

STEPHANIE J. SPIELMAN

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CONTACT INFORMATION

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EDUCATION

The University of Texas at Austin	2011 - present
Ph.D. in Ecology, Evolution and Behavior (expected May 2016)	
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

Graduate Student Professional Development Award	2015
Office of Graduate Studies, UT Austin	
Graduate Dean's Prestigious Fellowship Supplement Award	2015
Office of Graduate Studies, UT Austin	
EEB Blair Endowment Travel Award	2015
Department of Integrative Biology, UT Austin	
Ruth L. Kirschstein NRSA Predoctoral Fellowship (NIGMS/NIH)	2015 – 2017
University of Texas at Austin	
Outstanding Teaching Award	2014
Biology Instructional Office, UT Austin	
EEB Travel Award	2013
Department of Integrative Biology, UT Austin	
SMBE Graduate Student Travel Award	2013
Society for Molecular Biology and Evolution	
Integrative Biology Graduate Recruitment Fellowship	2011
Department of Integrative Biology, UT Austin	

PEER-REVIEWED PUBLICATIONS

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

2. **Spielman SJ**, Wan S, and Wilke CO. 2015. *One-rate models outperform two-rate models in site-specific dN/dS estimation*. bioRxiv. <http://dx.doi.org/10.1101/032805>.

1. **Spielman SJ[†]**, Meyer, AG[†], 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>.

[†]Authors contributed equally.

PRESENTATIONS AND POSTERS

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

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

Big Data 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