

STEPHANIE J. SPIELMAN, PHD

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CONTACT INFORMATION

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ACADEMIC APPOINTMENTS

Assistant Professor Department of Biological Sciences, Rowan University	2018 – Present
Research Assistant Professor (Postdoctoral level) Institute for Evolutionary Genomics and Medicine, Temple University	2016–2018

EDUCATION

The University of Texas at Austin Ph.D. in Ecology, Evolution, and Behavior, Department of Integrative Biology Research focus in Computational Molecular Evolution Advisor: Claus O. Wilke, PhD	2011–2016
Brown University Sc.B. in Biology, with Honors Concentration in Ecology and Evolutionary Biology Advisor: Daniel M. Weinreich, PhD	2006–2010

PEER-REVIEWED PUBLICATIONS

25. **SJ Spielman** and EK Moore. 2020. “dragon: A New Tool for Exploring Redox Evolution Preserved in the Mineral Record.” *Frontiers in Earth Science*. 8:414.
24. **SJ Spielman**. 2020. “Relative Model Fit Does Not Predict Topological Accuracy in Single-Gene Protein Phylogenetics.” *Molecular Biology and Evolution*. 37(7):2110-2123.
23. EK Moore, J Hao, **SJ Spielman**, and N Yee. 2020. “The Evolving Redox Chemistry and Bioavailability of Vanadium in Deep Time.” *Geobiology*. 00:1-12.

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*. 37(1): 295-299.
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

2. N Srivastava, **SJ Spielman**, S Morrison, and EK Moore. 2020. "Geological factors that impacted cadmium availability to be used as an alternative cofactor for zinc in the carbon fixation pathways of marine diatoms." *Earth and Space Science Open Archive*. <https://doi.org/10.1002/essoar.10503716.1>.
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

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

ACTIVE FUNDING AND GRANTS

NSF EAR2020520 CO-PI (\$319,227; 50%). “dragon-phire: Deep-time Redox Analysis of the Geobiology Ontology Network - Protein Hardware Integrates Redox Evolution.”	08/2020 – 07/2023
Alex’s Lemonade Stand Foundation PI (\$16,760.00; 100%). “OpenPBTA Analysis Site.”	1/15/2020 – 7/15/2021

PREVIOUS FUNDING AND GRANTS

Rowan University Seed Funding Program CO-PI (\$10,000; 50%). “Developing and Applying a New Web-Based Platform for Investigating the Coevolution of the Geosphere and Biosphere.” <i>Award rescinded due to COVID-19 before funds were applied to research.</i>	7/2019 – 6/2020
NIGMS/NIH F31-GM113622 (NRSA) PI. “Software development and application of a simulation framework for protein evolution.”	2015–2016

PRESENTATIONS AND POSTERS

Leveraging population-genetics-informed models to improve the reliability of simulation studies in molecular evolution Contributed Poster at <i>SMBE 2020</i> <i>Conference canceled due to COVID-19</i>	July 2020
Cautionary tales in phylogenetic model selection. Invited Research Seminar at Rutgers University New Brunswick, NJ 2019.	
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

Protein models affect measures of evolutionary divergence

Presented by undergraduate researcher Francis K. Picone

Contributed Poster at COURI 2019
Rowan University, Glassboro, NJ 2019.

Phylogenetic model selection is sensitive to alignment quality

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

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

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

Analysis of Motif Distributions in Regions of Endocytic Proteins

Presented by undergraduate researcher Chante Bethell
Contributed Poster at RUSSS 2019
Rowan University, Glassboro, NJ 2019.

TEACHING EXPERIENCE

Instructor, Instruction to Data Science in R Workshop Cumberland Bridges to Rowan (CB2R) Program, Rowan University	Summer 2020
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Instructor, Data Science for Biologists Rowan University	Spring 2020 – Present
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Guest Lecturer, Statistical Genetics Villanova University	November 6, 2019
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Instructor, Introduction to Evolution and Scientific Inquiry Rowan University	Fall 2018 – Spring 2020
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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, 2018
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Instructor, Genomics and Evolutionary Medicine (Graduate Level) Temple University	Spring 2018
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Instructor, Biostatistics (Graduate Level) Temple University	Fall 2017
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Teaching Assistant, Computational Biology and Bioinformatics Department of Statistics and Data Science, The University of Texas at Austin	Spring 2015
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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

Invited Career Panelist, iEvoBio Meeting 2020

June 2020

Meeting canceled due to COVID-19

Invited Career Panelist, iEvoBio Meeting 2019

June 26, 2019

Providence, RI

Instructor, Introduction to Biocomputing Weekly Short Course

Fall 2018

Rowan University

PeerJ Ambassador for Open Science Advocacy

2018 – Present

Steering Committee Member and Advisor

Fall 2017 – Spring 2018

Professional Science Masters in Bioinformatics Program

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

Member, Society for Molecular Biology and Evolution

Peer Reviewer

Molecular Biology and Evolution, Systematic Biology, Genome Biology and Evolution, Virus 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