

# Josh Weinstock, Ph.D.

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## Education

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**Emory University** Atlanta, GA, USA  
*B.A., Department of Mathematics* 2015  
Summa Cum Laude

**University of Michigan** Ann Arbor, MI, USA  
*M.S., Department of Biostatistics* 2018

**University of Michigan** Ann Arbor, MI, USA  
*Ph.D., Department of Biostatistics* 2021  
Advisor: Goncalo Abecasis

## Research and Professional Experience

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### Academic

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**Johns Hopkins University, Department of Biomedical Engineering** Baltimore, MD  
*Assistant Research Scientist* July 2023–  
I am a research scientist in Alexis Battle's lab

**Stanford University, Department of Genetics** Stanford, CA  
*Post-Doctoral Scholar* August 2021–July 2023  
I worked jointly with Jonathan Pritchard (Stanford) and Alexis Battle (JHU) on using gene regulatory networks to elucidate the genomic mechanisms underlying complex traits

**Johns Hopkins University, Department of Biomedical Engineering** Baltimore, MD  
*Visiting Scientist* August 2021–July 2023

**University of Michigan, Department of Biostatistics** Ann Arbor, MI  
*Graduate Student Research Assistant* 2018–2021  
My dissertation committee included Goncalo Abecasis, Hyun Min Kang, Xiang Zhou, and Jun Li

**Emory University Psychology Department** Atlanta, GA  
*Undergraduate Research Assistant, Dr. Irwin Waldman's lab* 2012–2015

**Emory University Computer Science Department** Atlanta, GA  
*Undergraduate Research Assistant, Dr. Eugene Agichtein's lab* May 2014–August 2014

### Industry

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**Microsoft Research AI** Redmond, WA  
*Research Intern* June 2019–August 2019  
Developed machine learning applications for genomics deployed on Azure

**Washington Nationals Baseball Club** District of Columbia  
*Research and Development Analyst* May 2015–August 2016  
Developed machine learning applications for baseball

## Awards, Honors, and Fellowships

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- 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

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<b>Johns Hopkins University</b> <i>Guest lecturer, Department of Biomedical Engineering</i> Advanced Topics in Genomic Data Analysis	<b>Baltimore, MD, USA</b> March 27th 2023
<b>University of Michigan</b> <i>Advanced Inference I Tutor, Department of Biostatistics</i> I tutored students in the department's Ph.D. level probability theory course, Biostat 801	<b>Ann Arbor, MI, USA</b> Fall Semester 2019
<b>University of Michigan</b> <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	<b>Ann Arbor, MI, USA</b> July 2018-August 2018

## Service

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<b>Project SHORT</b> <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–
<b>NHLBI TOPMed Investigator Meeting</b> <i>Meeting Organizer Committee</i>	<b>Rockville, MD</b> January 26-27th 2023
<b>University of Michigan</b> <i>Curriculum Committee, Department of Biostatistics</i>	<b>Ann Arbor, MI, USA</b> September 2020-August 2021
<b>University of Michigan</b> <i>Student Representative, Department of Biostatistics</i> I and one other student represented the biostatistics student body at faculty meetings	<b>Ann Arbor, MI, USA</b> September 2019-August 2020
<b>Journal of Quantitative Analysis in Sports</b> <i>Ad-hoc reviewer</i>	

## Publications and Preprints

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- [1] **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.

- [2] 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.
- [3] 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.
- [4] 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.
- [5] **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.
- [6] 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.
- [7] **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.
- [8] L Alexander Liggett, Liam D Cato, **Joshua S Weinstock**, Yingze Zhang, S Mehdi Nouraei, 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).
- [9] 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).
- [10] 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.
- [11] 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.
- [12] 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.

- [13] 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).
- [14] 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.
- [15] 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.
- [16] 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.
- [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. "Bidirectional Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of intermediate potential". In: *medRxiv* (2021).
- [18] 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.
- [19] 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).
- [20] 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.
- [21] 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.
- [22] 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).
- [23] 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.

- [24] 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.
- [25] 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

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- [26] **J.S. Weinstock**. "A Survey of Somatic Point Mutations in TOPMed". In: NHLBI TOPMed Investigator Meeting. 2023.
- [27] **J.S. Weinstock**. "Structure Learning Using CRISPR Perturbations for Gene Regulatory Network Inference". In: Statistical Genetics Working Group, Department of Biostatistics, Johns Hopkins. 2022.
- [28] **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.
- [29] **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.
- [30] **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.
- [31] **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.