

# STEPHANIE J. SPIELMAN, PHD

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## CONTACT INFORMATION

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## ACADEMIC APPOINTMENTS

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

## EDUCATION

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**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

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**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

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

## PEER-REVIEWED PUBLICATIONS

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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

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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

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### 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

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**Instructor, Genomics and Evolutionary Medicine**

Spring 2018

Temple University

**Instructor, Biostatistics**

Fall 2017

Temple University

**Instructor, Functional Ecological Genomics Workshop**

May 24–26, 2017

Lacawac Sanctuary

**Co-instructor, Peer-led Introduction to Biocomputing**

Spring 2015, 2016

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

**Lead Instructor, Introduction to Python**

May 2015, 2016

Big Data in Biology Summer School

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

**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