

# STEPHANIE J. SPIELMAN

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## CONTACT INFORMATION

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## ACADEMIC APPOINTMENTS

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

<b>Outstanding Teaching Award</b> Biology Instructional Office, UT Austin	2014
<b>EEB Travel Award</b> Department of Integrative Biology, UT 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, UT Austin	2011
<b>Karen T. Romer Undergraduate Teaching and Research Award</b> Brown University	2009

## PEER-REVIEWED PUBLICATIONS

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10. **Spielman SJ** and Wilke CO. *Extensively parameterized mutation–selection reliably capture site-specific selective constraint*. Mol Biol Evol (In press).
9. 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.
8. Echave J, **Spielman SJ**, and Wilke CO. 2016. *Causes of evolutionary rate variation among protein sites*. Nature Rev Genet 17: 109 – 121.
7. **Spielman SJ** and Wilke CO. 2015. *Pyvolve: A flexible Python module for simulating sequences along phylogenies*. PLOS ONE 10(9): e0139047.
6. 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.
5. **Spielman SJ**, Kumar K\*, and Wilke CO. *Comprehensive, structurally-curated alignment and phylogeny of vertebrate biogenic amine receptors*. PeerJ 3: e773.
4. **Spielman SJ** and Wilke CO. *The relationship between dN/dS and scaled selection coefficients*. Mol Biol Evol 32(4): 1097 – 1108.
3. 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.
2. **Spielman SJ**, Dawson ET\*, and Wilke CO. 2014. *Limited utility of residue masking for positive-selection inference*. Mol Biol Evol 31(9): 2496 – 2500.

1. 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.
0. **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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### **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

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<b>Co-instructor, Peer-led Introduction to Biocomputing</b> Center for Computational Biology and Bioinformatics, UT Austin	Spring 2015, 2016
<b>Lead Instructor, Introduction to Python</b> Big Data in Biology Summer School Center for Computational Biology and Bioinformatics, UT Austin	May 2015, 2016
<b>Teaching Assistant, Computational Biology and Bioinformatics</b> Department of Statistics and Data Science, UT Austin Supervisor: Dr. Claus Wilke	Spring 2015
<b>Co-instructor, Introduction to Python</b> Big Data Summer School Center for Computational Biology and Bioinformatics, UT Austin	May 2014
<b>Teaching Assistant, Biostatistics</b> Department of Statistics and Data Science, UT Austin Supervisor: Dr. Claus Wilke	Fall 2013, 2012
<b>Teaching Assistant, Evolution</b> Department of Integrative Biology, UT Austin Supervisors: Dr. Mark Kirkpatrick and Dr. C. Randal Linder	Spring 2013
<b>Teaching Assistant, Evolutionary Biology</b> Department of Biology, Brown University Supervisor: Dr. Chris Organ	Fall 2009