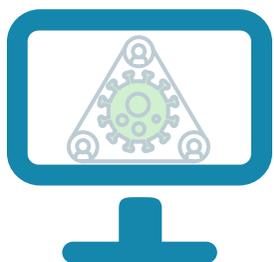


February 2021

CompEpi Quarterly

Newsletter of the Global Pervasive Computational Epidemiology project



computational-epidemiology.org

Annual Report due 30 March

This is a reminder that annual reports for Expeditions are DUE to NSF on **March 30, 2021!** The PI for each award is responsible for submitting the annual report for their institution (including any subcontracts) on Research.gov.

Golda will collect narrative reports (PDF or Word format) from each institution and combine these into a single PDF document. Each PI should upload this combined document into the Support Files under the “Accomplishments” section of the report.

The remainder of the report consists of text boxes to fill with short answers and additional sections for reporting on publications and personnel. The main sections are outlined below.

Accomplishments

This section contains text boxes for short answers on major accomplishments during Year 1.

- Major goals
- Accomplishments
- Opportunities for training and professional development
- Plans for future goals
- Support Files – upload
 - o Golda will provide a combined PDF with contributions from all institutions
 - o Each PI should upload this document to the annual report for their award

Products

- Publications and presentations that acknowledge your Expeditions grant
- You must upload your publication in PDF/A format to the NSF Public Access Repository [<https://par.nsf.gov/>]
- You can link all of the NSF grants you have in the PAR system

Participants & Other Collaborating Organizations

- REU information
- Personnel at your institution
 - o Include info on role, contributions, and person months worked
- Partner Organizations
 - o List other institutions involved in our Expeditions project

Impact

This section contains text boxes for short answers on impacts the Expeditions project has had on the areas below. (You may choose “nothing to report” for any of these areas.)

- Development of principal discipline of project
- Other disciplines
- Human resources
- Teaching/education
- Infrastructure
- Technology transfer
- Society beyond science and technology

Changes/Problems

This section contains text boxes for short answers on any major changes in approach to your project, and actual or anticipated delays.

If you have any questions on how to fill out your annual report, please contact Golda (ggh5e@virginia.edu) or Erin (er9ff@virginia.edu).

Overdue reports can cause delays for other NSF awards and projects. Please submit your annual report on time in order to avoid an overdue notice!



Golda & Erin

Seminar Series - 22 Oct 20

Machine-Learned Epidemiology

Work in computational epidemiology to date has been limited by coarseness and lack of timeliness of observational data. Most existing models are based on hand-curated statistics that are often delayed, expensive to collect, and cover only limited jurisdictions. Our goal is to lift the state of the art in epidemiology to a new qualitative state, where real-time health predictions become feasible and actionable. We do this at scale by applying machine learning and secure aggregation to online data to infer what likely contributed to the contagion. In this talk, I will sample current projects at Google focusing on privacy-first epidemiology research and recent publications.



Dr. Adam Sadilek

- nature.com/articles/s41467-019-12809-y
- nature.com/articles/s41746-018-0045-1
- science.sciencemag.org/content/sci/early/2020/07/16/science.abc5096
- nature.com/articles/s41562-020-0875-0
- nature.com/articles/s41746-020-0222-x



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Adam Sadilek is a senior scientist at Google, where he focuses on large-scale machine learning applied to health, speech understanding, and other domains. Prior to joining Google, Dr. Sadilek was the co-founder and chief executive officer of Fount.in, a machine learning startup providing automated text understanding. Dr. Sadilek obtained his Ph.D. in artificial intelligence from the University of Rochester. Advised by Henry Kautz, Dr. Sadilek led the development of nEmesis, a system that enables real-time epidemiological models. nEmesis demonstrated that the spread of flu and food-borne illness can be effectively predicted by mining online data. In parallel with his studies, Dr. Sadilek has done research and development work at eBay Research Labs, Google, and Microsoft Research, where he focused on optimization and novel applications of machine learning in the context of big data.

*Would you like to present at a future Seminar?
Email Golda and Erin with your availability, title, and abstract.*

Seminar Series - 5 Nov 20



Mobility network models of COVID-19 explain inequities and inform reopening

The COVID-19 pandemic dramatically changed human mobility patterns, necessitating epidemiological models which capture the effects of changes in mobility on virus spread. In this talk we introduce a metapopulation SEIR model that integrates fine-grained, dynamic mobility networks to simulate the spread of SARS-CoV-2 in 10 of the largest US metropolitan statistical areas. Derived from cell phone data, our mobility networks map the hourly movements of 98 million people from neighborhoods (census block groups, or CBGs) to points of interest (POIs) such as restaurants and religious establishments, connecting 57k CBGs to 553k POIs with 5.4 billion hourly edges. We show that by integrating these networks, a relatively simple SEIR model can accurately fit the real case trajectory, despite substantial changes in population behavior over time. Our model predicts that a small minority of “superspreader” POIs account for a large majority of infections and that restricting maximum occupancy at each POI is more effective than uniformly reducing mobility. Our model also correctly predicts higher infection rates among disadvantaged racial and socioeconomic groups solely from differences in mobility: we find that disadvantaged groups have not been able to reduce mobility as sharply, and that the POIs they visit are more crowded and therefore higher-risk. By capturing who is infected at which locations, our model supports detailed analyses that can inform more effective and equitable policy responses to COVID-19.



Dr. Jure Leskovec



Serina Chang



Jure Leskovec is an Associate Professor of Computer Science at Stanford University, and investigator at Chan Zuckerberg Biohub. His general research area is applied machine learning and data science for large interconnected systems. Focuses on modeling complex, richly-labeled relational structures, graphs, and networks for systems at all scales, from interactions of proteins in a cell to interactions between humans in a society. Applications include commonsense reasoning, recommender systems, computational social science, and computational biology with an emphasis on drug discovery.

Serina Chang is currently pursuing a PhD in Computer Science (CS) at Stanford University, advised by Prof. Jure Leskovec and Prof. Johan Ugander. Previously, she completed her undergrad at Columbia University, where she majored in CS and concentrated in Sociology, and was advised by Prof. Kathy McKeown. She's interested in developing methods to model and make predictions over complex systems of human behavior, with applications in computational epidemiology, (dis)information dynamics, political polarization, and recommendation systems. Her research is supported by the NSF Graduate Research Fellowship and the Stanford School of Engineering Finch Family Fellowship.

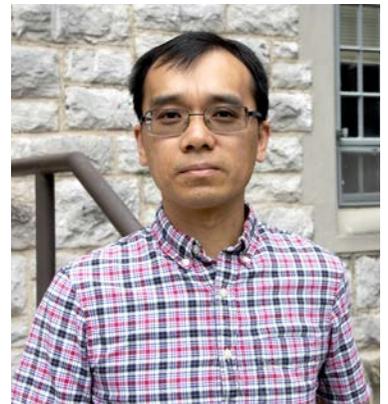


Seminar Series - 19 Nov 20

[Click here to watch on YouTube](#)

Modeling and Active Learning for Experiments with Quantitative-Sequence Factors

In this talk, we would like to discuss a new type of experiment involving a sequence of multiple components associated with their quantities. Such experiments and data are emerging in medical study, health care, logistics, and many other disciplines. It often require simultaneous optimization for both quantities and sequence-orders of several components, which is designed as a new type of factors: Quantitative-Sequence (QS) factors. Due to the large and semi-discrete input spaces for such experiments, it is non-trivial to efficiently identify optimal settings using only a small number of experimental runs. To address these challenges, we propose a novel active learning approach, denote as QS-learning, to enable effective modeling and efficient optimization for experiments with QS factors. The performance of the proposed method is elaborated by a real drug experiment on lymphoma treatment and several simulation studies.



Dr. Xinwei Deng



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Xinwei Deng is an associate professor in the Department of Statistics at Virginia Tech. He received his Bachelor's degree in mathematics from Nanjing University, and PhD degree in industrial engineering from Georgia Tech. His research interests focus on statistical modeling of complex data, design and analysis of experiments, and the interface between experimental design and machine learning.

Seminar Series - 14 Jan 21

Click here
to watch on
YouTube

Controlling epidemics on networks: a game theoretical perspective

While public health interventions such as social distancing and vaccination reduce the risk of infection for an individual, there can be different kinds of costs associated with complying with them--- these include the cost of the vaccination, cost of breaking social contacts, as well as possible peer pressure which leads to a cost of not conforming with one's neighbors. On the other hand, if an individual's neighbors comply, it reduces the infection risk for an individual, thereby reducing the risk of infection. This makes the problem of deciding whether an individual should comply with interventions to reduce the risk of infection a natural and interesting game-theoretic setting. In this talk, we will discuss a general network based framework to study how strategic decisions about such interventions impact the spread of epidemics on networks. We will discuss structural properties and computational complexity of Nash equilibria, and how they are affected by different components of the game, including network structure, information, peer effects and resource constraints. We show that there are tradeoffs between self-interest and an overall social optimum, and discuss different strategies to improve the strategic outcomes.



Dr. Anil Vullikanti

 UNIVERSITY of VIRGINIA

BIOCOMPLEXITY INSTITUTE



Anil Kumar S. Vullikanti is a professor in the Department of Computer Science and at the Biocomplexity Institute. Vullikanti received his undergraduate degree from the Indian Institute of Technology, Kanpur, and his Ph.D. from the Indian Institute of Science, Bangalore. He was a post-doctoral researcher at the Max-Planck Institute for Informatics, and a technical staff member at the Los Alamos National Laboratory.

Vullikanti's research interests are in the broad areas of approximation and randomized algorithms, dynamical systems, wireless networks, social networks, computation epidemiology and the modeling, simulation and analysis of socio-technical systems. His work has been published in journals and conferences in different areas, such as Nature, Journal of the ACM, IEEE/ACM Transactions on Networking, and the SIAM Journal on Computing and Transactions on Parallel and Distributed Computing. Vullikanti's name appears as V.S. Anil Kumar on most publications. He is the recipient of the NSF CAREER award and the DOE Early Career award.



Seminar Series - 28 Jan 21



Optimal COVID-19 quarantine and testing strategies

For COVID-19, it is vital to understand if quarantines shorter than 14 days can be equally effective with judiciously deployed testing. Here, we develop a mathematical model that quantifies the probability of post-quarantine transmission incorporating testing into travel quarantine, quarantine of traced contacts with an unknown time of infection, and quarantine of cases with a known time of exposure. We find that testing on exit (or entry and exit) can reduce the duration of a 14-day quarantine by 50%, while testing on entry shortens quarantine by at most one day. In a real-world test of our theory applied to offshore oil rig employees, 47 positives were obtained with testing on entry and exit to quarantine, of which 16 had tested negative at entry; preventing an expected nine offshore transmission events that each could have led to outbreaks. We show that appropriately timed testing can make shorter quarantines effective.



Dr. Jeffrey Townsend

Yale

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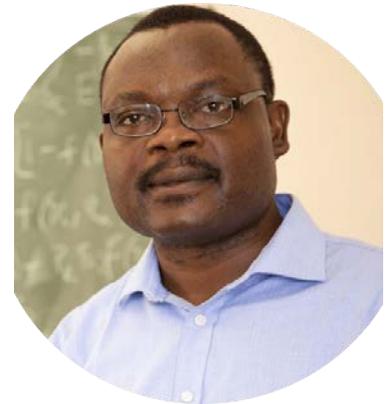
Professor Townsend received his Ph.D. in 2002 in organismic and evolutionary biology from Harvard University. After that, he was appointed as a Miller Fellow at the University of California-Berkeley in the Department of Plant and Microbial Biology. In 2004, he was appointed as an Assistant Professor in the Department of Molecular and Cell Biology at the University of Connecticut. In 2006 he moved to an Assistant Professorship the Department of Ecology and Evolutionary Biology at Yale University. In 2013 he began to work on statistical approaches to fit mathematical models of disease spread and emergence, and was appointed as an Associate Professor of Biostatistics and Ecology & Evolutionary Biology, in 2017 he was named Elihu Associate Professor of Biostatistics and Ecology & Evolutionary Biology, and in 2018 he was appointed Elihu Professor of Biostatistics and Ecology & Evolutionary Biology.

Seminar Series - 11 Feb 21



Searching for COVID-19 patients in a hypercube

We will present a new method for pooled testing, based on the geometry of a hypercube, which has significant advantages over alternatives. The method is already a key component of the national strategy for COVID-19 testing in Rwanda and is being trialed in other countries. We will describe the mathematical details of the method, including its theoretical failure rate, its advantages over alternatives, and its limitations. We will also describe beautiful experiments validating the method in the lab, attempts at its robotic automation, and real-time tests conducted on a South African rugby team. Based on joint work with Leon Mutesa, Neil Turok, Tulio de Oliveira et al.



Dr. Wilfred Ndifon



Dr. Lavanya Singh



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Wilfred Ndifon is Professor of Theoretical Biology at the African Institute for Mathematical Sciences (AIMS) and the Chief Scientific Officer for the AIMS Global Network. He took his PhD at Princeton, with Simon Levin, and did postdoctoral studies at the Weizmann Institute of Science.

Lavanya Singh is a postdoctoral fellow in the laboratory of Prof. Tulio de Oliveira at University of Kwazulu Natal (UKZN). She recently completed her PhD studies at UKZN, which focused on the development and evaluation of novel peptide inhibitors of HIV integrase using gold nanoparticles and targeted delivery. She currently leads lab work aimed at automating the hypercube-based testing method.



Our team has been busy supporting the challenges of real-time epidemic science, particularly pertaining to the COVID-19 Pandemic.

Publications & Preprints

-
- Prioritizing allocation of COVID-19 vaccines based on social contacts increases vaccination effectiveness.** *medRxiv*. Feb 15. Chen J, Hoops S, Marathe A, Mortveit H, Lewis B, Venkatramanan S, Haddadan A, Bhattacharya P, Adiga A, Vullikanti A, Srinivasan A, Wilson ML, Ehrlich G, Fenster M, Eubank S, Barrett C, Marathe M (2021)
- Persistence of anti-vaccine sentiment in social networks through strategic interactions.** *Proceedings of the Thirty-Fifth AAAI Conference on Artificial Intelligence*, Feb 9. Haque ASM, Thakur M, Bielskas M, Marathe A, Vullikanti A (2021)
- Trajectory of individual immunity and vaccination required for SARS-CoV-2 community immunity: a conceptual investigation.** *Journal of the Royal Society Interface*. Feb 3, 18(175):20200683. Saad-Roy CM, Levin SA, Metcalf CJ, Grenfell BT (2021)
- Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes.** *Science. In review. medRxiv*, Feb 3. Saad-Roy CM, Morris SE, Metcalf CJ, Mina MJ, Baker RE, Farrar J, Holmes EC, Pybus OG, Rambaut A, Graham AL, Levin SA, Grenfell BT, Wagner CE (2021)
- Supporting COVID-19 policy response with large-scale mobility-based modeling.** *Proceedings of the 27th ACM SIGKDD Conference on Knowledge Discovery and Data Mining (KDD), Applied Data Science Track. Submitted*. Chang S, Wilson ML, Lewis B, Mehrab Z, Dudakiya K, Pierson E, Koh PW, Gerardin J, Redbird B, Grusky D, Marathe M, Leskovec J (2021)
- All Models are Useful: Bayesian Ensembling for Robust High Resolution COVID-19 Forecasting.** *Proceedings of the 27th ACM SIGKDD Conference on Knowledge Discovery and Data Mining (KDD), Applied Data Science Track. Submitted*. Adiga A, Wang L, Hurt B, Peddireddy A, Porebski P, Venkatramanan S, Lewis B, Marathe M (2021)
- Adaptive human behavior in epidemics: the impact of risk misperception on the spread of epidemics.** *Nature Scientific Report. Submitted*. Espinoza B, Marathe M, Swarup S, Thakur M (2021)
- Superinfection and the evolution of an initial asymptomatic stage.** *Royal Society Open Science*. Jan 27, 8(1):202212. Saad-Roy CM, Grenfell BT, Levin SA, Pellis L, Stage HB, van den Driessche P, Wingreen NS (2021)
- Cross-country evidence on the association between contact tracing and COVID-19 case fatality rates.** *Scientific Reports*, Jan 25, 11(1):1-6. Yalaman A, Basbug G, Elgin C, Galvani AP (2021)
- Optimal COVID-19 quarantine and testing strategies.** *Nature Communications*, Jan 7, 12(1):1-9. Wells CR, Townsend JP, Pandey A, Moghadas SM, Krieger G, Singer B, McDonald RH, Fitzpatrick MC, Galvani AP (2021)
- Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes.** *medRxiv*. Jan 1. Saad-Roy CM, Morris SE, Metcalf CJ, Mina MJ, Baker RE, Farrar J, Holmes EC, Pybus O, Graham AL, Levin SA, Grenfell BT (2021)
- Incorporating Expert Guidance in Epidemic Forecasting.** *arXiv:2101.10247*, Dec 24. Rodríguez A, Adhikari B, Ramakrishnan N, Prakash BA (2020).
- Cohorting to isolate asymptomatic spreaders: An agent-based simulation study on the Mumbai Suburban Railway.** *arXiv:2012.12839*. Dec 23. Talekar A, Shriram S, Vaidhiyan N, Aggarwal G, Chen J, Venkatramanan S, Wang L, Adiga A, Sadilek A, Tendulkar A, Marathe M (2020)
- Economic and behavioral influencers of vaccination and antimicrobial use.** *Frontiers in Public Health*, Dec 21, 8: 614113. Wagner CE, Prentice JA, Saad-Roy CM, Yang L, Grenfell BT, Levin SA, Laxminarayan R (2020)
- Using Mobility Data to Understand and Forecast COVID19 Dynamics.** *medRxiv*, Dec 15. Wang L, Ben X, Adiga A, Sadilek A, Tendulkar A, Venkatramanan S, Vullikanti A, Aggarwal G, Talekar A, Chen J, Lewis B, Swarup S, Kapoor A, Tambe M, Marathe M (2020)

Publications & Preprints

Evolution of similar configurations in graph dynamical systems. *International Conference on Complex Networks and Their Applications*. Dec 1, 544-555. Priest J, Marathe M, Ravi SS, Rosenkrantz D, Stearns R (2020)

Blocking the Propagation of Two Simultaneous Contagions over Networks. *International Conference on Complex Networks and Their Applications*. Dec 1, 455-468. Carscadden H, Kuhlman C, Marathe M, Ravi SS, Rosenkrantz D (2020)

Epidemiological and Economic Impact of COVID-19 in the US. *medRxiv*. Nov 30. Chen J, Vullikanti A, Santos J, Venkatramanan S, Hoops S, Mortveit H, Lewis B, You W, Eubank S, Marathe M, Barrett C (2020)

High resolution proximity statistics as early warning for US universities reopening during COVID-19. *medRxiv*. Mehrab Z, Ranga A, Sarkar D, Venkatramanan S, Baek Y, Swarup S, Marathe M (2020)

Data-driven modeling for different stages of pandemic response. *Journal of the Indian Institute of Science*, Nov 16, 100:901-915. Adiga A, Chen J, Marathe M, Mortveit H, Venkatramanan S, Vullikanti A (2020)

Immune life history, vaccination, and the dynamics of SARS-CoV-2 over the next 5 years. *Science*, Nov 13, 370(6518):811-8. Saad-Roy CM, Wagner CE, Baker RE, Morris SE, Farrar J, Graham AL, Levin SA, Mina MJ, Metcalf CJ, Grenfell BT (2020)

Wisdom of the Ensemble: Improving Consistency of Deep Learning Models. *arXiv*, Nov 13. Wang L, Ghosh D, Gonzalez Diaz M, Farahat A, Alam M, Gupta C, Chen J, Marathe M (2020)

Mobility network models of COVID-19 explain inequities and inform reopening. *Nature*, Nov 10, 1-6. Chang S, Pierson E, Koh PW, Gerardin J, Redbird B, Grusky D, Leskovec J (2020)

PREEMPT: Scalable Epidemic Interventions Using Sub-Modular Optimization on Multi-GPU Systems. *Proceedings of SC20: International Conference for High Performance Computing, Networking, Storage, and Analysis (IEEE)*, Nov 9, 765-779. Minutoli M, Sambaturu P, Halappanavar M, Tumeo A, Kalyanaraman A, Vullikanti A (2020)

Epidemiology and transmission dynamics of COVID-19 in two Indian states. *Science*, Nov 6, 370(6517):691-697. Laxminarayan R, Wahl B, Reddy Dudala S, Gopal K, Mohan C, Neelima S, Jawahar Reddy KS, Radhakrishnan J, Lewnard J (2020)

Medical costs of keeping the US economy open during COVID-19. *Scientific Reports*. Oct 28, 10(1):1-0. Chen J, Vullikanti A, Hoops S, Mortveit H, Lewis B, Venkatramanan S, You W, Eubank S, Marathe M, Barrett C, Marathe A (2020)

Mathematical Models for COVID-19 Pandemic: A Comparative Analysis. *Journal of the Indian Institute of Science*, Oct 30, 100:793-807. Adiga A, Dubhashi D, Lewis B, Marathe M, Venkatramanan S, Vullikanti A (2020)

Examining Deep Learning Models with Multiple Data Sources for COVID-19 Forecasting. *arXiv*, Oct 27. Wang L, Adiga A, Venkatramanan S, Chen J, Lewis B, Marathe M (2020)

AIcov: An Integrative Deep Learning Framework for COVID-19 Forecasting with Population Covariates. *arXiv:2010.03757*, Oct 8. Fox GC, von Laszewski G, Wang F, Pyne S (2020)

Commentary on Ferguson, et al, "Impact of Non-pharmaceutical Interventions (NPIs) to Reduce COVID-19 Mortality and Healthcare Demand. *Bulletin of Mathematical Biology* 82, Oct 7. Eubank S, Eckstrand I, Lewis B, Venkatramanan S, Marathe M, Barrett C (2020)

Broadcasting on two-dimensional regular grids. *arXiv:2010.01390*, Oct 3. Makur A, Mossel E, Polyanskiy Y (2020)



In the news

Repeated Testing for COVID-19 is Vital, Economic and Public Health Analysis Shows.

UT News. 5 February 2021.

Where COVID is on the Menu: Failed Contact Tracing Leaves Diners in the Dark.

Almendrala A. CapRadio. 30 November 2020.

Q&A: A Pandemic Modeler Looks Back - and Forward.

Samarrai F. UVA Today. 10 December 2020.

COVID-19: California plays the card of appeasement and deconfine.

Desk. Inspired Traveler. 29 January 2021.

Steering the Future of Women in Science: The Institutional Wizardry of Microbiologist Rita Colwell.

Debakcsy D. Women You Should Know. 2 December 2020.

University of Virginia Biocomplexity Institute Launches National COVID-19 Medical Resource Demand Dashboard.

Globe Newswire. 15 December 2020.

Here's how infectious disease doctors and public health experts are safely celebrating Thanksgiving this year.

Stieg C. CNBC Make It. 22 November 2020.

India's COVID-19 'human barricade' to keep cases under control, say experts.

Ravikumar S, Jamkhandikar S. Reuters. 17 February 2021.



Researcher Spotlight: Rita Colwell, Univ of Maryland

 We asked Rita Colwell how she got her start. To see her full interview, click here to visit our YouTube channel.

Well, that's a kind of zigzag course. It was not a straight downfield run. I started out heading to medical school at Purdue University where I attended as an undergraduate. In the spring of my senior year, I met my husband to be. We got married - it was a whirlwind romance - we were married within two months. It was a 62 year very happy marriage and I lost him two years ago, so I miss him terribly. But we worked together over the years, raising two terrific children. We got our PhDs together, and the interesting thing was that in that senior year I was accepted to medical school. I was heading to medical school, met Jack, got married, went to the department chairman and said "Look. He's been here. He's a returning veteran from serving in the Army, and he will lose a year if we move on. So why don't I stay, get a master's, he gets his master's, then we'll go on to med school," and the med school agreed to keep my appointment open.

But the department chairman said **"We don't waste fellowships on women."**

So I went to my undergraduate advisor, Dr. Alan Burdick who was a geneticist. He said, "Oh, well, their loss is my gain." He said, "I have a research assistantship - you can do a master's in genetics." So that's what I did. And it turned out to be the most fortuitous because it wasn't that much later than the discovery of the DNA helix and a whole molecular revolution.

And so my husband got accepted as a graduate student at the University of Washington. I applied to medical school, I was accepted but got another letter saying you have to be a resident for a year and then you can go to medical school. So I ended up going into microbiology. So it's been a very zigzagging course and I finally, became probably the first officially trained marine microbiologist in the US. And embryos are very common in the aquatic environment. I made the discovery that *Vibrio cholerae* is an aquatic bacterium. And that it can never be eradicated, it can be well controlled, as we know, in the US, by safe drinking water. So that's how I arrived where I am.



Do what you like, do what you love - work on that which really excites you and interests you

Student Spotlight: Serina Chang, Stanford (pt 2)

 *We weren't able to release Serina's full interview last time due to an embargo - here's the rest of the story. To see her full interview, visit our YouTube channel.*

The goal of [this paper](#) is really to look at the relationship between human mobility and disease spread – specifically the spread of COVID-19. And so using mobility, we have this really rich detailed mobility data set from this company SafeGraph and using their data we were able to estimate these networks. And so the network here is, on one hand, we have these local neighborhoods, which are called census block groups. It's approximately 600 to 3000 people or so. And so we have all the census block groups in the United States. And then we know based on our networks their hourly movements to specific points of interest. So these points of interest might be restaurants or cafes or bars or fitness centers or grocery stores, etc.

Based on this hourly movement of these pretty fine grained populations to these individual points of interest we are able to model the spread of disease. And so for example if you have two populations gathering at one restaurant, and it's a small restaurant and they're spending a long time there, then our model will predict a certain number of infections coming out of that hour.

Using our model we're able to really estimate, who is getting infected, where they're getting infected, and when they're getting infected down to great granularity. So using this model, it's really quite powerful. You can ask a lot of questions.

The first area of questions is around reopening. And so we asked, which places should we reopen? What is the distribution of infections over places? So are there super spreader places, for example. And when should we reopen and how should we be open? So to give you a little bit of insight into the findings one finding that we have is there do seem to be points of interest that are super spreaders, and one statistic that can show that is, for example 10% of the super spreaders in every city that we model account for over 80% of the infections over the three month period that we model. So that's really quite extreme - 10% to 85% and this is true basically across the 10 cities that we model, which are 10 of the largest metropolitan areas in the United States. And so that's one finding that we have. And knowing that there are super spreader locations kind of flips the script a little bit because I think there's been more of a conversation around super spreader individuals. And that's a really important conversation to have.

But to think about locations themselves that might be super spreaders - that might also be something that's easier to tackle from a policy standpoint.



From the admin team



We are excited to be a part of this team and community. Please let us know about your publications and presentations, if you'd like to present at our Seminar Series, or if you want to share the progress your group has made. Building a community on this scale requires an intentional effort and commitment, and we are here to support you in any way we can.

Golda Barrow {ggh5e@virginia.edu} & Erin Raymond {er9ff@virginia.edu}

Social media

We are always looking for content, so please let us know if there is a link, comment, or video we can share on social media.



Collaboration opportunities

Don't forget about these great team resources!



Join our Seminar Series the 2nd & 4th Thursday of every month!

Feb. 25: Rajesh Sundaresan (Indian Institute of Science, Bangalore)

Mar. 11: Natarajan Meghanathan (Jackson State University)

NSF acknowledgement

Remember to acknowledge NSF in your publications. Check with your grant manager for the appropriate number.

- In any publication (including web pages) of any material based on or developed under this project: "This material is based upon work supported by the National Science Foundation under Grant No. [CCF-xxxxxxx]."
- All publications except scientific articles or papers appearing in scientific, technical or professional journals: "Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation."
- NSF support must be orally acknowledged during all news media interviews, including popular media such as radio, television and news magazines.

