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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

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), Veterans Affairs (VA) Phoenix Healthcare System, 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	Fellow, American College of Medical Informatics
2024	Member, Advanced Leadership Initiative (ALI), Arizona State University
2018	Awardee, Endeavour Research Fellowship (Australian Government)
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

PUBLICATIONS-ORIGINAL INVESTIGATIONS

1. Chung JR, Price AM, Zimmerman RK, Moehling Geffel K, House SL, Curley T, Wernli KJ, Phillips CH, Martin ET, Vaughn IA, Murugan V, **Scotch M**, Saade EA, Faryar KA, Gaglani M, Ramm JD, Williams OL, Walter EB, Kirby M, Keong LM, Kondor R, Ellington SR, Flannery B; US Flu VE Network Investigators. *Influenza vaccine effectiveness against medically attended outpatient illness, United States, 2023-24 season.* Clin Infect Dis. 2025 Jan 6:ciae658. doi: 10.1093/cid/ciae658.
2. Faleye TOC, Skidmore P, Elyaderani A, Adhikari S, Kaiser N, Smith A, Yanez A, Perleberg T, Driver EM, Halden RU, Varsani A, **Scotch M**. *Adenovirus 41 diversity in Arizona (USA) using wastewater-based epidemiology, long-range PCR, and pathogen sequencing between October 2019 and March 2020.* Epidemiol Infect. 2024 Nov 18;152:e142.
3. Bermudez-Rivera B*, Hampton B*, Wheeler C*, Vargas J*, Swaminathan S, Driver EM, Halden RU, Varsani A, **Scotch M**, Faleye TOC. *Nine rhizobium phage genomes recovered from wastewater in Tempe, AZ, October 2019-March 2020.* Microbiol Resour Announc. 2024 Oct 10;13(10):e0068024.
4. Wang X*, Walker G, Kim KW, Stelzer-Braid S, **Scotch M**, Rawlinson WD. *The resurgence of influenza A/H3N2 virus in Australia after the relaxation of COVID-19 restrictions during the 2022 season.* J Med Virol. 2024 Sep;96(9):e29922.
5. Faleye TOC, Skidmore P, Elyaderani A, Adhikari S, Kaiser N, Smith A, Yanez A, Perleberg T, Driver EM, Halden RU, Varsani A, **Scotch M**. *Exploring canine picornavirus diversity in the USA using wastewater surveillance: from high-throughput genomic sequencing to immuno-informatics and capsid structure modeling. Viruses. 2024 Jul 24;16(8):1188.*
6. Wu Y, Namilae S, Srinivasan A, Mubayi A, **Scotch M**. *Parametric analysis of SARS-CoV-2 dose-response models in transportation scenarios.* PLoS One. 2024 Jun 12;19(6):e0301996.
7. Zufle A, Salim F, Anderson T, **Scotch M**, Xiong L, Sokol K, Xue H, Kong R, Heslop D, Paik H-Y, MacIntyre CR. *Leveraging Simulation Data to Understand Bias in Predictive Models of Infectious Disease Spread.* ACM Trans Spatial Algorithms Syst. 2024. doi: 10.1145/3660631.
8. 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.
9. 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.
10. **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.
11. 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.
12. 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.
13. 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.
14. 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.

15. 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.
16. 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.
17. 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.
18. 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.
19. 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.
20. 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.
21. 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.
22. 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.
23. 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.
24. 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.
25. 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.
26. 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.
27. 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.
28. 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.
29. 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.
30. Vaiente MA*, **Scotch M**. *Going back to the roots: Evaluating Bayesian phylogeographic models with discrete trait uncertainty*. Infect Genet Evol. 2020 Nov;85:104501.

31. 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.
32. 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.
33. 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.
34. **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.
35. 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.
36. 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.
37. 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.
38. Adam DC[*], MacIntyre CR[†], **Scotch M**[†]. *Phylodynamics 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.
39. **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.
40. 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.
41. 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.
42. 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.
43. 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.
44. Magee D[*], **Scotch M**. *The effects of random taxa sampling schemes in Bayesian virus phylogeography*. Infect Genet Evol. 2018 Oct;64:225-230.
45. 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.
46. 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.
47. 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.
48. 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.
49. 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.
50. 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.
51. 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.

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53. 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.
54. Jirjies S*, Wallstrom G, Halden RU, **Scotch M**. *pyJacqQ: python implementation of Jacquez's Q-statistics for space-time clustering of disease exposure in case-control studies*. J Stat Softw. 2016 Oct;74(6).
55. 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.
56. 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.
57. 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.
58. 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.
59. 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.
60. 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.
61. **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.
62. **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.
63. 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.
64. **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.
65. **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.
66. 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.
67. **Scotch M**, Rabinowitz P, Brandt C. *State-level zoonotic disease surveillance in the United States*. Zoonoses Public Health. 2011 Dec;58(8):523-8.
68. **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.
69. **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.
70. 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.
71. **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.
72. 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.
73. **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.
74. 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.

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76. 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.
77. **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.
78. 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.
79. **Scotch M**, Odofin L, Rabinowitz P. *Linkages between animal and human health sentinel data.* BMC Vet Res. 2009 Apr 23;5:15.
80. Rabinowitz, P, **Scotch M**, Conti L. *Human and animal sentinels for shared health risks.* Vet Ital. 2009 Jan-Mar;45(1):23-4.
81. **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.
82. 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.
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84. 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.
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89. Parmanto B, **Scotch M**, Ahmad S. *A framework for designing a healthcare outcome data warehouse.* Perspect Health Inf Manag. 2005 Sep 6;2:3.

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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.
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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 AMIA-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.
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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.
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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.
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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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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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35. 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, California. 2012.
36. 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, District of Columbia. 2011.
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 VA.* 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* report*s.* 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.

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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

2412446 Berry (PI) 09/01/2024-08/30/2031
NSF/DBI
PIPP Phase II: Environmental Surveillance for Assessing Pathogen Emergence (ESCAPE)
The goal of this PIPP phase II center is to develop and implement environmental surveillance systems that work for everyone, anywhere while advancing public health intelligence through communication, community-based science, and workforce development to predict and prevent infectious disease pandemics.
Role: Co-PI

R21LM014467-01 Scotch, Gonzalez-Hernandez (PIs) 05/07/2024-04/30/2026
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.

U01IP001180 Murugan (PI) 09/30/2022-08/31/2027
CDC
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

2302969 Zufle (PI) 04/01/2023-03/31/2026
NSF/IIS
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

R01AI164481 Scotch, Gonzalez (PIs) 09/17/2021-08/31/2025
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.

R15LM013382 Namilae, Srinivasan (PIs) 08/05/2021–07/31/2025
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

2154934 Berry S (PI) 08/01/2022-01/31/2025
NSF/CCF
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: Senior personnel (ASU PI)

PENDING RESEARCH SUPPORT

None

PRIOR RESEARCH SUPPORT

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.

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

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

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

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

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.

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

2024– Member, Emerging Infectious Disease Committee, ASU

2023	Member, Research & Innovation Implementation Team, School of Medicine and Advanced Engineering, ASU
2022–	Chair, Research Council, College of Health Solutions, ASU
2020–2024	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 (*ad hoc*), 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

2024	Grant Reviewer (*Ad Hoc*), National Science Foundation (NSF), Human Networks and Data Science -- Infrastructure program.
2023–2024	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 (*Ad Hoc*), 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 (*Ad Hoc*), 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 (*Ad Hoc*), NIAID/NIH, Centers of Excellence for Influenza Research and Response (CEIRR)

2020	Grant Reviewer (*Ad Hoc*), NLM/NIH, NLM Grants for Scholarly Works in Biomedicine and Health (G13), 2020/10 ZLM1 ZH-P (01)
2019	Grant Reviewer (*Ad Hoc*), NLM/ NIH, BILDS 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

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

2024	Instructor, BMI 614 (graduate, online): *Current Perspectives in Health Informatics*
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

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.*

MENTORSHIP AND ADVISING-COMPLETED

2023–2024	Izabella Lach, Advisor, Creighton SOM summer research program, *Exploring the Recent Evolutionary Patterns of B/Victoria.*
2020–2024	Emma Wang, Doctoral Thesis Co-supervisor, University of New South Wales, *Influenza dynamics from pre- to post-pandemic periods: epidemiology and genetic characteristics*
2021–2024	Amir Elyaderani, Advisor, ASU Biomedical Informatics Masters in Passing from PhD program

2024	Ethan Leiter-Weintraub, Second Committee Member, Barrett, The Honors College Honors Thesis, *Genome-wide association analysis of response and remission to selective serotonin reuptake inhibitor treatment for major depressive disorder and seasonal depression pattern*
2024	Sadhana Pandarinathan, Second Committee Member, Barrett, The Honors College Honors Thesis, *Evaluating the heterogeneity of logistic regression models to predict coronary artery disease status.*
2012–2024	Rachel Beard, ASU Doctoral Dissertation Committee Chair-graduated with Masters in Passing, *Integration of geographic information systems and molecular epidemiological techniques into spatial decision support for outbreaks of zoonotic diseases*
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, *Rs-fMRI independent component analysis and dual regression to find surgical targets to stop seizures in TSC*
2021	Jordy Cevallos-Chavez, Masters in Passing Committee Member, *The impact of mobility on the dynamics of COVID-19 outbreak in provinces of Ecuador*
2021	Carlos Bustamante Orellana, Masters in Passing Committee Member, *Modeling and preparedness: the transmission dynamics of COVID-19 outbreak in provinces of Ecuador*
2016–2020	Matteo Vaiente, ASU Doctoral Dissertation Committee Chair, *Learning RNA viral disease dynamics from molecular sequence data*
2017–2020	Dillon Adam, Doctoral Dissertation Committee Chair (joint with Raina MacIntyre from UNSW), *The molecular epidemiology, evolution and phylogeography of pathogens of public health significance*
2020	Rahim Taghikhani, Doctoral Dissertation Committee Member, *Mathematics of Dengue transmission dynamics and assessment of Wolbachia-based interventions*
2020	Maryl Harris, Barrett Honors College Undergraduate Thesis Co-Advisor, *Effects of LCMV infection on murine fetal development in immunized mothers*
2020	Mina Soliman, Biomedical Informatics Undergraduate Capstone Chair, *Digital epidemiology and its many methods*
2020	Kaysap Kondury, Barrett Honors College Undergraduate Thesis Advisor, *The essential factors that influence and impact type 2 diabetes mellitus prevalence in Pima Indian populations*
2020	Komal Agrawal, Master's Thesis Committee Chair, *Predictive modeling of RNAs for permanent shunt placement in pediatric intraventricular hemorrhage*
2016–2019^	Tasnia Tahsin, ASU Doctoral Dissertation Committee Chair (joint with Graciela Gonzalez-Hernandez from University of Pennsylvania), *Knowledge-driven approaches for geographic information extraction from biomedical literature*
2016–2019	Arjun Magge, ASU Doctoral Dissertation Committee Chair (joint with Graciela Gonzalez-Hernandez from University of Pennsylvania), *Biomedical information extraction pipelines for public health in the age of deep learning*
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, Master's Thesis Committee Chair*, Common variants and their impact on autism*

2014–2016	Wenzhe Xue, ASU Doctoral Dissertation Committee Member, *A new image quantitative method for diagnosis and therapeutic response*
2012–2016	Azadeh Nikfarjam, ASU Doctoral Dissertation Committee Member, *Health information extraction from social media*
2012–2016	Ehsan Emadzadeh, ASU Doctoral Dissertation Committee Member, *Context-aware adaptive hybrid semantic relatedness in biomedical science*
2016	Alex Halloran, ASU Master's Thesis Committee Chair, *Specialist Finder: A clinical decision support tool for primary care physicians*
2016	Kate Goodin, ASU Master's Thesis Committee Chair, *Evaluation of health information exchange connection for a local public health department*
2015-2016	Divya Mahendra, ASU Master's Thesis Committee Chair, *Identifying differential dependencies associated with drug response across cancer cell lines*
2015–2016	Marcus Naymik, Master's Thesis Committee Member, *A comparison of obese and lean human epigenetics*
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 Jacquez'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

2024	Research Lab Lightning Talk. Giants Among Us Symposium. Mayo Clinic and ASU Alliance for Health Care. Phoenix, Arizona.
2024	*Virus sequencing & bioinformatics of avian influenza viruses among wild birds in Arizona.* American Ornithological Society (AOS) Annual Meeting. Estes Park, Colorado.
2024	(Invited Presentation) *Leveraging NLP for Genomic Epidemiology and Virus Surveillance.* Computational Biomedicine Health Language Processing Annual Symposium. Cedars-Sinai Medical Center. Beverly Hills, California.
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 erro*r. 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, Cell Press Multi-Journal Submission
Journal, Computer and Electronics in Agriculture
Journal, Computer Methods and Programs in Biomedicine
Journal, eBioMedicine
Journal, Ecohealth

Journal, Emerging Microbes & Infections
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
Journal, Zoonoses and Public Health
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)
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)