

Nima Hejazi

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Curriculum Vitæ

updated: October 2018

Current Positions

- *Ph.D. Candidate*, Group in Biostatistics, University of California, Berkeley
Advisors: Mark van der Laan and Alan Hubbard

Research Interests

- Methodology causal inference, nonparametric statistics, machine learning, targeted loss-based estimation, semiparametric theory, survival analysis, statistical computing, reproducible research.
- Applications precision medicine, computational biology and bioinformatics, epidemiology, randomized clinical trials, vaccine efficacy trials, healthcare policy, public policy.

Education

- 2016–present **Doctor of Philosophy in Biostatistics**, *University of California, Berkeley*.
Designated emphasis (Ph.D. minor) in Computational and Genomic Biology
Committee: [Mark van der Laan](#) (co-chair), [Alan Hubbard](#) (co-chair), [Nicholas Jewell](#), [Fernando Pérez](#)
Dissertation: Topics in Robust Nonparametric Estimation, Causal Inference, and Statistical Computing
- 2016–2017 **Master of Arts in Biostatistics**, *University of California, Berkeley*.
Committee: Mark van der Laan (co-chair), Alan Hubbard (co-chair), Martyn Smith
Thesis: Generalized Application of Empirical Bayes Statistics to Asymptotically Linear Parameters
- 2011–2015 **Bachelor of Arts**, *University of California, Berkeley*.
Molecular & Cell Biology, Psychology, Public Health (triple major)

Accreditation, Open Education, and Training

- 10/2017 **Instructor Training Program Certification**, *Software Carpentry*.
- 04–11/2016 **Genomic Data Science Specialization**, *Johns Hopkins University via Coursera*.
- 02–12/2015 **Data Science Specialization**, *Johns Hopkins School of Public Health via Coursera*.

Research Experience

- 01/2017–present **Graduate Student Researcher**, *University of California, Berkeley, Berkeley, CA*.
Advisor: Prof. Mark J. van der Laan, Division of Biostatistics & Department of Statistics
- Theoretical and methodological developments for nonparametric statistical and causal inference in the assessment of effects based on stochastic interventions, coupled with software implementations.
 - Techniques for nonparametric estimation with functional constraints and targeted loss-based estimation over constraint-specific paths, with applications to algorithmic fairness and optimal treatments.
 - Development and implementation of robust, model-free methods for the identification of differentially methylated positions and regions using high-dimensional microarray data for methylation profiling.
 - Core developer and founding member of the [tlverse](#), a robust and centralized software ecosystem (in the R language) for statistical and causal inference within the framework of Targeted Learning.

- 08/2015–**Graduate Student Researcher**, *University of California, Berkeley*, Berkeley, CA.
present Advisor: Prof. Alan E. Hubbard, Division of Biostatistics
- Development of methods for robust statistical inference with applications in high-dimensional biology, including data-adaptive hypothesis testing and variance-moderated targeted loss-based estimation.
 - Statistical data analysis of high-dimensional genomics and epigenetics data, as well as collaborative bioinformatical support, for experimental efforts in molecular biology and toxicology.
- 03/2014–**Undergraduate Student Researcher**, *University of California, Berkeley*, Berkeley, CA.
05/2015 Lab of Prof. Mark T. D’Esposito, Helen Wills Neuroscience Institute & Department of Psychology
- Study of the properties of resting-state voxel connectivity in the visual system using fMRI data.
- 05/2012–**Undergraduate Student Researcher**, *UCSF Medical Center*, San Francisco, CA.
02/2015 Supervisor: Dr. Paul S. Larson, Department of Neurological Surgery
- Analysis of outcomes from deep brain stimulation surgery using interventional MR imaging.
- 08/2012–**Undergraduate Research Assistant**, *University of California, Berkeley*, Berkeley, CA.
05/2014 Lab of Prof. Robert T. Knight, Helen Wills Neuroscience Institute & Department of Psychology
- Study of disruptions in lexical selection from neurological disease based on human EEG recordings.
- 08/2011–**Undergraduate Research Assistant**, *University of California, Berkeley*, Berkeley, CA.
05/2013 Lab of Prof. Leslea J. Hlusko, Department of Integrative Biology
- Data collection for studies in quantitative genetics concerning the evolution of hominid dentition.

Industry Experience

- 08/2018–**Biostatistical Analyst (Intern)**, *Kaiser Permanente Division of Research*, Oakland, CA.
present Supervisor: Dr. Romain S. Neugebauer, Biostatistics Core, and Dr. Julie A. Schmittdiel
- Development and implementation of robust prediction methodology combining ensemble machine learning and causal inference, applied to massive longitudinal studies using electronic health records.
- 01/2016–**Data Scientist (Intern)**, *Cogitativo, Inc.*, Berkeley, CA.
03/2016
- Applied modern statistical methods, data analytic tools, and data product design to problems in the healthcare services space, producing client-side tools for interactive data mining and visualization.
- 03/2016–**Private Consultant**.
present
- Consultation on problems in statistics, data analysis, and software development for data science.

Awards, Honors, & Scholarships

- June 2018 Travel Scholarship, BioC 2018: Where Software and Biology Connect (annual conference), Bioconductor: Open Source Software for Bioinformatics
- March 2018 The Wellness Scholarship in Honor of Chin Long Chiang, School of Public Health, University of California, Berkeley
- 2017–2018 NIH BD2K Training Grant (T32LM012417-02), Biomedical Big Data Training Program, University of California, Berkeley
- July 2017 Travel Scholarship, Summer Institute in Statistics for Big Data, Department of Biostatistics, University of Washington
- May 2017 Honorable mention (rank 3–6), Thomas R. Ten Have Award for junior researchers, for the poster “Nonparametric variable importance for continuous exposures with applications in high-dimensional biology”, Atlantic Causal Inference Conference
- June 2015 Travel Scholarship, Summer Institute in Biostatistics, Department of Biostatistics & Medical Informatics, University of Wisconsin — Madison

Publications

Statistical Applications

- [1] **N. Hejazi**, C. Schiffman, and X. Zhou, "Review of 'statistical analysis of numerical preclinical radiobiological data'," *ScienceOpen Research*, 2017. doi: 10.14293/s2199-1006.1.sor-stat.afhtwc.v1.rxidzs. [Online]. Available: <https://dx.doi.org/10.14293%2Fs2199-1006.1.sor-stat.afhtwc.v1.rxidzs>
- [2] A. Sobh, A. Loguinov, G. Naz Yazici, **N.S. Hejazi**, A.E. Hubbard, M. Smith, L. Zhang, and C.D. Vulpe, "Functional profiling identified determinants of arsenic trioxide cellular toxicity," *submitted*, 2018.

Refereed Statistical Software

- [1] **N.S. Hejazi**, W. Cai, and A.E. Hubbard, "biotmle: Targeted Learning for biomarker discovery," *The Journal of Open Source Software*, vol. 2, no. 15, 2017. doi: 10.21105/joss.00295. [Online]. Available: <https://dx.doi.org/10.21105/joss.00295>
- [2] J.R. Coyle and **N.S. Hejazi**, "origami: A generalized framework for cross-validation in R," *The Journal of Open Source Software*, vol. 3, no. 21, 2018. doi: 10.21105/joss.00512. [Online]. Available: <https://dx.doi.org/10.21105/joss.00512>
- [3] **N.S. Hejazi**, R.V. Phillips, A.E. Hubbard, and M.J. van der Laan, "methyvim: Targeted, robust, and model-free differential methylation analysis in R," *F1000Research*, vol. 7, no. 1424, 2018. doi: 10.12688/f1000research.16047.1. [Online]. Available: <https://dx.doi.org/10.12688/f1000research.16047.1>
- [4] W. Cai, A. Hubbard, and **N.S. Hejazi**, "adapttest: Data-adaptive statistics for high-dimensional multiple hypothesis testing in R," *The Journal of Open Source Software*, submitted.

Currently in Preparation

- [1] **N.S. Hejazi**, S. Kherad-Pajouh, M.J. van der Laan, and A.E. Hubbard, "Variance moderation of locally efficient estimators in high-dimensional biology." [Online]. Available: <https://arxiv.org/abs/1710.05451>
- [2] **N.S. Hejazi**, K. Benac, and N.P. Jewell, "Immortal time bias analyses: Time-varying survival regression models and delayed entry approaches."
- [3] **N.S. Hejazi**, M.J. van der Laan, H.E. Janes, P.B. Gilbert, and D.C. Benkeser, "Efficient estimation of and robust inference on the effects of stochastic interventions under two-phase sampling."
- [4] **N.S. Hejazi** and M.J. van der Laan, "Optimal nonparametric estimation of constrained functional parameters."
- [5] —, "Targeted maximum likelihood estimation with constraint-specific paths."
- [6] I. Díaz and **N.S. Hejazi**, "Causal mediation analysis for stochastic interventions."
- [7] D.C. Benkeser, A. Chambaz, and **N.S. Hejazi**, "A guided tour in Targeted Learning territory."
- [8] W. Cai, **N.S. Hejazi**, and A.E. Hubbard, "Data-adaptive statistics for multiple hypothesis testing in high-dimensional settings." [Online]. Available: <https://arxiv.org/abs/1704.07008>

Dissertations and Theses

- [1] **N.S. Hejazi**, “Generalized application of empirical Bayes statistics to asymptotically linear parameters,” Master’s thesis, University of California, Berkeley, 2017.

Software

Open Source Software and Projects

- [1] **N.S. Hejazi** and A.E. Hubbard, “biotmle: Targeted Learning with moderated statistics for biomarker discovery,” <https://bioconductor.org/packages/biotmle>, R package version 1.4.0. [Online]. Available: <https://dx.doi.org/10.18129/B9.bioc.biotmle>
- [2] **N.S. Hejazi** and M.J. van der Laan, “methyvim: Targeted, robust, and model-free differential methylation analysis,” <https://bioconductor.org/packages/methyvim>, R package version 1.2.0. [Online]. Available: <https://dx.doi.org/10.18129/B9.bioc.methyvim>
- [3] D.C. Benkeser and **N.S. Hejazi**, “survtmle: Compute targeted minimum loss-based estimates in right-censored survival settings,” <https://CRAN.R-project.org/package=survtmle>, R package version 1.1.0. [Online]. Available: <https://dx.doi.org/10.5281/zenodo.835868>
- [4] J.R. Coyle and **N.S. Hejazi**, “origami: Generalized framework for cross-validation,” <https://CRAN.R-project.org/package=origami>, R package version 1.0.0. [Online]. Available: <https://dx.doi.org/10.5281/zenodo.1155901>
- [5] J.R. Coyle, **N.S. Hejazi**, I. Malenica, and O. Sofrygin, “sl3: Pipelines for machine learning and Super Learning,” <https://github.com/tlverse/sl3>, R package version 1.1.0. [Online]. Available: <https://dx.doi.org/10.5281/zenodo.1342294>
- [6] W. Cai, A.E. Hubbard, and **N.S. Hejazi**, “adapttest: Data-adaptive statistics for high-dimensional multiple testing,” <https://bioconductor.org/packages/adapttest>, R package version 1.0.0. [Online]. Available: <https://dx.doi.org/10.18129/B9.bioc.adapttest>
- [7] J.R. Coyle, **N.S. Hejazi**, and M.J. van der Laan, “hal9001: The scalable Highly Adaptive Lasso,” <https://github.com/tlverse/hal9001>, R package version 0.2.0.
- [8] **N.S. Hejazi**, M.J. van der Laan, and D.C. Benkeser, “txshift: Targeted Learning of the causal effects of stochastic interventions,” <https://github.com/nhejazi/txshift>, R package version 0.2.0.
- [9] **N.S. Hejazi**, J.R. Coyle, and M.J. van der Laan, “tmle3shift: Targeted maximum likelihood estimation of the effects of stochastic shift interventions,” <https://github.com/tlverse/tmle3shift>, R package version 0.1.5.

Presentations

Talks — Invited and Contributed

- [1] **N.S. Hejazi**, “Fair inference through semiparametric-efficient estimation over constraint-specific paths,” August 2018, Joint Statistical Meetings (contributed). [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2018_jsm_fairtmle.pdf
- [2] **N.S. Hejazi**, A.E. Hubbard, and M.J. van der Laan, “Data-adaptive estimation and inference for differential methylation analysis,” July 2018, BioC 2018: Where Software and Biology Connect, Bioconductor (contributed). [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2018_bioc_methyvim/2018_bioc_methyvim.html

- [3] **N. Hejazi**, “Robust nonparametric inference for stochastic interventions under multi-stage sampling,” April 2018, Biostatistics Seminar Series, Division of Biostatistics, UC Berkeley (contributed). [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2018_berkeley_txshift.pdf
- [4] **N. Hejazi** and K. Benac, “Efficient estimation of survival prognosis under immortal time bias,” March 2018, Berkeley Statistics Annual Research Symposium, Department of Statistics, UC Berkeley (contributed). [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2018_itb_bstars.pdf
- [5] **N. Hejazi**, “Data-adaptive estimation and inference for differential methylation analysis,” November 2017, Annual Computational and Genomic Biology Retreat, Center for Computational Biology, UC Berkeley (contributed). [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2017_berkeley_methyvim.pdf
- [6] —, “Finite-sample inference and moderated statistics for asymptotically linear parameters,” March 2017, Biostatistics Seminar Series, Division of Biostatistics, UC Berkeley (contributed). [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2017_berkeley_biotmle.pdf
- [7] A.E. Hubbard, **N. Hejazi**, W. Cai, and A. Decker, “Targeted learning for high-dimensional variable importance,” July 2016, Statistical Causal Inference and Applications to Genetics, Centre de Recherches Mathématiques (invited). [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2016_crm_limmatmle.pdf

Posters — Invited and Contributed

- [1] **N.S. Hejazi**, M.J. van der Laan, and D.C. Benkeser, “Robust nonparametric inference for stochastic interventions under multi-stage sampling,” May 2018, Atlantic Causal Inference Conference. [Online]. Available: https://statistics.berkeley.edu/~nhejazi/posters/2018_acic.pdf
- [2] **N. Hejazi**, K. Benac, and N.P. Jewell, “Efficient estimation of survival prognosis under immortal time bias,” March 2018, Berkeley Statistics Annual Research Symposium. [Online]. Available: https://statistics.berkeley.edu/~nhejazi/posters/2018_bstars.pdf
- [3] **N.S. Hejazi**, I. Malenica, A.K. Waschka, A.E. Hubbard, and M.J. van der Laan, “Nonparametric variable importance for continuous exposures with applications in high-dimensional biology,” May 2017, Atlantic Causal Inference Conference. [Online]. Available: https://statistics.berkeley.edu/~nhejazi/posters/2017_acic.pdf
- [4] **N. Hejazi** and A.E. Hubbard, “Super Learner for optimal prediction,” July 2016, Statistical Causal Inference and Applications to Genetics, Centre de Recherches Mathématiques. [Online]. Available: https://statistics.berkeley.edu/~nhejazi/posters/2016_crm-comp.pdf

Other Talks and Presentations

- [1] **N. Hejazi**, “Towards the realistic, robust, and efficient assessment of causal effects with stochastic shift interventions,” September 2018, Ph.D. Qualifying Examination, Graduate Group in Biostatistics, UC Berkeley. [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2018_phd_qual.pdf
- [2] —, “Targeted biomarker discovery,” April 2018, Career Exploration Committee, Statistics Undergraduate Student Association, UC Berkeley. [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2018_susa_berkeley/2018_susa_berkeley.html

- [3] —, “Targeted biomarker discovery,” March 2017, Graduate Student Admit Day, Group in Biostatistics, UC Berkeley. [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2017_admitday_berkeley/2017_admitday_berkeley.html
- [4] **N. Hejazi** and E. Muzzall, “Ensemble machine learning with Super Learner and h2o in R,” December 2016, The Hacker Within, Berkeley Institute for Data Science, UC Berkeley. [Online]. Available: https://statistics.berkeley.edu/~nhejazi/present/2016_talk_h2oSL_THW.pdf

Activities, Service, & Affiliations

Ad-Hoc Reviewer

- 2018–present IEEE/ACM Transactions on Computational Biology and Bioinformatics
 2018–present The Journal of Open Source Software

Education and Outreach

- 2018–present Lesson Maintainer, “Version Control with Git” (workshop materials), Software Carpentry

University and Departmental Committees

- Aug. 2018–present Member of Executive Board, Biostatistics Graduate Student Association, Graduate Group in Biostatistics, University of California, Berkeley; Berkeley, CA, USA
 Feb. 2018 Invited Member, Admissions Committee for Graduate Studies (M.A./Ph.D.), Graduate Group in Biostatistics, University of California, Berkeley; Berkeley, CA, USA

Affiliations

- 2017–present International Biometric Society (Western North American Region)
 2016–present Berkeley Institute for Data Science
 2016–present American Statistical Association

Teaching Experience

Teaching Assistantship

- Spring 2018 *Targeted Learning in Biomedical Big Data* (PBHLTH 290), with Prof. Mark J. van der Laan, Division of Biostatistics, University of California, Berkeley
- o Developed all laboratory materials and homework assignments, provided weekly laboratory instruction, and supervised course projects, as the sole graduate student instructor for the pilot offering of this course.
 - Course website: <https://vanderlaan-group.github.io/tlbbd-sp2018/>
 - Laboratory materials: <https://github.com/tlbbd-sp2018>

Short Course and Workshop Instructorship

- 2017–present *Software Carpentry* — workshop instruction aiming to promote and foster skills, best practices, and workflows for software development and scientific computing in research settings.
- o Jul. 2018; “Scientific Computing with Bash, Git, and Python”; workshop instructor (co-instructor: K. Marwaha); Berkeley Institute for Data Science; website: <https://bids.github.io/2018-07-16-bids/>
 - o Jan. 2018; “Scientific Computing with Bash, Git, and R”; workshop helper with K. Ottoboni & T. Hart; Berkeley Institute for Data Science; website: <http://www.kellieottoboni.com/2018-01-11-bids/>

- 2017–present *Data Carpentry* — workshop instruction centering on core skills and best practices for the application of data analytic principles and tools for scientific computing in research.
- o May 2018; “Software Tools for Genomic Data Analysis”; workshop instructor (co-instructor: A. Orr); Lawrence Berkeley National Laboratory; website: <https://code.nimahejazi.org/2018-05-03-LBNL/>
 - o Aug. 2017; “Software Tools for Genomic Data Analysis”; workshop helper with K. Hertweck & E. Becker; Lawrence Berkeley National Laboratory; website: <https://k8hertweck.github.io/2017-08-07-LBNL/>
- Aug. 2018 Module Instructor, R Bootcamp, with Dr. Christopher J. Paciorek, Department of Statistics, University of California, Berkeley
- o Presented modules on modern data manipulation (via the tidyverse suite of packages) and data visualization, contributed new instructional materials, and assisted in one-on-one instruction of participants.
 - Short course description: <https://statistics.berkeley.edu/computing/r-bootcamp>
 - Workshop materials: <https://github.com/berkeley-scf/r-bootcamp-2018>
- Aug. 2017 Module Instructor, R Bootcamp, with Dr. Christopher J. Paciorek, Department of Statistics, University of California, Berkeley
- o Presented a module on programming concepts in R (iteration, flow control, writing functions), contributed new materials on modern functional programming, and assisted in one-on-one instruction of participants.
 - Short course description: <https://statistics.berkeley.edu/computing/r-bootcamp>
 - Workshop materials: <https://github.com/berkeley-scf/r-bootcamp-2017>

Miscellaneous Teaching

- 2017–present Private Tutor in Statistics (introductory, computing, and intermediate-level theory courses)
 2015–2016 Tutor in Mathematics & Statistics, Athletic Study Center, University of California, Berkeley
 2013–2015 Tutor in General Chemistry, Student Learning Center, University of California, Berkeley

Computing Skills

- Systems: Linux (Ubuntu/Debian, Red Hat, Arch), macOS, UNIX
 Languages: R, PYTHON, JULIA, C++, SQL, L^AT_EX, MATLAB, shell scripting
 Apps/Other: Git/GitHub, Amazon Web Services (EC2), Google Compute Engine, Microsoft Office

Selected Courses (credit or audit)

- 2016–??? **Berkeley (graduate):** Theoretical Stat. I (W. Fithian), Theoretical Stat. II (M.I. Jordan), Applied Stat. I (P.B. Stark), Applied Stat. II (J. McAuliffe), Stat. Genomics (S. Dudoit), Causal Inference (M. Petersen), Causal Inference & Sensitivity Analysis (S. Pimentel), Experimental Design (S. Pimentel), Fairness in Machine Learning (M. Hardt), Machine Learning in Bio. (J. Listgarten), Targeted Learning (M.J. van der Laan), Adaptive Designs (M.J. van der Laan), Convex Optim. (B. Recht)
- 2011–2015 **Berkeley (undergraduate):** Modern Biostat. Theory (M.J. van der Laan & A.E. Hubbard), Survival Analysis & Causality (M.J. van der Laan), Computational Biostat. (S. Dudoit), Longitudinal Data Analysis (N.P. Jewell), Stat. Data Science (K.J. Millman), Multivar. Stat. (L. Li), Big Data in Public Health (L. Li), Fourier Analysis (J.A. Strain), Mathematical Bio. (L. Pachter)

Distractions

2007–??? Endurance Sports: Distance Running

- Half marathons: Berkeley (2018)
- Trail running: 20–40 miles per week.
- Cross Country (2007, 2008, 2010)