

Andrew C. Bergen

Curriculum Vitae

Andrew Bergen, Ph.D.
Assistant Professor of Biology
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Education

Ph.D. in Molecular Genetics and Genomics – Washington University in St. Louis (August, 2015)

B.S. in Biology – University of Missouri-Kansas City (July, 2007) (Summa cum laude)

Academic and Industry Experience

Laboratory Methods Coordinator – Analytical Scientist, 2023 - 2024

Perrigo Company – Eau Claire, Wisconsin

I worked as the laboratory methods coordinator of analytical methods for the pharmaceutical and nutritional company Perrigo. I develop new laboratory methods and incorporate statistical approaches for validation of all lab data. I also develop statistical methods for analysis of results and train lab members in the proper execution of lab protocols.

Application Engineer, January 2022 – December 2022

arivis – a ZEISS company

I provided image analysis solutions for researchers using ZEISS arivis image analysis software. I worked with researchers at top universities (such as Harvard, Yale, MIT) and pharmaceutical companies (such as AstraZeneca, Novartis, Eli Lilly) that needed computational analysis solutions for their microscopy image datasets. I also wrote Python code to extend the current capabilities of the software.

Postdoctoral research, 2018 – 2021

Lab of Audrey Gasch, Laboratory of Genetics, University of Wisconsin – Madison

My research in the Gasch lab elucidated how variation in signaling and transcription factor dynamics result in heterogeneity in cell response to harmful environments. To study these areas, I used time-lapse microscopy to follow the signaling dynamics in individual yeast cells. I also wrote MATLAB analysis pipelines to automate the process of identifying important single-cell features from these datasets.

Postdoctoral research, 2015 – 2018

Lab of John Reinitz and Martin Kreitman, Department of Ecology & Evolution, University of Chicago

My research in the Reinitz and Kreitman lab focused on applying statistical models of gene regulation to understand the functional consequences of enhancer evolution in the *Drosophila* segmentation network. I also designed and wrote simulations in C++ to evolve *Drosophila* enhancers within a population *in silico* and predict the impact of mutations in specific transcription factor binding sites.

Graduate Research, 2008 – 2015

Lab of Justin Fay (Ph.D. Advisor), Department of Genetics, Washington University in St. Louis

My research in the lab of Justin Fay utilized yeast as a model system to understand the functional consequences of cis-regulatory evolution. My research also focused on theoretical models and computer simulations that addressed the effects of deleterious mutations in populations when there is epistasis between the fitness effects of mutations.

Teaching

Biology Program, Taylor University

- Introduction to Cell Biology & Genetics Lab (BIO201L) - Fall 2024
- Introduction to Cell Biology & Genetics (BIO201) – Spring, 2025
- Principles of Genetics (BIO203 & BIO203L) – Fall, 2024 & Spring 2025
- Introduction to Bioinformatics (BIO370) – Spring, 2025

Publications

Bergen, A.C., Kocik, R.A., Hose, J., McClean, M.N. and Gasch, A.P., 2022. Modeling single-cell phenotypes links yeast stress acclimation to transcriptional repression and pre-stress cellular states. *eLife*, 11, p.e82017. [[link](#)]

Bergen, A.C., Olsen, G.M. and Fay, J.C., 2016. Divergent MLS1 promoters lie on a fitness plateau for gene expression. *Molecular biology and evolution*, 33(5), pp.1270-1279. [[link](#)]

Bergen, A.C., 2015. Mutation load under additive fitness effects. *Genetics Research*, 97, p.e2. [[link](#)]

Levine, B., Hackney, J.F., **Bergen, A.**, Dobens, L. and Truesdale, A., 2010. Opposing interactions between *Drosophila* Cut and the C/EBP encoded by Slow Border Cells direct apical constriction and epithelial invagination. *Developmental Biology*, 344(1):196-209. [[link](#)]

Other Publications

Bergen, A.C., “Numerous epistatic fitness functions greatly reduce mutation load with no detectable linkage disequilibrium” (in preparation)

Bergen, A.C., *et al.* 2022. “Scalable and Automated AI Image Analysis for Volume Electron Microscopy” [[link](#)] (online research article, non-peer-reviewed)