

Sheila M. Gaynor, PhD

BIostatISTICS POSTDOCTORAL FELLOW • NHLBI BIODATA CATALYST FELLOW

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Summary

Biostatistician working at the intersection of statistical genetics and genomics, data science, and statistical computing.

Expertise in data-driven science (*high-dimensional data modeling, large-scale sequencing analyses, functional data integration, genomic networks*), statistics (*mixed models, statistical learning, multivariate analysis*), cross-functional collaboration, and research leadership.

Technical skills including R, WDL, Linux, cluster and cloud computing, GitHub.

Experience

Harvard University

Boston, MA

POSTDOCTORAL FELLOW IN THE DEPARTMENT OF BIostatISTICS

2018 - Present

- Develop cloud-based computational pipelines for large-scale, reproducible rare variant analyses incorporating functional annotations
- Lead rare variant analysis of whole genome sequencing (WGS) data from the Trans-Omics for Precision Medicine (TOPMed) Program to study lung diseases, diabetes and glycemic traits, and inflammation biomarkers
- Develop inferential methods to improve statistical power for rare variant analysis using auxiliary phenotypes and functional data
- Improve fine-mapping methods and applications to identify likely causal genetic variants associated with lung cancer
- Mentor students, serve on thesis committees, prepare grants, and build scientific collaborations

Duke University

Durham, NC

STATISTICAL CONSULTANT FOR THE CENTER FOR TRANSLATIONAL PAIN MEDICINE

2017 - 2020

- Conducted and validated clustering analyses on individuals from multiple cohorts with broad pain phenotyping
- Created clinically-implemented algorithm for pain subtyping to identify patients with increased risk status

Boston University

Boston, MA

VISITING RESEARCHER IN BEHAVIORAL SCIENCE RESEARCH

2015 - 2017

- Led statistical analysis of a cohort study to identify latent classes of smokers not motivated to quit within 30 days
- Executed analysis plan in R and identified three distinct subtypes of unmotivated smokers

McLean Hospital

Belmont, MA

VISITING RESEARCHER IN NEUROBIOLOGY OF FEAR LABORATORY

2015 - 2017

- Performed network and mediation analyses to identify biological mechanisms and mutations characterizing PTSD
- Contributed to book chapter on gene-environment interaction with applications to trauma disorders

Education

Harvard University

Cambridge, MA

PH.D. IN BIostatISTICS, A.M. IN BIostatISTICS

2013 - 2018

- Dissertation entitled "Statistical Methods for Integratively Characterizing Genetic and Genomic Data"
- Co-advised by Dr. Xihong Lin and Dr. John Quackenbush
- Developed statistical methods to perform mediation analysis with common binary outcomes, build and analyze tissue-specific eQTL networks, and detect community structure in regression-based networks

University of North Carolina

Chapel Hill, NC

B.S.P.H. IN BIostatISTICS, B.A. IN MATHEMATICS

2009 - 2013

- With highest honors and highest distinction

Awards

Fellowships

- 2020 **BioData Catalyst Fellowship in Cloud-based Biomedical Research**, NHLBI
- 2017 **F31 Kirschstein Predoctoral Individual National Research Service Award**, NHLBI
- 2013 **National Science Foundation Graduate Research Fellowship**, NSF
- 2013 **T32 NIH HIV/AIDS Training Grant Fellowship**, NIAID

Honors

- 2020 **Rising Star in Computational and Data Science Award**, University of Texas at Austin
2017 **Summer Institute in Statistical Genetics Scholarship**, University of Washington
2017 **Program in Quantitative Genomics Travel Award**, Harvard University
2016 **XSEDE Computation Allocation**, NSF
2016 **Certificate of Distinction in Teaching**, Harvard University Department of Biostatistics

Selected publications

- Gaynor, S.M.**, Fillingim, R.B., Zolnoun, D.A., Slade, G.D., ... & Bair, E. (2021). Association between craniofacial pain and hormonal contraceptive use: The OPPERA study. *Journal of Oral & Facial Pain and Headache*.
- Gaynor, S.M.**, Bortsov, A.V., Bair, E., Fillingim, R.B., ... & Smith, S. (2021). Phenotypic profile clustering pragmatically identifies diagnostically and mechanistically informative subgroups of chronic pain patients. *PAIN*.
- Sun, R., Xu, M., Li, X., **Gaynor, S.**, ... & Lin, X. (2021). Integration of multiomic annotation data to prioritize and characterize inflammation and immune-related risk variants in squamous cell lung cancer. *Genetic epidemiology*, 45(1), 99-114.
- Raffield, L.M., Iyengar, A.K., Wang, B., **Gaynor, S.M.**, ... & Auer, P.L. (2020). Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. *American Journal of Human Genetics*, 106(1), 112-120.
- Li, X.* , Li, Z.* , Zhou, H., **Gaynor, S.M.**, ... & Lin, X. (2020). Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. *Nature genetics*, 52(9), 969-983.
- Gaynor, S.M.***, Sun, R.* , Lin, X. & Quackenbush, J. (2019). Identification of differentially expressed gene sets using the Generalized Berk-Jones statistic. *Bioinformatics*.
- Gaynor, S.M.**, Schwartz, J., & Lin, X. (2019). Mediation analysis for common binary outcomes. *Statistics in Medicine*, 38(4), 512-529.
- Borrelli, B., **Gaynor, S.**, Tooley, E., Armitage, C.J., Wearden, A., & Bartlett, Y.K. (2018). Identification of three different types of smokers who are not motivated to quit: Results from a latent class analysis. *Health Psychology*, 37(2), 179.
- Gaynor, S.**, & Bair, E. (2017). Identification of relevant subtypes via preweighted sparse clustering. *Computational Statistics & Data Analysis*, 116, 139-154.
- Bair, E., **Gaynor, S.**, Slade, G.D., Ohrbach, R., Fillingim, R.B., Greenspan, J.D., ... & Maixner, W. (2016). Identification of clusters of individuals relevant to temporomandibular disorders and other chronic pain conditions: the OPPERA study. *Pain*, 157(6), 1266.

Under Review and Preprints

- Gaynor, S.M.***, DiCorpo, D.* , Westerman, K., Russell, E., ... & Manning, A. Whole Genome Sequence Association Analysis of Fasting Glucose and Fasting Insulin Levels in Diverse Cohorts from the NHLBI TOPMed Program. medRxiv [Preprint]. January 4, 2021. Available from: <https://doi.org/10.1101/2020.12.31.20234310>.
- Li, D., **Gaynor, S.M.**, Quick, C., Chen, J. T., ... & Lin, X. Identifying US Counties with High Cumulative COVID-19 Burden and Their Characteristics. medRxiv [Preprint]. January 12, 2021. Available from: <https://doi.org/10.1101/2020.12.02.20234989>.
- McCaw, Z.R., **Gaynor, S.M.**, Sun, R., and Lin, X. Cross-tissue eQTL Calling via Surrogate Expression Analysis.
- Gaynor, S.M.**, Fagny, M., Lin, X., Platig, J., Quackenbush, J. Connectivity of variants in eQTL networks dictates reproducibility and functionality. bioRxiv 515551 [Preprint]. January 9, 2019. Available from: <https://doi.org/10.1101/515551>.
- Gaynor, S.M.**, Lin, X., Quackenbush, J. Spectral clustering in regression-based biological networks. bioRxiv 651950 [Preprint]. May 27, 2019. Available from: <https://doi.org/10.1101/651950>.