BIOGRAPHICAL SKETCH

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NAME: Brown, Grant

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

B. Positions 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
International Biometric Society (ENAR)

C. Contribution to Science

The role of a Biostatistician is often that of consultant, and as such many of my contributions to science have been in a supporting role to other researchers. In this capacity I've helped to investigate fields as diverse as public policy impacts on opioid prescription doses and duration, race and gender disparities in alcohol treatment utilization, and evaluating programs designed to reduce antipsychotic prescriptions in elderly populations. For my own methodological research, I have focused on a class of techniques known as compartmental epidemic models, which divide 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. My recent focus has been on approximate Bayesian computing techniques to improve efficiency and accuracy of these models.

- Brown, Grant D, Oleson, Jacob J, Porter, Aaron T. (2015) An empirically adjusted approach to reproductive number estimation for stochastic compartmental models: A case study of two Ebola outbreaks. Biometrics. doi: 10.1111/biom.12432
- 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. doi: 10.1016/j.sste.2017.11.001

- Oleson, Jacob J, Cavanaugh, Joseph E, McMurray, Bob, Brown, Grant. (2015) Detecting time-specific differences between temporal nonlinear curves: Analyzing data from the visual word paradigm. Statistical Methods in Medical Research. doi:10.1177/0962280215607411
- Carnahan, R.M., Brown, G.D., Letuchy, E.M., et. al. (2017) Impact of programs to reduce antipsychotic and anticholinergic use in nursing homes. Alzheimers Dement. doi: 10.1016/j.trci.2017.02.003

Spatial SEIR Models

SEIR models are named for the disease states they define. Individuals in a population are assumed to be either susceptible to a pathogen, exposed to one but not yet infectious, infectious, or removed from the infectious population by mortality or recovery with immunity. My thesis work in this area developed a general spatial parameterization of these models defined for discrete spatial locations such as counties, provinces, farms, and cities. This development enables investigators to explore complex hypotheses about the spatial, temporal, and demographic factors affecting spread of pathogens.

Subsequent methodological work in this area has demonstrated the applicability of both empirical likelihood techniques and approximate Bayesian computation to spatial SEIR models. The former approach has the attractive property of relaxing the assumption that the modeler knows the spatial mixing structure/network through which a disease spreads. The latter family of techniques dramatically reduces the required computation time to fit spatial SEIR models, and provides a natural mechanism to evaluate evidence for particular modes of spread.

I have applied spatial SEIR models and the previously mentioned related techniques to a variety of human diseases. In my thesis work, I addressed two distinct outbreaks of Ebola Virus Disease in Africa, the spread of methicillin resistant Staphylococcus Aureus in Iowa communities, and annual outbreaks of Influenza. I have additionally performed analyses of household smallpox data from Nigeria, as well as the 2010 cholera epidemic in Haiti and the Dominican Republic.

- 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. doi: 10.1016/j.sste.2017.11.001
- Brown, G. D., Oleson, J. J. and Porter, A. T. (2015). An empirically adjusted approach to reproductive number estimation for stochastic compartmental models: a case study of two Ebola outbreaks. Biometrics. DOI: 10.1111/biom.12432
- Ozanne, M.V., Oleson, J.J., Brown, G.D. et. al. (2017). 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. Under review at Stat. Methods Med. Res.
- Brown G. (2015) Application of Heterogeneous Computing Techniques to Compartmental Spatiotemporal Epidemic Models. Thesis Manuscript. http://ir.uiowa.edu/etd/1554/

Reproductive Numbers

The basic reproductive number is a fundamental concept in Epidemiology, and captures the expected number of secondary infections an infectious individual will produce in a completely susceptible population. This measure conveys the likelihood that a particular disease will continue to spread, and is often the target of public health intervention efforts. Despite the obvious utility of such a quantity, implementation and interpretation varies widely between models and analyses, and the usual formulation suffers from limitations which can lead to unrealistic estimates in practice. In order to address this concern, I developed a quantity known as the empirically adjusted reproductive number which better captures reproductive behavior in real populations. Moreover, this work demonstrated that comparisons between adjusted and non-adjusted reproductive numbers can profitably motivate model selection concerns.

- Brown, G. D., Oleson, J. J. and Porter, A. T. (2015). An empirically adjusted approach to reproductive number estimation for stochastic compartmental models: a case study of two Ebola outbreaks. Biometrics. DOI: 10.1111/biom.12432
- Ozanne, M.V., Oleson, J.J., Brown, G.D. et. al. (2017). 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. Under review at Stat. Methods Med. Res.
- 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. doi: 10.1016/j.sste.2017.11.001

Software Development

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 the following four R packages:

The libSpatialSEIR package provides the implementation of spatial SEIR models as described in my thesis work. This R package is written as a mixture of R and C++ code, and employs tuned MCMC sampling techniques to perform Bayesian inference for spatial SEIR and SEIRS models.

EARNMC stands for Empirically-Adjusted-Reproductive-Number-Manuscript-Companion, and provides both code and data to implement all analyses in the associated manuscript. This package uses libSpatialSEIR to perform the analyses, and is focused on reproducible research.

The RcppCAF library was inspired by packages like RcppEigen, which provide additional C++ functionality to package developers. In particular, RcppCAF provides an easy way to call the open source C++ Actor Framework software from C++ code included in an R package. This parallel framework can be used as a simple way to distribute computing work between the cores of a multi-core processor, or as a flexible basis for asynchronous statistical computing algorithms.

ABSEIR efficiently implements Approximate Bayesian Computing techniques for spatial SEIR models, improving upon the SEIR model specification tools first provided by libSpatialSEIR. ABSEIR is faster, easier to use, and more flexible than this previous work.

I have also created and contributed to a number of other open source projects, including laspy, RcppEigen, ncvreg, bigrf, and rCharts.

D. Research Support

Ongoing Research Support

Contract #5889NB90 (PI: Oleson, Jacob) 8/1/95-6/29/22
IDPH FY19 Screening Data Management
Iowa Department of Public Health
Breast and Cervical Cancer Early Detection Program, Data and Entry Analysis; WISEWOMAN Enhanced Design, Data Entry and Analysis; Data Management subcontract. Subcontract studies design, data management, and analysis on this project.
Role: Biostatistician

5 R01 TW010500 (PI: Oleson, Jacob) 7/20/16-6/30/21
Epidemic Modeling Framework for Complex, Multi-Species Disease Processes and the Impact of Vertical and Vector Transmission: A Study of Leishmaniasis in Peri-Urban Brazil
NIH
Despite knowledge of vertical transmission for multiple infectious diseases for at least three-quarters of a century, we do not know how vertical transmission impacts the basic reproductive number (R0) of classically vector-borne infections. In addition, multi-species diseases are likely to persist through both vertical and horizontal transmission, and not enough is known about their collective impact on R0. Vertical transmission of VL was previously discounted, but this EEID collaborative group has demonstrated that vertical transmission maintains endemic canine VL within US hunting hounds (6). We use this unique cohort to measure the infective capacity of vertical transmission in VL. With understanding gained from this study, we will be able to interpret how vertical transmission and horizontal transmission impact R0 separately, and we will quantify their interactive effect on R0.
Role: Co-Investigator

1 P20 NR018081 (PI: Gardner, Sue & Rakel, Barbara) 8/13/18-5/31/23
Center for Advancing Multimorbidity Science: Profiling risk and symptom expression to develop customized therapies for adults with multiple chronic conditions (CAMS)
NIH/NINR
The Center aims to accelerate the realization of precision health by: a) broadening the conceptual model of multimorbidity science to include symptoms/ symptom clusters; b) training new investigators in multimorbidity science and advanced data analytics; and c) mentoring new investigators from pilot projects through the established programs of research in multimorbidity and precision science.
Role: Center Affiliated Faculty

1 R25 HL147231 (PI: Zamba, Gideon) 3/1/19-2/28/22
Iowa Summer Institute for Research Education in Biostatistics (ISIREB)
NIH
This is a proposal to the National Institutes of Health (NIH), National Heart, Lung and Blood Institute (NHLBI), from the University of Iowa, in response to RFA-HL-19-019 for an Iowa Summer Institute for Research Education in Biostatistics (ISIREB), Summer Programs 2019, 2020, & 2021.
Role: Co-Investigator

Completed Research Support

No Contract # (PI: Carnahan, Ryan) 5/1/13-4/30/16
Extension Connection: Advancing Dementia Care for Rural and Hispanic Populations
Patient-Centered Outcomes Research Institute (PCORI)

Role: Co-Investigator

5 R25 HL131467 (PI: Zamba, Gideon) 2/15/16-1/31/19
Iowa Summer Institute for Research Education in Biostatistics
NIH
This is a proposal to the National Institutes of Health (NIH), National Heart, Lung and Blood Institute (NHLBI), from the University of Iowa, in response to RFA-HL-16-017 for a Summer Institute for Research Education in Biostatistics. The ultimate vision of our proposed research education program is to increase the number of undergraduates who enter graduate programs in Biostatistics and to maintain a solid underrepresented minority pipeline into biostatistics graduate programs. The proposal is for the University of Iowa (UI) Department of Biostatistics to recruit a diverse group of 18 trainees each year, from 2016 to 2018, with focus on minority, underrepresented and disadvantaged students who would not have otherwise been exposed to the field of biostatistics.
Role: Co-Investigator

5 R21 AA023878 (PI: Gilbert, Paul) 4/1/16-3/31/18
Factors Responsible for Racial-Gender Disparities in Alcohol Services Use
NIH
Alcohol abuse and dependence are responsible for considerable public health harms; yet, the majority of people with an alcohol use disorder do not receive treatment, and some social groups are less likely than others to receive alcohol services. In addition, there are gender differences. Among those with alcohol use disorders, women are less likely to obtain treatment, more likely to present with comorbid conditions, and remain in treatment for shorter durations than men. Furthermore, gender may exacerbate racial/ethnic disparities. We will identify predisposing, enabling/inhibiting, and need factors associated with alcohol services use. Findings will extend current knowledge about the mechanisms responsible for disparities and may identify leverage points for interventions to increase alcohol services use.
Role: Co-Investigator