STEPHANIE J. SPIELMAN, PHD

Science Hall 201D ⋄ 201 Mullica Hill Road
Rowan University, Glassboro, NJ 08028

CONTACT INFORMATION

Email	spielman@rowan.edu
ORCID	http://orcid.org/0000-0002-9090-4788
Website	https://spielmanlab.github.io
Personal Github	https://www.github.com/sjspielman
Lab Github	https://www.github.com/spielmanlab

ACADEMIC APPOINTMENTS

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

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

26. N Srivastava*, **SJ Spielman**, S Morrison, and EK Moore. 2021. "Geological factors that impacted cadmium availability to be used as an alternative cofactor for zinc in the carbon fixation pathways of marine diatoms." *Journal of Geophysical Research: Biogeosciences*. 126(2): e2020JG005966. *Highlighted "Research Spotlight" article in* Eos: Science News by AGU.

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 accessibilites 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

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

President's Award for Excellence in Innovative Instructional Delivery 2021
Faculty Center for Teaching Excellence, Rowan University

Outstanding Dissertation Award 2016
Office of Graduate Studies, The University of Texas at Austin
Awarded to top dissertation across all of science, math, and engineering

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 2014
Biology Instructional Office, The University of Texas at Austin

EEB Travel Award 2013
Department of Integrative Biology, The University of Texas at Austin

SMBE Graduate Student Travel Award 2013
Society for Molecular Biology and Evolution

Integrative Biology Graduate Recruitment Fellowship 2011
Department of Integrative Biology, The University of Texas at Austin

Karen T. Romer Undergraduate Teaching and Research Award 2009
Brown University

ACTIVE FUNDING AND GRANTS

NSF EAR2020520 08/2020 – 07/2023
CO-PI ($319,227; 50%). "dragon-phire: Deep-time Redox Analysis of the Geobiology Ontology Network - Protein Hardware Integrates Redox Evolution."

Rowan University Seed Funding Program 07/2019 – 06/2021
CO-PI ($10,000; 50%). "Developing and Applying a New Web-Based Platform for Investigating the Coevolution of the Geosphere and Biosphere."

Alex's Lemonade Stand Foundation 1/15/2020 – 7/15/2021
PI ($16,760.00; 100%). "OpenPBTA Analysis Site."

PREVIOUS FUNDING AND GRANTS

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

PRESENTATIONS AND POSTERS

Leveraging population-genetics–informed models to improve the reliability of simulation studies in molecular evolution
Accepted Poster at SMBE 2020.
Conference canceled due to COVID-19.

Cautionary tales in phylogenetic model selection.
Invited Research Seminar at Rutgers University, 2019.
Rutgers University, New Brunswick, NJ.

Cautionary tales in protein phylogenetic modeling.
Invited Research Seminar at West Chester University, 2019.
West Chester University, West Chester, PA.

Testing the role of model selection in phylogenetic accuracy.
Contributed Talk at Evolution 2019.
Providence, RI.

dragon: An interactive web-based platform to explore mineral-chemistry networks in deep-time.
Contributed Talk at ENIGMA Astrobiology Symposium, 2019.

Rutgers University, New Brunswick, NJ.

Possibilities, pitfalls, and practical consequences of model selection procedures in phylogenetics.
Invited Research Seminar at Dalhousie University, 2019.
Halifax, Nova Scotia, Canada.

Introduction to Computational Molecular Evolution
"Research Spotlight" Invited Seminar at the Rowan University Biology Club, 2018.
Rowan University, Glassboro, NJ.

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

Uncovering the properties and limitations of models of sequence evolution.
Invited CIDID Seminar at Fred Hutchinson Cancer Research Center, 2016.
Seattle, Washington.

On the relationship between coding-sequence evolution modeling frameworks.
Contributed talk at *SMBE 2015*
Vienna, Austria.

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*, 2014.
Georgia Institute of Technology, Atlanta, GA.

Limited utility of residue masking for positive-selection inference.
Contributed poster at *2nd Annual Symposium on Big Data in Biology*, 2014.
UT Austin, Austin, TX.

The molecular evolution of membrane proteins.
Contributed talk at *SMBE Satellite Meeting MPEII*, 2013.
University of Colorado, Aurora, CO.

Membrane environment imposes unique selection pressures on GPCRs.
Contributed poster at *Annual BEACON Congress*, 2013.
Michigan State University, East Lansing, MI.

UNDERGRADUATE STUDENT POSTER PRESENTATIONS

Analysis of the genetic diversity of *Caulobacter crescentus* Phickviruses using *phoH* and thymidylate synthase as signature genes.
A Cruz, V Vincent, SJ Spielman, MA Randa, and GB Hecht.

Contributed Poster at *ABRCMS 2020*.
Virtual Conference.

Protein models affect measures of evolutionary divergence.
FK Picone and SJ Spielman.
Contributed Poster at *COURI 2019*.
Rowan University, Glassboro, NJ.

Phylogenetic model selection is sensitive to alignment quality.
M Miraglia and SJ Spielman.
Contributed Poster at *COURI 2019*.
Rowan University, Glassboro, NJ.

Investigating the role of Cadmium within the biosphere and geosphere in deep tume.
N Srivastava, SJ Spielman, and EK Moore.
Contributed Posters at *RUSSS 2019* and *COURI 2019*.
Rowan University, Glassboro, NJ.

Analysis of motif distributions in regions of endocytic proteins.
C Bethell and SJ Spielman.
Contributed Poster at *RUSSS 2019*.
Rowan University, Glassboro, NJ.

Bolded names indicate undergraduate student presenters.

TEACHING EXPERIENCE

Instructor, Instruction to Data Science in R Workshop Summer 2020
Cumberland Bridges to Rowan (CB2R) Program, Rowan University

Instructor, Data Science for Biologists Spring 2020 – Present
Rowan University

Guest Lecturer, Statistical Genetics November 6, 2019
Villanova University

Instructor, Introduction to Evolution and Scientific Inquiry Fall 2018 – Spring 2020
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

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
eLife, *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*