William Michael Landau

Education

- PhD Statistics, Iowa State U, 2016
- MS Statistics, Iowa State U 2013
- BS Math, U of Chicago 2011

Contact

- will.landau@gmail.com
- wlandau.github.io
- linkedin.com/in/wlandau
- github.com/wlandau

Publications

- Landau, W., Niemi, J., and Nettleton, D., "Fully Bayesian analysis of RNA-seq counts for the detection of gene expression heterosis". *Journal of the American Statistical Association*, https://doi.org/10.1080/01621459.2018.1497496.
- Landau, W. (2018), "The drake R package: a pipeline toolkit for reproducibility and high-performance computing". *Journal of Open Source Software*, 3(21), 550, https://doi.org/10.21105/joss.00550.
- Niemi, J., Mittman, E., Landau, W., and Nettleton, D. (2015), "Empirical Bayes Analysis of RNA-seq Data for Detection of Gene Expression Heterosis," *Journal of Agricultural*, *Biological*, and *Environmental Statistics*, 20, 1-15. Available at link.springer.com.
- Landau, W. and Liu, P. (2013), "Dispersion Estimation and Its Effect on Test Performance in RNA-seq Data Analysis: A Simulation-Based Comparison of Methods," *PLOS One*, 8. Available at journals.plos.org.
- Ratliff, B., Womack. C., Tang, X., Landau, W., Butler, L., and Szpunar, D. (2010), "Modeling the Rovibrationally Excited C2H4OH Radicals from the Photodissociation of 2-Bromoethanol at 193 nm," *Journal of Physical Chemistry*, 114, 4934-4945. Available at ncbi.nlm.nih.gov.

Open Source Software

- drake, an R-focused pipeline toolkit for reproducible computation and high-performance computing. Part of rOpenSci.
- txtq, a minimalist, serverless, socketless message queue for interprocess communication.
- downsize, and R package to toggle between the test and production versions of large workflows.
- R packages fbseq, fbseqCUDA, and fbseqOpenMP. A toolkit for the fully Bayesian analysis
 of genomic count data.

Awards

- 2017 Lilly Innovator Award. Awarded for leading a successful team effort to modernize Lilly's internal process for contributing open source software.
- Student Paper Award, American Statistical Association Section on Statistical Computing, Jan 2016. Awarded for an early draft of the preprint at arxiv.org/abs/1606.06659.
- Vince Sposito Statistical Computing Award, Iowa State University, Aug 2013.
- GlaxoSmithKline Industrial Scholarship, Iowa State University, Sep 2011.
- Alumni Scholarship, Iowa State University, Aug 2011.

Skills

- Reproducible research, statistical computing, hierarchical models, Bayesian methods, Markov chain Monte Carlo, high-dimensional data analysis, genomics data analysis, exploratory analysis, visualization, linear and nonlinear models, data mining, machine learning, predictive modeling, multivariate analysis.
- High-performance computing, R, R package development, general-purpose graphics processing unit (GPU) computing, CUDA, shell scripting, LaTeX, HTML, CSS.
- Past experience with C/C++, MPI, OpenMP, Python, JavaScript, AWK, Fortran.

Research statistician

- October 2016 Present
- Eli Lilly and Company
- Developed internal statistical tools and capabilities for the design, simulation, and analysis
 of clinical trials.
- Served as the lead statistician in early-phase autoimmune asset teams.
- Supported late-phase clinical trial teams with advanced analytics, including clinical program simulation and tailored therapeutics.
- Published open-source software packages drake and txtq to improve reproducibility and high-performance computing in R.

Research assistant

- May 2013 Aug 2016
- RNA-sequencing Working Group, Department of Statistics, Iowa State University.
- Funded by NIH grant R01GM109458 with Drs. Dan Nettleton and Jarad Niemi.
- Developed a new fully Bayesian analysis method for high-dimensional genomic datasets using hierarchical models.
- Implemented massively parallelized Markov chain Monte Carlo.
- Created the fbseq R package to distribute the analysis method.
- Implemented and distributed parallel computing backends for CUDA GPUs (fbseqCUDA) and OpenMP (fbseqOpenMP).

 Created the remakeGenerator, parallelRemake, and downsize packages to manage, ameliorate, expedite, and accelerate computationally heavy reproducible workflows that are under heavy development.

Seminar instructor

- Aug Dec, 2012 and 2013.
- Department of Statistics, Iowa State University.
- GPU computing seminar series at wlandau.github.io/gpu.
- Educated faculty and graduate students on massively parallel computing with generalpurpose graphics processing units.
- Constructed, curated, and distributed slides, video, and example code at wlandau.github.io/gpu and on YouTube.

Course instructor

- Jan May, 2012 and 2013.
- Department of Statistics, lowa State University.
- STAT 305: Engineering Statistics (wlandau.github.io/stat305).

Grader

- Aug Dec, 2011.
- Department of Statistics, lowa State University.
- STAT 231: Engineering Probability.
- STAT 105: Introduction to Engineering Statistics.

Leadership at Eli Lilly and Company

- Led a successful team effort to modernize Lilly's internal procedure for contributing open source software.
- Served as a volunteer moderator in the 2017 National Science Bowl (high school Indiana Regionals).

Leadership at Iowa State University

- Founder and leader, Cloud Computing Working Group, Sep Dec 2015.
- Member, Computation Advisory Committee, Sep 2015 May 2016.
- Volunteer instructor, Office of Precollegiate Programs for Talented and Gifted (OPPTAG), Mar 13, 2014.
- Fellow, Preparing Future Faculty, Aug 2013 May 2014.

• Assistant Coach, Boxing Club, Aug 2013 - Dec 2013.

References

- Jarad Niemi, PhD advisor and major professor, niemi@iastate.edu.
- Dan Nettleton, lead principal investigator of the RNA-sequencing Working Group (Iowa State Department of Statistics), dnett@iastate.edu.
- Peng Liu, MS advisor and major professor, pliu@iastate.edu.
- Additional references available on request.

Hobbies

• Climbing, Brazillian Jiu Jitsu, sailing, windsurfing