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 titled "Statistical Methods for Integratively Characterizing Genetic and Genomic Data" Co-advised by Dr. Xihong Lin and Dr. John Quackenbush **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** Cambridge, MA POSTDOCTORAL FELLOW 2018 - Present Develop methods for whole genome sequencing and multi-omics data Analyze massive whole genome sequencing data from the TOPMed study Durham, NC **Duke University** STATISTICAL CONSULTANT FOR THE CENTER FOR TRANSLATIONAL PAIN MEDICINE 2017 - Present Conduct clustering analyses on individuals from multiple cohorts with pain phenotyping • Perform descriptive analyses on cohort studies across different pain conditions **Boston University** Boston, MA VISITING RESEARCHER IN BEHAVIORAL SCIENCE RESEARCH 2015 - 2017 • Led statistical analysis of identifying latent classes of smokers unmotivated to quit from a cohort study • 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 PTSD studies • Contributed to book chapter on gene-environment interaction **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 statistical methods for complementary and supervised clustering Analyzed subtypes of temporomandibular disorder **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 **Washington University in St. Louis** St. Louis, MO

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2010-2011

STATISTICAL CONSULTANT & INTERN FOR THE OUTCOMES RESEARCH OFFICE

• Performed prognostic modeling of cancer survival in hospital databanks

Evaluated 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., Schwartz, J., & Lin, X. (2018). Mediation analysis for common binary outcomes. Statistics in Medicine.

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.

Kallogjeri, 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.

Submitted

Gaynor, S. M.*, Sun, R.*, Lin, X, & Quackenbush, J. Identification of differentially expressed gene sets using the Generalized Berk-Jones statistic.

Gaynor, S.M., Fillingim, RB., Zolnoun, DA., Slade, GD., Ohrbach, R., Greenspan, JD., Maixner, W., Bair, E. Association between craniofacial pain and hormonal contraceptive use: The OPPERA study.

Sun, R.*, Xu, M.*, Li, X., **Gaynor, S.M.**, Zhou, H., Bosse, Y., Lam, S., Tsao, MS., Tardon, A., Chen, C., Doherty, J., Goodman, G., Bojesen, SE., Landi, MT., Johansson, M., Field, JK., Bickelboller, H., Wichmann, HE., Risch, A., Rennert, G., Arnold, S., Wu, X., Melander, O., Brunnstrom, H., Marchand, LL., Liu, G., Andrew, A., Duell, E., Kiemeney, LA., Shen, H., Haugen, A., Johansson, M., Grankvist, K., Caporaso, N., Woll, P., Teare, MD., Scelo, G., H, YC., Y, JM., Lazarus, P., Schabath, MB., Aldrich, MC., Albanes, D., Mak, R., Barbie, D., Brennan, P., Hung, RJ., Amos, Cl., Christiani, DC., Lin, X. Identification of Inflammation and Immune-Related Risk Variants Associated with Squamous Cell Lung Cancer.

Professional Involvement

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
2017	Graduate Mentor, Harvard Summer Program in Biostatistics & Computational Biology
2016-2018	Co-organizer, Harvard Biostatistics-Biomedical Informatics Big Data Seminar
2015-2017	Member, Harvard Biostatistics Student Advising Committee
2015-2016	Organizer & Coordinator, Harvard Big Data Seminar
2015	Chair, ENAR Session on Graphical Modeling
2014	Judge, Harvard School of Public Health Poster Day

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Presentations

ORAL PRESENTATIONS

- 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. Preweighted 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
- UNC Celebration of Undergraduate Research, 2013. The association between oral contraceptive use and painful conditions.
- International Pelvic Pain Society Conference, 2012. OPPERA 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

· Led weekly lab sessions and graded homework

Harvard University Department of Biostatistics Boston, MA TEACHING ASSISTANT, ID 201: PRINCIPLES OF BIOSTATISTICS AND EPIDEMIOLOGY 2017 Led weekly lab sessions and graded homework **Harvard University Department of Biostatistics** Boston, MA HEAD TEACHING ASSISTANT, ID 201: PRINCIPLES OF BIOSTATISTICS AND EPIDEMIOLOGY 2015 Developed new lab sessions and homework assignments for new course Managed teaching staff of six biostatistics teaching assistants Led weekly lab sessions and graded homework **Harvard University Department of Biostatistics** Boston, MA INDEPENDENT STUDY IN BIOSTATISTICS DIRECTOR 2016 • Met weekly to teach and review topics in introductory biostatistics Conducted assessments and evaluated student progress Harvard University Commonwealth Fund Fellowship in Minority Health Policy Boston, MA BIOSTATISTICS AND EPIDEMIOLOGY PROGRAM TUTOR 2015-2016 Reviewed and instructed on course materials • Guided problem sessions and assisted in assignment and test preparation **Harvard University Department of Biostatistics** Boston, MA TEACHING ASSISTANT, BIO 200: PRINCIPLES OF BIOSTATISTICS 2014

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