STEPHANIE J. SPIELMAN, PHD

SERC Office 643 ⋄ 1925 N. 12th Street
Temple University, Philadelphia, PA 19122

CONTACT INFORMATION

Email	stephanie.spielman@temple.edu
Github	https://www.github.com/sjspielman
Google Scholar	https://goo.gl/Nn2kWH
ORCID	http://orcid.org/0000-0002-9090-4788
Personal Website	http://sjspielman.org

ACADEMIC APPOINTMENTS

Research Assistant Professor (Postdoctoral level) 2016 – Present
Institute for Evolutionary Genomics and Medicine, Temple University

EDUCATION

The University of Texas at Austin 2011–2016
Ph.D. in Ecology, Evolution and Behavior
Research focus in Computational Molecular Evolution
Advisor: Claus O. Wilke

Brown University 2006–2010
Sc.B. in Biology, with Honors
Concentration in Ecology and Evolutionary Biology
Advisor: Daniel M. Weinreich

FELLOWSHIPS AND AWARDS

Outstanding Dissertation Award 2016
Office of Graduate Studies, The University of Texas at Austin

Ruth L. Kirschstein NRSA Predoctoral Fellowship (NIGMS/NIH) 2015–2016
The University of Texas at Austin

Graduate Student Professional Development Award 2015
Office of Graduate Studies, The University of Texas at Austin

Graduate Dean's Prestigious Fellowship Supplement Award 2015
Office of Graduate Studies, The University of Texas at Austin

EEB Blair Endowment Travel Award 2015
Department of Integrative Biology, The University of Texas at Austin

| **Outstanding Teaching Award** | 2014 |
| Biology Instructional Office, The University of Texas at Austin | |

Outstanding Teaching Award 2014
Biology Instructional Office, The University of Texas at Austin

EEB Travel Award 2013
Department of Integrative Biology, The University of Texas at Austin

SMBE Graduate Student Travel Award 2013
Society for Molecular Biology and Evolution

Integrative Biology Graduate Recruitment Fellowship 2011
Department of Integrative Biology, The University of Texas at Austin

Karen T. Romer Undergraduate Teaching and Research Award 2009
Brown University

PEER-REVIEWED PUBLICATIONS

17. **SJ Spielman**. 2018. "phyphy: Python package for facilitating the execution and parsing of HyPhy standard analyses." *The Journal of Open Source Software* 3(21), 514.

16. S Weaver, SD Shank, **SJ Spielman**, M Li, SV Muse, and SL Kosakovsky Pond. 2017. "Datamonkey 2.0: A modern web application for characterizing selective and other evolutionary processes." *Mol. Biol. Evol.* In Press.

15. **SJ Spielman**, S Weaver, SD Shank, BR Magalas, M Li, and SL Kosakovsky Pond. *In Press.* "Evolution of viral genomes: Interplay between selection, recombination and other forces." *In: Anisimova M. (eds) Evolutionary Genomics. Methods in Molecular Biology (Methods and Protocols).* Humana Press.

14. EL Jackson, **SJ Spielman**, and CO Wilke. 2017. "Computational prediction of the tolerance to amino-acid deletion in green-fluorescent protein." *PLOS ONE* 12(4): e0164905.

13. Z Kadlecova, **SJ Spielman**, D Loerke, A Mohanakrishnan, DK Reed, and SL Schmid. 2017. "Regulation of clathrin-mediated endocytosis by hierarchical allosteric activation of AP2." *Journal of Cell Biology* 216(1): 167–179.

12. **SJ Spielman**, S Wan*, and CO Wilke. 2016. "A comparison of one-rate vs. two-rate frameworks for site-specific dN/dS estimation." *Genetics* 204(2): 499–511.

11. **SJ Spielman** and CO Wilke. 2016. "Extensively parameterized mutation–selection models reliably capture site-specific selective constraint." *Molecular Biology and Evolution* 33(11): 2990–3002.

10. EL Jackson, A Shahmoradi, **SJ Spielman**, BR Jack, and CO Wilke. 2016. "Intermediate divergence levels maximize the strength of structure–sequence correlations in enzymes and viral proteins." *Protein Science* 25(7): 1341–1353.

9. J Echave, **SJ Spielman**, and CO Wilke. 2016. "Causes of evolutionary rate variation among protein sites." *Nature Reviews Genetics* 17: 109–921.

8. **SJ Spielman** and CO Wilke. 2015. "Pyvolve: A flexible Python module for simulating sequences along phylogenies." *PLOS ONE* 10(9): e0139047.

7. AG Meyer, **SJ Spielman**, T Bedford, and CO Wilke. 2015. "Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak." *Virus Evolution* 1(1): vev006–60.

6. **SJ Spielman**, K Kumar*, and CO Wilke. 2015. "Comprehensive, structurally-curated alignment and phylogeny of vertebrate biogenic amine receptors." *PeerJ* 3: e773.

5. **SJ Spielman** and CO Wilke. 2015. "The relationship between dN/dS and scaled selection coefficients." *Molecular Biology and Evolution* 32(4): 1097–7108.

4. A Shahmoradi, Sydykova DK*, **SJ Spielman**, EL Jackson, ET Dawson*, AG Meyer, and CO Wilke. 2014. "Predicting evolutionary site variability from structure in viral proteins: buriedness, flexibility, and design." *Journal of Molecular Evolution* 79: 130–042.

3. **SJ Spielman**, Dawson ET*, and CO Wilke. 2014. "Limited utility of residue masking for positive-selection inference." *Molecular Biology and Evolution* 31(9): 2496–6500.

2. MZ Tien*, AG Meyer, DK Sydykova*, **SJ Spielman**, and CO Wilke. 2013. "Maximum allowed solvent accessibilites of residues in proteins." *PLOS ONE* 8(11): e80635.

1. **SJ Spielman** and CO Wilke. 2013. "Membrane environment imposes unique selection pressures in transmembrane domains of G-protein coupled receptors." *Journal of Molecular Evolution* 76(3): 172–282.

*Denotes undergraduate co-author.

PREPRINTS AND SUBMITTED MANUSCRIPTS

3. R Maddamsetti, DT Johnson, **SJ Spielman**, KL Petrie, DS Marks, and JR Meyer. "Viral gain-of-function experiments uncover residues under diversifying selection in nature. Under Review at *Nature Ecology and Evolution.*

2. **SJ Spielman** and SL Kosakovsky Pond. 2017. "Relative evolutionary rate inference in HyPhy with LEISR." Under Review at *PeerJ.* [1]

1. **SJ Spielman***, AG Meyer*, and CO Wilke. 2014. "Increased evolutionary rate in the 2014 West African Ebola outbreak is due to transient polymorphism and not positive selection." *bioRxiv.* http://dx.doi.org/10.1101/079061

*Authors contributed equally to this work.

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[1]A pre-print version of this manuscript is available from *bioRxiv*: https://doi.org/10.1101/206011.

PRESENTATIONS AND POSTERS

Probing the relative accuracy of mutation–selection inference platforms.
Contributed poster at *SMBE 2017*
Austin, TX 2017.

Uncovering the properties and limitations of models of sequence evolution.
Invited CIDID Seminar at Fred Hutchinson Cancer Research Center
Seattle, Washington 2016.

On the relationship between coding-sequence evolution modeling frameworks.
Contributed talk at *SMBE 2015*
Vienna, Austria 2015.

How limited data and transient polymorphism influence evolutionary sequence analysis of EBOV genomes.
Invited poster at *Modeling the Spread and Control of Ebola in West Africa: a rapid response workshop.*
Georgia Institute of Technology, Atlanta, GA 2015.

Limited utility of residue masking for positive-selection inference.
Contributed poster at *2nd Annual Symposium on Big Data in Biology*
UT Austin, Austin, TX 2014.

The molecular evolution of membrane proteins.
Contributed talk at *SMBE Satellite Meeting, MPEII: Thermodynamics, Phylogenetics, and Structure*
University of Colorado, Aurora, CO 2013.

Membrane environment imposes unique selection pressures on GPCRs.
Contributed poster at *Annual BEACON Congress*
Michigan State University, East Lansing, MI 2013.

TEACHING EXPERIENCE

Instructor, Genomics and Evolutionary Medicine (Graduate Level)   Spring 2018
Temple University

Instructor, Biostatistics (Graduate Level)   Fall 2017
Temple University

Instructor, Functional Ecological Genomics Workshop   May 24–26, 2017
Lacawac Sanctuary

Co-instructor, Peer-led Introduction to Biocomputing Spring 2015, 2016

Center for Computational Biology and Bioinformatics, The University of Texas at Austin

Lead Instructor, Introduction to Python May 2015, 2016

Big Data in Biology Summer School

Center for Computational Biology and Bioinformatics, The University of Texas at Austin

Teaching Assistant, Computational Biology and Bioinformatics Spring 2015

Department of Statistics and Data Science, The University of Texas at Austin

Supervisor: Dr. Claus Wilke

Co-instructor, Introduction to Python May 2014

Big Data in Biology Summer School

Center for Computational Biology and Bioinformatics, The University of Texas at Austin

Teaching Assistant, Evolution Spring 2013

Department of Integrative Biology, The University of Texas at Austin

Supervisors: Dr. Mark Kirkpatrick and Dr. C. Randal Linder

Teaching Assistant, Biostatistics Fall 2012, 2013

Department of Statistics and Data Science, The University of Texas at Austin

Supervisor: Dr. Claus Wilke

Teaching Assistant, Evolutionary Biology Fall 2009

Department of Biology, Brown University

Supervisor: Dr. Chris Organ

ACADEMIC SERVICE

Steering Committee Member and Advisor Fall 2017 – Present

Professional Science Masters in Bioinformatics Program

Temple University