

# Sheila M. Gaynor

## BIostatISTICS POSTDOCTORAL FELLOW

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## Education

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### 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

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### 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

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### 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

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**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

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

## Presentations

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### 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

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