

# STEPHANIE J. SPIELMAN, PHD

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

## CONTACT INFORMATION

---

Email [stephanie.spielman@temple.edu](mailto: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

<b>Outstanding Teaching Award</b> Biology Instructional Office, The University of Texas at Austin	2014
<b>EEB Travel Award</b> Department of Integrative Biology, The University of Texas at Austin	2013
<b>SMBE Graduate Student Travel Award</b> Society for Molecular Biology and Evolution	2013
<b>Integrative Biology Graduate Recruitment Fellowship</b> Department of Integrative Biology, The University of Texas at Austin	2011
<b>Karen T. Romer Undergraduate Teaching and Research Award</b> Brown University	2009

## PEER-REVIEWED PUBLICATIONS

---

19. **SJ Spielman** and SL Kosakovsky Pond. 2018. “Relative evolutionary rate inference in HyPhy with LEISR.” *PeerJ*. In Press.
18. **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.
17. S Weaver, SD Shank, **SJ Spielman**, M Li, SV Muse, and SL Kosakovsky Pond. 2018. “Datamonkey 2.0: A modern web application for characterizing selective and other evolutionary processes.” *Mol. Biol. Evol.* In Press.
16. **SJ Spielman**, S Weaver, SD Shank, BR Magalas, M Li, and SL Kosakovsky Pond. 2018. “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. In Press.
15. DK Sydykova, BR Jack, **SJ Spielman**, and CO Wilke. 2017. “Measuring evolutionary rates of proteins in a structural context.” *F1000Research* 6:1845.
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 accessibilities 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

---

2. 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*.
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.

## 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