

STEPHANIE J. SPIELMAN, PHD

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CONTACT INFORMATION

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ACADEMIC APPOINTMENTS

Research Assistant Professor (Postdoctoral level)	2016 – Present
Institute for Evolutionary Genomics and Medicine, Temple University	

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, The University of Texas at Austin

Ruth L. Kirschstein NRSA Predoctoral Fellowship (NIGMS/NIH) 2015–2016
The University of Texas at Austin

Graduate Student Professional Development Award 2015
Office of Graduate Studies, The University of Texas at Austin

Graduate Dean's Prestigious Fellowship Supplement Award 2015
Office of Graduate Studies, The University of Texas at Austin

EEB Blair Endowment Travel Award 2015
Department of Integrative Biology, The University of Texas at Austin

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

PEER-REVIEWED PUBLICATIONS

15. **Spielman SJ**, Weaver S, Shank SD, Magalas BR, Li M, and Kosakovsky Pond SL. *In Press*. “Evolution of viral genomes: Interplay between selection, recombination and other forces.” *In: Anisimova M. (eds) Evolutionary Genomics. Methods in Molecular Biology (Methods and Protocols)*. Humana Press.
14. Jackson EL, **Spielman SJ**, and CO Wilke. 2017. “Computational prediction of the tolerance to amino-acid deletion in green-fluorescent protein.” *PLOS ONE* 12(4): e0164905.
13. Kadlecova Z, **Spielman SJ**, Loerke D, Mohanakrishnan A, Reed DK, and Schmid SL. 2017. “Regulation of clathrin-mediated endocytosis by hierarchical allosteric activation of AP2.” *Journal of Cell Biology* 216(1): 167–179.
12. **Spielman SJ**, Wan S*, and Wilke CO. 2016. “A comparison of one-rate vs. two-rate frameworks for site-specific dN/dS estimation.” *Genetics* 204(2): 499–511.
11. **Spielman SJ** and Wilke CO. 2016. “Extensively parameterized mutation–selection models reliably capture site-specific selective constraint.” *Molecular Biology and Evolution* 33(11): 2990–3002.
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 Science* 25(7): 1341–1353.
9. Echave J, **Spielman SJ**, and Wilke CO. 2016. “Causes of evolutionary rate variation among protein sites.” *Nature Reviews Genetics* 17: 109–921.
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. 2015. “Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak.” *Virus Evolution* 1(1): vev006–60.

6. **Spielman SJ**, Kumar K*, and Wilke CO. 2015. “Comprehensive, structurally-curated alignment and phylogeny of vertebrate biogenic amine receptors.” *PeerJ* 3: e773.
5. **Spielman SJ** and Wilke CO. 2015. “The relationship between dN/dS and scaled selection coefficients.” *Molecular Biology and Evolution* 32(4): 1097–7108.
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.” *Journal of Molecular Evolution* 79: 130–042.
3. **Spielman SJ**, Dawson ET*, and Wilke CO. 2014. “Limited utility of residue masking for positive-selection inference.” *Molecular Biology and Evolution* 31(9): 2496–6500.
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.” *Journal of Molecular Evolution* 76(3): 172–282.

*Denotes undergraduate co-author.

PREPRINTS AND SUBMITTED MANUSCRIPTS

4. **Spielman SJ**. 2017. “phyphy: Python package for facilitating the execution and parsing of HyPhy standard analyses” *The Journal of Open Source Software*. Under Review.
3. Weaver S, Shank SD, **Spielman SJ**, Li M, Muse SV, and Kosakovsky Pond SL. 2017. “Datamonkey 2.0: A modern web application for characterizing selective and other evolutionary processes.” *Mol. Biol. Evol.* Under Review.
2. **Spielman SJ** and Kosakovsky Pond SL. 2017. “Relative evolutionary rate inference in HyPhy with LEISR.” *bioRxiv*. <https://doi.org/10.1101/206011>
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/10.1101/079061>

*Authors contributed equally to this work.

PRESENTATIONS AND POSTERS

Probing the relative accuracy of mutation–selection inference platforms.
 Contributed poster at *SMBE 2017*

Austin, TX 2017.

Uncovering the properties and limitations of models of sequence evolution.

Invited CIDID Seminar at Fred Hutchinson Cancer Research Center
Seattle, Washington 2016.

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*
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

Instructor, Genomics and Evolutionary Medicine

Temple University

Spring 2018

Instructor, Biostatistics

Temple University

Fall 2017

Instructor, Functional Ecological Genomics Workshop

Lacawac Sanctuary

May 24-26, 2017

Co-instructor, Peer-led Introduction to Biocomputing

Center for Computational Biology and Bioinformatics, The University of Texas at Austin

Spring 2015, 2016

Lead Instructor, Introduction to Python

Big Data in Biology Summer School

Center for Computational Biology and Bioinformatics, The University of Texas at Austin

May 2015, 2016

Teaching Assistant, Computational Biology and Bioinformatics

Spring 2015

Department of Statistics and Data Science, The University of Texas at Austin

Supervisor: Dr. Claus Wilke

Co-instructor, Introduction to Python

May 2014

Big Data in Biology Summer School

Center for Computational Biology and Bioinformatics, The University of Texas at Austin

Teaching Assistant, Evolution

Spring 2013

Department of Integrative Biology, The University of Texas at Austin

Supervisors: Dr. Mark Kirkpatrick and Dr. C. Randal Linder

Teaching Assistant, Biostatistics

Fall 2012, 2013

Department of Statistics and Data Science, The University of Texas at Austin

Supervisor: Dr. Claus Wilke

Teaching Assistant, Evolutionary Biology

Fall 2009

Department of Biology, Brown University

Supervisor: Dr. Chris Organ