

# Gregory Darnell

Institute Post-Doctoral Fellow  
Institute for Computational and Experimental Research in Mathematics  
Brown University

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## Education

2014–2019	Ph.D. Quantitative and Computational Biology	Princeton University
2015	M.A. Quantitative and Computational Biology	Princeton University
2013–2014	Ph.D. Student Computational Biology & Bioinformatics	Duke University
2008–2013	B.S. Computer Science, <i>minor</i> Bioinformatics	University of California, Los Angeles

## Postdoctoral Fellowship Research

*My post-doctoral research continues the theme from my dissertation research (described below) of building high-dimensional models for understanding vast genomic data. I am co-advising on projects at the intersection of computation, statistics, and genomics. These projects include: [1] design of a novel model for interpretable and robust estimation of genetic effect sizes using biologically annotated neural networks; [2] development of a novel framework for variational autoencoders using interpretable priors and latent space representation that helps mitigate mode-collapse; and [3] estimation of a gene and biological pathway-based aggregated statistic for pathway-trait associations. Additionally, I am leading a project on developing methodologies for imputing unobserved non-linear interactions between genetic variants in genetic association studies using only observed summary statistics.*

## Publications

### Dissertations

- [1] **Gregory Darnell**. Associations and Confounding in High-Dimensional Genomics, Princeton University, Ann Arbor, 2019. ProQuest, <https://search.proquest.com/pqdtglobal/docview/2245698877/D7786861C23647ABPQ/1>

*The promise of curing many human diseases has become within reach as a result of development in gene-editing techniques such as CRISPR. However, before creating therapeutic techniques it is necessary to understand the genetic architecture of complex traits. My dissertation research develops novel statistical and machine learning techniques for understanding genotype-phenotype associations in complex traits such as: autoimmune diseases, gene expression, and tissue morphology. My results have shown that by properly controlling for confounding, it is possible to maintain interpretability, increase statistical power, and gain insight into the genetic architecture of complex traits.*

### Journals

\*Indicates equal authorship.

- [1] Jordan Ash\*, **Gregory Darnell**\*, Daniel Munro, Barbara Engelhardt. "Joint analysis of gene expression levels and histological images identifies genes associated with tissue morphology." *accepted. Nature Communications*. May, 2019  
*First computational pipeline to estimate genotype-image associations using neural networks.*
- [2] Bianca Dumitrascu, **Gregory Darnell**, Julien Aroyles, Barbara E Engelhardt. "Statistical tests for detecting variance effects in quantitative trait studies." *Bioinformatics*. July, 2018  
*A novel regression framework to estimate genetic variant effect on the variance of a phenotype.*
- [3] **Gregory Darnell**, Stoyan Georgiev, Sayan Mukherjee, Barbara E Engelhardt. "Adaptive Randomized Dimension Reduction on Massive Data." *Journal of Machine Learning Research (JMLR)*. 18(140):1-30, 2017  
*A solution to large inverse problems in linear mixed models using random projections.*
- [4] **Gregory Darnell**, Dat Duong, Buhm Han, Eleazar Eskin. "Incorporating Prior Information into Association Studies." *Bioinformatics*. 28(12):i47-53, *Special Issue of the Proceedings of the Nineteenth International Conference on Intelligent Systems in Molecular Biology (ISMB-2012)* Long Beach, CA: July 15-27, 2012  
*Increasing power in association studies by re-prioritizing variants based on prior information.*

## Archival

- [1] Li-Fang Cheng, **Gregory Darnell**, Corey Chivers, Michael E Draugelis, Kai Li, Barbara E Engelhardt. "Sparse Multi-Output Gaussian Processes for Medical Time Series Prediction." *arXiv preprint arXiv:1703.09112*. March, 2017  
*Efficient prediction of sparsely sampled biomarkers in a hospital setting using Gaussian Process regression.*

## Professional Experience

2019–2020	Institute Postdoctoral Fellow, <b>ICERM, Brown University</b> (Sept - June) Institute for Computational and Experimental Research in Mathematics Mentors: Professors Sohini Ramachandran, Lorin Crawford, Sigal Gottlieb, Yanlai Chen Program: Model and dimension reduction in uncertain and dynamic systems
2017	Research Internship, <b>Microsoft Research New England</b> (Sept - Dec) Mentors: Dr. Nicolo Fusi Project: Automated machine learning using parameter-free optimization
2016	Research Internship, <b>Microsoft Research New England</b> (June - Sept) Mentors: Professor Jennifer Listgarten and Dr. Nicolo Fusi Project: Output warping for improved prediction in machine learning models
2012	Research Assistant, <b>Rockefeller University</b> (June - Sept) Mentors: Professors Robert Darnell and Chaolin Zhang Projects: Accurate and efficient RNA-Seq read mapping & Prediction of binding specificity of RNA-binding proteins
2009	Research Assistant, <b>Harvard School of Public Health</b> (June - Sept) Mentor: Professor Alkes Price Project: Geographical ancestry prediction using principal components analysis on genotypes
2008–2013	Research Assistant, <b>University of California, Los Angeles</b> Mentor: Professor Eleazar Eskin Projects: Improving power in association study methods in Bioinformatics & Data compression schemes in computational genetics

## Invited Talks

- "The path to exciting research directions and fulfilling mentorship in Bioinformatics" UCLA Bioinformatics Graduation Keynote Speaker. Los Angeles, California. June 7, 2017
- "Winner's Curse in Quantitative Genomics Studies" *Biological Data Science*. Cold Spring Harbor, NY. Oct 28, 2016
- "Winner's Curse in Quantitative Genomics Studies" *New York Area Population Genomics Workshop 2016*. Princeton University, NJ. Jan 21, 2016

## Teaching

Summer 2016	Computer Science: Undergraduate Mentorship	Princeton University
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	Project: Analyzing the link between ancestry and morphology in sea urchin embryo images	
Fall 2015	COS 513: Foundations of Probabilistic Modeling Assistant in Instruction	Princeton University
Fall 2014	COS 375: Computer Architecture and Organization Assistant in Instruction	Princeton University
Spring 2012	Computer Science CM124. Computational Genetics Grader, Homework office hours, Test administration	University of California, Los Angeles

## Technical Reviewing and Committees

2019 Program Committee Member IEEE International Conference on Bioinformatics and Biomedicine.

2016, 2017, 2018 Reviewer for the journal of *Bioinformatics*, Oxford Academics.

## Academic Awards & Accreditations

- Selected for Institute Postdoctoral Fellowship at ICERM, 2019 (Institute for Computational and Experimental Research), Brown University
- Selected for the 2017 NBA Hackathon, New York, NY
- Travel Fellowship to ISMB 2012, Long Beach, CA
- Microsoft Certified Professional, 2006
- COMPTIA A+ (Hardware and Software), 2006
- COMPTIA Network+, 2006

## Skills

Python, PyTorch, R, Linux/Unix

## Leadership

- Student leader of statistics/machine learning reading group at Princeton.
- Co-founder and president of the UCLA Powerlifting Club Sport Team.