

Brian Lohman, Ph.D.

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<https://brianlohman.github.io>

Summary:

I am interested the development and application of bioinformatics tools for complex problems in –omics data. I enjoy crafting software solutions and workflows for use at scale in the cluster and the cloud. My diverse experiences and strong statistical skills enable me to contribute to a wide variety of projects.

Education:

The University of Utah School of Medicine (current)

Postdoctoral Scholar

Advisor: Dr. Aaron Quinlan

The University of Texas at Austin (May 2017)

Ph.D., Evolutionary Genomics

Advisor: Dr. Daniel Bolnick

University of Idaho (2011)

B.S. Biology, Minor: Psychology

Technical Skills:

Programming Languages: Python, R, Unix, Nim, JavaScript

Software packages/libraries: Python data stack (Pandas, Numpy, sklearn), Plotly, cyvcf2, R/qlt, DESeq2, limma, WGCNA, topGO, WGCNA, Bootstrap, DataTables, JQuery, Bedtools, BWA, Plink, PRSice

Computational: Linux-based HPC systems, SLURM, Nextflow, Amazon Web Services, Docker, Github

Statistics: Identify and carry out the correct statistical test for given problems (R or Python), drawing on a strong background in statistics and machine learning. Able to collaborate on diverse projects, (social sciences, epidemiology, genomics) contributing sound statistical advice.

Scientific Training:

Postdoctoral Research, University of Utah. Advisor: Dr. Aaron Quinlan (2017-present)

- Under minimal supervision, design and carry out original research on the genetics of autism spectrum disorder. Merge traditional statistical models, machine learning methods, and polygenic risk scores to identify and describe sub-populations of autistic individuals.
- Design and build new software solutions as necessary. Implement my own Python and R code in HPC and cloud environments as both stand-alone programs and as part of terabyte scale workflows.
- Collaborate with diverse research groups, guiding statistical analyses and project design.
- Build and present interactive HTML reports to a diverse group of supervisors and collaborators.

Dissertation Research, University of Texas at Austin. Advisor: Dr. Daniel Bolnick (2012-2017)

- Developed and validated a new high-throughput, low-cost RNAseq library build that allowed me to increase sample sizes and detect subtle patterns in gene expression. This effort resulted in a publication and initiated the Bolnick lab's work on transcriptomics.
- Built RNAseq libraries, sequenced, and analyzed data from a large lab-cross infection experiment. I merged my own data with existing immunological data, including flow cytometry, and identified candidate genes for multiple immune phenotypes. This work is published at Frontiers in Immunology.
- Generated, sequenced, and analyzed RNAseq data from a large reciprocal transplant experiment. I identified changes in gene expression associated with novel biotic and abiotic stressors. The resulting manuscript is published at Molecular Ecology.

- Fine mapped candidate genes by RFLP and QTL analysis, increasing our confidence in a gene-trait association. Built CRISPR/Cas9 constructs to make knockouts and validated by embryo injection.
- Built a simulation in R to explore the effects of evolutionary forces on traits across an environmental gradient. I combined these simulated data with my own reanalysis of previously published trait data. Published in the American Naturalist, this manuscript emphasizes the importance of dimensionality in evolutionary studies.

Other formal training and coursework:

University of Utah Department of Biomedical Informatics' 2019 DeCART Summer School

Statistical Natural Language Processing

Machine Learning for Healthcare

University of Washington's 2015 Summer Institute in Statistical Genetics

Quantitative Genetics

Gene Expression Profiling

Association Mapping: GWAS and Sequence Data

Selected Publications:

Lohman, B.K., Weber, J.N., Steinel, N.C., and Bolnick, D.I. (2017) Gene expression contributes to the recent evolution of host resistance in a model host parasite system. *Frontiers in Immunology*.

Lohman, B.K., Stutz, W., and Bolnick, D.I. (2017) Gene expression stasis and plasticity following migration into a foreign environment. *Molecular Ecology*.

Lohman, B.K., Berner, D., and Bolnick, D.I. (2017) Clines arc through multivariate morphospace. *The American Naturalist*.

Lohman, B.K., Weber, J.N., Matz, M.V, and Bolnick, D.I. (2016) Evaluation of TagSeq, a reliable low-cost alternative for RNAseq. *Molecular Ecology Resources*.

Selected grants, fellowships, and awards:

2016 University of Texas at Austin College of Natural Sciences C.P "Pete" Oliver Memorial Endowed Research Award

2016 National Science Foundation East Asia Pacific Institute (EAPSI) Fellowship

2016 University of Texas at Austin College of Natural Sciences Continuing Fellowship

2015 University of Texas at Austin College of Natural Sciences Summer Fellowship

2015 University of Washington Summer Institute in Statistical Genetics Scholarship

2014 National Science Foundation GRFP Honorable Mention

2014 University of Texas at Austin Department of Ecology, Evolution, and Behavior DDIG-like Grant

2013 National Science Foundation GRFP Honorable Mention

2012 University of Texas at Austin Department of Ecology, Evolution, and Behavior Start-up Grant

2010 National Science Foundation Research Experience for Undergraduates Fellowship at University of Alaska Anchorage

Teaching and Mentoring:

Teaching Assistant at the University of Texas at Austin (2012-2016)

Mentored four undergraduates and two K-12 teachers in modern molecular biology (2012-2016)

References Available Upon Request