# Aaron J. Fisher

Biostatistics & Machine Learning Researcher

② aaronjfisher.com | ☑ afishe27@alumni.jh.edu | Ў @ajfishr | ♥ Boston, MA

### **Education**

**PhD** in Biostatistics (2016), Johns Hopkins Bloomberg School of Public Health, Baltimore, MD

- Advisors: Vadim Zipunnikov & Brian Caffo
- Awards & Scholarships:
  - Margaret Merrell Award for outstanding research by a Biostatistics doctoral student
  - June B. Culley Award for outstanding achievement on an oral examination paper
  - Doctoral Training Grant in Environmental Biostatistics

**BA** in Economics (2010), *University of Rochester*, Rochester, NY

Summa cum laude

### **Professional experience**

**Principal Statistician** (2019-Present), *Takeda Pharmaceuticals*, *Statistics and Quantitative Sciences*, Boston, MA

- o Analysis of wearable devices in early-stage clinical trials (with Dmitri Volfson) **Postdoctoral Research Fellow** (2016-2019), *Dept of Biostatistics at the Harvard T.H. Chan School of Public Health*, Boston, MA
- Advisors: Francesca Dominici & Cynthia Rudin
   Statistical Consultant (2016), Pfizer, Boston, MA
- o Analysis of wearable devices and temperature probes in human sleep studies

Intern Analyst (2010), Structured Decisions Corporation, Newton, MA

o Background research project for a linear programming application

#### **Skills**

**Statistics & Machine Learning**: Causal inference, matrix decompositions, regression in a RKHS, Bayesian regression trees, random forests, neural networks, finite sample bounds, adaptive clinical trials, non-convex quadratic programming, functional data analysis

**Computing**: R package development, git, Python, PyTorch, MATLAB, Stata, shell scripting, LATEX

### Summary of selected projects

Fast bootstrap PCA for millions of covariates: When analyzing high dimensional brain MRI data, with millions of voxels measured for each patient, principal component analysis is commonly used to reduce dimension. However, bootstrapping such analyses can be computationally time-intensive. We developed a procedure that reduces this time from the order of days to the order of minutes, with no loss in accuracy. Our work was published in JASA T&M, and my associated R package (bootSVD) has been downloaded over 23,000 times.

**Interpretability for machine learning models**: Uninterpretable, black-box prediction mod-

els can provoke distrust, and their predictions can be difficult to combine with supplementary information in order to make decisions. We proposed a formalization of existing methods for summarizing how much a given black-box model uses different covariates to gain prediction accuracy, and also developed a novel method for estimating how much *unknown proprietary* models rely on different covariates. We applied this method to study the dominant predictive factors in the criminal recidivism model COMPAS. The technical aspects of this paper combined approaches from finite sample theory, U-statistics, covering numbers, and non-convex quadratic programming. Our paper was published in JMLR, and has been cited over 169 times (link), including citations to previous arXiv versions.

In more recent work, I have been developing machine learning methods for wearable device data that balance accuracy with interpretability.

**Influence functions for causal inference**: Influence functions have emerged as a popular framework for combining machine learning with statistical inference, especially within the field of causal inference. Unfortunately, the technical theory underlying influence functions intimidates many researchers away from the subject. My educational paper on this topic attempts to make influence functions more approachable and intuitive. The paper, published in The American Statistician, is built around rigorous, visual illustrations, which we hope can be similarly useful to illustrations of a standard derivative as the "slope at a point."

**Fast prognostic scores for prostate cancer screening**: As part of a team developing Bayesian risk scores that inform decisions on whether to pursue invasive diagnostic tests, I implemented an importance sampling approach to obtain fast, in-clinic risk updates in response to new patient information.

## Selected academic papers (see Google Scholar for full list)

Submitted

**A. J. Fisher** (2020). Treatment effect bias from sample snooping: blinding outcomes is neither necessary nor sufficient. ( $\underline{link}$ .)

#### Peer-Reviewed Publications...

- **A. J. Fisher,** E. H. Kennedy (2020). Visually Communicating and Teaching Intuition for Influence Functions. *The American Statistician*. (<u>link</u>.)
- **A. J. Fisher,** C. Rudin, F. Dominici (2019). All Models are Wrong, but Many are Useful: Learning a Variable's Importance by Studying an Entire Class of Prediction Models Simultaneously. *The Journal of Machine Learning Research*. (paper link; 169 citations as of July 16, 2020, including citations to previous arXiv versions)
- **A. J. Fisher**, M. Rosenblum (2018). Stochastic Optimization of Adaptive Enrichment Designs for two Subpopulations. *Journal of Biopharmaceutical Statistics*. (<u>link</u>.)
- R. Y. Coley, **A. J. Fisher**, M. Mamawala, H. B. Carter, K. J. Pienta, S. L. Zeger (2017). A Bayesian Hierarchical Model for Prediction of Latent Health States from Multiple Data Sources with Application to Active Surveillance of Prostate Cancer. *Biometrics*. (<u>link</u>.)
- **A. J. Fisher**, B. Caffo, B. Schwartz, V. Zipunnikov (2016). Fast, Exact Bootstrap Principal Component Analysis for p > 1 million. *Journal of the American Statistical Association TM*. (link.)
- **A. J. Fisher**, G. B. Anderson, R. Peng, J. Leek (2014). A randomized trial in a massive online open course shows people don't know what a statistically significant relationship looks like, but they can learn. *PeerJ.* (<u>link</u>; 10,610 unique visitors as of July 16, 2020.)