

# STEPHANIE J. SPIELMAN, PHD

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## CONTACT INFORMATION

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## ACADEMIC APPOINTMENTS

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**Assistant Professor** 2018 – Present  
Department of Biological Sciences, Rowan University

**Research Assistant Professor (Postdoctoral level)** 2016–2018  
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, PhD

**Brown University** 2006–2010  
Sc.B. in Biology, with Honors  
Concentration in Ecology and Evolutionary Biology  
Advisor: Daniel M. Weinreich, PhD

## PEER-REVIEWED PUBLICATIONS

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22. SL Kosakovsky Pond, AFY Poon, R Velazquez, S Weaver, N Lance Hepler, B Murrell, SD Shank, B Rife Magalis, D Bouvier, A Nekrutenko, S Wisotsky, **SJ Spielman**, SDW Frost, SV Muse. 2019. “HyPhy 2.5 – a customizable platform for evolutionary hypothesis testing using phylogenies.” *Molecular Biology and Evolution*. In Press.
21. **SJ Spielman**, S Weaver, SD Shank, BR Magalas, M Li, and SL Kosakovsky Pond. 2019. “Evolution of viral genomes: Interplay between selection, recombination and other forces.” *Evolutionary Genomics. Methods in Molecular Biology*, vol 1910. Humana Press, New York, NY.

20. R Maddamsetti, DT Johnson, **SJ Spielman**, KL Petrie, DS Marks, and JR Meyer. 2018. “Viral gain-of-function experiments uncover residues under diversifying selection in nature.” *Evolution*. 72: 2234–2243.
19. **SJ Spielman** and SL Kosakovsky Pond. 2018. “Relative evolutionary rates in proteins are largely insensitive to the substitution model.” *Molecular Biology and Evolution*. 35(9): 2307–2317.
18. **SJ Spielman** and SL Kosakovsky Pond. 2018. “Relative evolutionary rate inference in HyPhy with LEISR.” *PeerJ* 6: e4339.
17. **SJ Spielman**. 2018. “phyphy: Python package for facilitating the execution and parsing of HyPhy standard analyses.” *Journal of Open Source Software* 3(21): 514.
16. S Weaver, SD Shank, **SJ Spielman**, M Li, SV Muse, and SL Kosakovsky Pond. 2018. “Datamonkey 2.0: A modern web application for characterizing selective and other evolutionary processes.” *Molecular Biology and Evolution* 35(3): 773–777.
15. DK Sydykova, BR Jack, **SJ Spielman**, and CO Wilke. 2018. “Measuring evolutionary rates of proteins in a structural context.” *F1000Research* 6:1845.
14. EL Jackson, **SJ Spielman**, and CO Wilke. 2017. “Computational prediction of the tolerance to amino-acid deletion in green-fluorescent protein.” *PLOS ONE* 12(4): e0164905.
13. Z Kadlecova, **SJ Spielman**, D Loerke, A Mohanakrishnan, DK Reed, and SL Schmid. 2017. “Regulation of clathrin-mediated endocytosis by hierarchical allosteric activation of AP2.” *Journal of Cell Biology* 216(1): 167–179.
12. **SJ Spielman**, S Wan\*, and CO Wilke. 2016. “A comparison of one-rate vs. two-rate frameworks for site-specific dN/dS estimation.” *Genetics* 204(2): 499–511.
11. **SJ Spielman** and CO Wilke. 2016. “Extensively parameterized mutation–selection models reliably capture site-specific selective constraint.” *Molecular Biology and Evolution* 33(11): 2990–3002.
10. EL Jackson, A Shahmoradi, **SJ Spielman**, BR Jack, and CO Wilke. 2016. “Intermediate divergence levels maximize the strength of structure–sequence correlations in enzymes and viral proteins.” *Protein Science* 25(7): 1341–1353.
9. J Echave, **SJ Spielman**, and CO Wilke. 2016. “Causes of evolutionary rate variation among protein sites.” *Nature Reviews Genetics* 17: 109–921.
8. **SJ Spielman** and CO Wilke. 2015. “Pyvolve: A flexible Python module for simulating sequences along phylogenies.” *PLOS ONE* 10(9): e0139047.
7. AG Meyer, **SJ Spielman**, T Bedford, and CO Wilke. 2015. “Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak.” *Virus Evolution* 1(1): vev006–60.
6. **SJ Spielman**, K Kumar\*, and CO Wilke. 2015. “Comprehensive, structurally-curated alignment and phylogeny of vertebrate biogenic amine receptors.” *PeerJ* 3: e773.
5. **SJ Spielman** and CO Wilke. 2015. “The relationship between  $dN/dS$  and scaled selection coefficients.” *Molecular Biology and Evolution* 32(4): 1097–7108.
4. A Shahmoradi, Sydykova DK\*, **SJ Spielman**, EL Jackson, ET Dawson\*, AG Meyer, and CO Wilke. 2014. “Predicting evolutionary site variability from structure in viral proteins: buriedness, flexibility, and design.” *Journal of Molecular Evolution* 79: 130–042.
3. **SJ Spielman**, Dawson ET\*, and CO Wilke. 2014. “Limited utility of residue masking for positive-selection inference.” *Molecular Biology and Evolution* 31(9): 2496–6500.
2. MZ Tien\*, AG Meyer, DK Sydykova\*, **SJ Spielman**, and CO Wilke. 2013. “Maximum allowed solvent accessibilities of residues in proteins.” *PLOS ONE* 8(11): e80635.

1. **SJ Spielman** and CO Wilke. 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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5. N Srivastava, **SJ Spielman**, and EK Moore. Under Review. “Geological factors that impacted cadmium availability to be used as an alternative cofactor for zinc in the carbon fixation pathways of marine diatoms.”
4. **SJ Spielman** and EK Moore. Under Review. “dragon: A New Tool for Exploring Redox Evolution Preserved in the Mineral Record.”
3. EK Moore, J Hao, **SJ Spielman**, and N Yee. Under Review. “The Evolving Redox Chemistry and Bioavailability of Vanadium in Deep Time.”
2. **SJ Spielman**. 2019. “Model fit does not predict accuracy in single-gene protein phylogenetics.” *bioRxiv*. <https://doi.org/10.1101/698860>.
1. **SJ Spielman\***, AG Meyer\*, and CO Wilke. 2014. “Increased evolutionary rate in the 2014 West African Ebola outbreak is due to transient polymorphism and not positive selection.” *bioRxiv*. <https://doi.org/10.1101/011429>.

\*Authors contributed equally to this work.

## AWARDS AND HONORS

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<b>Outstanding Dissertation Award</b> Office of Graduate Studies, The University of Texas at Austin <i>Awarded to top dissertation across all of science, math, and engineering</i>	2016
<b>Graduate Student Professional Development Award</b> Office of Graduate Studies, The University of Texas at Austin	2015
<b>Graduate Dean’s Prestigious Fellowship Supplement Award</b> Office of Graduate Studies, The University of Texas at Austin	2015
<b>EEB Blair Endowment Travel Award</b> Department of Integrative Biology, The University of Texas at Austin	2015
<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

## ACTIVE FUNDING AND GRANTS

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- Alex's Lemonade Stand Foundation** 1/2020 – 12/2020  
PI (\$16,760.00; 100%). “OpenPBTA Analysis Site.”
- NSF XSEDE DEB190018** 11/2019 – 11/2020  
PI. “Investigating the impact of different evolutionary models on estimating divergence times.”
- Rowan University Seed Funding Program** 7/2019 – 6/2020  
co-PI (\$10,000; 50%). “Developing and Applying a New Web-Based Platform for Investigating the Coevolution of the Geosphere and Biosphere.”

## PREVIOUS FUNDING AND GRANTS

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- NIGMS/NIH F31-GM113622 (NRSA)** 2015–2016  
PI. “Software development and application of a simulation framework for protein evolution.”

## PRESENTATIONS AND POSTERS

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- Cautionary tales in protein phylogenetic modeling.**  
Invited Research Seminar at West Chester University  
West Chester, PA 2019.
- Testing the role of model selection in phylogenetic accuracy.**  
Contributed Talk at Evolution 2019  
Providence, RI 2019.
- dragon: An interactive web-based platform to explore mineral-chemistry networks in deep-time.**  
Contributed Talk at ENIGMA Astrobiology Symposium  
Rutgers University, New Brunswick, NJ 2019.
- Possibilities, pitfalls, and practical consequences of model selection procedures in phylogenetics.**  
Invited Research Seminar at Dalhousie University  
Halifax, Nova Scotia, Canada 2019.
- Introduction to Computational Molecular Evolution**  
“Research Spotlight” Invited Seminar at the Rowan University Biology Club  
Rowan University, Glassboro, NJ 2018.
- 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.

## STUDENT POSTER PRESENTATIONS

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**Protein models affect measures of evolutionary divergence**

Contributed Poster at COURI 2019  
Presented by undergraduate researcher Francis K. Picone  
Rowan University, Glassboro, NJ 2019.

**Phylogenetic model selection is sensitive to alignment quality**

Contributed Poster at COURI 2019  
Presented by undergraduate researcher Molly Miraglia  
Rowan University, Glassboro, NJ 2019.

**Investigating the Role of Cadmium within the Biosphere and Geosphere in Deep Time**

Contributed Poster at RUSSS 2019 and COURI 2019  
Presented by undergraduate researcher Naman Srivastava (jointly advised by Eli K. Moore, PhD)  
Rowan University, Glassboro, NJ 2019.

## **Analysis of Motif Distributions in Regions of Endocytic Proteins**

Contributed Poster at RUSSS 2019

Presented by undergraduate researcher Chante Bethell

Rowan University, Glassboro, NJ 2019.

## **TEACHING EXPERIENCE**

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**Instructor, Introduction to Evolution and Scientific Inquiry** Fall 2018 – Present  
Rowan University

**Lead Instructor, Introduction to Python** May 2015, 2016, 2018  
Big Data in Biology Summer School  
Center for Computational Biology and Bioinformatics, The University of Texas at Austin

**Instructor, Genomics and Evolutionary Medicine (Graduate Level)** Spring 2018  
Temple University

**Instructor, Biostatistics (Graduate Level)** Fall 2017  
Temple University

**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

## **ACADEMIC SERVICE AND OUTREACH**

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**Invited Career Panelist, iEvoBio Meeting 2019**  
Providence, RI

June 26, 2019

**Instructor, Introduction to Biocomputing Weekly Short Course**  
Rowan University

Fall 2018

**PeerJ Ambassador for Open Science Advocacy**

2018 – Present

**Steering Committee Member and Advisor**  
Professional Science Masters in Bioinformatics Program  
Temple University

Fall 2017 – Spring 2018

**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

**Member, Society for Molecular Biology and Evolution**

**Peer Reviewer**

*Molecular Biology and Evolution, Systematic Biology, Genome Biology and Evolution, Molecular Phylogenetics and Evolution, PLoS Computational Biology, Bioinformatics, BMC Evolutionary Biology, BMC Bioinformatics, PeerJ, Philosophical Transactions of the Royal Society B, Genes, Journal of Molecular Evolution*