

Jordan Creed

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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

- I. 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.
 8. Hernandez-Prera J, Valderrabano P, **Creed J**, Iglesia J, Slebo R, Centeno BA, Tarasova V, Hallanger-Johnson J, Veloski C, Otto KJ, Wenig BM, Yoder S, Lam C, Park DS, Anderson AR, Raghunand N, Berglund A, Caudell J, Gerke TA, Chung CH. Molecular determinants of thyroid nodules with indeterminate cytology and RAS mutations. *Thyroid* 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.
- 2020 Creating R packages. In: BioData Club: 2020 July 17; 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/aebergl/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