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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), 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, <i>Enhancing phylogeography by improving geographical information from GenBank</i> , American Medical Informatics Association (AMIA) Joint Summits

- 2007 Awardee, Tuition and Travel, Cold Spring Harbor Laboratory Workshop on Infectious Disease Ontology, Supported by the Burroughs Wellcome Fund
- 2002 Winner, Best Paper, *Sublanguage of cross coverage*, AMIA Fall Symposium

PUBLICATIONS-ORIGINAL INVESTIGATIONS

1. **Scotch M**, Faley TO, Urquidez-Negrete A, Bobbett B, Boyle V, Conard K, Sublasky-Rodriguez L, Murugan V. *Influenza A(H3N2) subclade K (J.2.4.1) viruses associated with a surge at a university health clinic, Arizona, the United States, November to early December 2025*. Euro Surveill. 2026 Feb;31(7). doi: 10.2807/1560-7917.ES.2026.31.7.2600111.
2. **Scotch M**, Faley TOC, Wright JM, Finnerty S, Halden RU, Varsani A. *Campus-based genomic surveillance uncovers early emergence of a future dominant A(H3N2) influenza clade*. iScience. 2025 Nov 4;28(12):113941. doi: 10.1016/j.isci.2025.113941.
3. Vargas J*, Bermudez-Rivera B*, Block I, Shaffer G, Estrada L, Dadd T, Dickerson T, Curtis C, Woods C, Driver EM, Halden RU, Varsani A, **Scotch M**, Faley TOC. *Canine Parvovirus and Vaccine-Origin Feline Panleukopenia Virus in Wastewater, Arizona, USA: July 2022-June 2023*. Microorganisms. 2025 Sep 11;13(9):2124.
4. Negrete AU, Nelson S, **Scotch M**, Faley TOC. *Influenza B virus from respiratory samples of individuals with influenza-like illness in a university campus in Arizona USA, in February 2025*. Microbiol Resour Announc. 2025 Jul 7:e0034425.
5. Strike W*, Faley TOC, Lubega B, Rockward A, Torabi S, Noble A, Banadaki MD, Keck J, Mugerwa H, **Scotch M**, Berry S. *Implementing wastewater-based epidemiology for long-read metagenomic sequencing of antimicrobial resistance in Kampala, Uganda*. Microorganisms. 2025 May 28;13(6):1240.
6. Wang X*, Sevendal AT, Kamalakkannan A, Stelzer-Braid S, Kim KW, **Scotch M**, Walker GJ, Rawlinson WD. *Influenza epidemiology and co-infections within New South Wales-based multicentre health districts between 2018 and 2023*. Pathology. 2025 Apr 22:S0031-3025(25)00158-8. doi: 10.1016/j.pathol.2025.02.009.
7. O'Connor K, Weissenbacher D, Elyaderani A*, Lautenbach E, **Scotch M**, Gonzalez-Hernandez G. *Patient-related metadata reported in sequencing studies of SARS-CoV-2: protocol for a scoping review and bibliometric analysis*. JMIR Res Protoc. 2025 Apr 22;14:e58567.
8. 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.
9. Faley 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.
10. Bermudez-Rivera B*, Hampton B*, Wheeler C*, Vargas J*, Swaminathan S, Driver EM, Halden RU, Varsani A, **Scotch M**, Faley TOC. *Nine rhizobium phage genomes recovered from wastewater in Tempe, AZ, October 2019-March 2020*. Microbiol Resour Announc. 2024 Oct 10;13(10):e0068024.
11. 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.
12. Faley 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.
13. 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.
14. 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.
15. 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.

16. 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 Mar;118:105550.
17. **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.
18. 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.
19. 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.
20. 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.
21. 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.
22. 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.
23. 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.
24. 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.
25. 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.
26. 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.
27. 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.
28. 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.
29. 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.
30. 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.

31. 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.
32. 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.
33. 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.
34. 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.
35. 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.
36. 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.
37. Vaiente MA*, **Scotch M**. *Going back to the roots: Evaluating Bayesian phylogeographic models with discrete trait uncertainty*. *Infect Genet Evol*. 2020 Nov;85:104501.
38. 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.
39. 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.
40. 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.
41. **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.
42. 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.
43. 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.
44. 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.
45. 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.
46. **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.
47. 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.
48. 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.
49. 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.

50. 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.
51. Magee D*, **Scotch M**. *The effects of random taxa sampling schemes in Bayesian virus phylogeography*. Infect Genet Evol. 2018 Oct;64:225-230.
52. 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.
53. 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.
54. 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.
55. 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.
56. 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.
57. 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.
58. 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.
59. 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.
60. 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.
61. 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).
62. 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.
63. 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.
64. 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.
65. 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.
66. 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.
67. 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.
68. **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.
69. **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.
70. 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.
71. **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.
72. **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.

73. 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.
74. **Scotch M**, Rabinowitz P, Brandt C. *State-level zoonotic disease surveillance in the United States*. Zoonoses Public Health. 2011 Dec;58(8):523-8.
75. **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.
76. **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.
77. 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.
78. **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.
79. 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.
80. **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.
81. 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.
82. 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.
83. 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.
84. **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.
85. 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.
86. **Scotch M**, Odofin L, Rabinowitz P. *Linkages between animal and human health sentinel data*. BMC Vet Res. 2009 Apr 23;5:15.
87. Rabinowitz, P, **Scotch M**, Conti L. *Human and animal sentinels for shared health risks*. Vet Ital. 2009 Jan-Mar;45(1):23-4.
88. **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.
89. 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.
90. Boulos MNK, **Scotch M**, Cheung K, Burden D. *Web GIS in practice VI: a demo "playlist" of geo-mashups for public health neogeographers*. Int J Health Geogr. 2008 Jul 18;7:38.
91. 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.
92. **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.
93. **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.
94. **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.
95. **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.
96. 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

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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.
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. Yeh KB, Bahnfleth WP, Bradforda E, Cardona C, Coleman KK, Hudson PJ, Dadonaite B, Hutchins RJ, Maresso A, MacIntyre CR, **Scotch M**. *Three things we can do now to reduce the risk of avian influenza spillovers*. Proc Natl Acad Sci U S A. 2025 Aug 5;122(31):e2503565122.
2. 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.
3. 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.
4. 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. Kong R, Anderson T, **Scotch M**, Heslop DJ, Khaokaew Y, Xue H, Xiong L, MacIntyre CR, Salim FD, Züfle A. *Simulated Infectious Diseases Datasets with Controlled Data Bias*. Proceedings of the 31st ACM SIGKDD Conference on Knowledge Discovery and Data Mining V2; Toronto ON, Canada: Association for Computing Machinery; 2025. p. 5551–9.
2. Eluru M, Potturu AS, **Scotch M**, Allen L, Osgood N, Tello A, Grando A. *Development and usability testing of a web-based research guide for health solutions grant writing*. AMIA Annu Symp Proc. 2025 May 22;2024:378-387.
3. 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.
4. 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.
5. 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.
6. 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.
7. 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)
8. 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.

9. **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.
10. 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.
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*. AMIA 2014 Joint Summits on Translational Science; 2014:102-111.
12. 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.
13. 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.
14. Rabinowitz P, Vegso S, Chudnov, Odojin L, **Scotch M**, Wilcox M. *The 'Canary Database': Assembling Evidence for One Health Linkages between Human, Animal, and Environmental Health*. 2013 Annual Meeting and Exhibition of the Medical Library Association (MLA '13).
15. **Scotch M**, Parmanto B. *SOVAT: Spatial OLAP Visualization and Analysis Tool*. Proc HICSS-38; 2005:142.2.
16. Parmanto B, **Scotch M**. *Mining Information from Mountains of Electronic Health Record: Unique Challenges and Solutions*. Proc AHIMA National Convention. 2003.
17. Stetson, PD, Johnson SB, **Scotch M**, Hripcsak, G. *The Sublanguage of Cross Coverage*. Proc AMIA Symp. 2002:742-6.

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CONFERENCE ABSTRACTS

1. Faley TOC, Skidmore P*, Elyaderani A*, Adhikari S, Kaiser NA*, Smith A*, Yanez A, Perleberg T, Driver EM, Halden RU, Varsani A, **Scotch M**. *Towards determining canine picornavirus diversity in the USA using wastewater-based genomic epidemiology*. American Society for Virology (ASV) Annual Meeting. Athens, Georgia. 2023.
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. Faley 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**, Faley 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. Faley 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. Faley 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. Faley 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.
20. **Scotch M**, Beard R, Tahsin T, Weissenbacher D, Suchard MA, Gonzalez G. *Incorporating geospatial observation error in discrete Bayesian virus phylogeography*. MEEGID-13. Antwerp, Belgium. 2016.
21. **Scotch M**, Beard R, Pahle R, Mubayi A, Namilae S, Srinivasan A. *The spread of the 2014 Ebola Zaire virus in West Africa*. Pacific Symposium on Biocomputing. Big Island, Hawaii. 2016.
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.
25. Beard R, **Scotch M**. *Identification of zoonotic disease clusters by integrating phylogeography*. The International Society for Evolution, Medicine, & Public Health. Tempe, Arizona. 2015.
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.
29. Veljkovic V, Veljkovic N, Perovic V, Sencanski M, **Scotch M**, Glisic S. *Antimalarials repositioning as a route to discovery of drugs for treatment of Ebola virus disease*. COST CM1307 conference on Targeted chemotherapy towards diseases caused by endoparasites. Calvi, France. 2014.
30. Martins S, Tu S, Martinello R, Rubin M, Foulis P, Luther S, Forbush T, **Scotch M**, Doebbellling B, Goldstein MK. *Creating a MRSA Ontology to Support Categorization of MRSA Infections*. AMIA Annual Symposium. Washington, District of Columbia. 2013.

31. **Scotch M**, Pabilonia K, Anderson T, Baroch J, Kohler D, DeLiberto TJ, Espy M, Pritt B, Black K, Seville MT. *Phylogeography of avian and human influenza in the Southwest United States*. 10th Annual Rocky Mountain Bioinformatics Conference. Aspen, Colorado. 2012.
32. **Scotch M**, Pabilonia K, Anderson T, Baroch J, Kohler D, DeLiberto TJ, Espy M, Pritt B, Seville MT. *Phylogeography of influenza A in human and avian species in the southwest United States*. 11th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID-11). New Orleans, Louisiana. 2012.
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.
34. O'Rourke T, Joly DO, Palmer J, Olson S, Manhas M, O'Rourke D, Rabinowitz P, **Scotch M**, Goldstein T, Kreuder Johnson C, Wolking D, Lebreton M, Karesh W, Mazet J. *Data standardization is critical to ensure wildlife health data quality*. 2012 Wildlife Disease Association Conference. Lyon, France.
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 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.

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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) 09/17/2021-08/31/2026

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.

PRIOR RESEARCH SUPPORT

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)
- 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.

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

2026 Member, PROMOTE Initiative Advisory Council, ASU
2025 Member, Executive Committee, Principled Innovation Infrastructure (PII) initiative, ASU
2025 Member, Steering Committee, *Giants Among Us*, Mayo Clinic and ASU Alliance for Health Care
2025– Member, Research Council, School of Medicine and Advanced Medical Engineering, ASU
2024– Member, Emerging Infectious Disease Committee, 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 (*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

- 2026 Grant Reviewer (*Ad Hoc*), National Institutes of Health (NIH) / Center for Scientific Review (CSR), GVE: Genetic Variation and Evolution Study Section
- 2026– Member, Executive Committee, AMIA Academic Forum
- 2026– Chair, Baccalaureate Educators Community, AMIA Academic Forum
- 2026 Grant Reviewer (*Ad Hoc*), NIH/CSR, PRID: Population-based Research in Infectious Diseases Study Section
- 2025 Chair (*Ad Hoc*), NIH/CSR, Special Emphasis Panel, R03 Small Grant Program for the NCATS Clinical and Translational Science Award (CTSA) Program, ZTR1 CI 8(01)
- 2024 Grant Reviewer (*Ad Hoc*), National Science Foundation (NSF), Human Networks and Data Science - Infrastructure program
- 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 (*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*), National Institute of Allergy and Infectious Diseases (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*), NIAID/NIH, Collaborative Influenza Vaccine Innovation Centers (CIVIC), Special Emphasis Panel ZAI1- EC-M-C1
- 2019 Grant Reviewer (*Ad Hoc*), 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

- 2025 Instructor, CHS 494 (undergraduate): *Health Research Scholars, Undergraduate Research Initiatives Program*

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*
2016–2017 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

2025 Founder and co-developer, *CHS Undergraduate Research Initiatives Program (URIP)*. Includes courses *CHS 280: Intro to Health Research* and *CHS 494: Health Research Scholars*
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

2025– Ainsley Atherton, Advisor, Biomedical Informatics PhD Program
2025– Kamyab Keshtkar, Doctoral Dissertation Committee Member, Biomedical Informatics PhD Program
2024– Joe Sneddon, Advisor, Biomedical Informatics PhD Program
2022– Diego Olivio, Doctoral Dissertation Committee Member, *Surveillance of avian circoviridae in North America*, School of Life Sciences (SOLS)

MENTORSHIP AND ADVISING-COMPLETED

2023–2024 Izabella Lach, Advisor, Creighton SOM summer research program, *Exploring the Recent Evolutionary Patterns of B/Victoria*
2022–2024 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*
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*
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, *R_s-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 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

- 2012–2024 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*
- 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

- 2026 *Rapid expansion of HPAI H5 clade 2.3.4.4b genotype D1.1 across North American flyways during fall 2024 avian migration.* Symposium on AI for Outbreak Forecasting: Are we seeing the full picture? University of New South Wales, Sydney, Australia.
- 2025 *Redefining PhD education in health informatics: addressing core training challenges in the AI-era.* Panel session. American Medical Informatics Association (AMIA) Annual Conference. Atlanta, Georgia.
- 2025 *Desert birds, global threats: tracking avian influenza in the pacific flyway.* ASM Microbe. Los Angeles, California
- 2025 New Fellow Presentation. AMIA FACMI Retreat. San Juan, PR, USA
- 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. 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 (LAV) 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

- 2025 Session Organizer, *One health and genomic epidemiology: innovations in pathogen surveillance*. ASM Microbe. Los Angeles, California
- 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, Genome Medicine
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)