BIOGRAPHICAL SKETCH

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NAME: Grant D. Brown

eRA COMMONS USER NAME (credential, e.g., agency login): GDBROWN1

POSITION TITLE: Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Iowa	B.A.	05/2010	International Studies
University of Iowa	B.S.	05/2010	Statistics
University of Iowa	M.S.	05/2012	Biostatistics
University of Iowa	Ph.D.	05/2015	Biostatistics

A. Personal Statement

In my role as Assistant Professor of Biostatistics at the University of Iowa, I have contributed to a wide range of projects, analyses, and efforts from the institutional level to international collaboration. Both my applied work and methodological research emphasize computational techniques; qualifications include extensive work with Bayesian hierarchical models, spatial statistics, statistical software development, and machine learning. In addition, over the last six years I have mentored numerous MS and MPH students in applied research roles, as well as supervised three PhD students to completion. I continue to advise students in all these roles, as well also to provide guidance to students in other departments and institutions.

Ongoing projects to highlight:

Contract #5881NB90   8/1/95-6/29/22
Iowa Department of Public Health
IDPH FY21 Screening Data Management
PI: Jacob Oleson; Role: Co-Investigator

1 R01 AA0272667-01A1   9/20/19-8/31/24
NIH
Recovery Definitions and Behavior Change Processes in Recovery Outside of Treatment
PI: Paul Gilbert; Role: Co-Investigator

4 R01 TW010500-05   7/20/16-6/30/21

NIH
Epidemic Modelling and Vector Transmission: Study of Leishmaniasis in Peri-Urban Brazil
PI: Jacob Oleson; Role: Co-investigator

Citations:
- Seedorff, N., Brown, G. (2021) totalvis: A Principal Components Approach to Visualizing Total Effects in Black Box Models. SN Computer Science. 2:141. DOI: 10.1007/s42979-021-00560-5. No PMCID.

- Ward C., Brown, G., Oleson, J. (2021) An Individual Level Infectious Disease Model in the Presence of Uncertainty from Multiple, Imperfect Diagnostic Tests. Under revision for Biometrics. No PMCID.
- Han et. al (2020) Key Positions of HIV-1 Env and Signatures of Vaccine Efficacy Show Gradual Reduction of Population Founder Effects at the Clade and Regional Levels. mBio. 11(3): e00126-20. DOI: 10.1128/mBio.00126-20. PMCID: PMC7373194.
- Ozanne, M.V., Oleson, J.J., Brown, G.D. et. al. (2019). Bayesian compartmental model for an infectious disease with dynamic states of infection: analyzing infection due to Leishmania infantum, the protozoan parasite causing Visceral Leishmaniasis in Brazil. Journal of Applied Statistics, 46(6):1043-1065. DOI: 10.1080/02664763.2018.1531979. PMCID: PMC6752225.

B. Positions, Scientific Appointments, and Honors

Positions and Employment

2009-2015	Research Assistant, Center for Public Health Statistics, University of Iowa
2012	Programmer, HOBU Inc.
2013	Team Teacher, Department of Biostatistics, University of Iowa
2013-2014	Statistical Consultant, College of Nursing, University of Iowa
2015-Present	Assistant Professor, Department of Biostatistics, University of Iowa

Professional Memberships

American Statistical Association(ASA)
International Biometric Society (ENAR)

C. Contributions to Science

In my collaborative role as a Biostatistician, I've supported investigations into problems as diverse as public policy impacts on opioid prescription doses and duration, race and gender disparities in alcohol treatment utilization, the population scale evolution of HIV, and evaluating programs designed to reduce antipsychotic prescriptions in elderly populations. For much of my own methodological research, I have focused on a class of techniques known as compartmental epidemic models, which model the complex, spatiotemporal dynamics of infectious disease epidemics by subdividing infectious processes into discrete states (e.g., susceptible, infectious, and removed). In this setting, I have developed a flexible class of spatial models, introduced an empirically adjusted estimator of pathogen reproductive numbers, and developed several statistical software packages. In addition, both in my own work and in supervision of graduate students, I have worked on computational statistics problems, with a particular focus has been on Approximate Bayesian Computing (ABC) techniques. Several of my current and former PhD students have published actively in this area.

- Ward C., Brown, G., Oleson, J. (2021) An Individual Level Infectious Disease Model in the Presence of Uncertainty from Multiple, Imperfect Diagnostic Tests. Under revision for Biometrics. No PMCID.
- Ozanne, M., Brown, G., Toepp, A., et. al. (2019) Bayesian compartmental models and associated reproductive numbers for an infection with multiple transmission modes. Biometrics. 76(3):711-721. DOI: 10.1111/biom.13192. PMCID: PMC7673222.
- Brown, G. D., Porter, A. T., Oleson, J.J., Hinman, J.A. (2017). Approximate Bayesian Computation for Spatial SEIR(S) Epidemic Models. Spat. Spatiotemporal Epidemiol. 42:27-37. DOI: 10.1016/j.sste.2017.11.001. PMCID: PMC5806152.
- Ranapurwala S., Carnahan, R., Brown,G. et.al. (2018). Impact of Iowa's prescription monitoring program on opioid pain reliever prescribing patterns: An interrupted time series study 2003-2014. Pain Medicine. 20(2):290-300. DOI: 10.1093/pm/pny029. No PMCID.

Models for infectious diseases have formed the organizing principal of much of my methodological research as well as the diverse network of collaborations I have developed, even beyond my focus on Bayesian compartmental modelling techniques and their associated computational challenges. This work has led to

domain collaboration in the area of HIV evolution, the zoonotic environment and transmission of visceral leishmaniasis, and efforts to improve Lyme Disease surveillance, among other areas.

- O'Connell et. al. (2021) Maternal transfer of neutralizing antibodies to OspA after oral vaccination of the rodent reservoir. Under review for Journal of Infectious Diseases. DOI: 10.1101/2021.01.27.428441. No PMCID.
- Han et. al (2020) Key Positions of HIV-1 Env and Signatures of Vaccine Efficacy Show Gradual Reduction of Population Founder Effects at the Clade and Regional Levels. mBio. 11(3): e00126-20. DOI: 10.1128/mBio.00126-20. PMCID: PMC7373194.
- Mahachi et. al. (2020) Predominant risk factors for tick-borne co-infections in hunting dogs from the USA. Parasites and Vectors.13(13): 247. DOI: 10.1186/s13071-020-04118-x. No PMCID.
- Toepp et. al. (2019) Comorbid infections induce progression of visceral leishmaniasis. Parasites and Vectors. 12(1):54. DOI: 10.1186/s13071-019-3312-3. PMCID: PMC6345068.

Beyond infectious diseases, I have contributed analyses and methodology to a wide variety of important public health problems. Most recently, I worked with one of my PhD. advisees to develop visualization techniques for black-box machine learning models which can enhance interpretability, as well as provide a basis for causal exploration of complex, nonlinear effects. In addition, I have worked collaboratively with experts in Alcohol Use Disorder to study disparities in treatment service utilization, and have an ongoing collaboration to study the impact of the COVID-19 pandemic on individuals in recovery for alcoholism. I have also contributed to an evaluation of statistical techniques in the speech language and hearing sciences, as well as promoted modern statistical approaches.

- Seedorff, N., Brown, G. (2021) totalvis: A Principal Components Approach to Visualizing Total Effects in Black Box Models. SN Computer Science. 2:141. DOI: 10.1007/s42979-021-00560-5. No PMCID.
- Gilbert. Et. al (2019) Gender Differences in Use of Alcohol Treatment Services and Reasons for Non-Use in a National Sample. Alcoholism Clinical and Experimental Research. 43(4):722-731. DOI: 10.1111/acer.13965. PMCID: 30807660.
- Oleson, J., Brown, G., McCreery, R. (2019) The Evolution of Statistical Methods in Speech, Language, and Hearing Sciences. Journal of Speech, Language and Hearing Research. 62(3):498-506. DOI: 10.1044/2018_JSLHR-H-ASTM-18-0378. PMCID: PMC6802898.
- Polgreen, P.M., Brown, G.D., Hornick, D.B. et. al. (2018) CFTR Heterozygotes Are at Increased Risk of Respiratory Infections: A Population-Based Study. Open Forum Infectious Diseases. 5(11):ofy219. DOI: 10.1093/ofid/ofy219. PMCID: PMC6210382.

As a strong proponent of open source software for reproducible research, I strive to provide working and comprehensive source code with every analysis I perform. I am particularly enthusiastic about R package development, as it provides a user friendly vehicle to encapsulate both methods and data. I have, thus far, written and published a number of general purpose and manuscript specific R packages. Most prominently, I have released ABSEIR, which implements fast and parallel Approximate Bayesian Computing algorithms for spatiotemporal epidemic models, and have used this package to support state-level COVID-19 modelling efforts. In addition, our recent manuscript concerning visualization and interpretation of black-box models is implemented as an open source R package: totalvis.