

Matthew Laurence Scotch, PhD, MPH

Associate Professor of Biomedical Informatics, College of Health Solutions;
Assistant Director, Center for Environmental Health Engineering, Biodesign Institute
Arizona State University

Biodesign Center for Environmental Health Engineering
P.O. Box 878101
Tempe, Arizona USA 85287-8101

PHONE: 480.727.2985

EMAIL: matthew.scotch@asu.edu

WEB: <https://isearch.asu.edu/profile/1615221>

EDUCATION and TRAINING

Years	Institution	Degree	Field
2006–2008	Yale University, New Haven, CT	Postdoc	Biomedical Informatics
2006–2007	Yale University, New Haven, CT	MPH	Public Health
2002–2006	University of Pittsburgh, Pittsburgh, PA	PhD	Biomedical Informatics
2000–2002	Columbia University, New York, NY	MA	Medical Informatics
1994–1998	University of Rochester, Rochester, NY	BA	Health & Society

PROFESSIONAL APPOINTMENTS

2017–	Senior Visiting Fellow, University of New South Wales (UNSW), Sydney, Australia
2016–	Associate Professor (with tenure), College of Health Solutions, Arizona State University (ASU)
2016–	PLuS Alliance Fellow, ASU, King's College London, University of New South Wales
2015–	Assistant Director, Biodesign Center for Environmental Security, Biodesign Institute, ASU
2015–	Faculty Advisor, Barrett, the Honors College at ASU
2015–2016	Without Compensation (WOC) - Research, Veterans Affairs (VA) Phoenix Healthcare System, Phoenix, Arizona
2013–	Research Affiliate, Mayo Clinic Arizona, Phoenix, Arizona
2012–2015	Assistant Professor, Center for Environmental Security, Biodesign Institute, ASU
2010–2016	Assistant Professor, Department of Biomedical Informatics, College of Health Solutions, ASU
2010–	Visiting Scholar, Yale School of Medicine, Yale University, New Haven, Connecticut
2008–2010	Associate Research Scientist, Yale Center for Medical Informatics, Yale School of Medicine, Yale University, New Haven, Connecticut
2008–2015	WOC – Research Service, VA Connecticut Healthcare System, West Haven, Connecticut

HONORS and AWARDS

2018	Awardee, Endeavour Research Fellowship (Australian Government)
2014	Nominee, New York Academy of Sciences Blavatnik Award for Young Scientists
2013	Nominee, Pew Biomedical Scholars Program (Limited Submission)
2011	Finalist, Best Paper, <i>Enhancing phylogeography by improving geographical information from GenBank</i> , American Medical Informatics Association (AMIA) Joint Summits
2007	Awardee, Tuition and Travel, Cold Spring Harbor Laboratory Workshop on Infectious Disease Ontology, Supported by the Burroughs Wellcome Fund
2002	Winner, Best Paper, <i>Sublanguage of cross coverage</i> , AMIA Fall Symposium
2002	Nominee, Homer R. Warner Award, <i>Sublanguage of cross coverage</i> , AMIA Fall Symposium

PUBLICATIONS-ORIGINAL INVESTIGATIONS

1. Stelzer-Braid S, Wynn M, Chatoor R, **Scotch M**, Ramachandran V, Teoh HL, Farrar MA, Sampaio H, Andrews PI, Craig ME, MacIntyre CR, Varadhan H, Kesson A, Britton PN, Newcombe J, Rawlinson WD. *Next generation sequencing of human enterovirus strains from an outbreak of enterovirus A71 shows applicability to outbreak investigations.* J Clin Virol. 2020 Jan;122:104216.
2. Beard R*, **Scotch M**. *Identifying current and emerging resources and tools utilized for detection, prediction, and visualization of viral zoonotic disease clusters: a Delphi study.* JAMIA Open. 2019 Oct; 2(3): 306–311.
3. Adam DC*, MacIntyre CR†, **Scotch M**†. *Phylogenetics of influenza A/H1N1pdm09 in India reveals circulation patterns and increased selection for clade 6b residues and other high mortality mutants.* Viruses. 2019 Aug 27;11(9). pii: E791.
4. **Scotch M**, Tahsin T*, Weissenbacher D, O'Connor K, Magge A*, Vaiente M*, Suchard MA, Gonzalez-Hernandez G. *Incorporating sampling uncertainty in the geospatial assignment of taxa for virus phylogeography.* Virus Evol. 2019 Feb 28;5(1):vey043.
5. Magee HY, Maurer MM, Cobos A, Pycke BFG, Venkatesan AK, Magee D, **Scotch M**, Halden RU. *U.S. nationwide reconnaissance of ten infrequently monitored antibiotics in municipal biosolids.* Sci Total Environ. 2018 Dec 1;643:460-467.
6. Bui CM*, Adam DC*, Njoto E*, **Scotch M**, MacIntyre CR. *Characterising routes of H5N1 and H7N9 spread in China using Bayesian phylogeographical analysis.* Emerg Microbes Infect. 2018 Nov 21;7(1):184.
7. Adam DC*, MacIntyre CR†, **Scotch M**†. *Bayesian phylogeography and pathogenic characterisation of smallpox based on HA, ATI and CrmB genes.* Mol Biol Evol. 2018 Nov 1;35(11):2607-2617.
8. Beard R*, Wentz E, **Scotch M**. *A systematic review of spatial decision support systems in public health informatics supporting the identification of high risk areas for zoonotic disease outbreaks.* Int J Health Geogr. 2018 Oct 30;17(1):38.
9. Magee D*, **Scotch M**. *The effects of random taxa sampling schemes in Bayesian virus phylogeography.* Infect Genet Evol. 2018 Oct;64:225-230.
10. Magee A*, Weissenbacher D, Sarker A, **Scotch M**, Gonzalez-Hernandez G. *Deep neural networks and distant supervision for geographic location mention extraction.* Bioinformatics. 2018 Jul 1;34(13):i565-i573.
11. Tahsin T*, Weissenbacher D, O'Connor K, Magge A, **Scotch M**, Gonzalez-Hernandez G. *GeoBoost: accelerating research involving the geospatial metadata of virus GenBank records.* Bioinformatics. 2018 May 1;34(9):1606-1608.
12. Njoto EN*, **Scotch M**, Bui CM*, Adam DC*, Chughtai AA*, MacIntyre CR. *Phylogeography of H5N1 avian influenza virus in Indonesia.* Transbound Emerg Dis. 2018 Apr 24.
13. Magee D*, Taylor JE, **Scotch M**. *The effects of sampling location and predictor point estimate certainty on posterior support in Bayesian phylogeographic generalized linear models.* Sci Rep. 2018 Apr 12;8(1):5905.
14. Tahsin T*, Weissenbacher D, Jones-Shargani D*, Magee D*, Vaiente M*, Gonzalez G, **Scotch M**. *Named entity linking of geospatial and host metadata in GenBank for advancing biomedical research.* Database. 2017 Dec 28; bax093.
15. Namilae S, Derjany P, Mubayi A, **Scotch M**, Srinivasan A. *Multiscale model for pedestrian and infection dynamics during air travel.* Phys Rev E. 2017 May;95(5-1):052320.
16. Magee D*, Suchard MA, **Scotch M**. *Bayesian phylogeography of influenza A/H3N2 for the 2014-15 season in the United States using three frameworks of ancestral state reconstruction.* PLoS Comput Biol. 2017 Feb 7;13(2):e1005389.
17. Namilae S, Srinivasan A, Mubayi A, **Scotch M**, Pahle R. *Self-propelled pedestrian dynamics model: Application to passenger movement and infection propagation in airplanes.* Physica A. 2017 Jan 1; 465(1):248-260.
18. Jirjies S*, Wallstrom G, Halden RU, **Scotch M**. *pyJacqQ: python implementation of Jacques's Q-statistics for space-time clustering of disease exposure in case-control studies.* J Stat Softw. 2016 Oct;74(6).
19. Tahsin T*, Weissenbacher D, Rivera R*, Beard R*, Firago M*, Wallstrom G, **Scotch M**, Gonzalez G. *A high-precision rule-based extraction system for expanding geospatial metadata in GenBank records.* J Am Med Inform Assoc. 2016 Sep;23(5):934-41.
20. Sarker A, O'Connor K*, Ginn R*, **Scotch M**, Smith K, Malone D, Gonzalez G. *Social media mining for toxicovigilance: automatic monitoring of prescription medication abuse from Twitter.* Drug Saf. 2016 Mar;39(3):231-40.
21. Veljkovic V, Paessler S, Glisic S, Prljic J, Perovic VR, Veljkovic N, **Scotch M**. *Evolution of 2014/15 H3N2 influenza viruses circulating in US: consequences for vaccine effectiveness and possible new pandemic.* Front Microbiol. 2015 Dec 22;6:1456.

22. Weissenbacher D, Tahsin T*, Beard R*, Figaro M*, Rivera R*, **Scotch M**, Gonzalez G. *Knowledge-driven geospatial location resolution for phylogeographic models of virus migration*. Bioinformatics. 2015 Jun 15;31(12):i348-i356. ISMB/ECCB 2015 Proceedings.
23. Veljkovic V, Glisic S, Muller CP, **Scotch M**, Branch DR, Perovic VR, Sencanski M, Veljkovic N, Colombatti A. *In silico analysis suggests interaction between Ebola virus and the extracellular matrix*. Front Microbiol. 2015 Feb 19;6:135.
24. Magee D*, Beard R*, Suchard MA, Lemey P, **Scotch M**. *Combining phylogeography and spatial epidemiology to uncover predictors of H5N1 influenza A virus diffusion*. Arch Virol. 2015 Jan;160(1):215-24.
25. Kane MJ, Price N, **Scotch M**, Rabinowitz P. *Comparison of ARIMA and random forest time series models for prediction of avian influenza H5N1 outbreaks*. BMC Bioinformatics. 2014 Aug 13;15(1):276.
26. **Scotch M**, Lam TT, Pabilonia KL, Anderson T, Baroch J, Kohler D, DeLiberto TJ. *Diffusion of influenza viruses among migratory birds with a focus on the Southwest United States*. Infect Genet Evol. 2014 Aug;26:185-193.
27. **Scotch M**, Mei C, Makonnen YJ, Pinto J, Ali A, Vegso S, Kane M, Sarkar IN, Rabinowitz P. *Phylogeography of influenza A H5N1 clade 2.2.1.1 in Egypt*. BMC genomics. 2013 Dec 10;14(1):871.
28. Womack JA, **Scotch M**, Leung S, Brandt CA. *Use of structured and unstructured data to identify contraceptive use in women veterans*. Perspect Health Inf Manag. 2013. Summer: 1-15.
29. **Scotch M**, Baarson B*, Beard R*, Lauder R*, Varman A*, Halden RU. *Examining the differences in format and characteristics of zoonotic virus surveillance data on state agency websites*. J Med Internet Res. 2013;15(4):e90.
30. **Scotch M**, Mei C. *Phylogeography of swine influenza H3N2 in the United States: translational public health for zoonotic disease surveillance*. Infect Genet Evol. 2013 Jan;13:224-9.
31. Rabinowitz PM, Galusha D, Vegso S, Michalove J*, Rinne S, **Scotch M**, Kane M. *Comparison of human and animal surveillance data for H5N1 influenza A in Egypt 2006-2001*. PLoS One. 2012;7(9):e43851. Epub 2012 Sep 27.
32. **Scotch M**, Brownstein JS, Vegso S, Galusha D, Rabinowitz P. *Human vs. animal outbreaks of the 2009 swine-origin H1N1 influenza A epidemic*. Ecohealth. 2011 Sep;8(3):376-80.
33. **Scotch M**, Sarkar IN, Mei C, Leaman R, Cheung KH, Ortiz P*, Singraur A*, Gonzalez G. *Enhancing phylogeography by improving geographical information from GenBank*. J Biomed Inform. 2011;44(S1):S44-47.
34. Garla V, Re VL 3rd, Dorey-Stein Z, Kidwai F, **Scotch M**, Womack J, Justice A, Brandt C. *The Yale cTAKES extensions for document classification: architecture and application*. J Am Med Inform Assoc. 2011. 18(5):614-20.
35. **Scotch M**, Rabinowitz P, Brandt C. *State-level zoonotic disease surveillance in the United States*. Zoonoses and Public Health. 2011;58(8):523-8.
36. **Scotch M**, Mattocks K, Rabinowitz P, Brandt C. *A qualitative study of state-level zoonotic disease surveillance in New England*. Zoonoses and Public Health. 2011;58(2):131-139.
37. Womack JA, **Scotch M**, Gibert C, Chapman W, Yin M, Justice AC, Brandt C. *A comparison of two approaches to text processing: facilitating chart reviews of radiology reports in electronic medical records*. Perspect Health Inf Manag. 2010; Oct 1;7:1a.
38. **Scotch M**, Mei C, Brandt C, Sarkar IN, Cheung K. *At the intersection of public-health informatics and bioinformatics: Using advanced Web technologies for phylogeography*. Epidemiology. 2010; 21(6):764-8.
39. Konovalov S, **Scotch M**, Post L, Brandt C. *Biomedical informatics techniques for processing and analyzing web blogs of military service members*. J Med Internet Res. 2010; 12(4):e45.
40. Rabinowitz PR, **Scotch M**, Conti LA. *Animals as sentinels: using comparative medicine to move beyond the laboratory*. Institute for Laboratory Animal Research Journal. 2010; 51(3):262-267.
41. Ohl M, Tate J, Duggal M, Skanderson M, **Scotch M**, Kaboli P, Vaughan-Sarrazin M, Justice A. *Rural residence is associated with delayed care entry and increased mortality among veterans with Human Immunodeficiency Virus (HIV) infection*. Medical Care. 2010 Dec;48(12):1064-1070.
42. **Scotch M**, Duggal M, Brandt C, Lin Z, Shiffman R. *Use of statistical analysis in the biomedical informatics literature*. Journal of the American Medical Informatics Association. 2010; 17(1):3-5.
43. Liu A, Lee V, Galusha D, Slade MD, Diuk-Wasser M, Andreadis T, **Scotch M**, Rabinowitz P. *Risk factors for human infection with West Nile virus in Connecticut: a multi-year analysis*. International Journal of Health Geographics. 2009, 8:67.
44. **Scotch M**, Odofin L, Rabinowitz P. *Linkages between animal and human health sentinel data*. BMC Veterinary Research. 2009, 5:15.

45. Rabinowitz, P, **Scotch M**, Conti L. *Human and animal sentinels for shared health risks*. Veterinaria Italiana. 2009; 45(1):23-34.
46. Boulos MNK, **Scotch M**, Cheung K, Burden D. *Web GIS in practice VI: a demo "playlist" of geo-mashups for public health neogeographers*. International Journal of Health Geographics. 2008, 7:38.
47. **Scotch M**, Yip K, Cheung K. *Development of grid-like applications for public health using Web 2.0 mashup techniques*. Journal of the American Medical Informatics Association. 2008;15(6):783-786.
48. Cheung K, Yip K, Townsend JP, **Scotch M**. *HCLS 2.0/3.0: Health care and life sciences data mashup using Web 2.0/3.0*. Journal of Biomedical Informatics. 2008;41(5):694-705.
49. **Scotch M**, Parmanto B, Monaco V. *Evaluation of SOVAT: an OLAP-GIS decision support system for community health assessment data analysis*. BMC Medical Informatics and Decision Making. 2008; 8(1):22.
50. Parmanto B, Paramita M, Sugiantara W, Pramana G, **Scotch M**, Burke DS. *Spatial and multidimensional visualization of Indonesia's village health statistics*. International Journal of Health Geographics. 2008; 7:30.
51. **Scotch M**, Parmanto B, Monaco V. *Usability evaluation of the Spatial OLAP Visualization and Analysis Tool (SOVAT)*. Journal of Usability Studies. 2007;2(2):76-95.
52. **Scotch M**, Parmanto B, Gadd CS, Sharma RK. *Exploring the role of GIS during community health assessment problem solving: experiences of public health professionals*. International Journal of Health Geographics. 2006;5:39.
53. **Scotch M**, Parmanto B. *Development of SOVAT: A numerical-spatial decision support system for community health assessment research*. International Journal of Medical Informatics. 2006;75(10-11):771-84.
54. Parmanto B, **Scotch M**, Ahmad S. *A framework for designing a healthcare outcome data warehouse*. Perspectives in Health Information Management. 2005; 2:3.

†Joint senior authorship; order switched to facilitate counting

*Student authors

PUBLICATIONS-REVIEWS

1. Morin CW, Stoner-Duncan B, Winker K, **Scotch M**, Hess JJ, Meschke JS, Ebi KL, Rabinowitz PM. *Avian influenza virus ecology and evolution through a climatic lens*. Environ Int. 2018 Jul 3;119:241-249.
2. MacIntyre RC, Engells TE, **Scotch M**, Heslop DJ, Gumel AB, Poste G, Chen X, Herche W, Steinhöfel K, Lim S, Broom A. *Converging and emerging threats to health security*. Environ Syst Decis. 2018 Jun; 38(2):198–207.

PUBLICATIONS-COMMENTARY

1. Adam DC*, Magee DJ*, Bui CM*, **Scotch M**, MacIntyre CR. *Does influenza pandemic preparedness and mitigation require gain-of-function research?*. Influenza Other Respir Viruses. 2017 May 14.
2. Braithwaite RS, **Scotch M**. *Using value of information to guide evaluation of decision supports for differential diagnosis: is it time for a new look?* BMC Med Inform Decis Mak. 2013 Sep 11;13(1):105.

*Student authors

CONFERENCE PROCEEDINGS

1. Magge A*, Weissenbacher D, Sarker A, **Scotch M**, Gonzalez-Hernandez G. *Bi-directional Recurrent Neural Network Models for Geographic Location Extraction in Biomedical Literature*. Pac Symp Biocomput. 2019;24:100-111.
2. Magge A*, **Scotch M**, Gonzalez-Hernandez G. *Clinical NER and Relation Extraction using Bi-Char-LSTMs and Random Forest Classifiers*. Proceedings of Machine Learning Research 90:25–30, 2018 Medication and Adverse Drug Event Detection Workshop.
3. Weissenbacher D, Sarker A, Tahsin T*, **Scotch M**, Gonzalez G. *Extracting geographic locations from the literature for virus phylogeography using supervised and distant supervision methods*. AMIA Jt Summits Transl Sci Proc. 2017 Jul 26;2017:114-122.

4. Magge A, **Scotch M**, Gonzalez G. *CSaRUS-CNN at AMLA-2017 tasks 1, 2: under sampled CNN for text classification*. In: Proceedings of the Second Workshop on Social Media Mining for Health Research and Applications Workshop Co-located AMIA 2017; 2017: 76–78.
5. Paul MJ, Sarker A, Brownstein JS, Nikfarjam A*, **Scotch M**, Smith KL, Gonzalez G. *Social media mining for public health monitoring and surveillance*. Pac Symp Biocomput. 2016;21:468-79. (Review)
6. Magee D*, Beard R*, **Scotch M**. *Analyses of Merging Clinical and Viral Genetic Data for Influenza Surveillance*. AMIA Annu Symp Proc. 2015 Nov 5;2015:1995-2004.
7. **Scotch M**, Suchard MA, Rabinowitz P. *Analysis of viral genetics for estimating diffusion of influenza A H6N1*. AMIA 2015 Joint Summits on Translational Science; 2015:36-40.
8. Magee D*, **Scotch M**. *Conceptualizing a Novel Quasi-Continuous Bayesian Phylogeographic Framework for Spatiotemporal Hypothesis Testing*. AMIA 2015 Joint Summits on Translational Science; 2015:212-216.
9. Tahsin T*, Rivera R*, Beard R*, Lauder R*, Weissenbacher D, **Scotch M**, Wallstrom G, Gonzalez G. *Natural language processing methods for enhancing geographic metadata for phylogeography of zoonotic viruses*. AMIA 2014 Joint Summits on Translational Science; 2014:102-111.
10. Beard R*, Magee D*, Suchard MA, Lemey P, **Scotch M**. *Generalized Linear Models for Identifying Predictors of the Evolutionary Diffusion of Viruses*. AMIA 2014 Joint Summits on Translational Science; 2014:23-28.
11. Tahsin T*, Rivera R*, Beard R*, Lauder R*, Weissenbacher D, **Scotch M**, Wallstrom G, Gonzalez G. *Natural language processing methods for enhancing geographic metadata for phylogeography of zoonotic viruses*. Proceedings of the 2014 Workshop on Biomedical Natural Language Processing (BioNLP 2014); 2014:1-9.
12. Rabinowitz P, Vegso S, Chudnov, Odofin L, **Scotch M**, Wilcox M. *The 'Canary Database': Assembling Evidence for One Health Linkages between Human, Animal, and Environmental Health*. 2013 Annual Meeting and Exhibition of the Medical Library Association (MLA '13).
13. **Scotch M**, Parmanto B. *SOVAT: Spatial OLAP Visualization and Analysis Tool* in Proceedings of HICSS-38; 2005;142.2.
14. Parmanto B, **Scotch M**. *Mining Information from Mountains of Electronic Health Record: Unique Challenges and Solutions* in Proceedings of AHIMA National Convention. 2003.
15. Stetson, PD, Johnson SB, **Scotch M**, Hripcsak, G. *The Sublanguage of Cross Coverage* in Proceedings of AMIA Fall Symposium. 2002;742-746.

*Student authors

CONFERENCE ABSTRACTS

1. Yoo W, **Scotch M**. *Patterns in HPV vaccine uptake for young female adolescents using NIS teen data*. American Public Health Association Annual Meeting. 2019. Philadelphia, PA.
2. **Scotch M**, Tahsin T, Weissenbacher D, O'Connor K, Magge A, Vaiente M, Suchard MA, Gonzalez G. *Sampling uncertainty for virus phylogeography*. Intelligent Systems for Molecular Biology. 2019. Basel, Switzerland.
3. **Scotch M**, Magge A, Vaiente M. *ZooPhy: A bioinformatics pipeline for virus phylogeography and surveillance*, International Society for Disease Surveillance Annual Conference. San Diego, California. 2019. Also published in Online J Public Health Inform. 2019; 11(1): e301.
4. Halden R, Terlinden E, Kraberger S, **Scotch M**, Steele J, Varsani A. *Tracking harmful chemicals and pathogens using the Human Health Observatory at ASU*. International Society for Disease Surveillance Annual Conference. San Diego, California. 2019. Also published in Online J Public Health Informatics, 2019;11(1): e369.
5. **Scotch M**, Gonzalez G. *ZooPhy and ZoDo: Bringing virus phylogeography to the public health epidemiologist*. 14th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID-14). Sitges, Spain. 2018.

6. Vaiente M, **Scotch M**. *Avian contact transmission underlies early epidemic expansion of West Nile virus in the US*. MEEGID-14. Sitges, Spain. 2018
7. Vaiente M, **Scotch M**. *Combining GoogleTrends and viral genetic data for public health surveillance: The case of Influenza A/H3N2 in Arizona*. MEEGID-14. Sitges, Spain. 2018
8. Magee D, **Scotch M**. *A pipeline for production of BEAST XML files with generalized linear model specifications*. Great Lakes Bioinformatics Conference (GLBIO). Chicago, IL. 2017.
9. **Scotch M**, Suchard MA, Rabinowitz P. *Phylogeography of 2014-2015 highly pathogenic avian influenza H5N2 in North America*. Options IX for the Control of Influenza. Chicago, IL. 2016
10. Magee D, **Scotch M**. *Algorithmic prediction of virus outbreak locales using past geospatial references*. MEEGID-13. Antwerp, Belgium. 2016.
11. **Scotch M**, Beard R, Pahle R, Mubayi A, Namilae S, Srinivasan A. *Combining human movement models with phylogeography for airplane policy options during Ebola outbreaks*. MEEGID-13. Antwerp, Belgium. 2016.
12. **Scotch M**, Beard R, Tahsin T, Weissenbacher D, Suchard MA, Gonzalez G. *Incorporating geospatial observation error in discrete Bayesian virus phylogeography*. MEEGID-13. Antwerp, Belgium. 2016.
13. **Scotch M**, Beard R, Pahle R, Mubayi A, Namilae S, Srinivasan A. *The spread of the 2014 Ebola Zaire virus in West Africa*. Pacific Symposium on Biocomputing. Big Island, HI. 2016.
14. Beard R, **Scotch M**. *Identification of zoonotic disease clusters by integrating phylogeography*. AMIA 2015 Joint Summits on Translational Science. San Francisco, CA. 2015.
15. **Scotch M**, Rivera R, Tahsin T, Beard R, Firago M, Weissenbacher D, Wallstrom G, Gonzalez G. *Addressing geospatial observation error for virus phylogeography*. The International Society for Evolution, Medicine, & Public Health Inaugural Meeting. Tempe, AZ. 2015.
16. Magee D, **Scotch M**. *Introducing the generalized linear model to continuous phylogeography: a novel quasi-continuous model*. The International Society for Evolution, Medicine, & Public Health Inaugural Meeting. Tempe, AZ. 2015.
17. Beard R, **Scotch M**. *Identification of zoonotic disease clusters by integrating phylogeography*. The International Society for Evolution, Medicine, & Public Health. Tempe, AZ. 2015.
18. **Scotch M**, Rivera R, Tahsin T, Beard R, Firago M, Weissenbacher D, Wallstrom G, Gonzalez G. *A pipeline for virus phylogeography that accounts for geospatial observation error*. 12th Annual Rocky Mountain Bioinformatics Conference. Aspen, CO. 2014.
19. Beard R, **Scotch M**. *Interpolating Genetic Characteristics of Zoonotic Viruses for Cluster modeling*. 12th Annual Rocky Mountain Bioinformatics Conference. Aspen, CO. 2014.
20. Magee D, **Scotch M**. *Comparison of Phylogeographic Node Flux with Local Disease Trends*. 12th Annual Rocky Mountain Bioinformatics Conference. Aspen, CO. 2014.
21. Veljkovic V, Veljkovic N, Perovic V, Sencanski M, **Scotch M**, Glisic S. *Antimalarials repositioning as a route to discovery of drugs for treatment of Ebola virus disease*. COST CM1307 conference on Targeted chemotherapy towards diseases caused by endoparasites. Calvi, France. 2014.
22. Martins S, Tu S, Martinello R, Rubin M, Foulis P, Luther S, Forbush T, **Scotch M**, Doebbellling B, Goldstein MK. *Creating a MRSA Ontology to Support Categorization of MRSA Infections*. AMIA Annual Symposium. Washington, DC. 2013.
23. **Scotch M**, Pabilonia K, Anderson T, Baroch J, Kohler D, DeLiberto TJ, Espy M, Pritt B, Black K, Seville MT. *Phylogeography of avian and human influenza in the Southwest United States*. 10th Annual Rocky Mountain Bioinformatics Conference. Aspen, CO. 2012.
24. **Scotch M**, Pabilonia K, Anderson T, Baroch J, Kohler D, DeLiberto TJ, Espy M, Pritt B, Seville MT. *Phylogeography of influenza A in human and avian species in the southwest United States*. 11th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID-11). New Orleans, LA. 2012.
25. **Scotch M**, Womack J, Leung S, Brant C. *An NLP Framework for Classifying Contraception Use among US Women Veterans*. AMIA 2012 Joint Summits on Translational Science. San Francisco, CA. 2012.

26. O'Rourke T, Joly DO, Palmer J, Olson S, Manhas M, O'Rourke D, Rabinowitz P, **Scotch M**, Godlstein T, Kreuder Johnson C, Wolking D, Lebreton M, Karesh W, Mazet J. *Data standardization is critical to ensure wildlife health data quality*. 2012 Wildlife Disease Association Conference. Lyon, France.
27. Womack JA, **Scotch M**, Leung S, Brandt C. *Analysis of contraceptive use among female veterans at the VA*. AMIA Joint Summits on Translational Science, San Francisco, CA. 2012.
28. Ortiz P, **Scotch M**, Taylor J. *Use of the Bayesian skyline plot to inform a prediction model of zoonotic infection in animal and human hosts*. AMIA Annual Symposium. Washington, DC. 2011.
29. Singraur A, **Scotch M**. *Integration of disparate genomic sequences for phylogeography of influenza*. AMIA Annual Symposium. Washington, DC. 2011.
30. Konovalov S, **Scotch M**, Brandt C. *An ontology-aware application for military blog analysis*. AMIA Annual Symposium. Washington, DC. 2010.
31. **Scotch M**, Martinello R, Mutalik P, Brandt C. *Use of natural language processing and machine learning for surveillance of MRSA at the VA*. AMIA Annual Symposium. Washington, DC. 2010.
32. Sint K, Rabinowitz P, **Scotch M**. *Human cases and bird outbreaks of avian influenza in Vietnam*. American Public Health Association (APHA) Annual Conference. Denver, CO. 2010.
33. Duggal M, Ebisu K, **Scotch M**, Anderson D, Brandt C, Justice A. *Geographic variation of missed visits among HIV infected veterans*. Society of General Internal Medicine 33rd Annual Meeting. Minneapolis, MN. 2010.
34. Womack J, **Scotch M**, Brandt C, Chapman W, Justice AC. *A comparison of two approaches for identifying negations in radiology reports*. AMIA Annual Symposium. San Francisco, CA. 2009.
35. Duggal M, Ebisu K, **Scotch M**, Brandt C, Cohen D, Skanderson M, Mattocks K, Levin F, Justice AC. *Use of GIS to examine outpatient clinic access at veterans health administration facilities among HIV veterans*. AMIA Annual Symposium. San Francisco, CA. 2009.
36. **Scotch M**, Konovalov S, Rajeevan N, Brandt C, Cheung K. *Using Web 2.0 tools and content mining in clinical and health services research*. Clinical Research Informatics Working Group Expo at AMIA Annual Symposium. San Francisco, CA. 2009.
37. **Scotch M**, Parmanto B. *Combining OLAP and GIS for community health assessments*. MedInfo Conference. San Francisco, CA. 2004.
38. **Scotch M**, Parmanto B, Sharma R, Meit M. *Development of a multidimensional data warehouse for community health assessment*. APHA Annual Meeting. San Francisco, CA. 2003.
39. **Scotch M**, Parmanto B, Sharma R, Meit M. *Constructing a community health database*. Pittsburgh Public Health Association Annual Conference. Pittsburgh, PA. 2003.

BOOK CHAPTERS

Scotch M, Brandt C, Leung S, Womack J. *Natural language processing for understanding contraceptive use at the VA*. In A. Gupta, V. L. Patel, & R. A. Greenes (Eds.), *Advances in Healthcare Informatics and Analytics* (Vol. 19, pp. 249-259). *Annals of Information Systems*: Springer International Publishing. 2016.

NOTABLE MEDIA MENTIONS

Barras, C. *Going to waste: Virologists say sewage systems are flush with opportunity*. *Nature Medicine*. 2018 Oct; 24(10):1484-1487.

ACTIVE RESEARCH SUPPORT

OAC 1931560
NSF

Scotch (PI)

11/01/2019–10/31/2022

Collaborative:Elements:Cyberinfrastructure for Pedestrian Dynamics-Based Analysis of Infection Propagation Through Air Travel

The goal of this project is to develop a novel software to simulate the movement of people in order to understand how movement patterns influence transmission of infection at local as well as global scales.

R01LM013129 Scotch, Halden, Varsani (PIs) 06/03/2019-05/31/2023
NIH/NLM

Bioinformatics Framework for Wastewater-based Surveillance of Infectious Diseases

The goal of this project is to develop and evaluate a bioinformatics framework that uses metagenomic data generated from sampling of wastewater to monitor local epidemics and outbreaks of infectious diseases.

R01AI117011 Scotch, Gonzalez-Hernandez (PIs) 04/01/2016–03/31/2020
NIH/NIAID

Tracking Evolution and Spread of Viral Genomes by Geospatial Observation Error

The goal of this project is to enhance the geospatial data used for the phylogeography of zoonotic viruses by applying natural language processing techniques to biomedical text and statistical phylogeography to viral genetic data.

PENDING RESEARCH SUPPORT

1R21AI154848-01 Scotch, Gonzalez (PIs) 07/01/2020-06/30/2022
NIH/NIAID

Estimating Influenza Vaccine Effectiveness through Social Media Mining

The goal of this project is to use social media mining to estimate seasonal influenza vaccine effectiveness by examining Twitter posts that are determined to be related to influenza illness and seasonal vaccination and compare these to Center for Disease Control and Prevention estimates.

1R01AI149718-01A1 Scotch, MacIntyre, Nguyen (PIs) 07/01/2020-06/30/2025
NIH/NIAID

Development of a risk assessment tool for emergence of human transmissible avian influenza using phylodynamic and stochastic modelling in Vietnam

The goal of this project is to develop and evaluate a risk assessment tool that uses phylogeography and epidemic modeling to identify high risk areas of human-to-human transmission of highly pathogenic avian influenza H5N1 virus.

1R15LM013382-01 Namilae, Srinivasan (PIs) 04/01/2020–03/31/2023
NIH/NLM

A data analytics framework for the application of pedestrian dynamics to public health

The goal of this project is to develop and evaluate an agnostic data analytics framework for the application of pedestrian dynamics to address a wide range of public health applications.

Role: Co-investigator

1R01AI151137-01A1 Scotch, Mubayi, Gonzalez (PIs) 07/01/2020–06/30/2024
NIH/NIAID

Early assessment of Dengue in Andean Latin America: Integrating Social Media and Population Mobility Information in Reducing Uncertainty in Surveillance and Preparedness Efforts

The goal of this project to use social media and epidemic models to improve surveillance of neglected tropical diseases including Dengue virus.

PRIOR RESEARCH SUPPORT

PA18A02 Accelerator Award Scotch, MacIntyre, Steinhofel (PIs) 07/01/2018-12/31/2019

PLuS Alliance

Enhancing Global Health Security through Avian Influenza Genomic Models

The goal of this PLuS Alliance Accelerator Award is to develop and evaluate models to identify risk factors associated with outbreaks of avian influenza viruses in human populations.

ACI 1640911 Scotch (PI) 09/01/2016–08/31/2019

NSF

Collaborative Research: Petascale Simulation of Viral Infection Propagation Through Air Travel

The goal of this project is to create a massively parallel simulation infrastructure using the Blue Waters supercomputing infrastructure that will provide useful insight to decision makers dealing with virus spread by modeling human movement in planes, modeling the spread of infections, software infrastructure for decision support, and massively parallel computing.

R01LM012080 Scotch (PI) 04/06/2015–03/31/2019

NIH/NLM

Merging Viral Genetics with Climate and Population Data for Zoonotic Surveillance

The goal of this project is to develop and evaluate a bioinformatics infrastructure to merge viral genetics with climate and population data for phylogeography and zoonotic surveillance.

F31LM012176-01 Beard (PI) 12/21/2015–12/20/2018

NIH/NLM

Integrating Bioinformatics and Clustering Analysis for Disease Surveillance

The major goal of this research fellowship award is to support pre-doctoral dissertation research in the integration of bioinformatics and geospatial clustering approaches for infectious disease surveillance.

Role: Sponsor

PA014 Seed Grant Scotch, MacIntyre, Steinhofel (PIs) 08/01/2016–07/31/2017

PLuS Alliance

Reducing the Risk of a Human-to-Human Transmissible Form of Highly Pathogenic Avian Influenza H5N1

The goal of this project is to develop and evaluate a model to identify risk factors associated with the evolution of a human-to-human form of highly pathogenic avian influenza.

ACI 1525012 Scotch (PI) 04/01/2015–12/31/2016

NSF

Collaborative Research: Simulation-Based Policy Analysis for Reducing Ebola Transmission Risk in Air Travel

The goal of this project is to create a massively parallel simulation infrastructure that will provide useful insight to decision makers dealing with Ebola by modeling human movement in planes, modeling the spread of infections, software infrastructure for decision support, and massively parallel computing.

R01LM011176-04 Gonzalez-Hernandez (PI) 09/10/2012–08/31/2016

NIH/NLM

Mining Social Network Postings for Mentions of Potential Adverse Drug Reactions

The goal of this project is to use natural language processing and information extraction techniques to identify adverse drug reactions from Web blogs.

Role: Co-Investigator

Regents Innovation Fund Merchant (PI) 05/24/2013–12/31/2015

Arizona Board of Regents

Arizona Environmental Grid Infrastructure Service

The goal of this project is to develop a technological infrastructure to support data sharing and collaboration across the three universities in Arizona in support of environmental health research.

Role: Co-Investigator

HIR 09-004 Doebbeling (PI) 04/01/2009–09/30/2015

VA/HSRD

Consortium for Healthcare Informatics Research: MRSA

The goal of this applied project is to develop and validate a model for automatic identification of MRSA status from clinical free text notes in the VA electronic medical record system.

Role: Co-Investigator (via either Intergovernmental Personnel Act or Government Contract)

R56AI102559 Scotch, Gonzalez-Hernandez (PIs) 08/02/2013–07/31/2015

NIH/NIAID

Text Processing and Geospatial Uncertainty for Phylogeography of Zoonotic Viruses

The goal of this project is to enhance the geospatial data used for the phylogeography of zoonotic viruses by applying natural language processing techniques to biomedical text.

R00LM009825 Scotch (PI) 09/30/2010–09/29/2014

NIH/NLM

Informatics for zoonotic disease surveillance: combining animal and human data

The goal of this career development award is to use informatics methods to link health data on animals and humans for automated surveillance of zoonotic diseases.

Seed Grant Scotch, Seville (PIs) 01/01/2011–06/30/2012, 01/31/2013–12/31/2013

Arizona State University/Mayo Clinic

Genetic characterization and phylogeography of influenza A virus found in animals and humans in Arizona.

The goal of this seed grant is to perform genetic characterization and phylogeography of influenza A virus found in animals and humans in Arizona using a combination of molecular biology and bioinformatics approaches.

PREDICT Rabinowitz (PI) 08/01/2011–09/30/2011

Yale University

Bioinformatics Functionality for GAINS

The goal of this project is to add bioinformatics functionality to the Wildlife Conservation Society's GAINS database in order to support genomic sequences generated as part of the USAID PREDICT project.

Role: PI (Subcontract)

HIR 09-007 Goldstein (PI) 08/01/2010–07/31/2011
VA/HSRD

Consortium of Healthcare Informatics Research: Translational Use Case Projects

The goal of this translation use case project is to develop and validate an on ontology for contraceptive use through information retrieval of clinical free text notes in the VA electronic medical record system.

Role: Co-Investigator (Intergovernmental Personnel Act)

K99LM009825-S1 Scotch (PI) 10/01/2009–09/30/2010
NIH/NLM

Informatics for zoonotic disease surveillance: combining animal and human data

ARRA Administrative Supplement to K99 award.

K99LM009825 Scotch (PI) 09/30/2008–09/29/2010
NIH/NLM

Informatics for zoonotic disease surveillance: combining animal and human data

The goal of this career development award is to use informatics methods to link health data on animals and humans for automated surveillance of zoonotic diseases.

SERVICE – UNIVERSITY

2019 Chair, Search Committee, Associate Professor of Biomedical Informatics, College of Health Solutions, ASU
2019 Member, Chalk Talk Faculty Committee, Biodesign Institute, ASU
2019– Chair, Academic Programs Committee, Biomedical Informatics, College of Health Solutions
2019– Degree Coordinator, Bachelor of Science in Biomedical Informatics, College of Health Solutions
2018– Member, President's Academic Council, ASU
2017– Member, Executive Visioning Team, College of Health Solutions, ASU
2017 Chair, Research Integrity Committee (*ad hoc*), ASU
2016– Member, Institutional Biosafety Committee, ASU
2016–2019 Member, Personnel Committee, Department of Biomedical Informatics, ASU
2016 Member, Promotion & Tenure Committee, School for the Science of Healthcare Delivery ASU
2016 Member, Review Committee, ASU-Mayo Seed Grant Program
2016 Member, Search Committee, Director of International School of Biomedical Diagnostics, ASU
2016– Member, Research Council, College of Health Solutions, ASU
2012 Member, Search Committee, Director of Center for Health Information & Research, ASU
2011–2014 Chair, Graduate Admissions, Department of Biomedical Informatics, ASU
2011–2013 Member, Marketing/Media Team, Department of Biomedical Informatics, ASU
2010, 2014–15 Member, Graduate Admissions Committee, Department of Biomedical Informatics, ASU
2010–2018 Member, Academic Programs Committee, Department of Biomedical Informatics, ASU

SERVICE – NATIONAL

2019 Grant Reviewer (*Ad Hoc*), National Library of Medicine (NLM)/National Institutes of Health (NIH), Biomedical Informatics, Library and Data Sciences Review Committee (x2; June and November meetings)

- 2019 Grant Reviewer (*Ad Hoc*), National Institute of Allergy and Infectious Diseases (NIAID)/NIH, Collaborative Influenza Vaccine Innovation Centers (CIVIC), Special Emphasis Panel ZAI1- EC-M-C1.
- 2019 Grant Reviewer (*Ad Hoc*), Center for Scientific Review (CSR)/NIH, Eukaryotic Parasites and Vectors, 2019/05 ZRG1 IDM-M (02)
- 2018 Grant Reviewer (*Ad Hoc*), CSR, Global Infectious Disease Research Training / Planning Program, 2019/01 ZRG1 IDM-Z (55)
- 2017 Grant Reviewer (*Ad Hoc*), NLM/NIH, Conflicts, R01/F31/K01/K99, 2018/01 ZLM1 ZH-C (01)
- 2017 Grant Reviewer (*Ad Hoc*), CSR, Global Infectious Disease Research Training / Planning Program, 2018/01 ZRG1 IDM-Z (55)
- 2017 Grant Reviewer (*Ad Hoc*), CSR, Health Informatics Special Emphasis Panel SBIR/STTR, 2017/08 ZRG1 HDM-A (11) B
- 2017 Grant Reviewer (*Ad Hoc*), CSR, Conflicts, K01/K99/R21/R01, ZRG1 ETTN-A (02)
- 2017 Grant Reviewer (*Ad Hoc*), CSR, Health Informatics Special Emphasis Panel SBIR/STTR, ZRG1 HDM-G (11)
- 2017 Grant Reviewer (*Ad Hoc*), NLM/NIH, Information Resource Grants to Reduce Health Disparities (G08), Special Emphasis Panel, ZLM1 ZH-G
- 2016 Grant Reviewer (*Ad Hoc*), NLM/NIH, Conflicts R01/R21/K01/K99, ZLM1 ZH-C (01)
- 2016 Grant Reviewer (*Ad Hoc*), NLM/NIH, Conflicts R01/R13/R21/K01/K99/F31, ZLM1 ZH-C (01)
- 2016 Grant Reviewer (*Ad Hoc*), NLM/NIH, Conflicts R01/R21/K99/K01, ZLM1 ZH-C (01)
- 2015 Grant Reviewer (*Ad Hoc*), NLM/NIH, Conflicts R01/R21/R13/K99/F31, ZLM1 ZH-C (01)
- 2015 Grant Reviewer (*Ad Hoc*), NLM/NIH, Conflicts R01/R21/R13, ZLM1 ZH-C (01)
- 2015 Grant Reviewer (*Ad Hoc*), NIAID/NIH, Development of Novel Therapeutics for Select Pathogens (R21/R03): Influenza, ZAI1 LR-M (M2) 01
- 2014 Grant Reviewer (*Ad Hoc*), NLM/NIH, Information Resource Grants to Reduce Health Disparities (G08), Special Emphasis Panel, ZLM1 ZH-G
- 2014 Grant Reviewer (*Ad Hoc*), NLM/NIH, Special Emphasis Panel, ZLM1 ZH-C 01
- 2013–2015 User Advisory Group, Influenza Research Database/Virus Pathogen Resource, Northrop Grumman/JCVI/Vecna/SAGE Analytica/Los Alamos National Lab
- 2012 Grant Reviewer (*Ad Hoc*), NLM/NIH, Information Resource Grants to Reduce Health Disparities (G08), Special Emphasis Panel, ZLM1 ZH-G
- 2012 Grant Reviewer (*Ad Hoc*), NIAID/NIH, Bioinformatics Integration Support Contract, Special Emphasis Panel ZAI1 QV-I C1
- 2011 Grant Reviewer (*Ad Hoc*), NLM/NIH, Loan Repayment (L30), Special Emphasis Panel ZLM1 ZH-L 08 1
- 2011 Past Chair, Public Health Informatics Working Group, AMIA
- 2009–2010 Chair, Public Health Informatics Working Group, AMIA
- 2008–2010 Member-at-Large, Executive Committee, Student Working Group, AMIA
- 2008 Chair-elect, Public Health Informatics Working Group, AMIA

SERVICE – INTERNATIONAL

- 2019 Council Member, International Society for Influenza and other Respiratory Virus Diseases (ISIRV)
- 2019 Grant Reviewer, Sir Henry Dale Fellowship, Wellcome Trust
- 2017– Scientific Advisory Board Member, NHMRC Centre for Research Excellence: Integrated Systems for Epidemic Response, Sydney, Australia
- 2016– Journal Editorial Board Member, Scientific Reports (Nature Publishing Group)
- 2015 Grant Reviewer, European Science Foundation, AXA Research Fund Postdoctoral Fellowships
- 2015–2016 Grant Reviewer, Swiss National Science Foundation (SNSF)
- 2013– Journal Editorial Board Member, Infection, Genetics and Evolution (Elsevier)
- 2012 Grant Reviewer, Medical Research Council, London, England

2012 Grant Reviewer, SNSF

TEACHING EXPERIENCE

2019 Instructor, BMI 461 (undergraduate): *Advanced topics in biomedical informatics I*, ASU
 2018 Instructor, BMI 601 (graduate, online): *Health Informatics*, ASU
 2017 Instructor, BMI 570 (graduate): *Biomedical informatics journal club/symposium*, ASU
 2016–2018 Instructor, BMI 102 (undergraduate): *Introduction to public health informatics/imaging informatics*, ASU
 2015–2016 Instructor, BMD 502 (graduate, online): *Foundations of biomedical informatics methods I*, ASU
 2015 Co-Instructor, BMI 102 (undergraduate): *Introduction to public health informatics/imaging informatics*, ASU
 2013–2014 Instructor, BMI/BIO 591 (graduate): *NIH grant writing*, ASU
 2013–2014 Co-Instructor, HCD 501 (graduate): *Health behavior and statistical tools in health environments*, ASU
 2013– Instructor, BMI 502 (graduate): *Foundations of biomedical informatics methods I*, ASU
 2012 Instructor, BMI 591 (graduate): *NIH grant writing*, ASU
 2011 Instructor, BMI 540 (graduate): *Problem solving in biomedical informatics*, ASU
 2011 Instructor, BMI 505 (graduate): *Foundations of biomedical informatics methods II* (databases module)
 2010–2012 Instructor, BMI 591/570 (graduate): *Biomedical informatics journal club/symposium*, ASU
 2009 Instructor, *Biomedical informatics journal club*, Yale University and VA Connecticut
 2005 Teaching Assistant, *Introduction to biomedical informatics*, University of Pittsburgh
 2003 Teaching Assistant, *Problem-oriented programming*, University of Pittsburgh
 2001 Teaching Assistant, *Economics of medical informatics*, Columbia University

ONLINE COURSE DEVELOPMENT

2017 Class presenter, PHCM9788 (PLuS Alliance course), *Geographic information systems: informatics and spatial intelligence surveillance*. Online course presentation, *Demystifying phylogenetic trees*.
 2017 Class presenter, PHCM9788 (PLuS Alliance course), *Infectious diseases intelligence*. Online course presentation, *Demystifying phylogenetic trees*.
 2014 Developer, BMD 502, *Foundations of biomedical informatics methods I*, ASU and Dublin City University, Dublin, Ireland
 2014 Developer, HCD 501, *Health behavior and statistical tools in health environments*, ASU

MENTORSHIP AND ADVISING-ONGOING

2017– Dillon Adam, Doctoral Dissertation Committee Co-Chair (with Raina MacIntyre from UNSW)
 2012–[^]Barrie Bradley, Doctoral Dissertation Committee Chair, *Development of an immunization registry for clinical and public health*
 2016– Matteo Vaiente, Doctoral Dissertation Committee Chair
 2012– Rachel Beard, Doctoral Dissertation Committee Chair, *Integration of geographic information systems and molecular epidemiological techniques into spatial decision support for outbreaks of zoonotic diseases*

[^]Temporarily Interrupted

MENTORSHIP AND ADVISING-COMPLETED

2016–2019[^] Tasnia Tahsin, Doctoral Dissertation Committee Co-Chair (with Graciela Gonzalez-Hernandez from University of Pennsylvania), *Knowledge-driven approaches for geographic information extraction from biomedical literature*
 2016–2019 Arjun Magee, Doctoral Dissertation Committee Co-Chair (with Graciela Gonzalez-Hernandez from University of Pennsylvania)

- 2018–2019 Komal Agrawal, Barrett Honors College Undergraduate Thesis Advisor, *The relationship between wastewater toxic substances and Alzheimer's disease*
- 2018–2019 Lydia Mendoza, Barrett Honors College Undergraduate Thesis Advisor, *Surveillance of influenza virus spread on the Arizona State University campus*
- 2017–2018 Meghana Nandan, Barrett Honors College Undergraduate Thesis Advisor, *Analysis of HIV risk groups using Bayesian phylogenetics*
- 2017–2018 George Karway, Barrett Honors College Undergraduate Thesis Advisor, *Making data collection entirely mobile*
- 2013–2017 Daniel Magee, Doctoral Dissertation Committee Chair, *Generalized linear models in Bayesian phylogeography*
- 2016–2017 Demetrius Jones-Shargani, Barrett Honors College Undergraduate Thesis Advisor, *MosquitoDB*
- 2017 Howard Lanus, Masters Thesis Committee Chair, *Common variants and their impact on autism*
- 2014–2016 Wenzhe Xue, Doctoral Dissertation Committee Member, *A new image quantitative method for diagnosis and therapeutic response*
- 2012–2016 Azadeh Nikfarjam, Doctoral Dissertation Committee Member, *Health information extraction from social media*
- 2012–2016 Ehsan Emadzadeh, Doctoral Dissertation Committee Member, *Context-aware adaptive hybrid semantic relatedness in biomedical science*
- 2016 Alex Halloran, Masters Thesis Committee Chair, *Specialist Finder: A clinical decision support tool for primary care physicians*
- 2016 Kate Goodin, Masters Thesis Committee Chair, *Evaluation of health information exchange connection for a local public health department*
- 2015–2016 Divya Mahendra, Masters Thesis Committee Chair, *Identifying differential dependencies associated with drug response across cancer cell lines*
- 2015–2016 Marcus Naymik, Masters Thesis Committee Member, *A comparison of obese and lean human epigenetics*
- 2015–2016 Brian Hanratty, Masters Thesis Committee Member, *An improved workflow for bisulfite sequencing analysis utilizing cpg filtering and gene detection*
- 2013–2015 Sen Peng, Doctoral Dissertation Committee Member, *Comprehensive genomic characterization of glioblastoma multiforme*
- 2015 Eric Buckland, Masters Thesis Committee Member, *Building a classifier to identify high grade, or muscle invasive, bladder cancer*
- 2015 Tasnia Tahsin, BMI 790 Reading and Conference Advisor, *Natural language processing methods for infectious disease surveillance*
- 2015 Rachel Beard, BMI 790 Reading and Conference Advisor, *Integrating molecular epidemiology and spatiotemporal analysis*
- 2015 Daniel Magee, BMI 790 Reading and Conference Advisor, *Statistical distributions and methods*
- 2013–2015 Saman Jirjies, Masters Thesis Committee Chair, *Open source implementation of Jacques's Q statistics for space-time clustering in case-control studies*
- 2013–2015 Mari Firago, Masters Thesis Committee Chair, *Exploring genetic diversity as a leading indicator of influenza outbreaks shown by Google flu trends*
- 2012–2015 Nima Tajbakhsh, Doctoral Dissertation Committee Member, *Ensuring high-quality colonoscopy by reducing polyp miss-rates*
- 2014 Neel Mehta, BMI 790 Reading and Conference Advisor (and temporary doctoral dissertation advisor), *Data mining in clinical medicine*
- 2014 Emily Crawford, MIC 495 Undergraduate Research, *Sequencing and analysis of human influenza neuraminidase gene*
- 2014 Emily Crawford, MIC 401 Undergraduate Senior Paper, *Surveillance of oseltamivir and zanamivir resistance in influenza A*
- 2012–2014 Aarthi Varman, Masters Thesis Committee Chair, *Identifying climate factors associated with valley fever clusters in Arizona using spatial scan statistics and geographic information systems*

- 2012–2014 Shobana Sekar, Masters Thesis Committee Member, *Study of batch-to-batch reproducibility in nucleic acid programmable protein array*
- 2012–2014 Brittany Baarson, Masters Thesis Committee Chair, *Examining climate influences on zip code level coccidioidomycosis for Arizona 2009-2012*
- 2011–2014 Venkata Yellapantula, Doctoral Dissertation Committee Member, *Informatics approaches for integrative analysis of disparate high-throughput genomic datasets in cancer*
- 2011–2014 Sheetal Shetty, Doctoral Dissertation Committee Member, *Structural variant detection: a novel algorithmic approach*
- 2012–2013 Sen Peng, Masters Thesis Committee Member, *Identification of aberrant splice variants associated with non small cell lung carcinoma*
- 2012–2013 Adam Turnock, Barrett Honors College Undergraduate Thesis Advisor, *The evolution of influenza throughout the southwest*
- 2012–2013 Rob Lauder, Masters Thesis Committee Chair, *Evaluation of unstructured reports from HealthMap as a leading indicator for West Nile virus cases reported by the Centers for Disease Control and Prevention*
- 2012 Ryan Sullivan, BMI 790 Reading and Conference Advisor, *Semi-supervised learning and bioNLP*
- 2012 Azadeh Nikfarjam, BMI 790 Reading and Conference Advisor, *Machine learning for natural language processing*
- 2012 Ehsan Emadzadeh, BMI 590 Reading and Conference Advisor, *Finding and linking geographical entities in biomedical text*
- 2012 Laura Wojtulewicz, BMI 590 Reading and Conference Advisor, *NIH grant writing*
- 2011–2012 Ryan Sullivan, Masters Thesis Committee Member, *Graph-based gene normalization*
- 2011–2012 Kathikraja Velmurugan, Masters Thesis Committee Member, *Investigation of genomic aberration events in MCF-7 Tamoxifen-resistant and sensitive subclones*
- 2011–2012 Bryan Hendrickson, Masters Thesis Committee Member, *Evaluation of data completeness within a large community health care system exchanging data with a state immunization information system: a cross-sectional study*
- 2011–2012 Kiran Mankar, Masters Thesis Committee Member, *A survey of state and city immunization information systems*
- 2011–2012 Nate Sutton, Masters Thesis Committee Member, *Automatic approaches for gene-drug interaction extraction from biomedical text: corpus and comparative evaluation*
- 2011–2012 Immanuel Purushothaman, Masters Thesis Committee Member, *Bioinformatics to explore the distinctions between high and low risk human papilloma virus*
- 2010–2012 Pierina Ortiz, Masters Thesis Committee Chair, *Use of Bayesian coalescence models to inform prediction models of zoonotic disease in animals*
- 2010–2012 Ashutosh Singraur, Masters Thesis Committee Chair, *Use of influenza sequence data for predicting location of cases*
- 2011 Xiaoxiao Wang, Masters Thesis Committee Member, *A corpus-based learning for co-reference resolution*

^Temporarily Interrupted

MENTORSHIP AND ADVISING-INCOMPLETED

- 2011–2018 Robert Yao, Doctoral Dissertation Committee Member, *Development of a rule-based computational framework for epilepsy*
- 2015–2019 Ryan Sullivan, Doctoral Dissertation Committee Member, *Using biomedical ontologies as structured background knowledge for hierarchical topic modeling*

PRESENTATIONS

- 2019 *Bioinformatics framework for wastewater-based surveillance of infectious diseases*. The National Academies of Sciences, Engineering, and Medicine. Board on Life Sciences Fall Meeting. Tempe, Arizona.

- 2019 *An online end-to-end pipeline for virus phylogeography that leverages natural language processing for finding host locations.* Rocky Mountain Bioinformatics Conference. Aspen, Colorado.
- 2019 *Informatics for genomics-informed surveillance of RNA viruses,* NLM Informatics and Data Science Lecture Series, National Library of Medicine, National Institutes of Health, Bethesda, Maryland.
- 2019 *Virus phylogeography for public health surveillance,* Computer Science Colloquium, University of West Florida, Pensacola, Florida.
- 2019 *Use of Sampling Uncertainty in Virus Phylogeography.* Yale Center for Biomedical Data Science Seminar Series. Yale University School of Medicine. New Haven, Connecticut.
- 2019 *ZooPhy: A bioinformatics pipeline for virus phylogeography and surveillance,* International Society for Disease Surveillance Annual Conference. San Diego, California.
- 2018 (Keynote) *Avian influenza virus ecology and evolution.* Egyptian Society of Virology. 7th International Conference on Emerging and Re-Emerging Viral Diseases. Hurghada, Red Sea Governorate, Egypt.
- 2018 *ZooPhy and ZoDo: Bringing virus phylogeography to the public health epidemiologist.* MEEGID-14. Sitges, Spain.
- 2018 *Use of genetic data in the grey zone & global security PLS,* Public Health Laboratory Network meeting. Australian Department of Health. Canberra, Australian Capital Territory.
- 2018 *NLP and phylogeography: studying the evolution and spread of viruses by finding locations of the infected host.* Seminar Series. School of Civil and Environmental Engineering, UNSW. Sydney, NSW, Australia.
- 2018 *Use of genetic data in the grey zone.* Seminar Series. Kirby Institute, UNSW. Sydney, NSW, Australia.
- 2018 *NLP and phylogeography: studying the evolution and spread of viruses by finding locations of the infected host.* University of Pennsylvania Health Language Processing Forum. Philadelphia, Pennsylvania.
- 2018 *Incorporating observation error in the geospatial assignment of taxa for virus phylogeography.* AMIA 2018 Informatics Summit. San Francisco, California.
- 2017 *Demystifying the genetic evolution of pathogens.* Arizona Biosecurity Workshop. Arizona State University. Tempe, Arizona
- 2017 *Influenza phylogeography for public health surveillance.* INFORMS Annual Conference. Houston, TX
- 2017 *Linking geospatial mentions in journal articles to GenBank records for virus phylogeography.* Great Lakes Bioinformatics Conference. Chicago, Illinois
- 2017 *Merging viral genetics with climate and population data for zoonotic surveillance.* NIH/NLM Board of Regents (Council). Bethesda, Maryland
- 2017 *Surveillance of RNA viruses using discrete Bayesian phylogeography.* Fusion 2017: ASU Biodesign Institute Scientific Retreat. Carefree, Arizona
- 2016 *Population health surveillance of RNA viruses through phylogeography.* The Kirby Institute, UNSW. Sydney, Australia
- 2016 *Incorporating geospatial observation error in discrete Bayesian virus phylogeography.* MEEGID-13. Antwerp, Belgium
- 2015 *Analysis of viral genetics for estimating diffusion of influenza A H6N1.* AMIA 2015 Joint Summits on Translational Science. San Francisco, California
- 2014 *A pipeline for virus phylogeography that accounts for geospatial observation error.* Rocky Mountain Bioinformatics Conference. Aspen, Colorado
- 2014 *Text processing and geospatial uncertainty for phylogeography of zoonotic viruses.* Webinar on NIH-funded projects on spatial uncertainty, surveillance research program of the National Cancer Institute (NCI) Division of Cancer Control and Population Sciences
- 2014 *Challenges and promises of bioinformatics for translational applications.* Lecture to first-year medical students. University of Arizona College of Medicine-Phoenix, Arizona
- 2014 *Tracking the spread of viruses.* Spirit of the senses salon. Tempe, Arizona
- 2014 *Phylogeographic generalized linear model for identifying predictors driving H5N1 diffusion within Egypt.* Intelligent Systems for Molecular Biology (ISMB). Boston, Massachusetts
- 2014 *Translational public health: using viral sequence data for zoonotic disease surveillance.* Epi Presents! Series. Maricopa County Department of Public Health. Phoenix, Arizona

- 2013 *Phylogeography of avian and human influenza in the Southwest United States*. Influenza2013: one influenza, one world, one health. Oxford, United Kingdom
- 2012 *Phylogeography of avian and human influenza in the southwest United States*. Rocky Mountain Bioinformatics Conference. Aspen, Colorado
- 2012 *Phylogeography of influenza A in human and avian species in the southwest United States*. MEEGID-11. New Orleans, Louisiana
- 2012 *Public health informatics to support public health decision making*. Society for Medical Decision Making (SMDM). Phoenix, Arizona
- 2011 *ZooPhy: an informatics system for phylozoonoses*. Translational Genomics Research Institute (TGen) weekly bioinformatics seminar. Phoenix, Arizona
- 2010 *Integrated human-animal surveillance systems for emerging threats to health*. Cummings School of Veterinary Medicine Symposium on The Electronic Medical Records. Grafton, Massachusetts
- 2010 *Using advanced web technologies to combine disparate data for public health research*. Society for Epidemiologic Research (SER). Seattle, Washington
- 2009 *Advanced web technologies for translational informatics across different biomedical domains*. AMIA Joint Summits on Translational Science. San Francisco, California
- 2009 *A mashup to help public health professionals*. NIH/NLM Board of Regents (Council). Bethesda, Maryland
- 2008 *Informatics for zoonotic disease surveillance: combining animal and human data*. NLM Training conference. Bethesda, Maryland
- 2007 *Informatics for zoonotic disease surveillance: combining animal and human data*. University of Pittsburgh Department of Biomedical Informatics lecture series. Pittsburgh, Pennsylvania
- 2005 *Usability assessment of the Spatial OLAP Visualization and Analysis Tool (SOVAT)*. NIH/NLM training conference. Bethesda, Maryland
- 2004 *A GIS tool for community health assessments*. Pennsylvania Rural Health Association. State College, Pennsylvania
- 2003 *Constructing a community health database: an early demonstration*. Pennsylvania Public Health Association. Harrisburg, Pennsylvania

CONFERENCE RESPONSIBILITIES

- 2019 Chair, Scientific Program Committee, ASU Biodesign Institute Fusion Retreat, Phoenix, Arizona
- 2019 Scientific Program Committee, Great Lakes Bioinformatics Conference, Madison, Wisconsin
- 2018 Scientific Program Committee, AMIA 2019 Informatics Summit, San Francisco, California
- 2018 Scientific Review Committee, 14th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID), Sitges, Spain.
- 2017 Co-Chair, Workshop, *New approaches to risk analysis in human biosecurity*, Society for Risk Analysis Annual Meeting, Arlington, Virginia
- 2017 Organizer and Chair, Special Session, *Phylogeography of viruses*, Great Lakes Bioinformatics Conference (ISCB), Chicago, Illinois
- 2017 Member, Scientific Program Committee, Great Lakes Bioinformatics Conference, Chicago, Illinois
- 2017 Chair, Scientific Paper Session, *Text mining*, AMIA Joint Summits on Translational Science, San Francisco, California
- 2017 Judge, Student Paper Competition, AMIA Joint Summits on Translational Science, San Francisco, California
- 2016 Member, Scientific Program Committee, MEEGID-13, Antwerp, Belgium
- 2016 Co-Chair, Special Session, *Social media mining for public health monitoring and surveillance*, Pacific Symposium on Biocomputing, Big Island, Hawaii
- 2014 Judge, Posters, AMIA Annual Conference, Washington, District of Columbia
- 2012 Organizer and Chair, Special Session, *Biomedical informatics to enhance clinical and public health decision making*, Society for Medical Decision Making Annual Conference, Phoenix, Arizona

2008 Chair, Scientific Paper Session, *Tools and systems for infection control*, AMIA Annual Conference, Washington, District of Columbia

MANUSCRIPT and BOOK REVIEWS

Journal, Applied Clinical Informatics
Journal, Applied and Environmental Microbiology
Journal, BMC Evolutionary Biology
Journal, BMC Genomics
Journal, BMC Infectious Diseases
Journal, BMC Medical Informatics and Decision Making
Journal, BMC Medical Research Methodology
Journal, Computer and Electronics in Agriculture
Journal, Computer Methods and Programs in Biomedicine
Journal, Ecohealth
Journal, IEEE Access
Journal, Infection, Genetics, and Evolution
Journal, International Journal of Environmental Research and Public Health
Journal, International Journal of Health Geographics
Journal, International Journal of Medical Informatics
Journal, Journal of Biomedical Informatics
Journal, Journal of Mass Communication & Journalism
Journal, Journal of Medical Internet Research
Journal, Journal of the American Medical Informatics Association
Journal, Medical Care
Journal, Methods of Information in Medicine
Journal, PeerJ
Journal, Pharmacoepidemiology and Drug Safety
Journal, PLoS ONE
Journal, PLoS Computational Biology
Journal, Royal Society Open Science
Journal, The Science of the Total Environment
Journal, Transboundary and Emerging Diseases
Journal, Viruses
Conference, AMIA Fall Symposium
Conference, AMIA Joint Summits on Translational Science
Conference, Hawaii International Conference on System Sciences
Conference, Pacific Symposium on Biocomputing (PSB)
Conference, Workshop on Biomedical and Health Informatics
Book, Human-Animal Medicine: Clinical Approaches to Zoonoses, Toxicants and Other Shared Health Risks

CURRENT SOCIETY MEMBERSHIPS

American Medical Informatics Association (AMIA)
International Society for Computational Biology (ISCB)
International Society for Influenza and other Respiratory Virus Diseases (ISIRV)
International Society for Disease Surveillance (ISDS)