

Jordan Creed

Research Data Analyst II, Department of Biostatistics and Bioinformatics

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Education

2015 B.H.S. (Public Health), University of Florida, Gainesville, FL

2016 M.P.H. (Biostatistics), University of Florida, Gainesville, FL

Academic appointments and employment

2013-2014 Undergraduate Intern, Maru Diagnostic Imaging Services, Tampa, FL

2014 Undergraduate Intern, The Kyle Practice, Belfast, Northern Ireland, UK

2016 Graduate Intern, Department of Biostatistics, H. Lee Moffitt Cancer Center & Research Institute, Tampa, FL

2016-2018 Research Data Analyst I (Bioinformatics), Department of Cancer Epidemiology, H. Lee Moffitt Cancer Center & Research Institute, Tampa, FL

2018- Research Data Analyst II (Bioinformatics), Department of Cancer Epidemiology, H. Lee Moffitt Cancer Center & Research Institute, Tampa, FL

Service

Moffitt Cancer Center

2017 Member, Bioinformatics Interest Meeting

2018- Member, Bio-Data Club

2019- Member, Hackathon Organizing Committee

University of Florida

2013-2015 Member, Health Occupations Students of America

2014-2015 Member, Health Science Students Organization

2014-2016 Secretary, Public Health Students Association

Professional

2017-2018 Co-Organizer, Tampa Bay R Users Group, Tampa, FL

2018- Organizer, Tampa Bay R Users Group, Tampa, FL

2018- Affiliate Member, American Association of Cancer Research (AACR)

2019- Member, R-Ladies Tampa, Tampa, FL

2020- Ad hoc reviewer, American Medical Informatics Association Annual Symposium (x2)

Peer-reviewed publications

1. Miller B, Peeri NC, Nabors LB, **Creed JH**, Thompson ZJ, Rozmeski CM, LaRocca RV, Chowdhary S, Olson JJ, Thompson RC, Egan KM. Handedness and the risk

of glioma. *J Neurooncol.* 2018 May;137(3):639-644. doi: 10.1007/s11060-018-2759-y. Epub 2018 Jan 13. PubMed PMID: 29332185; PubMed Central PMCID: PMC5924459.

2. Peeri NC*, **Creed JH***, Anic GM, Thompson RC, Olson JJ, LaRocca RV, Chowdhary SA, Brockman JD, Gerke TA, Nabors LB, Egan KM (*co-first authors). Toenail selenium, genetic variation in selenoproteins and risk and outcome in glioma. *Cancer Epidemiology* 2018; DOI:10.1016/j.canep.2018.02.002
3. **Creed JH**, Aden-Buie G, Monteiro AN, Gerke TA. epiTAD: a web application for visualizing chromosome conformation capture data in the context of genetic epidemiology. *Bioinformatics* 2019; DOI: 10.1093/bioinformatics/btz387
4. **Creed JH***, Peeri NC*, Anic GM, Thompson RC, Olson JJ, LaRocca RV, Chowdhary SA, Brockman JD, Gerke TA, Nabors LB, Egan KM (*co-first authors). Methylmercury exposure, genetic variation in metabolic enzymes, and the risk of glioma. *Sci Rep* 2019; DOI: 10.1038/s41598-019-47284-4
5. **Creed JH**, Berglund AE, Rounbehler RJ, Awasthi S, Cleveland JL, Park JY, Yamoah K, Gerke TA. Commercial gene expression tests for prostate cancer prognosis provide paradoxical estimates of race-specific risk. *Cancer Epidemiol Biomarkers Prev* 2019; DOI: 10.1158/1055-9965.EPI-19-0407
6. **Creed JH**, Gerke TA, Berglund AE. MatSurv: Survival analysis and visualization in MATLAB. *Journal of Open Source Software* 2020, 5(46), 1830; DOI: 10.21105/joss.01830
7. **Creed JH**, Smith-Warner SA, Gerke TA, Egan KM. A prospective study of coffee and tea consumption and the risk of glioma in the UK Biobank. *Eur J Cancer* 2020; In press.

Preprints

1. **Creed JH**, Monteiro AN, Gerke TA. epiTAD: a web application for visualizing high throughput chromosome conformation capture data in the context of genetic epidemiology. bioRxiv 243840. <https://www.biorxiv.org/content/early/2018/01/05/243840>
2. **Creed JH**, Berglund AE, Rounbehler RJ, Awasthi S, Cleveland JL, Park JY, Gerke TA. Commercial gene expression tests for prostate cancer prognosis provide paradoxical estimates of race-specific risk. bioRxiv 604058. <https://www.biorxiv.org/content/10.1101/604058v1.full>

Manuscripts In Prep

1. **Creed JH**, Nwogu O, Gerke TA. Distribution of effect estimates and p-values estimated from the top medical literature, 2000-2010.

Book Chapters

1. Berglund AE, Putney RM, **Creed JH**, Aden-Buie G, Gerke TA, Rounbehler RJ. Accessible pipeline for translational research using TCGA: Examples of relating gene mechanism to disease specific outcomes. Submitted 2019, In Press

Conference presentations

** denotes oral presentation, – denotes poster presentation*

- **Creed JH**, Chi YY, Chen DT. Interactive analysis of cancer genomics and clinical outcomes for the NanoString nCounter platform. In: Public Health Day: 2016 August; Gainesville, FL.
- **Creed JH**, Gerke T, Monteiro A. EpiTAD Viewer: A Software Application for Visualizing and Contextualizing HI-C Data in Genetic Epidemiology. In: Moffitt Scientific Symposium: 2017 May 4; Tampa, FL. Award: **Population Science Poster Winner**.
- Gerke T, Tyekucheva S, **Creed JH**, Penney KL, Sinnott JA, Ebot E, Berglund AE, Loda M, Stampfer MJ, Kraft P, Parmigiani G, Mucci LA. All happy families are alike: Transcriptomic homogeneity in indolent prostate tumors is a useful prognostic biomarker. In: Prostate Cancer: Advances in Basic, Translational, and Clinical Research (AACR Special Conference): 2017 Dec 2–5; Orlando, FL.
- **Creed JH**, Berglund AE, Yamoah KJ, Gerke TA. Ancestry informative eQTLs in prostate tumor tissue: implications for observed cancer disparities. In: USF Health Research Day: 2018 Feb 23; Tampa, FL.
- Nwogu O, **Creed JH**, Egan KM, Gerke TA. Leveraging eQTL Analysis to Identify Genes Associated with Glioblastoma Multiforme Survival. In: USF Health Research Day: 2018 Feb 23; Tampa, FL.
- Berglund A, Putney R, **Creed J**, Aden-Buie G, Gerke T, Rounbehler R. Accessible pipeline for translational research using TCGA: Tristetraprolin as an example relating gene mechanism to disease specific outcomes. In: TCGA Legacy: Multi-Omic Studies in Cancer: 2018 Sep 27–29; Washington, DC.
- Laajala TD, Aden-Buie G, Gerke T, **Creed J**, Berglund A, Stopsack K, Cramer SD, Tyekucheva S, Aittokallio T, Costello JC. Identifying genetic interactions that drive aggressive prostate cancer using an ensemble of penalized Cox regression models. In: AACR Convergence: Artificial Intelligence, Big Data, and Prediction in Cancer: 2018 Oct 14–17; Newport, RI.
- **Creed JH**, Awasthi S, Yamoah KJ, Gerke TA. Gleason grade progresses in a race-dependent manner. In: 43rd Annual Society of Preventive Oncology Conference: 2019 Mar 10–12; Tampa, FL.
- Awasthi S, **Creed JH**, Williams V, Gerke TA, Yamoah K. Treatment related race disparities in long term survival among very low risk prostate cancer patients. In: 43rd Annual Society of Preventive Oncology Conference: 2019 Mar 10–12; Tampa, FL.
- * **Creed JH**, Berglund AE, Rounbehler RJ, Awasthi S, Cleveland JL, Park JY, Gerke TA. Commercial gene expression tests for prostate cancer prognosis provide paradoxical estimates of race-specific risk. In: AACR Annual Meeting - Factors influencing cancer outcomes minisymposium: 2019 March 29–April 3; Atlanta, GA.
- Awasthi S, **Creed JH**, Asamoah F, Williams VL, Fink AK, Dhillon J, Park J, Gerke TA, Yamoah K. Rethinking early intervention for healthy young men with very low risk prostate cancer; does race matter? In: Moffitt Scientific Symposium: 2019 May 2; Tampa, FL.

– Aden-Buie G, **Creed JH**, Gerke TA. A web application and software package for analysis and exploration of the FCDS Florida Cancer Registry Data. In: Moffitt Scientific Symposium: 2019 May 2; Tampa, FL.

* **Creed JH**, Gerke TA. Global ancestry estimation and data repository for the TCGA pan-cancer resource. In: Moffitt Scientific Symposium: 2019 May 2; Tampa, FL.

– Carvajal R, Gonzalez-Calderon G, Betin-Montes M, Gai-Cherry R, **Creed JH**, Gerke TA, Eschrich S, Berglund A. Patient Timelines for Research-Oriented Exploration of Longitudinal Cancer Patient Data: PT Explorer. In: American Medical Informatics Association (AMIA) 2019 Annual Symposium: 2019 Nov 16–20; Washington, DC. Award: **Distinguished Poster**.

* **Creed JH**, Gerke, TA. mediator: an R package for causal mediation analysis. In: 2020 Statistical Practice in Cancer Conference: 2020 February 28; Tampa, FL.

* **Creed JH**, Shahla B, Aden-Buie G, Yamoah K, Gerke, TA. A framework to reduce analytic complexity for longitudinal data. In: 2020 Moffitt Scientific Symposium: 2020 May 20; Tampa, FL.

Conferences and Workshops

- 2018 Frontiers in Statistics: Data Science across Disciplines. University of South Florida, Tampa, FL. Health Science Chair.
- 2018 Data Analysis Using R. University of South Florida, Tampa, FL. R Meetup Chair
- 2019 Intermediate Shiny Workshop. rstudio::conf January 15–16; Austin, TX.
- 2019 Integrative Molecular Epidemiology: Bridging Cancer Biology and Precision Medicine. AACR July 14–19; Boston, MA.
- 2020 Building Tidy Tools Workshop. rstudio::conf January 27–28; San Francisco, CA.

Presentations and Talks

- 2018 Introduction to Shiny. In: R Meetup Tampa: 2018 March 29; Tampa, FL.
- 2018 Introduction to R. In: Data Analysis Using R: 2018 November 5; Tampa, FL.
- 2018 Improving reproducible research with shiny. In: Data Analysis Using R: 2018 November 9; Tampa, FL.
- 2019 Visualizing genomic data with karyoploteR. In: BioData Club: 2019 June 21; Tampa, FL.
- 2019 Navigating Maps in R. In: R Ladies Tampa: 2019 September 14; Tampa, FL.

Software development

Creed JH, Aden-Buie G, Monteiro AN, Gerke TA. epiTAD: A web application for visualizing high throughput chromosome conformation capture data in the context of genetic epidemiology, <https://apps.gerkelab.com/epiTAD/>. R Shiny Application 2018; latest development version <https://github.com/GerkeLab/epiTAD>.

Creed JH, Gerke TA, Berglund AE. MatSurv: Survival analysis and visualization in MatLab. MatLab package 2019; latest development version <https://github.com/aeberg/MatSurv>.

Creed JH, Aden-Buie G, Gerke TA. ShinyDAG: A web application for building, analyzing, and visualizing directed acyclic graphs (DAGs), <https://apps.gerkelab.com/shinyDAG/>. R Shiny Application 2018; latest development version <https://github.com/GerkeLab/ShinyDAG>.

Creed JH, Aden-Buie G, Gerke TA. mediator: An R package for implementing causal mediation analyses. R package 2019; latest development version <https://github.com/GerkeLab/mediator>.

Support

Date: 10/08/2019
Funding Source: R Consortium
Title: Bad Idea Hackathon 2019
Role: Organizer
Amount: \$200

Awards

2018 rstudio::conf Diversity Scholarship

Other education

Principles of Molecular Medicine : 2017 Aug 21 - Dec 4; Department of Medical Sciences, University of South Florida, Tampa, FL

Applied Bioinformatics : 2017 Aug 22 - Dec 5; Department of Medical Sciences, University of South Florida, Tampa, FL

Genome Data Analysis Course: 2017 Sept 20 - Nov 15; Department of Bioinformatics, Moffitt Cancer Center, Tampa, FL

Special Topics in Statistics : 2018 Jan 17 - May 2; Department of Mathematics and Statistics, University of South Florida, Tampa, FL