STEPHANIE J. SPIELMAN

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CONTACT INFORMATION

Email: stephanie.spielman@utexas.edu
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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

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 Grant 2013
Department of Integrative Biology, UT Austin

SMBE Graduate Student Travel Grant 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

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. 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 accessibilites 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.

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 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 Short Course May 2014
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