

STEPHANIE J. SPIELMAN

The University of Texas at Austin
2500 Speedway, Austin, TX 78712

CONTACT INFORMATION

Email: stephanie.spielman@utexas.edu
Website: <http://sjspielman.org>
Github: <https://www.github.com/sjspielman>

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 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	
Karen T. Romer Undergraduate Teaching and Research Award	2009
Brown University	

PEER-REVIEWED PUBLICATIONS

7. Meyer AG, **Spielman SJ**, Bedford T, and Wilke CO. *The time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak*. Virus Evolution. In Press.
6. **Spielman SJ**, Kumar K*, and Wilke CO. *Comprehensive, structurally-curated alignment and phylogeny of vertebrate biogenic amine receptors*. PeerJ 3:e773 <http://dx.doi.org/10.7717/peerj.773>
5. **SJ Spielman** and CO Wilke. *The relationship between dN/dS and scaled selection coefficients*. Mol Biol Evol 32(4):1097-1108.
4. **Spielman SJ**, Dawson ET*, and Wilke CO. 2014. *Limited utility of residue masking for positive-selection inference*. Mol Biol Evol 31(9):2496 - 2500.
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. 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** and Wilke CO. 2015. *Pyvolve: A flexible Python module for simulating sequences along phylogenies*. bioRxiv doi: 10.1101/020214.
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 doi: 10.1101/011429. [†]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*
The University of Texas at 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

Lead Instructor, Introduction to Python

May 2015

Big Data Summer School

Center for Computational Biology and Bioinformatics, UT Austin

Co-instructor, Peer-led Introduction to Biocomputing

Spring 2015

Center for Computational Biology and Bioinformatics, UT Austin

Teaching Assistant, Computational Biology and Bioinformatics

Spring 2015

Department of Statistics and Data Science, UT Austin

Co-instructor, Introduction to Python

May 2014

Big Data Summer School

Center for Computational Biology and Bioinformatics, UT Austin

Teaching Assistant, Biostatistics

Fall 2013

Department of Statistics and Data Science, UT Austin

Teaching Assistant, Evolution

Spring 2013

Department of Integrative Biology, UT Austin

Teaching Assistant, Biostatistics

Fall 2012

Department of Statistics and Data Science, UT Austin

Teaching Assistant, Evolutionary Biology

Fall 2009

Department of Biology, Brown University