

Sheila M. Gaynor

BIostatISTICS POSTDOCTORAL FELLOW

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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

Experience

Harvard University

Boston, MA

POSTDOCTORAL FELLOW IN THE DEPARTMENT OF BIostatISTICS

2018 - Present

- 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
- Fine-map genetic loci associated with lung cancer to identify likely causal genetic variants
- Transition to independent research by mentoring students, preparing grants, and building scientific collaborations

Duke University

Durham, NC

STATISTICAL CONSULTANT FOR THE CENTER FOR TRANSLATIONAL PAIN MEDICINE

2017 - Present

- Conduct and validate clustering analyses on individuals from multiple cohorts with broad pain phenotyping
- Create 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 who are 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 on the Grady Trauma Project to identify biological mechanisms and mutations to better biologically characterize post-traumatic stress disorder
- Contributed to book chapter on gene-environment interaction with applications to trauma and stress-related disorders

Harvard University

Boston, MA

ROTATION STUDENT IN THE DEPARTMENT OF BIOMEDICAL INFORMATICS PARK LAB

2014

- Implemented open-source bioinformatics tools across programming languages to call copy number variants
- Compared copy number calls between array and sequencing data from The Cancer Genome Atlas (TCGA)

University of North Carolina

Chapel Hill, NC

HONORS UNDERGRADUATE RESEARCHER IN THE DEPARTMENT OF BIostatISTICS

2011-2013

- Developed sparse clustering method to identify secondary clusters in data with high-variance features or clusters associated with an outcome of interest in supervised settings
- Classified clinically-relevant subtypes of temporomandibular disorder based on anatomical and etiological criteria

University of North Carolina

Chapel Hill, NC

SUMMER UNDERGRADUATE RESEARCH FELLOW IN THE DEPARTMENT OF BIostatISTICS

2012

- Evaluated the association between hormonal contraceptive use and pain conditions in a multi-site cohort study

Washington University in St. Louis

St. Louis, MO

STATISTICAL CONSULTANT & INTERN FOR THE SCHOOL OF MEDICINE OUTCOMES RESEARCH OFFICE

2010-2011

- Generated prognostic models and nomograms for cancer survival in hospital databanks
- Compared chart-based and claims-based comorbidity scoring methods across institutions for individuals with cancer

Awards

Fellowships

- 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
- 2012 **Summer Undergraduate Research Fellowship**, UNC

Honors

- 2017 **Program in Quantitative Genomics Travel Award**, Harvard University Department of Biostatistics
- 2016 **XSEDE Computation Allocation**, NSF
- 2016 **Certificate of Distinction in Teaching**, Harvard University Department of Biostatistics
- 2013 **Delta Omega Undergraduate Award**, Delta Omega Public Health Honors Society
- 2013 **Carolina Research Scholar**, UNC Office of Undergraduate Research
- 2013 **Buckley Public Service Scholar**, UNC Carolina Center for Public Service
- 2012 **Phi Beta Kappa**, University of North Carolina

Publications

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.

Kalogjeri, D., **Gaynor, S. M.**, Piccirillo, M. L., Jean, R. A., Spitznagel, E. L., & Piccirillo, J. F. (2014). Comparison of comorbidity collection methods. *Journal of the American College of Surgeons*, 219(2), 245-255.

Under Review

Gaynor, S.M., Fillingim, R.B., Zolnoun, D.A., Slade, G.D., Ohrbach, R., Greenspan, J.D., Maixner, W., Bair, E. Association between craniofacial pain and hormonal contraceptive use: The OPPERA study.

Sun, R.*, Xu, M.*, Li, X., **Gaynor, S.M.**, ... & Lin, X. Identification of inflammation and immune-related risk variants associated with squamous cell lung cancer.

Li, X.*, Li, Z.*, Zhou, H., **Gaynor, S.M.**, ... & Lin, X. Dynamic incorporation of multiple in-silico functional annotations empowers rare variant association analysis of large whole genome sequencing studies at scale.

Preprints

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>.

Book Chapters

Klengel, T., Lebois, L.A.M., **Gaynor, S.M.**, Guffanti, G. (2018). Genetics and Gene-Environment Interaction. In Stoddard Jr, F.J., Benedek, D.M., Milad, M.R., & Ursano, R. J. (Eds.). *Trauma-and stressor-related disorders*. Oxford University Press. (198-210).

Professional Involvement

2019	Mentor of Undergraduate Independent Study , Harvard University Department of Biostatistics
2018-2019	Co-mentor of Master's Research Assistant , Harvard University Department of Biostatistics
2012-2019	Member , ENAR Section of the International Biometrics Society
2018	Co-mentor & Master's Thesis Committee Member , Harvard University Department of Biostatistics
2017-2018	Member , Harvard Biostatistics Colloquium Committee
2016-2018	Co-organizer , Harvard Biostatistics-Biomedical Informatics Big Data Seminar
2017	Graduate Mentor , Harvard Summer Program in Biostatistics & Computational Biology
2015-2017	Member , Harvard Biostatistics Student Advising Committee
2016	Graduate Participant , International High Performance Computing Summer School
2015-2016	Organizer & Coordinator , Harvard Big Data Seminar
2015	Chair , ENAR Session on Graphical Modeling
2014	Judge , Harvard School of Public Health Poster Day

Presentations

ORAL PRESENTATIONS

- *Framingham Heart Study FOCuS Seminar Series*, 2019. Dynamic incorporation of functional annotations in rare variant analysis.
- *NHLBI TOPMed In-Person Meeting*, 2019. Identification of rare variant sets associated with lung function via set-based analyses incorporating in-silico functional annotations.
- *Joint Statistical Meetings*, 2018. Degree centrality of SNPs in eQTL networks.
- *ENAR Spring Meeting*, 2017. Error quantification in biologically relevant eQTL network metrics.
- *Massachusetts General Hospital Trauma Genomics Group*, 2017. Mediation analysis of pathways to PTSD diagnosis.
- *Broad Institute Statistical Genetics Seminar*, 2017. Causal mediation analysis for genomic data.
- *Biostatistics Student Seminar*, 2016. Graduate Research Fellowships.
- *Joint Statistical Meetings*, 2016. Genomic analysis with common binary outcomes via mediation.
- *ENAR Spring Meeting*, 2016. Mediation methods for case-control settings with applications to genomics.
- *Harvard Medical School Epigenetics Symposium*, 2015. Integrating epigenetic and genomic analyses via mediation analysis.
- *Joint Statistical Meetings*, 2015. Mediation-based integrative genomic analysis.
- *Biostatistics Student Seminar*, 2015. A mediation-based integrative genomic analysis of lung cancer.
- *ENAR Spring Meeting*, 2015. Mediation-based integrative genomic analysis.
- *International Association for Dental Research Epi-Forum*, 2015. Prewighted sparse clustering with applications to temporomandibular disorder.
- *ENAR Spring Meeting*, 2014. Identification of biologically relevant subtypes via preweighted sparse clustering.

POSTER PRESENTATIONS

- *ENAR Spring Meeting*, 2018. Assessing the Effective Degree of SNPs in eQTL Networks. Oral poster.
- *American Society for Human Genetics Annual Meeting*, 2016. Mediation methods applied to post-traumatic stress disorder to identify genomic effects.
- *Harvard Graduate Women in Science and Engineering Symposium*, 2015. A mediation-based integrative genomic analysis of lung cancer.
- *UNC Celebration of Undergraduate Research*, 2013. The association between oral contraceptive use and painful conditions.
- *International Pelvic Pain Society Conference*, 2012. OPFERA Study Identifies an Association Between the Use of Hormonal Contraceptives and Orofacial Pain and Headaches. Prepared poster, First place in poster competition.
- *ENAR Spring Meeting*, 2012. Identification of clinically relevant disease subtypes using supervised sparse clustering.

Teaching

2017	Teaching Assistant, ID 201: Principles of Biostatistics and Epidemiology , Harvard University Department of Biostatistics
2016	Director of Independent Study in Biostatistics , Harvard University Department of Biostatistics
2015-2016	Biostatistics and Epidemiology Program Tutor , Harvard University Commonwealth Fund Fellowship in Minority Health Policy
2015	Founding Head Teaching Assistant, ID 201: Principles of Biostatistics and Epidemiology , Harvard University Department of Biostatistics
2014	Teaching Assistant, BIO 200: Principles of Biostatistics , Harvard University Commonwealth Fund Fellowship in Minority Health Policy