

STEPHANIE J. SPIELMAN

CONTACT INFORMATION

Email stephanie.spielman@gmail.com
Website http://sjspielman.org
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EDUCATION

The University of Texas at Austin 2011 – 2016
Ph.D. in Ecology, Evolution and Behavior
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

Outstanding Dissertation Award 2016
Office of Graduate Studies, UT Austin

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 – 2016
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

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. *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**[†], 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, 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

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, 2016

Big Data in Biology 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