

Samuel V. Scarpino

Assistant Professor at Northeastern University; Chief Data Scientist at Dharma Platform

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Lab web page

Twitter - @svscarpino

LinkedIn

Google Scholar Profile

updated - Sept. 2017

education

- 2013 **Ph.D. Ecology, Evolution, & Behavior** The University of Texas at Austin
Drs Lauren Ancel Meyers & Mark Kirkpatrick, advisors
- 2010 **Complex Systems Summer School** Santa Fe Institute
- 2007 **B.Sc. Biology, honors** Indiana University, Bloomington

professional experience

- Sept. 2017 **Assistant Professor** Northeastern University, Boston, MA, USA
I am an Assistant Professor of Marine & Environmental Sciences and Physics & a core faculty member in the Network Science Institute at Northeastern University. My group's research focuses on the socio-biological dynamics of disease, with an overarching goal to construct a complex systems theory of disease.
- Ongoing **Chief Data Scientist** Dharma Platform, Washington, D.C., USA
I am the Chief Data Science Officer at Dharma Platform.
<http://www.dharmaplatform.com/>
- Ongoing **Strategic Advisor** BioFire Diagnostics, ThinkMD, ILiAD Biotechnologies
Provide guidance on analytics associated with epidemiology and disease surveillance.
- 2016–2017 **Assistant Professor** University of Vermont, Burlington, VT, USA
Held a tenure-track Assistant Professorship in Mathematics and Statistics and was a core faculty member in the Complex Systems Center at the University of Vermont.
- 2013–2015 **Omidyar Fellow** Santa Fe Institute, Santa Fe, NM, USA
Held an Omidyar postdoctoral fellowship at the Santa Fe Institute. As an Omidyar Fellow, I had Principle Investigator status through the SFI.
- 2014 & 2015 **Research Experience for Undergraduates: Organizer and Mentor** Santa Fe Institute
Twice assisted in organizing the Santa Fe Institute's N.S.F. funded Research Experience for Undergraduates program, which targeted underrepresented minorities in S.T.E.M..
- 2010–2013 **R Instructor** S.S.C, The University of Texas at Austin
Taught a four day, intensive introduction to R programming course during three Summer Statistics Institutes. Served for four years as the sole instructor for "An Introduction to R" and "R Graphics" in the Division of Statistics and Scientific Computation.
- 2007–2011 **National Science Foundation Graduate Research Fellow** The University of Texas at Austin
Held a competitive research fellowship from the NSF. Responsible for full time research towards my dissertation.

grants

Profit (PI), Horbar (Co-PI), **Scarpino, SV (Co-PI)** - *in review* - "Quantifying Regionalized Care Delivery and Outcomes." National Institutes of Health

B Kirkpatrick (PI), **Scarpino, SV (Co-I)** - *in review* - "Integrating epidemiological and genetic data to uncover mechanisms of hidden disease transmission." National Institutes of Health COBRE.

B Kirkpatrick (PI), **Scarpino, SV (I)** - *in review* - "A Phase II Evaluation of the Safety and Protective Efficacy of a Single Dose of the Live Attenuated Tetravalent Dengue Vaccine TV005 to Protect against Infection with Attenuated DENV-2 (rDEN Δ 30-7169) or DENV-3 (rDEN3 Δ 30) Challenge Viruses in a Dengue Endemic Population in South Asia." National Institutes of Health U01.

Scarpino, SV (PI) & Diehl, S (PI) - *ongoing* - "Integrating 'omics and clinical data to study dengue infection." Biomedical Engineering Pilot Project, College of Medicine, University of Vermont, \$40,000 (2017).

Scarpino, SV (PI) - *ongoing* - "Web Based Neural Network Tools to Forecast Antigenic Relatedness of Viruses from Genomic Sequences." Centers for Disease Control and Prevention, \$100,500 (2016 - 2017).

AP Galvani (PI), LA Meyers (PI), & **Scarpino, SV (consultant)** - *ongoing* - "Dynamic Data-driven Decision Models for Infectious Disease Control." National Institutes of Health MIDAS U01, \$20,000 (2014 - 2018).

Barber, S (PI) , LA Meyers (Co-PI), & **Scarpino, SV (CO-PI, SFI)** - *completed* - "Surety BioEvent App." Defense Threat Reduction Agency - Chemical and Biological Defense Program, \$20,000 (2014–2016).

Scarpino, SV (PI) & BM Althouse (PI) - *completed* - "Next Generation Surveillance for the Next Pandemic." Santa Fe Institute & MIDAS Center for Communicable Disease Dynamics-Harvard, \$82,794 (2014).

LA Meyers (PI) & **Scarpino, SV (consultant)** - *completed* - "Arbovirus Surveillance and Control: Optimizing the Detection and Mitigation of West Nile Virus, Dengue Fever, and Chikungunya Outbreaks." Texas Department of State Health Services - Public Health Emergency Preparedness Funds, \$5,000 (2014).

LA Meyers (PI) & **Scarpino, SV (consultant)** - *completed* - "Right Sizing Influenza Virologic Surveillance Project." Association of Public Health Laboratories, \$5,000 (2014).

M Kirkpatrick (PI) & **Scarpino, SV (CO-PI)** - *completed* - "Sexually Antagonistic Selection and Speciation in the Platyfish." National Science Foundation, Doctoral Dissertation Improvement Grant, \$13,895 (2011–2013).

Scarpino, SV (PI) - *completed* - "Speciation in the Platyfish." Department of Ecology, Evolution, and Behavior, The University of Texas at Austin, Doctoral Dissertation Improvement Grant, \$7,800 (2011–2013).

patents

Utility Patent - Berezin AB, Birmingham JR, Robinson M, **Scarpino SV**, Simmons JW, Smith C. 2014. Energy Deposit Discovery System and Method - 20140142906.

publications

27. Allard A, Althouse BM, **Scarpino SV**, Hébert-Dufresne L. *in press*. Asymmetric percolation drives a double transition in sexual contact networks. *Proceedings of the National Academy of Sciences USA*.
26. Des Marais DL, Guerrero RF, Lasky JR, **Scarpino SV***. 2017. Topological features of a gene co-expression network predict patterns of natural diversity in environmental response. *Proceedings of the Royal Society B* 284: 20170914.
25. **Scarpino SV**, Meyers LA, Johansson MA. 2017. Design strategies for efficient arbovirus surveillance. *Emerging Infectious Diseases* 23(4): 642–644.
24. Levin DA and **Scarpino SV**. 2017. On the young age of intraspecific herbaceous taxa. *New Phytologist* 213:1513–1520.
23. **Scarpino SV***, Allard A, Hébert-Dufresne L. 2016. The effect of a prudent adaptive behaviour on disease transmission. *Nature Physics* 12: 1042–1046. **Press - Article in the 99th percentile as measured by Altmetric.**
22. DeAngelis H, **Scarpino SV**, and Althouse BM. 2016. Modeling the Effects of Priming With the Whole-Cell Bordetella Pertussis Vaccine—Reply. *JAMA Pediatrics*. 170(12):1229–1229.
21. Fitzpatrick MC, Wenzel NS, **Scarpino SV**, Althouse BM, Galvani AP, and Townsend JP. 2016. Cost-effectiveness of a next-generation pertussis vaccine. *Vaccine*. 34: 3405–3411.
20. DeAngelis H, **Scarpino SV**, Fitzpatrick MC, Galvani AP, and Althouse BM. 2016. Epidemiological and economic effects of priming with the whole-cell *Bordetella pertussis* vaccine. *JAMA Pediatrics*. 170(5):459–65.
19. **Scarpino, SV***. 2016. Evolutionary Medicine IV. Evolution and Emergence of Novel Pathogens. In: Kliman, R.M. (ed.), *Encyclopedia of Evolutionary Biology*. vol. 2, pp. 77–82. Oxford: Academic Press.
18. **Scarpino SV***, Davies SW, Pongwarin T, Scott J, Matz MV. 2015. Estimating trait heritability in highly fecund species. *Genes|Genomes|Genetics*. 5(12): 2639–2645. **Award - Selected as one of the top published articles in 2016 by Genes|Genomes|Genetics.**
17. **Scarpino SV**, Althouse BM, and the participants of the Santa Fe Institute Workshop Next Generation Surveillance for the Next Pandemic. 2015. Enhancing disease surveillance with novel data streams. *EPJ Data Science*. 4(1): 1–8. **Press - Article in the 95th percentile as measured by Altmetric.**
16. Shrestha M, **Scarpino SV**, and Moore C. 2015. A message-passing approach for recurrent-state epidemic models on networks. *Physical Review E* 92: 022821.
15. von Hippel P, **Scarpino SV**, and Holas I. 2015. Robust estimation of inequality from binned incomes. *Sociological Methodology* 10.1177/0081175015599807.
14. Althouse BM and **Scarpino SV**. 2015. Asymptomatic transmission and the resurgence of *Bordetella pertussis*. *BMC Medicine* 13(146): 2–12. **Press - Article in the 95th percentile as measured by Altmetric.**
13. **Scarpino SV**, Iamarino A, Wells C, Yamin D, Ndeffo-Mbah M, Wenzel N, Fox SJ, Nyenswah T, Altice FL, Galvani A, Meyers LA, Townsend JP. 2015. Epidemiological and viral genomic sequence analysis of the 2014 Ebola outbreak reveals clustered transmission. *Clinical Infectious Diseases* 60(7):1079–1082. **Press - Article in the 98th percentile as measured by Altmetric.**
12. Lofgren ET, Halloran ME, Rivers CM, Drake JM, Porco TC, Lewis BL, Yang W, Vespignani A, Shaman J, Eisenberg JNS, Eisenberg MC, Marathe MV, **Scarpino SV**, Alexander KA, Meza R, Ferrari MJ, Hyman JM, Meyers LA, Eubank SG. 2014. Mathematical models: A key tool for outbreak response. *Proc. Natl. Acad. Sci. USA* 111(51): 18095–18096.
11. **Scarpino SV***, Levin DA, and Meyers LA. 2014. Polyploid formation shapes flowering plant diversity. *American Naturalist* 184 (4): 456–465.

10. Rivers C, Alexander K, Bellan S, Del Valle S, Drake JM, Eisenberg JN, Eubank S, Ferrari M, Halloran ME, Galvani A, Lewis BL, Lewnard J, Lofgren E, Macal C, Marathe M, Ndeffo Mbah M, Meyers LA, Meza R, Park A, Porco T, **Scarpino SV**, Shaman J, Vespignani A, Yang W. 2014. Ebola: models do more than forecast. *Nature* 515(7528): 492.
9. Halloran EM, Vespignani A, Bharti N, Feldstein LR, Alexander K, Ferrari M, Shaman J, Drake JM, Porco T, Eisenberg J, DeValle S, Lofgren E, **Scarpino SV**, Eisenberg M, Gao D, Hyman JM, Eubank S, Longini IM. 2014. Ebola: Mobility data. *Science* 346(6208): 433.
8. **Scarpino SV***, Hunt PJ, Garcia-De-Leon FJ, Juenger TE, Scharl M, Kirkpatrick M. 2013. Evolution of a genetic incompatibility in the genus *Xiphophorus*. *Molecular Biology and Evolution* 30 (10): 2301-2310.
7. Crews D, Gillette R, **Scarpino SV**, Manikkam M, Savenkova MI, Skinner MK. 2012. Epigenetic transgenerational alterations to stress response in brain gene networks and behavior. *Proceedings of the National Academy of Sciences USA* 109 (23): 9143 - 9148.
6. **Scarpino SV***, Dimitrov NB, Meyers LA. 2012. Optimizing provider recruitment for influenza surveillance networks. *PLoS Comp. Biol.* 8 (4): e1002472.
5. Otto SP, Pannell JR, Peichel CL, Ashman TL, Charlesworth D, Chippindale AK, Delph LF, Guerrero RF, **Scarpino SV**, McAllister BF. 2011. About PAR: The distinct evolutionary dynamics of the pseudoautosomal region. *Trends in Genetics* 27(9): 358 - 367.
4. Delph LF, Andicoechea J, Steven J, Herlihy C, **Scarpino SV**, Bell D. 2011. Environment-dependent intralocus sexual conflict in a dioecious plant. *New Phytologist* 192(2): 542-552.
3. Caillaud D, Crofoot MC, **Scarpino SV**, Jansen P, Garzon-Lopez CX, Winkelhagen A, Bohlman SA, Walsh PD. 2010. Modeling the spatial distribution and fruiting pattern of a key tree species in a neotropical forest: methodology and potential applications. *PLoS ONE* 5(11): e15002.
2. Kirkpatrick M, Guerrero RF, **Scarpino SV**. 2010. Patterns of neutral genetic variation on recombining sex chromosomes. *Genetics* 184: 1141-1152.
1. Pourbohloul B, Ahued A, Davoudi B, Meza R, Meyers LA, Skowronski DM, Villasenor I, Galvan F, Cravioto P, Earn DJ, Dushoff J, Fisman D, Edmunds WJ, Hupert N, **Scarpino SV**, Trujillo J, Lutzow M, Morales J, Contreras A, Chavez C, Patrick DM, Brunham RC. 2009. Initial human transmission dynamics of the pandemic (H1N1) 2009 virus in North America. *Influenza and Other Respiratory Viruses* 3(5): 215-222.

*denotes corresponding author

books

Rohani P & **Scarpino SV**. The integrative biology of Pertussis: epidemiology, immunology & evolution. Oxford University Press. *Under contract*.

outreach publications

3 graphs that help show why Ebola goes viral or dies out. 2015. **Scarpino SV**. [Nautilus](#).

The mathematics of stopping Ebola. 2014. **Scarpino SV**. [Santa Fe New Mexican Front Page](#) - Nov. 24th 2014.

preprints

Scarpino SV & Petri G. On the predictability of infectious disease outbreaks. [arXiv](#)

Allard A, Althouse BM, Hébert-Dufresne L, **Scarpino SV**. The risk of sustained sexual transmission of Zika is underestimated. [bioRxiv](#)

Meyers L, Ginocchio CC, Faucett AN, Nolte FS, Gesteland PH, Leber A, Janowiak D, Donovan V, Bard JD, Spitzer S, Stellrecht KA, Salimnia H, Selvarangan R, Juretschko S, Daly JA, Wallentine JC, Lindsey K, Moore F, Reed SL, Agüero-Rosenfeld M, Fey PD, Storch GA, Melnick SL, Cook CV, Nelson RK, Jones JD, **Scarpino SV**, Althouse BM, Ririe KM, Malin BA, Poritz MA. Automated collection of pathogen-specific diagnostic data for real-time syndromic epidemiological studies. [bioRxiv](#)

Otero G, Althouse BM, McTavish EJ, **Scarpino SV***. Analysis of clinical *Bordetella pertussis* isolates using whole genome sequences reveals novel genomic regions associated with recent outbreaks in the United States. [bioRxiv](#)

Scarpino SV*, Guerrero RF, Scarpino, PV. The moose of Isle Royale: An unnatural condition? [bioRxiv](#)

Scarpino SV*, Gillette R, Crews D. multiDimBio: An R package for the design, analysis, and visualization of systems biology experiments. [arXiv](#)

mentoring

High School: Meghan Hill (SFI), Sergio Mata (SFI), & John Chan (UT Austin), .

Undergraduate: Sophia Novarre (UVM), George Chrisafis (UVM), Haedi DeAngelis (SFI), Cody O'Ferrall (SFI), Gillia Patterson (SFI), Patrick Hunt (UT Austin), & Garrett Johnson (UT Austin).

Graduate: Chia-Hung Yang (Northeastern), Deven Gokhale (UVM), & Tandin Dorji (UVM).

Thesis Committees: Amanda Northrop (Biology - UVM), Melanie Kazenel (Plant biology - UVM), Lauren Ash (Biology - UVM), & Andy Reagan (Mathematical Sciences - UVM).

Postdoctoral: Munik Shrestha (Northeastern & UVM).

teaching

Stat 201: Computational Statistics and Data Analysis. University of Vermont.

Stat 295/CS 295a: Introduction to Statistical Learning. University of Vermont.

invited seminars - thirty six

2017 **Network Heterogeneity Induces Entropy Barriers in Social Contagion**

Keynote, CompleNet18, Boston, MA, USA

2017 **On the Predictability of Infectious Disease Outbreaks**

Contagion Satellite, Conference on Complex Systems, Cancun, MX

2017 **Complexity and Disease**

Young Researchers Network on Complex Systems Warm Up, Conference on Complex Systems, Cancun, MX

- 2011 **Polyploidy and Diversification in Angiosperms**
Physiological Chemistry, University of Wurzburg, Biocenter, Am Hubland, Wurzburg, Germany
- 2010 **Effectiveness of the Influenza-Like Illness Surveillance Network (ILINet) in Texas**
Texas Department of State Health Services Influenza Surveillance Coordinators Conference, Austin, TX, USA

conference session organizer

- 2017 **Contagion on Networks**
NetSci, Indianapolis, IN, USA
- 2015 **The Evolutionary Importance of Polyploidy**
Botany Society of America, Edmonton, Alberta, Canada
- 2014 **Next Generation Decision Support for the Next Pandemic**
INFORMS, San Francisco, CA, USA

professional presentations - forty two

- 2017 **The Interhospital Transfer Network for Very Low Birth Weight Infants in the United States**
Podium presentation at the Conference on Complex Systems 2017, Cancun, Mexico
- 2017 **The Interhospital Transfer Network for Very Low Birth Weight Infants in the United States**
Podium presentation at Pediatric Academic Societies 2017, San Francisco, CA, USA
- 2017 **Topological features of gene regulatory networks predict patterns of natural diversity in environmental stress response**
Podium presentation at NetSci X, Tel Aviv, Isreal
- 2016 **On the Unpredictability of Outbreaks**
Podium presentation at the Conference on Complex Systems 2016, Amsterdam, Netherlands
- 2016 **Universal Limits to Predictability of Infectious Disease Outbreaks**
Podium presentation at the Limits to Prediction in Complex Systems Workshop, Santa Fe, NM, USA
- 2016 **A Prudent Adaptive Behaviour Accelerates Disease Transmission on Networks**
Podium presentation at the Contagion'16 CCS Satellite, Amsterdam, Netherlands
- 2016 **The Network Topology of Natural Variation in Abiotic Stress-Responsive Gene Expression**
Podium presentation at Evolution 2016, Austin, TX, USA
- 2016 **On the Unpredictability of Outbreaks**
Podium presentation in Mathematics & Foundation of Complex Systems seminar series, Turin, Italy

- 2016 **A Prudent Behavior Accelerates Disease Transmission on Networks**
Podium presentation at NetSci 2016, Seoul, South Korea
- 2016 **The Coalescent and Infectious Diseases**
Podium presentation in the Mathematics Colloquium Series, Burlington, VT, USA
- 2016 **The Resurgence and Persistence of Whooping Cough**
Podium presentation at the Infectious Disease Research Conference, College of Medicine, University of Vermont, Burlington, VT, USA
- 2016 **A Prudent Behavior Accelerates Disease Transmission**
Podium presentation in the IGERT Smart Grid Seminar Series, Burlington, VT, USA
- 2016 **The Network Topology of Natural Variation in Abiotic Stress-Responsive Gene Expression**
Podium presentation in the EEEB Seminar Series, Burlington, VT, USA
- 2016 **The Resurgence of Whooping Cough**
Podium presentation at the American Society of Naturalists Meeting, Asilomar, CA, USA
- 2015 **Data Blindspots: High-tech Disease Surveillance Misses the Poor**
Podium presentation at the International Society for Disease Surveillance, Denver, CO, USA
- 2015 **Social Network Clustering and Ebola Virus Transmission**
Podium presentation at Ecology & Evolution of Infectious Diseases, Athens, GA, USA
- 2015 **Designing Multifaceted Dengue Surveillance Systems**
Podium presentation at the International Symposium on Mathematical Programming, Pittsburgh, PA, USA
- 2015 **Polyploid Formation Shapes Flowering Plant Diversity**
Podium presentation at Evolution, Sao Paulo, Brazil
- 2015 **Data Blindspots: High-tech Disease Surveillance Misses the Poor**
Webinar presentation to the NIH MIDAS MISSION, Pittsburgh, PA, USA
- 2015 **Enhancing Disease Surveillance with Novel Data Streams**
Podium presentation at 3rd International Digital Disease Detection Conference , Florence, Italy
- 2015 **Polyploid Formation Shapes Flowering Plant Diversity**
Podium presentation at Botany, Edmonton, Alberta, Canada
- 2014 **A Primer on Network Epidemiology**
Podium presentation at Dynamics Of and On Networks, Santa Fe, NM, USA
- 2014 **An Integrative Surveillance System for Influenza-associated Hospitalizations in at Risk Populations**
Podium presentation at INFORMS, San Francisco, CA, USA
- 2014 **Evolution of a Genetic Incompatibility in the Genus *Xiphophorus***
Podium presentation at Evolution, Raleigh, NC, USA

- 2014 **Goal-Oriented Optimization of Surveillance Systems**
Podium presentation at the National Association of County and City Health Officials Preparedness Summit, Atlanta, GA, USA
- 2014 **The Texas Pandemic Influenza Preparedness Toolkit**
Podium presentation at the National Association of County and City Health Officials Preparedness Summit, Atlanta, GA, USA
- 2013 **Interactive Pandemic Exercise Toolkit**
Podium presentation at the American Public Health Association Annual Meeting, Boston, MA, USA
- 2013 **Within Host Evolution of Antiviral Resistance**
Podium presentation at the National Evolutionary Synthesis Center, Durham, NC, USA
- 2013 **Optimizing Provider Recruitment for Public Health Surveillance Networks**
Podium presentation at the INFORMS Annual Operations Research Meeting, Minneapolis, MN, USA
- 2013 **The Texas Pandemic Influenza Preparedness Exercise Toolkit**
Podium presentation at the NIH MIDAS Mission Meeting, Austin, TX, USA
- 2012 **Forecasting Influenza Hospitalizations**
Podium presentation at the NIH MIDAS Network Meeting, Washington, DC, USA
- 2012 **The Texas Pandemic Influenza Preparedness Toolkit**
Podium presentation at the NIH MIDAS Mission Meeting, Washington, DC, USA
- 2012 **The Evolution of a Cancer Suppressor in the Genus *Xiphophorus***
Podium presentation at Evolution, Ottawa, Canada
- 2011 **Optimizing Provider Recruitment for Public Health Surveillance Networks**
Podium presentation at Epidemics³ - Third International Conference on Infectious Disease Dynamics, Boston, MA, USA
- 2011 **Optimizing Provider Recruitment for Influenza Surveillance Networks**
Podium presentation at Influenza 2011, Oxford, UK
- 2011 **Polyploidy and Diversification in Angiosperms**
Podium presentation in the Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland
- 2010 **Computational Models for Designing Optimal Influenza Surveillance Networks**
Podium presentation at the INFORMS Annual Operations Research Meeting, Austin, TX, USA
- 2010 **Polyploidy and Speciation in Angiosperms**
Podium presentation at Evolution, Portland, OR, USA
- 2010 **Geographic Optimization of Influenza Surveillance Networks**
Podium presentation at the NIH MIDAS Network Meeting, Washington, DC, USA
- 2010 **The Polyploidy Ratchet: Using ABC to Estimate Rates of Speciation and Hybridization in Angiosperms**
Podium presentation in Population Biology Seminar Series, The University of Texas at Austin, Austin, TX, USA

- 2009 **The Polyploidy Ratchet: Using ABC to Estimate Rates of Speciation and Hybridization in Angiosperms**
Podium presentation at Evolution, Moscow, ID, USA

outreach - thirty seven

- 2017 **Cascading Information Enhances Network-Constrained Routing in Real-World Traffic Systems**
Data science team, Lyft, San Francisco, CA, USA
- 2017 **The Social Computome and Fractal Foraging**
Salon, Blue Cat Wine Bar, Burlington, VT, USA
- 2017 **Diseases are Complex Systems**
The Pursuit of Knowledge, Honors college plenary lecture, University of Vermont, Burlington, VT, USA
- 2017 **The Predictability of Complex Systems**
Gund Institute research "slam", University of Vermont, Burlington, VT, USA
- 2016 **Poverty and Public Health**
Gund Institute for Ecological Economics, University of Vermont, Burlington, VT, USA
- 2016 **Data Blindspots: High-tech Disease Surveillance Misses the Poor**
Data Science Meetup, Burlington, VT, USA
- 2016 **Data Modeling for Disease Prediction and Surveillance in [R]**
International Society of Disease Surveillance, Public Health R Working Group, Online Webinar
- 2016 **A Complex Systems Approach to Disease**
Board of Advisors Meeting, College of Engineering & Mathematical Sciences, University of Vermont, Burlington, VT, USA
- 2015 **Evolution and the Emergence of Novel Pathogens**
Computational Biology Seminar Series for Undergraduates, Louisiana State University, Baton Rouge, LA, USA
- 2015 ***On Immunity: an Inoculation* by Eula Biss**
I590 - Special Seminar in the Cognitive and Social Sciences, Indiana University, Bloomington, IN, USA
- 2015 **The Complexity of Disease** Complexity: Out of the Box Thinking: Touching the World with Today's Science, Santa Fe, NM, USA
- 2015 **Methods for Designing Efficient and Effective Disease Surveillance Networks**
State of New Mexico Quarterly Epidemiology Meeting, Santa Fe, NM, USA
- 2015 **Forecasting Infectious Diseases**
Business Network Meeting, Santa Fe, NM, USA
- 2015 **Horror of Dracula**
Science on the Screen, Santa Fe, NM, USA
- 2015 **The Science of Data-Driven Decisions**
EE Ford Summer Leadership Session, Santa Fe, NM, USA
- 2015 **Poverty and Disease**
Creative Mornings, Santa Fe, NM, USA
- 2014-15 **Science Fair Judge**
Santa Fe Public Schools, Santa Fe, NM, USA

2013-15	Advisory board member	Art Science Gallery, UT Austin, USA
2014	Income Inequality and Influenza	American Philosophical Society, Santa Fe Institute, Santa Fe, NM, USA
2014	Complexity Science and Ebola	Santa Fe Radio Cafe - KSFR, Santa Fe, NM, USA
2014	Fighting Ebola with Math	Science Cafe for Young Thinkers - Santa Fe, NM, USA
2014	The Ongoing Ebola Outbreak	Rotary Club Lecture Series - Santa Fe, NM, USA
2014	Evolutionary and Population Dynamics of the Ongoing Ebola Outbreak	Public Seminar Series - Santa Fe Institute, USA
2014	Mathematical Modeling for Public Health	N.S.F. - Mentoring through Critical Transitions in Mathematics, University of New Mexico, USA
2014	The Ongoing Ebola Outbreak	Rotary Club Lecture Series - Los Alamos, NM, USA
2014	What Inspired Me to Pursue Science	High School Prize for Scientific Excellence award ceremony, Santa Fe Institute, USA
2014	Evolution of Antiviral Resistance in Influenza	Biology 472 Seminar Series, Northern New Mexico College, USA
2014	Surveillance for Antiviral Resistant Influenza	Slice of Science, Santa Fe Institute, USA
2013	Genes, Cancer, and Evolution	UT FORUM Osher Lifelong Learning Institute, UT Austin, USA
2012	Cancerous Fish in Mexico: How Evolutionary Biologists Study Cancer	O'Henry Middle School, Austin, TX, USA
2011	Sexual Conflict and the Evolution of Sex Chromosomes	St Edwards University, Austin, TX, USA
2011	Zombies: Mathematical Epidemiology and Popular Culture	Science in the Pub, Austin, TX, USA
2010	Influenza Biology and Transmission	Science Under the Stars, Brackenridge Field Laboratory, The University of Texas at Austin
2010	Influenza in Texas	She Blinded Me With Science, KVRX 91.7FM, Austin, TX, USA
2009	Zombies: Mathematical Epidemiology and Popular Culture	Science Study Break, University of Texas Life Sciences Library
2009	Land Use Patterns and Disease Emergence	Nerd Nite, Austin, TX, USA
2009	SPORE: The Science Behind the Video Game	Charles Darwin's 200th Birthday, University of Texas Libraries

editor

Ongoing	Deputy Editor	PLoS Neglected Tropical Diseases
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2014–16 **Associate Editor** PLoS Neglected Tropical Diseases

2014 **Guest Editor** PLoS Neglected Tropical Diseases

reviewer - thirty six unique venues

American Journal of Botany, American Naturalist, Annals of Applied Statistics, Annals of Internal Medicine, BMC Bioinformatics, BMC infectious diseases, Chapman and Hall, Environmental Biology of Fishes, Evolution, Genetics, Informatics in Medicine Unlocked, Interdisciplinary Perspectives on Infectious Disease, International Journal of Infectious Diseases, Journal of Theoretical Biology, Lancet Infectious Diseases, Molecular Ecology, Nature Communications, Nature Physics, Nature Scientific Data, Nature Scientific Reports, Network Science, PeerJ, Physica A, PLoS Biology, PLoS Computational Biology, PLoS Neglected Tropical Diseases, PLoS One, PLoS Pathogens, Predictive Medicine, Preventative Medicine, Proceedings of the National Academy of Sciences USA, Proceedings of the Royal Society B, Royal Society Open Science, Science, Science Advances, Springer Nature.

awards and honors

2017 **Research Fellow** Institute for Scientific Interchange Foundation, Turin, Italy.

2017 **Top Publication Award** Davies and Scarpino et al. (2016) was selected by G3 as one of its top 15 articles published in 2016.

2012 **Course Transformation Fellowship** Division of Statistics and Scientific Computation, The University of Texas at Austin
Worked as a part of a collaborative effort in the Division of Statistics and Scientific Computation to redesign the undergraduate level, biostatistics course.

2012 **Graduate Research Fellowship** Graduate School, The University of Texas at Austin

2008 **Analysis and Consulting Fellowship** Division of Statistics and Scientific Computation, The University of Texas at Austin

2007 **Dean's Excellence Award** 2007 entering Ph.D. class, The University of Texas at Austin

2007 **Houston Livestock Show and Rodeo Fellowship** 2007 entering Ph.D. class, The University of Texas at Austin

grant reviewer

Medical Research Council, Skills Development Fellowship; Medical Research Council, Research Grant.

developed code

multiDimBio: An R Package for the Design, Analysis, and Visualization of Systems Biology Experiments. [CRAN](#)

binequality: An R Package for Performing Multimodel Estimation of Inequality from Binned Incomes. [CRAN](#)

Miscellaneous code associated with publications can be found on my [website](#) .

working groups and workshops (*organizer*)

2016	Re-emerging Infectious Diseases: The Challenge of Pertussis	Santa Fe Institute
2016	Non-Equilibrium Versus Optimization Approaches to the Origin of Social Groups	IMeRA - Aix Marseille Universite
2015	Molecular Networks and Evolution Across Biological Scales	Santa Fe Institute
2015	EpiHack: Analytics	Skoll Global Threats Fund
2015	Dynamic Primate Contact Networks and Disease Risk	Santa Fe Institute
2014	Next Generation Surveillance for the Next Pandemic	Santa Fe Institute
2014	Molecular Network Topology and Local Adaptation	Santa Fe Institute

working groups and workshops (*participant*)

2017	Measuring and Modeling Community Engagement in Health Emergencies	Bill and Melinda Gates Foundation
2017	Cyber-Social Learning Systems Workshop 3	Computing Community Consortium
2016	Cyber-Social Learning Systems Workshop 2	Computing Community Consortium
2016	Limits to Prediction	Santa Fe Institute
2016	Population Models in the 21st Century	Mathematical Biosciences Institute
2016	The Future of Digital Data for Use in Disease Detection	Chatham House
2015	NIH Disaster Research Response Project Exercise	The University of Texas Health Science Center
2014	Dynamics Of and On Networks	Santa Fe Institute
2014	Network on Inequality, Complexity & Health	Santa Fe Institute
2013	From Co-Infection to Cultural Dissonance: New Challenges for Biological and Cultural Evolution	Santa Fe Institute
2013	Gateways to Emergence	Santa Fe Institute
2013	Influenza and Twitter Hackathon	NIH MIDAS Mission Group
2012	Evolution of Sex-Determination Mechanisms	Universitaire de Suisse Occidentale, La Sage, Switzerland

public health interface

- 2016 **Epihack:Denver** Council of State and Territorial Epidemiologists
This two-day event, bringing together epidemiologists, researchers, software developers, and other stakeholders, will explore the use of Flu Near You and other emerging tools for public health surveillance in the United States. It was organized in partnership with National Association of County and City Health Officials, HealthMap of Boston Children's Hospital, and the Skoll Global Threats Fund.
- 2016 **Early Warning for Asthma Exacerbation** Defense Threat Reduction Agency
In collaboration with the International Society of Disease Surveillance, I am taking part in a consultancy on predicting early warnings for asthma exacerbation. The end goal is to deliver a concrete action plan to the City of Boston Health Department for predicting and responding to asthma exacerbations caused by both infectious disease outbreaks and environmental factors.
- 2015 **Council of State and Territorial Epidemiologists - Webinar** US CSTE
I delivered a webinar to over 300 state and territorial epidemiologists with the following goal, participants will be able to: 1. Demonstrate how an integrative surveillance system can be used to improve situational awareness and early detection; 2. Assess the performance of various data sources, e.g. primary health care providers, laboratory data, emergency department chief complaints, and Google Flu Trends, for surveillance; and 3. Evaluate the utility of primary health care providers and emergency department chief complaints for predicting influenza-associated hospitalizations in at risk populations.
- 2015 **Chikungunya Surveillance in Puerto Rico** US CDC
In response to the recent chikungunya outbreak in Puerto Rico, we are collaborating with the CDC to select clinics for enhanced chikungunya surveillance. The system design algorithms we developed for influenza have been adapted to interrogate data from Dengue virus, whose dynamics are highly correlated with chikungunya in countries where both viruses are endemic.
- 2015 **Chikungunya Risk Mapping in Texas** Texas Department of State Health Services
In response to recent, large chikungunya outbreaks in the Caribbean, we are collaborating with the Texas Department of State Health Services to improve surveillance for the virus in mosquitoes and humans.
- 2013–15 **Right Sizing Influenza Virologic Surveillance Project** Association of Public Health Labs & US CDC
This work is an extension of the previous "right-size" project with APHL and CDC. Here, we will develop an enhanced suite of sample size calculators to guide state-level laboratory influenza testing by addressing biases within the current influenza surveillance system, anti-viral resistance, and vaccine strain selection. The project has three specific objectives: (1) detection of rare/novel influenza strains including confirmation of the Influenza Virologic Surveillance Right Size Roadmap thresholds, (2) improve surveillance for vaccine virus selection, (3) enhance monitoring for antiviral resistance.
- 2012–13 **Influenza Surveillance Right Size Sample Size Calculators** Association of Public Health Labs & US CDC
This project had three objectives: (1) to evaluate the representativeness of CDC influenza laboratory surveillance data, (2) to develop a statistical tool to guide state-level laboratory sampling strategies, and (3) to develop recommendations for modifying the national laboratory-based influenza surveillance system to improve the power and representativeness of lab surveillance data. The calculators are web-based and currently hosted on the APHL [website](#).

2012–13 **Augmentation and Use of BioSense 2.0 in Texas**

Texas Department of State Health Services

This project had three objectives: (1) to assess the performance of current BioSense 2.0 for early detection of infectious disease outbreaks and surveillance of epidemic transmission, morbidity and mortality throughout the state, (2) to develop criteria for targeting additional hospitals for inclusion in BioSense 2.0 to improve surveillance in at risk populations, and (3) to develop strategic guidelines for augmentation of BioSense 2.0.

2011–13 **The Texas Pandemic Flu Toolkit**

Texas Department of State Health Services

The Texas Pandemic Flu Toolkit is a collection of tools developed by the Meyers Research Group at the University of Texas at Austin for the Texas Department of State Health services. These tools include: an antiviral distribution optimizer, a vaccine allocation optimizer, a pandemic influenza simulator, a pandemic influenza exercise tool, and a ventilator stockpiler. The tools are available at the [Texas Pandemic Flu Toolkit Website](#).

organization membership

American Society of Naturalists and the Complex Systems Society