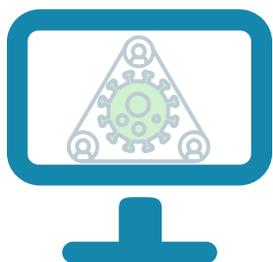
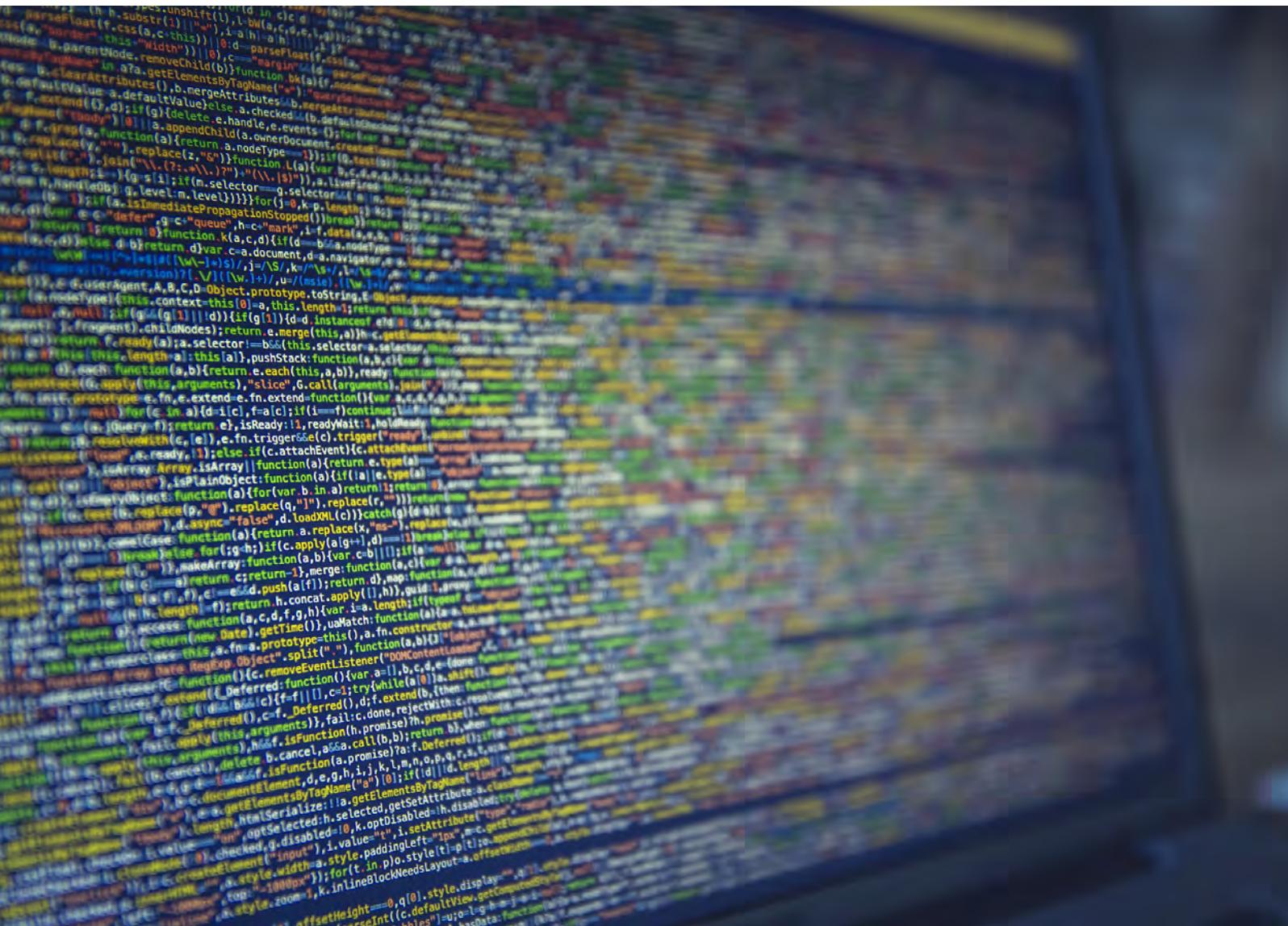


February 2022

CompEpi Quarterly

Newsletter of the Global Pervasive Computational Epidemiology project



computational-epidemiology.org

SAVE THE DATE: GPCE TEAM MEETING MAY 23-25



REVIEW

Learn about the fantastic work the team has accomplished.



COLLABORATE

Discuss future collaborations.



ENGAGE

Design programs to engage student researchers.



PREPARE

Make sure we're ready for our NSF Site Visit.



MEETING AGENDA

We'll plan on meeting for an informal dinner on Monday night, then working all day Tuesday and finishing Wednesday by noon.

We need Program Committee members! Email Golda (ggh5e@virginia.edu) or Erin (er9ff@virginia.edu) to help out!



computational-epidemiology.org/



Annual Report due March 30

This is a reminder that annual reports for Expeditions are DUE to NSF on **March 30, 2022!** 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 - 9 Sep 21

Click here to watch on YouTube

All Models Are Useful: Bayesian Ensembling for Robust High Resolution COVID-19 Forecasting

Timely, high-resolution forecasts of infectious disease incidence are useful for policy makers in deciding intervention measures and estimating healthcare resource burden. Although multiple methods have been explored for this task, their performance has varied across space and time due to noisy data and the inherent dynamic nature of the pandemic. In this talk, we discuss our efforts towards forecasting COVID-19 confirmed cases which has continued to serve local, state and multinational health agencies for over a year. We present a forecasting pipeline which incorporates probabilistic forecasts from multiple statistical, machine learning and mechanistic methods through a Bayesian ensembling scheme and is able to produce forecasts at different resolutions: county, state, and national level. In terms of forecast evaluation, while showing that the Bayesian ensemble is at least as good as the individual methods, we also show that each individual method contributes significantly for different spatial regions and time points. We compare our model's performance with other similar models being integrated into CDC-initiated COVID-19 Forecast Hub. In addition, we have developed a public-access interactive dashboard for visualizing and evaluating our model forecasts and will discuss some of its functionalities.



Dr. Aniruddha Adiga

UNIVERSITY of VIRGINIA

BIOCOMPLEXITY INSTITUTE



Aniruddha Adiga is a Research Scientist at the NSSAC Division of the Biocomplexity Institute and initiative, UVA. He completed his Ph.D. from the Department of Electrical Engineering, Indian Institute of Science (IISc), Bangalore, India and has held the position of Postdoctoral fellow at IISc, North Carolina State University, and UVA. His research areas include signal processing, machine learning, data mining, forecasting and big data analysis. At NSSAC, his primary focus has been the analysis and development of forecasting systems for epidemiological signals such as influenza-like illness and COVID-19 using auxiliary data sources.

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

Seminar Series - 23 Sep 21



Immunopectidomics: A Personalized Medicine Approach to Antigen Discovery, Characterization, and Treatment of Autoimmune Inflammatory Disease

Peptide antigens bound to HLA molecules and presented to T-lymphocytes are a critical initial step to facilitate the response of the adaptive immune system in the eradication of pathogen-infected or cancerous cells, and the production of antibodies. However, in the context of immune mediated disease, antigens may be inappropriately presented, initiating an aberrant immune response that contributes to the pathogenesis of chronic inflammatory diseases. Immunopectidomics is an emerging field of proteomics that utilises mass spectrometry to identify such antigens. Here, we present robust methodology for the identification of HLA-bound peptides, particularly in those individuals with very strong, but thus far unexplained HLA-specific genetic predisposition to the mucosal inflammatory disorders, Crohn’s disease and ulcerative colitis. We further demonstrate the use of prediction algorithms and the potential of mucosal modelling to identify antigen candidates most likely to induce essential T-cell activity, informing downstream pathogenesis of disease.



Dr. Rebecca Powell Doherty



Dr Rebecca Powell Doherty is a senior research fellow in the Antigen Discovery Group at the University of Oxford. She completed her PhD in interdisciplinary biology and immunology in 2010 from UNC Charlotte, and graduated with an MPH from Virginia Tech in 2017. Her research focuses on the link between specific HLA/MHC molecular polymorphisms and the progression of autoimmune disease, including type 1 diabetes, Crohn’s disease, and ulcerative colitis.

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

Seminar Series - 7 Oct 21

[Click here to watch on YouTube](#)

Modeling SARS-CoV-2 immuno-epidemiological dynamics

The COVID-19 pandemic is a global emergency with significant morbidity and mortality. In this talk, we use models to investigate the potential future SARS-CoV-2 transmission dynamics, landscapes of immunity, and the effect of vaccination. Since there are substantial uncertainty on the strength and duration of immunity following natural infection or vaccination, we examine a range of scenarios. Through a general framework, we also explore the potential epidemiological and evolutionary considerations of various vaccine dosing regimes. Finally, we examine the impact of vaccine nationalism on SARS-CoV-2 immuno-epidemiological dynamics and control.



Chadi Saad-Roy



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Chadi Saad-Roy is a Ph.D. candidate in Quantitative and Computational Biology at Princeton University. Broadly, he is interested in mathematical biology, epidemiology, and evolutionary biology. He has worked on various topics at the interface of these disciplines, including influenza eco-evolutionary dynamics, evolutionary theory for the evolution of an asymptomatic infectious stage, and, during the COVID-19 pandemic, modeling SARS-CoV-2 immuno-epidemiological dynamics.

Seminar Series - 21 Oct 21

[Click here to watch on YouTube](#)

Machine Learning Research Applications During the COVID-19 Pandemic

In this lecture, Dr. Majumder will discuss three foci of her team's COVID-19-related research during the first year of the pandemic, including agent-based modeling for epidemic dynamics, natural language processing for bibliometric analysis, and novel digital data sources for misinformation surveillance. She will also briefly cover her team's more recent investigations, including an analysis of county-level risk factors for COVID-19-related case fatality in the United States and an assessment of psychological responses to the pandemic among telehealth patients, among others.



Dr. Maia Majumder



Dr. Maimuna (Maia) Majumder is a member of the ladder-rank faculty at Harvard Medical School and Boston Children's Hospital's Computational Health Informatics Program. Her current research interests involve artificial intelligence and machine learning approaches in the context of public health, with a focus on infectious disease surveillance using digital disease data (e.g., search trends; news and social media). Since January 2020, she and her team have been actively responding to the ongoing COVID-19 pandemic.

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

Seminar Series - 4 Nov 21

[Click here to watch on YouTube](#)

COVID-19 and Challenges to the Classical Theory of Epidemics

The standard theory of infectious diseases, tracing back to the work of Kermack and McKendrick nearly a century ago, has been a triumph of mathematical biology, a rare marriage of theory and application. Yet the limitations of its most simple representations, which has always been known, have been laid bare in dealing with COVID-19, sparking a spate of extensions of the basic theory to deal more effectively with aspects of viral evolution, asymptotic stages, heterogeneity of various kinds, the ambiguities of notions of herd immunity, the role of social behaviors and other features. This lecture will address some progress in addressing these, and open challenges in expanding the mathematical theory.



Dr. Simon Levin



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Simon A. Levin is the James S. McDonnell Distinguished University Professor in Ecology and Evolutionary Biology at Princeton University and the Director of the Center for BioComplexity in the Princeton Environmental Institute. His research examines the structure and functioning of ecosystems, the dynamics of disease, and the coupling of ecological and socioeconomic systems. Levin is a Fellow of the American Academy of Arts and Sciences and the American Association for the Advancement of Science, a Member of the National Academy of Sciences and the American Philosophical Society, and a Foreign Member of the Istituto Veneto di Scienze, Lettere ed Arti, and the Istituto Lombardo (Milan). He has over 500 publications and is the editor of the *Encyclopedia of Biodiversity* and the *Princeton Guide to Ecology*. Levin's awards include: the Heineken Prize for Environmental Sciences, Kyoto Prize in Basic Sciences, Margalef Prize for Ecology, the Ecological Society of America's MacArthur and Eminent Ecologist Awards, the Luca Pacioli Prize (Ca'Foscari University of Venice), the Tyler Prize for Environmental Achievement, and the National Medal of Science.

Seminar Series - 18 Nov 21



Towards Rapid Vaccine Development & Deployment

Using the technology being developed in the Zeichner lab, it should be possible to move from the identification of a protein antigen vaccine target to a testable vaccine in 3 weeks. In this new platform, DNA encoding the antigen is synthesized, and then cloned into a synthetic plasmid that has an inducible surface express cassette employing a Gram-negative autotransporter, which is then transformed into *E. coli* strains that have had a large fraction of the genes that encode proteins expressed on their surfaces. Antigens expressed on the surfaces of these genome-reduced *E. coli* are much better recognized by the immune system than antigens expressed on the surfaces of wild-type *E. coli*. The bacteria are inactivated with formalin, producing a killed whole cell bacterial vaccine. The Zeichner lab has used the platform to make coronavirus vaccines targeting the fusion peptide and stalk regions of the viral spike protein and, with Virginia Tech collaborators, has shown that an early version of the vaccine can provide broad protection against clinical disease in an animal model, raising the prospects that we can produce a universal coronavirus vaccine. Killed whole cell bacterial vaccines are a >100 year-old technology. There are currently many approved killed whole cell bacterial vaccines in use around the world, for example the WHO-prequalified killed whole cell cholera vaccine. Using the cholera vaccine as a benchmark, the cost of production of a killed whole cell bacterial vaccine should be less than US\$ 1 per dose. Factories that are currently producing killed whole cell bacterial vaccine exist around the world, including in many low and middle income countries, so such vaccines should be able to be rapidly deployed around the world.



Dr. Steven Zeichner



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Steve is the McLemore Birdsong Professor in the departments of Pediatrics and Microbiology, Immunology, and Cancer Biology. He obtained his MD and PhD in Microbiology at the University of Chicago as a student in the Medical Scientist Training Program. He completed a residency in Pediatrics and fellowship in Pediatric Infectious Diseases at the Children’s Hospital of Philadelphia and affiliate of the University of Pennsylvania. Steve was a principal investigator in the NIH Intramural Program for several years, and then moved to Children’s National Medical Center and George Washington University School of Medicine. He came to UVA about 6 years ago. Steve has worked in several areas, ranging from basic HIV and herpesvirus molecular biology and control of gene expression to early phase antiretroviral drug development in children. Among other projects, his lab is currently developing a new, rapid, inexpensive, synthetic biology-based, globally appropriate, vaccine technology useful for pandemic and biothreat response, which is the subject of his talk.



Seminar Series - 27 Jan 22

[Click here to watch on YouTube](#)

Computational Epidemiology at the time of COVID-19

The data science revolution is finally enabling the development of large-scale data-driven models that provide real- or near-real-time forecasts and risk analysis for infectious disease threats. These models also provide rationales and quantitative analysis to support policy-making decisions and intervention plans. At the same time, the non-incremental advance of the field presents a broad range of challenges: algorithmic (multiscale constitutive equations, scalability, parallelization), real-time integration of novel digital data streams (social networks, participatory platform, human mobility etc.). I will review and discuss recent results and challenges in the area, and focus on ongoing work aimed at responding to the COVID-19 pandemic.



Dr. Alessandro Vespignani



Alessandro Vespignani is the Director of the Network Science Institute and Sternberg Family Distinguished University Professor at Northeastern University. He is a professor with interdisciplinary appointments in the College of Computer and Information Science, College of Science, and the Bouvé College of Health Sciences. Dr. Vespignani's work focuses on statistical and numerical simulation methods to model spreading phenomena, including the realistic and data-driven computational modeling of biological, social, and technological systems. For several years his work has focused on the spreading of infectious diseases, working closely with the CDC and the WHO.

Seminar Series - 10 Feb 22

Click here
to watch on
YouTube

Presentation of the EU project Livestock Disease Surveillance Knowledge Integration (LIDISKI)

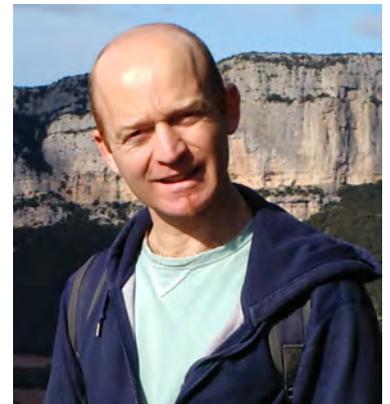
Livestock diseases and their related costs of management are ranked as the biggest economic threat to the livelihood of poor rural farmers and livestock owners. Diseases are mitigated by setting up and maintaining surveillance and control systems. However many countries, including Nigeria, need technological inputs, improved animal health services, and better disease surveillance infrastructure, vaccines production systems, and research data.

To tackle these issues, the EU funded, 4 years long, LIDISKI project aims to Integrate Knowledge collected from actors in the animal health sector to provide tools and know-how to implement sustainable Surveillance and control strategies against Livestock Diseases (www.lidiski.org).

The project focuses on two of the most impacting diseases in Nigeria: peste des petits ruminants (PPR) and Newcastle disease (ND). The whole methodology of the project is based on two central tenets:

1) local actors need to gain competency and benefit from new tools to maintain sustainable surveillance and control of diseases; 2) participatory approaches, integrating local culture and knowledge and socio-economic context are fundamental to engage communities and ensure success of surveillance and control strategies. Based on this, the project is developed in four actions: 1) Capacity building of animal health actors, 2) Engaging communities in surveillance and control, 2) Understanding the epidemiological and socio-economic context, 4) Developing tools and guidelines to scale-up strategies.

After 2 years of implementation, results and impact of the project are starting to take form and provide exciting perspectives.



Dr. Arnaud Bataille



Dr Arnaud Bataille | Researcher in Virology, CIRAD

Arnaud Bataille has obtained his PhD at the University of Leeds (UK) on population genetics and disease ecology. He has worked in multiple countries (Ecuador, Netherlands, South Korea) on the evolutionary and ecological processes associated with animal disease emergence before joining CIRAD (Montpellier, France) in November 2015. His work focuses principally on the Peste des Petits Ruminants virus (PPRV). He investigates the transmission and evolutionary dynamics of PPRV with the aim of elaborating better control strategies. He also contributes to the development of new diagnostic tools and of vaccines against PPR and is co-head of OIE/FAO and EU reference laboratories for PPR.

Publications & Preprints



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

-
- A Markov Decision Process Framework for Efficient and Implementable Contact Tracing and Isolation.** arXiv preprint arXiv:2112.15547. 2021 Dec 31. Li G, Haddadan A, Li A, Marathe M, Srinivasan A, Vullikanti A, Zhao Z.
- Spatiotemporal Pattern Mining for Nowcasting Extreme Earthquakes in Southern California.** arXiv preprint arXiv:2012.14336. 2021 Dec 20. Feng B, Fox G.
- Earthquake Nowcasting with Deep Learning.** arXiv preprint arXiv:2201.01869. 2021 Dec 18. Fox G, Rundle J, Donnellan A, Feng B.
- AI-Driven Agent-Based Models to Study the Role of Vaccine Acceptance in Controlling COVID-19 Spread in the US.** Proceedings of the 2021 IEEE International Conference on Big Data (Big Data) 2021 Dec 15, 1566-1574. Bhattacharya P, Machi D, Chen J, Hoops S, Lewis B, Mortveit H, Venkatramanan S, Wilson ML, Marathe A, Porebski P, Klahn B.
- On Efficient Design of Pilot Experiment for Generalized Linear Models.** *Journal of Statistical Theory and Practice.* 2021 Dec 15; (4):1-21. Li Y, Deng X.
- Link recommendation algorithms and dynamics of polarization in online social networks.** Proceedings of the National Academy of Sciences. 2021 Dec 14;118(50). Santos FP, Lelkes Y, Levin SA.
- Theoretical and computational characterizations of interaction mechanisms on Facebook dynamics using a common knowledge model.** *Social Network Analysis and Mining.* 2021 Dec; 11(1):1-9. Kuhlman CJ, Korkmaz G, Ravi SS, Vega-Redondo F.
- M2p2: Multimodal persuasion prediction using adaptive fusion.** *IEEE Transactions on Multimedia.* 2021 Dec 9. Bai C, Chen H, Kumar S, Leskovec J, Subrahmanian VS.
- Modeling Heterogeneous Hierarchies with Relation-specific Hyperbolic Cones.** *Advances in Neural Information Processing Systems.* 2021 Dec 6; 34. Bai Y, Ying Z, Ren H, Leskovec J.
- Neural Distance Embeddings for Biological Sequences.** *Advances in Neural Information Processing Systems.* 2021 Dec 6; 34. Corso G, Ying Z, Pándy M, Veličković P, Leskovec J, Liò P.
- Combiner: Full attention transformer with sparse computation cost.** *Advances in Neural Information Processing Systems.* 2021 Dec 6; 34. Ren H, Dai H, Dai Z, Yang M, Leskovec J, Schuurmans D, Dai B.
- The durability of immunity against reinfection by SARS-CoV-2: a comparative evolutionary study.** *The Lancet Microbe.* 2021 Dec 1;2(12):e666-75. Townsend JP, Hassler HB, Wang Z, Miura S, Singh J, Kumar S, Ruddle NH, Galvani AP, Dornburg A.
- Realistic Commodity Flow Networks to Assess Vulnerability of Food Systems.** Proceedings of the International Conference on Complex Networks and Their Applications 2021 Nov 30; 168-179. Springer, Cham.
- Versatile Uncertainty Quantification of Contrastive Behaviors for Modeling Networked Anagram Games.** Proceedings of the International Conference on Complex Networks and Their Applications 2021 Nov 30; 644-656. Springer, Cham. Hu Z, Deng X, Kuhlman CJ.
- A framework for simulating multiple contagions over multiple networks.** Proceedings of the International Conference on Complex Networks and Their Applications 2021 Nov 30; 241-252. Springer, Cham. Kishore A, Machi L, Kuhlman CJ, Machi D, Ravi SS.



Publications & Preprints



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

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Racism is a virus: anti-Asian hate and counterspeech in social media during the COVID-19 crisis.

Proceedings of the 2021 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining 2021 Nov 8; 90-94. He B, Ziems C, Soni S, Ramakrishnan N, Yang D, Kumar S.

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Graphs. arXiv:2110.14890. 2021 Oct 28. Ren H, Dai H, Dai B, Chen X, Zhou D, Leskovec J, Schuurmans D.

Actionable Insights in Urban Multivariate Time-series. Proceedings of the 30th ACM International Conference on Information & Knowledge Management 2021 Oct 26; 1774-1783. Tabassum A, Chinthavali S, Tansakul V, Prakash BA.

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Chen J, Vullikanti A, Santos J, Venkatramanan S, Hoops S, Mortveit H, Lewis B, You W, Eubank S, Marathe M, Barrett C.

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8. Sadilek A, Liu L, Nguyen D, Kamruzzaman M, Serghiou S, Rader B, Ingerman A, Mellem S, Kairouz P, Nsoesie EO, MacFarlane J.

HySec-Flow: Privacy-Preserving Genomic Computing with SGX-based Big-Data Analytics Framework.

Proceedings of the 2021 IEEE 14th International Conference on Cloud Computing (CLOUD) 2021 Sep 5; 733-743. Widanage C, Liu W, Li J, Chen H, Wang X, Tang H, Fox J.

HPTMT: Operator-Based Architecture for Scalable High-Performance Data-Intensive Frameworks.

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prospective, active surveillance study. The Lancet Infectious Diseases. 2021 Dec 1; 21(12):1665-76.

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All-cause mortality during the COVID-19 pandemic in Chennai, India: an observational study. The

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SARS-CoV-2 Testing Strategies for Outbreak Mitigation in Vaccinated Populations. medRxiv. 2022 Jan

1. Kumar CK, Balasubramanian R, Ongarello S, Carmona S, Laxminarayan R.



Researcher Spotlight: Anuj Mubayi, The Public Health Company

 We asked Anuj Mubayi about the **vulnerabilities in our healthcare system** that have been exposed by the COVID-19 pandemic. His answer highlighted the importance of health economics, too. To see the full interview, [click here to visit our YouTube channel](#).

The pandemic has highlighted vulnerabilities in the healthcare system - highlighted gaps. And we are realizing that. It is opening up a can of worms where the challenges that we face on a day to day basis, our capabilities in handling mass larger scale health care problems in general. So we are looking at those in a much more broader setting in public health, rather than just looking at COVID. But definitely the pandemic has guided us in that direction. I'm an applied mathematician by training, so I use mathematical models - I build and then link them to real life and translate the results into community-level understanding for interventions or various things.

So that is the work that I am part of with The Public Health Company, but with my collaborators I am doing things in health economics. A lot of time we build disease models - infectious disease models - and we project trends and interventions, but "how many cases will occur in a few weeks time" has less importance if you do not talk about the cost of controlling it. Economic aspects and the disease burden should go hand in hand, and that is a field called health economics, where we study the economic burden. The value of some interventions for one person may not be the same value for another person, and how do you evaluate that?



And we are realizing that we have to bring different systems together so that there is a smooth flow of information, both in terms of data and modeling results, and implications in the decision making process.

Student Spotlight: Ann Li/UVA and George Li/UMD



We asked Ann and George to **talk about their award winning research** - we think you'll be as impressed with these young scientists as we are! To see the full interview, visit our YouTube channel.

George: The Virginia Department of Health has recently funded some vaccine distribution sites in order to increase accessibility to the vaccines, but of course there is only a limited number of sites that you can place around the state. So our paper studies how to optimally place these sites across the State in order to maximize some notion of accessibility and at the same time, of course, we have some guarantees with respect to fairness because there's disparities between different demographic groups in terms of vaccine accessibility.

Ann: I really didn't have much familiarity with the research process going into this, and so a lot of it has just been familiarizing myself with how research works as a whole.



**Before going to college I focused a lot on math, and there was always that lingering worry that math was really cool to me, but no one cares.
George**

Li G, Li A, Marathe M, Srinivasan A, Tsepenekas L, Vullikanti A. *Deploying Vaccine Distribution Sites for Improved Accessibility and Equity to Support Pandemic Response*. arXiv:2202.04705. 2022 Feb 9. Best Student Paper Award, AAMAS 2022.

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*Would you like us to feature one of your students in the Spotlight?
Email Erin (er9ff@virginia.edu) and we'll make it happen!*

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.



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

Here's the schedule for the next few months - stay tuned for more details!

- 10 Mar - David Swerdlow, Harvard
- 24 Mar - TBD
- 14 Apr - TBD
- 28 Apr - Dylan George, CDC

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.

