

CONTACT INFORMATION	Department of Statistics and Data Science Carnegie Mellon University Pittsburgh, PA USA	website: willtownes.github.io email: ftownes@andrew.cmu.edu
SUMMARY	I am an applied statistician working primarily with biomedical data. I am involved with infectious disease as part of the Delphi Group and have developed methods for spatial and single-cell genomics. I am also interested in wearable devices, ecology, and economics. I strive to produce open source software implementations to help scientists achieve their research goals more effectively.	
PROFESSIONAL EXPERIENCE	2022 - present	Assistant Professor , Department of Statistics and Data Science Carnegie Mellon University, Pittsburgh, PA
	2019 - 2022	Postdoctoral Researcher , Department of Computer Science Princeton University, Princeton, NJ (advisor: Barbara Engelhardt)
	2011 - 2014	Software Test Engineer , SRA International, Arlington, VA
	2008 - 2010	Software Analyst , Perrin Quarles Associates, Charlottesville, VA
	2007 - 2008	Fulbright Scholar , University of the Philippines Conducted independent forest ecology research while living with an indigenous <i>Aeta</i> community in Bataan Province.
EDUCATION	2019	Ph.D. Biostatistics , Harvard University, Cambridge, MA USA <i>Dissertation Committee: Rafael Irizarry (Dana-Farber Cancer Institute, Data Science)</i> <i>Jeff Miller (Harvard University, Biostatistics)</i> <i>Martin Aryee (Massachusetts General Hospital, Pathology)</i>
	2013	M.S. Mathematics & Statistics , Georgetown University, Washington, DC USA
	2007	B.S. Biology , Washington & Lee University, Lexington, VA USA
RESEARCH	In Review	
	[1] Jones A, Townes FW , Li D, Engelhardt BE. Alignment of spatial genomics and histology data using deep Gaussian processes (2022). Preprint: doi: 10.1101/2022.01.10.475692 .	
	[2] Verpeut JL, Bergeler S, Kislin M, Townes FW , Klibaite U, Dhanerawala ZM, Hoag A, Jung C, Lee J, Pisano TJ, Seagraves KM, Shaevitz JW, Wang SSH. Cerebellar contributions to a brainwide network for flexible behavior (2021). Preprint: doi: 10.1101/2021.12.07.471685 .	
	In Press	
	[1] Townes FW , Engelhardt BE. Nonnegative spatial factorization. <i>Nature Methods</i> (2022). Preprint: https://arxiv.org/abs/2110.06122 .	
	Peer-reviewed Journal Articles	
	[1] Gewirtz ADH, Townes FW , and Engelhardt BE. Telescoping bimodal latent Dirichlet allocation to identify expression QTLs across tissues. <i>Life Science Alliance</i> (2022). doi: 10.26508/lsa.202101297 .	
	[2] Jones A, Townes FW , Li D, Engelhardt BE. Contrastive latent variable modeling with application to case-control sequencing experiments. <i>Annals of Applied Statistics</i> (2022). doi: 10.1214/21-AOAS1534 .	
	[3] Hecker J, Townes FW , Kachroo P, Lasky-Su J, Ziniti J, Cho MH, Weiss ST, Laird NM, Lange C. A unifying framework for rare variant association testing in family-based designs, including higher criticism approaches, SKATs, and burden tests. <i>Bioinformatics</i> (2020). doi: 10.1093/bioinformatics/btaa1055 .	
	[4] Townes FW , Carr K, Miller JW. Identifying longevity associated genes by integrating gene expression and curated annotations. <i>PLOS Computational Biology</i> (2020). doi: 10.1371/journal.pcbi.1008429 .	

- [5] **Townes FW**, Irizarry RA. Quantile normalization of single-cell RNA-seq read counts without unique molecular identifiers. *Genome Biology* (2020). doi:10.1186/s13059-020-02078-0.
- [6] **Townes FW**, Hicks SC, Aryee MJ, Irizarry RA. Feature selection and dimension reduction for single-cell RNA-Seq based on a multinomial model. *Genome Biology* (2019). doi:10.1186/s13059-019-1861-6.
- [7] Marsh DM, **Townes FW**, Cotter K, Farroni K, McCreary K, Petry R, Tilghman J. Thermal Preference and Species Range in Mountaintop Salamanders and Their Widespread Competitors. *Journal of Herpetology* (2019). doi:10.1670/18-110.
- [8] Hicks SC, **Townes FW**, Teng M, Irizarry RA. Missing Data and Technical Variability in Single-Cell RNA-Sequencing Experiments. *Biostatistics* (2018). doi:10.1101/025528.
- [9] Hecker, J, Xu X, **Townes FW**, Fier HL, Corcoran C, Laird N, Lange C. Family-Based Tests for Associating Haplotypes With General Phenotype Data: Application to Asthma Genetics. *Genetic Epidemiology* (2017). doi:10.1002/gepi.22094.
- [10] Valeri L, Patterson-Lomba O, Gurmu Y, Abloh A, Bobb J, **Townes FW**, Harling G. Predicting Subnational Ebola Virus Disease Epidemic Dynamics from Sociodemographic Indicators. *PLOS One* (2016). doi:10.1371/journal.pone.0163544.
- [11] **Townes W**. Seed dispersal of the genus *Leea* in forest patches of Bataan, Philippines. *Ecotropica* (2010).

Technical Reports

- [1] **Townes FW**. Review of Probability Distributions for Modeling Count Data. *arXiv* (2020). <https://arxiv.org/abs/2001.04343>.
- [2] **Townes FW**. Generalized Principal Component Analysis. *arXiv* (2019). <https://arxiv.org/abs/1907.02647>.

TALKS

Invited

- [1] Biomedical Informatics Department, University of Colorado Anschutz Medical Center. October 2022.
- [2] Advanced Biomedical Computation Seminar, Computational Pathology Department, Brigham and Women's Hospital. March 2022.
- [3] Statistics and Data Science Department, Carnegie Mellon University. March 2022.
- [4] Biomedical Data Science Department, Stanford University. February 2022.
- [5] Biostatistics Department, University of Michigan. January 2022.
- [6] Population and Public Health Sciences Department, University of Southern California. January 2022.
- [7] Emerging Concepts in Microbial Informatics, Molecular Medicine and Biotechnology (panelist). Trinity University of Asia. November 2021.
- [8] Don't Normalize: the GLM-PCA approach to normalization. *Normjam*, New York Genome Center. November 2019.
- [9] Biostatistics and Data Science as a Career Path. Biology Department, Washington & Lee University. October 2019.

Contributed Talks

- [1] Latent factorization methods for genomics. *New England Statistical Symposium* (virtual presenter). May 2022.

- [2] Nonnegative process factorization for multivariate spatial count data. *Joint Statistical Meetings* (virtual conference). August 2021.
- [3] Quantile normalization of single-cell RNA-seq read counts without unique molecular identifiers. *Joint Statistical Meetings* (virtual conference). August 2020.
- [4] Dimension reduction for massive single-cell datasets. *Bioconductor Annual Meeting* (virtual conference). July 2020. slides doi:10.7490/f1000research.1118084.1
- [5] Dimension Reduction for Single Cell RNA-Seq based on a Multinomial Model. *Joint Statistical Meetings* (Denver, CO). August 2019.
- [6] Varying-Censoring Aware Matrix Factorization for Single Cell RNA-Sequencing. *Bioconductor Annual Meeting* (Boston, MA). July 2017.

Seminars

- [1] Human tumor atlas network steering committee meeting. April 2022.
- [2] Nonnegative spatial factorization. *Hansen and Hicks labs, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health*. November 2021.
- [3] Primer: Generalized linear models and latent factor models. *Broad Institute Models, Inference, and Algorithms*. October 2020.
- [4] Feature Selection and Dimension Reduction for Single Cell RNA-Seq. *Greene Lab, Department of Systems Pharmacology and Translational Therapeutics, Perelman School of Medicine, University of Pennsylvania*. February 2019.
- [5] Unsupervised Learning for Single Cell Gene Expression. *Harvard Biostatistics Cancer Working Group*. September 2018.
- [6] Single Cell Housekeeping Genes and Normalization. *Dana-Farber Cancer Institute cBio Seminar*. April 2018.
- [7] Informative Missing Data in Single Cell RNA-Seq. *Dana-Farber Cancer Institute Genomics Seminar*. October 2016.
- [8] Family Based Association Tests for Rare Variants. *Brigham & Women's Hospital Channing Network Medicine Seminar*. September 2015.

Interviews

- [1] The Bioinformatics Chat. March 2020. <https://bioinformatics.chat/glm-pca>

Posters

- [1] Townes FW, Shukla C. Gene Expression Autoencoders. *Harvard Biomedical Informatics 707 (Deep Learning in Healthcare)*. April 2018.
- [2] Townes FW, Marquez-Luna C. Mixture of Experts Analysis of Infectious Disease Outbreak Characteristics. *Harvard Computer Science 281 (Advanced Machine Learning)*. December 2015.
- [3] Townes FW, Karaayvaz M, Gillespie S, Bernstein B, Ellisen L, Aryee M. Single Cell RNA-Seq Technical and Biological Confounders. *Program in Quantitative Genomics Conference, Harvard Medical School*. November 2015.

PEER REVIEW **Journals:** *American Journal of Human Genetics, Bioinformatics, Biostatistics, Genome Biology, NAR Genomics and Bioinformatics, Nature Communications*

FUNDING
PROFESSIONAL SOCIETIES American Statistical Association, International Society for Computational Biology

2018 - 2019 NIH T32 Training Grant: Cancer
 2017 Chan-Zuckerberg Foundation Travel Grant
 Human Cell Atlas Jamboree. European Bioinformatics Institute, Hinxton, UK
 2016 - 2018 NIH T32 Training Grant: Big Data to Knowledge
 2016 NSF-CBMS Travel Award: Topology, Geometry, and Statistics
 2014 - 2016 NIH T32 Training Grant: Clinical Epidemiology of Lung Diseases

TEACHING EXPERIENCE

2021 Fall **Guest lecture**, Advanced Computational Genomics (Princeton - COS 597D)
 2020 Fall **Guest lecture**, Computational Biology of Single Cells (Princeton - COS 597F)
 2018 Fall **Teaching Assistant**, Applied Regression (Harvard - BST 210)
 Grade homeworks, hold office hours, and teach a weekly lab section.
 2018 Summer **Co-Instructor**, StatStart (Harvard)
 Statistics program for under-represented high school students.
 Gave two interactive lectures on graphing data and regression.
 2017 Fall **Teaching Assistant**, Applied Bayesian Analysis (Harvard - BST 228)
 Grade homeworks, provide solutions, and hold office hours.
 2017 Summer **Lead Instructor**, Introduction to Data Science (PARSE Ltd.)
 Nonprofit, week-long statistics program for high school students.
 Developed course material and gave interactive lectures using R.
 2017 Spring **Teaching Assistant**, Applied Longitudinal Analysis (Harvard - BST 226)
 Grade homeworks and hold office hours.
 2016 Fall **Teaching Assistant**, Intro to Statistical Methods (Harvard - BST 201)
 Grade homeworks, provide solutions, hold office hours, and teach a weekly lab section.
 2016 Summer **Project Mentor**, Pipelines into Biostatistics (Harvard)
 Program for under-represented undergraduates.
 Guided three students on a pharmacogenomics data analysis.
 2016 Spring **Teaching Assistant**, Rates and Proportions (Harvard - BST 210)
 Grade homeworks, provide solutions, hold office hours, and teach a weekly lab section.

SOFTWARE PACKAGES

- [1] **glmpca**: dimension reduction for non-normally distributed data. R package: <https://cran.r-project.org/package=glmpca>, python package: <https://pypi.org/project/glmpca/>
- [2] **scry**: Small-Count Analysis Methods for High-Dimensional Data. Bioconductor R package: <https://bioconductor.org/packages/release/bioc/html/scry.html>
- [3] **quminorm**: Quantile normalization of non-UMI single cell read counts. R package: <https://github.com/willtownes/quminorm>
- [4] **spatial-factorization**: Spatially-aware probabilistic factor models. Python package: <https://github.com/willtownes/spatial-factorization-py>

TECHNICAL SKILLS

Programming: R, Python, SQL, Git, L^AT_EX, Shell
Operating Systems: MacOS, Linux, Windows
Machine Learning Frameworks: Caret, Scikit-learn, Keras, Tensorflow, Stan