

Sheila M. Gaynor

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EDUCATION

Harvard University

Ph.D. in Biostatistics, May 2018

- Dissertation Title: “Statistical Methods for Integratively Characterizing Genetic and Genomic Data”
- Advisors: Dr. John Quackenbush and Dr. Xihong Lin

A.M. in Biostatistics, May 2015

08/2013-05/2018

Cambridge, MA

University of North Carolina at Chapel Hill

B.S.P.H in Biostatistics and B.A. in Mathematics, May 2013

- Honors Thesis Title: “Identification of Biologically Relevant Subtypes via Preweighted Sparse Clustering”
- With highest honors and highest distinction

08/2009-05/2013

Chapel Hill, NC

ACADEMIC APPOINTMENT

Harvard T.H. Chan School of Public Health

Postdoctoral Fellow, Department of Biostatistics

- Fellowship with Dr. Xihong Lin
- Develop statistical and computational methods to analyze whole genome sequencing, genomic, and clinical data
- Collaborate on large-scale studies including the NHLBI Trans-Omics for Precision Medicine (TOPMed) Program
- Focus on rare variant, fine mapping, and functional annotation methods and applications

06/2018-Present

Boston, MA

EXPERIENCE

Center for Translational Pain Medicine, Duke University

Statistical Consultant

Analysis of patients with pain phenotyping and development of clinically-implemented algorithm of pain subtyping

2017-Present

Durham, NC

Behavioral Science Research, Boston University

Visiting Researcher

Modeled a study of smokers unmotivated to quit using latent class analysis

2015-2017

Boston, MA

Neurobiology of Fear Laboratory, McLean Hospital

Visiting Researcher

Analyzed a study of post-traumatic stress disorder using network and mediation analysis

2015-2018

Belmont, MA

Department of Biomedical Informatics, Harvard University

Rotation Student

Implemented bioinformatics tools to call copy number variants in The Cancer Genome Atlas (TCGA)

2014

Boston, MA

Department of Biostatistics, University of North Carolina

Honors Undergraduate Researcher

Developed sparse clustering method for data with high-variance features or an outcome in supervised settings

2011-2013

Chapel Hill, NC

Department of Biostatistics, University of North Carolina

Summer Undergraduate Research Fellow

Analyzed the association between hormonal contraceptive use and pain conditions

2012

Chapel Hill, NC

Outcome Research Office, Washington University in St. Louis	2010-2011
Statistical Consultant and Intern	St. Louis, MO
<i>Investigated comorbidity scoring methods and prognostic models for cancer survival in hospital biobanks</i>	

Department of Biostatistics, Washington University in St. Louis	2010
Summer Institute for Training in Biostatistics Trainee	St. Louis, MO
<i>Learned and applied principles of applied biostatistics</i>	

FELLOWSHIPS AND GRANTS

Awarded

NIH F31 Kirschstein Predoctoral Individual National Research Service Award	09/17-05/18
NIH/NHLBI HL138832	
<ul style="list-style-type: none"> • <i>Integrative analysis of lung disease genotypes and gene expression</i> • Goal: To develop statistical methods and open source tools for jointly analyzing genetic and genomic data to understand the genetic basis of lung diseases 	

NSF Graduate Research Fellowship	08/13-05/18
NSF DGE1144152, DGE1745303	
<ul style="list-style-type: none"> • <i>Graduate Research Fellowship Program in Mathematical Sciences - Biostatistics</i> • Goal: To obtain training in biostatistical theory, methods, and computation and support doctoral research 	

Under Review

K99/R00 Pathway to Independence Award	Submitted 03/20
NIH/NHLBI	
<ul style="list-style-type: none"> • <i>Statistical methods to integrate rich functional and phenotypic data in whole genome sequencing analyses</i> • Goal: To develop statistical and computational methods for massive whole genome sequencing data and transition to independent research 	

HONORS AND AWARDS

2020	Rising Star in Computational and Data Science Award, University of Texas at Austin
2017	Summer Institute in Statistical Genetics Scholarship, University of Washington Department of Biostatistics
2017	Program in Quantitative Genomics Travel Award, Harvard T.H. Chan School of Public Health
2016	XSEDE Computation Allocation, NSF
2016	Certificate of Distinction in Teaching, Harvard University Department of Biostatistics
2013	T32 NIH HIV/AIDS Training Grant Fellowship, NIAID
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
2012	Summer Undergraduate Research Fellowship, University of North Carolina

PUBLICATIONS

Peer-Reviewed

1. Kallogjeri, D., **Gaynor, S.M.**, Piccirillo, M.L., Jean, R.A., Spitznagel Jr, E.L., & Piccirillo, J.F. (2014). Comparison of comorbidity collection methods. *Journal of the American College of Surgeons*, 219(2), 245-255.
2. Bair, E., **Gaynor, S.**, Slade, G.D., Ohrbach, R., Fillingim, R.B., Greenspan, J.D., Dubner, R., Smith, S.B., Diatchenko, L., and Maixner, W. (2016). Identification of clusters of individuals relevant to temporomandibular disorders and other chronic pain conditions: the OPPERA study. *Pain*, 157(6), 1266.

3. **Gaynor, S.**, and Bair, E. (2017). Identification of relevant subtypes via preweighted sparse clustering. *Computational Statistics and Data Analysis*, 116, 139-154.
4. 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.
5. **Gaynor, S.M.**, Schwartz, J., and Lin, X. (2019). Mediation analysis for common binary outcomes. *Statistics in Medicine*, 38(4), 512-529.
6. **Gaynor, S.M.***, Sun, R.*, Lin, X., and Quackenbush, J. (2019). Identification of differentially expressed gene sets using the Generalized Berk-Jones statistic. *Bioinformatics*.
7. Raffield, L.M., Iyengar, A.K., Wang, B., **Gaynor, S.M.**, Spracklen, C.N., Kowalski, M.H., Salimi, S., Polfus, L.M., Benjamin, E.J., Bis, J.C., Bowler, R., Cade, B.E., Comellas, A.P., Correa, A., Durda, P., Gogarten, S., Jain, D., Kral, B.G., Lange, L.A., Larson, M.G., Laurie, C., Lee, J., Lewis, J.P., Mitchell, B., Pankratz, N., Rich, S.S., Rotter, J.I., Ryan, K., Tracy, R.P., Yanek, L.R., Zhao, L.P., Lin, X., Li, Y., Dupuis, J., Reiner, A.P., Mohlke, K.L., Auer, P.L., TOPMed Inflammation Working Group, and NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium. Allelic heterogeneity at CRP locus identified by whole-genome sequencing in multi-ancestry cohorts. *To appear, American Journal of Human Genetics*.
8. **Gaynor, S.M.**, Fillingim, R.B., Zolnoun, D.A., Slade, G.D., Ohrbach, R., Greenspan, J.D., Maixner, W., and Bair, E. Association between craniofacial pain and hormonal contraceptive use: The OPPERA study. *To appear, Journal of Oral Facial Pain and Headache*.
9. Sun, R., Xu, M., Li, X., **Gaynor, S.M.**, Zhou, H., Bosse, Y., Lam, S., Tsao, M., Tardon, A., Chen, C., Doherty, J., Goodman, G., Egil Bojesen, S., Teresa, M.T., Johansson, M., Field, J.K., Bickeboller, H., Wichmann, H., Risch, A., Rennert, G., Arnold, S., Wu, X., Melander, O., Brunnstrom, H., Marchand, L.L., Zong, X., Liu, G., Andrew, A., Duell, E., Kiemeny, L.A., Shen, H., Haugen, A., Johansson, M., Grankvist, K., Caporaso, N., Woll, P., Teare, M.D., Scelo, G., Hong, Y., Yuan, J., Lazarus, P., Schabath, M.B., Aldrich, M.C., Albanes, D., Brennan, P., Barbie, D., Mak, R., Hung, R.J., Amos, C.I., Christiani, D.C and Lin, X. Identification of inflammation and immune-related risk variants associated with squamous cell lung cancer. *To appear, Genetic Epidemiology*.
10. Li, X.*, Li, Z.*, Zhou, H., **Gaynor, S.M.**, Liu, Y., Chen, H., Sun, R., Dey, R., Arnett, D.K., Aslibekyan, S., Ballantyne, C.M., Bielak, L.F., Blangero, J., Boerwinkle, E., Bowden, D.W., Broome, J.G., Conomos, M.P., Correa, A., Curran, J.E., Cupples, L.A., Freedman, B.I., Guo, X., Kardia, S.L.R., Kathiresan, S., Khan, A.T., Kooperberg, C.L., Irvin, M.R., Laurie, C.C., Manichaikul, A.W., Mahaney, M.C., Mathias, R.A., Morrison, A.C., Martin, L.W., McGarvey, S.T., Mitchell, B.D., Montasser, M.E., Moore, J., O'Connell, J.R., Palmer, N.D., Pampuna, A., Peralta, J.M., Peyser, P.A., Psaty, B.M., Vasan, R.S., Redline, S., Rice, K.M., Rich, S.S., Smith, J.A., Tsai, M., Tiwari, H.K., Wang, F.F., Weeks, D.E., Weng, Z., Wilson, J.G., Yanek, L.R., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Lipids Working Group, Neale, B.M., Sunyaev, S.R., Abecasis, G.R., Rotter, J.I., Willer, C.J., Peloso G.M., Natarajan, P., and Lin, X. Dynamic incorporation of multiple in-silico functional annotations empowers rare variant association analysis of large whole genome sequencing studies at scale. *To appear, Nature Genetics*.

Submitted and Preprints

1. **Gaynor, S.M.**, Fagny, M., Lin, X., Platig, J., and Quackenbush, J. Connectivity of variants in eQTL networks dictates reproducibility and functionality. bioRxiv 515551 [Preprint].
2. **Gaynor, S.M.**, Lin, X., and Quackenbush, J. Spectral clustering in regression-based biological networks. bioRxiv 651950 [Preprint].
3. **Gaynor, S.M.**, Bortsov, A., Maixner, W., and Smith, S.B. Pragmatic patient profile clustering identifies diagnostically and prognostically informative subgroups.
4. McCaw, Z.R., **Gaynor, S.M.**, Sun, R., and Lin, X. Cross-tissue eQTL Calling via Surrogate Expression Analysis.

5. Li, D., **Gaynor, S.M.**, Quick, C., Chen, J.T., Stephenson, B.J.K, Coull, B.A., and Lin, X. Unraveling US National COVID-19 Racial/Ethnic Disparities using County Level Data Among 328 Million Americans.

* Indicates equal contribution as first authors

Book Chapters

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

EDUCATIONAL CONTRIBUTIONS

Teaching

2017	Teaching Assistant, ID 201: Principles of Biostatistics and Epidemiology, Harvard University Department of Biostatistics
2017	Guest Lecturer, BST 254: Effective Grant & Research Proposal Writing for Biostatistics Research, 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
2015	Guest Lecturer, ID 201: Principles of Biostatistics and Epidemiology, Harvard University Department of Biostatistics
2014	Teaching Assistant, BIO 200: Principles of Biostatistics, Harvard University Department of Biostatistics

Advising and Mentorship

2019	Claire Tseng, <i>Undergraduate Independent Study, Biostatistics, Harvard University</i>
2018-2019	Wenying Deng, <i>Master's Research Assistantship, Biostatistics, Harvard University</i>
2018	Mengting Li, <i>Master's Thesis Committee, Biostatistics, Harvard University</i>
2017	<i>Graduate Mentor, Harvard Summer Program in Biostatistics & Computational Biology</i>

PRESENTATIONS

Oral Presentations

06/2019 Dynamic incorporation of functional annotations in rare variant analysis. *Framingham Heart Study FOCuS Seminar Series*.

04/2019 Identification of rare variant sets associated with lung function via set-based analyses incorporating in-silico functional annotations. *NHLBI TOPMed In-Person Meeting*.

07/2018 Degree centrality of SNPs in eQTL networks. *Joint Statistical Meetings*.

04/2017 Reframing eQTL Networks to account for intermediate analyses. *Biostatistics Student Seminar*.

03/2017 Error quantification in biologically relevant eQTL network metrics. *ENAR Spring Meeting*.

03/2017 Mediation analysis of pathways to PTSD diagnosis. *Massachusetts General Hospital Trauma Genomics Group*.

02/2017 Causal mediation analysis for genomic data. *Broad Institute Statistical Genetics Seminar*.

10/2016 Graduate Research Fellowships. *Biostatistics Student Seminar*.

07/2016 Genomic analysis with common binary outcomes via mediation. *Joint Statistical Meetings*.

03/2016 Mediation methods for case-control settings with applications to genomics. *ENAR Spring Meeting*.

10/2015 Integrating epigenetic and genomic analyses via mediation analysis. *Harvard Medical School Epigenetics Symposium*.

08/2015 A mediation-based integrative genomic analysis of lung cancer. *Biostatistics Student Seminar*.

07/2015 Mediation-based integrative genomic analysis. *Joint Statistical Meetings*.

03/2015 Mediation-based integrative genomic analysis. *ENAR Spring Meeting*.

03/2015 Prewighted sparse clustering with applications to temporomandibular disorder. *International Association for Dental Research Epi-Forum*.

03/2014 Identification of biologically relevant subtypes via preweighted sparse clustering. *ENAR Spring Meeting*.

Poster Presentations

07/2019 Rare variant association analysis for studies with rich phenotyping subject to missingness. *American Society for Human Genetics Annual Meeting*.

07/2019 Fine mapping causal variants with functional annotations. *Joint Statistical Meetings*. Oral poster.

03/2018 Assessing the Effective Degree of SNPs in eQTL Networks. *ENAR Spring Meeting*. Oral poster.

10/2016 Mediation methods applied to post-traumatic stress disorder to identify genomic effects. *American Society for Human Genetics Annual Meeting*.

04/2015 A mediation-based integrative genomic analysis of lung cancer. *Harvard Graduate Women in Science and Engineering Symposium*.

04/2013 The association between oral contraceptive use and painful conditions. *UNC Celebration of Undergraduate Research*.

10/2012 OPPERA Study Identifies an Association Between the Use of Hormonal Contraceptives and Oro-facial Pain and Headaches. *International Pelvic Pain Society Conference*. Prepared poster, First place in poster competition.

04/2012 Identification of clinically relevant disease subtypes using supervised sparse clustering. *ENAR Spring Meeting*.

PROFESSIONAL SERVICE

2018-2019 Organizer, Harvard Biostatistics Postdoctoral Mental Health Study

2017-2018 Member, Harvard Biostatistics Colloquium Committee

2016-2018 Co-organizer, Harvard Biostatistics-Biomedical Informatics Big Data Seminar

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

TECHNICAL SKILLS

Statistical Software	R, Experience in: SAS, STATA, Python
Genetics Software	PLINK, GCTA
Other Software	Linux computing, GitHub, L ^A T _E X, Microsoft Office, Cytoscape

REFERENCES

Xihong Lin, Professor
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John Quackenbush, Henry Pickering Walcott Professor of Computational Biology and Bioinformatics. Chair
Department of Biostatistics
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William Maixner, Joannes H. Karis M.D. Professor of Anesthesiology
Department of Anesthesiology
Duke University School of Medicine
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Paige Williams, Senior Lecturer and Director of Graduate Studies
Department of Biostatistics and Department of Epidemiology
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