

# STEPHANIE J. SPIELMAN

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## CONTACT INFORMATION

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Github <https://www.github.com/sjspielman>

## ACADEMIC APPOINTMENTS

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

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<b>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

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<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

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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." *Molecular Biology and Evolution* (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 Science* 25(7): 1341–1353.
9. Echave J, **Spielman SJ**, and Wilke CO. 2016. "Causes of evolutionary rate variation among protein sites." *Nature Reviews Genetics* 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." *Molecular Biology and Evolution* 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." *Journal of Molecular Evolution* 79: 130–042.

3. **Spielman SJ**, Dawson ET\*, and Wilke CO. 2014. "Limited utility of residue masking for positive-selection inference." *Molecular Biology and Evolution* 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." *Journal of Molecular Evolution* 76(3): 172–282.

\*Denotes undergraduate co-author.

## SUBMITTED MANUSCRIPTS

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2. Jackson EL, **Spielman SJ**, and Wilke CO. 2016. "Computational prediction of the tolerance to amino-acid deletion in green-fluorescent protein." bioRxiv <http://dx.doi.org/10.1101/079061>. *Under Review*.
1. Kadlecova Z, **Spielman SJ**, Loerke D, Mohanakrishnan A, Reed DK, and Schmid SL. 2016. "Regulation of clathrin-mediated endocytosis by hierarchical allosteric activation of AP2." *Under Review*.

## PRESENTATIONS AND POSTERS

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### 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

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**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, 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