

Samuel V. Scarpino

Assistant Professor of Network Science at Northeastern University

contact

Northeastern University
210-177
360 Huntington Avenue
Boston, MA 02115
U.S.A.

tel.
+1 (617) 373-4222

s.scarpino@
northeastern.edu

Lab web page

Twitter - @svscarpino

LinkedIn

Google Scholar Profile

updated - Jan. 2019

education

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

professional experience

- | | | |
|-------------|---|---|
| Ongoing | Assistant Professor I am a core faculty member in the Network Science Institute, an Assistant Professor of Marine & Environmental Sciences and Physics, & an Affiliated Assistant Professor in the Health Sciences Department at Northeastern University. My group's research takes a complex systems approach to advancing our scientific understanding of biology & health. | Northeastern University, Boston, MA, USA |
| Ongoing | Chief Data Scientist I am the Chief Data Scientist at Dharma Platform, a technology start-up that provides data management solutions to social impact organizations. | Dharma Platform, Washington, D.C., USA |
| Ongoing | Strategic Advisor Provide guidance on analytics associated with epidemiology and disease surveillance. | BioFire Diagnostics, ThinkMD, ILiAD Biotechnologies |
| 2016–2017 | Assistant Professor 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. | University of Vermont, Burlington, VT, USA |
| 2013–2015 | Omidyar Fellow Held an Omidyar postdoctoral fellowship at the Santa Fe Institute. As an Omidyar Fellow, I had Principle Investigator status through the SFI. | Santa Fe Institute, Santa Fe, NM, USA |
| 2014 & 2015 | Research Experience for Undergraduates: Organizer and Mentor 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.. | Santa Fe Institute |
| 2010–2013 | R Instructor 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. | S.S.C, The University of Texas at Austin |
| 2007–2011 | National Science Foundation Graduate Research Fellow Held a competitive research fellowship from the NSF. Responsible for full time research towards my dissertation. | The University of Texas at Austin |

grants

Scarpino, SV (PI) - *Recommended for funding* - "Machine learning and clinical decision making." Gates Foundation, \$100,000 (2019).

Scarpino, SV (PI) - *in review* - "Integrating epidemiological and genetic data to uncover mechanisms of hidden disease transmission." National Institutes of Health - NIAID - R21.

Scarpino, SV (Co-I) - *in review* - "A prospective study of social networks and smoking behavior among adults with tobacco-related cancers." National Institutes of Health - R01.

Scarpino, SV (Co-I) - *in review* - "Transmission dynamics of virulence traits in *Vibrio cholerae*: a paradigm for disease emergence." National Science Foundation - EEID.

Scarpino, SV (Co-I) - *in review* - "Health Care Markets and Patient Outcomes for VLBW Infants." National Institutes of Health - R01.

Pespeni, M (PI), **Scarpino, SV (Former Co-PI)**, et al. - *In Progress** - "NRT: Quantitative & Evolutionary STEM Training (QUEST): An Integrative Training Program for Versatile STEM Professionals to Solve Environmental and Global Health Problems" National Science Foundation, \$2,999,999 (2017-2022).

Kirkpatrick, B (PI), **Scarpino, SV (Former Co-I)**, et al. - *In Progress** - "Translational Global Infectious Disease Research Center" National Institutes of Health - COBRE, \$12,300,000 (2018-2023).

Scarpino, SV (PI) & Diehl, S (PI) - *Completed* - "Integrating 'omics and clinical data to study dengue infection." Biomedical Engineering Pilot Project, College of Medicine, University of Vermont, \$40,000 (2017 - 2018).

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

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

Barber, S (PI), Meyers, LA (Co-PI), **Scarpino, SV (CO-PI, SFI), et al.** - *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).

Kirkpatrick, M (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).

*Awarded at the University of Vermont and could not be transferred to Northeastern University.

patents

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

peer-reviewed publications

28. **Scarpino SV**^{*,†} & Petri G[†]. *In press*. On the predictability of infectious disease outbreaks. *Nature Communications*.
27. Baltrusaitis K, Brownstein JS, **Scarpino SV**, Bakota E, Crawley A, Conidi G, Gunn J, Gray J, Zink A, and Santillana M. 2018. Comparison of crowd-sourced, electronic health records based, and traditional health-care based influenza-tracking systems at multiple spatial resolutions in the United States of America. *BMC Infectious Diseases* 8:403.
26. Shrestha M, **Scarpino SV**, Edwards EM, Greenberg LT, and Horbar JD. 2018. The interhospital transfer network for very low birth weight infants in the United States. *EPJ Data Science* 7:27.
25. 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, Aguero-Rosenfeld M, Fey PD, Storch GA, Melnick SL, Cook CV, Nelson RK, Jones JD, **Scarpino SV**, Althouse BM, Ririe KM, Malin BA, Poritz MA. 2018. Automated collection of pathogen-specific diagnostic data for real-time syndromic epidemiological studies. *Journal of Medical Internet Research* 4(3):e59.
24. Allard A, Althouse BM, Hébert-Dufresne L, **Scarpino SV**[†]. 2017. The risk of sustained sexual transmission of Zika is underestimated. *PLoS Pathogens* 13(9): e1006633.
23. Allard A, Althouse BM, **Scarpino SV**, Hébert-Dufresne L. 2017. Asymmetric percolation drives a double transition in sexual contact networks. *Proceedings of the National Academy of Sciences USA* 114(34): 8969-8973.
22. 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.
21. **Scarpino SV**, Meyers LA, Johansson MA. 2017. Design strategies for efficient arbovirus surveillance. *Emerging Infectious Diseases* 23(4): 642-644.
20. Levin DA and **Scarpino SV**. 2017. On the young age of intraspecific herbaceous taxa. *New Phytologist* 213:1513-1520.
19. **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.**
18. 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.
17. 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.
16. 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.
15. **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.**
14. **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.**

13. Shrestha M, **Scarpino SV**, and Moore C. 2015. A message-passing approach for recurrent-state epidemic models on networks. *Physical Review E* 92: 022821.
12. von Hippel P, **Scarpino SV**, and Holas I. 2015. Robust estimation of inequality from binned incomes. *Sociological Methodology* 10.1177/0081175015599807.
11. 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.**
10. **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.**
9. **Scarpino SV***, Levin DA, and Meyers LA. 2014. Polyploid formation shapes flowering plant diversity. *American Naturalist* 184 (4): 456-465.
8. **Scarpino SV***, Hunt PJ, Garcia-De-Leon FJ, Juenger TE, Schartl 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.

†all authors contributed equally to this work

books and book chapters

4. Rohani P & **Scarpino SV**. *In press*. The integrative biology of Pertussis: epidemiology, immunology & evolution. Oxford University Press.
3. Rohani P & **Scarpino SV**. *In press*. Basics of pertussis transmission dynamics. In: Rohani P & Scarpino SV (ed.). The integrative biology of Pertussis: epidemiology, immunology & evolution. Oxford University Press.

2. Althouse BM & **Scarpino SV**. *In press*. Contrasting ecological & evolutionary signatures of whooping cough epidemiological dynamics. In: Rohani P & Scarpino SV (ed.). *The integrative biology of Pertussis: epidemiology, immunology & evolution*. Oxford University Press.
1. **Scarpino, SV***. 2016. Evolutionary Medicine IV. Evolution and Emergence of Novel Pathogens. In: Kliman, RM (ed.), *Encyclopedia of Evolutionary Biology*. vol. 2, pp. 77–82. Oxford: Academic Press.

outreach publications

8. Modelling the trajectory of disease outbreaks works. 2018. Rivers CM and **Scarpino SV** [Nature](#).
7. Epidemic Spreading: Don't Close the Gates. 2018. **Scarpino SV**. [Nature Physics](#).
6. The flu vaccine is effective. 2017. **Scarpino SV**. [Medium](#).
5. 3 graphs that help show why Ebola goes viral or dies out. 2015. **Scarpino SV**. [Nautilus](#).
4. The mathematics of stopping Ebola. 2014. **Scarpino SV**. [Santa Fe New Mexican Front Page](#) - Nov. 24th 2014.
3. 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. [PNAS](#).
2. 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](#).
1. 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](#).

awards and honors

| | | |
|------|--|---|
| 2018 | Scientific Steering Committee Member | Trend Surveillance, BioFire Diagnostics, Salt Lake City, UT, USA. |
| 2017 | Fellow | Institute for Scientific Interchange Foundation, Turin, Italy. |
| 2017 | Junior Scientific Award - Complex Systems Society | Recognizes extraordinary scientific achievements by a CSS researchers within 7 years of PhD completion. |
| 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 |
| 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 |

editorial boards

| | | |
|---------|------------------------------|----------------------------------|
| Ongoing | Deputy Editor | PLoS Neglected Tropical Diseases |
| Ongoing | Guest Academic Editor | PLoS Computational Biology |
| Ongoing | Guest Academic Editor | PLoS One |
| 2014–16 | Associate Editor | PLoS Neglected Tropical Diseases |
| 2014 | Guest Editor | PLoS Neglected Tropical Diseases |

invited seminars - forty six

| | | |
|------|--|---|
| 2019 | Gene Interaction Networks and Speciation | Keynote, Latin American Conference of Complex Networks, Cartagena, Colombia |
| 2019 | Machine Learning and Clinical Decision Making | Global Infectious Disease Institute Seminar Series, University of Vermont, Burlington, VT, USA |
| 2018 | The Eco-Evolutionary Dynamics of Gene Interaction Networks | Statistical Physics of Networks and Phase Transitions Workshop, Seoul National University, Seoul, South Korea |
| 2018 | Speciation and Gene Network Evolution | Biology Department Seminar, Boston University, Boston, MA, USA |
| 2018 | Networks and Evolution | Complex Networks Winter Workshop, Québec City, Québec, Canada |
| 2018 | Network Heterogeneity Induces Entropy Barriers in Social Contagion | NetSci2018, Paris, France |
| 2018 | On the Predictability of Infectious Disease Outbreaks | Center for Communicable Disease Dynamics Seminar, Harvard School of Public Health, Boston, MA, USA |
| 2018 | The Risk of Sustained Sexual Transmission of Zika is Underestimated | CompleNet18, Boston, MA, USA |
| 2018 | Digital Health Data for Public Health: Friend or Foe? | Debate on Big Data, Digital Health 2018, Lyon, France |
| 2017 | On the Predictability of Complex Adaptive Systems | Condensed Matter/Biophysics Seminar, Brown University, Providence, RI, USA |
| 2017 | Topological Variation in Gene Expression | Biostatistics and Computational Biology Seminar, Dana-Farber Cancer Institute, 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
- 2017 **Entropy Barriers in Social Contagion**
Institute on Complex System, Northwestern University, Evanston, IL, USA
- 2017 **Panel discussion - Community engagement and behavior change in disease modeling**
IMeasuring and Modeling Community Engagement in Health Emergencies, Bill & Melinda Gates Foundation, Washington, DC, USA
- 2017 **Network Heterogeneity Induces Entropy Barriers in Social Contagion**
Network Science Institute, Northeastern University, Boston, MA, USA
- 2017 **On the Unpredictability of Outbreaks: The Role of Ecology, Evolution, and Behavior**
Center for Infectious Disease Dynamics, Pennsylvania State University, State College, PA, USA
- 2017 **The Integrative Biology of Disease**
Biofrontiers Institute, University of Colorado Boulder, Boulder, CO, USA
- 2017 **Topological Features of Gene Regulatory Networks Predict Patterns of Natural Diversity in Environmental Response**
Department Seminar, Department of Biology, University of Vermont, Burlington, VT, USA
- 2016 **The Predictability Horizon for Infectious Diseases**
Population Models in the 21st Century, Mathematical Biosciences Institute, Columbus, OH, USA
- 2016 **On the Limits to Predictability, Or How Big Data Alone Can't Solve Our Problems**
New-Regime Management in the Era of Big Data, Morgan Stanley, New York City, NY, USA
- 2016 **A Complex Systems View of Infectious Disease Outbreaks**
Oppenheim Symposium, Oberlin College, Oberlin, OH, USA
- 2016 **Data Blindspots: High-tech Disease Surveillance Misses the Poor**
Disease Modeling Symposium, Institute for Disease Modeling, Bellevue, WA, USA
- 2016 **The Network Topology of Natural Variation in Abiotic Stress-Responsive Gene Expression**
Evolutionary Genomics Supergroup Seminar Series, Harvard University, Cambridge, MA, USA
- 2016 **Predicting Infectious Disease Outbreaks**
Vermont Complex Systems Speaker Series, University of Vermont, Burlington, VT, USA
- 2016 **Modeling Infectious Disease Outbreaks on Social Networks**
Department of Mathematics, St. Michaels College, Winooski, VT, USA
- 2015 **The Ecological and Evolutionary Dynamics of Whooping Cough**
Department of Ecology and Evolutionary Biology, the University of Arizona, Tucson, AZ, USA

-
- 2015 **Network Structure, Subclinical Infection, and Ebola**
Institute for Disease Modeling, Bellevue, WA, USA
- 2015 **Emergent Epidemics**
Complex Systems Summer School, Santa Fe Institute, Santa Fe, NM, USA
- 2015 **Network Structure, Subclinical Infection, and Ebola**
ISI Foundation, Turin, Italy
- 2015 **Asymptomatic Transmission and the Resurgence of *Bordetella pertussis***
Computational Ecology & Epidemiology Study Group, University of Georgia, Athens, GA, USA
- 2015 **Toward a Complex Systems Theory of Disease**
Vermont Complex Systems Center, University of Vermont, Burlington, VT, USA
- 2015 **The Role of Social Network Clustering in Ebola Virus Transmission**
Modeling the Spread and Control of Ebola in W. Africa, Atlanta, GA, USA
- 2014 **Epidemiological and Phylodynamic Analysis of the 2014 Ebola Outbreak Reveals Clustered Transmission**
Center for Computational, Evolutionary and Human Genomics, Stanford University, Stanford, CA, USA
- 2014 **Optimizing Outbreak Surveillance**
Healthcare Modeling, Multi-scale Challenges and Methods, MITRE, McLean, VA, USA
- 2014 **Using Your Digital Footprint to Track the Next Pandemic**
Santa Fe Institute Business Network Meeting, Palo Alto, CA, USA
- 2014 **Data-driven Modeling**
Graduate Workshop in Computational Social Science Modeling and Complexity, Santa Fe Institute, Santa Fe, NM, USA
- 2014 **The Evolution of Antiviral Resistance in Influenza**
Complex Systems Summer School, Santa Fe Institute, Santa Fe, NM, USA
- 2014 **Stronger Together: Modeling Lessons for Success--Public Health Practitioners' Collaboration with Computational Modelers**
Panel discussion at the National Association of County and City Health Officials Preparedness Summit, Atlanta, GA, USA
- 2014 **Goal-oriented Design of Surveillance Systems**
Centers for Disease Control and Prevention, San Juan, Puerto Rico, USA
- 2014 **Local and Nonlocal Information in a Traffic Network: How Important is the Horizon?**
American Mathematical Society, Joint Mathematics Meeting, Albuquerque, New Mexico, USA
- 2013 **Goal-oriented Design of Influenza Surveillance Systems**
Center for Nonlinear Studies, Los Alamos National Labs, Los Alamos, NM, USA

- 2013 **The Texas Pandemic Flu Toolkit**
Public Health Capabilities: Bridging the Gap Between Planning and Preparedness, Tyler, TX, USA
- 2013 **Public Health Surveillance: Network Design and Outbreak Prediction**
Network Dynamics and Simulation Science Laboratory, Virginia Tech Bioinformatics Institute, USA
- 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

- 2018 **Contagion on Networks II**
NetSci, Paris, France
- 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 seven

- 2018 **Empowering Robust and Effective Local Public Health Infrastructure and Governance Through Cloud and Mobile-based Technology**
Podium presentation at NACCHO Public Health Informatics, Atlanta, GA, USA
- 2018 **Hard Talk: Will Technology and Big Data Replace Monitoring Evaluation, Research and Learning?**
Podium presentation at MERL Tech DC 2018, Washington, D.C., USA
- 2018 **Real-time Phenotype Prediction From Unaligned Whole Genome Sequencing Data Using Deep Learning**
Podium presentation at the Society for Molecular Biology and Evolution Annual Meeting, Yokohama, Japan
- 2018 **On the Predictability of Infectious Disease Outbreaks**
Podium presentation at the Center for the Ecology of Infectious Diseases, University of Georgia, Athens, GA, USA
- 2018 **On the Predictability of Infectious Disease Outbreaks**
Podium presentation at the American Naturalist 150th Anniversary Meeting, Asilomar, CA, USA

- 2017 **Data Blindspots: High-tech Disease Surveillance Misses the Poor**
Podium presentation at the Data and Algorithm Bias Conference 2017, Singapore
- 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 eight

- 2018 **Paper Unwind: The Real Story Behind the Moose of Isle Royale National Park**
NetSci Graduate Student Symposium, Northeastern University, Boston, MA, USA
- 2018 **Advisor**
Hack for Humanity, Brown University, Providence, RI, USA
- 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 | 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 | <i>On Immunity: an Inoculation</i> 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 |

reviewer - forty seven unique venues

American Journal of Botany, American Naturalist, American Society of Tropical Medicine and Hygiene, Annals of Applied Statistics, Annals of Internal Medicine, Applied Network Science, BMC Bioinformatics, BMC Medicine, BMC infectious diseases, Bulletin of Mathematical Biology, Chapman and Hall, Environmental Biology of Fishes, EPJ Data Science, Evolution, Genetics, IEEE Transactions on Control Systems Technology, Informatics in Medicine Unlocked, Interdisciplinary Perspectives on Infectious Disease, International Journal of Infectious Diseases, Journal of Medical Internet Research, Journal of Theoretical Biology, Lancet Infectious Diseases, Molecular Biology & Evolution, 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, Physical Review X, 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, Systematic Biology, Vaccine.

grant reviewer

National Science Foundation (2019 panelist); Medical Research Council, Skills Development Fellowship; Medical Research Council, Research Grant; Vermont Genetics Network, 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](#) .

preprints

Guerrero RF, **Scarpino SV**, Rodrigues JV, Hartl D, Ogbunugafor DB. Proteostasis environment shapes higher-order epistasis operating on antibiotic resistance. [bioRxiv](#)

Scarpino SV, Scott JG, Eggo RM, Clements B, Dimitrov NB, Meyers LA. Socioeconomic bias in influenza surveillance. [arXiv](#)

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: Ezra Levy (Northeastern University), Sophia Novarre (UVM), George Chrisafis (UVM), Haedi DeAngelis (SFI), Cody O’Ferrall (SFI), Gilia Patterson (SFI), Patrick Hunt (UT Austin), & Garrett Johnson (UT Austin).

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

Thesis Committees: Brennan Klein (Network Science - Northeastern), Dina Mistry (Physics - Northeastern), Lauren Ash (Biology - UVM), & Andy Reagan (Mathematical Sciences - UVM).

Postdoctoral: Munik Shrestha (Northeastern & UVM).

teaching

ENVR 2900: Networks and Biology. Northeastern University.

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

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

service

- Program Committee for Web Conference's Health Track, San Francisco, CA, USA (2019).
- Scientific Committee for CompleNet 2019, Tarragona, Catalonia, Spain (2019).
- Conference Program Committee: NERCCS 2019, Binghamton, NY, USA (2019).
- School Organizing Committee: NetSci, Burlington, VT, USA (2019).
- Conference Program Committee: NERCCS 2019, Binghamton, NY, USA (2019).
- Conference Program Committee: ICCS 2018, Boston, MA, USA (2018).
- Conference Workshop Program Committee: SIAM Network Science Workshop, Portland, OR, USA (2018).
- Conference Program Committee: NERCCS 2018, Binghamton, NY, USA (2018).
- Conference Program Committee: NetSci, Indianapolis, IN, USA (2017).
- Complex Systems Society Governing Council (2017–2019).
- Conference Workshop Program Committee: SIAM Network Science Workshop, Pittsburgh, PA, USA (2017).
- Statistics undergraduate and graduate curriculum committees, University of Vermont (2017).
- Search committee member, Four Tenure-Track Hires in Complex Systems, University of Vermont (2016).
- Health Service Research Center Steering Committee, College of Medicine, University of Vermont (2016-17).
- Bioinformatics Working Group, College of Medicine, University of Vermont (2016-17).
- Conference Session Reviewer: Computational health track, 26th WWW Conference, Perth, Australia (2016).
- Conference Session Reviewer: Contagion 2015, Conference on Complex Systems, Tempe, AZ, USA (2015).
- Slice of Science seminar series chair, Santa Fe Institute (2014-15).
- Organizing committee: Integrative Biology Graduate Research Symposium (2008-13).
- Research and Educational Technology Committee (2009-13).
- Graduate Student Assembly and Center for Teaching and Learning T/AI Panel (2013).
- Regent's outstanding teaching award committee (2011-12).
- University Health Services Committee (2011-12).
- Parking and Transportation Services Appeals Committee (2010-11).
- Provost's Student Advisory Committee (2010-11).
- Dean of the Graduate Schools Student Advisory Committee (2010-11, 2011-12).
- Graduate Student Assembly - Student Affairs Director (2010-11).
- Graduate Student Assembly - Department Representative (2009-10, 2011-12).
- Graduate student representative to the Integrative Biology Faculty: (2009).

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*)

| | | |
|------|---|---|
| 2019 | Scaling Limits of Dynamical Processes on Random Graphs | BIRS - Casa Matematica Oaxaca |
| 2018 | Data Innovations for Epidemic Readiness | World Economic Forum |
| 2018 | Digital Economy and Society Community Meeting | World Economic Forum |
| 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 |

- 2010 **Emergence of Gender and Sex Chromosomes: Evolutionary Insights from a Diversity of Taxa**
National Evolutionary Synthesis Center
- 2009 **Investigative Workshop on Modeling Transmission Dynamics of Bovine Tuberculosis**
National Institute for Mathematical and Biological Synthesis
- 2008–10 **Efficient Wildlife Vaccination**
National Center for Ecological Analysis and Synthesis

public health interface

- 2018 **Neural Networks and Lab Testing** US CDC
I am an advisor to a small working group at the CDC exploring how convolutional neural networks, i.e. deep learning, can be applied to laboratory prioritization decisions.
- 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, Complex Systems Society, Ecological Society of America, Society for Molecular Biology and Evolution, Society for the Study of Evolution.