

MATTHEW LEVENTHAL

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Research Interests

I am PhD student in MIT's program in Computational and Systems Biology advised by Professor of Biological Engineering Ernest Fraenkel. With my background as a BA in biological science and mathematics from Bowdoin College, I excel in communicating my research to both biological and computational scientists in public and in one-on-one settings. My experience as a computational associate prepared me for my current work: leveraging and developing methods for integrating multiple modes of sequencing data in order to understand the molecular mechanisms and therapeutic targets of Alzheimer's Disease as well as shared mechanisms of neurodegeneration across diseases. Through my work as a PhD student I aim to develop the independent research experience that will prepare me to lead a research group of my own.

Education

Massachusetts Institute of Technology, Cambridge, MA
PhD, Computational and Systems Biology. Entry year 2019.
Thesis advisor: Ernest Fraenkel

Relevant Coursework: Advanced Computational Biology, Graduate Genetics, Topics in Computational and Systems Biology, Bayesian Modeling and Inference, Molecular Biology, Cellular and Molecular Neuroscience Core I, and Topics in Computational Molecular Biology.

Bowdoin College, Brunswick, ME
Bachelor of the Arts, Biology and Mathematics. May 2017.

Relevant Coursework: Linear Algebra, Biostatistics, Number Theory and Cryptography, Neurobiology, Evolution, Biochemistry and Cell Biology, Genetics of Human Disease, Ordinary Differential Equations, Non-Euclidean Geometry, Microbiology, Molecular Evolution, Probability, Real Analysis, Partial Differential Equations, Advanced Cell and Molecular Biology, Computational Genomics, Statistics

Research Experience

Graduate Research Assistant, April 1, 2020-Present

Massachusetts Institute of Technology, Cambridge, Massachusetts
Mentor: Ernest Fraenkel

- Utilized methods that integrate high-throughput sequencing technologies to discover biological mechanisms shared across neurodegenerative diseases
- Collaboratively designed biological experiments with faculty and researchers from Brigham and Women's Hospital based on hypotheses generated from network analyses
- Developed methods to quantify and reduce latent space uncertainty of Variational Autoencoders to better identify the biological pathways underlying disease pathology
- Presented results of the Variational Autoencoder project at the Learning Meaningful Representations of Life workshop at NeurIPS
- Presented work at Fraenkel lab meeting and the Computational and Systems Biology Seminar at MIT

Computational Associate, June 3, 2017-August 2, 2019

The Broad Institute of Harvard and MIT, Cambridge, Massachusetts
Co-Mentors: Benjamin Ebert, Gad Getz

- Developed a method in Python to estimate the degree of clonal hematopoiesis in 78,000 healthy blood exomes

- Analyzed Target-Capture, Whole Exome, Chip-seq and RNA-seq data of human blood samples in a Cloud-Based analysis platform to identify drivers of clonal hematopoiesis, the results of which were published in *Science*, *Blood Advances* and *Nature Communications* among other journals
- Presented results frequently at both Ebert and Getz lab meetings
- Presented results the Broad Retreat Poster Session in 2017 and 2018

Computational Associate, June 13, 2016-August 6, 2016

The Broad Institute of Harvard and MIT, Cambridge, Massachusetts

Mentor: Gad Getz

- Worked with the Cancer Genome Analysis team
- Moved the Pan Cancer Analysis of Whole Genomes pipeline to a cloud computing environment called FireCloud
- Attended weekly cancer research seminars and weekly journal clubs on applying computational methods to cancer biology

Research Assistant, June 1 2015-September 1 2015

University of Michigan-Ann Arbor, Ann Arbor, Michigan

Mentor: Ivo Dinov

- Developed a dynamic web application modeling brain signaling over time hosted on the SOCR server
- Presented work in weekly lab meetings
- Gained experience in web design, coding in Javascript, HTML5 and CSS
- Learned how to collaborate using GitHub on computational projects

Research Assistant, June 2014-September 2014

Bowdoin College, Brunswick, Maine

Mentor: Vladimir Douhovnikoff

- Used Hardy-Weinberg Model assumptions to model how clonal plant growth changes genetic diversity in plant populations
- Prepared and presented a poster at the President's Science Symposium
- Presented research in an informal 10 minute talk
- Continued research as an independent study in the Fall 2014 semester

Skills

Analytical skills: Differential RNA-seq expression analysis (EdgeR, DeSeq2), Whole-Exome, Whole-Genome and Target-Capture sequencing analysis, ChIP-seq analysis (transcription factor peak calling, motif analysis), single-cell RNA-seq clustering, Mutational Signature Analysis

Computer skills: Java, R, Prism 6, LaTeX, Javascript, GitHub, HTML5, CSS, Python, Bash/Shell, Google Cloud analysis of Next-Generation Sequencing

Fellowships and Grants

- Computational and Systems Biology T32 Training Grant 2019-2020
- Bowdoin College National Merit Scholarship 2013-2017
- Bowdoin College Computational Sustainability Grant 2014
- Bowdoin College Alumni Council Fund 2015
- Society of Applied and Industrial Mathematics 2015-2016

Teaching Experience

Teaching assistant, February 2021-May 2021

MIT Department of Biological Engineering, Cambridge Massachusetts

- Served as a teaching assistant for 20.440 (Analysis of Biological Networks) in the spring 2021 semester
- Prepared lectures for recitation
- Held small group office hours sections twice a week
- Graded problem sets and helped in re-designing problem sets with the other course staff members

Study Group Leader, January 2016-May 2016

Bowdoin College Center for Learning and Teaching, Brunswick, Maine

- Led study sessions for a section of Scientific Reasoning in Biology to provide one-on-one instruction
- Assisted undergraduate students with reading and interpreting scientific literature
- Clarified and explained introductory biology concepts

Drop-In Tutor, September 2016-December 2016

- Tutored introductory biology and chemistry for three hours at a time for students seeking extra help in understanding course material

Activities and Interests

Cross Country, Track and Field, September 2013-2017

Bowdoin College Athletics, Brunswick, Maine

- NESCAC All-Academic Cross Country Team 2014-2016
- NESCAC All-Academic Track and Field Team 2017
- NESCAC All-Sportsmanship Track and Field Team 2017
- Independently developed a statistical model that predicts which teams are selected to race at the Division III Cross-Country National Championships

Co-president of the Bowdoin Music Collective, September 2016-May 2017

Bowdoin Student Activities, Brunswick, Maine

- Organized and led weekly meetings
- Organized weekly student musical performances on campus
- Communicated and met with the Director of Student Activities weekly

Publications

(In Preparation) **Leventhal, Matthew**, Joseph Benetatos, Camilla A Zanella, Byungk Kang, Christopher Ng, David Housman, Clemens R Scherzer, Mel B Feany, Ernest Fraenkel. A systems biology approach reveals common pathways of neurodegeneration

(In Preparation) Tariq, Ifrah, **Matthew Leventhal**, Diep Nguyen, Ernest Fraenkel. Estimating the latent space uncertainty of Variational Autoencoders improves integration of multi-omic sequencing data.

Ellen Beauchamp, **Matthew Leventhal**, Elsa Bernard, Emma Hoppe, Gabriele Todisco Maria Creignou, Anna Galli, Cecilia Castelano, Marie McConkey, Akansha Tarun, Waihay Wong, Monica Schenone, Caroline Stanclift, Benjamin Tanenbaum, Edyta Malolepsza, Björn Nilsson, Alexander Bick, Joshua Weinstock, Mendy Miller, Abhishek Niroula, Andrew Dunford, Amaro Taylor-Weiner, Timothy Wood, Alex Barbera, Shankara Anand, Bruce Psaty, Pinkal Desai, Michael Cho, Andrew Johnson, Ruth Loos, Daniel MacArthur, Monkol Lek, Donna Neuberg, Kasper Lage, Steven Carr, Eva Hellström-Lindberg, Luca Malcovati, Elli Papaemmanuil, Chip Stewart, Gad Getz, Robert Bradley, Siddhartha Jaiswal and Benjamin Ebert. 2021. ZBTB33 is Mutated In clonal hematopoiesis and myelodysplastic syndromes and impacts RNA Splicing. *Blood Cancer Discovery*.

Bick, Alex G, Joshua S Weinstock, Satish K Nandakumar, Charles P Fulco, Erik L Bao, Seyedeh M Zekavat, Mindy D Szeto, Xiotian Liao, **Matthew J Leventhal**, Joseph Nasser, Kyle Chang, Cecelia Laurie, Bala Bharathi Burugula, Christopher J Gibson, Amy E Lin, Margaret A Taub, Francois Aguet, Kristin Ardlie, Braxton D Mitchell, Kathleen C Barnes, Arden Moscatti, Myriam Fornage, susan Redline, Bruce M Psaty, Edwin K Silverman, Scott T Weiss, Nicholette D Palmer, Ramachandran S Vasan, Esteban G Burchard, Sharon LR Kardia, Jiang He, Robert C Kaplan, Nicholas L Smith, Donna K Arnett, David A Schwartz, Adolfo Correa, Mariza de Andrade, Xiuqing Guo, Barbara A Konkle, Brian Custer, Juan M Peralta, Hongsheng Gui, Deborah A Meyers, Stephen T McGarvey, Ida Yii-Der Chen, M. Benjamin Shoemaker, Patricia A Peyser, Jai G Broome, Stephani M Gogarten Fei Fei Wang, Quenna Wong, May E Montasser, Michelle Daya, Eimear E Kenny, Kari E North, Lenore J Launer, Brian E Cade, Joshua C Bis, Michael H Cho, Jessica Lasky-Su, Donald W Bowden, L. Adrienne Cupples, Angel CY Mak, Lewis C Becker, Jennifer A Smith, Tanika N Kelly, Stella Aslibekyan, Susan R Heckbert, Hemant K Tiwari, Ivana V Yang, John A Heit, Steven A Lubitz, Jill M Johnsen, Joanne E Curran, Sally E Wenzel, Daniel E Weeks, Dabeeru C Rao, Dawood Darbar, Jee-Young Moon, Russell P Tracy, Erin J Buth, Nicholas Rafaels, Ruth JF Loos, Peter Durda, Yongmei Liu, Lifang Hou, Jiwon Lee, Priyadarshini Kachroo, Barry I Freedman, Daniel Levy, Lawrence F Bielak, James E Hixson, James S Floyd, Eric A Whitsel, Patrick T Ellinor, Marguerite R Irvin, Tasha E Fingerlin, Laura M Raffield, Sebastian M Armasu, Marsha M Wheeler, Ester C SabinoJohn Blangero, Keoki L Williams, Bruce D Levy, Wayne Huey-Herng Sheu, Dan M Roden, Eric Boerwinkle, JoAnn E Manson, Rasika A Mathias, Pinkal Desai, Kent D Taylor, Andrew D Johnson, Paul L Auer, Charles Kooperberg, Cathy C Laurie, Thomas W Blackwell, Albert V Smith, Hongyu Zhao, Ethan Lange, Leslie Lange, Stephen S Rich, Jerome I Rotter, James G Wilson, Paul Scheet, Jacob O Kitzman, Eric S Lander, Jesse M Engreitz, Benjamin L Ebert, Alexander P Reiner, Siddhartha Jaiswal, Goncalo Abecasis, Vijay G Sankaran, Sekar Kathiresan and Pradeep Natarajan. 2020. Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*. 586: 763-768.

Mouhieddine, Tarek H, Adam S Sperling, Robert Redd, Jihye Park, **Matthew Leventhal**, Christopher J. Gibson, Salomon Manier, Amin H Nassar, Marzia Capelletti, Daisy Huynh, Mark Bustoros, Romanos Sklavenitis-Pistofidis, Sabrin Tahri, Klavis Hornburg, Henry Dumke, Muhieddine M Itani, Cody J Boehner, Chia-Jen Liu, Saud H AlDubayan, Brendan Reardon, Eliezer M Van Allen, Jonathan J Keats, Chip Stewart, Shaadi Mehr, Daniel Auclair, Robert L Schlossman, Nikhil C Munshi, Kenneth C Anderson, David P Steensma, Jacob P Laubach, Paul G Richardson, Jerome Ritz, Benjamin L Ebert, Robert J Soiffer, Lorenzo Trippa, Gad Getz, Donna S Neuberg and Irene M Ghobrial. 2020. Clonal hematopoiesis is associated with adverse outcomes in multiple myeloma patients undergoing transplant. *Nature Communications*. 11: 1-9.

Sperling, Adam S, **Matthew Leventhal**, Christopher J. Gibson, Benjamin L. Ebert, and David Steensma. 2019. Myelodysplastic syndromes (MDS) occurring in Agent Orange exposed individuals carry a mutational spectrum similar to that of de novo MDS. *Leukemia and Lymphoma*. 61 (3): 728-731.

Boettcher, Steffen, Peter G. Miller, Rohan Sharma, Marie McConkey, **Matthew Leventhal**, Xiaoping Yang, Federica Piccioni, Jesi Kim, Sherry Chao, Andrei V. Krivtsov, Andrew O. Giacomelli, William C. Hahn, Tyler Jacks, Hartmut Doehner, Scott A. Armstrong, Benjamin L. Ebert. 2019. A dominant-negative effect drives selection of TP53 missense mutations in acute myeloid leukemia. *Science*. 365 (6453): 599-604.

Jan, Max, **Matthew J Leventhal**, Elizabeth A Morgan, Jordan C Wengrod, Anewsha Nag, Samantha D Drinian, Bruce M Wollison, Matthew D Ducar, Aaron R Thorner, Natasha Kekre, Vincent T Ho, John Koreth, Corey S Cutler, Sarah Nikiforow, Edwin P Alyea III, Joseph H Antin, Robert J Soiffer, Jerome Ritz, R. Coleman Lindsley, and Benjamin L Ebert. 2019. Recurrent genetic HLA loss in Acute Myeloid Leukemia relapsed after matched unrelated allogeneic hematopoietic cell transplant. *Blood Advances*. 3 (14): 2199–2204.

Douhovnikoff, Vladimir, and **Matthew Leventhal**. 2016. The use of Hardy Weinberg Equilibrium in clonal plant systems. *Ecology and Evolution*. <http://onlinelibrary.wiley.com/doi/10.1002/ece3.1946/full>.

Presentation Abstracts

Jan, Max, **Matt J Leventhal**, Elizabeth A Morgan, Jordan C Wengrod, Anewsha Nag, Samantha D Drinian, Bruce M Wollison, Matthew D Ducar, Aaron R Thorner, Natasha Kekre, Vincent T Ho, John Koreth, Corey S Cutler, Sarah Nikiforow, Edwin P Alyea III, Joseph H Antin, Robert J Soiffer, Jerome Ritz, R. Coleman Lindsley, and Benjamin L Ebert. Recurrent genetic HLA loss in Acute Myeloid Leukemia relapsed after matched unrelated allogeneic hematopoietic cell transplant. American Society of Hematology. December 1, 2018. <https://ash.confex.com/ash/2018/webprogram/Paper113911.html>

Matthew Leventhal. Improving the efficiency of statistical analysis of cancer genomes through the development of cloud-based software. American Mathematical Society Special Session on Undergraduate Research. September 24, 2016. http://www.ams.org/amsmtgs/2238_abstracts/1121-92-218.pdf

Conference Posters

Tariq, Ifrah, **Matthew Leventhal**, Diep Nguyen. Estimating Latent Space Uncertainty to Improve Integration of Multi-Omic Sequencing Data. Learning Meaningful Representations of Life Workshop at the Conference on Neural Information Processing Systems (NeurIPS).