

# STEPHANIE J. SPIELMAN

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## CONTACT INFORMATION

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

## EDUCATION

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

<b>Brown University</b>	2006 - 2010
Sc.B. in Biology, with Honors	
Concentration in Ecology and Evolutionary Biology	
Advisor: Daniel M. Weinreich	

## FELLOWSHIPS AND AWARDS

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<b>Outstanding Dissertation Award</b>	2016
Office of Graduate Studies, UT Austin	
<b>Graduate Student Professional Development Award</b>	2015
Office of Graduate Studies, UT Austin	
<b>Graduate Dean's Prestigious Fellowship Supplement Award</b>	2015
Office of Graduate Studies, UT Austin	
<b>EEB Blair Endowment Travel Award</b>	2015
Department of Integrative Biology, UT Austin	
<b>Ruth L. Kirschstein NRSA Predoctoral Fellowship (NIGMS/NIH)</b>	2015 – 2016
University of Texas at Austin	
<b>Outstanding Teaching Award</b>	2014
Biology Instructional Office, UT Austin	
<b>EEB Travel Award</b>	2013
Department of Integrative Biology, UT Austin	
<b>SMBE Graduate Student Travel Award</b>	2013
Society for Molecular Biology and Evolution	

**Integrative Biology Graduate Recruitment Fellowship**

2011

Department of Integrative Biology, UT Austin

**Karen T. Romer Undergraduate Teaching and Research Award**

2009

Brown University

## PEER-REVIEWED PUBLICATIONS

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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 (In press).
9. Echave J, **Spielman SJ**, and Wilke CO. 2016. *Causes of evolutionary rate variation among protein sites*. Nature Rev Genet 17: 109–121.
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. *Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak*. Virus Evolution 1(1): vev006–10.
6. **Spielman SJ**, Kumar K\*, and Wilke CO. *Comprehensive, structurally-curated alignment and phylogeny of vertebrate biogenic amine receptors*. PeerJ 3: e773.
5. **Spielman SJ** and Wilke CO. *The relationship between dN/dS and scaled selection coefficients*. Mol Biol Evol 32(4): 1097–1108.
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: 130–142.
3. **Spielman SJ**, Dawson ET\*, and Wilke CO. 2014. *Limited utility of residue masking for positive-selection inference*. Mol Biol Evol 31(9): 2496–2500.
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): 172–182.

\*Denotes undergraduate co-author.

## PREPRINTS AND OPINIONS

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2. **Spielman SJ**, Wan S, and Wilke CO. 2015. *A comparison of one-rate and two-rate inference frameworks for site-specific dN/dS estimation*. bioRxiv. <http://dx.doi.org/10.1101/032805>.

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

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### **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, CCBB*

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, UT Austin

### **Lead Instructor, Introduction to Python**

May 2015, 2016

Big Data in Biology Summer School

Center for Computational Biology and Bioinformatics, UT Austin

### **Teaching Assistant, Computational Biology and Bioinformatics**

Spring 2015

Department of Statistics and Data Science, UT Austin

Supervisor: Dr. Claus Wilke

**Co-instructor, Introduction to Python**

May 2014

Big Data Summer School

Center for Computational Biology and Bioinformatics, UT Austin

**Teaching Assistant, Biostatistics**

Fall 2013, 2012

Department of Statistics and Data Science, UT Austin

Supervisor: Dr. Claus Wilke

**Teaching Assistant, Evolution**

Spring 2013

Department of Integrative Biology, UT 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