

# STEPHANIE J. SPIELMAN

SERC Building, 1835-1899 N. 12th Street  
Temple University, Philadelphia, PA 19122

## CONTACT INFORMATION

---

Email [stephanie.spielman@temple.edu](mailto:stephanie.spielman@temple.edu)  
Website <http://sjspielman.org>  
Github <https://www.github.com/sjspielman>

## ACADEMIC APPOINTMENTS

---

<b>Research Assistant Professor/Postdoc</b> Institute for Evolutionary Genomics and Medicine, Temple University	2016 – Present
--------------------------------------------------------------------------------------------------------------------	----------------

## EDUCATION

---

<b>The The University of Texas at Austin</b> Ph.D. in Ecology, Evolution and Behavior Research focus in Computational Molecular Evolution Advisor: Claus O. Wilke	2011–2016
<b>Brown University</b> Sc.B. in Biology, with Honors Concentration in Ecology and Evolutionary Biology Advisor: Daniel M. Weinreich	2006–2010

## FELLOWSHIPS AND AWARDS

---

<b>Outstanding Dissertation Award</b> Office of Graduate Studies, The University of Texas at Austin	2016
<b>Ruth L. Kirschstein NRSA Predoctoral Fellowship (NIGMS/NIH)</b> The University of Texas at Austin	2015–2016
<b>Graduate Student Professional Development Award</b> Office of Graduate Studies, The University of Texas at Austin	2015
<b>Graduate Dean's Prestigious Fellowship Supplement Award</b> Office of Graduate Studies, The University of Texas at Austin	2015
<b>EEB Blair Endowment Travel Award</b> Department of Integrative Biology, The University of Texas at Austin	2015

<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

---

12. **Spielman SJ**, Wan S, and Wilke CO. 2016. *A comparison of one-rate vs. two-rate frameworks for site-specific dN/dS estimation*. Genetics (In press).
11. **Spielman SJ** and Wilke CO. 2016. *Extensively parameterized mutation–selection models reliably capture site-specific selective constraint*. Mol Biol Evol (In press).
10. Jackson EL, Shahmoradi A, **Spielman SJ**, Jack BR, and Wilke CO. 2016. *Intermediate divergence levels maximize the strength of structure–sequence correlations in enzymes and viral proteins*. Protein Sci 25(7): 1341–1353.
9. Echave J, **Spielman SJ**, and Wilke CO. 2016. *Causes of evolutionary rate variation among protein sites*. Nature Rev Genet 17: 109–921.
8. **Spielman SJ** and Wilke CO. 2015. *Pyvolve: A flexible Python module for simulating sequences along phylogenies*. PLOS ONE 10(9): e0139047.
7. Meyer AG, **Spielman SJ**, Bedford T, and Wilke CO. 2015. *Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak*. Virus Evolution 1(1): vev006–60.
6. **Spielman SJ**, Kumar K\*, and Wilke CO. 2015. *Comprehensive, structurally-curated alignment and phylogeny of vertebrate biogenic amine receptors*. PeerJ 3: e773.
5. **Spielman SJ** and Wilke CO. 2015. *The relationship between dN/dS and scaled selection coefficients*. Mol Biol Evol 32(4): 1097–7108.
4. Shahmoradi A, Sydykova DK\*, **Spielman SJ**, Jackson EL, Dawson ET\* Meyer AG, and Wilke CO. 2014. *Predicting evolutionary site variability from structure in viral proteins: buriedness, flexibility, and design*. J Mol Evol 79: 130–042.

3. **Spielman SJ**, Dawson ET\*, and Wilke CO. 2014. *Limited utility of residue masking for positive-selection inference*. Mol Biol Evol 31(9): 2496–6500.
2. Tien MZ\*, Meyer AG, Sydykova DK\*, **Spielman SJ**, and Wilke CO. 2013. *Maximum allowed solvent accessibilities of residues in proteins*. PLOS ONE 8(11): e80635.
1. **Spielman SJ** and Wilke CO. 2013. *Membrane environment imposes unique selection pressures in transmembrane domains of G-protein coupled receptors*. J Mol Evol 76(3): 172–282.

\*Denotes undergraduate co-author.

## PREPRINTS AND OPINIONS

---

1. **Spielman SJ**<sup>†</sup>, Meyer, AG<sup>†</sup>, and Wilke CO. 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/10.1101/01142>.

<sup>†</sup>Authors contributed equally.

## PRESENTATIONS AND POSTERS

---

### 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, CCB*  
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

---

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

**Teaching Assistant, Biostatistics** Fall 2013, 2012  
Department of Statistics and Data Science, The University of Texas at Austin  
Supervisor: Dr. Claus Wilke

**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, Evolutionary Biology** Fall 2009  
Department of Biology, Brown University  
Supervisor: Dr. Chris Organ