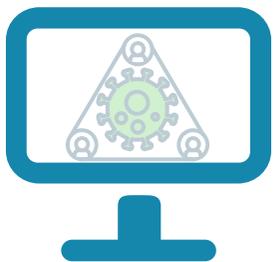


May 2021

CompEpi Quarterly

Newsletter of the Global Pervasive Computational Epidemiology project



computational-epidemiology.org

Seminar Series Updates

One of the highlights of this Expeditions program is undoubtedly the twice-monthly Seminar Series. This window into your research has been essential to building our community and planting the seeds for the next cutting-edge idea in computational epidemiology.

If you have missed any of the previous seminars, or would like to refresh your memory on what has been presented so far, you can find all of the speakers on our [YouTube channel](#).

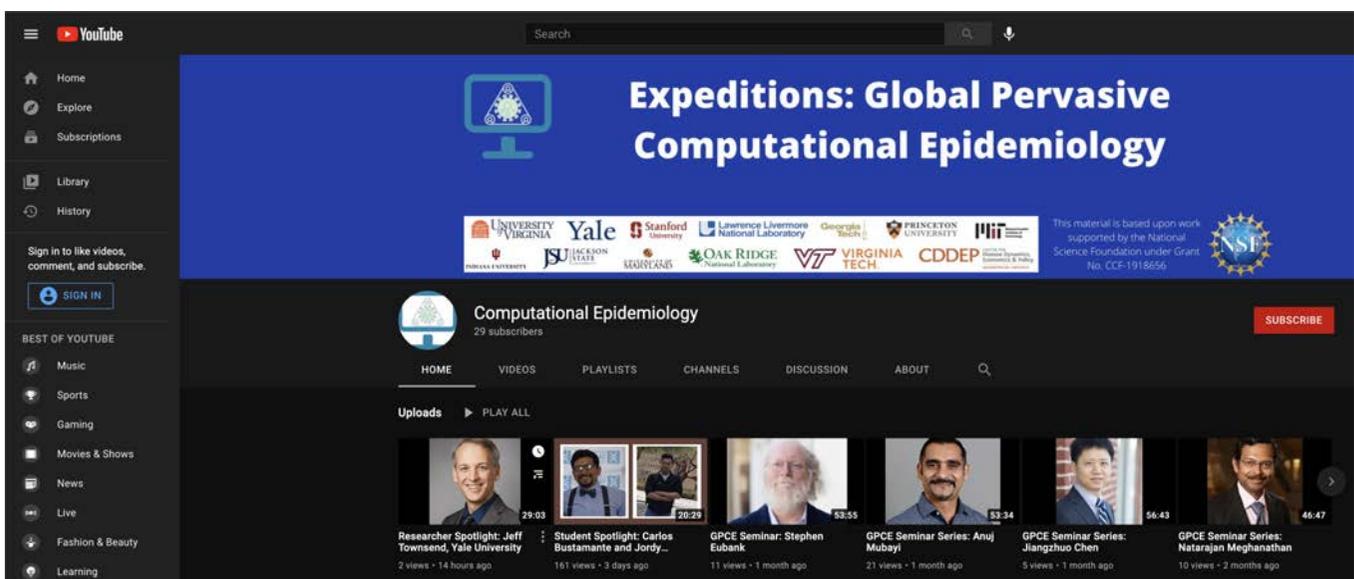
Are you ready to present your latest research? Do you have a colleague you would like to invite to speak? Your support of this program might be the catalyst for a critical and novel contribution to computational epidemiology.

What are you waiting for?

To reserve your spot on the speaker schedule, contact Golda (ggh5e@virginia.edu) or Erin (er9ff@virginia.edu).



Golda & Erin

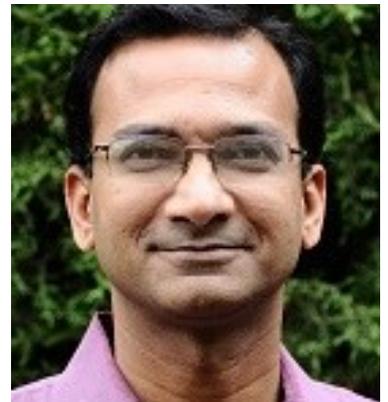


Seminar Series - 25 Feb 21

Click here
to watch on
YouTube

Optimal design of serosurveys for disease burden estimation

The first state-wide COVID-19 serosurvey in Karnataka, a state in India with a population of about 70 million, was done in September 2020 when the infection was near a peak. For accurate total disease-burden estimation at such times, one needs to estimate the active infection in the population along with the seroprevalence of antibodies to the virus. This entails the use of multiple tests for the detection of antigens, viral RNA, and antibodies. Given a family of such tests, their sensitivities, specificities, and costs, what are good survey designs? In this talk, we will discuss a model for disease prevalence, the so-called c-optimal design criterion, and its solution. We will also discuss other criteria and their use in Karnataka's second state-wide serosurvey which concluded only recently.



Dr. Rajesh Sundaresan



The talk is based on joint work with collaborators from the Indian Institute of Public Health, Indian Statistical Institute, Strand Life Sciences, and the Indian Institute of Science.



Rajesh Sundaresan is Professor at the Indian Institute of Science. He is currently on sabbatical leave visiting Strand Life Science and the Indian Statistical Institute. His research interests are in communication, computation, and control over networks. For some recent COVID-19 modelling and epidemiological work, please visit his webpage: <https://ece.iisc.ac.in/~rajeshs>

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

Seminar Series - 11 Mar 21



A Novel Approach to Quantify the Intra-Cluster Density of the Blocking Cluster of a Complex Network

We first propose a binary search algorithm to determine the minimum fraction of nodes in a network to be used as initial adopters (f_{IA}^{min}) for a particular threshold fraction (q) of adopted neighbors (related to the cascade capacity of the network) leading to a complete information cascade. We observe the q vs. f_{IA}^{min} distribution for several complex real-world networks to exhibit a step function pattern wherein there is an abrupt increase in f_{IA}^{min} beyond a certain value of q (q_{step}); the f_{IA}^{min} values at q_{step} and the next measurable value of q are represented as $\underline{f_{IA}^{min}}$ and $\overline{f_{IA}^{min}}$ respectively. The difference $\overline{f_{IA}^{min}} - \underline{f_{IA}^{min}}$ is observed to be significantly high (a median of 0.44 for a suite of 40 real-world networks studied in this research) such that we claim the $1-q_{step}$ value (we propose to refer $1-q_{step}$ as the Cascade Blocking Index, CBI) for a network could be perceived as a measure of the intra-cluster density of the blocking cluster of the network that cannot be penetrated without including an appreciable number of nodes from the cluster to the set of initial adopters (justifying a relatively larger $\overline{f_{IA}^{min}}$ value).



Dr. Natarajan Meghanathan



Dr. Natarajan Meghanathan is a tenured Full Professor of Computer Science at Jackson State University, Jackson, MS. He graduated with a Ph.D. in Computer Science from The University of Texas at Dallas in May 2005. Dr. Meghanathan has published more than 150 peer-reviewed articles (more than half of them being journal publications). He has also received federal education and research grants from the U. S. National Science Foundation, Army Research Lab and Air Force Research Lab. Dr. Meghanathan has been serving in the editorial board of several international journals and in the Technical Program Committees and Organization Committees of several international conferences. His research interests are Wireless Ad hoc Networks and Sensor Networks, Systems and Software Security, Graph Theory Algorithms, Machine Learning, Cloud Computing and Computational Biology.



Seminar Series - 25 Mar 21

Click here
to watch on
YouTube

Efficient Vaccination in a Volatile Pandemic

Vaccines have begun to play an important role for mitigating the ongoing COVID-19 pandemic. While vaccines are being administered, more infectious new variants continue to spread in the population and may soon become dominant; people start reducing social distancing and gradually return to their normal activities. These changes will potentially increase the effective reproduction number R of the disease. On the other hand, it takes time to vaccinate all those who are willing; and for some places in the world it's challenging to obtain a sufficient vaccine supply for all people. Due to the fast changing nature of the disease and human behavior, we need more efficient vaccination strategies to achieve optimal results in terms of reducing infections/hospitalizations/deaths. In this work, we take into account the volatile nature of the COVID-19 pandemic including new variants, relaxation of non-pharmaceutical interventions, and vaccine hesitancy, and use an agent based model to study how speedup of vaccination can help to nullify the impact of these factors; and to compare different strategies of COVID-19 vaccine allocation to individuals, including age based schemes and schemes based on structural properties of the underlying social contact network.



Dr. Jiangzhuo Chen

 UNIVERSITY of VIRGINIA

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Jiangzhuo Chen is a research associate professor in the Network Systems Science and Advanced Computing division. Chen received his BA in Economics from Nanjing University, MA. in Economics from Boston College, and PhD in Computer Science from Northeastern University. Dr. Chen's dissertation explores confluent flows. Chen was a post-doctoral researcher and a senior research associate at VT before moving to NSSAC, Biocomplexity Institute, UVA in 2018. His current projects include: high-performance simulation of social network dynamics; modeling of synthetic population and social network; and forecasting of epidemics.

Seminar Series - 8 Apr 21



Ecological Complexity, Thresholds, and Risk Tradeoff in the Dynamics of Neglected Vector Borne Diseases

Vector-borne infectious disease systems are inherently multiscale complex systems. In this talk, I will describe examples from my research on neglected vector-borne disease systems to show how ecological complexity and epidemiological risks are captured in a modeling framework. The model dynamics of such system is governed by multitude of factors including host competence, host population size, vector feeding preference, spatial heterogeneity, biting heterogeneity and control efforts. The vector borne model often exhibits critical bifurcations, where it has a human infection and a vector population threshold, characterized by a bi-stable region, that describe potential for elimination of the disease beyond its threshold value. In this case, if control is applied through human treatment a new and lower human infection threshold is created, making elimination difficult to achieve, before eventually the human infection threshold no longer exists, making it impossible to control the disease by only reducing the human infection levels below a certain threshold.



Dr. Anuj Mubayi



Anuj Mubayi is an Associate Director at *PRECISIONheor* and Instructional Assistant Professor at the *Department of Mathematics, Illinois State University*. He currently also holds adjunct faculty position at College of Health Solutions, Arizona State University and at the Precision Research Center-Berkeley. He is an applied and computational mathematical scientist, whose research is driven by the quantitative modeling of problems of interest to the public health or social sciences communities.

He has extensive experience in the health decision analysis and in successful development of strong mathematical sciences training programs. He is also a research fellow at the *Center for Collaborative Studies in Mathematical Biology of the Intercollegiate Biomathematics Alliance (IBA)*. His research interests include the development of new cost-effective tools for ameliorating the impact of infectious diseases while increasing our understanding of mechanisms that drive their prevalence and mitigating morbidity related consequences. He is currently working alongside with researchers of *Viral Infection Propagation be Through Air-Travel (VIPRA)* and *Global Pervasive Computational Epidemiology (GPCE)* projects.



Seminar Series - 22 Apr 21



Perturbative approximations to stochastic satisfiability problems

Determining optimal interventions in a network-based epidemiology model can be cast as a stochastic satisfiability (SSAT) problem: What is the total probability that any of a large number of sets of random events occurs? The SSAT construct appears in many guises in many domains, e.g., as Moore-Shannon network reliability in network science or as partition functions in statistical mechanics and field theory. Solving this problem even approximately is notoriously hard, and the solutions themselves are specific to the problem instance, sensitive to small changes in its global structure, and unlikely to lead to feasible interventions in epidemiology. Nevertheless, it is interesting and important to be able to compare the optima found using various heuristics to the true optimum. Here I will describe work in progress applying perturbative methods from statistical physics in combination with tools from computer-aided design to yield approximations of controllable computational complexity with tight error bounds (but in an unusual sense) that respect important symmetries of the true solution.



Dr. Stephen Eubank



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Stephen Eubank is deputy director in the Network Systems Science and Advanced Computing division and a tenured professor, Department of Public Health Sciences. Eubank has previously researched fluid turbulence, nonlinear dynamics and chaos, time series analysis of markets (as a founder of Prediction Company), natural language processing (as Visiting Scientist at ATR in Kyoto, Japan), and simulations of large interaction-based systems. Eubank has been with the Biocomplexity Institute since January 2005, and pursued interests both in developing advanced technology for the study of realistic socio-technical systems and also in understanding how the dynamics of diffusive processes on networks, such as disease transmission, are related to the structure of the underlying networks.





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

Publications & Preprints

- Optimal, near-optimal, and robust epidemic control.** *Communications Physics*. Apr 20, 4(78). Morris D, Rossine F, Plotkin JB, Levin SA (2021)
- Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes.** *Science*. Mar 9, 10.1126/science.abg8663. Saad-Roy C, Morris S, Metcalf CJ, Mina M, Baker R, Farrar J, Holmes E, Pybus O, Graham A, Levin SA, Grenfell B, Wagner C (2021)
- Leveraging a multiple-strain model with mutations in analyzing the spread of COVID-19.** *ICASSP 2021-2021 IEEE International Conference on Acoustics, Speech and Signal Processing*. Jun 6, 8163-8167. Sridhar A, Yağan O, Eletreby R, Levin SA, Plotkin JB, Poor HV (2021)
- Social Network Interventions to Prevent Reciprocity-driven Polarization.** *Proceedings of the 20th International Conference on Autonomous Agents and MultiAgent Systems*. May 3, 1643-1645. Santos FP, Santos FC, Pacheco JM, Levin SA (2021)
- Analysis of the potential impact of durability, timing, and transmission blocking of COVID-19 vaccine on morbidity and mortality.** *EClinicalMedicine*. May 1, 35:100863. Haghpanah F, Lin G, Levin SA, Klein E (2021)
- Scalable epidemiological workflows to support covid-19 planning and response.** *medRxiv*. Feb 26. Machi D, Bhattacharya P, Hoops S, Chen J, Mortveit H, Venkatramanan S, Lewis B, Wilson M, Fadikar A, Maiden T, Barrett CL (2021)
- Evaluation of COVID-19 vaccination strategies with a delayed second dose.** *PLoS Biology*. Apr 21, 19(4):e3001211. Moghadas SM, Vilches TN, Zhang K, Nourbakhsh S, Sah P, Fitzpatrick MC, Galvani AP (2021)
- Simulated identification of silent COVID-19 infections among children and estimated future infection rates with vaccination.** *JAMA Network Open*. Apr 23, 4(4):e217097. Moghadas SM, Fitzpatrick MC, Shoukat A, Zhang K, Galvani AP (2021)
- The impact of vaccination on coronavirus disease 2019 (COVID-19) outbreaks in the United States.** *Clinical Infectious Diseases*. Jan 30. Moghadas SM, Vilches TN, Zhang K, Wells CR, Shoukat A, Singer BH, Meyers LA, Neuzil KM, Langley JM, Fitzpatrick MC, Galvani AP (2021)
- Racial disparities in COVID-19 mortality across Michigan, United States.** *EClinicalMedicine*. Mar 1, 33:100761. Parpia AS, Martinez I, El-Sayed AM, Wells CR, Myers L, Duncan J, Collins J, Fitzpatrick MC, Galvani AP, Pandey A (2021)
- Quantifying the potential for dominant spread of SARS-CoV-2 variant B. 1.351 in the United States.** *medRxiv*. May 12. Sah P, Vilches TN, Shoukat A, Pandey A, Fitzpatrick MC, Moghadas SM, Galvani AP (2021)
- Timing is everything: the relationship between COVID outcomes and the date at which mask mandates are relaxed.** *medRxiv*. Apr 6. Shoukat A, Galvani AP, Fitzpatrick MC (2021)
- Comparison of Regression Approaches for Analyzing Survival Data in the Presence of Competing Risks.** *Letters in Biomathematics*. Apr 15, 8(1):29-47. Ghosh S, Samanta GP, Mubayi A (2021)
- WiFi mobility models for COVID-19 enable less burdensome and more localized interventions for university campuses.** *medRxiv*. Mar 24. Swain VD, Xie J, Madan M, Sargolzaei S, Cai J, De Choudhury M,



Researcher Spotlight: Jeff Townsend, Yale University

 *We asked Jeff Townsend motivating the next generation of scientists, and we loved his answer. To see the full interview, [click here to visit our YouTube channel](#).*

They [the town of Woodbridge Board of Education] were starting this outside seminar series from experts in the town just talking to kids – K to six year olds - and so I gave a talk about the COVID pandemic. And one of the kids asked me a question to which I didn't know the answer, and I said “I don't know the answer to that question” and it was just a really great moment. And the superintendent afterwards said you know, I loved everything you had to say but that was the part he liked the most, was the fact that it became clear to the kids that the scientist doesn't necessarily know the answer to everything and that there's research to be done to figure out that answer. And so that was an exciting moment for me as well and I'm really glad that that moment came through because I certainly had answers for a lot of questions, but not all of them. The ones that aren't answered are the ones that are the next science questions for people to go forward and do more work.

Somehow, it's very hard in educating about science because there's so much to know. I realized what you actually do as a scientist is trying to figure out things you have no idea about. You're really working to get an understanding of things that you really don't understand and that's so much more exciting than learning a whole another set of facts. So I hope that we can convey to young scientists, the degree to which science is not sort of a dry boring execution affair, but really something that thrills the mind. It's just so exciting to try to be in on the pursuit of new knowledge.



Science is not a dry boring execution affair, but really something that thrills the mind

Student Spotlight: Carlos Bustamante & Jordy Cevallos, Arizona St U

 We asked Carlos and Jordy **how they would explain their research to a 3rd grader**, and we think you'll like what they had to say! To see the full interview, visit our [YouTube channel](#).

Carlos Bustamante: Regarding my research I would say we just try to understand the problems that we face in our life. For example, with our COVID 19 pandemic, we have adults being worried about this disease, about how they might get sick. So what we want to study is the effect of staying home in the reduction of the number of people to go to hospital, the number of people that might die from the disease. And we know at the beginning, we didn't have any interventions that we might enact. We didn't have medicine, we didn't have vaccines, because we didn't know much about it. So what we wanted to study is, what if we stay at home? If we stay at home then the virus will be so bored that it will just go away from our neighborhood, because it wouldn't have anyone to infect. It would just go away, it has no one to play with.



If we stay at home then the virus will be so bored that it will just go away from our neighborhood



Jordy Cevallos: I would say we study the effect of staying home with your mom, your dad, your little brothers and sisters, and how these actions reduce the number of deaths in the neighborhood. The number of deaths and the number of people that get infected, that get sick with this COVID 19, which is a very small enemy that we cannot see, but we need a microscope to see these little agents. So that if we're staying in our homes, the virus will be so bored that he will go away, far away from our neighborhood so that we will be safe.

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!

Bryan Lewis (UVA), Judy Fox (UVA), and Lenny Heath (VT) are on the schedule for the coming months - stay tuned for more details!

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.

