

EXHIBIT A

**Declaration of
Nina H. Fefferman, Ph.D**

**IN THE UNITED STATES DISTRICT COURT
FOR THE NORTHERN DISTRICT OF GEORGIA
ATLANTA DIVISION**

RHONDA JONES *et al.*,

Plaintiffs,

v.

VICTOR HILL *et al.*,

Defendants.

CIVIL ACTION

NO. 1:20-CV-2791-ELR-CCB

DECLARATION OF NINA H. FEFFERMAN

1. I, Nina Fefferman, being competent to make this declaration and having personal knowledge of the matters stated herein, declare under penalty of perjury that the following is true and correct:

2. I am over 21 years of age. The statements contained in this declaration are based on my personal knowledge, or on information that experts in the field of infectious disease epidemiology would reasonably rely on in forming an opinion, and are true and correct to the best of my knowledge.

I. Expert Qualifications

3. I am a full Professor at the University of Tennessee, Knoxville in both the Department of Ecology and Evolutionary Biology and the Department of

Mathematics. I am also the Director of the Mathematical Modeling Consulting Center at the National Institute for Mathematical and Biological Synthesis, and the Associate Director of the University of Tennessee One Health Initiative. My research focuses on complex adaptive systems, with a focus on the interplay between individual behavior and infectious disease epidemiology.

4. I have worked for the past 16 years as a researcher of the epidemiology, ecology, and evolution of infectious disease, pandemic preparedness, national biosecurity, and infrastructure protection. I hold a Master's degree in mathematics from Rutgers University and a PhD in Biology from Tufts University.

5. For over a decade, I was one of the primary researchers of the Command, Control, and Interoperability Center for Advanced Data Analytics, a U.S. Department of Homeland Security ("DHS") Center of Excellence, where I ran a research group focusing on the mathematics of both biosecurity and cybersecurity. As part of my role in that center, I contributed models and policy recommendations to DHS and its affiliate agencies for how to manage and mitigate pandemic threats from H1N1 2009 flu, Ebola in West Africa, and Zika virus. I have also consulted for various additional state and federal agencies and private companies, domestically and abroad, in the area of outbreak management since 2004.

6. My C.V., attached as **Exhibit A**, includes a full list of my honors, experience, and publications.

7. I am not being compensated for my work reviewing materials and preparing this report. Any live testimony I provide will also be provided *pro bono*.

8. I have reviewed and relied upon the following documents in forming the opinions set forth below:

- a. Report by the Georgia Department of Community Affairs listing the Clayton County Jail capacity and population (dated June 2020);
- b. Documents from the Georgia Department of Public Health regarding the nature and scope of the COVID-19 outbreak at the Clayton County Jail (dated June 11, 2020 and July 9, 2020);
- c. Declarations by current and former Clayton County Jail detainees, including the following:
 - i. Declaration of Barry Watkins, dated June 21, 2020;
 - ii. Declaration of Randolph Mitchell, dated June 21, 2020;
 - iii. Declaration of Rhonda Jones, dated June 21, 2020;
 - iv. Declaration of Michael Singleton, dated June 24, 2020;
 - v. Declaration of C.C., dated June 25, 2020;
 - vi. Declaration of J.H., dated June 25, 2020.

- vii. Declaration of M.B., dated June 3, 2020;
- viii. Declaration of F.S., dated June 18, 2020;
- ix. Declaration of A.W., dated June 21, 2020;
- x. Declaration of W.L.M., dated July 7, 2020;
- xi. Declaration of D.H., dated July 14, 2020.

d. Other Documents

- i. Centers for Disease Control and Prevention, *Interim Guidance on Management of Coronavirus Disease 2019 (COVID-19) in Correctional and Detention Facilities* (Mar. 23, 2020), available at <https://www.cdc.gov/coronavirus/2019-ncov/downloads/guidance-correctional-detention.pdf>.
- ii. Centers for Disease Control and Prevention, *Interim Guidance on Management of Coronavirus Disease 2019 (COVID-19) in Correctional and Detention Facilities* (July 22, 2020), <https://www.cdc.gov/coronavirus/2019-ncov/community/correction-detention/guidance-correctional-detention.html>.
- iii. Centers for Disease Control and Prevention, *Interim Considerations for SARS-CoV-2 Testing in Correctional and Detention Facilities* (July 7, 2020) <https://www.cdc.gov/coronavirus/2019-ncov/community/correction-detention/testing.html>.
- iv. Robert Weidner & Jennifer Schultz, *Examining the Relationship Between US Incarceration Rates and Population Health at the County Level*, 13 SSM Pop. Health 1 (2019).
- v. Susan Kelley, *Study: Nearly Half of Americans Have Had a Family Member Jailed, Imprisoned*, 47 Hum. Ecology 15 (2019).

- vi. Hugh Lester & Martin Miller, *Discrete Event Simulation of Jail Operations in Pursuit of Organizational Culture Change*, in *COMPUTER SECURITY* 307-322 (Springer 2019).
- vii. Joseph A. Bick, *Infection Control in Jails and Prisons*, 45 *Clinical Infectious Diseases* 1047 (2007).
- viii. Charles Hoge, et al., *An Epidemic of Pneumococcal Disease in an Overcrowded, Inadequately Ventilated Jail*, 331 *New Eng. J. Med.* 643 (1994).
- ix. Kathryn Nowotny, *Health Care Needs and Service Use Among Male Prison Inmates in the United States: A Multi-Level Behavioral Model of Prison Health Service Utilization*, 5 *Health Just.* 9 (2017).

II. Opinion

9. Based on my expertise in the epidemiology of infectious pandemics and my understanding of the conditions within the Clayton County Jail from the declarations and other documents listed above, I conclude that unsafe conditions within the jail are exacerbating the spread of disease. As a consequence, detainees in the facility, as well as the corrections and medical staff, their families, and the broader community, are being put at unnecessary risk of severe harm from COVID-19.

10. In response, it is my opinion as an expert in infectious disease dynamics that individuals who are already detained in the facility—particularly individuals

who are susceptible to complications from COVID-19—should be evaluated for release. Additionally, at a minimum, the jail’s administrators should take immediate steps to:

- a. Provide detainees with clear information about COVID-19, including methods for prevention, recognizing symptoms, and reporting symptoms;
- b. Enforce and allow for social distancing among detainees during all activities, including those involving meals, medical care, and court appearances;
- c. Provide adequate masks that are cleaned or replaced regularly;
- d. Implement an enhanced cleaning protocol that includes providing disinfectant materials to detainees so that they may clean out their cells;
- e. Implement an enhanced personal hygiene protocol that includes providing hand sanitizer to detainees, as well as increased quantities of soap and more frequent laundry services;
- f. Screen all incoming detainees and staff for symptoms and quarantine all incoming detainees for at least 14 days;
- g. Test anyone who displays any of the most common symptoms associated with COVID-19;
- h. Act promptly to isolate individuals who report symptoms or who have been in recent close contact with those who have reported symptoms; and
- i. Ensure that sick individuals have access to supportive medical monitoring and care during the entire period they are symptomatic.

The jail should incorporate these recommendations into clear and formal guidelines to adequately protect those who remain in jail facilities and ensure that these steps are being followed by all staff. These steps should be maintained until

at least such time as the epidemic in the broader community has been contained and social distancing and other prevention and mitigation measures are no longer recommended.

11. By adopting these recommendations—to both release as many people as possible and to implement urgently needed protective measures within the jail—the jail could substantially reduce the number of COVID-19 infections in both the jail and the surrounding Clayton County community, and reduce the risk that the Clayton County healthcare system becomes overwhelmed.

A. Risk of COVID-19 Within Jails and the Wider Community

12. The health of persons in jail and the health of the rest of the community are inherently linked. The two populations must interact because jails constantly release people into the wider community, admit new people from the wider community, and rely on staff and vendors who regularly mix with the wider community. Further, many jails rely on local hospitals to treat incarcerated persons requiring advanced medical care, adding to the burden on the limited resources of local healthcare systems.

13. Unmitigated spread of disease within jails results in worse health outcomes for the entire population. Cases of infection occurring within a jail cause

additional cases of infection, hospitalization, and deaths in the wider community.¹ This link is not surprising. Studies show that the conditions inherent to all jails degrade the health of incarcerated people, leaving them more vulnerable to infection and severe outcomes from infection.² As an epidemiological result of increasing individual vulnerability to disease, the vulnerability of the whole jail population increases.

14. Jails with disease prevalence higher than the general populations they serve—like the Clayton County Jail—will therefore act as sources of infection. Jails with high infection rates will continue to re-seed infection into the wider community, undermining the wider community’s efforts to contain or mitigate outbreaks, and can even introduce disease into otherwise non-infected communities.

¹ Eric Lofgren, Kristian Lum, Aaron Horowitz, Brooke Madubuonwu & Nina Fefferman, *The Epidemiological Implications of Incarceration Dynamics in Jails for Community, Corrections Officer, and Incarcerated Population Risks from COVID-19*, medRxiv (May 4, 2020) (submitted for review), <https://www.medrxiv.org/content/10.1101/2020.04.08.20058842v2>.

² David C. McClelland, et al., *The Need for Power, Stress, Immune Function, and Illness Among Male Prisoners*, 91 *J. of Abnormal Psych.* 61, 68 (1982); Elizabeth T. Jacobs & Charles J. Mullany, *Vitamin D Deficiency and Inadequacy in a Correctional Population*, 31 *Nutrition* 659 (2015); Fiona G. Kouyoumdjian, et al., *Do People Who Experience Incarceration Age More Quickly? Exploratory Analyses Using Retrospective Cohort Data on Mortality from Ontario*, 12 *PLOS One* 1, 7 (2017); U.S. Dep’t of Justice, *Special Report, Medical Problems of State and Federal Prisoners and Jail Inmates 2011–12* (Revised Oct. 4, 2016) <https://www.bjs.gov/content/pub/pdf/mpsfj1112.pdf>.

15. Outbreaks of disease in jails are exacerbated by three dynamics: (1) the continuous introduction of potential new sources of infection (for example, as a result of new admissions or by staff); (2) the high density of jail living arrangements (such as bunks and cells), which creates more physical proximity and contact among susceptible incarcerated people; and (3) often inadequate protocols for mitigating the spread of infection within the facility. Any intervention calculated to slow or halt the outbreak of disease in jails will rise or fall on its capacity to meaningfully shift one or more of these three powerful factors.

B. Failure to Mitigate COVID-19 Infection Inside the Clayton County Jail

16. Based on the declarations I have reviewed, it is clear that the Clayton County Jail has not taken basic steps recommended by authoritative public health entities to respond to the COVID-19 pandemic and protect the health and safety of people inside and outside its walls. The lack of action by officials with the Clayton County Sheriff's Office contravenes public health guidance and common sense. The result is a jail environment that is already in the midst of a recorded outbreak and, with every passing day that allows the continuation of these conditions, continues to risk further viral transmission both within the jail and spilling out into the broader community.

i. Exposure Conditions Within the Housing Unit Cells

17. Conditions within the jail's cells pose a substantial risk of infection due to crowding and lack of adequate hygiene materials provided by the jail. The cornerstone of COVID-19 prevention is social distancing, a practice that is effectively impossible in a small jail cell that holds more than one person. Making matters worse, Declarants report that most if not all of the two-person cells in the jail house three people. Thus, within a given cell, there is no possibility of social distancing that would offer any protection from transmission between cellmates. This problem is worsened further by detainees' lack of access to appropriate masks.

18. Further, detainees' lack of sufficient access to cleaning products and personal sanitary products also contribute to the potential for transmission. There is an apparent insufficiency in the surfactants/disinfectants and cleaning materials with which the jail provides detainees to maintain personal hygienic practice for themselves and their surroundings. Detainees receive only a single 4 oz. bottle of soap per week, no hand sanitizer, insufficient access to disinfectant, and no sponges or rags. This lack of cleaning materials would be problematic under standard conditions and is even more so during a pandemic. Although the primary routes of infection in normal circumstances outside a jail are from droplets in the air, there are

still known risks from contaminated surfaces being touched and then transferred by touch of unclean hands to the face. Current evidence suggests that the virus causing COVID-19 may remain alive on hard surfaces like those common to a jail for hours or even days.³ For this reason, the CDC recommends that regularly touched surfaces be frequently cleaned and disinfected.⁴ In the circumstances described in the detainee statements, there are insufficient cleaning supplies to clean either surfaces or hands. This failure is unacceptable, easily remedied by the jail, and likely to further the spread of infection if not corrected.

ii. Exposure Conditions Outside of Housing Unit Cells

19. The jail's practice of requiring detainees to congregate in large groups—sometimes multiple times per day—fosters easy transmission of COVID-19 infection. Declarants report that they must stand in a line to obtain their second

³ The CDC recommends sanitizing frequently touched surfaces multiple times a day in the household setting. The jail setting is riskier than the household setting due to increased human density, and thus an increased sanitization regime is appropriate. See Centers for Disease Control and Prevention, *Cleaning and Disinfection for Households* (July 10, 2020) <https://www.cdc.gov/coronavirus/2019-ncov/prevent-getting-sick/cleaning-disinfection.html>.

⁴ Centers for Disease Control and Prevention, *Interim Guidance on Management of Coronavirus Disease 2019 (COVID-19) in Correctional and Detention Facilities* (July 22, 2020), <https://www.cdc.gov/coronavirus/2019-ncov/community/correction-detention/guidance-correctional-detention.html>.

meal of the day.⁵ At pill call, the daily distribution of medication to detainees, jail staff require detainees to line up to receive their medications from a nurse in the middle of the housing unit.⁶ They are further made to congregate in holding cells awaiting courtroom appearances and in the medical wing with people from other housing.⁷ Each time detainees are instructed to line up close together, if any one person in the group is infected, the infection can easily spread to all persons in the group. The jail can and should reduce the risk of infection by no longer making detainees congregate in large groups (in fact, such congregation of large groups should be actively prohibited), by ensuring the wearing of masks during all activities involving contact with others not housed in the same room together, and by disinfecting high-touch surfaces regularly.

20. Further, depriving incarcerated people of access to the outdoors is known to contribute to immunocompromise, which will increase susceptibility to infection and thereby make it easier to transmit infection to others.⁸ Nevertheless,

⁵ See, e.g., Decl. of Randolph Mitchell ¶ 7.

⁶ See, e.g., Decl. of Barry Watkins ¶¶ 13-14.

⁷ See, e.g., Decl. of J.H. ¶¶ 31-32 (detailing forced congregation at video court); Decl. of Barry Watkins ¶¶ 26-27 (detailing forced congregation during trips to the medical wing).

⁸ See Elizabeth T. Jacobs & Charles J. Mullany, *Vitamin D Deficiency and Inadequacy in a Correctional Population* 31 Nutrition 659 (2015).

declarants describe receiving no access at all to the outdoors, or even to an open-air “yard,” despite it also being a space where detainees can maintain more distance between themselves and others.⁹ The jail should therefore allow as many detainees as possible to have time outdoors regularly with access rotated through small groups to limit potential spread due to congregation.

21. Ensuring that every detainee has (and uses) a mask would also decrease transmission risks. Masks have been shown to be effective at decreasing the likelihood of spread of COVID-19 infection from a sick person to a healthy person. Consequently, the jail should issue a mask to each staff person and detainee, and ensure that each person in the jail always has a clean mask. Paper masks should be replaced on a daily basis and cloth masks should be “routinely” laundered.¹⁰ The jail should require that all individuals (detainees and staff) always wear appropriate masks. This is not a protocol taken to protect oneself; it is taken to protect others,

⁹ See, e.g., Decl. of Randolph Mitchell ¶ 8.

¹⁰ Edward M. Fisher & Ronald E. Shaffer, *Considerations for Recommending Extended Use and Limited Reuse of Filtering Facepiece Respirators in Health Care Settings*, 11 J. Occup. & Environ. Hyg. D115 (2014), <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4610368/> (summarizing studies suggesting that facemask protection can be reduced by multiple donnings or uses); Centers for Disease Control and Prevention, *Interim Guidance on Management of Coronavirus Disease 2019 (COVID-19) in Correctional and Detention Facilities* (July 22, 2020), <https://www.cdc.gov/coronavirus/2019-ncov/community/correction-detention/guidance-correctional-detention.html>.

and when everyone is protected, every individual benefits.

22. The jail has also failed to provide education regarding protocol for personal protection from COVID-19 infection and how to interrupt the spread (as described in detainee declarations). This shortcoming is an epidemiologically unsupportable scenario with no discernable justification. Knowledge is a powerful tool for modifying behavior, and disseminating information about how to recognize and prevent the spread of COVID-19 would cost little if anything.¹¹ The jail should make every effort to provide written, verbal, and demonstration-based explanations for best practices about social distancing, personal hygienic practices, and signs and symptoms that should be immediately reported to officers and/or medical staff.

iii. Unclear and Unsafe Intake Protocols

23. The statements from detainees indicate that the jail's standard operating procedure includes a protocol of quarantining new detainees for up to 7 days before they are sent to general population. However, even if new arrivals are isolated for 7 days, that period of time is epidemiologically insufficient to prevent them from

¹¹ See Robert Hornik, *PUBLIC HEALTH COMMUNICATION: EVIDENCE FOR BEHAVIOR CHANGE* (Routledge 2002); see also, Centers for Disease Control and Prevention, *Interim Guidance on Management of Coronavirus Disease 2019 (COVID-19) in Correctional and Detention Facilities* (July 22, 2020), <https://www.cdc.gov/coronavirus/2019-ncov/community/correction-detention/guidance-correctional-detention.html> (providing sample signage).

carrying infection into the jail system. The etiology of COVID-19 is such that individuals can begin to show symptoms anywhere from 2 to 14 days after exposure to infection.¹² If, as appears to be the case, new detainees are released into the general population fewer than 14 days after their arrival, they may carry pre-symptomatic infection with them into the general population during this known window of potential duration before symptom onset. This jail protocol poses a risk to the entire area in which they are housed and in which they move.

iv. Failure to Examine, Isolate, or Provide Adequate Medical Care to Symptomatic Individuals

24. Based on my review of the declarations, the jail is committing critical failures by not responding promptly to reported symptoms, and by failing to isolate or provide adequate medical care to symptomatic individuals. Identifying and isolating symptomatic individuals is one of the most important steps the jail should be taking to mitigate transmission. Individuals with any detected sign or symptom not explained by another clinically diagnosed condition should be removed from the rest of the population, tested, and only returned to the rest of the population upon receiving a negative test result. They should have access to supportive medical

¹² Centers for Disease Control and Prevention, *Symptoms of Coronavirus* (May 13, 2020), <https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html>.

monitoring and care during the entire period they are symptomatic. The jail's failure to follow these commonsense procedures ensures the infection will continue to spread unabated.

25. Declarants describe long delays between reporting symptoms consistent with COVID-19 infection and receiving medical attention. Some report filing medical requests and waiting over a week to be seen by a medical professional.¹³ Others report that, even after notifying multiple members of the jail staff that they are unwell, they were never seen by medical staff.¹⁴ Still another reported no access to the system that allows for communications with the medical staff.¹⁵ Particularly during a pandemic, no detainee should be prohibited or delayed in any way from receiving medical care, yet such delays appear to be routine at the jail. Immediate attention to symptomatic individuals is key to controlling the spread of the virus and should be a priority of jail staff.

26. Multiple declarations also state that sick individuals are only removed a substantial time after their symptoms are first reported, or that the sick people are not isolated at all.¹⁶ These responses from the jail are both medically and

¹³ See, e.g., Decl. of F.S. ¶ 26.

¹⁴ See, e.g., Decl. of W.L.M. ¶¶ 29-34; Decl. of J.H. ¶¶ 30-31.

¹⁵ See Decl. of M.B. ¶ 19.

¹⁶ See, e.g., Decl. of F.S. ¶¶ 23-24; Decl. of W.L.M. ¶ 18-21.

epidemiologically unsupportable. As soon as a person develops any sign or symptom of COVID-19 infection they should be separated from others who have not yet developed any symptoms. All symptomatic individuals should be tested immediately, and those who have been in close contact with the symptomatic person should be quarantined and monitored regularly. The symptomatic person should be isolated and monitored closely in a medical environment, especially if they are older or have any of the medical conditions that predispose someone to severe COVID-19 outcomes (*e.g.*, diabetes, hypertension, etc.).

27. Detainees further describe that the identification of active infection in certain dormitories did not lead to isolation of individuals housed in those units from interaction with other detainees. Most critically, detainees acting in their capacity as trustees were still sent to perform duties in housing units with either confirmed or suspected cases of active COVID-19 infection, thereby exposing to infection themselves, the other detainees with whom they are housed, and as a consequence, all areas of the facility served by trustee labor.¹⁷ The jail's failure to isolate individuals who are presenting with COVID-19 signs and symptoms, whether or not they have yet received a positive COVID-19 test, substantially undermines the

¹⁷ See Decl. of D.H. ¶¶ 13-25.

efficacy of any other efforts to mitigate the spread of infection. It exposes the entirety of the facility and the broader community to ongoing infection.

28. Finally, the jail must ensure that sick individuals receive supportive medical monitoring and care during the entire period they are symptomatic. Based on my review of the declarations, it appears that the jail is largely failing to provide supportive medical care and oversight to symptomatic individuals, even when the individual has been acknowledged by jail staff to be symptomatic and placed into a form of “medical isolation.” One man reported that, 14 days into his “quarantine,” he still had not been seen by a doctor or received any medical treatment.¹⁸ Another reported his symptoms to medical staff and had a COVID-19 test pending, yet he received no medical care and was unable to access help as he experienced a symptomatic attack one night.¹⁹ Finally, a third reported an entire dorm being “locked down” for 17 days, during which time nobody in the dorm received any monitoring of, or treatment for, their symptoms.²⁰ Providing continuous medical

¹⁸ See Decl. of C.C. ¶ 6 (“I never saw a doctor, and I never received any medicine or other medical treatment.”).

¹⁹ See Decl. of W.L.M. ¶ 29 (“At approximately 1:00 a.m., I began to feel severe pain in my lungs; it felt as if my lungs were going to collapse. I could not breathe. I began to bang on my cell door because the emergency call button in my cell does not work. My cellmate, E.R., told me that banging on the door would not work either: no one was coming to help. I believed I was going to die that night.”).

²⁰ Decl. of D.H. ¶¶ 27-28.

care is critical to preventing harm to detainees, and does not apply any less to people who are quarantined or isolated. The jail's medical staff should evaluate all known symptomatic individuals at least once per day and should apply "close monitoring" to all individuals who are at least moderately ill.²¹ Any appropriate evaluation and treatment (such as pulmonary imaging, antibiotics, or oxygen therapy) should be administered without delay.

v. Insufficient Testing Protocols for Reactive Epidemiological Interventions

29. The jail's testing is woefully insufficient to allow for effective epidemiological interventions. It has been shown that individuals may transmit COVID-19 infection prior to the onset of symptoms. In an ideal scenario, the jail would test each individual daily and remove anyone with a positive test from the rest of the population immediately. Due to practical constraints, such as test availability, an acceptable best practice would be to test a random sample of 10% of individuals present in the jail each week (whether symptomatic or not) as an indication of prevalence and an early warning of increased transmission risks. (Note that this would include detainees and staff and the choice of individuals comprising the 10%

²¹ National Institute of Health, *Management of Persons with COVID-19* (June 11, 2020), <https://www.covid19treatmentguidelines.nih.gov/overview/management-of-covid-19/>.

should be newly randomly selected each week.) If conditions in the jail prevent adopting this best practice, an alternative best practice should at least be to monitor the daily temperature of each seemingly healthy detainee and to perform a more thorough test (which could include a breathing test, test of ability to smell, and lung scan) on any individual showing *any* symptoms consistent with COVID-19. Jail staff should actively query individuals regarding the onset of new symptoms, rather than relying only on general surveillance testing or medical requests that involve slow processing times.

30. The jail appears to take a haphazard approach to testing people who are symptomatic. Detainees describe being unable to get tested, even when they are experiencing symptoms and bring those symptoms to the attention of the medical staff.²² The jail's standards for testing people appear to be keyed to temperature.²³ Performing a COVID-19 test only on those detainees who have an elevated body temperature is epidemiologically unsupportable. Some studies have concluded that, early in the progression of symptomatic infection, only 44% of patients exhibited

²² See, e.g., Decl. of D.H. ¶ 23; Decl. of J.H. ¶¶ 30-31; Decl. of Randolph Mitchell ¶¶ 16-17.

²³ See, e.g., Decl. of Barry Watkins ¶ 41 (“The nurse told me I couldn’t receive a test if I wasn’t running a fever. She did not take my temperature to see if I was feverish.”).

fever as a symptom.²⁴ Lack of fever should not be used as a disqualification from being tested for active infectious status. Ideally, testing should be based on identification of exposure to a confirmed COVID-19 case via contact tracing but, at minimum, testing should be employed anytime an individual experiences novel and otherwise medically unexplained presentation of any of the most common symptoms associated with COVID-19.²⁵

C. Conclusion and Recommendation

31. It is my professional judgment that the people incarcerated in the Clayton County Jail are facing risks of exposure to COVID-19 that are drastically higher than those faced by members of the broader community. These risks could be mitigated by a set of minor and reasonable steps consistent with community- and correctional facility-focused recommendations by public health authorities including (but not limited to) the CDC; however the jail has thus far failed to take these steps to prevent the spread and resultant harms of COVID-19. Based on the extensive work I have done on mitigation and containment strategies for infectious disease, it

²⁴ Wei-jie Guan, et al., *Clinical Characteristics of Coronavirus Disease 2019 in China*, 382 *New Eng. J. Med.* 1708 (2020), <https://www.nejm.org/doi/full/10.1056/NEJMoa2002032>.

²⁵ Centers for Disease Control and Prevention, *Symptoms of Coronavirus* (May 13, 2020), <https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html>.

is my opinion that reducing the population of the Clayton County Jail by releasing people who are at heightened risk of harm from COVID-19 and implementing the recommended procedures for mitigating the risk of infection within the facility will substantially reduce the number of COVID-19 infections in the jail. Successful implementation of these strategies will also clearly yield a reduction in the source of risk to the families of jail staff and incarcerated individuals, as well as to the broader community.

32. It is my professional opinion that these steps are both necessary and urgent. Each additional day the jail continues under current operational standards will cost lives in both the incarcerated population and the broader Clayton County community it serves.

33. The health of people in jails and prisons, whether incarcerated or employed within, is inextricably linked with community health. It is essential to protect the health of individuals who are detained in and work in these facilities, for their sake and the sake of the wider community.

I swear under penalty of perjury that the information given herein is true and correct, and I understand that a false answer to any item may result in a charge of false swearing.



Nina H. Fefferman, PhD
Name

July 23, 2020
Date

Knoxville, TN

The University of Tennessee, Knoxville
447 Hesler Biology Building, 1406 Circle Dr.
Knoxville, TN 37996
Phone: 781 710 5025
Fax: 865-974-3067
E-mail: nina.h.fefferman@gmail.com

EXHIBIT A

Nina H. Fefferman

<http://feffermanlab.org>

Nationality: United States of America
Telephone: 781 710 5025
e-mail: nina.h.fefferman@gmail.com

Departments: Ecology and Evolutionary Biology &
Mathematics
Address: 447 Hesler Biology Building
University of Tennessee
Knoxville, TN 37996

Education

- 2005 PhD in Mathematical Biology from the Department of Biology, Tufts University.
Advisor: J. Michael Reed
- 2001 MS in Mathematics from the Department of Mathematics, Rutgers University.
Advisor: J. Beck
- 1999 AB in Mathematics from Princeton University

Positions

- 2020- Associate Director, UT One Health Initiative, University of Tennessee, Knoxville
- 2018- Director, Mathematical Modeling Consulting Center, University of Tennessee, Knoxville
- 2018 - Professor, Depts. of Mathematics & Ecology and Evolutionary Biology, University of Tennessee, Knoxville
- 2016 - 2018 Associate Professor, Depts. of Mathematics & Ecology and Evolutionary Biology, University of Tennessee, Knoxville
- 2015 - 2016 Program Director, Graduate Program in Ecology and Evolution, Rutgers University
- 2012 - 2016 Associate Professor, Dept. of Ecology, Evolution, and Natural Resources, Rutgers University
- 2011 - 2016 Assistant/Associate Professor, School of Public Health, University of Medicine and Dentistry of New Jersey
- 2008 - 2012 Assistant Professor, Dept. of Ecology, Evolution, and Natural Resources, Rutgers University
- 2007 - 2016 Research Assistant/Associate Professor, The Center for Discrete Mathematics and Theoretical Computer Science, Rutgers University
- 2005 - present Co-Director, Tufts University Initiative for the Forecasting and Modeling of Infectious Disease (InForMID), Tufts University School of Medicine
- 2005 - 2007 Visiting Research Associate, Center for Discrete Math and Theoretical Computer Science (DIMACS), Rutgers University
- 2005 Short Term Visitor, School of Natural Sciences, Institute for Advanced Study

Honors/Awards

- 2019 Invited Participant of the 11th. Triennial Invitational Choice Symposium
- 2019 Invited Performer/Participant, Stand Up Science – a public performance featuring stand-up comics and scientists discussing their work
- 2017 Invited Research Team Leader: AWM Women in Mathematical Biology Workshop
- 2016 Invited Speaker at the National Academy of Sciences Sackler Colloquium
- 2015 Coauthored an article chosen for the cover of *Phil Trans Roy Soc B* (issue 370.1665)
- 2012 Invited to Health Foo 2012

- 2011 Shared the Virginia Governor's Technology Award in the category of ‘Cross-Boundary Collaboration in Modeling & Simulation’ for our study ‘Strategic Default in the Context of a Social Network: An Epidemiological Approach’.
- 2010 Speaker at TEDx Midatlantic
- 2009 Rutgers University Packard Fellow Nominee
- 2007 Coauthored an article chosen for the cover of *The Lancet Infectious Diseases* (vol. 7)
- Invited to give 22 Keynote, Plenary, or Public Lectures (see Invited Talks for details), over three continents

Media Coverage (interviews and coverage):

Television/Online Video Broadcasts:

- The Washington Post, 2020
- BBC International, 2020
- WBIR News, 2019
- NJTV News, 2015
- Discovery Channel “How Stuff Works” (Season 2: “Games Unboxed”), 2011
- BBC World News Aug 21, 2007
- CBS News Aug 22, 2007
- Canada Television (CTV) Aug 21, 2007
- AT&T Tech Channel Sept, 2007

Radio Broadcasts:

- NPR Marketplace, Mar 2020
- NPR WUOT Knoxville, Mar 2017
- PRI Studio 360, Sept 2016
- New Tech City, WNYC, Oct 2014
- PRI Studio 360, Sept 2014
- PRI Studio 360, Jan 2013
- BBC UK News, Aug 2007
- National Public Radio Podcast “Science Friday”, Sept 2007
- AM900 CHML, Sept 2007
- National Public Radio “All Things Considered”, Oct 2005

Print/Online Media (2005-present):

ABC News, ABS CBN News, ARS Technical, Canadian Press (via CBC), Cell, The Daily Mail (UK), The Daily Telegraph (Australia), The Economist, Forbes, Fox News, G1.com.br (Brazil), The Gist (Slate.com), O Globo (Brazil), Gazet Van Antwerpen (Belgium), La Jornada (Mexico), KevinMD, Knox News, Medical News Today, New Scientist, NU.nl (Netherlands), PC Gamer, Politico.com, Reuters, TIME, The Washington Post, Science News, Slate.com, the South African Star, Tech News World, Wired, Yahoo! Entertainment, You Made I *and many more...*

Research Support (reverse chronological order by start date)

Active

2020-2021	\$198,932	NSF RAPID – DEB Coupled Social and Epidemiological Networks and COVID-19	PI
2020-2022	\$359,849	DoD Minerva DECUR - The Topology of Interdependent Multi-Domain Behavioral Systems	PI
2017-2022	\$138,964	NSF IOS - Melding Mathematical and Theoretical	UT-PI

Models of Stress			
2017-2021	\$2,498,876	NSF EEID – Co-evolutionary Epidemiology of Avian Malaria	UT-PI
Completed			
2018-2020	\$196,628	SESYNC/NIMBioS Modeling Risk Perception, Vector-borne Diseases, and Environmental Integrity	PI
2018-2019	\$2,000	Haines Morris Grant – Internal UTK Competition	Co-PI
2017	\$30,000	Syngenta – Workshop Grant – Math of Agribusiness	Co-I
2016-2019	\$99,938	NSF EAGER – CISE – Distributed Anomaly Detection	PI
2016-2018	\$50,000	US - Israel Binational Science Foundation (BSF)	Co-PI
2016-2018	\$190,000	NSF RAPID – DEB – Modeling Zika Virus Control	PI
2016-2017	\$75,000	US START Center – Leadership in Social Networks	PI
2016-2017	\$100,000	National Academies Keck Futures Initiative	Co-PI
2015-2018	\$292,804	USFWS – White-Nose Syndrome Open Grant	Co-PI
2015-2017	\$21,003	NSF RAPID – Information & Intelligent Systems – Virtual Worlds and Experiential Learning	PI
2015-2017	\$130,000	NSF EAGER – DEB – Machine Learning for Co-Evolutionary Systems	Co-PI
2014-2016	\$100,000	Dept. of Homeland Security – Next Generation Communications and Interoperability	Project PI
2011-2014	\$3,853,332	NSF EASM – Ocean Sciences – SocioEconomic Systems and Climate Change	Co-PI
2011-2012	\$22,500	UCDPER – Emergency Preparedness	Co-PI
2010-2012	\$384,000	Dept. of Homeland Security – Virtual Worlds and Experiential Education	Project PI
2010-2011	\$99,944	Dept. of Homeland Security – Self-Organizing Surveillance Systems	Project PI
2010	\$22,500	Dept. of Homeland Security – BioSecurity	Co-PI
2009-2012	\$299,886	NSF – DEB – ULTRA-Ex	Co-PI
2009-2011	\$89,318	UCDPER – Emergency Preparedness	PI
2009-2010	\$10,000	USDA CSREES Multi-State Research Fund – Vector-borne Disease Control	Co-I
2008	\$99,990	NIH NAID SBIR – Epidemiological Surveillance	PI
2008	\$5,000	Rutgers Climate and Environmental Change Initiative	PI
2008	\$75,000	Rutgers Academic Excellence Fellowship, Climate and Health Research Initiative	Co-I
2007	\$22,500	Dept. of Homeland Security – BioSecurity	PI
2007	\$22,500	Dept. of Homeland Security – BioSecurity	PI
2006	\$5,000	Tufts Summer Scholars Award – Epidemiology	PI
2003-2004	\$42,000	NIH R01 Supplement - Epidemiology	Co-PI
2003-2004	\$1,500	Tufts Institute of the Environment	Co-I
2003	\$500	MASI Student Travel Award	PI
2003	\$1,500	TIES Student Travel Award	PI

Consultancies

2020	American Civil Liberties Union (ACLU)
2020	The State of Vermont, Department of Education
2018	Ogilvy

2017-present	Humane Society International
2009-present	US Centers for Disease Control
2011-2012	Research Institute for Housing America Trust Fund
2006-2007	New Jersey, Department of Corrections
2004-2009	NIH U19 (Center PI: Gorski) T-cell Mediated Immunity
2004	National Defense University
2004	DARPA

Participation in Research Centers

Center	Position	Description of Role
NIMBioS (National Institute for Mathematical and Biological Synthesis)	Leadership Team	Active participant in working group, organizer of multiple tutorials, mentor for summer research experience for undergraduates, and founding director of the Mathematical Modeling Consulting Center
InForMID (Tufts University Initiative for the Forecasting and Modeling of Infectious Diseases)	Center Co-Director	Researcher and Administrative lead in the area of mathematical modeling of infectious disease epidemiology
CCICADA (US Dept of Homeland Security Command, Control, and Interoperability Center for Advanced Data Analysis)	Project PI	Principle Investigator into data analysis relating to social behavior in virtual/technologically enable environments, bio-security, and bio-inspired algorithms in cyber-security
DIMACS (The Center for Discrete Mathematics and Theoretical Computer Science)	Member	Active participant in working groups, collaborations, and conferences (including acting as organizer for multiple workshops/conferences/tutorials) in all areas of mathematical macrobiology
START (US Dept of Homeland Security Center for the Study of Terrorism and Responses to Terrorism)	Project PI	Principle Investigator working on understanding social behavior and algorithms driving the emergence of extremism and leadership in

Publications (peer reviewed):

* = a student or post-doctoral researcher advised by Fefferman during the research effort reported

Journal Articles:

Published or In Press

70. Udiani*, O. and N.H. **Fefferman**. (In press) How Disease Risk Constrains the Evolution of Social Systems. *Proceedings of the Royal Society, B*.

69. Jiao*, J., M. Gilchrist, and N.H. **Fefferman**. (In press) The Impact of Host Metapopulation Structure on Short-term Evolutionary Rescue in the Face of a Novel Pathogenic Threat. *Global Ecology and Conservation*.
68. Lemanski*, N., S. Schwab, D. Fonseca, and N.H. **Fefferman**. 2020. Coordination Among Neighbors Improves the Efficacy of the Zika Control Despite Economic Costs. *PLoS Neglected Tropical Diseases*. 14(6): e0007870.
67. Wilson, S., S. Sindi, H. Brooks, M. Hohn, C. Price, A. Radunskaya, N. Williams, and N.H. **Fefferman**. 2020. How Emergent Social Patterns in Allogrooming Combat Parasitic Infections. *Frontiers in Ecology and Evolution*. 8:54.
66. DeNegre*, A., Myers*, K., and N.H. **Fefferman**. 2020. Impact of Strain Competition on Bacterial Resistance in Immunocompromised Populations. *Antibiotics*. 9(3):114
65. Myers*, K., A. Redere*, and N.H. **Fefferman**. 2020. How Resource Limitations and Household Economics May Compromise Efforts to Safeguard Children During Outbreaks. *BMC Public Health*. 20(1):1-14.
64. Suarez*, G., O. Udiani*, B. Allan, C. Price, S. Ryan, E. Lofgren, A. Coman, C. Stone*, L. Gallos*, and N.H. **Fefferman**. 2020. A Generic Arboviral Model Framework for Exploring Trade-offs Between Vector Control and Environmental Concern. *Journal of Theoretical Biology*. 490 (2020) 110161.
63. DeNegre*, A., Myers*, K., and N.H. **Fefferman**. 2020. Impact of Chemoprophylaxis Policy for AIDS-immunocompromised Patients on Emergence of Bacterial Resistance. *PLoS One*. 15(1): e0225861.
62. Gallos*, L., S. Havlin, G. Stanley, and N.H. **Fefferman**. 2019. Proximity drives the emergence of network structure and density. *Proceedings of the National Academy of Sciences*. 116(41):20360-20365.
61. Stone*, C., S. Schwab*, D. Fonseca, and N.H. **Fefferman**. 2019. Contrasting the Value of Targeted vs. Area-Wide Mosquito Control Scenarios to Limit Arbovirus Transmission for Different Tropical Urban Population Centers. *PLoS Neglected Tropical Diseases*. 13.7: e0007479.
60. Myers*, K, A. DeNegre*, L.K. Gallos*, N. Lemanski*, A. Mayberry, A. Redere*, S. Schwab*, O. Stringham, & N.H. **Fefferman**. 2019. Dynamic Ad Hoc Social Networks in Improvised Intelligence / Counter-Intelligence Exercises: A Department of Homeland Security Red-Team Blue-Team Live-Action Roleplay. *Journal of Homeland Security and Emergency Management*. <https://doi.org/10.1515/jhsem-2018-0027>.
59. Suarez*, G.P., L.K. Gallos, and N.H. **Fefferman**. 2019. A Case Study in Tailoring a Bio-Inspired Cyber-Security Algorithm: designing anomaly detection for multilayer networks. *Journal of Cyber Security and Mobility*. 8(1):113-132.
58. DeNegre*, A., K. Myers*, M. Ndeffo, and N.H. **Fefferman**. 2019. Emergence of Antibiotic Resistance in Immunocompromised Host Populations. *PLoS One* 14 (2), e0212969.
57. Schwab*, S., C. Stone*, D. Fonseca, and N.H. **Fefferman**. 2019. (Meta)population Dynamics Determine Effective Spatial Distributions of Mosquito-Borne Disease Control. *Ecological Applications* 29(3): e01856.
56. Kebir*, A., N.H. **Fefferman**, and S.B. Miled. 2018. A general structured model of a hermaphrodite population. *Journal of Theoretical Biology*. 449:53-59.
55. Lemanski*, N.J. and N.H. **Fefferman**. 2018. Expanding the evolutionary theory of aging: honeybees as a test case for an optimal decision making model of senescence. *American Naturalist*. 191(6):756-766.

54. Schwab*, S., C. Stone*, D. Fonseca, and N.H. **Fefferman**. 2018. The importance of being urgent: the impact of surveillance target and scale on mosquito-borne disease control. *Epidemics*. 23:55-63.
53. Beckage, B., L. Gross, S. Metcalf, E. Carr, K. Lacasse, J. Winter, P. Howe, N. **Fefferman**, A. Zia, and T. Franck. 2018. Integrating human behavior and risk perception into a climate model. *Nature Climate Change*. 8:79–84.
52. Maslo, B., O. Stringham, A. Bevan, A. Brumbaugh, C. Sanders, M. Hall, and N.H. **Fefferman**. 2017. High Survival of Some Infected Bat Populations Veils a Persistent Extinction Risk from White-nose Syndrome. *Ecosphere*. 8(12):e02001.10.1002/ecs2.2001.
51. Stone*, C.M., S.R. Schwab*, D.M. Fonseca, N.H. **Fefferman**. 2017. Human movement, cooperation, and the effectiveness of coordinated vector control strategies. *Journal of the Royal Society Interface*. 14(133):20170336.
50. Lemanski*, N.J. and N.H. **Fefferman**. 2017. Coordination Between the Sexes Constrains the Optimization of Reproductive Timing in Honey Bee Colonies *Nature Scientific Reports*. 7:2740.
49. Egizi, A., N.H. **Fefferman**, and R. Jordan. 2017. Relative Risk of Infection with Ehrlichiosis Agents and Lyme Disease in an Area Where Both Vectors are Sympatric. *Emerging Infectious Diseases*. 23(6):939-945.
48. Greenbaum*, G. and N.H. **Fefferman**. 2017. Application of network methods for understanding evolutionary dynamics in discrete habitat. *Molecular Ecology*. DOI: 10.1111/mec.14059
47. Maslo, B., R. Valentin, K Leu, K Kerwin, A Bevan, G.C. Hamilton, N.H. **Fefferman**, and D.M. Fonseca. 2017. ChiroSurveillance: The Use of Native Bats to Detect Invasive Agricultural Pests. *PLoS One*. 12(3), e0173321.
46. Robinson*, O.J., O.P. Jensen, M.M. Provost, S. Huang, N.H. **Fefferman**, A. Kebir and J.L. Lockwood. 2017. Evaluating the vulnerability of sex-changing fish to harvest: A game-theoretic approach. *ICES Journal of Marine Science*. 74(3):652-659.
45. Gallos*, L., M. Korczynski*, and N.H. **Fefferman**. 2017. Anomaly Detection Through Information Sharing Under Different Topologies. *EURASIP Journal on Information Security*. 2017:5. DOI:10.1186/s13635-017-0056-5.
44. Maslo, B., S. Gignoux-Wolfsohn, and N.H. **Fefferman**. 2017. Success of Wildlife Disease Treatment Depends on Host Immune Response. *Frontiers in Ecology and Evolution*. 5(28).
43. Lofgren*, E., A. Egizi, and N.H. **Fefferman**. 2016. Patients as Patches: Ecology and Epidemiology in Healthcare Environments. *Infection Control and Hospital Epidemiology*. 37(12):1507-1512.
42. Korczynski*, M., A. Hamieh*, J. H. Huh, H. Holm, S. R. Rajagopalan, and N. H. **Fefferman**. 2016. Hive Oversight for Network Intrusion Early Warning Using DIAMoND: A Bee-Inspired Method for Fully Distributed Cyber Defense. *IEEE Communications Magazine* 54(6):60-67.
41. Gallos*, L. and N.H. **Fefferman**. 2015. Simple and efficient self-healing strategy for damaged complex networks. *Physical Reviews E*. 92(5):052806.
40. Kebir*, A., N.H. **Fefferman**, S. Ben Miled. 2015. Understanding hermaphrodite species through game theory. *Journal of Mathematical Biology*. 71(6-7):1505-1524.
39. Gallos*, L., and N.H. **Fefferman**. 2015. The Effect of Disease-Induced Mortality on Structural Network Properties. *PLoS One*. DOI: 10.1371/journal.pone.0136704
37. Burkhalter*, J.C., N.H. **Fefferman**, and J.L. Lockwood. 2015. The impact of personality on the success of prospecting behavior in changing landscapes. *Current Zoology*. 61:557-568.

36. Robinson*, O., J. Lockwood, O. Stringham*, and N.H. **Fefferman**. 2015. A Novel Tool for Making Policy Recommendations Based on PVA:Helping Theory Become Practice. *Conservation Letters*. 8(3):190-198.
35. **Fefferman**, N.H. and E.N. Naumova. 2015. Dangers of vaccine refusal near the herd immunity threshold: a modelling study. *Lancet Infectious Diseases*. S1473-3099(15)70130-1
34. Maslo, B. and N.H. **Fefferman**. 2015. A Case Study of Bats and White-Nose Syndrome Demonstrating How to Model Population Viability with Evolutionary Effects. *Conservation Biology*. 29(4):1176-1185. DOI: 10.1111/cobi.12485.
33. Parham, P E. J. Waldoock, G.K. Christophides, D. Hemming, F. Agosto, K. J. Evans, N.H. **Fefferman**, H. Gaff, A. Gumel, S. LaDeau, S. Lenhart, R.E. Mickens, E. Naumova, R. Ostfeld, P. Ready, M. Thomas, J. Velasco-Hernandez, E. Michael. 2015. Climate, Environmental, and Socioeconomic Change – Weighing up the Balance in Vector-Borne Disease Transmission. *Philosophical Transactions of the Royal Society B*. 370.1665 (2015): 20130551.
32. Egizi, A., N.H. **Fefferman**, and D. M. Fonseca. 2015. Evidence that implicit assumptions of “no evolution” of disease vectors in changing environments can be violated on a rapid timescale. *Philosophical Transactions of the Royal Society B*. 370.1665 (2015): 20140136.
31. Greening*, B., N. Pinter-Wollman, and N.H. **Fefferman**. 2015. Higher-Order Analysis of Information Sharing and Knowledge Capacity in Animal Social Groups *Current Zoology*. 61(1): 114–127.
30. Gallos*, L. and N.H. **Fefferman**. 2014. Revealing effective classifiers through network comparison. *Europhysics Letters*. 108(3): 38001.
29. Lofgren*, E.T., R.W. Moehring, D.J. Anderson, D.J. Weber, and N.H. **Fefferman**. 2014. A Mathematical Model to Evaluate the Routine Use of Fecal Microbiota Transplantation to Prevent Incident and Recurrent *Clostridium difficile* Infection. *Infection Control and Hospital Epidemiology*. 35(1):18-27.
28. Greening*, B. and N.H. **Fefferman**. 2014. Evolutionary Significance of the Role of Family Units in a Broader Social System. *Nature Scientific Reports*. 4: 3608
27. Seiler, M.J., Collins, A.J., and N.H. **Fefferman**. 2013. Strategic Mortgage Default in the Context of a Social Network: An Epidemiological Approach. *Journal of Real Estate Research* 35(4).
26. Robinson*, O.J., N.H. **Fefferman**, and J.L. Lockwood. 2013. How to effectively manage invasive predators to protect their native prey. *Biological Conservation* 165: 146-153.
25. **Fefferman**, N.H., and L.M. Romero. 2013. Can physiological stress alter population persistence? A model with conservation implications. *Conservation Physiology*. 1(1): cot012. doi: 10.1093/conphys/cot012
24. Moorthy, M., D. Castronovo, A. Abraham, S. Bhattacharyya, S. Gradus, J. Gorski, Y.N. Naumov, N.H. **Fefferman**, and E.N. Naumova. 2012. Deviations in influenza seasonality: odd coincidence or obscure consequence? *Clinical Microbiology and Infection*. 18(10):955-962.
23. Hock*, K. and N.H. **Fefferman**. 2012. Social organization patterns can lower disease risk without associated disease avoidance or immunity. *Ecological Complexity*. 12:34–42.
22. Hock*, K. and N.H. **Fefferman**. 2011. Violating Social Norms when Choosing Friends: How Rule-Breakers Affect Social Networks. *PLoS One*. 2011; 6(10): e26652
21. Hock*, K. and N.H. **Fefferman**. 2011. Extending the role of social networks to study social organization and interaction structure of animal groups. *Annales Zoologici Fennici*. 48(6):365-370.

20. Kafai, Y.B. and N.H. **Fefferman**. 2010. Virtual Epidemics as Learning Laboratories in Virtual Worlds. *Journal of Virtual Worlds Research*. 3(2):2-15.
19. Hock*, K., K.L. Ng, and N.H. **Fefferman**. 2010. Systems approach to studying animal sociality: individual position versus group organization in dynamic social network models. *PLoS One*. 5(12): e15789.
18. **Fefferman**, N.H. and E.N. Naumova. 2010. Innovation in Observation: A Vision for Early Outbreak Detection. *Emerging Health Threats*. 3:e6. doi: 10.3134/ehjt.10.006
17. Lofgren*, E.T., J.B. Wenger, N.H. **Fefferman**, D. Bina, S Gradus, S. Bhattacharyya, Y.N. Naumov, J. Gorski, E.N. Naumova. 2010. Disproportional Effects in Populations of Concern for Pandemic Influenza: Insights from Seasonal Epidemics in Wisconsin, 1967-2004. *Influenza and Other Respiratory Diseases*. 4:205-212.
16. Phan, L., N.H. **Fefferman**, D. Hui, and D. Brugge. 2010. Impact of Street Crime on Boston Chinatown. *Local Environment*. 15(5):481-491.
15. Reed, J.M., N.H. **Fefferman**, and R.C. Averil-Murray. 2009. Vital Rate Sensitivity Analysis and Management Implications for Desert Tortoise. *Biological Conservation*. 14(12): 2813-3222.
14. Wilson-Rich, N., Spivak, M., **Fefferman**, N.H., Starks, P.T. 2009. Genetic, Individual, and Group Facilitation of Disease Resistance in Insect Societies. *Annual Reviews of Entomology*. 54:405-23.
13. **Fefferman**. N.H. 2008. Biological Experimentation *in silico*. *Annales Zoologici Fennici*, 45: 367-368.
12. Lofgren*, E., M. Senese*, J. Rogers* and N.H. **Fefferman**. 2008. Pandemic Preparedness Strategies for School Systems: Is Closure Really the Only Way? *Annales Zoologici Fennici*, 45: 449-458.
11. **Fefferman**, N.H. and K.L. Ng*. 2007. How Disease Models on Static Graphs Fail to Approximate Epidemics in Shifting Social Networks. *Physical Review E*. 76:031919. (This article was selected for reprinting by the *Virtual Journal of Biological Physics Research 2007*)
10. Lofgren*, E. and N.H. **Fefferman**. 2007. The Untapped Potential of Virtual Game Worlds to Shed Light on Real World Epidemics. *The Lancet Infectious Diseases*. 7:625–629. (article content was the cover of the journal)
9. Lofgren*, E., N.H. **Fefferman**, Y.N. Naumov, J. Gorski and E.N. Naumova. 2007. Influenza Seasonality: Underlying Causes and Modeling Theories. *Journal of Virology*, 81(11):5429-5436.
8. Lofgren*, E., N.H. **Fefferman**, M. Doshi and E.N. Naumova. 2007. Assessing Seasonal Variation in Multisource Surveillance Data: Annual Harmonic Regression. *Lecture Notes in Computer Science*. BioSurveillance 2007. eds D. Zeng et al. 4506:114-123.
7. **Fefferman**, N.H. and K.L Ng*. 2007. The role of individual choice in the evolution of social complexity. *Annales Zoologici Fennici*, 44:58-69.
6. **Fefferman**, N.H., J.F.A. Traniello, R.B. Rosengaus and D.V. Calleri. 2007. Disease Prevention and Resistance in Social Insects: Modeling the Survival Consequences of Immunity, Hygienic Behavior and Colony Organization. *Behavioral Ecology and Sociobiology*, 61:565-577.
5. Starks, P.T.B. and N.H. **Fefferman**. 2006. Polistes Nest Founding Behavior: a Model for the Selective Maintenance of Alternative Behavioral Phenotypes. *Annales Zoologici Fennici*, 43:456-467.
4. **Fefferman**, N.H., and E.N. Naumova. 2006. Combinatorial Decomposition of an Outbreak Signature. *Mathematical Biosciences*, 202(2):269-287.

3. **Fefferman**, N.H. and J.M. Reed. 2006. A Vital Rate Sensitivity Analysis that is Valid for Non-Stable Age Distributions and for Short-Term Planning. *The Journal of Wildlife Management*, 70(3):649-656.
2. **Fefferman**, N.H., and P.T.B. Starks. 2006. A Modeling Approach to Swarming in Honey Bees. *Insectes Sociaux*, 53(1):37-45.
1. **Fefferman**, N.H., E.A. O'Neil, and E.N. Naumova. 2005. Confidentiality vs Confidence: The aggravation of aggregation as a remedy in public health. *Journal of Public Health Policy*, 26(4):430-449.

Under Review:

13. Carrignon, S., R.A. Bentley, M.J. Silk, and N.H. **Fefferman**. The 'Icarus Effect' of Preventative Health Behaviors. (Under Review)
12. Silk, M.J., S. Carrignon, R.A. Bentley, and N.H. **Fefferman**. Improving Pandemic Mitigation Policies Across Communities Through Coupled Dynamics of Risk Perception and Infection (Under Review)
11. **Fefferman**, N.H., E.T. Lofgren, N. Li, P. Blue, D.J. Weber, and A.A. Yakubu. Fear, Access, and the Real-Time Estimation of Etiological Parameters for Outbreaks of Novel Pathogens. (Under Review)
10. **Fefferman**, N.H., S. DeWitte, S.S. Johnson, and E.T. Lofgren. Leveraging Insight from Centuries of Outbreak Preparedness to Improve Modern Planning Efforts. (Under Review)
9. **Fefferman**, N.H. and O. Udiani. Workforce Training, Deployment, Protection, and Management in the Wake of a Pandemic. (Under Review).
8. Lofgren, E. K. Lum, A. Horowitz, B. Madubonwu, K. Myers, and N. H. **Fefferman**. The Epidemiological Implications of Jails for Community, Corrections Officer, and Incarcerated Population Risks from COVID-19. (Under Review).
7. Feinberg, F., A. Patania, B. McShane, B. Falk, D. Larremore, E. Feit, J. Helveston, M. Small, M. Braun, N. **Fefferman**, and E. Bruch. A Framework for Studying Choices in Networks. (Under Review)
6. Beckage, B., K. Lacasse, J.M. Winter, N.H. **Fefferman**, F.M. Hoffman, L.J. Gross, S.S. Metcalf, T. Franck, E. Carr, A. Zia, and A. Kinzig. The Earth has humans, so why don't our climate models? (Under Review)
5. Udiani*, O., K. Lacasse, A. Zia, L. Gallos*, P. Zhong*, B. Beckage, E. Carr, T. Franck, L. Gross, F. Hoffman, P. Howe, A. Kinzig, S. Metcalf, J. Winter, and N.H. **Fefferman**. Recruitment and Mobilization for Social Movements: implications from network modeling. (Under Review)
4. Udiani*, O., and N.H. **Fefferman**. Could the Need for Rest Provide a Pathway for the Evolution of Division of Labor in Social Species? (Under Review)
3. Gignoux-Wolfsohn, S.A., Pinsky, M.L., Kerwin, K., Herzog, C., Hall, M., Bennett, A.B., **Fefferman**, N.H. and Maslo, B., Genomic signatures of evolutionary rescue in bats surviving white-nose syndrome. (Under Review)
2. Hobson, E.A., M.J. Silk, N.H. **Fefferman**, D.B. Larremore, P. Rombach, S. Shai, and N. Pinter-Wollman. What Are Your Social Questions? Identifying Appropriate Reference Models When Animals Don't Live in Asymptopia. (Under Review)
1. Siewe*, N., B. Greening*, and N.H. **Fefferman**. The Potential Role of Asymptomatic Infection in Outbreaks of Emerging Pathogens (Under Review)

Book Chapters:

Published or In Press

10. **Fefferman**, N.H. When to Turn to Nature-Inspired Solutions for Cyber Systems. 2019. in Nature-Inspired Security and Resilience. eds. Eltoweissy, Elalfy, Fulp, and Mazurczyk. pp 29-50. The Institution of Engineering and Technology, London, UK.
9. Price, C.R. and N.H. **Fefferman**. 2019. A Preliminary Exploration of the Professional Support Networks the EDGE Program Creates. in A Celebration of the EDGE Program's Impact on the Mathematics Community and Beyond (pp. 317-325). Springer, Cham.
8. Brooks. H.Z., M.E. Hohn, C. Price, A.E. Radunskaya, S.S. Sindi, N.D. Williams, S.N. Wilson, N.H. **Fefferman**. 2018. Mathematical Analysis of the Impact of Social Structure on Ectoparasite Load in Allogrooming Populations. in Understanding Complex Biological Systems with Mathematics eds. A. Radunskaya, R. Segal, B. Shtylla. Association for Women in Mathematics Series, vol 14. pp 47-61. Springer
7. Williams, N.D., H.Z. Brooks, M.E. Hohn, C. R. Price, A.E. Radunskaya, S.S. Sindi, S.N. Wilson, and N. H. **Fefferman**. 2018. How Disease Risks Can Impact the Evolution of Social Behaviors and Emergent Population Organization. in Understanding Complex Biological Systems with Mathematics eds. A. Radunskaya, R. Segal, B. Shtylla. Association for Women in Mathematics Series, vol 14. pp 31-46. Springer
6. Korczynski*, M., A. Hamieh*, J.H. Huh, H. Holm, S. R. Rajagopalan, and N.H. **Fefferman**. 2017. DIAMoND: Distributed Intrusion/Anomaly Monitoring for Nonparametric Detection (invited extended version). in Security, Privacy and Reliability in Computer Communications and Networks. eds. K. Sha, A Striegel, and M Song. River Publishers Series in Communications. River Publishers.
5. **Fefferman**, N.H. and L.M. Fefferman. 2011. Mathematical Macrobiology: An Unexploited Opportunity in High School Education. in Biomath in the Schools. eds. M.B. Cozzens, and F.S. Roberts. DIMACS Series in Discrete Mathematics and Theoretical Computer Science. Vol 76. American Mathematical Society.
4. Jagai, J., N.H. **Fefferman** and E.N. Naumova. 2011. Waterborne Disease Surveillance. in Encyclopedia of Environmental Health. eds. J. Nriagu, S. Kcew, T. Kawamoto, J. Patz, and D. Rennie. Elsevier Science. 1st edition
3. Ji, S., W.A. Chaovalitwongse, N.H. **Fefferman**, W. Yoo, and J.E. Perez-Ortin. 2009. Mechanism-based Clustering of Genome-wide RNA Levels: Roles of Transcription and Transcript-Degradation Rates. in Clustering Challenges in Biological Networks. eds. S. Butenko, P.M. Pardalos, and W.A. Chaovalitwongse. World Scientific Publishing Company.
2. **Fefferman**, N.H. and J.F.A. Traniello. 2008. Social Insects as Models in Epidemiology: Establishing the Foundation for an Interdisciplinary Approach to Disease and Sociality. in Organization of Insect Societies: From Genome to Sociocomplexity eds J. Gadau and J. Fewell. Harvard University Press
1. MacLeod, N., N. Ortiz, N.H. **Fefferman**, W. Clyde, C. Schuller, and J. MacLean. 2000. Phenotypic Response of Foraminifera to episodes of global environmental change. in Biotic Response to Global Change. eds S.J. Culver and P. Rawson. Cambridge University Press

Edited Volumes:

1. **Fefferman**, N.H. (Ed.) (2008) *Annales Zoologici Fennici* 45(5)

Peer Reviewed Contributed Conference Papers:

8. Suarez*, G.P., L.K. Gallos, and N.H. **Fefferman**. 2018. A Case Study in Tailoring a Bio-Inspired Cyber-Security Algorithm: designing anomaly detection for multilayer networks. *2018 IEEE Security and Privacy Workshops (SPW)*. IEEE, 2018.

7. Fields, D. A., Kafai, Y. B., Giang, M. T., **Fefferman**, N., & Wong, J. 2017. Plagues and people: Mass community participation in a virtual epidemic within a tween online world. *Proceedings of the 12th International Conference on the Foundations of Digital Games*. DOI: 10.1145/3102071.3102108
6. Kafai, Y. B., Fields, D. A., Giang, M. T., **Fefferman**, N., Sun, J., Kunka, D., & Wong, J. 2017. Designing for massive engagement in a tween community: Participation, prevention, and philanthropy in a virtual epidemic. In *Interaction Design & Children Conference*. New York: ACM, 365-370. ISBN: 978-1-4503-4921-5
5. Fields, D. A., Kafai, Y. B., Giang, M. T., **Fefferman**, N., & Wong, J. 2017. The Dragon Swooping Cough: Mass community participation in a virtual epidemic within a tween online world. In B. Smith, M. Borge, E. Mercier & K. Y. Lim (Eds.) *Proceedings of the 12th International Conference on Computer Supported Collaborative Learning*, Volume 2 (pp. 865-866). Philadelphia, PA: International Society of the Learning Sciences.
4. Fields, D. A., Kafai, Y. B., Sun, J., **Fefferman**, N., Ellis, E., DeVane, B., Giang, M. T., & Wong, J. 2016. The great dragon swooping cough: Stories about learning designs in promoting participation and engagement with a virtual epidemic. In Barany, A., Slater, S., & C. Steinkuehler (Eds.), *Proceedings of the Games + Learning + Society (GLS) 12.0 Conference* (pp. 419-424). Pittsburgh, PA: ETC Press.
3. Verma, S., A. Hamieh*, J. H. Huh, H. Holm, S. R. Rajagopalan, M. Korczynski*, and N. H. **Fefferman**. 2016. Stopping Amplified DNS DDoS Attacks Through Query Rate Sharing Between DNS Resolvers, to appear in the International Conference on Availability, Reliability and Security (ARES). (Note: this is the proceeding of a conference, not a journal, but is equivalent to journal publication for the field of computer science, however in keeping with the conventions of Biology, Fefferman is last author as PI on the sponsoring grant that funded the research.)
2. Korczynski*, M., A. Hamieh*, J.H. Huh, H. Holm, S. R. Rajagopalan, and N.H. **Fefferman**. 2015. DIAMoND: Distributed Intrusion/Anomaly Monitoring for Nonparametric Detection. *CCCN 2015: 24th International Conference on Computer Communications and Networks, IEEE, 2015*. (Note: this is the proceeding of a conference, not a journal, but is equivalent to journal publication for the field of computer science, however in keeping with the conventions of Biology, Fefferman is last author as PI on the sponsoring grant that funded the research.)
1. **Fefferman**, N.H., J. Jagai, and E.N. Naumova. 2004. Two - Stage Wavelet Analysis Assessment of Dependencies in Time Series of Disease Incidence. *Proceedings of the 2004 Conference of the International Environmetrics Society*

Research Mentoring

(bold = current)

Undergraduate Researchers:

Shyretha Brown, Danika Chari, Kaige Chen, Ian Clark, Liz Davis, Anne Eaton, Taylor Eisenstein, Brandon Grandison, Derek Hansen, David Haycraft, John Huffman, Ana Kilgore, John Kim, Edward Lee, Somair Malik, Andrew McConvey, Jeffrey Mandell, Zain Paracha, Luke Postle, Lauren Prince, Asya Pritsker, Cathy Reis, Jeremiah Rogers, Bolanle Salaam, Nicole Scholtz, Margaret Senese, Joshua Smith, Andrew Sohn, Kim Stanek, Johanna Tam, Colleen Thiersch, Elena Tsvetkova, Barton Willage, Immanuel Williams, Nakeya Williams, Barry Walker, Hannah Yin, Yi Ming Yu, Yongqing Yuan, Stefanie Yuen, James Xue, Bobby Zandstra

Graduate Researchers:

*(Committee Member, or Advisor for work on funded research projects – not primary dissertation advisor; * = special case)*

Kevin Aagard, Emma Bell, Carissa Bleker, Curtis Burkhalter, Jordan Bush, Huilan Chang, Erick Chastain, Fnu Eric Ngang Che, **Brittany Coppinger**, Ashley Crump, Kathryn Fair, Alison Golinski, **Stephen Grady**, Gili Greenbaum, Candice JeanLouis, **Hwayoung Jung**, Ariel Kruger, Di Li, Eric Lofgren*, Nicholas Lorusso, Adam Marszalek, Benjamin McClendon, Anthony Ogbuka, Paul Raff, Orin Robinson, Margarete Romero, Rajat Roy, Liliana Salvador, **Shelby Scott**, Tinevimbo Shiri, Brittany Stephenson, Alex Thorn, Rafael Valentine, Alex Villiard, Orion Weldon

(primary research advisor to)

Jessica Beck, **Kelly Buch**, Ashley DeNegre, **Jeff DeSalu**, Brad Greening, Natalie Lemanski, **Agnesa Redere**, Samantha Schwab, **Anna Sisk** (co-advised), Oliver Stringham, Karen Wylie

Post-Doctoral Researchers:

Dr. Erick Chastain, Dr. Lazaros Gallos, Dr. Manuel Garcia-Quisimondo, Dr. Ali Hamieh, Dr. Karlo Hock, Dr. Cindy Hui, **Dr. Jing Jiao**, Dr. Amira Kebir, Dr. Maciej Korczynski, Dr. Natalie Lemanski, Dr. Kellen Myers, Dr. Kah Loon Ng, Dr. Chris Stone, Dr. Nourridine Siewe (co-advised by Prof. S. Lenhart), Dr. Gonzalo Suarez, **Dr. Oyita Udiani**, Dr. Peng Zhong

Courses Developed and Taught (all courses developed from scratch)

- Advanced Mathematical Ecology II (MAT/EEB 682 – University of Tennessee, Knoxville) Spring 2017 and 2019
- Evolution, Disease, and Medicine (ENR110 – Rutgers University / EEB 310 – UT, Knoxville) Fall each year 2009 – 2014, Spring 2018 and 2020
- Conversational Bio-Mathematical Modeling (ENR 428 – Rutgers University/ EEB 475 – UT, Knoxville) Spring 2011 – 2014, 2020
- Problems in Ecology: Academic Pedagogy (ENR 601 – Rutgers University) Fall 2015
- *(Co-Developed and Taught)* Ethics & Professional Development in Ecology and Evolution (ENR 602 01 – Rutgers University) Spring 2013-2016 (exception – sabbatical Fall 2014-Spring 2015)
- Introduction to Modeling Ecology, Evolution, and Epidemiology (ENR 604 – Rutgers University) Spring each year 2010 – 2016 (exception – sabbatical Fall 2014-Spring 2015)
- Introduction to Epidemiological Modeling (ENR 603 – Rutgers University) Fall each year 2009 – 2012
- Elements of Data Analysis and Epidemiology (CMPH 343 – Tufts University School of Medicine) Spring 2006

Professional Memberships

Association for Women in Mathematics (AWM)
Association for Women in Science (AWIS)
Complex Systems Society (CSS)
Institute of Electrical and Electronics Engineers (IEEE)
International Union for the Study of Social Insects (IUSSI)
Society for Industrial and Applied Mathematics (SIAM)
Society for Mathematical Biology (SMB)

Invited Presentations

2020

Session Keynote: “Logic, Equations, Data: From each according to their ability,” Intelligent Systems for Molecular Biology (ISMB) 2020, COVID-19 Session (conference shifted to virtual meeting)

Public Webinar: “Invasive Species Policy and COVID-19,” Panel Participant, Ecological Society of America, Webinar Series

Public Interview: “Nina Fefferman,” You Made it Weird podcast

Public Lecture: “The Role of Applied Math in Real-time Pandemic Response: How Basic Disease Models Work,” NIMBioS Webinar Series, Knoxville, TN

Public Interview: “Math + Virus + Us,” Here We Are podcast and YouTube video.

2019

Public Lecture: “Vaccine Acceptance and Epidemic Risks,” Infinite Futures Event Series, Museum of Science and Industry, Chicago, IL.

“When to Turn to Biology for Inspiration in Systems Design,” DIMACS 30th Anniversary Conference, New Brunswick, NJ.

“Patients as patches: Ecological challenges from the epidemiology of healthcare environments,” ESA 2019, Louisville, KY.

“Math and Disease,” Possibilities in Postsecondary Education and Science (PIPES), UTK, Knoxville, TN.

Keynote Address: “Evolving Efficient Solutions: How simple natural systems solve the most complicated problems,” MBI Capstone Conference 2019, Columbus, OH (virtual)

Plenary Talk: “How AIDS prevalence impacts the emergence of antibiotic resistance in bacterial infections,” SIAM BMM 2019, Richmond, VA.

Public Lecture: “Math and Disease,” Stand Up Science, Farragut, TN.

“Biosurveillance and Homeland Security,” Princeton University, NJ.

“Understanding Social Communication Systems with Homology Theory,” Complex Systems Seminar, University of Michigan, Ann Arbor, MI.

“Going Against the Grain,” Women Empowered in STEM (WeSTEM) 2019, Champaign, IL.

“You’re Worth It: Job Negotiations,” Women Empowered in STEM (WeSTEM) 2019, Champaign, IL.

2018

“Math: A Critical, Treacherous Bridge Between Scientific Disciplines,” American Geophysical Union (AGU 2018), Washington DC.

“The Evolution of Social Complexity as Multi-Scale Feedback Control on Networks,” Systems Theory Lunch Colloquium, Harvard Medical School, Boston, MA.

“Saving Bats from Fungal Diseases with Linear Algebra,” Claremont Center for Mathematical Sciences Colloquium, Claremont, CA.

Plenary Talk: “Evolving Efficient Solutions: How simple natural systems solve the most complicated problems,” NIMBioS Undergraduate Research Conference 2018, Knoxville, TN.

Plenary Talk: “Linking Local Decisions with Global Outcomes in Networks: Case Studies in Behavior and Population Health” SIAM Life Sciences 2018, Minneapolis, MN.

“The mathematical biology of networks: from disease outbreaks to cyber-attacks,” TN Governor’s School, University of Tennessee, Knoxville, TN.

“Trans-disciplinary adventures in the mathematical biology of networks: from disease outbreaks to cyber attacks,” DIMACS REU, Rutgers University, Piscataway, NJ.

Public Webinar: “Social and Biological Networks: The Evolution of Social Systems,” US National Academies of Sciences, Engineering, and Medicine: Math Frontiers Webinar Series

2017

“Self-Diagnosing Networks,” Data Institute San Francisco Conference (DSCO17), San Francisco, CA.

Keynote: “Evolving Efficient Solutions: How simple natural systems solve the most complicated problems,” Workshop on Bio-Inspired Security, Trust Assurance, and Resilience (BioSTAR 2017), San Jose, CA.

“Wildlife Disease Management Outcomes May Depend on the Mechanism of Host Immune Response,” Distinguished Lecture Series in Immunology and Infectious Diseases, Center for Emerging & Re-emerging Infectious Diseases, School of Medicine, University of Washington, Pullman, WA.

2016

“Evolving Healthy Populations,” International Symposium on Biomathematics and Ecology Education and Research 2016, Charlseton, SC.

“Individuals, Societies, and Climate: Modeling motivations to change,” Oak Ridge National Laboratory Workshop on Human Activity at Scale in Earth System Models, Oak Ridge, TN.

“Network Models in Epidemiology,” US-Canadian Institutes Epidemiology Summer School: Mathematical Modeling of Infectious Disease Spread, MBI, Columbus, OH.

“The Invasion Ecology of Diseases in a Human Environment,” Arthur M. Sackler Colloquia of the National Academy of Sciences, Coupled Human and Environmental Systems, Washington DC.

“Global Feedback Control on Centrality in Self-Organizing Systems”, Mathematical Biosciences Institute Workshop on the Control and Observability of Network Dynamics, MBI, Columbus, OH.

“Zika Control: More Complicated than Hoped?” Next Einstein Forum, Dakar, Senegal.

2015

“Linear Algebraic Tools in Conservation Ecology,” Simon A. Levin Mathematical, Computational and Modeling Sciences Center Seminar, Tempe, AZ.

“Applications of Homology Theory to Animal Communication Systems,” Mathematics and Statistics Colloquium, Arizona State Univ., Tempe, AZ.

“Trade-offs Between Collaboration and Infection Risk: Can ‘social distancing’ improve colony function?” Conference on Complex Systems 2015, Tempe, AZ.

“The Benefits of Ongoing Dynamics in Self-Organizing Social Systems,” Conference on Collective Dynamics and Evolving Networks, Bath, UK.

Plenary Talk: Exploiting the Complexity of Identity to Infiltrate Clandestine Groups – Lessons from a LARP, CyDentity Conference, CCICADA, New Brunswick, NJ.

“Incorporating Evolutionary Rescue into Population Viability Models,” Mathematics of Planet Earth: Workshop on Management of Natural Resources, Washington D.C.

“Distributed Detection Algorithms for Real-Time Maritime CyberSecurity,” Joint CCICADA & AMU Conference on Maritime CyberSecurity, New Brunswick, NJ.

“The Definition of Communication: One way biology and math people accidentally talk past each other and what we might be able to do to fix it,” Annual Meeting, Society for Integrative and Comparative Biology, West Palm Beach, FL.

2014

“BioInspired Anomaly Detection: Social Insects and Network Security,” Dept. of Homeland Security Science and Technology HSARPA CyberSecurity Division Research and Development Showcase and Technical Workshop, Washington D.C.

“n-TANGLE: a new method for comparing networks across scales” Workshop on Advances in Discrete Networks, Dept. of Mathematics, Univ. of Pittsburgh, Pittsburgh, PA.

Keynote Address: “Virtual Worlds Helping Public Health Preparedness,” New Jersey Health Care Quality Institute Annual Meeting, Trenton, NJ.

“A Mathematician’s Role in Fighting Ebola,” Saint Ann’s School, Brooklyn, NY.

“Provable Boundaries on Disease Outbreaks in Self-Organizing Social Networks,” The Duke University Mathematical Biology Colloquium, Durham, NC.

Keynote Address: “Designing your own role: Women in STEM,” Tufts University Graduate Student Luncheon for Women in Science, Medford, MA.

“Division of Labor as an Adaptation to Combat Disease Risks?” The Seventh International Symposium on Biomathematics and Ecology: Education and Research (BEER), Claremont, CA.

“How dynamic networks affect disease transmission,” The BioCircuits Institute, UCSD, San Diego, CA.

“The Evolution of Social Complexity,” Plant Biology Dept. Seminar, Univ. of Vermont, Burlington, VT.

“Provable Boundaries on Disease Outbreaks in Self-Organizing Social Networks,” Math Dept. Seminar, Univ. of Tennessee at Knoxville, TN.

“Mathematics, Optimization, and the Evolution and Behavior of Social Insects,” Math Dept. Junior Colloquium, Univ. of Tennessee at Knoxville, TN.

“The Life of a Mathematical Researcher,” Saint Ann’s School, Brooklyn, NY.

“Mathematics, Optimization, and the Evolution and Behavior of Social Insects,” Social Insect Research Group Seminar, School of Life Sciences, Arizona State Univ., AZ.

“N-tangle: A Network Comparison Method,” Workshop on Animal Social Networks, NIMBioS, TN
2013

“Evolutionary pressures, Infectious Diseases, and Self-Organizing Social Systems,” Evolutionary Studies Seminar, Co-Sponsored by the Collective Dynamics of Complex Systems Research Group, the Undergraduate Math Club, Upsilon Pi Epsilon, and Pi Mu Epsilon, SUNY Binghamton, NY.

“BioInspired Anomaly Detection,” DHS CyberSecurity PI Meeting, Arlington, VA.

“Mathematics, Evolutionary Biology, Epidemiology, and National Security”, Saint Ann’s School, Brooklyn, NY.

“Evolution of Reproductive Timing and Social Organization in Honey Bees,” Scientific Learning Forum at FMC, Ewing, NJ.

“Crowd Sourcing WoW: A Case Study in Improving Pandemic Preparedness,” Annual George M. Sideris Biology Conference, LIU, Brooklyn, NY.

2012

Public Lecture: “Math, Complexity, and Social Groups: Using math to understand the nature of society,” Campus Life Enrichment Committee (CLEC) Lecture, Georgia Southern Univ., GA.

“How and Why Static Approximations Can Fail to Give Adequate Insight into Processes on Dynamic Networks,” Math Dept. Colloquium, Georgia Southern Univ., GA.

“Theoretical Worlds: An Exploration of Models and Model Systems,” Tufts Univ, Dept. of Civil and Environmental Engineering Seminar Series, Medford, MA.

“Help, my avatar is sick!” Panel Talk, SXSW, Austin, TX.

“WISE – Women, Ignore Silly Expectations!” 2012 WISE Conference, Texas A&M, TX.

2011

“The Evolution of Social Complexity,” CUNY Initiative for the Theoretical Sciences Workshop on A Unified Theory of Evolution, CUNY, NY.

“Balancing Workforce Productivity Against Disease Risks for Environmental and Infectious Epidemics,” Math Dept. Seminar, Univ. of Ghana, Legon, Ghana.

“Selective Pressures from Disease on Social Behavior in Hosts,” DIMACS/MBI US - African BioMathematics Initiative: Workshop on Genetics and Disease Control, Elmina, Ghana.

Plenary Address: “The Future of Technology and Knowledge,” Next-Generation Communications Interoperability Workshop, Chicago, IL.

“Virtual Worlds and Real Epidemics - Insights from WoW's Corrupted Blood Plague,” E-Virtuoses International Conference on Serious Games, Valenciennes, France.

Plenary Address: “Disease Robustness and Evolutionary Selective Pressures on Social Organization in Eusocial Insects,” Mathematical Biosciences Institute Workshop on Insect Self-Organization and Swarming, Ohio State Univ., OH.

“Hakkar’s Corrupted Blood Plague: How an Outbreak in WoW is Helping Epidemiologists Create Better Disease Models,” Game Developer’s Conference 2011, San Francisco, CA

“Exploring the Role of Behavior in Infectious Disease Dynamics: Mathematical Insights from World of Warcraft and other Virtual Worlds,” DIMACS/CCICADA Student Workshop on Where the Mathematical and Computational Sciences Meet Society, Rutgers University, NJ

“Multi-Dimensional Data and the Influence of Human Behavior in Biosurveillance for Infectious Disease Outbreaks,” Global Biosurveillance Conference: Enabling Science and Technology – 2nd Meeting in the Biological Threat Non-Proliferation Conference Series, Santa Fe, NM

2010

“Distributed Algorithms for Collective Visualization of Data,” Visualanalytics Workshop 2010, Imperial College London, UK

“The Importance of Behavioral Dynamics on Disease Burden,” Southern African Wildlife College, South Africa

“The Impact of Stress on Populations,” DIMACS Advanced Study Institute on Conservation Biology, Limpopo, South Africa

“Social Behavior in Virtual Worlds,” Panel Discussant – InPlay 2010, Toronto, Canada

“Self-Organizing Networks, Social Complexity, and Disease Dynamics,” Rensselaer Polytechnic Institute, NY

“Playing with Plague: Exploring Disease Dynamics from Within,” 2010 AAAS Annual Meeting, San Diego, CA

“Epidemiological Pressures on the Evolution of Social Complexity,” Mathematical Methods in Systems Biology, Tel Aviv, Israel

2009

“Information Theoretic Tool for Biosurveillance,” CCICADA Kickoff Meeting, Rutgers Univ., NJ

“Perspectives, Challenges, and Creativity in Understanding Behavioral Epidemiology,” Workshop on Behavioral Epidemiology, Rutgers Univ., NJ

“Evolutionary Implications of Epidemics on Social Behavior,” Evolutionary Genetics and Genomics at Rutgers, Rutgers Univ., NJ

Panel participant and Speaker on Popular Culture and Science, Sheffield Documentary Film Festival '09, Sheffield, United Kingdom

Keynote Address: “Epidemiological Insights from Virtual Worlds,” Life Science Dialogue Heidelberg, - Inaugural Conference, Germany

“Social Stability and Success: A new concept in self-organizing systems and preferential attachment,” Office of Naval Research Workshop on Complex Systems, Institute for Pure and Applied Mathematics, Los Angeles, CA

“The Impact of Household Capital Models on Targeted Epidemiological Control Strategies for Diseases with Age-Based Etiologies,” Makerere Univ., Kampala, Uganda

Keynote Address: “Hakkar's Corrupted Blood Plague: How an Outbreak in World of Warcraft is Helping Epidemiologists Create Better Disease Models,” Games for Health – Virtual Worlds, Boston, MA

“Network Representations and the Evolution of Social Complexity,” Frontiers in Applied and Computational Mathematics, New Jersey Institute of Technology, NJ

“Mathematical Optimization, Evolutionary Sociobiology, and Eusocial Insects,” Conference on The Power of Analysis, Princeton Univ., NJ

“Mathematical Insights into Behavioral Epidemiology,” Univ. of Texas Health Science Center, Houston, TX

“Basics of Mathematical Modeling,” Mosquito Modeling Made Easy Day, Center for Vector Biology, Rutgers Univ., NJ

“Mathematical and Computational Methods in Epidemiology and BioSurveillance,” Jackson State University, MS

“Mathematics, Optimization, and the Evolution and Behavior of Social Insects,” UNC, Chapel Hill, Applied Math, NC

“Network models in Epidemiology and Sociobiology: Introduction, Overview, and Recent Advances,” Mathematical Sciences, RPI, NY

2008

“Social Behavior and the Dynamics of Corrupted Blood,” Rice University/Games for Health, Houston, TX

“Possible Selective Mechanisms for the Evolution of Disease-defensive Social Organizations,” Ecology and Evolution Seminar, Boston Univ., MA

“Behavioral Epidemiology in Virtual Worlds: Exploiting the virtual experience,” Advanced Technology Applications for Combat Casualty Care 08; Telemedicine and Advanced Technologies Research Center Medical Simulation & Training Technology

“Recent Advances in the What, How and When of Network Models in Infectious Disease Epidemiology,” SIAM 2008, CA

“World of Warcraft Corrupted Blood Disease: Epidemiological Observations and Findings,” Games for Health, Baltimore, MD

“Computational Ecology: The Evolution of Sociality,” Frontiers in Applied and Computational Mathematics, New Jersey Institute of Technology, NJ

Plenary Talk: “Self-organizing social behavior and disease-defensive organizational strategies in social species,” Complexity 2008, Univ. Illinois Urbana, IL

“From the Individual to the Population: Modeling the many levels of evolutionary fitness in social species,” Dept. of Ecology and Evolution and Natural Resources, Rutgers Univ., NJ

“Individual Decisions, Group Efficiency,” ExxonMobil, Clinton, N.J.

2007

Public Lecture: “Virtual Games, Real Epidemics: Can We Learn Real-Life Lessons in BioDefense from Online Games?” Biosecurity, Biotechnology and Global Health Seminar Series, Program on Science and Global Security, Princeton Univ., NJ

- “Disease on Networks: Can Static Representations Capture the Full Complexity of a Dynamic Process?” NDSSL Seminar Series, Virginia Bioinformatics Institute, Virginia Tech, VA
- Public Lecture:** “Real People, Virtual Worlds: Watching a Plague Unfold,” Institute for Mathematical Sciences, National Univ. of Singapore
- “The Continued Mystery of Regular, Old, Annual Flu,” Workshop on Mathematical models for the Study of the Infection Dynamics of Emergent and Re-emergent Diseases in Humans, Institute for Mathematical Sciences, National Univ. of Singapore
- “Epidemics and the Evolution of Social Complexity,” Program in Ecology and Evolution Seminar Series, Rutgers Univ., NJ
- “Playing Games at School: Parents, Public Schools, and Children's Health,” DIMACS Workshop on Game Theory in Epidemiology and Ecology, Rutgers Univ., NJ
- “Analyzing Entropy in Biosurveillance,” U.S. Dept. of Homeland Security research briefing, Washington D.C.
- “Fantastic Problems in Mathematical Ecology,” DIMACS Bio-Math Connection Field Testers Workshop, Rutgers Univ., NJ
- “Does Securing Infrastructure Against Workforce-Depletion Depend on Whether the Risk is Environmental or Infectious?” DIMACS Workshop on Mathematical Modeling of Infectious Diseases in Africa, Univ. of Stellenbosch, South Africa
- “Social interaction and disease dynamics,” Workshop on Analysis of Time Series Data in Epidemiology, Tufts Univ. School of Medicine, Boston, MA
- “The Behaviors of Individuals and Populations,” Working Group on Spatio-Temporal and Network Modeling of Diseases, ICMS, Edinburgh, Scotland
- “The Evolution of Complexity in Already Social Groups,” Dept. of Ecology and Evolutionary Biology, Princeton Univ., NJ
- “Disease as a Selective Pressure and the Evolution of Social Complexity,” Applied Biomathematics, Stony Brook, NY
- “Vital Rate Sensitivity Analysis: A new method for population viability analysis - Two examples of its use,” Applied Biomathematics, Stony Brook, NY
- “Disease as a Selective Pressure and the Evolution of Social Complexity,” Morin Lab, Dept. of Ecology, Evolution and Natural Resources, Rutgers Univ., NJ
- 2006
- “The Role of Individual Choice in the Evolution of Social Complexity and its Implications Towards the Emergence of Zoonotic Infections,” DIMACS Computational and Mathematical Epidemiology Seminar, Rutgers Univ., NJ
- “Preparing Societal Infrastructure Against Disease-Related Workforce Depletion,” DIMACS Workshop on Facing the Challenge of Infectious Diseases in Africa, University of the Witwatersrand, South Africa
- “Fantastic Problems in Mathematical Ecology,” DIMACS Bio-Math Connect Institute for High School Teachers, Denver, CO
- “Societal Bio-defense - How Can we Accomplish Safety, Stability and Efficiency?” SIAM Annual Meeting, Boston, MA
- “When females should stop supporting lazy males: mathematics and honey bees?” DIMACS REU Seminar Series, Rutgers Univ., NJ
- “Selected Problems in Epidemiology.” DIMACS Tutorial on Data Mining and Epidemiology, NJ
- “How Would Termites Prepare for Pandemic Bird Flu and What Should We Learn From Them?” Joint Dept. of Entomology and Center for Infectious Disease Dynamics Seminar, Penn State Univ., PA

“Different Scales of BioDefense - Can societies be both safe and efficient?” DIMACS Computational and Mathematical Epidemiology Seminar, Rutgers Univ., NJ

2005

“Termites in the Nation’s Service,” DIMACS Computational and Mathematical Epidemiology Seminar, Rutgers Univ., NJ

“Applications of Self-Organizing Systems to Epidemiology.” DIMACS Mixer Series, Rutgers Univ., NJ

“Disease Signatures: A New Combinatorial Method for Epidemiology,” DIMACS Computational and Mathematical Epidemiology Seminar, Rutgers Univ., NJ

“Fantastic Problems in Mathematical Ecology,” DIMACS Bio-Math Connect Institute for High School Teachers, Rutgers Univ., NJ

“How Complex Systems Can Simplify a Complex Problem: What Epidemiologists Can Learn From Insects,” Institute for Advanced Study, Center for Systems Biology Seminar Series, NJ

2004

“Incorporating Behavior and Social Structure into Pathogen Defense Strategies. Conference on Innate Immunity for Biodefense,” National Defense University's Center for Technology and National Security Policy (CTNSP) & the Department of Defense, Washington D.C.

Keynote Address: “Social Insects, Immunocompetence and Epidemiology: A Model System for Systems Modelers,” Vanderbilt Medical School, Dept. of Microbiology and Immunology Annual Retreat, TN

“Disease and Immunocompetence in Group-Living Animals: Implications for Human Epidemiology,” DARPA/DSO Workshop on Endogenous Defense, VA

Contributed Presentations

2008. “An Interdisciplinary Framework for Defining and Distinguishing Security Desiderata for Personally Sensitive Information,” DIMACS/DyDAn Workshop on Internet Privacy: Facilitating Seamless Data Movement with Appropriate Controls

2006. “A Vital Rate Sensitivity Analysis (VRSA) for Non-stable Age Distributions and Short-term Planning,” North American Ornithological Conference

2004. “A Mathematical Analysis of Reproductive Fission,” North American Section of the International Union for the Study of Social Insects (with published abstract)

2004. “Two-stage Wavelet Analysis Assessment of Dependencies in Time Series of Disease Incidence,” The 2004 Conference of the International Environmetrics Society (with published abstract)

2004. “Mathematical Modeling of Behavior and Ecology in Social Insects: Social mechanisms of pathogen control in termite colonies,” Departmental Research Seminar, Tufts Univ.

2003. “Modeling Waterborne Infectious Outbreaks: When, where and how bad will they be?” The 2003 Conference of the International Environmetrics Society (with published abstract)

2003. “Modeling Disease Resistance through Social Interactions in Termites,” The 2nd Conference on the Mathematics and Algorithms of Social Insects (with published abstract)

Service (external to Home Institution)

Ongoing Referee of papers for *American Naturalist*, *Annales Zoologici Fennici*, *Behavioral Ecology and Sociobiology*, *Biological Conservation*, *BMC Evolutionary Biology*, *Bulletin for Mathematical Biology*, *Canadian Biosystems Engineering*, *Conservation Letters*, *IMA Journal of Applied Mathematics*, *Journal of Biological Dynamics*,

- Journal of Infectious Diseases, Journal of Insect Science, Journal of Nonlinear Dynamics, Mathematical Biosciences, Journal of Medical Internet Research, Journal of the Royal Society Interface, Malaria Journal, Nature, Nature Scientific Reports, Parasites and Vectors, PeerJ, Physical Reviews X, PLoS Computational Biology, PLoSOne, PLoS Medicine, PNAS, Vaccine, Vector-Borne and Zoonotic Diseases*
- 2020-cont. Reviewer/Fact Checker for Health Feedback (a not-for-profit organization verifying the credibility of influential claims and media coverage that claims to be scientific, most often on topics of climate and health)
- 2020-cont. Deputy Editor *PLOS Computational Biology*
- 2019-2021 Director of Development, Enhancing Diversity in Graduate Education (EDGE) Foundation
- 2019 Guest Editor *PLOS Computational Biology*
- 2019 Co-Organizer SIAM Network Science Annual Meeting (NS 19)
- 2018 NSF ad hoc proposal reviewer
- 2018 Burroughs Wellcome Fund grant proposal reviewer
- 2018 Co-Organizer IEEE Symposium on Security and Privacy, entitled: 3rd Workshop on Bio-inspired Security, Trust, Assurance and Resilience (BioSTAR 2018)
- 2017-cont. Member of the Leadership Team of the National Institute for Mathematical and Biological Synthesis
- 2017 Co-Organizer NIMBioS Workshop on Applying Optimization Techniques to Agricultural Problems
- 2017 ARO grant proposal reviewer
- 2016 Co-Organizer MBI (the Mathematical Biosciences Institute at Ohio State) Workshop on Generalized Network Structures and Dynamics
- 2016 Co-Organizer MBI (the Mathematical Biosciences Institute at Ohio State) Emphasis Semester on Dynamics of Biologically Inspired Networks
- 2014 ARO grant proposal reviewer
- 2013- 2016 Member of Scientific Advisory Board for MBI (the Mathematical Biosciences Institute at Ohio State)
- 2013 NIH grant proposal reviewer
- 2013-2016 Co-Organizer NIMBioS Working Group on Climate Change and Vector-borne Diseases
- 2013-2019 Invited Participant Joint NIMBioS-SESYNC Working Group on Human Risk Perception and Climate Change
- 2012 Invited Grant Proposal Reviewer for the United States – Israel Binational Science Foundation
- 2012 US Environmental Protection Agency FIFRA Scientific Advisory Panel (SAP) on Pollinator Risk Assessment Framework
- 2011 Invited Participant - External Expert Review Panel for Bioscience Research and Development at Los Alamos National Laboratory
- 2011 Program Committee Member, The Third International UKVAC Workshop on Visual Analytics (VAW 2011)
- 2011 NSF grant proposal reviewer
- 2011 Co-Organizer DIMACS/MBI US - African BioMathematics Initiative: Advanced Study Institute and Workshop on Genetics and Disease Control
- 2010 Organizer of the DIMACS Mini-Workshop on ‘Emergent Properties of Dynamic Biological Networks’
- 2010 Lecturer at DIMACS/MBI US - African BioMathematics Initiative: Workshop and Advanced Study Institute on Conservation Biology

- 2010 Organizer of the DIMACS Mini-Workshop on ‘Game-theoretic Approaches to Medical Prognosis’
- 2010 NSF grant reviewer/panel participant
- 2010 Invited International Reviewer for Centre of Excellence Grants for the Australian Research Council
- 2010 Co-Organizer of the DIMACS Workshop on Modeling and Mitigation of the Impacts of Extreme Weather Events to Human Health Risks
- 2009 Co-Organizer DIMACS Workshop on Economic Epidemiology, Makerere Univ., Kampala, Uganda
- 2009 NSF grant reviewer/panel participant
- 2009 Co-Organizer/ Program Co-Chair Workshop on Economic Epidemiology, Makerere Univ., Kampala, Uganda
- 2009 Co-Organizer Mosquito Modeling Made Easy Day at the N.J. Center for Vector Biology
- 2008-2010 Member Chief Editorial Committee for the DIMACS Book Series
- 2008-2010 Member Editorial Board of DIMACS Educational Modules Series
- 2008 Invited organizer SIAM mini-symposium on Network Models of Infectious Disease
- 2008 Ran the Reconnect Program on Biosurveillance at DIMACS – a week long short course for teaching faculty at liberal arts institutions on an advanced topic to expand their own and their students research opportunities
- 2007 Mentor to two teams of researchers for Department of Homeland Security funded Research Experience for those at Minority Serving Institutions
- 2006-2016 Advisory/Editorial Board Member for the journal *Annales Zoologici Fennici*
- 2004 Subject Matter Expert on Innate Immunity and Biodefense, National Defense University
- 2004 Research Consultant, DARPA (via Strategic Analysis, INC.)
- 2003 Developed algorithm for Managing Endangered Species Habitat in Hawaii - MESH software package (Reed, J.M., N.H. Fefferman, C.S. Elphick, and M. Silbernagle. 2004)
- 2000-2002 Technical Editor (Cryptography) to MacMillan Press
- 1999 Invited Reviewer of AES submission to the National Institute of Standards and Technology, later published as The Twofish Encryption Algorithm, Schneier, et al, 1999, John Wiley & Sons Inc.

Service (internal to Home Institution)

- 2020 Advisor to the COVID-19 Re-Imagining Fall Task Force
- 2019-cont. Head of Graduate Admissions, Program in Ecology and Evolutionary Biology
- 2019 Research Mentor for the NIMBioS Summer Research Experiences (SRE) for Undergraduates
- 2019 Co-Organizer Tutorial on Networks at NIMBioS
- 2018 Serve on departmental Promotion and Tenure Committee for Prof. O’Meara
- 2018-cont. Serve on Faculty Mentoring Committee for Prof. Kivlin
- 2017-cont. Served as Departmental Coordinator for University Future Faculty Program
- 2017 Research Mentor for the NIMBioS Summer Research Experiences (SRE) for Undergraduates
- 2017 Lecturer for Joint 2017 MBI-NIMBioS-CAMBAM Summer Graduate Program
- 2016-2017 University of Tennessee, Knoxville Department of Ecology and Evolutionary Biology Search Committee Member and Diversity Advocate (Ecosystem Ecology Search)
- 2016-2017 University of Tennessee, Knoxville Department of Mathematics Search Committee Member (Mathematical Biology Search)

- 2016-cont. University of Tennessee, Knoxville Program in Ecology and Evolutionary Biology
Graduate Affairs Committee Member
- 2015-2016 Rutgers University Biological Sciences Area Committee Member
- 2014 Rutgers University EENR Department Wildlife Biology Faculty Search Committee
Member
- 2010 Co-Mentor to a team of researchers for Department of Homeland Security funded
Research Experience for those at Minority Serving Institutions
- 2009-2010 Organizer of the EENR seminar series
- 2009 Organizer of the DIMACS Workshop on Behavioral Epidemiology
- 2009-2010 Member E&E Executive Committee
- 2008-2012 Member of EENR Curriculum Committee
- 2008-2010 Member Chief Editorial Committee for the DIMACS Book Series
- 2008-2010 Member Editorial Board of DIMACS Educational Modules Series
- 2007-2009 Member of the Rutgers University Advisory Board to the Office for the Promotion of
Women in Science, Engineering and Mathematics
- 2006-2015 Research Advisor for Rutgers Univ. DIMACS REU
- 2005-2007 Co-organizer DIMACS seminar series Mathematical and Computational Epidemiology