

Stephanie J. Spielman, PhD

DATA SCIENTIST

Childhood Cancer Data Lab, Alex's Lemonade Stand Foundation 3 Bala Plaza, Bala Cynwyd, PA 19004

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I am a computational biologist and data scientist focused on developing open-source products to accelerate pediatric cancer research.

Education

The University of Texas at Austin

PH.D., INTEGRATIVE BIOLOGY

Austin, Texas, USA

2016

Brown University

B.S., BIOLOGY WITH HONORS

Providence, RI, USA

2010

Positions

Alex's Lemonade Stand Foundation

DATA SCIENTIST, CHILDHOOD CANCER DATA LAB

Bala Cynwyd, PA, USA

2022–Present

- Develop open-source tools and data repositories, and lead training workshops to support pediatric cancer researchers

Rowan University

ASSISTANT PROFESSOR

Glassboro, New Jersey, USA

2018–2022

Temple University

RESEARCH ASSISTANT PROFESSOR

Philadelphia, Pennsylvania, PA

2016–2018

- Developed research in methods for quantifying protein evolution and taught graduate-level courses in Biostatistics and Evolutionary Medicine.

The University of Texas at Austin

GRADUATE RESEARCH ASSISTANT

Austin, Texas, USA

2011–2016

- Computational molecular evolution research, including phylogenetic modeling and virus evolution.

The University of Texas at Austin

GRADUATE TEACHING ASSISTANT

Austin, Texas, USA

2011–2016

- Supported undergraduate level courses in Biostatistics, Computational Biology and Bioinformatics, and Evolutionary Biology

Honors and Awards

President's Award for Excellence in Innovative Instructional Delivery

ROWAN UNIVERSITY

Glassboro, NJ, USA

2021

- Awarded by the Faculty Center for Teaching Excellence

Outstanding Dissertation Award

THE UNIVERSITY OF TEXAS AT AUSTIN

Austin, Texas, USA

2016

- Awarded by the Office of Graduate Studies to the top dissertation among all of science, math, and engineering

Ruth L. Kirschstein National Research Service Award (F31)

THE UNIVERSITY OF TEXAS AT AUSTIN

Austin, Texas, USA

2015

- Pre-doctoral fellowship awarded by NIH/NIGMS

Outstanding Teaching Award

THE UNIVERSITY OF TEXAS AT AUSTIN

Austin, Texas, USA

2014

- Awarded by the Biology Instructional Office

Selected Publications

- Hawkins, A. G., Shapiro, J. A., Spielman, S. J., Mejia, D. S., Prasad, D. V., Ichihara, N., Yakovets, A., Wheeler, K. G., Bethell, C. J., Foltz, S. M., O'Malley, J., Greene, C. S., & Taroni, J. N. (2024). The single-cell pediatric cancer atlas: Data portal and open-source tools for single-cell transcriptomics of pediatric tumors. *bioRxiv*. <https://doi.org/10.1101/2024.04.19.590243>

2. Shapiro, J. A., Gaonkar, K. S., Spielman, S. J., Savonen, C. L., Bethell, C. J., Jin, R., Rathi, K. S., Zhu, Y., Egolf, L. E., Farrow, B. K., Miller, D. P., Yang, Y., Koganti, T., Noureen, N., Koptyra, M. P., Duong, N., Santi, M., Kim, J., Robins, S., ... Taroni, J. N. (2023). OpenPBTA: The open pediatric brain tumor atlas. *Cell Genomics*, 3(7), 100340. <https://doi.org/10.1016/j.xgen.2023.100340>
3. Spielman, S. J., & Miraglia, M. L. (2021). *Relative model selection of evolutionary substitution models can be sensitive to multiple sequence alignment uncertainty*. <https://doi.org/10.1186/s12862-021-01931-5>
4. Spielman, S. J. (2020). Relative model fit does not predict topological accuracy in single-gene protein phylogenetics. *Molecular Biology and Evolution*, 37(7), 2110–2123. <https://doi.org/10.1093/molbev/msaa075>
5. Spielman, S. J., & Moore, E. K. (2020). dragon: A new tool for exploring redox evolution preserved in the mineral record. *Frontiers in Earth Science*. <https://doi.org/10.3389/feart.2020.585087>
6. Spielman, S. J., & Kosakovsky Pond, S. L. (2018). Relative evolutionary rates in proteins are largely insensitive to the substitution model. *Molecular Biology and Evolution*, 35(9), 2307–2317. <https://doi.org/10.1093/molbev/msy127>
7. Echave, J., Spielman, S. J., & Wilke, C. O. (2016). Causes of evolutionary rate variation among protein sites. *Nature Reviews Genetics*, 17(2), 109–121. <https://doi.org/10.1038/nrg.2015.18>
8. Meyer, A. G., Spielman, S. J., Bedford, T., & Wilke, C. O. (2015). Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak. *Virus Evolution*, 1(1), vev006. <https://doi.org/10.1093/ve/vev006>
9. Spielman, S. J., & Wilke, C. O. (2015). pyvolve: A flexible python module for simulating sequences along phylogenies. *PLOS ONE*, 10(9), e0139047. <https://doi.org/10.1371/journal.pone.0139047>
10. Spielman, S. J., & Wilke, C. O. (2015). The relationship between dN/dS and scaled selection coefficients. *Molecular Biology and Evolution*, 32(4), 1097–1108. <https://doi.org/10.1093/molbev/msv003>