David Gerard

American University
Department of Mathematics and Statistics
4400 Massachusetts Avenue NW, Room 106E
Don Myers Building
Washington, DC 20016-8050
U.S.A.

Phone: +1-202-885-3022
Email: dgerard@american.edu
Homepage: https://dcgerard.github.io/
Github: https://github.com/dcgerard

Education

Ph.D. Statistics, University of Washington, June 2015.

M.S. Statistics, The Ohio State University, June 2012.

B.S. Mathematics, The Ohio State University, June 2010.

B.S. Molecular Genetics, The Ohio State University, June 2010.

Articles

Published

Gerard, D., & Stephens, M. (2018). Empirical Bayes Shrinkage and False Discovery Rate Estimation, Allowing For Unwanted Variation. *To appear in Biostatistics.* [Link to Biostatistics] [Link to arXiv]

Gerard, D., & Hoff, P. (2017). Adaptive higher-order spectral estimators. *Electronic Journal of Statistics*, 11(2), 3703-3737. [Link to EJS] [Link to arXiv]

Gerard, D., & Hoff, P. (2016). A higher-order LQ decomposition for separable covariance models. *Linear Algebra and its Applications*, 505, 57-84. [Link to LAA][Link to arXiv]

Gerard, D., & Hoff, P. (2015). Equivariant minimax dominators of the MLE in the array normal model. *Journal of Multivariate Analysis*, 137, 32-49. [Link to JMVA] [Link to arXiv]

Pollack, J. D., **Gerard, D.**, & Pearl, D. K. (2013). Uniquely Localized Intra-Molecular Amino Acid Concentrations at the Glycolytic Enzyme Catalytic/Active Centers of Archaea, Bacteria and Eukaryota are Associated with Their Proposed Temporal Appearances on Earth. *Origins of Life and Evolution of Biospheres*, 43(2), 161-187. [Link to Springer]

Gerard, D., Gibbs, H. L., & Kubatko, L. (2011). Estimating hybridization in the presence of coalescence using phylogenetic intraspecific sampling. *BMC evolutionary biology*, 11(1), 291. [Link to BMC]

Preprints

Gerard, D., & Stephens, M. (2017). Unifying and Generalizing Methods for Removing Unwanted Variation Based on Negative Controls. *arXiv preprint arXiv:1705.08393.* [Link to arXiv]

Gerard, D., Ferrão, L. F. V., Garcia, A. A. F., & Stephens, M. (2018). Genotyping Polyploids from Messy Sequencing Data. *bioRxiv* [Link to bioRxiv]

Teaching Experience

Lecturer of introductory statistics 09/2017 - 12/2017

Developed my own lectures, homeworks, and exams.

This course was intended to be a standard introduction to Statistics for non-majors plus some light mathematical theory. The content included introductions to probability, inference, and the R statistical computing language.

Lecturer of introductory statistics 06/2013 - 09/2013

Developed my own lesson plans and slides from which I lectured three times a week.

Created material for two teaching assistants during their small-group sections.

Course content included comparisons of good sampling designs versus bad sampling designs, conditions under which claims of causality may be made, confounding variables, good and bad measures for answering questions of interest, describing relationships between variables, and good and bad graphics to describe data.

Graduate Teaching Assistant 09/2012 - 06/2013

Led four one-hour recitation sections of introductory statistics every week.

These were small group discussions that acted primarily as support for the main content taught during lecture.

Lecturer of introductory statistics 09/2011 - 12/2011

Lectured to large groups of students using a pre-defined course plan.

Created my own slides to follow along with the lesson plans.

Phylogenetic Workshop Assistant 06/2011 - 08/2011

Led a group of undergraduate researchers studying HIV. We studied the association between evolutionary distance (measured by branch distance along estimated trees) and clinical variables collected by an HIV treatment center in Belgium.

Phylogenetic Workshop Assistant 06/2010 - 08/2010

Led lab sessions on Unix and various phylogenetic program packages.

Led a group of undergraduates researching the evolutionary origins of flightless birds.

Individually mentored an undergraduate student on phylogenetic research and statistical analysis with R. We tried to incorporate protein structure into our gene tree estimates while studying the evolutionary relationships of HPV.

Undergraduate Teaching Assistant: 09/2008 - 12/2008

Taught four one-hour recitation sections of intermediate algebra every week.

Research Experience

Postdoctoral Scholar under Professor Matthew Stephens: 09/2015 - 07/2018

Developed empirical Bayes methods to account for hidden confounding in large scale gene expression studies.

Efficiently implemented these methods in R and C++.

Rigorously tested these methods using Monte Carlo methods.

Lead/mentored graduate students on their individual projects.

Authored reports and academic papers.

Research Assistant Under Professor Peter Hoff: 09/2013 - 06/2015

Studied optimal estimation of covariance matrices in Gaussian arrays using the notions of equivariance.

Developed novel tensor decompositions, creating higher-order versions of well-known matrix decompositions.

Developed singular value shrinkage mean estimators for tensor-variate data.

Research Assistant Under Professor Joe Verducci: 09/2011 - 06/2012

Studied monotone association between gene expression and drug resistance within unspecified subtypes of cancer.

Undergraduate Research Fellow Under Professors Laura Kubatko and H. Lisle Gibbs: 04/2009 - 06/2010

Studied the hybridization of two subspecies of Missouri Rattlesnakes and two populations of Black Ratsnakes.

Duties included sequencing work in the lab, computer programming using Perl, and data analysis with various programs.

Awards

Z.W. Birnbaum Award for the best general exam of the 2013-2014 academic year. This is the only research award presented by the University of Washington Statistics Department.

Distinguished University Fellowship (September 2010 - June 2012).

Graduated Summa Cum Laude (June 2010).

Medalist Scholarship (September 2006 - June 2010).

Coding

R Packages: `tensr`, `hose`, `vicar`, `seqgendiff`, `updog`.

Advanced training: R, LaTeX.

Intermediate training: C++, Shell.

Familiar: Python, Matlab/Octave, Mathematica.

Data Analysis

Data Munging (tidyverse).

Data Visualization (ggplot2).

Reproducible Data Analysis (rmarkdown/make).

Version Control (Git/Github).

Continuous Integration (Travis CI/AppVeyor).

R package development.