

CURRICULUM VITAE
ASHLEY I. TEUFEL, Ph.D.
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EDUCATION

Ph.D., Molecular Biology , University of Wyoming Advisor: David Liberles	2015
B.S., Mathematics , Minor: Bioinformatics, New Mexico State University	2007
B.S., Computer Science , Minor: Mathematics, New Mexico State University	2006

ACADEMIC POSITIONS

Assistant Professor of Bioinformatics , Texas A&M - San Antonio	2021–present
Omidyar Fellow , Santa Fe Institute	2019–2021
Postdoctoral Fellow , Dept. of Integrative Biology, The University of Texas at Austin Advisor: Claus Wilke	2015–2018
Research Fellow , Dept. of Biology, Temple University	2015
M.S., Biology student , Minor: Mathematics, New Mexico State University	2008-2010

TEACHING

Gen Biology I - Attributes of Living Systems , Instructor, Texas A&M - San Antonio	2022 - present
Seminar - Cell/Molecular Biology , Instructor, Texas A&M - San Antonio	2022 - present
Seminar - Integrative Biology , Instructor, Texas A&M - San Antonio	2021
Statistics in Biology and Medicine , Instructor, Texas A&M - San Antonio	2021-present
Science Sprint: Building models to detect, project, and combat COVID-19 , Mentor, The University of Texas at Austin (virtual event)	2020
Biostatistics , Instructor, The University of Texas at Austin	2018
Computational Biology & Bioinformatics , Guest Lecturer, The University of Texas at Austin	2017
Gene Family Analysis Workshop , Teaching Assistant, New Mexico State University	2014
Bioinformatics , Guest Lecturer & Teaching Assistant, University of Wyoming	2012, 2014
Computers in Biology , Teaching Assistant, University of Wyoming	2011, 2013
Mathematics in Biology , Developer & Teaching Assistant, New Mexico State University	2009
Computer Science , Laboratory Proctor & Tutor, New Mexico State University	2005–2010

EXTERNAL FUNDING

\$3,550 Working group “Capturing the Evolutionary Capacity to Innovate via Novel Interactions in Protein Interaction Networks” funded by Santa Fe Institute Education	2019
\$6,383 Working group “The Point of No Return” funded by Santa Fe Institute	2019
\$53,505 Grant “Master Key vs. Extra Key: Testing competing lock-and-key hypothesis for constrained protein-protein evolution” funded by BEACON an NSF center	2018
\$2,898 “Seeing the Tree and the Forest: Understanding Individual and Population Variation in Biology, Medicine, and Society” fellowship funded by The University of Texas at Austin	2017

PUBLICATIONS

24. Liberles, D. A., Meyer, M. M., Rest, J. S., and **Teufel**, A. I. (2021). 2021 zuckerkandl prize. *Journal of Molecular Evolution*, to appear in volume 90(1):1
23. Klein, B., Holmér, L., Smith, K. M., Johnson, M. M., Swain, A., Stolp, L., **Teufel**, A. I., and Kleppe, A. S. (2021). A computational exploration of resilience and evolvability of protein–protein interaction networks. *Communications Biology*, 4(1):1352
22. **Teufel**, A. I., Liu, W., Draghi, J. A., Cameron, C. E., and Wilke, C. O. (2021). Modeling poliovirus replication dynamics from live time-lapse single-cell imaging data. *Scientific reports*, 11(1):1–15
21. Ahrens, J. B., **Teufel**, A. I., and Siltberg-Liberles, J. (2020). A phylogenetic rate parameter indicates different sequence divergence patterns in orthologs and paralogs. *Journal of Molecular Evolution*, pages 1–11
20. Shoemaker, L. G., Barner, A. K., Bittleston, L. S., and **Teufel**, A. I. (2020). Quantifying the relative importance of variation in predation and the environment for species coexistence. *Ecology Letters*, 23(6):939–950
19. Laurent, J. M., Garge, R. K., **Teufel**, A. I., Wilke, C. O., Kachroo, A. H., and Marcotte, E. M. (2020). Humanization of yeast genes with multiple human orthologs reveals functional divergence between paralogs. *PLoS Biology*, 18(5):e3000627
18. **Teufel**, A. I. (2019). Spire: R package for single-cell population infection replication estimation. *Zenodo*, page 10.5281/zenodo.3366146
17. Liberles, D. A. and **Teufel**, A. I. (2018). Evolution and structure of proteins and proteomes. *Genes*, 9(12):583
16. **Teufel**, A. I., Johnson, M. M., Laurent, J. M., Kachroo, A. H., Marcotte, E. M., and Wilke, C. O. (2018). The many nuanced evolutionary consequences of duplicated genes. *Molecular Biology and Evolution*, 36(2):304–314
15. **Teufel**, A. I., Ritchie, A. M., Wilke, C. O., and Liberles, D. A. (2018). Using the mutation-selection framework to characterize selection on protein sequences. *Genes*, 9(8):409
14. Jiang*, Q., **Teufel***, A. I., Jackson, E. L., and Wilke, C. O. (2018). Beyond thermodynamic constraints: evolutionary sampling generates realistic protein sequence variation. *Genetics*, 208(4):1387–1395
13. Caglar, M. U., **Teufel**, A. I., and Wilke, C. O. (2018). Sicegar: R package for sigmoidal and double-sigmoidal curve fitting. *PeerJ*, 6:e4251
12. **Teufel**, A. I. and Wilke, C. O. (2017). Accelerated simulation of evolutionary trajectories in origin-fixation models. *Journal of The Royal Society Interface*, 14(127):20160906
11. Orlenko*, A., **Teufel***, A. I., Chi, P. B., and Liberles, D. A. (2016). Selection on metabolic pathway function in the presence of mutation-selection-drift balance leads to rate-limiting steps that are not evolutionarily stable. *Biology Direct*, 11(1):31
10. **Teufel**, A. I., Liu, L., and Liberles, D. A. (2016). Models for gene duplication when dosage balance works as a transition state to subsequent neo-or sub-functionalization. *BMC Evolutionary Biology*, 16(1):45
9. Zhao, J., **Teufel**, A. I., Liberles, D. A., and Liu, L. (2015). A generalized birth and death process for modeling the fates of gene duplication. *BMC Evolutionary Biology*, 15(1):275

8. **Teufel**, A. I., Masel, J., and Liberles, D. A. (2015). What fraction of duplicates observed in recently sequenced genomes is segregating and destined to fail to fix? *Genome Biology and Evolution*, 7(8):2258–2264
7. **Teufel**, A. I. (2015). *Mechanistic Models of the Evolutionary Dynamics of Duplicated Genes*. (Dissertation) University of Wyoming
6. **Teufel**, A. I., Zhao, J., O'Reilly, M., Liu, L., and Liberles, D. A. (2014). On mechanistic modeling of gene content evolution: birth-death models and mechanisms of gene birth and gene retention. *Computation*, 2(3):112–130
5. Jones, M. R., Forester, B. R., **Teufel**, A. I., Adams, R. V., Anstett, D. N., Goodrich, B. A., Landguth, E. L., Joost, S., and Manel, S. (2013). Integrating landscape genomics and spatially explicit approaches to detect loci under selection in clinal populations. *Evolution*, 67(12):3455–3468
4. Liberles, D. A., **Teufel**, A. I., Liu, L., and Stadler, T. (2013). On the need for mechanistic models in computational genomics and metagenomics. *Genome Biology and Evolution*, 5(10):2008–2018
3. **Teufel**, A. I., Grahnen, J. A., and Liberles, D. A. (2012). Modeling proteins at the interface of structure, evolution, and population genetics. In *Computational Modeling of Biological Systems*, pages 347–361. Springer
2. Liberles, D. A., Teichmann, S. A., Bahar, I., Bastolla, U., Bloom, J., Bornberg-Bauer, E., Colwell, L. J., de Koning, A. P. J., Dokholyan, N. V., Echave, J., Elofsson, A., Gerloff, D. L., Goldstein, R. A., Grahnen, J. A., Holder, M. T., Lakner, C., Lartillot, N., Lovell, S. C., Naylor, G., Perica, T., Pollock, D. D., Pupko, T., Regan, L., Roger, A., Rubinstein, N., Shakhnovich, E., Sjölander, K., Sunyaev, S., **Teufel**, A. I., Thorne, J. L., Thornton, J. W., Weinreich, D. M., and Whelan, S. (2012). The interface of protein structure, protein biophysics, and molecular evolution. *Protein Science*, 21(6):769–785
1. Konrad*, A., **Teufel***, A. I., Grahnen, J. A., and Liberles, D. A. (2011). Toward a general model for the evolutionary dynamics of gene duplicates. *Genome Biology and Evolution*, 3:1197–1209

PRESENTATIONS

27. “Using Big Data to Examine How Anti-Viral Drugs Impact Viral Replication and Potentially Viral Evolution” Texas A&M International University, virtual (February, 2021)
26. “Using Big Data to Examine How Anti-Viral Drugs Impact Viral Replication and Potentially Viral Evolution” Texas A&M University - San Antonio, virtual (February, 2021)
25. “Modeling Covid-19 Spread in Long Term Care Facilities in the Greater Austin, TX Region” University of Texas at Austin Covid Modeling Consortium, virtual (August, 2020)
24. “Uncovering Viral Replication Dynamics from High-throughput Single-cell Experiments” Center for Computation and Technology, Louisiana State University, Baton Rouge, LA (February, 2020)
23. “The Many Nuanced Evolutionary Consequences of Protein Functional Divergence” Department of Biological Sciences, Louisiana State University, Baton Rouge, LA (February, 2020)
22. “Translational Efficiency and The Evolution of Position-Dependent Codon Usage” Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Manchester, England (July, 2019)
21. “The Point of No Return: Entrenchment in Molecular, Technological, and Social Systems” JSMF- SFI Postdocs in Complexity V, Santa Fe, NM (March, 2019)
20. “Is Evolution Irreversible?” JSMF- SFI Postdocs in Complexity IV, Santa Fe, NM (September, 2018)

19. "The Many Nuanced Consequences of Gene Duplication" BEACON Center for the Study of Evolution in Action, Lansing, MI (August, 2018)
18. "The Many Nuanced Consequences of Gene Duplication" Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Yokohama, Japan (July, 2018)
17. "How Does Complex Life Functionally Diversify?" The University of Arizona, Tucson, AZ (February, 2018)
16. "How Does Complex Life Functionally Diversify?" The Santa Fe Institute, Santa Fe, NM (January, 2018)
15. "A Protein's Guide to Losing Friends and Alienating Partners" University of Central Florida, Orlando, FL (November, 2017)
14. "Functional Shifts in Duplicated Genes via Specialization of Interacting Partners" BEACON Center for the Study of Evolution in Action, Lansing, MI (August, 2017)
13. "Uncovering Replication Principles from Single-cell Virology Experiments" Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Austin, TX (July, 2017)
12. "Protein Flexibility and the Irreversibility of Evolution" Texas Protein Folders Meeting, Cleveland, TX (April, 2017)
11. "Functional Retention of Protein-Protein Interactions Despite Substantial Sequence Divergence" BEACON Center for the Study of Evolution in Action, Lansing, MI (August, 2016)
10. "Functional Retention of Protein-Protein Interactions Despite Substantial Sequence Divergence" Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Gold Coast, Australia (July, 2016)
9. "What Fraction of Gene Duplicates Observed in Recently Sequenced Genomes is Segregating and Destined to Fail to Fix?" Lehigh Valley Ecology and Evolution Symposium, Allentown, PA (April, 2015)
8. "Selective Pressures on Amino Acid Substitutions During Human-Chimpanzee Divergence" Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Chicago, IL (July, 2013)
7. "Selective Pressures on Amino Acid Substitutions During Human-Chimpanzee Divergence" Quantitative Laws of Genome Evolution, Lake Como, Italy (July, 2013)
6. "Towards a General Model for the Evolutionary Dynamics of Gene Duplicates" Stockholm Bioinformatics Center, Stockholm University, Stockholm, Sweden (August, 2012)
5. "The Interface of Evolutionary Dynamics of Gene Duplicates and Landscape Genetics" Symposium on Landscape Genetics, University of Toronto, Toronto, Canada (May, 2012)
4. "Towards a General Model for the Evolutionary Dynamics of Gene Duplicates" Mechanisms of Protein Evolution, University of Colorado Health Sciences Center, Denver, CO (December, 2011)
3. "Lineage-Specific Substitution Patterns at the Interface of Effective Population Size, Linkage, and Biochemistry" Synthesis Meeting on Modeling Protein Structural and Energetic Constraints on Sequence Evolution, NIMBioS, Durham, NC (October, 2011)
2. "Unifying Models for Estimating Population Size and Demography" New Mexico State University Bio-Symposium, Las Cruces, NM (April, 2010)

1. “Spatial-Temporal Models of Primate Behavior” New Mexico State University, Las Cruces, NM (May, 2009)

POSTERS

5. “Translational Efficiency and The Evolution of Position-Dependent Codon Usage” Molecular Mechanisms in Evolution Gordon Research Conference, Easton, MA (June, 2019)
4. “Translational Efficiency and The Evolution of Position-Dependent Codon Usage” (presented by undergraduate trainee) Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Austin, TX (July, 2017)
3. “Accelerated Simulation of Evolutionary Trajectories in Origin-Fixation Models” Institute for Cellular and Molecular Biology at The University of Texas at Austin Retreat, Horseshoe Bay, TX (September, 2016)
2. “Selective Pressures on Amino Acid Substitutions During Human-Chimpanzee Divergence” NSF Bioinformatics Workshop, Little Rock, AR (March, 2013) (3rd place poster award)
1. “Simulation of Evolutionary Dynamics of Gene Duplicates” New Mexico Bioinformatics Science and Technology Symposium, Santa Fe, NM (October, 2012)

JOURNAL REVIEWER EXPERIENCE

Biophysical Journal, BMC Evolutionary Biology, Elife, Journal of Molecular Evolution, Journal of Theoretical Biology, Molecular Biology and Evolution, Molecular Ecology, PeerJ, PLoS ONE, PLoS Computational Biology, Systematic Biology, Theoretical Population Biology

AWARDS

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| Ecological Society of America (ESA), Theoretical Ecology Outstanding Paper Award Honorable Mention | 2021 |
| Registration and travel awards for Society for Molecular Biology and Evolution (SMBE) annual meeting, Manchester, England. Funded by SMBE | 2019 |
| Registration award for SMBE annual meeting, Yokohama, Japan. Funded by SMBE | 2018 |
| Registration award for SMBE annual meeting, Austin, TX. Funded by SMBE | 2017 |
| Registration award for SMBE annual meeting, Gold Cast, Australia. Funded by SMBE | 2016 |
| Travel award for SMBE annual meeting, Chicago, IL. Funded by SMBE | 2013 |
| Travel award for “Quantitative Laws of Genome Evolution”, Lake Como, Italy. Funded by Wyoming IDeA Networks for Biomedical Research Excellence (INBRE) | 2013 |
| Registration for “Quantitative Laws of Genome Evolution”, Lake Como, Italy. Funded by UniverLecco, an outreach program from the city of Lecco | 2013 |
| Travel award for “NSF Bioinformatics Workshop”, Little Rock, AR. Funded by Wyoming INBRE | 2013 |
| Travel award for “Symposium on Landscape Genetics” in Toronto, Canada. Funded by The University of Toronto Landscape Genetics Distributed Graduate Course | 2012 |

TRAINEES

Leina Gries, High School Student, Institute for Computing in Research	2019
Genevieve Mortensen, Undergraduate Student, The University of Texas at Austin	2018
Ayat Sharif, Undergraduate Student, The University of Texas at Austin	2017
Nelson Marrow, Undergraduate Student, The University of Texas at Austin	2016-2019
Qian Jiang, Ph.D. Student, visiting scholar at The University of Texas at Austin sponsored by the China Scholarship Council	2016-2017

PROFESSIONAL SERVICE

Zuckerlandl Prize Committee Member for the Journal of Molecular Evolution	2021
College of Arts and Sciences Curriculum Committee Member, Texas A&M - San Antonio	2021
Zuckerlandl Prize Committee Member for the Journal of Molecular Evolution	2020
Editorial Board Member for the journal BMC Ecology and Evolution	2020–present
Volunteer Lecturer & Mentor at the Institute for Computing in Research	2019
Associate Editor of the Journal of Molecular Evolution	2019–present
Symposium Chair of “Mechanisms of Protein Evolution” at SMBE annual meeting	2017

OTHER ACTIVITIES

Featured in Parallax article “The Point of no Return”	2019
Guest Editor for the journal Genes special issue “Evolution and Structure of Proteins and Proteomes”	2017
Second Place in Flaming Gorge Jalapeño Eating Contest held in Laramie, WY	2014
Summer Student of Computational Biology, University of Oxford	2012
Advisor: Jotun Hein	
Landscape Genetics Field School, Koffler Scientific Reserve	2012
Advisor: Melanie Murphy	
President of the New Mexico State University Association for Computing Machinery	2009-2010
Featured in New Mexico State University Young Women in Computing Fall newsletter	2009
Primate Behavior and Ecology Field School, Baboon Community Sanctuary La Milpa Belize	2009
Advisor: Brenda Benefit	
Vice President of the New Mexico State University Association for Computing Machinery	2008-2009
Member of the New Mexico State University Mathematics Honor Society, Pi Mu Epsilon	2005-2010