

**Matthew Laurence Scotch, PhD, MPH**

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

Department of Biomedical Informatics-ASU  
Mayo Clinic, Samuel C. Johnson Research Bldg  
13212 East Shea Boulevard, Scottsdale, Arizona 85259

PHONE: 480.884.0245 or 480.727.2985

EMAIL: [matthew.scotch@asu.edu](mailto:matthew.scotch@asu.edu)

<https://webapp4.asu.edu/directory/person/1615221>

**EDUCATION and TRAINING**

<u>Years</u>	<u>Institution</u>	<u>Degree</u>	<u>Major</u>
2006–2008	Yale University New Haven, Connecticut	Postdoctoral Fellow	Biomedical Informatics
2006–2007	Yale University New Haven, Connecticut	MPH	Public Health
2002–2006	University of Pittsburgh Pittsburgh, Pennsylvania	PhD	Biomedical Informatics
2000–2002	Columbia University New York, New York	MA	Biomedical Informatics
1994–1998	University of Rochester Rochester, New York	BA	Health & Society

**PROFESSIONAL EXPERIENCE**

2015–	Assistant Director, Center for Environmental Security, Biodesign Institute, Arizona State University (ASU)
2015–	Without Compensation (WOC) - Research, Veterans Affairs (VA) Phoenix Healthcare System, Phoenix, Arizona
2014–	WOC – Research Service, VA Salt Lake City Healthcare System, Salt Lake City, Utah
2013–	Research Affiliate, Mayo Clinic Arizona, Phoenix, Arizona
2012–2015	Assistant Professor, Center for Environmental Security, Biodesign Institute, ASU
2010–	Assistant Professor, Department of Biomedical Informatics, College of Health Solutions, ASU
2008–2015	WOC – Research Service, VA Connecticut Healthcare System, West Haven, Connecticut

## HONORS and AWARDS

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

## PUBLICATIONS

### (Peer Reviewed)

1. 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.
2. 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.
3. 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.
4. **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.
5. **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.
6. 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.
7. 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.
8. **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.
9. **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.
10. Rabinowitz, PM, Galusha D, Vegso S, Michalove S, Rinne S, **Scotch M**, Kane M. *Comparison of human and animal surveillance data for H5N1 influenza A in Egypt 2006-2001*. PLoS One. 2012;7(9):e43851. Epub 2012 Sep 27.
11. **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.
12. **Scotch M**, Sarkar IN, Mei C, Leaman R, Cheung KH, Ortiz P, Singraur A, Gonzalez G. *Enhancing phylogeography by improving geographical information from GenBank*. J Biomed Inform. 2011;44(S1):S44-47.

13. Garla V, Re VL 3<sup>rd</sup>, Dorey-Stein Z, Kidwai F, **Scotch M**, Womack J, Justice A, Brandt C. *The Yale eTAKES extensions for document classification: architecture and application*. J Am Med Inform Assoc. 2011. 18(5):614-20.
14. **Scotch M**, Rabinowitz P, Brandt C. *State-level zoonotic disease surveillance in the United States*. Zoonoses and Public Health. 2011;58(8):523-8.
15. **Scotch M**, Mattocks K, Rabinowitz P, Brandt C. *A qualitative study of state-level zoonotic disease surveillance in New England*. Zoonoses and Public Health. 2011;58(2):131-139.
16. 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.
17. **Scotch M**, Mei C, Brandt C, Sarkar IN, Cheung K. *At the intersection of public-health informatics and bioinformatics: Using advanced Web technologies for phylogeography*. Epidemiology. 2010; 21(6):764-8.
18. Konovalov S, **Scotch M**, Post L, Brandt C. *Biomedical informatics techniques for processing and analyzing web blogs of military service members*. J Med Internet Res. 2010; 12(4):e45.
19. 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.
20. Ohl M, Tate J, Duggal M, Skanderson M, **Scotch M**, Kaboli P, Vaughan-Sarrazin M, Justice A. *Rural residence is associated with delayed care entry and increased mortality among veterans with Human Immunodeficiency Virus (HIV) infection*. Medical Care. 2010 Dec;48(12):1064-1070.
21. **Scotch M**, Duggal M, Brandt C, Lin Z, Shiffman R. *Use of statistical analysis in the biomedical informatics literature*. Journal of the American Medical Informatics Association. 2010; 17(1):3-5.
22. Liu A, Lee V, Galusha D, Slade MD, Diuk-Wasser M, Andreadis T, **Scotch M**, Rabinowitz P. *Risk factors for human infection with West Nile virus in Connecticut: a multi-year analysis*. International Journal of Health Geographics. 2009, 8:67.
23. **Scotch M**, Odofin L, Rabinowitz P. *Linkages between animal and human health sentinel data*. BMC Veterinary Research. 2009, 5:15.
24. Rabinowitz, P, **Scotch M**, Conti L. *Human and animal sentinels for shared health risks*. Veterinaria Italiana. 2009; 45(1):23-34.
25. Boulos MNK, **Scotch M**, Cheung K, Burden D. *Web GIS in practice VI: a demo "playlist" of geo-mashups for public health neogeographers*. International Journal of Health Geographics. 2008, 7:38.
26. **Scotch M**, Yip K, Cheung K. *Development of grid-like applications for public health using Web 2.0 mashup techniques*. Journal of the American Medical Informatics Association. 2008;15(6):783-786.
27. Cheung K, Yip K, Townsend JP, **Scotch M**. *HCLS 2.0/3.0: Health care and life sciences data mashup using Web 2.0/3.0*. Journal of Biomedical Informatics. 2008;41(5):694-705.
28. **Scotch M**, Parmanto B, Monaco V. *Evaluation of SOVAT: an OLAP-GIS decision support system for community health assessment data analysis*. BMC Medical Informatics and Decision Making. 2008; 8(1):22.
29. Parmanto B, Paramita M, Sugiantara W, Pramana G, **Scotch M**, Burke DS. *Spatial and multidimensional visualization of Indonesia's village health statistics*. International Journal of Health Geographics. 2008; 7:30.
30. **Scotch M**, Parmanto B, Monaco V. *Usability evaluation of the Spatial OLAP Visualization and Analysis Tool (SOVAT)*. Journal of Usability Studies. 2007;2(2):76-95.
31. **Scotch M**, Parmanto B, Gadd CS, Sharma RK. *Exploring the role of GIS during community health assessment problem solving: experiences of public health professionals*. International Journal of Health Geographics. 2006;5:39.

32. **Scotch M**, Parmanto B. *Development of SOVAT: A numerical-spatial decision support system for community health assessment research*. International Journal of Medical Informatics. 2006;75(10-11):771-84.
  33. Parmanto B, **Scotch M**, Ahmad S. *A framework for designing a healthcare outcome data warehouse*. Perspectives in Health Information Management. 2005; 2:3.
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## CONFERENCE PROCEEDINGS

### (Peer Reviewed)

1. **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.
  2. 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.
  3. 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.
  4. 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.
  5. 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.
  6. 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).
  7. **Scotch M**, Parmanto B. *SOVAT: Spatial OLAP Visualization and Analysis Tool* in Proceedings of HICSS-38; 2005;142.2.
  8. Parmanto B, **Scotch M**. *Mining Information from Mountains of Electronic Health Record: Unique Challenges and Solutions* in Proceedings of AHIMA National Convention. 2003.
  9. Stetson, PD, Johnson SB, **Scotch M**, Hripcsak, G. *The Sublanguage of Cross Coverage* in Proceedings of AMIA Fall Symposium. 2002;742-746.
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## CONFERENCE ABSTRACTS

### (Peer Reviewed)

1. Beard R, **Scotch M**. *Identification of zoonotic disease clusters by integrating phylogeography*. AMIA 2015 Joint Summits on Translational Science. San Francisco, CA. 2015.
2. **Scotch M**, Rivera R, Tahsin T, Beard R, Firago M, Weissenbacher D, Wallstrom G, Gonzalez G. *Addressing geospatial observation error for virus phylogeography*. The International Society for Evolution, Medicine, & Public Health Inaugural Meeting. Tempe, AZ. 2015.
3. Magee D, **Scotch M**. *Introducing the generalized linear model to continuous phylogeography: a novel quasi-continuous model*. The International Society for Evolution, Medicine, & Public Health Inaugural Meeting. Tempe, AZ. 2015.
4. Beard R, **Scotch M**. *Identification of zoonotic disease clusters by integrating phylogeography*. The International Society for Evolution, Medicine, & Public Health Inaugural Meeting. Tempe, AZ. 2015.
5. **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*. 12<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference. Aspen, CO. 2014.
6. Beard R, **Scotch M**. *Interpolating Genetic Characteristics of Zoonotic Viruses for Cluster modeling*. 12<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference. Aspen, CO. 2014.
7. Magee D, **Scotch M**. *Comparison of Phylogeographic Node Flux with Local Disease Trends*. 12<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference. Aspen, CO. 2014.
8. 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.
9. Martins S, Tu S, Martinello R, Rubin M, Foulis P, Luther S, Forbush T, **Scotch M**, Doebbellling B, Goldstein MK. *Creating a MRSA Ontology to Support Categorization of MRSA Infections*. AMIA Annual Symposium. Washington, DC. 2013.
10. **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*. 10<sup>th</sup> Annual Rocky Mountain Bioinformatics Conference. Aspen, CO. 2012.
11. **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*. 11<sup>th</sup> International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases, New Orleans, LA. 2012.
12. **Scotch M**, Womack J, Leung S, Brant C. *An NLP Framework for Classifying Contraception Use among US Women Veterans*. AMIA 2012 Joint Summits on Translational Science. San Francisco, CA. 2012.
13. O'Rourke T, Joly DO, Palmer J, Olson S, Manhas M, O'Rourke D, Rabinowitz P, **Scotch M**, Godlstein T, Kreuder Johnson C, Wolking D, Lebreton M, Karesh W, Mazet J. *Data standardization is critical to ensure wildlife health data quality*. 2012 Wildlife Disease Association Conference. Lyon, France.
14. Womack JA, **Scotch M**, Leung S, Brandt C. *Analysis of contraceptive use among female veterans at the VA*. AMIA Joint Summits on Translational Science, San Francisco, CA. 2012.
15. Ortiz P, **Scotch M**, Taylor J. *Use of the Bayesian skyline plot to inform a prediction model of zoonotic infection in animal and human hosts*. AMIA Annual Symposium. Washington, DC. 2011.

16. Singraur A, **Scotch M**. *Integration of disparate genomic sequences for phylogeography of influenza*. AMIA Annual Symposium. Washington, DC. 2011.
17. Konovalov S, **Scotch M**, Brandt C. *An ontology-aware application for military blog analysis*. AMIA Annual Symposium. Washington, DC. 2010.
18. **Scotch M**, Martinello R, Mutalik P, Brandt C. *Use of natural language processing and machine learning for surveillance of MRSA at the VA*. AMIA Annual Symposium. Washington, DC. 2010.
19. Sint K, Rabinowitz P, **Scotch M**. *Human cases and bird outbreaks of avian influenza in Vietnam*. American Public Health Association (APHA) Annual Conference. Denver, CO. 2010.
20. Duggal M, Ebisu K, **Scotch M**, Anderson D, Brandt C, Justice A. *Geographic variation of missed visits among HIV infected veterans*. Society of General Internal Medicine 33rd Annual Meeting. Minneapolis, MN. 2010.
21. Womack J, **Scotch M**, Brandt C, Chapman W, Justice AC. *A comparison of two approaches for identifying negations in radiology reports*. AMIA Annual Symposium. San Francisco, CA. 2009.
22. Duggal M, Ebisu K, **Scotch M**, Brandt C, Cohen D, Skanderson M, Mattocks K, Levin F, Justice AC. *Use of GIS to examine outpatient clinic access at veterans health administration facilities among HIV veterans*. AMIA Annual Symposium. San Francisco, CA. 2009.
23. **Scotch M**, Konovalov S, Rajeevan N, Brandt C, Cheung K. *Using Web 2.0 tools and content mining in clinical and health services research*. Clinical Research Informatics Working Group Expo at AMIA Annual Symposium. San Francisco, CA. 2009.
24. **Scotch M**, Parmanto B. *Combining OLAP and GIS for community health assessments*. MedInfo Conference. San Francisco, CA. 2004.
25. **Scotch M**, Parmanto B, Sharma R, Meit M. *Development of a multidimensional data warehouse for community health assessment*. APHA Annual Meeting. San Francisco, CA. 2003.
26. **Scotch M**, Parmanto B, Sharma R, Meit M. *Constructing a community health database*. Pittsburgh Public Health Association Annual Conference. Pittsburgh, PA. 2003.

## ACTIVE RESEARCH SUPPORT

R01LM012080-01                      Scotch (PI)                                      04/06/2015–03/31/2018

NIH/NLM                                      \$332,295 (\$299,066)\*

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.

Role: PI

ACI 1525012                                      Srinivasan (PI)                                      04/01/2015–03/30/2016

NSF    \$200,000 (\$50,000)

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: Site PI

Regents Innovation Fund Merchant (PI) 05/24/2013–06/20/2015

Arizona Board of Regents \$860,000 (\$16,000)

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

R56AI102559-01A1 Scotch, Gonzalez (PIs) 08/02/2013–07/31/2015

NIH/NIAID \$451,478 (\$180,591)

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.

Role: PI (Multiple Principal Investigators (MPI)

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

NIH/NLM \$1,020,890 (\$153,134)

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

\*Dollar amounts in this section reflect the current total amount of awarded research. The amount in parenthesis reflects the amount of this recognized to Matthew Scotch.

## PRIOR RESEARCH SUPPORT

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

NIH/NLM \$722,862 (\$722,862)\*

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.

Role: PI

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

01/31/2013–12/31/2013 \$40,000 (\$37,796)

Arizona State University/Mayo Clinic

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

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

Role: PI (MPI)

HIR 09-004 Doebbeling (PI) 04/01/2009–09/30/2015  
 VA/HSRD \$1,200,000 (\$144,251)  
 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)

K99LM009825 Scotch (PI) 09/30/2008–09/29/2010  
 NIH/NLM \$180,000 (\$180,000)  
 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.  
 Role: PI

K99LM009825-02S1 Scotch (PI) 10/01/2009–09/30/2010  
 NIH/NLM \$50,000 (\$50,000)  
 Informatics for zoonotic disease surveillance: combining animal and human data  
 ARRA Administrative Supplement to K99 award.  
 Role: PI

HIR 09-007 Goldstein (PI) 08/01/2010–07/31/2011  
 VA/HSRD \$1,021,400 (\$37,000)  
 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)

PREDICT Rabinowitz (PI) 08/01/2011–09/30/2011  
 Yale University \$27,000  
 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)

\*Dollar amounts in this section reflect the total cost of the award and the amount in parenthesis reflects the total amount recognized to Matthew Scotch.

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**PENDING RESEARCH SUPPORT**

VA	Chapman (PI)	10/01/2015–09/30/2018
HSRD/VA	\$9,000	
Integrated NLP Platform for EHR Data Access and Visualization		
The goal of this project is to use visualization and natural language processing techniques to improve patient care at the VA.		
Role: Co-Investigator		
1R01AI117011-01	Scotch, Gonzalez (PIs)	04/01/2015–03/31/2019
NIH/NIAID	\$1,975,000	
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.		
Role: PI (MPI)		
Impact Score (percentile): 28 (20)		
1R01AI117011-01A1	Scotch, Gonzalez (PIs)	12/01/2015–11/30/2019
NIH/NIAID	\$1,970,000	
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.		
Role: PI (MPI)		

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**SERVICE – UNIVERSITY**

2012	Search Committee, Director of Center for Health Information & Research, ASU
2011–2014	Chair of Graduate Admissions, Department of Biomedical Informatics, ASU
2011–2013	Marketing/Media Team, Department of Biomedical Informatics, ASU
2010, 2014–	Member of Graduate Admissions, Department of Biomedical Informatics, ASU
2010–	Academic Programs Committee, Department of Biomedical Informatics, ASU

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**SERVICE – NATIONAL**

2015	Grant Reviewer, National Institute of Allergy and Infectious Diseases (NIAID)/National Institutes of Health (NIH), Development of Novel Therapeutics for Select Pathogens (R21/R3): Influenza, ZAI1 LR-M (M2) 01
2014	Grant Reviewer, National Library of Medicine (NLM)/NIH, Information Resource Grants to Reduce Health Disparities (G08), Special Emphasis Panel, ZLM1 ZH-G
2014	Grant Reviewer, NLM/NIH, Special Emphasis Panel, ZLM1 ZH-C 01
2013–	User Advisory Group, Influenza Research Database/Virus Pathogen Resource, Northrop Grumman/JCVI/Vecna/SAGE Analytica/Los Alamos National Lab

- 2012 Grant Reviewer, NLM/NIH, Information Resource Grants to Reduce Health Disparities (G08), Special Emphasis Panel, ZLM1 ZH-G
- 2012 Grant Reviewer, NIAID/NIH, Bioinformatics Integration Support Contract, Special Emphasis Panel ZAI1 QV-I C1
- 2011 Grant Reviewer, 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
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### **SERVICE – INTERNATIONAL**

- 2015 Grant Reviewer, European Science Foundation, AXA Research Fund Postdoctoral Fellowships
- 2013– Journal Editorial Board Member, *Infection, Genetics and Evolution* (Elsevier)
- 2012 Grant Reviewer, Medical Research Council, London, England
- 2012, 2015 Grant Reviewer, Swiss National Science Foundation
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### **TEACHING EXPERIENCE**

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

### **ONLINE COURSE DEVELOPMENT**

- 2014 Developer, *BMD 502, Foundations of biomedical informatics methods I*, ASU and Dublin City University, Dublin, Ireland
- 2014 Developer, *HCD 501, Health behavior and statistical tools in health environments*, ASU
-

**MENTORSHIP AND ADVISING-ONGOING**

- 2015– Eric Buckland, Masters Thesis Committee Member, *Classification of bladder cancer patients using a marker defined classifier*
- 2015– Marcus Naymik, Masters Thesis Committee Member, *A comparison of obese and lean human epigenetics*
- 2014– Wenzhe Xue, Doctoral Dissertation Committee Member, *A new method for precise, accurate, rapid, and simple tumor volume measurement on cancer therapeutic response*
- 2013– Daniel Magee, Doctoral Dissertation Committee Chair, *Conceptualization, implementation, and validation of a novel quasi-continuous phylogeographic model for RNA viruses*
- 2013– Sen Peng, Doctoral Dissertation Committee Member, *Comprehensive genomic characterization of glioblastoma multiforme*
- 2012– Barrie Bradley, Doctoral Dissertation Committee Chair, *Development of an immunization registry for clinical and public health*
- 2012– Rachel Beard, Doctoral Dissertation Committee Chair, *Integration of geographic information systems and molecular epidemiological techniques into spatial decision support for outbreaks of zoonotic diseases*
- 2012– Azadeh Nikfarjam, Doctoral Dissertation Committee Member, *Semi-supervised concept extraction from social media for post-marketing pharmacovigilance*
- 2012– Laura Wojtulewicz, Doctoral Dissertation Committee Member, *Use of gene pathways on predicting adverse drug reporting*
- 2011– Robert Yao, Doctoral Dissertation Committee Member, *Development of a rule-based computational framework for epilepsy*

**MENTORSHIP AND ADVISING-COMPLETED**

- 2013–2015 Saman Jirjies, Masters Thesis Committee Chair, *Open source implementation of Jacques's Q statistics for space-time clustering in case-control studies*
- 2015 Tasnia Tahsin, BMI 790 Reading and Conference Advisor, *Natural language processing methods for infectious disease surveillance*
- 2015 Rachel Beard, BMI 790 Reading and Conference Advisor, *Integrating molecular epidemiology and spatiotemporal analysis*
- 2015 Daniel Magee, BMI 790 Reading and Conference Advisor, *Statistical distributions and methods*
- 2012–2015 Nima Tajbakhsh, Doctoral Dissertation Committee Member, *Ensuring high-quality colonoscopy by reducing polyp miss-rates*
- 2013–2015 Mari Firago, Masters Thesis Committee Chair, *Exploring genetic diversity as a leading indicator of influenza outbreaks shown by Google flu trends*
- 2014 Neel Mehta, BMI 790 Reading and Conference Advisor (and temporary doctoral dissertation advisor), *Data mining in clinical medicine*
- 2011–2014 Venkata Yellapantula, Doctoral Dissertation Committee Member, *Informatics approaches for integrative analysis of disparate high-throughput genomic datasets in cancer*
- 2014 Emily Crawford, MIC 495 Undergraduate Research, *Sequencing and analysis of human influenza neuraminidase gene*
- 2014 Emily Crawford, MIC 401 Undergraduate Senior Paper, *Surveillance of oseltamivir and zanamivir resistance in influenza A*
- 2012–2014 Aarthi Varman, Masters Thesis Committee Chair, *Identifying climate factors associated with valley fever clusters in Arizona using spatial scan statistics and geographic information systems*

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

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## PRESENTATIONS

- 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*, Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID), 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*, NLM Board of Regents, 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)*, 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

- 2014 Poster Judge, AMIA Annual Conference
- 2012 Session Organizer, *Biomedical informatics to enhance clinical and public health decision making*, SMDM, Phoenix, Arizona
- 2008 Scientific Session Chair, *Tools and systems for infection control*, AMIA Annual Conference

## MANUSCRIPT and BOOK REVIEWS

- Journal, Applied Clinical Informatics
- Journal, BMC Evolutionary Biology
- Journal, BMC Genomics
- Journal, BMC Medical Informatics and Decision Making

Journal, BMC Medical Research Methodology  
Journal, Computer and Electronics in Agriculture  
Journal, Computer Methods and Program in Biomedicine  
Journal, Ecohealth  
Journal, International Journal of Environmental Research and Public Health  
Journal, International Journal of Health Geographics  
Journal, International Journal of Medical Informatics  
Journal, Journal of Biomedical Informatics  
Journal, Journal of Mass Communication & Journalism  
Journal, Journal of Medical Internet Research  
Journal, Journal of the American Medical Informatics Association  
Journal, Medical Care  
Journal, Methods of Information in Medicine  
Journal, Pharmacoepidemiology and Drug Safety  
Journal, PLoS ONE  
Journal, The Science of the Total Environment  
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*