

Matthew Laurence Scotch, PhD, MPH

Associate Dean of Research and 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: 1.480.727.2985

EMAIL: matthew.scotch@asu.edu

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

EDUCATION and TRAINING

<u>Years</u>	<u>Institution</u>	<u>Degree</u>	<u>Field</u>
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

2024–	Associate Dean of Research, College of Health Solutions, Arizona State University (ASU)
2022–2024	Assistant Dean of Research, College of Health Solutions, ASU
2022–	Visiting Professorial Fellow, University of New South Wales (UNSW), Sydney, Australia
2021–	Professor, College of Health Solutions, ASU
2015–	Assistant Director, Center for Environmental Health Engineering, Biodesign Institute, ASU
2015–	Faculty Advisor, Barrett, the Honors College at ASU
2013–	Research Affiliate, Mayo Clinic Arizona, Phoenix, Arizona
2022	Interim Assistant Dean of Research, College of Health Solutions, ASU
2017–2022	Senior Visiting Fellow, UNSW, Sydney, Australia
2016–2021	Associate Professor (with tenure), College of Health Solutions, ASU
2016–2022	PLuS Alliance Fellow, ASU, King's College London, University of New South Wales
2015–2016	Without Compensation (WOC) - Research, Veterans Affairs (VA) Phoenix Healthcare System, 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–	Lecturer, 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

2024	Member, Advanced Leadership Initiative (ALI), Arizona State University
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, *Enhancing phylogeography by improving geographical information from GenBank*, 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, *Sublanguage of cross coverage*, AMIA Fall Symposium
- 2002 Nominee, Homer R. Warner Award, *Sublanguage of cross coverage*, AMIA Fall Symposium

PUBLICATIONS-ORIGINAL INVESTIGATIONS

1. Wang X*, Kim KW, Walker G, Stelzer-Braid S, **Scotch M**, Rawlinson WD. *Genome characterization of influenza A and B viruses in New South Wales, Australia, in 2019: A retrospective study using high-throughput whole genome sequencing*. Influenza Other Respir Viruses. 2024 Jan;18(1):e13252.
2. Faleye TOC, Driver EM, Wright JM, Halden RU, Varsani A, **Scotch M**. *Direct detection of canine picornavirus complete coding sequence in wastewater using long-range reverse-transcriptase polymerase chain reaction and long-read sequencing*. Infect Genet Evol. 2024 Jan 8;118:105550.
3. **Scotch M**, Lauer K, Wieben ED, Cherukuri Y, Cunningham JM, Klee EW, Harrington JJ, Lau JS, McDonough SJ, Mutawe M, O'Horo JC, Rentmeester CE, Schlicher NR, White VT, Schneider SK, Vedell PT, Wang X, Yao JD, Pritt BS, Norgan AP. *Genomic epidemiology reveals the dominance of Hennepin County in the transmission of SARS-CoV-2 in Minnesota from 2020 to 2022*. mSphere. 2023 Oct 26:e0023223. doi: 10.1128/msphere.00232-23.
4. Faleye TOC, Driver EM, Bowes DA, Smith A, Kaiser NA, Wright JM, Chapman AR, Halden RU, Varsani A, **Scotch M**. *Canine parvovirus 2C identified in dog feces from poop bags collected from outdoor waste bins in Arizona USA, June 2022*. Transboundary and Emerging Diseases. 2023;2023:5596886. doi: 10.1155/2023/5596886.
5. Bowes DA, Henke KB, Driver EM, Newell ME*, Block I, Shaffer G, Varsani A, **Scotch M**, Halden RU. *Enhanced detection of mpox virus in wastewater using a pre-amplification approach: A pilot study informing population-level monitoring of low-titer pathogens*. Sci Total Environ. 2023 Dec 10;903:166230.
6. Fontenele RS, Yang Y, Driver EM, Magge A, Kraberger S, Custer JM, Dufault-Thompson K, Cox E*, Newell ME*, Varsani A, Halden RU, **Scotch M**, Jiang X. *Wastewater surveillance uncovers regional diversity and dynamics of SARS-CoV-2 variants across nine states in the USA*. Sci Total Environ. 2023 Jun 15;877:162862.
7. Chapman AR*, Wright JM, Kaiser NA*, Jones PM*, Driver EM, Halden RU, Varsani A, **Scotch M**, Faleye TOC. *Rhizobium Phage-Like Microvirus Genome Sequence Identified in Wastewater in Arizona, USA, in November 2020 Encodes an Endolysin and a Putative Multiheme Cytochrome c-like Protein*. Microbiol Resour Announc. 2023 May 17;12(5):e0006923.
8. Faleye TOC, Elyaderani A*, Skidmore P*, Adhikari S, Smith A*, Kaiser N*, Sandrolini H, Finnerty S, Halden RU, Varsani A, **Scotch M**. *Surveillance of rhinovirus diversity among a university community identifies multiple types from all three species including an unassigned rhinovirus A genotype*. Influenza Other Respir Viruses. 2023 Jan;17(1):e13057.
9. Bowes DA, Driver EM, Kraberger S, Fontenele RS, Holland LA, Wright J, Johnston B, Savic S, Engstrom Newell M, Adhikari S, Kumar R, Goetz H, Binsfeld A, Nessi K, Watkins P, Mahant A, Zevitz J, Deitrick S, Brown P, Dalton R, Garcia C, Inchausti R, Holmes W, Tian XJ, Varsani A, Lim ES, **Scotch M**, Halden RU. *Leveraging an established neighbourhood-level, open access wastewater monitoring network to address public health priorities: a population-based study*. Lancet Microbe. 2023 Jan;4(1):e29-e37.
10. Faleye TOC, Driver EM, Bowes DA, Holm RH, Talley D, Yeager R, Bhatnagar A, Smith T, Varsani A, Halden RU, **Scotch M**. *Detection of human, porcine and canine picornaviruses in municipal sewage sludge using pan-enterovirus amplicon-based long-read Illumina sequencing*. Emerg Microbes Infect. 2022 Dec;11(1):1339-1342.
11. Collins CL, Faleye TOC, Kraberger S, Fontenele RS, Adams D, Adhikari S, Sandrolini H, Finnerty S, Halden RU, **Scotch M**, Varsani A. *Complete Coding Sequences of Rhinovirus Types A46, A39, C56, and C48*. Microbiol Resour Announc. 2022 Nov 17;11(11):e0068022.
12. Smith A*, Kaiser N*, Yanez A, Perleberg T, Elyaderani A*, Skidmore P*, Adhikari S, Driver EM, Halden RU, Varsani A, **Scotch M**, Faleye TOC. *Genome Sequence of a Microvirus Recovered from Wastewater in Arizona, USA, in October 2020, Encodes a Previously Undescribed DNA-Binding Protein*. Microbiol Resour Announc. 2022 Oct 20;11(10):e0033722.

13. Collins CL, Kraberger S, Fontenele RS, Faleye TOC, Adams D, Adhikari S, Sandrolini H, Finnerty S, Halden RU, **Scotch M**, Varsani A. *Genome Sequences of Anelloviruses, Genomovirus, and Papillomavirus Isolated from Nasal Pharyngeal Swabs*. Microbiol Resour Announc. 2022 Sep 15;11(9):e0068122.
14. Faleye TOC, Skidmore PT*, Elyaderani A*, Smith A*, Kaiser N*, Adhikari S, Yanez A, Perleberg T, Driver EM, Halden RU, Varsani A, **Scotch M**. *Canine picornaviruses detected in wastewater in Arizona, USA 2019 and 2021*. Infect Genet Evol. 2022 Sep;103:105315.
15. Namilae S, Wu Y, Mubayi A, Srinivasan A, **Scotch M**. *Identifying mitigation strategies for COVID-19 superspreading on flights using models that account for passenger movement*. Travel Med Infect Dis. 2022 May-Jun;47:102313.
16. Fontenele RS, Kraberger S, Hadfield J, Driver EM, Bowes D, Holland LA, Faleye TOC, Adhikari S, Kumar R, Inchausti R, Holmes WK, Deitrick S, Brown P, Duty D, Smith T, Bhatnagar A, Yeager RA 2nd, Holm RH, von Reitzenstein NH, Wheeler E, Dixon K, Constantine T, Wilson MA, Lim ES, Jiang X, Halden RU, **Scotch M**, Varsani A. *High-throughput sequencing of SARS-CoV-2 in wastewater provides insights into circulating variants*. Water Res. 2021 Oct 15;205:117710.
17. Faleye TOC, Bowes DA, Driver EM, Adhikari S, Adams D, Varsani A, Halden RU, **Scotch M**. *Wastewater-based epidemiology and long-read sequencing to identify enterovirus circulation in three municipalities in Maricopa County, Arizona, Southwest United States between June and October 2020*. Viruses. 2021 Sep 10;13(9):1803. doi: 10.3390/v13091803.
18. Adam DC, Chen X, **Scotch M**, MacIntyre CR, Dwyer D, Kok J. *The molecular epidemiology and clinical phylogenetics of rhinoviruses among paediatric cases in Sydney, Australia*. Int J Infect Dis. 2021 Sep;110:69-74.
19. Faleye TOC, Adams D, Adhikari S, Sandrolini H, Halden RU, Varsani A, **Scotch M**. *Use of hemagglutinin and neuraminidase amplicon-based high-throughput sequencing with variant analysis to detect co-infection and resolve identical consensus sequences of seasonal influenza in a university setting*. BMC Infect Dis. 2021 Aug 13;21(1):810.
20. Islam T, Lahijani MS, Srinivasan A, Namilae S, Mubayi A, **Scotch M**. *From bad to worse: airline boarding changes in response to COVID-19*. R Soc Open Sci. 2021 Apr 28;8(4):201019.
21. Faleye TOC, Driver E, Bowes D, Adhikari S, Adams D, Varsani A, Halden RU, **Scotch M**. *Pan-Enterovirus Amplicon-Based High-Throughput Sequencing Detects the Complete Capsid of a EVA71 Genotype C1 Variant via Wastewater-Based Epidemiology in Arizona*. Viruses. 2021 Jan 7;13(1):E74. doi: 10.3390/v13010074.
22. Magge A, Weissenbacher D, O'Connor K, Tahsin T, Gonzalez-Hernandez G, **Scotch M**. *GeoBoost2: A natural language processing pipeline for GenBank metadata enrichment for virus phylogeography*. Bioinformatics. 2020 Dec 22;36(20):5120-5121.
23. Vaiente MA*, **Scotch M**. *Going back to the roots: Evaluating Bayesian phylogeographic models with discrete trait uncertainty*. Infect Genet Evol. 2020 Nov;85:104501.
24. Ngonghala CN, Iboi E, Eikenberry S, **Scotch M**, MacIntyre CR, Bonds MH, Gumel AB. *Mathematical assessment of the impact of non-pharmaceutical interventions on curtailing the 2019 novel Coronavirus*. Math Biosci. 2020 Jul;325:108364.
25. Holland LA, Kaelin EA, Maqsood R, Estifanos B, Wu LI, Varsani A, Halden RU, Hogue BG, **Scotch M**, Lim ES. *An 81 nucleotide deletion in SARS-CoV-2 ORF7a identified from sentinel surveillance in Arizona (Jan-Mar 2020)*. J Virol. 2020 Jul 1;94(14):e00711-20.
26. Yoo W, Koskan A, **Scotch M**, Pottinger H, Huh WK, Helitzer D. *Patterns and disparities in human papillomavirus (HPV) vaccine uptake for young female adolescents among us states: NIS-Teen (2008-2016)*. Cancer Epidemiol Biomarkers Prev. 2020 Jul;29(7):1458-1467.
27. **Scotch M**, Halden RU, Denton A, Sandrolini H, Fontenele RS, Varsani A. *Coding-complete genome sequence of a human respirovirus 1 strain from a clinical sample in Arizona*. Microbiol Resour Announc. 2020 Jun 11;9(24):e00465-20.
28. Chen X, Adam DC*, Chughtai AA, Stelzer-Braid S, **Scotch M**, MacIntyre CR. *The phylogeography of MERS-CoV in hospital outbreak-associated cases compared to sporadic cases in Saudi Arabia*. Viruses. 2020 May 14;12(5):E540.
29. 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.
30. 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.

31. 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.
32. **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.
33. 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.
34. 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.
35. 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.
36. 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.
37. Magee D*, **Scotch M**. *The effects of random taxa sampling schemes in Bayesian virus phylogeography*. *Infect Genet Evol*. 2018 Oct;64:225-230.
38. Njoto EN, **Scotch M**, Bui CM, Adam DC*, Chughtai AA*, MacIntyre CR. *Phylogeography of H5N1 avian influenza virus in Indonesia*. *Transbound Emerg Dis*. 2018 Oct;65(5):1339-1347.
39. Magge 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.
40. 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.
41. 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.
42. 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.
43. 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.
44. 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 (Oxford)*. 2017 Jan 1;2017:bax093.
45. 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.
46. 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.
47. 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).
48. 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.
49. 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.
50. 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.
51. 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.
52. 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.

53. 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.
54. **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.
55. **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.
56. 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.
57. **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.
58. **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.
59. 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 2006-2011*. PLoS One. 2012;7(9):e43851. Epub 2012 Sep 27.
60. **Scotch M**, Rabinowitz P, Brandt C. *State-level zoonotic disease surveillance in the United States*. Zoonoses Public Health. 2011 Dec;58(8):523-8.
61. **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 Dec;44 Suppl 1:S44-S47.
62. **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.
63. 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 Sep-Oct;18(5):614-20.
64. **Scotch M**, Mattocks K, Rabinowitz P, Brandt C. *A qualitative study of state-level zoonotic disease surveillance in New England*. Zoonoses Public Health. 2011 Mar;58(2):131-9.
65. 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*. Med Care. 2010 Dec;48(12):1064-70.
66. **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 Nov;21(6):764-8.
67. 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 Oct 5;12(4):e45.
68. 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.
69. 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.
70. **Scotch M**, Duggal M, Brandt C, Lin Z, Shiffman R. *Use of statistical analysis in the biomedical informatics literature*. J Am Med Inform Assoc. 2010 Jan-Feb;17(1):3-5.
71. 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*. Int J Health Geogr. 2009 Nov 27;8:67.
72. **Scotch M**, Odofin L, Rabinowitz P. *Linkages between animal and human health sentinel data*. BMC Vet Res. 2009 Apr 23;5:15.
73. Rabinowitz P, **Scotch M**, Conti L. *Human and animal sentinels for shared health risks*. Vet Ital. 2009 Jan-Mar;45(1):23-4.
74. **Scotch M**, Yip K, Cheung K. *Development of grid-like applications for public health using Web 2.0 mashup techniques*. J Am Med Inform Assoc. 2008 Nov-Dec;15(6):783-6.
75. 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*. J Biomed Inform. 2008 Oct;41(5):694-705.
76. Boulous MNK, **Scotch M**, Cheung K, Burden D. *Web GIS in practice VT: a demo "playlist" of geo-mashups for public health neogeographers*. Int J Health Geogr. 2008 Jul 18;7:38.

77. Parmanto B, Paramita M, Sugiantara W, Pramana G, **Scotch M**, Burke DS. *Spatial and multidimensional visualization of Indonesia's village health statistics*. Int J Health Geogr. 2008 Jun 11;7:30.
78. **Scotch M**, Parmanto B, Monaco V. *Evaluation of SOVAT: an OLAP-GIS decision support system for community health assessment data analysis*. BMC Med Inform Decis Mak. 2008 Jun 9;8:22.
79. **Scotch M**, Parmanto B, Monaco V. *Usability evaluation of the Spatial OLAP Visualization and Analysis Tool (SOVAT)*. J Usability Stud. 2007 Feb;2(2):76-95.
80. **Scotch M**, Parmanto B. *Development of SOVAT: A numerical-spatial decision support system for community health assessment research*. Int J Med Inform. 2006 Oct-Nov;75(10-11):771-84.
81. **Scotch M**, Parmanto B, Gadd CS, Sharma RK. *Exploring the role of GIS during community health assessment problem solving: experiences of public health professionals*. Int J Health Geogr. 2006 Sep 18;5:39.
82. Parmanto B, **Scotch M**, Ahmad S. *A framework for designing a healthcare outcome data warehouse*. Perspect Health Inf Manag. 2005 Sep 6;2:3.

†Joint senior authorship; order switched to facilitate counting

*Student authors

PUBLICATIONS-REVIEWS

1. Wang X, Stelzer-Braid S, **Scotch M**, Rawlinson WD. *Detection of respiratory viruses directly from clinical samples using next-generation sequencing: A literature review of recent advances and potential for routine clinical use*. Rev Med Virol. 2022 Jul 1:e2375.
2. 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 Oct;119:241-249.
3. 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. Khairat S, Feldman SS, Rana A, Faysel M, Purkayastha S, **Scotch M**, Eldredge C. *Foundational domains and competencies for baccalaureate health informatics education*. J Am Med Inform Assoc. 2023 Aug 10:ocad147.
2. 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 Jul;11(4):306-310.
3. 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.
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*Student authors

CONFERENCE ABSTRACTS

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2. Wang X*, **Scotch M**, Stelzer-Braid S, Kim KW, Rawlinson WD. *Genome characterization of seasonal influenza viruses in Australia in the 2019 influenza season*. Consortium of Universities for Global Health (CUGH) '23. Washington, District of Columbia. 2023.
3. Faleye TOC, Wright JM, Kaiser NA*, Chapman AR*, Islas M, Halden RU, Varsani A, **Scotch M**. *Influenza A virus (IAV) diversity and antiviral resistance profile in a large university community in southwest USA during the 2022-2023 Northern Hemisphere season*. 7th ISIRV-Antiviral Group (AVG) Conference. Seattle, Washington. 2023.
4. Namilae S, **Scotch M**, Mubayi A, Eddy B, Coffey J. *Collaborative: Elements: Cyberinfrastructure for Pedestrian Dynamics-Based Analysis of Infection Propagation Through Air Travel*. 2022 NSF Cyberinfrastructure for Sustained Scientific Innovation (CSSI) Principal Investigator Meeting: Towards a Sustainable Data and Software Cyberinfrastructure. Alexandria, Virginia. 2022.
5. **Scotch M**, Faleye TOC, Halden RU, Varsani. *Genomic epidemiology of the SARS-CoV-2 Delta variant in Arizona USA*. Annual Rocky Mountain Bioinformatics Conference. Aspen, Colorado. 2021.
6. Faleye TOC, Adams D, Adhikari S, Sandrolini H, Halden RU, Varsani A, **Scotch M**. *Comparison of amplicon-based conventional and long-read Illumina sequencing for high-resolution variant profiling of H3N2 Influenza A virus HA recovered from a clinical sample*. 8th ESWI Influenza Conference – virtual, 4-7 December 2021.
7. Faleye TOC, Bowes DA, Driver S, Adhikari S, Adams D, Varsani A, Halden R, **Scotch M**. *Preponderance of enterovirus c circulation in three municipalities in Maricopa County, Arizona, Southwest United States between June and October 2020*. World Microbe Forum – virtual, 20-24 June, 2021.

8. Faleye TOC, Adams D, Adhikari S, Sandrolini H, Halden RU, Varsani A, **Scotch M**. *Comparison of amplicon-based conventional and long-read Illumina sequencing for detection of minority variants with likely resistance to Neuraminidase inhibitors in a clinical sample*. International Society for Influenza and other Respiratory viruses and World Health Organization (ISIRV-WHO) Virtual Conference, 19-21 October, 2021.
9. 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, Pennsylvania.
10. **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.
11. **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.
12. 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.
13. **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.
14. Vaiente M, **Scotch M**. *Avian contact transmission underlies early epidemic expansion of West Nile virus in the US*. MEEGID-14. Sitges, Spain. 2018
15. Vaiente M, **Scotch M**. *Combining Google Trends and viral genetic data for public health surveillance: The case of Influenza A/H3N2 in Arizona*. MEEGID-14. Sitges, Spain. 2018
16. Magee D, **Scotch M**. *A pipeline for production of BEAST XML files with generalized linear model specifications*. Great Lakes Bioinformatics Conference (GLBIO). Chicago, Illinois. 2017.
17. **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, Illinois. 2016.
18. Magee D, **Scotch M**. *Algorithmic prediction of virus outbreak locales using past geospatial references*. MEEGID-13. Antwerp, Belgium. 2016.
19. **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.
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22. Beard R, **Scotch M**. *Identification of zoonotic disease clusters by integrating phylogeography*. AMIA 2015 Joint Summits on Translational Science. San Francisco, California. 2015.
23. **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, Arizona. 2015.
24. 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, Arizona. 2015.
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26. **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, Colorado. 2014.
27. Beard R, **Scotch M**. *Interpolating Genetic Characteristics of Zoonotic Viruses for Cluster modeling*. 12th Annual Rocky Mountain Bioinformatics Conference. Aspen, Colorado. 2014.
28. Magee D, **Scotch M**. *Comparison of Phylogeographic Node Flux with Local Disease Trends*. 12th Annual Rocky Mountain Bioinformatics Conference. Aspen, Colorado. 2014.

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33. **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, California. 2012.
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35. Womack JA, **Scotch M**, Leung S, Brandt C. *Analysis of contraceptive use among female veterans at the V.A.* AMIA Joint Summits on Translational Science, San Francisco, California. 2012.
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37. Singraur A, **Scotch M**. *Integration of disparate genomic sequences for phylogeography of influenza*. AMIA Annual Symposium. Washington, District of Columbia. 2011.
38. Konovalov S, **Scotch M**, Brandt C. *An ontology-aware application for military blog analysis*. AMIA Annual Symposium. Washington, District of Columbia. 2010.
39. **Scotch M**, Martinello R, Mutalik P, Brandt C. *Use of natural language processing and machine learning for surveillance of MRSA at the V.A.* AMIA Annual Symposium. Washington, District of Columbia. 2010.
40. Sint K, Rabinowitz P, **Scotch M**. *Human cases and bird outbreaks of avian influenza in Vietnam*. American Public Health Association (APHA) Annual Conference. Denver, Colorado. 2010.
41. 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, Minnesota. 2010.
42. 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, California. 2009.
43. 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, California. 2009.
44. **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, California. 2009.
45. **Scotch M**, Parmanto B. *Combining OLAP and GIS for community health assessments*. MedInfo Conference. San Francisco, California. 2004.
46. **Scotch M**, Parmanto B, Sharma R, Meit M. *Development of a multidimensional data warehouse for community health assessment*. APHA Annual Meeting. San Francisco, California. 2003.
47. **Scotch M**, Parmanto B, Sharma R, Meit M. *Constructing a community health database*. Pittsburgh Public Health Association Annual Conference. Pittsburgh, Pennsylvania. 2003.

*Student authors

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):1484-87.

ACTIVE RESEARCH SUPPORT

1U01IP001180-01

CDC

Murugan (PI)

09/30/2022-08/31/2027

Platform to Assess Influenza and COVID-19 Vaccine Effectiveness in Underserved Arizona Populations

The goal of this project is to assess seasonal influenza and SARS-CoV-2 vaccine effectiveness among diverse demographic and clinical populations in Arizona.

Role: Co-investigator

IIS 2302969

Zufle (PI)

04/01/2023-03/31/2026

NSF

Collaborative Research: NSF-CSIRO: HCC: Small: Understanding Bias in AI Models for the Prediction of Infectious Disease Spread

The goal of this study is to design, develop, and validate artificial intelligence models that consider various forms of bias in prediction of infectious disease spread.

Role: Co-PI

1R01AI164481-01A1

Scotch, Gonzalez (PIs)

09/17/2021-08/30/2024

NIH/NIAID

Enriching SARS-CoV-2 sequence data in public repositories with information extracted from full text articles

The goal of this project is to develop and evaluate a biomedical informatics framework for enriching SARS-CoV-2 sequence data in public repositories for studying genomic epidemiology and population health.

1R15LM013382-01A1

Namilae, Srinivasan (PIs)

08/05/2021-07/31/2024

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

U01LM013129

Scotch, Halden, Varsani (PIs)

06/03/2019-05/31/2024

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.

U01LM013129-04S1

Scotch, Halden, Varsani (PIs)

06/03/2022-05/31/2024

NIH/NLM

COVID-19 RADx-rad Administrative supplement to the parent award

The goal of this RADx-rad administrative supplement is to implement and evaluate a bioinformatics framework for wastewater-based epidemiology of SARS-CoV-2 across multiple cities in the United States of America.

AEGIS Scotch (PI) 06/01/2023-05/31/2024
University of Arizona

Genomic epidemiology of avian influenza viruses in the Southwest US

The goal of this study is to sequence avian influenza viruses from multiple species and the environment to study the evolution and spread of the viruses in Arizona.

PENDING RESEARCH SUPPORT

1R21LM014467-01 Scotch, Gonzalez-Hernandez (PIs) 12/01/2023-11/30/2025
NIH/NLM

Real-time estimation of influenza vaccine effectiveness through social media mining

The goal of this project is to use natural language processing (NLP) to estimate influenza vaccine effectiveness from social media posts in order to supplement traditional studies that rely on a test-negative design

Impact Score: 28

1R01AI174596-01A1 Scotch, MacIntyre, Pham (PIs) 04/01/2024-03/31/2029
NIH/NIAID

Development of a risk assessment tool for human transmissible avian influenza using phylodynamic and geospatial modeling in Vietnam

The goal of this project is to develop and evaluate a framework for predicting local risk of pandemic emergence of highly pathogenic avian influenza in Vietnam using genomic and geospatial epidemiology models informed by seroprevalence in humans and poultry.

PRIOR RESEARCH SUPPORT

CCF 2154934 Berry S (PI) 08/01/2022-01/31/2024
NSF

PIPP Phase I: Advancing Environmental Surveillance for Pandemic Prediction in Remote and Resource Poor Settings

The goal of this planning grant is the founding of the Center for the Discovery of Emerging Environmental Pathogens (C-DEEP). The vision of C-DEEP is to advance the science of environmental surveillance and metagenomics, specifically in regions where pandemics are likely to emerge and where current disease surveillance processes are inadequate.

Role: Co-investigator

OAC 1931560 Scotch (PI) 11/01/2019–10/31/2023
NSF

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.

OAC 2027529 Scotch (PI) 05/15/2020-12/31/2022
NSF

Collaborative:RAPID: Leveraging new data sources to analyze the risk of COVID-19 in crowded locations

The goal of this RAPID project is to utilize new data sources such as location-based services data and videos of pedestrian movement to develop local and global models of COVID-19 risk.

COVID-19 Seed Grant Scotch (PI) 06/01/2020-12/31/2021
ASU/CHS

Next-generation sequencing and genomic epidemiology of SARS-CoV-2 patients in Arizona

The goal of this seed grant is to use next-generation sequencing on processed clinical specimens of COVID-19 positive patients in Arizona seen at a Abrazo Health Network hospital and to link subsequent genetic sequence analysis to clinical phenotypes including disease severity.

3U01LM013129-02S1 Scotch, Halden, Varsani (PIs) 07/01/2020-09/30/2021
NIH/NLM

COVID-19 Administrative supplement to the parent award

The goal of this administrative supplement is to use Bayesian phylogeographic-generalized linear models (GLM) to link epidemiologic case data to virus sequence metadata to study genotype-phenotype relationships of SARS-CoV-2.

CBET 2028564 Halden (PI) 05/01/2020-04/30/2021
NSF

Collaborative:RAPID: COVID-19's impact on the urban environment, behavior, and wellbeing

The goal of this RAPID project is to leverage novel data sources from community wastewater including the concentrations of 130+ wastewater-borne biomarkers of environmental stress and human wellbeing and report the resultant data to city stakeholders via an online dashboard for public health decision-making during COVID-19.

Role: Co-PI

5R01AI117011-04 Scotch, Gonzalez-Hernandez (PIs) 04/01/2016–03/31/2021
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.

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 Srinivasan (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.

Role: Co-PI

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 Srinivasan (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.

Role: Co-PI

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
ASU/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

2023– Member, Research & Innovation Implementation Team, School of Medicine and Advanced Engineering, ASU
2022– Chair, Research Council, College of Health Solutions, ASU
2020– Member, Governance Board, ASU Research Computing Core
2018– Member, President's Academic Council, ASU
2016– Member, Institutional Biosafety Committee, ASU

2022–2023	Chair, Search Committee, Assistant Professor of Biomedical Informatics, College of Health Solutions, ASU
2022–2023	Faculty Advisor, Students of Biomedical Informatics (SoBMI)
2021	Member, Personnel Committee, College of Health Solutions
2020–2022	Chair, Search Committee, Associate Professor/Professor of Biomedical Informatics, College of Health Solutions, ASU
2020	Member, Search Committee, ASU Provost
2020	Member, Search Committee, Professor (all ranks) in Urban Health Engineering & Data Analytics, School of Sustainable Engineering and the Built Environment, ASU
2019	Chair, Search Committee, Associate Professor of Biomedical Informatics, College of Health Solutions, ASU
2019–2022	Member, Chalk Talk Faculty Committee, Biodesign Institute, ASU
2019–2020	Chair, Academic Programs Committee, Biomedical Informatics, College of Health Solutions
2019–2022	Degree Director, Bachelor of Science in Biomedical Informatics, College of Health Solutions
2018	Member, Search Committee, Professor (all ranks) in Microbial Risk Assessment, School of Sustainable Engineering and the Built Environment, ASU
2017–2020	Member, Executive Visioning Team, College of Health Solutions, ASU
2017	Chair, Research Integrity Committee (<i>ad hoc</i>), ASU
2016–2020	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
2016–2020	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
2010–2022	Member, Academic Programs Committee, Department of Biomedical Informatics, ASU

SERVICE – NATIONAL

2023–	Chair (Appointed), National Library of Medicine (NLM)/National Institutes of Health (NIH), Biomedical Informatics, Library and Data Sciences (BILDS) Review Committee
2021–	Member, Baccalaureate Educators Community, AMIA Academic Forum
2023	Chair (<i>Ad Hoc</i>), NLM/NIH, G08 Special Emphasis Panel, 2023/10 ZLM1 ZH-G (01)
2023	Member, Scientific Program Committee, Great Lakes Bioinformatics Conference, Montreal, QC.
2020	Grant Reviewer (<i>Ad Hoc</i>), NLM/NIH, Regional Medical Libraries for the Network of the National Library of Medicine (UG4) & Its Evaluation Center (U24), 2021/01 ZLM1 ZH-U (01)
2020–2024	Grant Reviewer (Appointed Member), NLM/NIH, Biomedical Informatics, Library and Data Sciences (BILDS) Review Committee
2020	Grant Reviewer (<i>Ad Hoc</i>), NIAID/NIH, Centers of Excellence for Influenza Research and Response (CEIRR)
2020	Grant Reviewer (<i>Ad Hoc</i>), NLM/NIH, NLM Grants for Scholarly Works in Biomedicine and Health (G13), 2020/10 ZLM1 ZH-P (01)
2019	Grant Reviewer (<i>Ad Hoc</i>), NLM/ NIH, BILDS Review Committee (x2; June and November meetings)
2019	Grant Reviewer (<i>Ad Hoc</i>), 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

- 2020– Journal Editorial Board Member, Environment International (Elsevier)
- 2013– Journal Editorial Board Member, Infection, Genetics and Evolution (Elsevier)
- 2021–2022 Topics Board Editor, Viruses (MDPI)
- 2020 Grant Reviewer, Swiss National Science Foundation (SNSF)
- 2019–2022 Council Member, International Society for Influenza and other Respiratory Virus Diseases (ISIRV)
- 2019 Grant Reviewer, Sir Henry Dale Fellowship, Wellcome Trust
- 2017–2019 Scientific Advisory Board Member, NHMRC Centre for Research Excellence: Integrated Systems for Epidemic Response, Sydney, Australia
- 2016–2019 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)
- 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*
 2020–2023 Instructor, CHS 791 (graduate): *F31 grant writing*
 2018 Instructor, BMI 601 (graduate, online): *Health Informatics*
 2017 Instructor, BMI 570 (graduate): *Biomedical informatics journal club/symposium*
 2016–2018 Instructor, BMI 102 (undergraduate): *Introduction to public health informatics/imaging informatics*
 2015–2016 Instructor, BMD 502 (graduate, online): *Foundations of biomedical informatics methods I*
 2015 Co-Instructor, BMI 102 (undergraduate): *Introduction to public health informatics/imaging informatics*
 2013–2014 Instructor, BMI/BIO 591 (graduate): *NIH grant writing*
 2013–2014 Co-Instructor, HCD 501 (graduate): *Health behavior and statistical tools in health environments*
 2013–2015 Instructor, BMI 502 (graduate): *Foundations of biomedical informatics methods I*
 2012 Instructor, BMI 591 (graduate): *NIH grant writing*
 2011 Instructor, BMI 540 (graduate): *Problem solving in biomedical informatics*
 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*

COURSE DEVELOPMENT

2020 Co-developer, CHS 791 (graduate): *F31 grant writing*
 2015 Developer, BMI 102 (undergraduate): *Introduction to public health informatics*
 2014 Developer, BMD 502 (graduate, online): *Foundations of biomedical informatics methods I*
 2014 Developer, HCD 501 (graduate, online): *Health behavior and statistical tools in health environment*
 2013 Co-developer, HCD 501 (graduate): *Health behavior and statistical tools in health environments*
 2012 Developer, BMI 591 (graduate): *NIH grant writing*

MENTORSHIP AND ADVISING-ONGOING

2023– Izabella Lach, Advisor, Creighton SOM summer research program, *Evolution of influenza B Yamagata and Victoria lineages*.
 2022– Diego Olivio, ASU Doctoral Dissertation Committee Member, *Surveillance of avian circoviridae in North America*
 2022– Peter Maxfield Jones, Advisor, University of Arizona College of Medicine-Phoenix, Medical School Scholarly Project, *Surveillance of avian influenza viruses in the Southwest United States*.
 2021– Mohamed Hamie, Advisor, University of Arizona College of Medicine-Phoenix, Medical School Scholarly Project, *Phylogenetics and molecular characterization of hepatitis C virus in the Medical East and North Africa*.
 2021– Amir Elyaderani, Advisor, ASU Biomedical Informatics PhD program
 2020– Emma Wang, Co-advisor, University of New South Wales
 2012– Rachel Beard, ASU Doctoral Dissertation Committee Chair, *Integration of geographic information systems and molecular epidemiological techniques into spatial decision support for outbreaks of zoonotic diseases*

MENTORSHIP AND ADVISING-COMPLETED

2023 Derek Anderson, Advisor, ASU BMI Master of Science capstone project.
 2022–2023 Daniel Mendoza, Second Committee Member, Barrett, The Honors College Honors Thesis, *A knowledge-driven, generalizable and automatic method to create medication code sets: opioids and antidepressants use case*
 2020–2021 Deborah Adams, Master of Public Health Thesis Chair, Equine Influenza, University of Arizona

2021	Matthew Nunez, ASU Master's Thesis Committee Chair, <i>Rs-fMRI independent component analysis and dual regression to find surgical targets to stop seizures in TSC</i>
2021	Jordy Cevallos-Chavez, Masters in Passing Committee Member, <i>The impact of mobility on the dynamics of COVID-19 outbreak in provinces of Ecuador</i>
2021	Carlos Bustamante Orellana, Masters in Passing Committee Member, <i>Modeling and preparedness: the transmission dynamics of COVID-19 outbreak in provinces of Ecuador</i>
2016–2020	Matteo Vaiente, ASU Doctoral Dissertation Committee Chair, <i>Learning RNA viral disease dynamics from molecular sequence data</i>
2017–2020	Dillon Adam, Doctoral Dissertation Committee Chair (joint with Raina MacIntyre from UNSW), <i>The molecular epidemiology, evolution and phylogeography of pathogens of public health significance</i>
2020	Rahim Taghikhani, Doctoral Dissertation Committee Member, <i>Mathematics of Dengue transmission dynamics and assessment of Wolbachia-based interventions</i>
2020	Maryl Harris, Barrett Honors College Undergraduate Thesis Co-Advisor, <i>Effects of LCMV infection on murine fetal development in immunized mothers</i>
2020	Mina Soliman, Biomedical Informatics Undergraduate Capstone Chair, <i>Digital epidemiology and its many methods</i>
2020	Kaysap Kondury, Barrett Honors College Undergraduate Thesis Advisor, <i>The essential factors that influence and impact type 2 diabetes mellitus prevalence in Pima Indian populations</i>
2020	Komal Agrawal, Master's Thesis Committee Chair, <i>Predictive modeling of RNAs for permanent shunt placement in pediatric intraventricular hemorrhage</i>
2016–2019 [^]	Tasnia Tahsin, ASU Doctoral Dissertation Committee Chair (joint with Graciela Gonzalez-Hernandez from University of Pennsylvania), <i>Knowledge-driven approaches for geographic information extraction from biomedical literature</i>
2016–2019	Arjun Magge, ASU Doctoral Dissertation Committee Chair (joint with Graciela Gonzalez-Hernandez from University of Pennsylvania), <i>Biomedical information extraction pipelines for public health in the age of deep learning</i>
2018–2019	Komal Agrawal, Barrett Honors College Undergraduate Thesis Advisor, <i>The relationship between wastewater toxic substances and Alzheimer's disease</i>
2018–2019	Lydia Mendoza, Barrett Honors College Undergraduate Thesis Advisor, <i>Surveillance of influenza virus spread on the Arizona State University campus</i>
2017–2018	Meghana Nandan, Barrett Honors College Undergraduate Thesis Advisor, <i>Analysis of HIV risk groups using Bayesian phylogenetics</i>
2017–2018	George Karway, Barrett Honors College Undergraduate Thesis Advisor, <i>Making data collection entirely mobile</i>
2013–2017	Daniel Magee, Doctoral Dissertation Committee Chair, <i>Generalized linear models in Bayesian phylogeography</i>
2016–2017	Demetrius Jones-Shargani, Barrett Honors College Undergraduate Thesis Advisor, <i>MosquitoDB</i>
2017	Howard Lanus, Master's Thesis Committee Chair, <i>Common variants and their impact on autism</i>
2014–2016	Wenzhe Xue, ASU Doctoral Dissertation Committee Member, <i>A new image quantitative method for diagnosis and therapeutic response</i>
2012–2016	Azadeh Nikfarjam, ASU Doctoral Dissertation Committee Member, <i>Health information extraction from social media</i>
2012–2016	Ehsan Emadzadeh, ASU Doctoral Dissertation Committee Member, <i>Context-aware adaptive hybrid semantic relatedness in biomedical science</i>
2016	Alex Halloran, ASU Master's Thesis Committee Chair, <i>Specialist Finder: A clinical decision support tool for primary care physicians</i>
2016	Kate Goodin, ASU Master's Thesis Committee Chair, <i>Evaluation of health information exchange connection for a local public health department</i>
2015–2016	Divya Mahendra, ASU Master's Thesis Committee Chair, <i>Identifying differential dependencies associated with drug response across cancer cell lines</i>
2015–2016	Marcus Naymik, Master's Thesis Committee Member, <i>A comparison of obese and lean human epigenetics</i>

- 2015–2016 Brian Hanratty, ASU Master's Thesis Committee Member, *An improved workflow for bisulfite sequencing analysis utilizing cpg filtering and gene detection*
- 2013–2015 Sen Peng, ASU Doctoral Dissertation Committee Member, *Comprehensive genomic characterization of glioblastoma multiforme*
- 2015 Eric Buckland, ASU Master's Thesis Committee Member, *Building a classifier to identify high grade, or muscle invasive, bladder cancer*
- 2015 Tasnia Tahsin, Reading and Conference Advisor, *Natural language processing methods for infectious disease surveillance*
- 2015 Rachel Beard, Reading and Conference Advisor, *Integrating molecular epidemiology and spatiotemporal analysis*
- 2015 Daniel Magee, Reading and Conference Advisor, *Statistical distributions and methods*
- 2013–2015 Saman Jirjies, Master's Thesis Committee Chair, *Open source implementation of Jacques's Q statistics for space-time clustering in case-control studies*
- 2013–2015 Mari Firago, Master's 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, Reading and Conference Advisor (and temporary doctoral dissertation advisor), *Data mining in clinical medicine*
- 2014 Emily Crawford, Undergraduate Research, *Sequencing and analysis of human influenza neuraminidase gene*
- 2014 Emily Crawford, Undergraduate Senior Paper, *Surveillance of oseltamivir and zanamivir resistance in influenza A*
- 2012–2014 Aarthi Varman, Master's 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, Master's Thesis Committee Member, *Study of batch-to-batch reproducibility in nucleic acid programmable protein array*
- 2012–2014 Brittany Baarson, Master's 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, Master's 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, Master's 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, Reading and Conference Advisor, *Semi-supervised learning and bioNLP*
- 2012 Azadeh Nikfarjam, Reading and Conference Advisor, *Machine learning for natural language processing*
- 2012 Ehsan Emadzadeh, Reading and Conference Advisor, *Finding and linking geographical entities in biomedical text*
- 2012 Laura Wojtulewicz, Reading and Conference Advisor, *NIH grant writing*
- 2011–2012 Ryan Sullivan, Master's Thesis Committee Member, *Graph-based gene normalization*
- 2011–2012 Kathikraja Velmurugan, Master's Thesis Committee Member, *Investigation of genomic aberration events in MCF-7 Tamoxifen-resistant and sensitive subclones*
- 2011–2012 Bryan Hendrickson, Master's 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, Master's Thesis Committee Member, *A survey of state and city immunization information systems*

- 2011–2012 Nate Sutton, Master's Thesis Committee Member, *Automatic approaches for gene-drug interaction extraction from biomedical text: corpus and comparative evaluation*
- 2011–2012 Immanuel Purushothaman, Master's Thesis Committee Member, *Bioinformatics to explore the distinctions between high and low risk human papilloma virus*
- 2010–2012 Pierina Ortiz, Master's Thesis Committee Chair, *Use of Bayesian coalescence models to inform prediction models of zoonotic disease in animals*
- 2010–2012 Ashutosh Singraur, Master's Thesis Committee Chair, *Use of influenza sequence data for predicting location of cases*
- 2011 Xiaoxiao Wang, Master's Thesis Committee Member, *A corpus-based learning for co-reference resolution*

^Student temporarily left program

MENTORSHIP AND ADVISING-INCOMPLETED

- 2015–2019 Ryan Sullivan, ASU Doctoral Dissertation Committee Member, *Using biomedical ontologies as structured background knowledge for hierarchical topic modeling*
- 2012–2021^ Barrie Bradley, ASU Doctoral Dissertation Committee Chair, *Development of an immunization registry for clinical and public health*
- 2011–2018 Robert Yao, ASU Doctoral Dissertation Committee Member, *Development of a rule-based computational framework for epilepsy*

^Student temporarily left program

ORAL PRESENTATIONS

- 2023 *Undergraduate health informatics accreditation: benefits, timeline, pathways, and milestones*. Panel session. American Medical Informatics Association (AMIA) Annual Conference. New Orleans, Louisiana.
- 2023 *Genomic epidemiology reveals the dominance of Hennepin County in transmission of SARS-CoV-2 in Minnesota from 2020-2022*. Great Lakes Bioinformatics Conference (GLBIO). Montréal, Québec.
- 2022 *Undergrad BMI education in the desert*. Panel on *Towards standards for undergraduate health informatics education*. Panel session. American Medical Informatics Association (AMIA) Annual Conference. Washington, District of Columbia.
- 2022 (Keynote) *Genomic epidemiology and bioinformatics for evolution and spread of RNA viruses*. SpatialEpi'22 Workshop at the 30th ACM SIGSPATIAL International Conference on Advances in Geographic Information Systems (ACM SIGSPATIAL 2022). Seattle, Washington. Virtual presentation.
- 2022 *Resurgence of H3N2 influenza A virus (IAV) on a university campus in Arizona, USA during the COVID-19 pandemic*. Options XI for the Control of Influenza Conference, Belfast, United Kingdom.
- 2022 *Genomic epidemiology and bioinformatics for RNA virus surveillance*, Honors College Symposium. Embry-Riddle Aeronautical University, Daytona Beach, Florida.
- 2022 *Wastewater-based epidemiology (WBE) and bioinformatics for surveillance of SARS-CoV-2 across US cities*, Biological Design Seminar Series, Arizona State University, Tempe, Arizona.
- 2021 *Genomic epidemiology of the SARS-CoV-2 Delta variant in Arizona USA*. Rocky Mountain Bioinformatics Conference. Aspen, Colorado.
- 2021 *High-throughput sequencing of SARS-CoV-2 in wastewater provides insights into circulating variants*. CIVV-olics Seminar Series. Biodesign Institute. Arizona State University. Tempe, Arizona.
- 2021 *High-throughput sequencing of SARS-CoV-2 in wastewater provides insights into circulating variants*. American Medical Informatics Association (AMIA) Annual Conference. San Diego, California.
- 2021 Panelist, *COVID-19 Variants: What Should You Know?* College of Health Solutions Health Talk, ASU.
- 2020 *Data-Driven Computing-Intensive Modeling*. Webinar on *Battling Emerging & Re-emerging Epidemics & Designing Mitigating Strategies - COVID-19*.
- 2020 *Bioinformatics framework for wastewater-based surveillance of infectious diseases*. Webinar on *Spirit of the Senses*.

- 2020 *Use of ZooPhy for neglected influenza viruses*. 5th International Symposium on Neglected Influenza Viruses. Columbus, Ohio. (Note: Postponed to 2021 due to COVID-19).
- 2020 *How will polar ice melt impact the migration of infectious disease?* Sip of Science Lecture Series hosted by the Biodesign Institute. The Henry Restaurant. Phoenix, Arizona.
- 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* PLuS, 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

- 2024 Scientific Program Committee, Great Lakes Bioinformatics (GLBIO) Conference, Pittsburgh, PA, USA
- 2022 Scientific Program Committee, OPTIONS for the Control of Influenza XI conference, Belfast, Northern Ireland, UK
- 2021 Scientific Program Committee, Great Lakes Bioinformatics Conference, Virtual
- 2021 Scientific Program Committee, AMIA 2021 Annual Symposium, San Diego, California
- 2020 Scientific Program Committee, AMIA 2021 Informatics Summit, Boston, Massachusetts
- 2020 Co-organizer, Workshop, *Epidemic Modeling and Pedestrian Dynamics*, University of West Florida, Pensacola, Florida
- 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, Bioinformatics
 Journal, BMC Evolutionary Biology
 Journal, BMC Genomics
 Journal, BMC Infectious Diseases
 Journal, BMC Medical Informatics and Decision Making
 Journal, BMC Medical Research Methodology
 Journal, Canadian Medical Association Journal (CMAJ)
 Journal, Computer and Electronics in Agriculture
 Journal, Computer Methods and Programs in Biomedicine
 Journal, eBioMedicine
 Journal, Ecohealth
 Journal, Environment International
 Journal, Eurosurveillance
 Journal, Frontiers in Cellular and Infection Microbiology
 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, Lancet Microbe
 Journal, Medical Care
 Journal, Methods of Information in Medicine
 Journal, Molecular Biology and Evolution
 Journal, Nature
 Journal, Nature Communications
 Journal, PeerJ
 Journal, Pharmacoepidemiology and Drug Safety

Journal, PLoS ONE
Journal, PLoS Computational Biology
Journal, PLoS Neglected Tropical Diseases
Journal, Royal Society Open Science
Journal, The Science of the Total Environment
Journal, Transboundary and Emerging Diseases
Journal, Virus Evolution
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 College of Epidemiology (ACE)
American Medical Informatics Association (AMIA)
American Ornithological Society (AOS)
American Society for Microbiology (ASM)
International Society for Computational Biology (ISCB)
International Society for Influenza and other Respiratory Virus Diseases (ISIRV)