnson & Johnson vaccine is less effective at preventing infection from the B.1.351 and B.1.1.7 variants,[51] and experts anticipate that the other vaccines may similarly be less effective against these and other variants. Given this uncertainty, routine testing of non-symptomatic people remains a necessary step to prevent outbreaks. Reflecting this reality, the Executive Office of Health and Human Services (EOHHS) continues to require bi-weekly testing of all vaccinated staff and weekly testing of all non-vaccinated staff.

[51] https://www.forbes.com/sites/williamhaseltine/2021/02/01/novavax-and-johnson--johnsons-vaccines-are-less-effective-against-the-uk-and-south-african-variants/?sh=b9fa66468e4f

The claim that individuals are more protected from COVID-19 infection within jails and prisons than in the community is unsupported and misleading.

60. Our understanding is that several Sheriffs have submitted affidavits suggesting that incarcerated individuals are safer within their facilities than in the general population. For example, Sheriff Cummings asserted, "it has been established that the inmates are far safer from the COVID-19 virus inside the Barnstable County Correctional Facility than in the community." Ex. 2a (Cummings Aff., ¶ 14). Similarly, Sheriff Quinn stated, "the inmates proved to be far safer inside the Berkshire County Jail and House of Correction than in the community." Ex 2a (Quinn Aff., ¶ 15).

61. To make these assertions, the Sheriffs largely rely on a comparison between the purportedly lower case rates within their facilities to the higher case rates in the general population. *See, e.g.*, Ex. 2a (Cummings Aff., ¶ 14); Ex 2a (Quinn Aff., ¶ 15). But for several reasons, this comparison does not demonstrate that individuals are more protected from COVID-19 within a carceral facility.

62. First, numerous facilities have such a low number of tests to render their case rates practically meaningless. For example, Barnstable has tested just four incarcerated individuals since October 14, 2020, and in the more than three months since this case was filed, Bristol, Hampshire, and Berkshire have tested only 99, 86, and 56 incarcerated individuals, respectively. Facilities cannot assert that incarcerated individuals and staff members are safe from a danger that they are not actually measuring.

63. Second, comparing the danger posed by COVID-19 within the general population to the danger posed by COVID-19 in prison is not an apples-to-apples comparison. That is because the risk and rate of spread in congregate settings are much higher than in the community, as has repeatedly been observed in nursing homes, long-term care facilities, and jails. As the Governor explained, the very reason that incarcerated individuals are included in phase one of the vaccination plan is "because of the possibility of outbreak and the heightened risk of close quarters."[52]

64. Third, because jails and prisons are not closed environments, spread in the surrounding community can meaningfully impact the introduction and spread of COVID-19 within the facility itself. Staff members from the surrounding communities enter the facilities every day, presenting daily opportunities for the virus to enter the facility. It is therefore not surprising that the CDC recommends that jurisdictions should consider expanding testing to individuals without symptoms in a variety of settings, including jails and prisons, when the case rates in the surrounding communities are high.[53]

[52] *Gov. Baker Defends Decision to Vaccinate Inmates Before General Public*, NBC Boston (Jan. 14, 2021), https://www.nbcboston.com/news/local/gov-baker-defends-decision-to-vaccinate-inmates-before-general-public/2280523.

[53] CDC, *CDC Guidance for Expanded Screening Testing to Reduce Silent Spread of SARS-CoV-2* (Jan. 21, 2021), https://www.cdc.gov/coronavirus/2019-ncov/php/open-america/expanded-screening-testing.html.

65. Given these issues, the suggestion that individuals are more protected from COVID-19 while incarcerated than in the community is unsupported and misleading.

Dr. Wurcel's January 14, 2021 affidavit does not provide any scientific or medical justification to support her decision not to recommend routine, comprehensive testing of non-symptomatic incarcerated individuals.

66. We have reviewed Dr. Alysse Wurcel's January 14, 2021 affidavit submitted in this case. (Ex. 3). In that affidavit, Dr. Wurcel states "[a]t this point, I have not recommended facility-wide repetitive surveillance testing in the jails." (Ex. 3 ¶9). In our professional opinion, there is no scientific or medical justification for this decision.

67. Dr. Wurcel's January 14, 2021 affidavit states that "[t]he CDC does not discuss or recommend for facility-wide repetitive surveillance testing in the most recent guidelines," (Ex. 3 ¶9), but that was not and is not correct.

68. At the time that Dr. Wurcel submitted her affidavit on January 14, 2021, the CDC's guidance for "Testing in Correctional and Detention Facilities" instructed that "correctional and detention facilities may consider testing asymptomatic individuals without known or suspected SARS-CoV-2 exposure in communities with moderate to substantial levels of community transmission."[54] Moreover, the CDC's "Guidance for Expanded Screening Testing to Reduce Silent Spread of SARS-CoV-2" similarly emphasized that jurisdictions should consider expanding testing of non-symptomatic individuals and explicitly included residents and staff in correctional facilities to prioritize for such expanded testing.[55]

69. Additionally, as explained above, the CDC's updated guidelines now strongly recommends that jails and prisons conduct routine, comprehensive testing of non-symptomatic incarcerated individuals and staff where there are no asserted resource constraints on testing.

70. Dr. Wurcel's January 14, 2021 affidavit suggests that her recommendations are in line with DPH recommendations. (Ex 3 ¶9). To our knowledge, DPH has not created or issued any guidelines regarding testing in Massachusetts jails and prisons, and Dr. Wurcel does not cite to any such guidance. Instead, Dr. Wurcel January 14, 2021 affidavit states, "I asked DPH if jails should consider universal screening, meaning testing each individual in the jail regardless of the conditions in the jail. At the time, during the spring of 2020, DPH did not recommend universal screening." (Ex. 3 ¶11).

71. Based on this statement, it is our understanding that as of January 14, 2021, Dr. Wurcel had not spoken to DPH about routine, comprehensive testing since this spring. If that is

[54] CDC, *Interim Considerations for SARS-CoV-2 Testing in Correctional and Detention Facilities*, (Dec. 3, 2020), https://www.cdc.gov/coronavirus/2019-ncov/community/correction-detention/testing.html.
[55] CDC, *CDC Guidance for Expanded Screening Testing to Reduce Silent Spread of SARS-CoV-2*, (Jan. 21, 2021), https://www.cdc.gov/coronavirus/2019-ncov/php/open-america/expanded-screening-testing.html.

the case, the advice is outdated and should no longer be relied upon for any medical decision.

72. Over the course of the last year, there has been a rapid evolution of testing recommendations based on our increased understanding about the asymptomatic spread of COVID-19, the growth of our testing capacity, and the explosion of community spread throughout the Commonwealth. Medical and scientific consensus no longer supports the recommendation to avoid routine, comprehensive testing where there have been no allegations that there are practical impediments to such testing.

The release of detained and incarcerated individuals is key to slowing the spread of COVID-19 within Massachusetts Houses of Correction, reducing strain on the healthcare infrastructure, and limiting the number of cases and deaths from COVID-19.

73. Slowing the spread of COVID-19 in jails is important to reduce the overall number of people infected, reduce the strain on the healthcare system, and provide time for the development of new therapies and interventions. This has become all the more important now that widespread availability of a vaccine is on the horizon within the next 6-12 months that could help save the lives that have not already been lost by that point.

74. It is our understanding that jails have an even higher turnover of individuals than prisons, as pre-trial admissions routinely enter the facilities. With more individuals coming and going, and more interactions among individuals, the risk of an outbreak increases as does the speed at which any outbreak would spread.

75. This is especially true because physical distancing, a cornerstone of reducing COVID-19 transmission, is exceptionally difficult within jails. Decreasing the incarcerated population is the only way to increase the ability of the remaining individuals to physically distance.

76. Release has the dual advantage of allowing for more space between people and reducing the overall number of individuals contacted by each person. For example, a person isolating at home can prepare meals, administer medications, and engage in most other activities of daily living without interacting with others. By reducing the contact rate and the number of contacts, the spread of COVID-19 will be limited.

77. Releasing prisoners whenever it is safe to do so is a key public health objective. In a piece published in the New England Journal of Medicine, Drs. Akiyama, Spaulding and Rich emphasized that jails and prisons need to decarcerate "as many people as possible" to "limit the impact of COVID-19 transmission," noting that "[e]ach person needlessly infected in the correctional setting who develops severe illness will be one too many."[56]

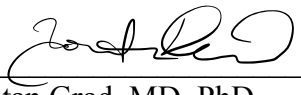
78. Similarly, a recent National Academies of Science, Engineering, and Medicine (NASEM) report concluded, "decarceration is an appropriate and necessary mitigation strategy to

[56] Matthew J. Akiyama et al., *Flattening the Curve for Incarcerated Populations — Covid-19 in Jails and Prisons*, New England Journal of Medicine (May 28, 2020), https://www.nejm.org/doi/full/10.1056/NEJMp2005687.

include in the COVID-19 response in correctional facilities" and would improve "the safety of incarcerated and detained people and correctional staff."[57]

79. It is our expert opinion that in the absence of decarceration efforts and extensive testing accompanied by case identification and isolation to block transmission, the ability of the virus to spread from asymptomatic and pre-symptomatic infected individuals means that outbreaks in the Houses of Correction increase in likelihood with rising community spread throughout the Commonwealth.

Signed under the pains and penalties of perjury on April 19, 2021.



Yonatan Grad, MD, PhD

Signed under the pains and penalties of perjury on April 19, 2021.

Emma Accorsi, BS

[57] National Academies of Sciences, Engineering, and Medicine, *Decarcerating Correctional Facilities during COVID-19: Advancing Health, Equity, and Safety* (2020), S-2, https://www.nap.edu/catalog/25945/decarcerating-correctional-facilities-during-covid-19-advancing-health-equity-and.

EXHIBIT A

YONATAN H. GRAD CURRICULUM VITAE

Date Prepared: 19 November 2020

NAME: Yonatan H. Grad
ACADEMIC TITLE: Melvin J. and Geraldine L. Glimcher Associate Professor of Immunology and Infectious Diseases
WORK ADDRESS: 665 Huntington Avenue
Building 1, Room 715
Boston, Mass. 02115
EMAIL: ygrad@hsph.harvard.edu

EDUCATION:

1996	Chemistry	B.A.	Johns Hopkins University
1997	Biological Sciences	M.Phil	Cambridge University
2004	Genetics	Ph.D.	Harvard Medical School
2006	Medicine	M.D.	Harvard Medical School

POSTDOCTORAL TRAINING:
Research Fellowships:

2010-2014	Dept of Epidemiology	Research Fellow	Harvard TH Chan School of Public Health

Internships and Residencies:

2006-2007	Internal Medicine	Intern	Brigham and Women's Hospital
2007-2009	Internal Medicine	Resident	Brigham and Women's Hospital
11/2008-2/2009	Internal Medicine	Chief Medical Resident	Faulkner Hospital
2009-2011	Infectious Diseases	Clinical Fellow	Brigham and Women's Hospital Massachusetts General Hospital

ACADEMIC APPOINTMENTS:

2012-Present	Instructor	Department of Medicine	Harvard Medical School
2015-2020	Assistant Professor	Department of Immunology and Infectious Diseases	Harvard T.H. Chan School of Public Health
2020-present	Associate Professor	Department of Immunology and Infectious Diseases	Harvard T.H. Chan School of Public Health

HOSPITAL/AFFILIATED INSTITUTIONAL APPOINTMENTS:

2011-Present	Associate Physician	Brigham and Women's Hospital
2011-2013	Associate Medical Staff	MIT Medical

LICENSURE AND CERTIFICATION:

2009	Massachusetts Medical License
2010	ABIM Board Certification in Internal Medicine
2011	ABIM Board Certification in Infectious Diseases

OTHER PROFESSIONAL APPOINTMENTS

2015-Present	Associate Member	Broad Institute of Harvard and MIT

COMMITTEE SERVICE:

DEPARTMENTAL/SCHOOL AND UNIVERSITY SERVICE:

1998 – 2001	Admissions Committee, Harvard-MIT Division of Health Science and Technology, Harvard Medical School
2008 - 2009	MD-PhD Grand Rounds, Brigham and Women's Hospital – Harvard Medical School, Resident organizer / Presenter
2013	Review of HST040 "Mechanisms of Microbial Pathogenesis", HST Curriculum Committee
2014 – Present	Interviewer, HMS MD-PhD Admissions Committee
2015 – Present	PQE Committee, Departments of Systems Biology and Immunology and Infectious Diseases
2015 – Present	Immunology and Infectious Diseases Department Dissertation Defense Committee
2015 – Present	Dissertation Advisory Committees for students at MIT (Biological Engineering) and Harvard (both Systems Biology and Biological Sciences in Public Health graduate programs)
2016 – Present	Biological Sciences in Public Health PhD Program Admissions Committee
2016 – 2018	Biological Sciences in Public Health Retreat Committee
2018 – Present	Harvard College Postgraduate Public Service Selection Committee
2018 – Present	Harvard College Evaluation Committee for the Fulbright Program
2018	Executive Committee of the Leadership Council presentation

2019 – Present	HSPH Faculty Council
2020 – Present	Committee on Microbiologic Safety

REGIONAL COMMITTEE SERVICE:

2020	Commonwealth of Massachusetts COVID-19 Task Force

NATIONAL COMMITTEE SERVICE:

2013 – Present	Infectious Disease Laboratory Working Group of the Board of Scientific Counselors, Office of Infectious Diseases, Centers for Disease Control and Prevention
2016	External review panel, Advanced Molecular Detection program of the US Centers for Disease Control and Prevention
2017	Invited member, US Centers for Disease Control and Prevention-Association for Public Health Laboratories "Gono-caucus 2017: Defining Multi-drug Resistant *Neisseria gonorrhoeae*"
2019 – 2020	Invited member, 2020 STD Prevention Conference Scientific Program committee (Clinical & Laboratory Domain)
2020 – 2024	NIH Study Section MIDS-B Standing Member

PROFESSIONAL SOCIETIES:

2011 – Present	Infectious Diseases Society of America
2012 – Present	American Society of Microbiology

HONORS AND DISTINCTIONS:

1994	Barry Goldwater Scholar	National
1995	Kilpatrick Prize	Johns Hopkins University
1995	Phi Beta Kappa	Johns Hopkins University
1996	Churchill Scholar	Winston Churchill Foundation
1997-2006	Medical Scientist Training Program Award	National Institutes of Health

2007	Resident/Mentor Teaching Award, Department of Medicine	BWH
2010	Fellowship Teaching Award, Department of Medicine	BWH
2012	Developmental Award	American Sexually Transmitted Diseases Association
2014	The Maxwell Finland Award for Excellence in Research	Massachusetts Infectious Disease Society
2016	ICAAC Young Investigator Award	American Society for Microbiology
2016	Clinical Scientist Development Award	Doris Duke Foundation
2016	Milton Fund Award	Harvard University
2019	ASTDA Young Investigator Award	American Sexually Transmitted Diseases Association

FUNDED GRANTS AND PROJECTS:

Completed Grants:

07/01/2013 – 09/30/2016
NIH
K08AI104767 (Grad)
Role: Principle Investigator
Total Direct Cost: $305,671
Genomic epidemiology of Neisseria gonorrhoeae with elevated MICs to cefixime
In this project, I aim to study the rising prevalence of gonococcal isolates with reduced susceptibility to the oral extended spectrum cephalosporin cefixime in the US.

05/01/2016 – 10/31/2017
Bill & Melinda Gates Foundation
OPP1151010 (Hanage)
Role: Principle Investigator
Total Direct Cost: $8,222
From Clinic to Cloud: Crowdsourcing resistance surveillance
The goal of this project is to develop a "clinic to cloud" approach for directly sequencing patient samples, inferring the presence of antibiotic resistance-associated sequencing, and collating that information for use in patient care and molecular epidemiology.

01/01/2016 – 12/31/2017
NIH (Broad Institute)
R21AI121932 (Blainey/Grad)
Role: Principle Investigator

Total Direct Cost: $49,641
Microfluidic sample preparation for genomic sequencing of clinical pathogen isolates
Our goal is to demonstrate the utility of a microfluidic device in pipelines for pathogen genome sequencing. To do so, we will sequence and analyze MRSA genomes obtained from Project CLEAR, a clinical trial investigating the impact of S. aureus decolonization protocols on S. aureus-associated morbidity and mortality.

07/01/16–06/30/19
CDC (Harvard Pilgrim Health Care Institute)
U54CK000484 (PI: Platt)
Role: Site PI
Total Direct Cost: $220,961 (subaward)
Epicenter IV: CLUSTER Trial for Outbreak Detection and Response
This project compares two approaches to predicting nosocomial pathogen outbreaks. We will use genome sequencing and analysis to quantify the mean pairwise genetic distance between outbreak isolates predicted by both methods and thereby assess the relative accuracy of the methods.

09/30/14–09/29/19
CDC (Stanford University)
NU38PS004644 (PI: Salomon)
Role: Co-Investigator
Total Direct Cost: $42,061 (subaward)
Prevention Policy Modeling Lab
Dr. Grad will contribute expertise in bioinformatics and genomics, particularly relating to gonorrhea projects. Responsibilities will include contribution to development of study questions, modeling strategies, data acquisition, parameterization of models, and interpretation of the results. He will contribute to preparation of manuscripts and modeling tools and dissemination of results and tools at scientific meetings, meetings with other stakeholders, and public release of modeling tools.

01/01/16 – 09/30/19
Richard and Susan Smith Family Foundation
No award No. (Grad)
Role: Principle Investigator
Total Direct Cost: $285,714
Genetic networks of antibiotic resistance in Neisseria gonorrhoeae
This project focuses on understanding the mechanisms of how strains of resistant bacteria emerge and spread, with the aim of developing novel strategies to prevent and treat resistant infections.

Active Grants:

07/01/18-01/07/2021
CDC (Social & Scientific System, Inc.)
Contract HHSN2722013000141, Task Order # HHSN27200011 (PI: Morris)

Role: Co-Investigator
Total Direct Cost: $171,834 (subaward)
Pilot Study of Whole Genomic Sequencing to Detect Reduced Antibiotic Susceptibility in Neisseria gonorrhoeae
For this proposal, the lab plans to culture isolates, and either generate the sequencing libraries in house or use local core facilities for library construction and sequencing. We will then analyze the results, linking the antibiotic susceptibility data (tests performed in another laboratory collaborating on this study) together with the genome sequences to define whether genetic elements known or suspected to contribute to resistance are present, and to determine the positive and negative predictive values of these elements.

07/01/16 – 12/31/20
Doris Duke Charitable Foundation – Clinical Scientist Development Award
Grant No. 2016092 (Grad)
Role: Principle Investigator
Total Direct Cost: $450,000
Using pathogen genomics and patient data to define determinants of persistent MRSA colonization and of success of decolonization
We aim to create a framework that considers factors from the patient and the colonizing MRSA strain to predict who is likely to benefit from decolonization protocols. To do so, we will analyze data from a randomized controlled clinical trial of decolonization that is unprecedented in its size and simultaneously examine host and pathogen attributes, including MRSA whole genome sequences and phenotypes. We will develop risk models for persistent MRSA carriage and MRSA infections and provide a framework to develop tools to assess and modify the factors that contribute to persistent colonization.

08/01/17 – 07/31/20
CDC (University of Utah)
U01CK000538 (Lipsitch)
Role: Co-Investigator
Total Direct Cost: $42,192 (subaward)
Modeling and Simulation to Support Antibiotic Stewardship and Epidemiological Decision-Making in Healthcare Settings
For project 1, we propose to obtain one or more data sets to estimate each quantity in the Bystander Selection Model, and will perform the analyses specified in the proposal. For project 2, working with Dr. Samore, we propose to define the most appropriate data sets from the VA database for analysis, and to select the alert threshold algorithms of greatest practical and clinical interest.

01/15/20 – 01/14/21
Harvard T.H. Chan School of Public Health
No award No. (Grad)
Role: Principle Investigator
Total Direct Cost: $100,000
Harvard Chan School of Public Health Acceleration Award

The two aims of this proposal are to define the drivers of the decline in outpatient antibiotic prescribing in a national dataset and to determine the drivers of geographic heterogeneity in antibiotic prescribing in the US.

03/01/20 – 02/28/22
Wellcome Trust
219812/Z/19/Z (Grad)
Role: Principle Investigator
Total Direct Cost: $300,517
Reducing antibiotic prescribing through a prioritized vaccination strategy
In this proposal, we will evaluate the association of PCV13 uptake on the recent declines in outpatient antibiotic prescribing in the US and estimate the antibiotic prescribing attributable to the most common pathogens and variation by age, demographic, and geography.

07/01/17 – 6/30/22
NIH/NIAID
R01AI132606 (Grad)
Role: Principle Investigator
Total Direct Cost: $1,250,000
Genomics approaches to elucidating pathways to antibiotic resistance in Neisseria gonorrhoeae
This project focuses on understanding the compensatory and enabling mutations that facilitate acquisition and maintenance of antibiotic resistance in the common pathogen Neisseria gonorrhoeae, the cause of the sexually transmitted disease gonorrhea.

07/01/20 – 6/30/25
NIH/NIAID
R01AI153521 (Grad)
Role: Principle Investigator
Total Direct Cost: $748,235
Identification and analysis of compensatory mutations that support the evolution of antibiotic resistance in Neisseria gonorrhoeae
This proposal will apply a synergistic combination of approaches to identify and characterize mutations that compensate for resistance mutations, using competitive co-infections in the mouse model of gonorrhea, application of systematic population genomics-informed methods to identify compensatory mutations in human isolates, and comprehensive experimental analysis to define their mechanisms.

07/01/20 – 05/31/25
NIH/NIAID (Yale University)
R01AI153351 (Yaesoubi)
Role: Co-Investigator
Total Direct Cost: $154,315 (subaward)
Enhancing surveillance systems to slow the spread of antimicrobial-resistant gonorrhea in the United States
This project aims to address the timely challenge of how to optimize surveillance for clinical and public health decision-making for gonorrhea.

03/25/17-04/30/22
Pfizer Pharmaceutical, Inc.
A31316 (Lipsitch/Grad)
Role: Co-PI
Total Direct Costs: $144,348
Quantifying pneumococcal conjugate vaccine impact against otitis media
This project will analyze epidemiological datasets of bacterial carriage and disease incidence to characterize changes in the relationship between disease and carriage that suggest vaccine impact on OM vaccine-targeted pneumococcal serotypes and other agents. The study assess whether early-life infection may be a causal factor in subsequent susceptibility based on epidemiological data, and model how this mechanism could impact OM burden under vaccination and serotype replacement scenarios.

08/15/20-08/14/21
Harvard T.H. Chan School of Public Health
No award # (Huttenhower)
Role: Co-Investigator
Total Direct Costs: $5,973
Dean's Fund for Scientific Advancement: Incubation Award
This project aims to provide first-in-kind discovery of DNA and RNA viruses throughout the human microbiome using the resources of the Harvard Chan Center for the Microbiome in Public Health, including over 10,000 existing human metagenomes and ~1,500 metatranscriptomes. These have been uniformly processed and curated by our standardized bioBakery computational platform, and here we will develop and apply new bioinformatic capabilities to detect and analyze viral members of the respiratory and gastrointestinal microbiome, including phage and eukaryotic viruses of relevance in population health.

*12/01/20-11/30/22
Richard and Susan Smith Family Foundation – Odyssey Award
No Award # (PI: Grad)
Role: Principal Investigator
Total Direct Costs: $285,714
Mechanisms of host-pathogen interactions from conditionally essential and deleterious genes
Our central hypothesis is that host niche-specific factors select for conditionally essential and against conditionally deleterious genes in N. gonorrhoeae. This project will leverage our large dataset of genome sequences from >12,000 clinical isolates and (1) use statistical association methods as the equivalent of a "natural screen" to identify conditionally essential and deleterious genes and use experimental methods to define the growth conditions that favor the loss-of-function and the wildtype forms, and (2) use these variants to learn the host selective pressures shaping N. gonorrhoeae evolution, starting with the pressures from cervical site of infection.
**Note: the sponsor allows award recipients to delay the project start-date; Dr. Grad officially delayed his start-date.*

TEACHING AND TRAINING:

TEACHING IN HARVARD CHAN SCHOOL COURSES:

2015-16	Epi519 – Evolutionary Epidemiology of Infectious Diseases	Guest Lecturer
2016-17	Epi260 – Mathematical Modeling of Infectious Diseases	Guest Lecturer
2014 -	Epi502 – Antibiotic Resistance	Guest Lecturer
2019 -	IID207 – Infectious Disease Outbreaks of the 20th and 21st Centuries: Strategies for Investigation and Control	Guest Lecturer
2019 -	MPH100e Essential Concepts in Infectious Disease	Guest Lecturer
2019 -	IID220 Topics in Immunology and Infectious Diseases	Course Director

TEACHING IN OTHER HARVARD COURSES:

2000	Computational Biology	Teaching Fellow
2008	Introduction to the Profession	Teaching Fellow
2011	Immunology, Microbiology, and Pathology	Instructor
2010-2012	The Impact of Infectious Diseases on History and Society	Instructor
2014-2016	Infectious Diseases Bootcamp	Instructor
2014-	Models of Diseases Bootcamp	Instructor
2014	MD-PhD Lunchtime Series	Instructor
2014-	HST040 – Mechanisms of Microbial Pathogenesis	Instructor

INVITED PRESENTATIONS:

2011	Genomic epidemiology of the *E. coli* O104:H4 Outbreaks in Europe	Boston, MA
2012	Comparative Genomics of *E. coli* O104:H4: Short-Term Evolution of an Emerging Pathogen	Newport, RI
2012	Technical Consultation of the Working Group on the Formation and Use of an Oral Cholera Vaccine Stockpile, World Health Organization	Geneva, Switzerland
2012	Chemotherapies: Common Challenges in Infectious Diseases and Cancer Biology, Broad Institute Retreat	Boston, MA
2013	Comparative Genomics of *E. coli* O104:H4: short-term evolution of an emerging Pathogen	Seattle, WA
2013	Two Stories of Pathogen Genomic, CDC	Atlanta, GA
2013	Genomic Epidemiology of *N. gonorrhoeae* with Reduced Susceptibility to Cefixime, CDC Division of Sexually Transmitted Diseases	Atlanta, GA
2014	Using Genomics to Study the Evolution and Spread of Pathogens: Examples from *N. gonorrhoeae* and RSV	Cambridge, MA
2014	Genomic Epidemiology of *N. gonorrhoeae* with Reduced Susceptibility to Cefixime, STD Prevention Conference / 15th IUSTI World Congress	Atlanta, GA

2014	Evolution and Spread of Pathogens, Wadsworth Center	Albany, NY
2015	Successful Lineages of Multidrug Resistant *N. gonorrhoeae*, IDWeek	San Diego, CA
2015	Worcester Polytechnic Institute	Worcester, MA
2015	Within-Host Deep Sequencing and Diversity Analysis of RSV Infection Reveals Dynamics of Genomic Diversity, RSV Vaccines for the World	La Jolla, CA
2015	Umass Medical School Invited Presentation	Boston, MA
2016	Society for Molecular Biology and Evolution	Japan
2016	The emergence and Spread of Antibiotic Resistant N. gonorrhoeae in the US	LAMG
2016	Invited Lecture, Ragon Institute and Center for AIDS Research at Harvard University 2016 Workshop on Microbial Genomics	Cambridge, MA
2016	Talk, 12th Annual Broad Institute Scientific Retreat	Boston, MA
2017	Invited seminar, Center for AIDS Research, Brigham and Women's Hospital,	Boston, MA
2017	Invited talk, United States Japan Cooperative Medical Sciences Program 19th International Conference on Emerging Infectious Diseases in the Pacific Rim	Seoul, S. Korea
2017	Invited talk, STAR STI CTG 2017 Programmatic Meeting on Antimicrobial Resistance in Neisseria gonorrhoeae	Silver Spring, MD
2017	Invited keynote talk, ASM Conference on Rapid Applied Microbial Next-Generation Sequencing and Bioinformatic Pipelines	Washington, DC
2017	Invited talk, Vaccine waning and mumps re-emergence in the United States, 116th International Titisee Conference: From pathogen evolution to microbiome dynamics	Titisee-Neustadt, Germany
2018	HSPH Forum panel member: The flu outbreak	Boston, MA
2018	Invited talk, Integrating genomics and epidemiology: examples of antibiotic resistant gonorrhea and the resurgence of mumps European Bioinformatics Institute	Hinxton, UK
2018	Invited talk, Integrating genomics and epidemiology: examples of antibiotic resistant gonorrhea and the	Waltham, MA

	resurgence of mumps North East section of the American Association of Clinical Chemistry / American Society for Microbiology Meeting	
2018	Invited talk, Integrating genomics and epidemiology: examples of antibiotic resistant gonorrhea and the resurgence of mumps Yale University	New Haven, CT
2018	Invited talk, Integrating genomics and epidemiology: examples of antibiotic resistant gonorrhea and the resurgence of mumps Brigham and Women's Hospital Clinical Pathology Conference Series	Boston, MA
2018	Invited talk, Epistasis in gonococcal antibiotic resistance, Conference – Antibiotic resistance: Evolutionary concepts versus clinical realities	Stockholm, Sweden
2018	Invited talk, Vaccine waning and the resurgence of mumps in the US Viral Genomics and Evolution conference	Hinxton, UK
2018	Invited talk, Modeling gonococcal antibiotic resistance STD Prevention Conference	Washington, DC
2018	Invited talk, Resurgence of mumps in highly vaccinated populations Massachusetts Department of Public Health Seminar series	Boston, MA
2018	Invited talk, Azithromycin resistance through interspecific acquisition of an epistasis dependent efflux pump component and transcriptional regulator in *Neisseria gonorrhoeae* International Pathogenic Neisseria Conference	Pacific Grove, CA
2018	Invited talk, Genomics and modeling to control gonococcal antibiotic resistance Microbiology Department Seminar	Indianapolis, IN
2018	Invited talk, MRSA colonization Doris Duke Charitable Foundation Meeting	New York City, NY
2018	Invited talk, Antibiotic resistance in gonococcus Society for Molecular Biology and Evolution	Kyoto, Japan
2018	Invited keynote talk, Antibiotic resistance in *Neisseria gonorrhoeae* Course on Antibiotics and Antibiotic Resistance	Hjortviken, Sweden
2018	Invited keynote talk (graduate student invitation)	Rehovot, Israel

	Integrating genomics and epidemiology to control antibiotic resistance Weizmann Institute, Systems Biology symposium	
2019	Invited talk, Addressing the challenges of antibiotic resistant *Neisseria gonorrhoeae* Institute for Microbiology and Infection, University of Birmingham	Birmingham, United Kingdom
2019	Invited keynote address, Infectious diseases genomic epidemiology and pathogen genomics Massachusetts Infectious Disease Society Spring Meeting	Boston, MA
2019	Invited talk, Genetics of development of gonococcal antimicrobial resistance at extragenital sites STI Clinical Trials Group Meeting on Extra-Genital Sexually Transmitted Infections	Washington, DC
2019	Invited talk, Selection, adaptation, and antibiotic resistance in the recombining bacterial pathogen *Neisseria gonorrhoeae* Boston Evolutionary Supergroup	Cambridge, MA
2019	Symposium talk: Quantifying the surveillance needed to sustain genetic marker- based antibiotic resistance diagnostics STI and HIV 2019 World Congress	Vancouver, Canada
2019	Conference talk: Novel pathway to ceftriaxone resistance in clinical isolates of *N. gonorrhoeae* via point mutations in the RNA polymerase STI and HIV 2019 World Congress	Vancouver, Canada
2019	Invited talk: Population genomics strategies for discovering pathways to the acquisition and maintenance of resistance in *Neisseria gonorrhoeae* IUSTI-Europe Congress 2019	Tallinn, Estonia
2019	Invited talk: Gonococcal genomics to improve surveillance and inform diagnostics IUSTI-Asia/Pacific Congress 2019	Shanghai, China
2019	Invited talk: Antibiotic use, resistance, and the example of *Neisseria gonorrhoeae* Department of Biomedical Informatics, Harvard Medical School	Boston, MA
2019	Invited talk: Discovery of modulators of antibiotic resistance in *Neisseria gonorrhoeae* through genomics National Consortium for Microbial Genomics Meeting Norwegian Institute of Public Health	Oslo, Norway
2020	Invited talk: *Neisseria gonorrhoeae* genomics and antibiotic resistance	Boston, MA

	Vincent Center for Reproductive Biology Massachusetts General Hospital	
2020	Invited webinar: *Neisseria gonorrhoeae* genomics and antibiotic resistance DMID project, NIH and international collaborators	Boston, MA
2020	Invited webinar: *Neisseria gonorrhoeae* genomics and antibiotic resistance London School of Hygiene and Tropical Medicine	London, UK
2020	Invited webinar: Navigating the Covid-19 pandemic: from life raft to dry land Broad Institute	Boston MA
2020	Invited talk: Getting to the post-pandemic period Broad-Israel Science Foundation Conference	Boston MA
2020	Invited talk: Genomics and antimicrobial resistance in *Neisseria gonorrhoeae* CDC STD Prevention Conference	Atlanta GA
2020	Invited talk: *Neisseria gonorrhoeae* Population Genomics for the Discovery of Genetic Modulators of Antimicrobial Resistance *N. gonorrhoeae* Research Society (NgoRS) Conference 2020	Chicago, IL
2020	Invited presentation: SARS-CoV-2 viral dynamics in acute infections FDA Evidence Accelerator	Washington, DC
2020	Invited talk: Using genomics to respond to antimicrobial resistant *N. gonorrhoeae* 2020 Joint Australasian HIV&AIDS and Sexual Health Conferences	Sydney, Australia
2020	Invited talk: Estimating SARS-CoV-2 seroprevalence and epidemiological parameters with uncertainty from serological surveys World Health Organization	Geneva, Switzerland
2020	Invited keynote: The challenges of antibiotic resistance in *Neisseria gonorrhoeae* CDC AMD conference	Atlanta, GA
2020	Invited panelist: COVID-19 and genome sequencing American Society for Microbiology Conference on Rapid Applied Microbial Next-Generation Sequencing and Bioinformatic Pipelines	Atlanta, GA
2020	Invited talk: Reducing antibiotic prescribing through a prioritized vaccination strategy Wellcome Trust Impact of Vaccines on AMR Researcher Meeting	London, UK
2020	Invited talk: The challenges of antibiotic resistance in *Neisseria gonorrhoeae* University of Washington Center for AIDS and STD	Seattle, WA

	Seminar Series	

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6. Bubar KM, Kissler SM, Lipsitch M, Cobey S, **Grad YH**, Larremore DB. Model-informed COVID-19 vaccine prioritization strategies by age and serostatus. *medRxiv*. 2020. In revision.

7. Brynildsrud OB, Osnes MN, Ma KC, **Grad YH**, Koomey JM, Caugant DA, Eldholm V. High-frequency phase-switching of *modB* methylase is associated with phenotypic ceftriaxone susceptibility in *Neisseria gonorrhoeae*. *bioRxiv*. 2020.

8. Sánchez-Busó L, Yeats CA, Taylor B, Goater R, Underwood A, Abudahab K, Argimon S, Ma KC, Mortimer TD, Cole MJ, **Grad YH**, Martin I, Raphael BH, Shafer WM, Spiteri G, Town K, Wi T, Harris SR, Unemo M, Aanensen D. A community-driven resource for genomic surveillance of *Neisseria gonorrhoeae* at Pathogenwatch. *bioRxiv*. 2020.

9. Yahara K, Ma KC, Mortimer TD, Shimuta K, Nakayama S, Hirabayashi A, Suzuki M, Jinnai M, Ohya H, Kuroki T, Watanabe Y, Yasuda M, Deguchi T, Eldholm V, Harrison OB, Maiden MCJ, **Grad YH**, Ohnishi M. Emergence and evolution of antimicrobial resistance genes and mutations in *Neisseria gonorrhoeae*. *bioRxiv.* 2020.

10. Ogbebor O, Mortimer TD, Fryling K, Zhang JJ, Bhanot N, **Grad YH**. Disseminated gonococcal infection complicated by prosthetic joint infection: case report and genomic and phylogenetic analysis. 2020. In review.

11. Kissler SM, Fauver JR, Mack C, Tai C, Shiue KY, Kalinich CC, Jednak S, Ott IM, Vogels CBF, Wohlgemuth J, Weisberger J, DiFiori J, Anderson DJ, Mancell J, Ho DD, Grubaugh ND*, **Grad YH***. Viral dynamics of SARS-CoV-2 infection and the predictive value of repeat testing. *medRxiv*. 2020. *co-senior authors.

12. Brown TS, Martinez de Salazar Munoz P, Bhatia A, Bunda B, Williams WK, Bor D, Miller JS, Mohareb A, Naranbai V, Beltran WG, Miller TE, Thierauf J, Yang W, Kress D, Stelljes K, Johnson K, Larremore D, Lennerz J, Iafrate AJ, Balsari S, Buckee CO*, **Grad YH***. GPS-estimated foot traffic data and venue selection for COVID-19 serosurveillance studies. *medRxiv.* 2020. *co-senior authors

13. Poyraz O, Sater MRA, Miller LG, McKinnell JA, Huang SS, **Grad YH***, Marttinen P*. The impact of site-specific clearance on Methicillin-resistant *Staphylococcus aureus* decolonization. *medRxiv*. 2020. *co-senior authors.

<u>Other peer reviewed publications</u>

1. **Grad YH**, Seifter JL, Levy B, and Loscalzo J. Clinical problem-solving. Bitter Pills. *N Engl J Med*. 2010. Nov 4;363(19):1847-51.

2. Schaffer A, **Grad Y**, and Ross J. Interactive medical case. Bitter Pills. *N Engl J Med*. 2010. Oct 14; 363(16):e26.

3. Croucher NJ, Harris SR, **Grad YH**, Hanage WP. Bacterial genomes in epidemiology--present and future. *Philos Trans R Soc Lond B Biol Sci*. 2013 Feb 4;368(1614):20120202. doi: 10.1098/rstb.2012.0202. Print 2013.

4. Wei K, Vaidya A, Rohloff PJ, Sun Y-P, **Grad YH**. A patient with fevers and fatigue. *N Engl J Med*. 2013 Feb 14;368(7):e9. doi: 10.1056/NEJMimc1208059.

5. **Grad YH**, Waldor MK. Deciphering the origins and tracking the evolution of cholera epidemics with whole-genome-based molecular epidemiology. *MBio*. 2013 Sep 10;4(5). doi:pii: e00670-13. 10.1128/mBio.00670-13.

6. **Grad YH**, Lispitch M. Epidemiologic data and pathogen genome sequences: a powerful synergy for public health. *Genome Biol*. 2014 Nov 18;15(11):538

7. Chang H, Cohen T, **Grad YH**, Hanage WP, O'Brien TF, Lispitch M. Origin and proliferation of multiple drug resistance in bacterial pathogens. *Microbiol Mol Biol Rev*. 2015 Mar;79(1):101-116.

8. **Grad YH**, Goldstein E, Lipsitch M, White P. Improving control of antibiotic resistant gonorrhea by integrating research agendas across disciplines: key questions arising from mathematical modeling. *J Infect Dis*. 2015.

9. **Grad YH**, Fortune SM. Biodiversity and hypervirulence of Listeria monocytogenes. *Nat Genet*. 2016. Mar 15

10. Mortimer T, **Grad YH**. Applications of genomics to slow the spread of MDR *Neisseria gonorrhoeae*. Antimicrobial Therapeutics Reviews. *Annals of the New York Academy of Sciences*. 2018.

11. Olesen SW and **Grad YH**. Deciphering the impact of bystander selection for antibiotic resistance in *Neisseria gonorrhoeae*. *Journal of Infectious Diseases*. 2019. 2019 Apr 8. pii: jiz156. doi: 10.1093/infdis/jiz156.

12. Rubin DHF, Ross JDC, **Grad YH**. The frontiers of addressing antibiotic resistance in Neisseria gonorrhoeae. *Translational Research*. 2020. 2020 Feb 28. pii: S1931-5244(20)30031-1. doi: 10.1016/j.trsl.2020.02.002.

13. Buckee CO, Balsari S, Chan J, Crosas M, Dominici F, Gasser U, **Grad YH**, Grenfell B, Halloran ME, Kraemer MUG, Lipsitch M, Metcalf CJE, Meyers LA, Perkins TA, Santillana M, Scarpino SV, Viboud C, Wesolowski A, Schroeder A. Aggregated mobility data could help fight COVID-19. *Science*. 23 Mar 2020: DOI: 10.1126/science.abb8021

14. Segal E, Zhang F, Lin X, King G, Shalem O, Shilo S, Allen WE, **Grad YH**, Greene CS, Alquaddoomi F, Anders S, Balicer R, Bauman T, Bonilla X, Booman G, Chan AT, Cohen O, Coletti S, Davidson N, Dor Y, Drew DA, Elemento O, Evans, G, Ewels P, Gale J, Gavrieli A, Geiger B, Hajirasouliha I, Jerala R, Kahles A, Kallioniemi O, Keshet A, Landau G, Meir T, Muller A, Nguyen LH, Oresic M, Ovchinnikova S, Peterson H, Rajagopal J, Ratsch G, Rossman H, Rung J, Sboner A, Sigaras A, Spector T, Steinherz R, Stevens I, Vilo J, Wilmes P. Building an international consortium for tracking coronavirus health status. *Nature Medicine.* 2020 Jun 2. doi: 10.1038/s41591-020-0929-x.

15. Lipsitch M, **Grad YH**, Sette A, Crotty S. Memory T cells and herd immunity to SARS-CoV-2. *Nature Reviews Immunology.* 2020. https://doi.org/10.1038/s41577-020-00460-4

Book Chapters

1. **Grad YH** and Ross J. Osteomyelitis and Septic Arthritis. In Principles and Practice of Hospital Medicine. McKean S, Ross J, Dressler D, Brotman D, and Ginsberg J, eds. New York: McGraw-Hill. 2012

2. Certain LK and **Grad YH**. Osteomyelitis and Septic Arthritis. In Principles and Practice of Hospital Medicine, 2nd Ed. McKean S, Ross J, Dressler D, Brotman D, and Ginsberg J, eds. New York: McGraw-Hill. 2017

3. Bhattacharyya RP, **Grad YH**, Hung DT. Chapter 146: Microbial genomics and infectious diseases. In Longo DL, Fauci AS, Kasper DL et al., eds. Harrison's Principles of Internal Medicine (19th edition). 2015. Updates 2018 and 2021.

Non-peer reviewed publications

1. **Grad Y**, Miller JC, Lipsitch M. Challenges to quantitative modeling of cholera disease transmission. SACEMA (South African Centre for Epidemiological Modelling and Analysis) Quarterly. Sept 2012.

Media and public engagement
Podcast interview, ThinkResearch, March 2020

Op-Ed, Washington Post, March 2020

Op-Ed, STAT, March 2020

Interview/podcast, Innovation Hub, April 2020

Podcast interview, "Deep Background" with Noah Feldman, May 2020

Podcast interview, ThinkResearch, September 2020

Op-Ed, Washington Post, September 2020

Thesis

1. **Grad Y**. (2004). *Computational analysis and prediction of regulatory sequences in bilaterians*. Ph.D. Thesis. Harvard University: Cambridge, MA, USA.

EXHIBIT B

E. K. Accorsi

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EDUCATION

Harvard University, Cambridge, Massachusetts — Sep 2016 – Present
Doctor of Philosophy in Infectious Disease Epidemiology
- Advisors: Dr. Marc Lipsitch, Dr. Curtis Huttenhower
- Thesis: Epidemiologic Studies of the Human Microbiome and of COVID-19
- Defended: March 15, 2021
- Degree conferral (expected): May 27, 2021
- Cumulative GPA: 4.0/4.0

Emory University, Atlanta, Georgia — Sep 2009 – May 2013
Bachelor of Science in Applied Mathematics
- Cumulative GPA: 4.0/4.0

ACADEMIC HONORS & AWARDS

Barry M. Goldwater Scholar — 2012
Nationally competitive award for excellence in research in science, mathematics, and engineering.

Jocelyn B. Taylor Scholar, Emory Scholars Program — 2009 – 2013
- One of Emory's premier merit awards, offered to 40 of 15,600 Emory applicants.
- Provides full tuition scholarship for undergraduate studies.

Deborah Jackson Award, Emory Department of Math/CS — 2013
Awarded to the most outstanding juniors and seniors in the Math and Computer Science Department.

Additional Awards: National Merit Scholar, Robert C. Byrd Honor Scholar, Phi Beta Kappa

PROFESSIONAL EXPERIENCE

Epic Systems Corporation, Verona, WI — Aug 2013 – Sep 2015
Technical Services Engineer, EpicCare Inpatient Team
Advised large health care organizations on how to configure and optimize Epic's electronic medical record software to improve patient outcomes and clinician efficiency; led large software install, upgrade, and optimization projects; worked closely with hospital leadership; liaised with software developers and clinicians to improve software quality.

RESEARCH EXPERIENCE

Harvard T.H. Chan School of Public Health, Boston, MA — Sep 2016 – Present
Graduate Research Assistant to Dr. Marc Lipsitch & Dr. Curtis Huttenhower
Conduct computational and epidemiological research on the human microbiome and COVID-19. My first project identifies species and genes associated with patterns of *S. aureus* carriage in the early infant nasal microbiome. My second project benchmarks statistical techniques for mediation analysis in microbiome data. My final project outlines epidemiological biases and possible solutions for important observational study designs for COVID-19.

NASA Ames Research Center DEVELOP Program, Moffet Field, CA — Jan 2016 – Aug 2016
Team Member, Contractor with SSAI
Worked collaboratively on a team using GIS and satellite remote sensing to study *Sargassum* seaweed over-proliferation in the Caribbean Sea, which causes both environmental and economic problems.

Emory Center for Mathematics & Computing in Medicine, Atlanta, GA — Jan 2013 – Jun 2013
Research Assistant to Dr. Alessandro Veneziani
Used computational fluid dynamics simulations to understand cerebral aneurysm pathogenesis and identify predictors of rupture in real patients and to study the long term effects of bicuspid aortic valve disease.

Centers for Disease Control (CDC), Atlanta, GA — Jan 2011 – Dec 2012
Guest Researcher, CDC Insectary
Conducted two independent research projects focusing on the fitness of transgenic mosquitoes and the implications of mosquito mating for genetic control strategies.

West Nile Virus Lab at Emory University, Atlanta, GA — Sep 2010 – Dec 2012
Research Assistant to Dr. Uriel Kitron
Performed field work studying the transmission dynamics of West Nile virus in urban Atlanta, including bird mist-netting, creek surveillance, and collection and identification of mosquitos.

NASA Student Airborne Research Program, Palmdale, CA — Jun 2012 – Aug 2012
Research Assistant to Dr. Raphael Kudela
Conducted remote sensing research on harmful algal bloom detection. Developed an algorithm that can be applied to satellite data to predict when blooms will become toxic based on their algal species composition.

Emory Undergraduate Research Programs, Atlanta, GA Sep 2010 – Dec 2011
Grant Recipient & Program Participant
Received competitive fellowships and grants (SIRE, SURE) in support of my research. Gained experience writing grant proposals, designing experiments, conducting literature reviews, creating posters, and presenting research.

Self-Organizing Lab at the University of Connecticut, Storrs, CT Jan 2008 – Aug 2009
Research Assistant to Dr. Whitney Tabor
Research explored the basis of the human ability to generalize. Data from anagram solution tasks and an artificial neural network suggested that self-organization allows for generalization in language processing.

PUBLICATIONS

1) Wang, Y., Yan, Y., Thompson, K. N., Bae, S., Accorsi, E.K., et al. (2021). Whole microbial community viability is not quantitatively reflected by propidium monoazide sequencing approach. *Microbiome*, *9*(17), 1-13. https://doi.org/10.1186/s40168-020-00961-3

2) Accorsi, E.K., Qiu, X., Rumpler, E., Kennedy-Shaffer, L., Kahn, R., et al. (2021). How to detect and reduce potential sources of biases in studies of SARS-CoV-2 and COVID-19. *European Journal of Epidemiology, 36*, 179–196. https://doi.org/10.1007/s10654-021-00727-7

3) Accorsi, E.K., Franzosa, E.A., Hsu, T., Joice Cordy, R., Maayan-Metzger, A., et al. (2020). Determinants of *Staphylococcus aureus* Carriage in the Developing Infant Nasal Microbiome. *Genome Biology*, *21*(1), 1-24. https://doi.org/10.1186/s13059-020-02209-7

4) Accorsi, E.K., Samples, J., McCauley, L.A., & Shadbeh, N. (2020). Sleeping Within Six Feet: Challenging Oregon's Labor Housing COVID-19 Guidelines. *Journal of Agromedicine*, 1–4. https://doi.org/10.1080/1059924X.2020.1815622

5) Kudela, R., Palacios, S., Austerberry, D., Accorsi, E.K., Guild, L., & Torres, J. (2015). Application of Hyperspectral Remote Sensing to Cyanobacterial Blooms in Inland Waters. *Remote Sensing of Environment, 167*, 196-205. http://dx.doi.org/10.1016/j.rse.2015.01.025

6) Henin, J., Accorsi, E.K., Cho, P., & Tabor, W. (2009). Extraordinary Natural Ability: Anagram Solution as an Extension of Normal Reading Ability. In the Proceedings of the 31st Annual Meeting of the Cognitive Science Society. Mahwah, New Jersey: *Lawrence Erlbaum Associates.*

MANUSCRIPTS IN REVIEW OR SUBMITTED

1) Niehus, R., Accorsi, E.K., Gweon, H., Turner, P., Tosas-Auguet, O., et al. (2021). The effect of antibiotics and probiotics on antibiotic resistance genes in the gut microbiome of newborn babies. [In review at *Antimicrobial Agents and Chemotherapy*]

2) Wong, S., Gold, S., Accorsi, E.K., Cowger, T.L., Wiseman, D., et al. (2021). Safety of administering biologics to IBD patients at an outpatient infusion center In New York City during the COVID-19 pandemic: Sars-CoV-2 seroprevalence and clinical and social characteristics. https://doi.org/10.1101/2021.03.15.21253615 [Submitted at *Inflammatory Bowel Diseases*]

1) Zhang, Y., Bhosle, A., Bae, S., McIver, L., Accorsi, E.K., et al. (2020) Identifying Novel Bioactive Microbial Gene Products in Inflammatory Bowel Disease. [In review at *Nature*]

2) Lopez, L., Nguyen, T., Weber, G., Kleimola, K., Bereda, M., Liu, Y., Accorsi, E.K., et al. (2020). Seroprevalence of anti-SARS-CoV-2 IgG Antibodies in the Staff of a Public School System in the Midwestern United States. https://doi.org/10.1101/2020.10.23.20218651 [In review at *PLOS ONE*]

MANUSCRIPTS IN PREPARATION

1) Accorsi, E.K., Franzosa, E.A., & Huttenhower, C. PERMANOVA, I hardly know 'ya: avoiding confounding through correct permutation specification when using PERMANOVA for longitudinal or batched microbiome data.

2) Accorsi, E.K., Franzosa, E.A., Gough, E.K., Ma, S., Manges, A., Lipsitch, M., et al. Detecting and quantifying mediation of phenotypes by microbial communities.

COVID-19 PROJECTS

Social Risk Factors for COVID-19 Exposure Questionnaire May 2020 – Present
Questionnaire developer
Created questionnaire for measuring social risk factors for COVID-19 exposure that can be used to understand disparities in infection risk and design better public health interventions. See: https://osf.io/a9xpd/

COVID-19 and Health Inequities Seminar Series, Virtual — Sep 2020 – Oct 2020
Organizer and moderator
Organized and moderated five-part seminar series focused on the factors driving inequalities in COVID-19 infection and mortality rates in the U.S. See: https://ccdd.hsph.harvard.edu/health-inequities-seminar-series/

PRESENTATIONS

Cold Spring Harbor Laboratory Microbiome Meeting – Virtual — 2020

Harvard Chan Center for the Microbiome in Public Health Symposium – Virtual — 2020

Harvard Chan Center for the Microbiome in Public Health Symposium – Boston, MA — 2019

17th Annual Jonathan Freeman Symposium – Boston, MA — 2019

Keystone Microbiome Symposium – Montreal, CA — 2019

4th Annual MIT-Harvard Microbiome Symposium – Cambridge, MA — 2019

NASA Annual Earth Science Application Showcase – Washington, DC — 2016

Society for Conservation GIS Annual Conference – Monterey, CA — 2016

11th Regular Session of CiiMAR-GoMC – Villahermosa, MX — 2016

Association of American Geographers – San Francisco, CA — 2016

Association for the Sciences of Limnology and Oceanography – New Orleans, LA — 2013

American Geophysical Union Fall Meeting – San Francisco, CA — 2013

Emory Fall 2012 Undergraduate Research Symposium – Atlanta, GA — 2012

UF-HHMI Science for Life Creativity in the Arts and Science Event – Gainesville, FL — 2012

60th Annual Meeting of the American Society of Tropical Medicine and Hygiene – Phil., PA — 2011

Emory SURE Poster Symposium – Atlanta, GA — 2011
- 3rd place poster (of 103)

Emory Spring 2011 Undergraduate Research Symposium – Atlanta, GA — 2011
- Best Poster, Natural Sciences

31st Annual Meeting of the Cognitive Science Society – Amsterdam, NL — 2009

TEACHING EXPERIENCE

Physalia Courses, Berlin, Germany — May 2019
Course Instructor
Co-taught a week-long intensive workshop for 40 PhD students and postdoctoral researchers entitled "Metagenomics, metatranscriptomics, and multi'omics for microbial community studies".

Harvard T.H. Chan School of Public Health, Boston, MA — Jul 2017 – Oct 2019
Teaching Fellow
Ran daily or weekly discussion sections and held office hours. Graded and provided feedback on homework assignments and exams.
- EPI 207: Advanced Epidemiologic Methods (Fall 2018, Fall 2019)
- EPI 203: Study Design in Epidemiologic Research (Spring 2019)
- EPI 201: Introduction to Epidemiology: Methods I (Fall 2017)
- EPI 202: Introduction to Epidemiology: Methods II (Fall 2017)
- EPI 500: Fundamentals of Epidemiology (Summer 2017)

Harvard T.H. Chan School of Public Health, Boston, MA — Sep 2018 – Dec 2018
Tutor
- EPI 201: Introduction to Epidemiology: Methods I (Fall 2018)
- EPI 202: Introduction to Epidemiology: Methods II (Fall 2018)

WORKSHOPS

Alan Turing Institute Epirecipes – London, UK — 2018

Marine Biological Laboratory STAMPS – Woods Hole, MA — 2017

LEADERSHIP EXPERIENCE

CCDD Student Journal Club, Boston, MA — Jan 2019 – May 2019
Organizer
Organized, and facilitated discussions for weekly graduate student journal club.

Emory Undergraduate Research Journal, Atlanta, GA — Sep 2009 – May 2013
Editor-in-Chief (Jan 2012 - May 2013), Social Sciences Section Head (Sep 2009 - Dec 2011)
Rebuilt and expanded the journal after it became inactive under previous leadership. Recruited, trained and managed a new 47 student staff. Increased student submissions to the journal, secured club funding, identified new ways to partner with faculty and staff, and produced a high-quality, peer-reviewed publication.

Emory Global Health Case Competition, Atlanta, GA — Sep 2010 – May 2013
Competition Co-Director (Sep 2010 - May 2011), Planning Committee (Sep 2011 - May 2013)
Led the group that organized the first global-health focused case competition to be held at a national level. Thirteen U.S. universities (120 students) competed, and full sponsorship ($70,000) was provided by General Electric. Coordinated all areas of the competition including case writing, funding, logistics and marketing.

ADDITIONAL SKILLS

Programming: R, SAS
Data Management: SQL, Excel
Able to learn new languages quickly as needed.