
BIOGRAPHICAL SKETCH

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NAME: Brunson, Jason Cory

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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
Virginia Tech, Blacksburg VA	B.S.	05/2004	Mathematics
Virginia Tech, Blacksburg VA	B.S.	08/2004	Statistics
Virginia Tech, Blacksburg VA	M.S.	05/2005	Mathematics
Virginia Tech, Blacksburg VA	Ph.D.	12/2013	Mathematics
UConn Health, Farmington CT	Postdoc	08/2017	Quantitative Medicine
UConn Health, Farmington CT	Postdoc	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”). I have worked at the University of Florida since 2020 as an Assistant Professor, during which time I have initiated collaborations with several colleagues. I arrived at the focus of this proposal through several strong connections within the Division of Pulmonary, Critical Care, and Sleep Medicine.

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 have maintained 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. This proposal comprises a specialization in lung transplant outcomes, which is a field rich with open questions and clinical and biological data suitable for new methodological approaches.

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. At the University of Florida, I am mentoring medical, graduate, and pre-med undergraduate students on projects related to this proposal. 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-based models, drawing from artificial intelligence and machine learning as well as classical statistics, 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 biological, clinical, psychosocial, and informatical characteristics and context of lung transplantation. 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 health-care 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.
5. **J.C. Brunson** (2020). ggalluvial: Layered Grammar for Alluvial Plots, *Journal of Open Source Software* 5(49): 2017.

Ongoing and recently completed projects that I would like to highlight include:

UF CTSI Precision Health Initiative Brunson (PI) 08/01/22–07/31/23

Efficient Modeling of Individualized COVID-19 Mortality Risk

This proposal leverages recent advances in scientific modeling software to more efficiently manage ensembles of individualized models to predict outcomes for COVID-19 patients in Florida and to augment these predictions with individualized risk assessments.

Role: PI

B. Positions, Scientific Appointments, and Honors

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

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** (2015), Triadic analysis of affiliation networks, *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. *Health informatics*. I self-trained at CQM as a data scientist, which entails a combination of statistical literacy, computational programming, and consultancy, with a focus on the pre-processing, analysis, and modeling of administrative healthcare data sets. I conducted a systematic review of studies that use network analysis to study healthcare data, a literature that contains myriad projects in diverse domains. My review synthesized this literature and taxonomized its methods in service to the field, but it also revealed to me that the increasingly popular use of “comorbidity networks” suffers from inconsistent methodology and uncertain validity. In response, and with a physician–informaticist colleague, we conducted a sensitivity analysis of techniques that have been used to study comorbidity networks, which we hope will encourage more consistent and transparent work in future. In addition to my scientific work, I completed a training collaboration with the Office of the State Comptroller of Connecticut, analyzing prescription patterns in claims data as part of an investigation into compound pharmacy fraud, and I collaborated with a pharmacist–scientist to develop a set of software packages to expedite comparative effectiveness research using claims databases.
- a. **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.
 - b. **J.C. Brunson**, T.P. Agresta, and R.C. Laubenbacher (2020). Sensitivity of comorbidity network analysis, *JAMIA Open* 3(1): 94–103.
 - c. **J.C. Brunson** (2020). ggalluvial: Layered Grammar for Alluvial Plots, *Journal of Open Source Software* 5(49): 2017.
3. *Descriptive and predictive modeling*. Since joining the University of Florida (UF), I have begun collaborations with several clinician–researchers, in Psychiatry, Psychology, and Family Medicine as well as in Pulmonary. My work includes some conventional statistical analysis, for example to describe determinants of healthcare worker burnout during the pandemic or to predict post-transplant outcomes among lung recipients, and I use my background in reproducibility to ensure in each case that my analysis is reproducible, auditable, and reusable. I have also worked to bring somewhat niche geometric and topological data analysis techniques into more mainstream use by way of open source software development. My primary methodological project, however, has been to couple an artificial intelligence approach called case-based reasoning into a machine learning framework in order to improve the predictive accuracy of models without cost to their interpretability. We are using these “localized” models to enhance mortality prediction in ICU and cardiac outcomes for COVID-19, using patient data obtained from electronic health records. Several manuscripts are submitted or in preparation, and this approach is the basis for my CTSI Precision Health Initiative pilot award.
- a. A.D. Guastello, **J.C. Brunson**, N. Sambuco, L.P. Dale, N.A. Tracy, B.R. Allen, C.A. Mathews (2022). Predictors of professional burnout and fulfillment in a longitudinal analysis on nurses and healthcare workers in the COVID-19 pandemic, *Journal of Clinical Nursing* Epub ahead of print.
 - b. **J.C. Brunson** and E. Paul (2022). ordr: A ‘tidyverse’ Extension for Ordinations and Biplots, R package version 0.1.0. <https://cran.r-project.org/package=ordr>
 - c. **J.C. Brunson** (2022). individuate: ‘tidymodels’ Extension for Individualized Models, R package version 0.0.1. <https://github.com/corybrunson/individuate>

Complete List of Published Work in MyBibliography:

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