BIOGRAPHICAL SKETCH

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NAME: Brunson, Jason Cory

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

POSITION TITLE: Research 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*)	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
Virginia Tech, Blacksburg	B.S.	08/2000	05/2004	Mathematics
Virginia Tech, Blacksburg	B.S.	08/2001	08/2004	Statistics
Virginia Tech, Blacksburg	M.S.	08/2004	05/2005	Mathematics
Virginia Tech, Blacksburg	Ph.D.	08/2005	12/2013	Mathematics
UConn Health, Farmington	Postdoc	06/2014	08/2017	Quantitative Medicine
UConn Health, Farmington	Postdoc	08/2017	04/2020	Network Modeling in Healthcare

A. Personal Statement

I recently completed two postdoctoral fellowships at UConn Health in the Center for Quantitative Medicine (CQM), following my PhD in Mathematics, a research assistantship in social network analysis, and an adjunct professorship. I was first hired in 2014 to train as a data scientist under the supervision of Dr. Reinhard Laubenbacher, and I pursued a variety of projects with different collaborators during this time. In 2017, I was awarded a fellowship with the UConn–NIDCR T90/R90 Research Training Program under Dr. Mina Mina. My project focused on network analysis and modeling of routinely-collected healthcare data sets ("health data").

My research focuses on predictive and exploratory modeling approaches to biomedical problems, in particular using health data. The complexity of these data and of the models trained on them can conspire to impede understanding and interpretation, and by exploiting tools from topology—the mathematical study of continuity, grounded in measures of distance or similarity—we are able in some settings to improve both the accuracy of predictions and the clinical value of the model components. This work in part responds to my previous efforts to synthesize and evaluate network models in systems medicine, which revealed important limitations of conventional approaches. Nevertheless, I maintain an active research program in network science fueled by collaborations with specialists in biological and clinical domains, including cell biology, immunology, and psychology. Most of my work includes a software development component, which has been important to its reproducibility and accessibility to trainees and collaborators as well as other researchers.

Dr. Laubenbacher also introduced me to research mentorship: I supervised four students on a Research Experience for Undergraduates (REU) during my doctoral program, perhaps my most rewarding experience as a PhD student. I continued the project alongside my dissertation, and since completing my degree I have taken every opportunity to involve students in research. At a summer REU at UConn Health, I mentored two students on several predictive modeling experiments using health data. I also initiated CQM's participation in the High School Mentorship Program, through which I mentored four student interns from two area high schools over three summers and helped connect several more with colleagues. These trainees participated in study design, data wrangling, software development, and computational experiments, and presented their work at symposia and conferences as well as coauthored journal articles, software packages, and software tutorials.

This background, in particular using network analysis and health data, has prepared me to design and implement rigorous and robust similarity- and topology-based models as outlined in the proposal. My experience working with medical and health researchers has enabled me to prepare a training plan to bridge my computational work with the specific clinical characteristics and study of COVID-19 and other disease-specific populations. Finally, my mentorship history has provided valuable experience toward organizing a research group oriented toward the aims of the proposal.

1. **J.C. Brunson**, X. Wang, and R.C. Laubenbacher (2017). Effects of research complexity and competition on the incidence and growth of coauthorship in biomedicine, *PLoS One* 12(3): e0173444.

2. **J.C. Brunson** and R.C. Laubenbacher (2018). Applications of network analysis to routinely collected healthcare data: a systematic review, *Journal of the American Medical Informatics Association* 25(2): 210–221.

3. **J.C. Brunson**, T.P. Agresta, and R.C. Laubenbacher (2019). Sensitivity of comorbidity network analysis. *JAMIA Open* 3(1): 94–103.

4. M. Terasaki, **J.C. Brunson**, and J. Sardi (2020). Analysis of the three dimensional structure of the kidney glomerulus capillary network, *Scientific Reports* 10, 20334.

B. Positions and Honors

Positions and Employment

2010–2013	Research Assistant, Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA
2014	Adjunct Professor, Department of Mathematics, Radford University, Radford, VA
2014–2017	Postdoctoral Fellow, Center for Quantitative Medicine, UConn Health, Farmington, CT
2017–2020	Postdoctoral Fellow, Skeletal, Craniofacial & Oral Biology Training Program, UConn Health, Farmington, CT
2020–	Research Assistant Professor, Laboratory for Systems Medicine, University of Florida, Gainesville, FL

Other Experience and Professional Memberships

2014–	Member, Society for Industrial and Applied Mathematics (SIAM)
2015–2020	Founding member, UConn Health–JAX-GM Postdoctoral Association (UJPDA)
2017–2018	President, UJPDA
2018–	Member, American Medical Informatics Association (AMIA)
2019–	Member, American Mathematical Society (AMS)

Professional Service

2010	Mentor, Research Experience for Undergraduates (REU) on Modeling and Simulation in Systems Biology
2015	Co-PI, ACSB 2015: A Conference on Algebraic and Combinatorial Approaches in Systems Biology, (NSF DMS-1503562, PI Vera–Licona)
2015–2017	Postdoc Representative and Negotiating Team Member, University Health Professionals AFT Local 3837 (UHP)
2015–2018	Front Desk & Clinical Support, Hartford Gay and Lesbian Health Collective
2016–	Reviewer, AMIA Annual Symposium
2016–2019	Mentor, High School Student Research Apprentice Program
2017–2020	Poster & digital presentation judge, Medical and Dental Student Research Day
2017	Co-organizer, Postdoc Research Day
2017	Mentor, REU on Modeling and Simulation in Systems Biology
2018	Organizer, Scientific Writing & Editing Support Group
2018–2019	Co-organizer & Matching Coordinator, UConn Health Speed Networking
2019–	Co-supervisor, Mathematics in Medicine Training Program
2019–2020	Editing & formatting, *The Ethical Challenges of the Stem Cell Revolution* (A.R. Chapman)
2019–	Host, "New Books in Mathematics", New Books Network (NBn)

2019	GitHub Coordinator, Medication Reconciliation Hackathon, Office of Health Strategy
2020–	Mentor, Computational Topology, Health Informatics, and Outcomes Research
2021–2022	Board Member, UF Carpentries Club
2021–	Substitute Representative, UF Faculty Council
2021–	Member, Faculty Council Research Task Force

Presentations

2012	"Evolution of the mathematics research collaboration network": Graduate Student Association Research Symposium, Virginia Tech
2012	Lecture series on Schubert calculus, Virginia Bioinformatics Institute
2013	"Caution in interpreting graph-theoretic diagnostics", SIAM Student Seminar
2014	"Surveying the Diagnostic Landscape", Mining Networks and Graphs: A Big Data Analytic Challenge, SIAM International Conference on Data Mining
2014	"Triad census for two-mode networks", SIAM Workshop on Network Science
2014	"Evolving Collaboration Patterns in Medical Research", AMIA Annual Symposium
2015	Tutorial on data analysis and visualization in R, Postdoctoral Seminar, UConn Health
2016	"Scientometrics in Space and Time", CQM Faculty/Staff seminar
2016	"Modulus on graphs as a generalization of standard graph theoretic quantities", Mathematics in Medicine (MiM) Journal Club
2016	"Emerging network methods in healthcare informatics", Connecticut Institute for Clinical and Translational Science (CICATS) methods seminar
2017	"RPKM versus TPM for comparing multiple gene expression across multiple RNA-seq samples", Laubenbacher Group meeting
2017	"Power-law distributions in empirical data", MiM Journal Club + CICATS methods seminar
2017	"Applications of network analysis to routinely collected health care data", CQM presentation, UConn Health
2017	"Modeling Incidence and Severity of Disease using Administrative Healthcare Data", Open Data in Action, Hartford Public Library
2018	"Co-occurrence Networks from Correlation Matrices", CICATS methods seminar
2018	"Conventional versus topological data analysis for disease subtyping: cases of type-2 diabetes mellitus", MiM Journal Club (scheduled)
2018	"Pairwise versus multivariate constructions of co-occurrence networks", SIAM Workshop on Network Science
2018	"Interrogating network models of epidemiological comorbidity", Skeletal, Craniofacial, & Oral Biology Training Program Symposium
2018	"Network analysis to measure disparities in professional healthcare infrastructure", MiM Journal Club
2019	"Network Analyses of Murine Glomeruli", π Day Research Roundtable, UConn
2019	"Network Analyses of Glomerular Capillaries", Biology and Medicine Through Mathematics (BAMM!) Conference, Virginia Commonwealth University
2019	"Network methods in biomedical research: 3 use cases", Postdoc Research Day, UConn Health
2019	"Network methods in biomedical research: 3 use cases", Skeletal, Craniofacial, & Oral Biology Training Program Symposium
2020	"Network analyses of murine glomeruli", SIAM Conference on the Life Sciences (cancelled)
2020	"Network analyses of murine glomeruli", BioMathematics seminar, UF
2021	"Measuring Patient Similarity and Individualizing Predictive Models", Division of Pulmonary, Critical Care, and Sleep Medicine seminar
2021	"Spatial graph analysis of glomerular capillaries", Special Session on Algebra, Combinatorics, and Topology in Biological Structures, AMS Fall Southeastern Sectional Meeting, University of South Alabama (moved online)
2021	"Toward tidy principles for matrix-decomposed data", Joint Statistical Meetings, Washington DC (invited)

C. Contribution to Science

1. *Network science.* As a Research Assistant and mentor, together with a team of undergraduates, I was introduced to network analysis and scientometrics at a summer program organized around systems biology. Our study of the mathematics literature, and a later collaboration focused on biomedicine, combined conventional and original tools to describe global changes in collaboration patterns in both communities over recent decades, and our results have been cited in both follow-up research and several commentaries on scientific practice. I have since kept up an active program of network science, which has involved collaborations with domain experts in immune response and cell biology on original applications of advanced graph theory to modeling cell signaling and capillary development. Network science has also been a major part of my more recent work involving administrative healthcare data, as detailed in the next section.

   a. **J.C. Brunson**, S. Fassino, A. McInnes, M. Narayan, B. Richardson, C. Frank, P. Ion, and R.C. Laubenbacher (2014). Evolutionary events in a mathematical sciences research collaboration network, *Scientometrics* 99(3): 973–998.
   b. **J.C. Brunson**, Triadic analysis of affiliation networks (2015). *Network Science* 3(4): 480–508.
   c. **J.C. Brunson**, X. Wang, and R.C. Laubenbacher (2017). Effects of research complexity and competition on the incidence and growth of coauthorship in biomedicine, *PLoS One* 12(3): e0173444.
   d. M. Terasaki, **J.C. Brunson**, and J. Sardi (2020). Analysis of the three dimensional structure of the kidney glomerulus capillary network, *Scientific Reports* 10, 20334.

2. *Administrative healthcare data.* My appointment at the Center for Quantitative Medicine entailed self-training as a "data scientist"—a combination of statistical literacy, computational programming, and consultancy—with a focus on the modeling and analysis of administrative data sets such as billing claims and electronic health records. One project in this role was a training collaboration with the Office of the State Comptroller of Connecticut, in which I combined pharmacy and insurance claims data provided by the state with publicly available healthcare survey data to describe how several out-of-state compound pharmacies pushed product to patients at exorbitant costs to the state. This project pushed me to adopt reproducible documentation as a research standard, which also proved useful for updating reports as new data became available, and the visualization software I wrote to communicate some results is used by thousands of users each month. I have also been engaged in software development with a pharmacist and medical researcher to expedite comparative effectiveness research using claims databases. Hundreds of validated specifications for index events, outcome measures, eligibility criteria, and covariates have been incorporated into a simple framework to extract and process the necessary data from standardized tables, substantially reducing the research overhead. More recently, I conducted a systematic review of studies that employ network analysis techniques for secondary use of healthcare data. This literature contains myriad projects in diverse domains that in several respects stand to benefit from sharing and combining techniques, and my supervisor and I brought them together into a single reference (and methodological synthesis) we hope will improve collaborations and accelerate advances. One lesson from this review was that the increasingly popular use of "comorbidity networks" suffers from inconsistent methodology and uncertain validity. In response, and with a family physician and health informaticist colleague, we conducted a sensitivity analysis of the comorbidity network construction and several network statistics that have been used to characterize them, which we hope will encourage more consistent and transparent use of this concept in the future.

   a. **J.C. Brunson** and C. Coleman. cerms: Efficient comparative effectiveness research using MarketScan, R package collection, in development. https://bitbucket.org/corybrunson/cerms/
   b. **J.C. Brunson** and R.C. Laubenbacher (2018). Applications of network analysis to routinely collected healthcare data: a systematic review, *Journal of the American Medical Informatics Association* 25(2): 210–221.
   c. **J.C. Brunson**, T.P. Agresta, and R.C. Laubenbacher (2020). Sensitivity of comorbidity network analysis. *JAMIA Open* 3(1): 94–103.
   d. **J.C. Brunson** (2020). ggalluvial: Layered Grammar for Alluvial Plots, *Journal of Open Source Software* 5(49): 2017.

Complete List of Published Work in MyBibliography:

https://www.ncbi.nlm.nih.gov/myncbi/browse/collection/47860258/?sort=date&direction=ascending

D. Research Support

Completed Research Support

508DE021989-07   Mina   07/01/2011–06/30/2021
NIDCR
Skeletal, Craniofacial, and Oral Biology Training Grant
The goal of this proposal is the continuation of the Institutional Training Program in Skeletal, Craniofacial and Oral Biology at the University of Connecticut School of Dental Medicine as a T90/R90 program. It is intended to help meet the substantial need for independent scientists trained in research related to improving oral, dental and craniofacial health in the United States.

Internal   Coleman   02/01/2018–07/31/2018
UConn School of Pharmacy
Developing a User-Friendly R Package Providing Standardized Coding and Analytic Methods for Comparative Effectiveness Research Using Administrative Healthcare Claims Data
We propose developing a user-friendly R package that will enable the building of a functional research database utilizing standardized covariate and outcomes coding and implement analytic methods for comparative effectiveness research using administrative healthcare claims data. Having such a package for the "R Project for Statistical Computing" platform would both reduce the burden on investigators in preparing administrative claims data for research studies and provide greater accountability and interpretability for end users of these real-world studies (including Bayer AG).