

# CURRICULUM VITAE

## ASHLEY I. TEUFEL

Institute for Cellular and Molecular Biology, Department of Integrative Biology

The University of Texas at Austin, Austin, TX 78712

Phone: 575-642-2920

E-Mail: ateufel@utexas.edu

### Research Interests

Computation and mathematical modeling at the interface of molecular evolution, population dynamics, and ecology.

### Education

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| 10/2015 | Ph.D., Molecular Biology, University of Wyoming<br>Laramie, WY<br>Advisor: Prof. David Liberles<br>Dissertation Title: "Mechanistic Models for Gene Duplication" |
| 12/2007 | B.S., Mathematics, Minor Bioinformatics, New Mexico State University<br>Las Cruces, NM   |
| 5/2006  | B.S., Computer Science, Minor Mathematics, New Mexico State University<br>Las Cruces, NM   |

### Experience

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| 11/2015-present | Postdoctoral Fellow, Department of Integrative Biology, The University of Texas at Austin<br>Austin, TX<br>Advisor: Prof. Claus Wilke |
| 2/2015-9/2015   | Visiting Research Fellow, Department of Biology, Temple University<br>Philadelphia, PA<br>Advisor: Prof. David Liberles               |
| 5/2012-8/2012   | Visiting Summer Student of Computational Biology, University of Oxford<br>Oxford, United Kingdom<br>Advisor: Prof. Jotun Hein         |
| 5/2012          | Landscape Genetics Field School, Koffler Scientific Reserve<br>Toronto, Canada<br>Advisor: Prof. Melanie Murphy                       |
| 3/2009          | Primate Behavior and Ecology Field School, Baboon Community Sanctuary<br>La Milpa, Belize<br>Advisor: Prof. Brenda Benefit            |
| 5/2008-5/2010   | M.S. Student, Biology, Minor Mathematics, New Mexico State University<br>Las Cruces, NM<br>Advisor: Prof. Brook Milligan              |

## Publications

Jiang, Q., **Teufel, A.I.**, Jackson, E.L., Wilke, C.O., 2017 “Beyond Thermodynamic Constraints: Evolutionary History Shapes Protein Sequence Variation” *Genetics* (submitted)

Caglar, M.U., **Teufel, A.I.**, Wilke, C.O., 2017 “Sicegar: R Package for Sigmoidal and Double-Sigmoidal Curve Fitting” *PeerJ* (submitted)

**Teufel, A.I.**, Wilke, C.O., 2017 “Accelerated Simulations of Evolutionary Trajectories in Origin-Fixation Models” *Journal of The Royal Society Interface*, 14:127

**Teufel, A.I.**, Liu, L., Liberles, D.A., 2016 “Models for Gene Duplication when Dosage Balance Works as a Transition State to Subsequent Neo or Subfunctionalization” *BMC Evolutionary Biology*, 16:45-51

Orlenko, A.\*, **Teufel, A.I.\***, Liberles, D.A., 2016 “Flux-dependent Selection on Metabolic Pathway Function in the Presence of Mutation-selection Balance Leads to Rate-limiting Steps that are not Evolutionary Stable” *Biology Direct*, 11:31

**Teufel, A.**, Masel, J., Liberles, D.A., 2015 “What Fraction of Duplicates Observed in Recently Sequenced Genomes of Segregating and Destined to Fail to Fix?” *Genome Biology and Evolution*, 7:2258-2264

Zhao, J., **Teufel, A.**, Liberles, D.A., Liu, L. 2015 “A Generalized Birth and Death Process for Modeling the Fates of Gene Duplication” *BMC Evolutionary Biology*, 15:275-286

**Teufel, A.I.**, Zhao, J., O'Reilly, M., Liu, L., Liberles, D.A., 2014. “On Mechanistic Modeling of Gene Content Evolution: Birth-Death Models and Mechanisms of Gene Birth and Gene Retention” *Computation* 2:112-130

Liberles, D. A., **Teufel, A.I.**, Liu, L., Stadler, T., 2013. “On the Need for Mechanistic Models in Computational Genomics and Metagenomics” *Genome Biology and Evolution*, 5:2008-2018

Jones, M.\*, Forester, B.\*, **Teufel, A.**, Adams, R., Anstett, D., Goodrich, B., Joost, S., Manel, S., 2013. “Integrating Landscape Genomics and Spatially Explicit Approaches to Detect Loci Under Selection in Clinal Population” *Evolution*, 67:3455-3468

Liberles, DA, Teichmann, S, Bahar I, Bastolla U, Bloom J, Bornberg-Bauer E, Colwell LJ, de Koning APJ, Dokholyan NV, Echave J, Elofsson A, Gerloff DL, Goldstein RA, Grahnen JA, Holder M, Lakner C, Lartillot N, Lovell S, Naylor G, Perica T, Pollock DD, Pupko T, Regan L, Roger A, Rubinstein N, Shakhnovich E, Sjolander E, Sunyaev S, **Teufel AI**, Thorne JL, Thornton JW, Weinreich DM, Whelan S. 2012. "The Interface of Protein Structure, Protein Biophysics, and Molecular Evolution" *Protein Science*, 21:769-785

**Teufel, A.I.**, Grahnen, J.A., and Liberles, D.A. “Modeling Proteins at the Interface of Structure, Evolution, and Population Genetics” in *Computational Modeling of Biological Systems: From Molecules to Pathways* (Ed: Dokholyan). New York: Springer-Verlag, 2012

Konrad, A.\*, **Teufel, A.I.\***, Grahnen, J.A., and Liberles, D.A. 2011. “Towards a General Model for the Evolutionary Dynamics of Gene Duplicates.” *Genome Biology and Evolution*, 3:1197-1209

## **Presentations**

“Functional Shifts in Duplicated Genes via Specialization of Interacting Partners” BEACON Center for the Study of Evolution in Action, Lansing, MI (August, 2017)

“Uncovering Replication Principles from Single-cell Virology Experiments” Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Austin, TX (July, 2017)

“Protein Flexibility and the Irreversibility of Evolution” Texas Protein Folders Meeting, Cleveland, TX (April, 2017)

“Functional Retention of Protein-Protein Interactions Despite Substantial Sequence Divergence” BEACON Center for the Study of Evolution in Action, Lansing, MI (August, 2016)

“Functional Retention of Protein-Protein Interactions Despite Substantial Sequence Divergence” Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Gold Coast, Australia (July, 2016)

“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)

“Selective Pressures on Amino Acid Substitutions During Human-Chimpanzee Divergence” Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Chicago, IL (July, 2013)

“Selective Pressures on Amino Acid Substitutions During Human-Chimpanzee Divergence” Quantitative Laws of Genome Evolution, Lake Como, Italy (July, 2013)

“Towards a General Model for the Evolutionary Dynamics of Gene Duplicates” Stockholm Bioinformatics Center, Stockholm University, Stockholm, Sweden (August, 2012)

“The Interface of Evolutionary Dynamics of Gene Duplicates and Landscape Genetics” Symposium on Landscape Genetics, University of Toronto, Toronto, Canada (May, 2012)

“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)

“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)

“Unifying Models for Estimating Population Size and Demography” New Mexico State University Bio-Symposium, Las Cruces, NM (April, 2010)

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

## Posters

“Translational Efficiency and The Evolution of Position-Dependent Codon Usage” Presented by undergraduate trainee: Nelson Morrow Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Austin, TX (July, 2017)

“Accelerated Simulation of Evolutionary Trajectories in Origin–Fixation Models” Institute for Cellular and Molecular Biology at UT Austin Retreat, Horseshoe Bay, TX (September, 2016)

“Selective Pressures on Amino Acid Substitutions During Human-Chimpanzee Divergence” NSF Bioinformatics Workshop, Little Rock, AR (March, 2013) (3rd place poster award)

“Simulation of Evolutionary Dynamics of Gene Duplicates” New Mexico Bioinformatics Science and Technology Symposium, Santa Fe, NM (October, 2012)

## External Funding and Awards

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| 4/2017 | Fellow of The University of Texas at Austin Pop-Up Institute "Seeing the Tree and the Forest: Understanding Individual and Population Variation in Biology, Medicine, and Society".<br>Total amount: \$2,898 |
| 7/2013 | Travel award for Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Chicago, IL.<br>Funded by SMBE   |
| 7/2013 | Travel award for “Quantitative Laws of Genome Evolution” in Lake Como, Italy.<br>Funded by Wyoming IDeA Networks for Biomedical Research Excellence (INBRE)  |
| 7/2013 | Registration for “Quantitative Laws of Genome Evolution” in Lake Como, Italy.<br>Funded by UniverLecco, an outreach program from the city of Lecco   |
| 5/2013 | Travel award for “NSF Bioinformatics Workshop” in Little Rock, AR.<br>Funded by Wyoming INBRE  |
| 5/2012 | Travel award for “Symposium on Landscape Genetics” in Toronto, Canada.<br>Funded by The University of Toronto Landscape Genetics Distributed Graduate Course   |

## Journals Reviewed For

Elife, PeerJ, PLoS ONE, BMC Evolutionary Biology, Journal of Molecular Evolution, Systematic Biology

## Teaching

- 1/2018-5/2018      Instructor, Biostatistics, The University of Texas at Austin  
- Basic theory of probability and statistics with practical applications with biological data. Includes fundamentals of probability, distribution theory, sampling models, data analysis, basics of experimental design, statistical inference, interval estimation and hypothesis testing.  
(Course to begin in the upcoming spring semester)
- 4/2017              Substitute Teacher, Computational Biology and Bioinformatics, The University of Texas at Austin  
- Computational-based data sorting, data transformation, and data analysis; programming in Python and R.  
(Gave lecture on sequence alignment methods)
- 5/2014              Teaching Assistant, Gene Family Workshop, New Mexico State University  
- Practical guide to phylogenetic program usage for analyzing phylogenomic and gene family datasets.
- 1/2014-5/2014      Teaching Assistant, Bioinformatics, University of Wyoming  
- Course topics range from classic algorithms in bioinformatics like multiple sequence alignment and phylogenetic tree construction to problems of functional analysis, including computational genomics, gene expression, protein structure, and systems biology analyses.  
(Gave lectures on machine learning)
- 8/2013-12/2013    Teaching Assistant, Computers in Biology, University of Wyoming  
- Prepares students to use existing internet resources as research tools in biology without the need to write or install software. Topics include literature searching, multiple sequence alignment and phylogenetic tree construction, primer design, protein homology modeling, and the use of model organism databases.
- 1/2012-5/2012      Teaching Assistant, Bioinformatics, University of Wyoming  
- See above for description.
- 8/2011-12/2011    Teaching Assistant, Computers in Biology, University of Wyoming  
- See above for description.
- 5/2009-7/2009      Teaching Assistant, Mathematics in Biology, New Mexico State University  
- Introduction to probability and deterministic models in ecology and epidemiology.
- 1/2009-5/2009      Course Development, Mathematics in Biology, New Mexico State University  
- See above for description.
- 1/2005-5/2010      Laboratory Proctor, Computer Science, New Mexico State University  
- Tutor for lower-division computer science courses.

## **Trainees**

9/2017-present	Ayat Sharif, Undergraduate Student, The University of Texas at Austin
8/2017-present	Mackenzie Johnson, Ph.D. Student, The University of Texas at Austin
1/2016-present	Nelson Marrow, Undergraduate Student, The University of Texas at Austin
1/2016-9/2017	Qian Jiang, Ph.D. Student, visiting scholar at The University of Texas at Austin sponsored by the China Scholarship Council

## **Other Awards and Activities**

10/2017	Guest editor of upcoming special issue on “Evolution and Structure of Proteins and Proteomes” in the journal Genes (IF: 3.600)
7/2017	Co-chair Society for Molecular Biology and Evolution (SMBE) “Mechanisms of Protein Evolution” Symposium
7/2014	Second Place in Flaming Gorge Jalapeno Eating Contest held in Laramie, WY
2009-2010	President of the New Mexico State University Association for Computing Machinery (ACM) chapter
2005-2010	Member of the New Mexico State University Mathematics Honor Society, Pi Mu Epsilon (PME)
2009	Featured in New Mexico State University Young Women in Computing (YWiC) Fall newsletter
2008-2009	Vice President of the New Mexico State University Association for Computing Machinery (ACM) chapter