

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 Ph.D. in Ecology, Evolution and Behavior (expected May 2016) Research focus in Computational Molecular Evolution Advisor: Claus O. Wilke	2011 - present
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Brown University Sc.B. in Biology, with Honors Concentration in Ecology and Evolutionary Biology Advisor: Daniel M. Weinreich	2006 - 2010
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AWARDS AND HONORS

Outstanding Teaching Award Biology Instructional Office, UT Austin	2014
EEB Travel Grant Department of Integrative Biology, UT Austin	2013
SMBE Graduate Student Travel Grant Society for Molecular Biology and Evolution	2013
Integrative Biology Graduate Recruitment Fellowship Department of Integrative Biology, UT Austin	2011
Karen T. Romer Undergraduate Teaching and Research Award Brown University	2009

PEER-REVIEWED PUBLICATIONS

6. **Spielman SJ**, Kumar K*, and Wilke CO. In press. *Comprehensive, structurally-curated alignment and phylogeny of vertebrate biogenic amine receptors*. PeerJ. Preprint: <https://peerj.com/preprints/571>.

5. **SJ Spielman** and CO Wilke. In press. *The relationship between dN/dS and scaled selection coefficients*. Mol Biol Evol.
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

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.

*Denotes undergraduate co-author.

PRESENTATIONS AND POSTERS

How limited data and transient polymorphism influence evolutionary sequence analysis of EBOV genomes.

Contributed 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

Co-instructor, Peer-led Introduction to Computational Biology Center for Computational Biology and Bioinformatics, UT Austin	Spring 2015
Teaching Assistant, Computational Biology and Bioinformatics Department of Statistics and Data Science, UT Austin	Spring 2015
Co-instructor, Introduction to Python Short Course Center for Computational Biology and Bioinformatics, UT Austin	May 2014
Teaching Assistant, Biostatistics Department of Statistics and Data Science, UT Austin	Fall 2013
Teaching Assistant, Evolution Department of Integrative Biology, UT Austin	Spring 2013
Teaching Assistant, Biostatistics Department of Statistics and Data Science, UT Austin	Fall 2012
Teaching Assistant, Evolutionary Biology Department of Biology, Brown University	Fall 2009