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CONTACT INFORMATION Department of Statistics and Data Science  
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SUMMARY I am an applied statistician working primarily with biomedical and public health data. I am involved with infectious disease projects 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.

PROFESSIONAL EXPERIENCE

2022 - present	<b>Assistant Professor</b> , Department of Statistics and Data Science Carnegie Mellon University, Pittsburgh, PA
2019 - 2022	<b>Postdoctoral Researcher</b> , Department of Computer Science Princeton University, Princeton, NJ (advisor: Barbara Engelhardt)
2011 - 2014	<b>Software Test Engineer</b> , SRA International, Arlington, VA
2008 - 2010	<b>Software Analyst</b> , Perrin Quarles Associates, Charlottesville, VA
2007 - 2008	<b>Fulbright Scholar</b> , University of the Philippines Conducted independent forest ecology research while living with an indigenous <i>Aeta</i> community in Bataan Province.

EDUCATION

2019	<b>Ph.D. Biostatistics</b> , Harvard University, Cambridge, MA USA <i>Dissertation Committee: Rafael Irizarry (Dana-Farber Cancer Institute, Data Science) Jeff Miller (Harvard University, Biostatistics) Martin Aryee (Massachusetts General Hospital, Pathology)</i>
2013	<b>M.S. Mathematics &amp; Statistics</b> , Georgetown University, Washington, DC USA
2007	<b>B.S. Biology</b> , 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](https://doi.org/10.1101/2022.01.10.475692).
- [2] Gewirtz ADH, **Townes FW**, Engelhardt BE. Expression QTLs in single-cell sequencing data (2022). Preprint: doi:[10.1101/2022.08.14.503915](https://doi.org/10.1101/2022.08.14.503915).
- [3] 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](https://doi.org/10.1101/2021.12.07.471685).

#### Peer-reviewed Journal Articles

- [1] **Townes FW**, Engelhardt BE. Nonnegative spatial factorization applied to spatial genomics. *Nature Methods* (2022). doi:[10.1038/s41592-022-01687-w](https://doi.org/10.1038/s41592-022-01687-w).
- [2] Gewirtz ADH, **Townes FW**, and Engelhardt BE. Telescoping bimodal latent Dirichlet allocation to identify expression QTLs across tissues. *Life Science Alliance* (2022). doi:[10.26508/lsa.202101297](https://doi.org/10.26508/lsa.202101297).
- [3] Jones A, **Townes FW**, Li D, Engelhardt BE. Contrastive latent variable modeling with application to case-control sequencing experiments. *Annals of Applied Statistics* (2022). doi:[10.1214/21-AOAS1534](https://doi.org/10.1214/21-AOAS1534).
- [4] 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. *Bioinformatics* (2020). doi:[10.1093/bioinformatics/btaa1055](https://doi.org/10.1093/bioinformatics/btaa1055).

- [5] **Townes FW**, Carr K, Miller JW. Identifying longevity associated genes by integrating gene expression and curated annotations. *PLOS Computational Biology* (2020). doi:10.1371/journal.pcbi.1008429.
- [6] **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.
- [7] **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.
- [8] 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.
- [9] 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.
- [10] 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.
- [11] 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.
- [12] **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] Biomedical Data Science Department, Stanford University. February 2022.
- [4] Biostatistics Department, University of Michigan. January 2022.
- [5] Population and Public Health Sciences Department, University of Southern California. January 2022.
- [6] Emerging Concepts in Microbial Informatics, Molecular Medicine and Biotechnology (panelist). Trinity University of Asia. November 2021.
- [7] Don't Normalize: the GLM-PCA approach to normalization. *Normjam*, New York Genome Center. November 2019.
- [8] 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] Wastewater based epidemiology. *Auton lab*. January 2023.
- [2] Human tumor atlas network steering committee meeting. April 2022.
- [3] Nonnegative spatial factorization. *Hansen and Hicks labs, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health*. November 2021.
- [4] Primer: Generalized linear models and latent factor models. *Broad Institute Models, Inference, and Algorithms*. October 2020.
- [5] 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.
- [6] Unsupervised Learning for Single Cell Gene Expression. *Harvard Biostatistics Cancer Working Group*. September 2018.
- [7] Single Cell Housekeeping Genes and Normalization. *Dana-Farber Cancer Institute cBio Seminar*. April 2018.
- [8] Informative Missing Data in Single Cell RNA-Seq. *Dana-Farber Cancer Institute Genomics Seminar*. October 2016.
- [9] 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, Journal of Machine Learning Research, NAR Genomics and Bioinformatics, Nature Communications, Nature Methods*

PROFESSIONAL SOCIETIES American Statistical Association, International Society for Computational Biology, Sigma Xi

FUNDING	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	2023 Spring	<b>Lead Instructor</b> , Introduction to Statistical Computing (CMU - 36-350)
	2021 Fall	<b>Guest lecture</b> , Advanced Computational Genomics (Princeton - COS 597D)
	2020 Fall	<b>Guest lecture</b> , Computational Biology of Single Cells (Princeton - COS 597F)
	2018 Fall	<b>Teaching Assistant</b> , Applied Regression (Harvard - BST 210) Grade homeworks, hold office hours, and teach a weekly lab section.
	2018 Summer	<b>Co-Instructor</b> , StatStart (Harvard) Statistics program for under-represented high school students. Gave two interactive lectures on graphing data and regression.
	2017 Fall	<b>Teaching Assistant</b> , Applied Bayesian Analysis (Harvard - BST 228) Grade homeworks, provide solutions, and hold office hours.
	2017 Summer	<b>Lead Instructor</b> , 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	<b>Teaching Assistant</b> , Applied Longitudinal Analysis (Harvard - BST 226) Grade homeworks and hold office hours.
	2016 Fall	<b>Teaching Assistant</b> , Intro to Statistical Methods (Harvard - BST 201) Grade homeworks, provide solutions, hold office hours, and teach a weekly lab section.
	2016 Summer	<b>Project Mentor</b> , Pipelines into Biostatistics (Harvard) Program for under-represented undergraduates. Guided three students on a pharmacogenomics data analysis.
	2016 Spring	<b>Teaching Assistant</b> , Rates and Proportions (Harvard - BST 210) Grade homeworks, provide solutions, hold office hours, and teach a weekly lab section.
SOFTWARE PACKAGES	<p>[1] <b>glmpca</b>: dimension reduction for non-normally distributed data. R package: <a href="https://cran.r-project.org/package=glmpca">https://cran.r-project.org/package=glmpca</a>, python package: <a href="https://pypi.org/project/glmpca/">https://pypi.org/project/glmpca/</a></p> <p>[2] <b>scry</b>: Small-Count Analysis Methods for High-Dimensional Data. Bioconductor R package: <a href="https://bioconductor.org/packages/release/bioc/html/scry.html">https://bioconductor.org/packages/release/bioc/html/scry.html</a></p> <p>[3] <b>quminorm</b>: Quantile normalization of non-UMI single cell read counts. R package: <a href="https://github.com/willtownes/quminorm">https://github.com/willtownes/quminorm</a></p> <p>[4] <b>spatial-factorization</b>: Spatially-aware probabilistic factor models. Python package: <a href="https://github.com/willtownes/spatial-factorization-py">https://github.com/willtownes/spatial-factorization-py</a></p>	
TECHNICAL SKILLS	<p><b>Programming</b>: R, Python, SQL, Git, L<sup>A</sup>T<sub>E</sub>X, Shell</p> <p><b>Operating Systems</b>: MacOS, Linux, Windows</p> <p><b>Machine Learning Frameworks</b>: Caret, Scikit-learn, Keras, Tensorflow, Stan</p>	