

Josh Weinstock, Ph.D.

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Education

Emory University <i>B.A., Department of Mathematics</i> Summa Cum Laude	Atlanta, GA, USA 2015
University of Michigan <i>M.S., Department of Biostatistics</i>	Ann Arbor, MI, USA 2018
University of Michigan <i>Ph.D., Department of Biostatistics</i> Advisor: Goncalo Abecasis	Ann Arbor, MI, USA 2021

Research and Professional Experience

Academic

Emory University, Department of Human Genetics <i>Incoming Assistant Professor</i>	Atlanta, GA August 2024–
Johns Hopkins University, Department of Biomedical Engineering <i>Assistant Research Scientist</i> I am a research scientist in Alexis Battle's lab	Baltimore, MD July 2023–July 2024
Stanford University, Department of Genetics <i>Post-Doctoral Scholar</i> I worked jointly with Jonathan Pritchard (Stanford) and Alexis Battle (JHU) on using gene regulatory networks to elucidate the genomic mechanisms underlying complex traits	Stanford, CA August 2021–July 2023
Johns Hopkins University, Department of Biomedical Engineering <i>Visiting Scientist</i>	Baltimore, MD August 2021–July 2023
University of Michigan, Department of Biostatistics <i>Graduate Student Research Assistant</i> My dissertation committee included Goncalo Abecasis, Hyun Min Kang, Xiang Zhou, and Jun Li	Ann Arbor, MI 2018–2021
Emory University Psychology Department <i>Undergraduate Research Assistant, Dr. Irwin Waldman's lab</i>	Atlanta, GA 2012–2015
Emory University Computer Science Department <i>Undergraduate Research Assistant, Dr. Eugene Agichtein's lab</i>	Atlanta, GA May 2014–August 2014

Industry

Microsoft Research AI <i>Research Intern</i> Developed machine learning applications for genomics deployed on Azure	Redmond, WA June 2019–August 2019
Washington Nationals Baseball Club <i>Research and Development Analyst</i> Developed machine learning applications for baseball	District of Columbia May 2015–August 2016

Awards, Honors, and Fellowships

- Reviewers' Choice Abstract, American Society of Human Genetics 2022 (Top 10% of poster abstracts)
- NHLBI BioData Catalyst Fellowship, Cohort III (\$69,733)
- NHGRI Institutional National Research Service Award (T32; Genome Science Training Program)
- Finalist for 2019 Charles J. Epstein Trainee Award at American Society of Human Genetics (One of ten pre-doctoral finalists)
- Rackham Travel Grant
- Henry L. Bowden Deans Achievement Scholarship (Merit Scholarship at Emory University)

Teaching

Johns Hopkins University <i>Guest lecturer, Department of Biomedical Engineering</i> Advanced Topics in Genomic Data Analysis	Baltimore, MD, USA March 27th 2023
University of Michigan <i>Advanced Inference I Tutor, Department of Biostatistics</i> I tutored students in the department's Ph.D. level probability theory course, Biostat 801	Ann Arbor, MI, USA Fall Semester 2019
University of Michigan <i>Graduate Student Instructor (TA), Department of Biostatistics</i> I mentored undergraduate students in the genomics section of the Big Data Summer Institute (BDSI) program	Ann Arbor, MI, USA July 2018-August 2018

Service

Project SHORT <i>Mentor</i> Project SHORT is a non-profit that offers pro-bono mentorship to undergraduate students from historically underrepresented groups who plan to apply to graduate programs.	September 2020–
NHLBI TOPMed Investigator Meeting <i>Meeting Organizer Committee</i>	Rockville, MD January 26-27th 2023
University of Michigan <i>Curriculum Committee, Department of Biostatistics</i>	Ann Arbor, MI, USA September 2020-August 2021
University of Michigan <i>Student Representative, Department of Biostatistics</i> I and one other student represented the biostatistics student body at faculty meetings	Ann Arbor, MI, USA September 2019-August 2020
Journal of Quantitative Analysis in Sports <i>Ad-hoc reviewer</i>	

Publications and Preprints

- [1] Yash Pershad, Taralynn Mack, Hannah Poisner, Yasminka A Jakubek, Adrienne M Stilp, Braxton D Mitchell, Joshua P Lewis, Eric Boerwinkle, Ruth JF Loos, Nathalie Chami, et al. "Determinants of mosaic chromosomal alteration fitness". In: *Nature Communications* 15.1 (2024), p. 3800.

- [2] Rebecca Keener, Surya B Chhetri, Carla J Connelly, Margaret A Taub, Matthew P Conomos, **Joshua S Weinstock**, Bohan Ni, Benjamin Strober, Stella Aslibekyan, Paul L Auer, et al. "Validation of human telomere length multi-ancestry meta-analysis association signals identifies POP5 and KBTBD6 as human telomere length regulation genes". In: *Nature Communications* 15.1 (2024), p. 4417.
- [3] Taralynn M Mack, Michael A Raddatz, Yash Pershad, Daniel C Nachun, Kent D Taylor, Xiuqing Guo, Alan R Shuldiner, Jeffrey R O'Connell, Eimear E Kenny, Ruth JF Loos, et al. "Epigenetic and proteomic signatures associate with clonal hematopoiesis expansion rate". In: *Nature Aging* (2024), pp. 1–10.
- [4] **Joshua S Weinstock***, Maya M Arce*, Jacob W Freimer, Mineto Ota, Alexander Marson, Alexis Battle, and Jonathan K Pritchard. "Gene regulatory network inference from CRISPR perturbations in primary CD4+ T cells elucidates the genomic basis of immune disease". In: *bioRxiv* (2023), pp. 2023–09.
- [5] Rebecca Keener, Surya B Chhetri, Carla J Connelly, Margaret A Taub, Matthew P Conomos, **Joshua S Weinstock**, Bohan Ni, Benjamin J Strober, Stella Aslibekyan, Paul L Auer, et al. "Validation of human telomere length trans-ancestry meta-analysis association signals identifies POP5 and KBTBD6 as novel human telomere length regulation genes". In: *bioRxiv* (2023), pp. 2023–07.
- [6] Zhi Yu, Amelie Vromman, Ngoc Quynh H Nguyen, Shamsudheen K Vellarikkal, Md Mesbah Uddin, Abhishek Niroula, Gabriel Griffin, Michael C Honigberg, Amy E Lin, Christopher J Gibson, et al. "Human Plasma Proteomic Profile of Clonal Hematopoiesis". In: *bioRxiv* (2023), pp. 2023–07.
- [7] Eric M Kernfeld, Yunxiao Yang, **Joshua S Weinstock**, Alexis Battle, and Patrick M Cahan. "A systematic comparison of computational methods for expression forecasting". In: *bioRxiv* (2023), pp. 2023–07.
- [8] **Joshua S Weinstock**, Cecilia A Laurie, Jai G Broome, et al. "The Genetic Determinants of Recurrent Somatic Mutations in 43,693 Blood Genomes". In: *Science Advances* 9.17 (2023), eabm4945.
- [9] Waihay J Wong, Connor Emdin, Alexander G Bick, Seyedeh M Zekavat, Abhishek Niroula, James P Pirruccello, Laura Dichtel, Gabriel Griffin, Md Mesbah Uddin, Christopher J Gibson, et al. "Clonal haematopoiesis and risk of chronic liver disease". In: *Nature* (2023), pp. 1–8.
- [10] **Joshua S Weinstock***, Jayakrishnan Gopakumar*, Bala Bharathi Burugula, Md Mesbah Uddin, Nikolaus Jahn, Julia A Belk, Hind Bouzid, Bence Daniel, Zhuang Miao, Nghi Ly, et al. "Aberrant activation of TCL1A promotes stem cell expansion in clonal haematopoiesis". In: *Nature* (2023), pp. 1–11.
- [11] L Alexander Liggett, Liam D Cato, **Joshua S Weinstock**, Yingze Zhang, S Mehdi Nouraie, Mark T Gladwin, Melanie E Garrett, Allison Ashley-Koch, Marilyn J Telen, Brian Custer, et al. "Clonal hematopoiesis in sickle cell disease". In: *The Journal of Clinical Investigation* 132.4 (2022).
- [12] Hind Bouzid, Julia A Belk, Max Jan, Yanyan Qi, Chloe Sarnowski, Sara Wirth, Lisa Ma, Matthew Chrostek, Herra Ahmad, Daniel Nachun, et al. "Clonal hematopoiesis is associated with protection from Alzheimer's disease". In: *medRxiv* (2021).

- [13] Margaret A Taub, Matthew P Conomos, Rebecca Keener, Kruthika R Iyer, **Joshua S Weinstock**, Lisa R Yanek, John Lane, Tyne W Miller-Fleming, Jennifer A Brody, Laura M Raffield, et al. "Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed". In: *Cell Genomics* 2.1 (2022), p. 100084.
- [14] Waihay J Wong, Connor Emdin, Alexander Bick, Seyedeh M Zekavat, Abhishek Niroula, James Pirruccello, Laura Dichtel, Gabriel Griffin, Md Mesbah Uddin, Christopher J Gibson, et al. "Clonal hematopoiesis and risk of chronic liver disease". In: *medRxiv* (2022), pp. 2022–01.
- [15] M Uddin, Ngoc Quynh H Nguyen, Bing Yu, Jennifer A Brody, Akhil Pampana, Tetsushi Nakao, Myriam Fornage, Jan Bressler, Nona Sotoodehnia, **Joshua S Weinstock**, et al. "Clonal hematopoiesis of indeterminate potential, DNA methylation, and risk for coronary artery disease". In: *Nature Communications* 13.1 (2022), pp. 1–16.
- [16] Caitlyn Vlasschaert, Taralynn Mack, Jonathan Brett Heimlich, Abhishek Niroula, Md Mesbah Uddin, **Joshua S Weinstock**, Brian Sharber, Alexander J Silver, Yaomin Xu, Michael R Savona, et al. "A practical approach to curate clonal hematopoiesis of indeterminate potential in human genetic datasets". In: *Blood* (2022).
- [17] Tetsushi Nakao, Alexander G Bick, Margaret A Taub, Seyedeh M Zekavat, Md M Uddin, Abhishek Niroula, Cara L Carty, John Lane, Michael C Honigberg, **Joshua S Weinstock**, et al. "Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential". In: *Science Advances* 8.14 (2022), eabl6579.
- [18] Md Mesbah Uddin, Zhi Yu, **Joshua S Weinstock**, Tetsushi Nakao, Abhishek Niroula, Sarah M Urbut, Satoshi Koyama, Seyedeh M Zekavat, Kaavya Paruchuri, Alexander J Silver, et al. "Germline genomic and phenomic landscape of clonal hematopoiesis in 323,112 individuals". In: *medRxiv* (2022), pp. 2022–07.
- [19] Bernhard Haring, Alexander P Reiner, Jingmin Liu, Deirdre K Tobias, Eric Whitsel, Jeffrey S Berger, Pinkal Desai, Sylvia Wassertheil-Smoller, Michael J LaMonte, Kathleen M Hayden, et al. "Healthy Lifestyle and Clonal Hematopoiesis of Indeterminate Potential: Results From the Women's Health Initiative". In: *Journal of the American Heart Association* 10.5 (2021), e018789.
- [20] Tetsushi Nakao, Alexander G Bick, Margaret A Taub, Seyedeh M Zekavat, Md M Uddin, Abhishek Niroula, Cara L Carty, John Lane, Michael C Honigberg, **Joshua S Weinstock**, et al. "Bidirectional Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of intermediate potential". In: *medRxiv* (2021).
- [21] Daniel Nachun, Ake T Lu, Alexander G Bick, Pradeep Natarajan, **Joshua S Weinstock**, Mindy D Szeto, Sekar Kathiresan, Goncalo Abecasis, Kent D Taylor, Xiuqing Guo, et al. "Clonal hematopoiesis associated with epigenetic aging and clinical outcomes". In: *Aging Cell* (2021), e13366.
- [22] L Alexander Liggett, Liam D Cato, **Joshua S Weinstock**, Yingze Zhang, Seyed Mehdi Nouraie, Mark T Gladwin, Melanie E Garrett, Allison Ashley-Koch, Marilyn Jo Telen, Brian Custer, et al. "Clonal hematopoiesis in sickle cell disease". In: *medRxiv* (2021).
- [23] Alexander G Bick*, **Joshua S Weinstock***, Satish K Nandakumar, Charles P Fulco, Erik L Bao, Seyedeh M Zekavat, Mindy D Szeto, Xiaotian Liao, Matthew J Leventhal, Joseph Nasser, et al. "Inherited causes of clonal haematopoiesis in 97,691 whole genomes". In: *Nature* (2020), pp. 1–7.

- [24] Wei Zhou*, Ben Brumpton*, Omer Kabil*, Julius Gudmundsson*, Gudmar Thorleifsson*, **Josh Weinstock**, Matthew Zawistowski, Jonas B Nielsen, Layal Chaker, Marco Medici, et al. “GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer”. In: *Nature Communications* 11.1 (2020), pp. 1–13.
- [25] Jeffrey A Goldstein*, **Joshua S Weinstock***, Lisa A Bastarache, Daniel B Larach, Lars G Fritsche, Ellen M Schmidt, Chad M Brummett, Sachin Kheterpal, Goncalo R Abecasis, Joshua C Denny, et al. “LabWAS: novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks”. In: *PLOS Genetics* (2020).
- [26] Diptavo Dutta, Sarah A Gagliano Taliun, **Joshua S Weinstock**, Matthew Zawistowski, Carlo Sidore, Lars G Fritsche, Francesco Cucca, David Schlessinger, Gonçalo R Abecasis, Chad M Brummett, et al. “Meta-MultiSKAT: Multiple phenotype meta-analysis for region-based association test”. In: *Genetic Epidemiology* 43.7 (2019), pp. 800–814.
- [27] Gregory JM Zajac, Lars G Fritsche, **Joshua S Weinstock**, Susan L Dagenais, Robert H Lyons, Chad M Brummett, and Gonçalo R Abecasis. “Estimation of DNA contamination and its sources in genotyped samples”. In: *Genetic Epidemiology* 43.8 (2019), pp. 980–995.
- [28] Dajiang J Liu, Gina M Peloso, Haojie Yu, Adam S Butterworth, Xiao Wang, Anubha Mahajan, Danish Saleheen, Connor Emdin, Dewan Alam, Alexessander Couto Alves, et al. “Exome-wide association study of plasma lipids in > 300,000 individuals”. In: *Nature Genetics* 49.12 (2017), pp. 1758–1766.

Selected Presentations

- [29] **J.S. Weinstock**. “A Survey of Somatic Point Mutations in TOPMed”. In: NHLBI TOPMed Investigator Meeting. 2023.
- [30] **J.S. Weinstock**. “Structure Learning Using CRISPR Perturbations for Gene Regulatory Network Inference”. In: Statistical Genetics Working Group, Department of Biostatistics, Johns Hopkins. 2022.
- [31] **J.S. Weinstock**, R.A. Mathias, A.P. Reiner, P. Natarajan, T.W. Blackwell, G.R. Abecasis, and A.G. Bick on behalf of the NHLBI TOPMed Consortium on behalf of the NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium. “A Compendium of Recurrent Somatic Variation in 46,080 TOPMed Whole Genomes”. In: American Society of Human Genetics Annual Meeting (Platform talk, PgmNr 1386). 2020.
- [32] **J.S. Weinstock***, A. Bick*, S.Nandakumar, V. Sankaran, A. Reiner, S. Jaiswal, G. Abecasis, P. Natarajan, and S. Kathiresan on behalf of the NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium. “Inherited Causes and Clinical Consequences of Clonal Hematopoiesis from 100,002 Whole Genomes”. In: American Society of Human Genetics Annual Meeting (Platform talk, PgmNr 344). 2019.
- [33] **J.S. Weinstock**, E.M. Schmidt, L.G. Fritsche, S. Kheterpal, C.M. Brummett, and G.R. Abecasis; “Large scale application of Mendelian Randomization to electronic health records yields novel causal inferences”. In: NHGRI Research Training and Career Development Annual Meeting (Lightning talk). 2018.

- [34] **J.S. Weinstock**, E.M. Schmidt, L.G. Fritsche, S. Kheterpal, C.M. Brummett, and G.R. Abecasis; "Large scale application of Mendelian Randomization to electronic health records yields novel causal inferences". In: American Society of Human Genetics Annual Meeting (Platform talk, PgmNr 135). 2017.