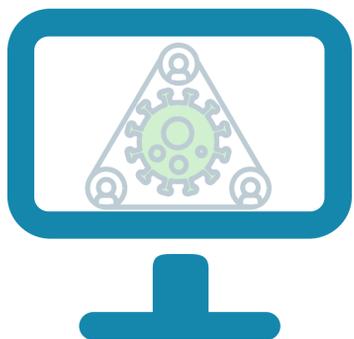


October 2020

CompEpi Quarterly

Newsletter of the Global Pervasive Computational Epidemiology project



computational-epidemiology.org

Fostering Diversity

We had the opportunity to attend the [2020 AAAS Science and Technology Policy forum](#) in early October, and a hot topic throughout the forum was addressing the racial inequality that exists in the US today, especially regarding STEM. As part of this NSF Expeditions grant, the UVA team has been actively working to partner with nearby Howard University and Norfolk State University in the creation of an undergraduate Journal Club. Our vision is a series of discussions and workshops to engage underrepresented students from UVA, Howard, and NSU in the research process. Some of the topics may include:

- How to choose a research topic
- How to define a research question and propose an experimental design
- Data collection and IRBs
- Experiments and data analysis
- Presenting research - talk or poster
- Publication overview

We are aiming to build relationships between faculty members of the schools, foster collaborations, and contribute to an inter-university network for students and researchers. We'll keep you updated as we make progress in this program - perhaps you can adapt it for your university!

And from Kristy Collins at Virginia Tech: I have presented the Virus Tracker-in-a-box program to teachers in Wythe and Smyth Counties as part of their virtual professional development workshops. The workshops were 50 min-1 hour long and we went through how teachers could use the program in their classrooms virtually, what a transmission tree was, talked about contact tracing. At the end of the workshop I pointed the teachers to the work that is being done associated to the grant.



Golda & Erin



Seminar Series - 24 Sept 20

[Click here to watch on YouTube](#)

Epidemiology and transmission dynamics of COVID-19 in two Indian states

Although most COVID-19 cases have occurred in low-resource countries, there is scarce information on the epidemiology of the disease in such settings. Comprehensive SARS-CoV-2 testing and contact-tracing data from the Indian states of Tamil Nadu and Andhra Pradesh reveal stark contrasts from epidemics affecting high-income countries, with 92.1% of cases and 59.7% of deaths occurring among individuals <65 years old. The per-contact risk of infection is 9.0% (95% confidence interval: 7.5-10.5%) in the household and 2.6% (1.6-3.9%) in the community. Superspreading plays a prominent role in transmission, with 5.4% of cases accounting for 80% of infected contacts. The case-fatality ratio is 1.3% (1.0-1.6%), and median time-to-death is 5 days from testing. Primary data are urgently needed from low- and middle-income countries to guide locally-appropriate control measures.



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Ramanan Laxminarayan is Senior Research Scholar and Lecturer at Princeton Environmental Institute and Director of the Center for Disease Dynamics, Economics & Policy in Washington DC. His research deals with the integration of economics and epidemiology to address global health problems. Since 2005, Laxminarayan has worked to improve the understanding of antibiotic resistance as a problem of managing a shared global resource and to bring this problem to the attention of national and global levels. His work encompasses extensive peer-reviewed research, public outreach, and direct country-level engagement through the Global Antibiotic Resistance Partnership. In 2003-04, he served on the National Academy of Science/Institute of Medicine Committee on the Economics of Antimalarial Drugs and subsequently helped create the Affordable Medicines Facility for malaria, a novel financing mechanism to delay resistance and improve access to antimalarial drugs. In 2014, Laxminarayan served on President Obama's Council of Advisors on Science and Technology's antimicrobial resistance working group and is a voting member of the U.S. Presidential Advisory Council on Combating Antimicrobial Resistance. He is a series editor of the Disease Control Priorities for Developing Countries, 3rd edition.

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

Seminar Series - 10 Sept 20

The durability of immunity following infection by SARS-CoV-2

Given the absence of direct data on reinfection, it has been widely reported that we know very little about the durability of immunity after infection by SARS-CoV-2. However, the durability of immunity among phylogenetically close coronavirus relatives of SARS-CoV-2 has been assayed, making it possible to estimate its duration of immunity by a comparative evolutionary analysis of related viruses SARS-CoV-1, MERS, HCoV-229E, HCoV-OC43, HCoV-HKU1, HCoV-NL63. We applied such a phylogenetic comparative approach and estimated the durability of immunity to be 78 weeks (1.5 years) for SARS-CoV-2 and 35 weeks for the seasonal coronavirus HCoV-NL63—results that were robust to multiple sensitivity analyses. By subsampling viral taxa and performing counterfactual estimations of the immunity durabilities, we demonstrated the high accuracy and precision of our approach. The estimated 1.5-year durability of protective immunity of SARS-CoV-2 is more than twice as long as for the seasonal coronaviruses circulating among humans. The ensuing timeframe for reinfection is vital to myriad components of public health decision-making. Most importantly, it suggests that the accumulation of herd immunity in the absence of an annual vaccine is not an effective strategy to forestall infection, morbidity, or deaths due to COVID-19.



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 - 27 Aug 20



Transforming Landscapes and the Ecology of Scale: Understanding Disease Emergence at the Human-Wildlife-Environmental Interface

From Dr. Alexander's talk: [This talk looks at the issue of] scale and health, and the sorts of challenges that face us in this respect. Africa is always viewed as this wonderful oasis of wildlife and picturesque natural landscapes, but the reality is quite different. People struggle quite substantially to have access to food and political stability, and HIV and all the other threats and impacts that have been imposed on people in Africa and now of course with COVID it's even worse. So we can still ask - and more importantly how do we prevent disease and improve public, animal, and ecosystem health? I thought there was some really interesting work here by Cohen and company, which just - I was fascinated by the work and it got me thinking about how we need to reframe a lot of what we do. What they did is they looked at three different important pathogen groups and they asked the question at what spatial scale were these predictors statistically significant? And the black dots in these circles indicate where that predictor actually became significant in chytrid fungus, West Nile Virus, and Lyme's disease. And you can see that at different spatial scales, that predictor had no relevance. And that meant that there was a lot of importance in determining what scale to operate. Now this example is looking at spatial, but I think that spatial obviously is as you know from host, from microbial levels to landscapes, or temporal from millennia to yesterday. And where and what should we be looking at? And what was important here is that there was no single scale that would have detected the importance of these three predictors, population density as a proxy for anthropogenic change, environmental factors, and host richness. And so that to me was really interesting and profound, and I think that it's important to recognize that factors become important at the scale in which they differ, so we won't see those factors if we don't have the correct scale. So the question is: What are we missing? And I think that becomes very important with regards to COVID because there just seems to be so many unknowns.

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Dr. Kathleen Alexander



Dr. Kathleen Alexander has been conducting research in East and Southern Africa for over thirty years. She has worked for the Government of Botswana as both the Chief of the Wildlife Veterinary Unit in the Department of Wildlife and National Parks and later, as the Ecological Advisor to the Office of the President of Botswana and the Attorney Generals Chambers. She presently serves as the Scientific Advisor to the Botswana Presidential COVID Task Force. She has spent most of her professional life studying the dynamics of infectious disease at the human-animal interface in Africa culminating in the creation of the Chobe Research Institute in Northern Botswana. She is a member of both the World Conservation Union's Wildlife Health Specialist Group as well as the Commission for Ecosystem Management. She moved to the Department of Fisheries and Wildlife Conservation at Virginia Tech in 2007 where she continues to conduct research in her long-term Botswana study site. Kathleen received both her PhD and veterinary degree from the University of California, Davis.

Seminar Series - 13 Aug 20

[Click here to watch on YouTube](#)

Automatic Extraction of Epidemiological Line Lists from Open Sources

Real-time monitoring and responses to emerging public health threats rely on the availability of timely surveillance data. During the early stages of an epidemic, the ready availability of line lists with detailed tabular information about laboratory-confirmed cases can assist epidemiologists in making reliable inferences and forecasts. Such inferences are crucial to understand the epidemiology of a specific disease early enough to stop or control the outbreak. However, construction of such line lists requires considerable human supervision and therefore, difficult to generate in real-time. We motivate Guided Epidemiological Line List (GELL), the first tool for building automated line lists (in near real-time) from open source reports of emerging disease outbreaks. Specifically, we focus on deriving epidemiological characteristics of an emerging disease and the affected population from reports of illness. GELL uses distributed vector representations (ala word2vec) to discover a set of indicators for each line list feature. This discovery of indicators is followed by the use of dependency parsing based techniques for final extraction in tabular form. We evaluate the performance of GELL on data from real outbreaks and show how these automatically extracted line list features can be used for making epidemiological inferences.



Dr. Naren Ramakrishnan



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Naren Ramakrishnan is the Thomas L. Phillips Professor of Engineering in the Department of Computer Science at Virginia Tech. He is also the director of the Discovery Analytics Center. He received his Ph.D. in computer sciences from Purdue University.

His research interests include data science, applied machine learning, and urban analytics. His work has been featured in the National Institutes of Health outreach publication Biomedical Computation Review, the National Science Foundation's Discoveries series, Wall Street Journal, Newsweek, Smithsonian Magazine, Chronicle of Higher Education, and Popular Science.

His research has been supported by NSF, DHS, NIH, NEH, IARPA, DARPA, DTRA, ONR, US Army Research Office, US Naval Surface Warfare Center (NSWC), Ford, General Motors, General Dynamics, HP Labs, L3 Communications, Lockheed Martin, Mayfair Group, Northrop Grumman, and NEC Labs.

Seminar Series - 23 Jul 20

[Click here to watch on YouTube](#)

Deep Learning Data-Driven Approaches for Epidemic Forecasting

The devastating impact of the currently unfolding global COVID-19 pandemic has sharply illustrated our enormous vulnerability to emerging infectious diseases. Forecasting disease trajectories is a non-trivial and important task. Estimating various measures related to the epidemic (such as future incidence over the next four weeks) gives policymakers valuable lead time to plan interventions and optimize supply chain decisions. In this talk we will talk about our data driven neural frameworks for epidemic forecasting for various targets, using seasonal influenza and the COVID-19 pandemic as examples. We first present our historical influenza model predicting influenza-like-illness symptomatic burden across the US, which has many desirable properties including interpretability. Next we show how to use new deep learning techniques to adapt our historical model to an emerging scenario (like COVID) leveraging auxiliary data sources. Finally we discuss our model for predicting COVID associated mortality and hospitalizations, which can handle noisy signals while propagating uncertainties. We utilize many data signals including mobility, social media and point-of-care datasets. Results from our real time predictions (shown on the CDC website and FiveThirtyEight.com) during the current pandemic since March indicates that our approaches are among the best performing ones, especially for short-term predictions.



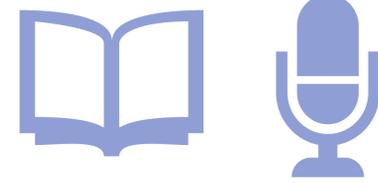
Dr. B. Aditya Prakash



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B. Aditya Prakash is an Associate Professor in the College of Computing at the Georgia Institute of Technology. He received a Ph.D. from the Computer Science Department at Carnegie Mellon University in 2012, and a B.Tech (in CS) from the Indian Institute of Technology (IIT) -- Bombay in 2007. He has published one book, more than 80 papers in major venues, holds two U.S. patents and has given four tutorials (SDM 2017, SIGKDD 2016, VLDB 2012 and ECML/PKDD 2012) at leading conferences. His work has also received a best paper award and five best-of-conference selections (AAMAS 2020, ICDM 2017, ASONAM 2013, CIKM 2012, ICDM 2012, ICDM 2011) and multiple travel awards. His research interests include Data Science, Machine Learning and AI, with emphasis on big-data problems in large real-world networks and time-series, with applications to computational epidemiology, urban computing, security and the Web. His work has been supported by the National Science Foundation (NSF), the Department of Energy (DoE), the National Security Agency (NSA), the National Endowment for Humanities (NEH) and various companies. Tools developed by his group have been in use in many places including ORNL, Walmart and Facebook. He received a Facebook Faculty Award in 2015, was named as one of 'AI Ten to Watch' 2017 by IEEE, and received the NSF CAREER award in 2018. He was previously on the faculty of Computer Science at Virginia Tech. He is also a member of the infectious diseases modeling MIDAS network and core-faculty at the Center for Machine Learning (ML@GT) and the Institute for Data Engineering and Science (IDEaS) at Georgia Tech. Aditya's Twitter handle is @badityap.





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

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A Lab of One's Own: One Woman's Personal Journey Through Sexism in Science. *Harvard Science Book Talk.* Colwell R (Sept 2020)

Representation Learning for Logical Reasoning in Knowledge Graphs. *Automated Knowledge Base Construction.* Leskovec J (June 2020)

Real-Time Computational Science for COVID-19 Pandemic Planning and Response. *ACM BCB 2020.* Marathe M (Sept 2020)

Projecting hospital utilization and assessing implications of silent transmission during the COVID-19 outbreak in the United States. *COVID-19 Consortium Colloquium Speaker Series, UT Austin.* Galvani A and Pandey A (Sept 2020)

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Towards real-time computational epidemiology. *Workshop on Knowledge Guided Machine Learning (KGML).* Marathe M (Aug 2020)

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In the news

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Researcher Spotlight: Simon Levin, Princeton

 We asked Simon Levin to define his overarching research goals. To see his full interview, visit our YouTube channel.

I began as a pure mathematician, but interested in applying it to problems of importance to the world which largely meant ecological, environmental problems, but quickly evolved to include infectious diseases. In general I think the unifying theme of my work has to do with trying to understand the unintended, emergent, macroscopic consequences of individual actions. To some extent, obviously, that includes how the decisions individuals made and the risks they take when it comes to the current pandemic, or any other outbreak of an infectious disease, and the implications for the spread in the population; it includes their decisions in terms of getting vaccinated and in terms of antibiotic use; but it also includes the other actions of individuals in our societies, even in terms of financial systems and the decisions we make there. It also extends all the way down to considering similar phenomena in ecological systems, all the way down to bacteria who engage in collective action.

So all of these are problems which first of all involve scaling and understanding from individuals up to collectives, and automatically that means conflicts between levels - what we call public goods problems - and they occupy a lot of my time. How do we protect society against the outbreak of disease? What are the incentives for individuals to get vaccinated? Of course, there are strong individual incentives in the case of something like COVID 19 or influenza where you want to protect yourself.

Well, we run in to similar conflicts when it comes to effects of climate change, pollution overuse of resources, where none of us perhaps has sufficient - unless we're very civic minded - individual incentive to take actions in the collective good. But if none of us does that then we're all in trouble. So how do we get individuals to cooperate and get us to the Social optimum or somewhere close to that? So those are the sorts of problems I worry about, everywhere from human societies all the way down to bacteria, and I work on microbial systems and other non-human animals systems because I want to gain insights to help me understand how to address these problems in human society.



I think that's the main thing that I've learned along the way is the importance of being adaptive. That lesson makes its way into all the research that I do.

Student Spotlight: Serina Chang, Stanford

 *We asked Serina Chang, a 2nd year PhD student at Stanford, about her research. To see her full interview, visit our YouTube channel.*

Another pretty different project, but also tied to my interest in complex systems, is looking at recommender systems. And so, in particular, there's been a lot of conversation around this concern that recommender systems - so, for example, Netflix or Facebook, where the algorithms you see on Twitter that recommend friends for you or recommend posts for you - there's a concern that they might be driving us into what's called "filter bubbles". And so filter bubbles is this idea that people are mostly only exposed to similar opinions to their own, and so they only see people who have the same ideology as them, and so it's this bubble that you're stuck in. And because of that, you might end up seeing society get more polarized, or at least people have a sense of - they lose perspective on what the entire country is thinking or even what the entire world is thinking. And so they only see that very unique perspective of their own and they're surrounded by all the time, so they're very convinced that it's correct.

There's a lot of concern around the impact of recommender systems on society and filter bubbles being one of them. But one of my recent works with my co-advisor Johan Ugander we were looking at basically the question of: if you want to say that recommender systems have this impact, the only way to really measure that impact is to measure what would have happened without recommender systems. And so you want to model a world in which people are still looking for items, so in order to really measure the impact of recommender systems, we want to know what would have happened without them.

And so what we did was we built these two models of the world. The first one was looking at what would happen if you have, for example, a user who is - let's take movies as an example. So let's say she gets on to a new platform. She wants to watch a movie for the night. And so in the world with a recommender system, maybe she gets onto this platform and the recommender system tries to estimate what her preferences are and then suggest some movies to her, and so it might ask her to rate a couple of movies or ask her "what is the movie that you enjoyed recently?" just to estimate her preferences and then suggest a movie to her.

Want to know how Serina got her start? Watch the full video here.



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}

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