

CONTACT INFORMATION	Department of Statistics and Data Science Carnegie Mellon University Pittsburgh, PA USA	website: <a href="https://willtownes.github.io">willtownes.github.io</a> email: <a href="mailto:ftownes@andrew.cmu.edu">ftownes@andrew.cmu.edu</a>
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	<b>In Review</b>	
	[1] Gewirtz ADH, <b>Townes FW</b> , Engelhardt BE. Expression QTLs in single-cell sequencing data (2022). Preprint: doi: <a href="https://doi.org/10.1101/2022.08.14.503915">10.1101/2022.08.14.503915</a> .	
	<b>Peer-reviewed Journal Articles</b>	
	[1] Jones A, <b>Townes FW</b> , Li D, Engelhardt BE. Alignment of spatial genomics and histology data using deep Gaussian processes. <i>Nature Methods</i> (2023). doi: <a href="https://doi.org/10.1038/s41592-023-01972-2">10.1038/s41592-023-01972-2</a>	
	[2] Verpeut JL, Bergeler S, Kislin M, <b>Townes FW</b> , Klibaite U, Dhanerawala ZM, Hoag A, Janarthanan S, Jung C, Lee J, Pisano TJ, Seagraves KM, Shaevitz JW, Wang SSH. Cerebellar contributions to a brainwide network for flexible behavior in mice. <i>Communications Biology</i> (2023). doi: <a href="https://doi.org/10.1038/s42003-023-04920-0">10.1038/s42003-023-04920-0</a>	
	[3] <b>Townes FW</b> , Engelhardt BE. Nonnegative spatial factorization applied to spatial genomics. <i>Nature Methods</i> (2023). doi: <a href="https://doi.org/10.1038/s41592-022-01687-w">10.1038/s41592-022-01687-w</a>	
	[4] Gewirtz ADH, <b>Townes FW</b> , and Engelhardt BE. Telescoping bimodal latent Dirichlet allocation to identify expression QTLs across tissues. <i>Life Science Alliance</i> (2022). doi: <a href="https://doi.org/10.26508/lsa.202101297">10.26508/lsa.202101297</a>	
	[5] Jones A, <b>Townes FW</b> , Li D, Engelhardt BE. Contrastive latent variable modeling with application to case-control sequencing experiments. <i>Annals of Applied Statistics</i> (2022). doi: <a href="https://doi.org/10.1214/21-AOAS1534">10.1214/21-AOAS1534</a>	
	[6] Hecker J, <b>Townes FW</b> , 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: <a href="https://doi.org/10.1093/bioinformatics/btaa1055">10.1093/bioinformatics/btaa1055</a>	

- [7] **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
- [8] **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
- [9] **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.
- [10] 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.
- [11] 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.
- [12] 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.
- [13] 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.
- [14] **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] Introduction to single cell genomics. (informal) *CMU Machine Learning Department lunch chats*. May 2023.
- [2] Wastewater based epidemiology. *Auton lab*. January 2023.
- [3] Human tumor atlas network steering committee meeting. April 2022.
- [4] Nonnegative spatial factorization. *Hansen and Hicks labs, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health*. November 2021.
- [5] Primer: Generalized linear models and latent factor models. *Broad Institute Models, Inference, and Algorithms*. October 2020.
- [6] 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.
- [7] Unsupervised Learning for Single Cell Gene Expression. *Harvard Biostatistics Cancer Working Group*. September 2018.
- [8] Single Cell Housekeeping Genes and Normalization. *Dana-Farber Cancer Institute cBio Seminar*. April 2018.
- [9] Informative Missing Data in Single Cell RNA-Seq. *Dana-Farber Cancer Institute Genomics Seminar*. October 2016.
- [10] 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>

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

THESIS  
COMMITTEES

- Aaron Rumack, CMU Machine Learning Department (2023)
- Timothy Barry, CMU Statistics Department (2023)

OTHER  
SERVICE  
ACTIVITIES

- Seminar Committee (2022-present)

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

- [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<sup>A</sup>T<sub>E</sub>X, Shell  
**Operating Systems:** MacOS, Linux, Windows  
**Machine Learning Frameworks:** Caret, Scikit-learn, Keras, Tensorflow, Stan