Jordan Creed

Data Scientist II, Department of Health Informatics

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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

On-going Education

2020–	PhD student (Epidemiology and Biostatistics), University of South Florida, Tampa, 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
2018–2021	Research Data Analyst II (Bioinformatics), Department of Cancer Epidemiology, H. Lee Moffitt Cancer Center & Research Institute, Tampa, FL
2020–	Graduate Research Assistant, College of Public Health, University of South Florida, Tampa, FL
2021–	Data Scientist II, Department of Health Informatics, H. Lee Moffitt Cancer Center & Research Institute, Tampa, FL
2022–	Data Science Mentor, RStudio Academy

Teaching

2021–	Instructor, BSC6939: Introduction to R Programming, University of South Florida
2022	Teaching Assistant, PHC6051: Biostatistics II, University of South Florida

Service

Moffitt Cancer Center

2017	Member, Bioinformatics Interest Meeting
2018–2020	Member, Bio-Data Club
2019–	Member, Hackathon Organizing Committee
2020–	Co-Organizer, Bio-Data Club

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; DOI: 10.1016/j.ejca.2020.01.012

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; DOI: 10.1089/thy.2019.0650

9. Cote DJ, Smith-Warner SA, **Creed JH**, Furtado J, Gerke TA, Wang M, Kim Y, Stampfer MJ, Egan KM. Circulating lipids and glioma risk: results from the UK

Biobank, Nurses' Health Study, and Health Professionals Follow-Up Study. Cancer Causes & Control 2021; DOI: 10.1007/s10552-021-01391-8

10. Yue Y, **Creed JH**, Cote DJ, Stampfer MJ, Wang M, Midttun O, McCann A, Ueland PM, Furtado J, Egan KM, Smith-Warner SA. Pre-diagnostic circulating concentrations of fat-soluble vitamins and risk of glioma in three cohort studies. SciRep 2021; DOI: 10.1038/s41598-021-88485-0

11. Samanic CM, Cote DJ, **Creed JH**, Stampfer MJ, Wang M, Smith-Warner SA, Egan KM. Prospective study of sleep duration and glioma risk. Cancer Causes Control; DOI: 10.1007/s10552-021-01447-9

12. Cote DJ, **Creed JH**, Samanic CM, Gerke TA, Stampfer MJ, Smith-Warner SA, Egan KM. A prospective study of inflammatory biomarkers and growth factors and risk of glioma in the UK Biobank. Cancer Epidemiology 2021; DOI: 10.1016/j.canep.2021.102043

13. **Creed JH**, Wilson CM, Soupir AC, Colin-Leitzinger CM, Kimmel GJ, Ospina OE, Chakiryan NH, Markowitz J, Peres LC, Coghill A, Fridley BL. spatialTIME and iTIME: R package and Shiny application for visualization and analysis of immunofluorescence data. Bioinformatics 2021; DOI: 10.1093/bioinformatics/btab757

14. Samanic CM, Teer JK, Thompson ZJ, **Creed JH**, Fridley BL, Nabros LB, Williams SL, Egan KM. Mitochondrial DNA sequence variation and risk of glioma. Mitochondrion 2022; DOI: 10.1016/j.mito.2022.01.002

15. Wilson C, Soupir AC, Thapa R, **Creed JH**, Nguyen J, Segura CM, Gerke TA, Schildkraut JM, Peres LC, Fridley BL. Tumor immune cell clustering and its association with survival in African American women with ovarian cancer. PLoS Computational Biology 2022; DOI: 10.1371/journal.pcbi.1009900

16. Awasthi S, Mahal BA, Park JY, **Creed JH**, Williams VL, Elkenawi A, Meadows SO, Pow-Sang JM, Lu-Yao G, Kelly WK, Lang DY, Zgibor J, Rebbeck TR, Yamoah K. Substantial Gleason reclassification in Black men with national comprehensive cancer network low-risk prostate cancer - A propensity score analysis. Prostate Cancer Prostatic Diseases 2022; DOI: 10.1038/s41391-022-00510-z

17. Awasthi S, Grass GD, Torres-Roca J, Johnstone PAS, Pow-Sang J, Dhillon J, Park J, Rounbehler RJ, Davicioni E, Hakansson A, Liu Y, Fink AK, Derenzis A, **Creed JH**, Poch M, Li R, Manley B, Fernandez D, Naghavi A, Gage K, Lu-Yao G, Katsoulakis E, Burri RJ, Leone A, Ercole CE, Palmer JD, Vapiwala N, Deville C, Rebbeck TR, Dicker AP, Kelly W, Yamoah K. Genomic testing in localized prostate cancer can identify subsets of African-Americans with aggressive disease. Journal of the National Cancer Institute September 2022; DOI: 10.1093/jnci/djac162

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. bioRvix 604058. https://www.biorxiv.org/content/10.1101/604058v1.full

3. Wilson C, Thapa R, **Creed JH** Nguyen J, Segura CM, Gerke TA, Schildkraut J, Peres L, Fridley BL. Statistical framework for studying the spatial architecture of the tumor immune microenvironment. medrvix
https://www.medrxiv.org/content/10.1101/2021.04.27.21256104v1

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. In: Markowitz J. (eds) Translational Bioinformatics for Therapeutic Development. Methods in Molecular Biology, vol 2194. Humana, New York, NY, 2021. https://doi.org/10.1007/978-1-0716-0849-4_8

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.

– Samanic C, Teer JK, Thompson ZJ, **Creed JH**, Nabros LB, Williams SL, Egan KM. Mitochondrial DNA Sequence Variation and Risk of Glioma. In: 2020 Society for Neuro-Oncology Annual Meeting.

– Howard R, **Creed JH**, Reisman P, Lewis P, Fellows K, Mason N, Challa C, Kulkarni K, Rollison D. Moffitt Cancer Analytics Platform (MCAP): A Cloud-Based Data Platform for Improved Data Curation, Integration, and Access. In: American Medical Informatics Association (AMIA) 2022 Informatics Summit: 2022 March 21-24; Chicago, IL.

– Hicks JK, **Creed JH**, Howard R, Szepietowski P, Reisman P, Rollison D. Leveraging a Cloud-Based Data Warehouse Coupled with a Precision Medicine Data Mart to Support Scalable Precision Medicine Consultation Services. In: 2022 Clinical Pharmacoge-

netics Implementation Consortium (CPIC) - Pharmacogenomics Global Research Network (PGRN) meeting: Diversifying PGx Science to Improve Implementation: 2022 May 10-12; Aurora, CO.

Certification

2020   Tidyverse Instructor Certification

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 Percision Medicine. AACR July 14 –19; Boston, MA.
2020   Building Tidy Tools Workshop. rstudio::conf January 27–28; San Francisco, CA.
2020   Rstudio Instructor Workshop. RStudio November 2–3; Tampa, FL (virtual Rstudio-led training).
2022   Causal Inference Workshop. rstudio::conf July 25–26; Washington, DC.

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.
2022   Spatial analysis of immune cells from multiplex immunofluorescence using the R package spatialTIME and iTIME Shiny application. In: Statistical Methods in Imaging Conference: 2022 May 25; Nashville, TN.

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.

Creed JH, Thapa R, Wilson C, Fridley B. `spatialTIME`: Spatial Analysis of Vectra Immunoflourescent Data. R package 2021; latest development version https://github.com/FridleyLab/spatialTIME.

Support

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

Awards

2018	rstudio::conf Diversity Scholarship
2020–2022	USF College of Public Health Doctoral Fellowship

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

Snowflake Fundamentals : 2021 May 12 - 13; Tampa, FL (virtual training)