Alexander L. Cope, PhD

Postdoctoral Associate Phone: (502) 542-9807 E-mail: alexander.cope@vanderbilt.edu Department of Biological Sciences, Vanderbilt University Nashville, Tennessee Website: acope3.github.io

Education

Ph.D. Graduate School of Genome Science and Technology

University of Tennessee, Knoxville, TN Dissertation: Maintaining protein localization, structure, and functional interactions via codon usage and coevolution of gene expression: Combining evolutionary bioinformatics with omics-scale data to test hypotheses related to protein function Advisors: Dr. Michael A. Gilchrist, Dr. Robert L. Hettich GPA: 3.910

B.Sc. Mathematics, Computer Science

Centre College, Danville, KY Advisors: Dr. Ellen Swanson (Mathematics), Dr. Christine Shannon (Computer Science) GPA: 3.738 (Magna Cum Laude)

Professional Appointments

Postdoctoral Associate

Vanderbilt University, Nashville, TN Advisor: Dr. Antonis Rokas, Dr. Matthew Pennell (co-advisor, USC)

- Linking genetic variation to phenotypic variation in fungi
- Learning about working with model and non-model fungi in a laboratory

Postdoctoral Researcher

Rutgers University, Piscataway, NJ Advisor: Dr. Premal Shah, Dr. Matthew Pennell (co-advisor since September 2022)

- NIH-IRACDA INSPIRE Fellow as of September 1st, 2021
- Use evolutionary and mechanistic models to study genome/proteome evolution
- Developer for riboviz 2 software package
- Assist collaborators in data analysis and visualization
- Mentoring high school, undergraduate, and graduate students

Graduate Research Assistant

University of Tennessee, Knoxville, TN

- Advisors: Dr. Michael A. Gilchrist, Dr. Robert L. Hettich
 - Combined mathematical models, evolutionary theory, and omics-scale data to answer key questions in genome and protein evolution
 - Worked with genomics, transcriptomic, and proteomic data
 - Worked closely with empirical and computational researchers
 - Software developer and maintainer of the AnaCoDa R package.

September 2024 – present

Aug. 2011 – May 2015

July 2020 - present

Aug. 2015 – May 2020

Aug. 2015 – May 2020

Grants/Fellowships/Awards

\$506 Codon Usage Bias Workshop Travel Award Awarded to support travel to the 2nd Workshop on Codon Usage Bias in Edinburgh, UK

Blavatnik Regional Awards for Young Scientists (Nominated)

- 1 of 15 postdoctoral fellows nominated by Rutgers University
- In competition with 158 total postdoctoral researchers from 26 of the New York region's academic and research institutions

\$185,000 NIH-IRACDA INSPIRE Fellowship

- 3-year postdoctoral fellowship at Rutgers University
- Received dedicated professional development in research, teaching, and mentoring
- Gained teaching experience via service as a co-instructor at minority serving institutions

\$2,500 NIMBioS Graduate Student Award

- NIMBioS National Institute for Mathematical and Biological Synthesis
- Awarded to University of Tennessee PhD students whose research reflects the mission of NIMBioS
- Funds were used to attend the Society for Molecular Biology and Evolution conference in 2019

\$64,000 James Graham Brown Colonel Scholar

Merit scholarship awarded to high-achieving students at Centre College

\$4,000 Combs Achievement Scholar

Merit scholarship awarded to high-achieving students at Centre College •

Publications/Manuscripts:

* indicates mentored undergraduate

+ indicates mentored high school student

- 1. A.L. Cope, D. Pak*, M.A. Gilchrist. The Importance of Nonsense Errors: Estimating the Rate and Implications of Drop-Off Errors during Protein Synthesis. bioRxiv (currently undergoing approval, link can be found at website in coming days) September 2024, (submitted to Nucleic Acids Research)
- 2. A.L. Cope, J.G. Schraiber, M.W. Pennell. Phylogenetic analysis reveals how selection and mutation shape coevolution protein abundances. bioRxiv. 2024, the of mRNA and July https://doi.org/10.1101/2024.07.08.602411 (in review at Science)
- 3. A.L. Cope, M.A. Gilchrist, P. Shah, E.W.J. Wallace. Evolutionary principles underpinning codon usage bias: patterns, functions, and mechanisms, EcoEvoRxiv, May 2024, https://doi.org/10.32942/X2802V
- 4. V. Jain⁺ and A.L. Cope. Examining the effects of temperature on the evolution of bacterial tRNA pools, Genome Biology and Evolution, May 2024, https://doi.org/10.1093/gbe/evae116

May 2024

Jan. 2022

Sep 2021 – present

Aug. 2011 – May 2015

Apr. 2019

- 5. O.J. Akeju^{*} and A.L. Cope. Re-examining correlations between synonymous codon usage and protein bond angles in E. coli., *Genome Biology and Evolution*, April 2024, https://doi.org/10.1093/gbe/evae080
- 6. D. Jiang, A.L. Cope, J. Zhang, M.W. Pennell. On the decoupling of evolutionary changes in mRNA and protein levels, *Molecular Biology and Evolution*, July 2023, <u>https://doi.org/10.1093/molbev/msad169</u>
- 7. J.S. Favate, S. Liang, A.L. Cope, S.S. Yadavalli, P. Shah. The landscape of transcriptional and translational changes over 22 years of bacterial adaptation, *eLife*, October 2022. https://doi.org/10.7554/eLife.81979
- A.L. Cope, P. Shah. Intragenomic variation in non-adaptive <u>nucleotide</u> biases causes underestimation of selection on synonymous codon usage, *PLOS Genetics*, Volume 18, Issue 6, e1010256, June 2022, https://doi.org/10.1371/journal.pgen.1010256
- 9. A.L. Cope, M.A. Gilchrist. Quantifying shifts in natural selection on codon usage between protein regions: a population genetics approach, *BMC Genomics*, Volume 23, Issue 408, May 2022, doi: https://doi.org/10.1186/s12864-022-08635-0
- I.A. Nikonorova, J. Wang, A.L. Cope, P.E. Tilton^{*}, K.M. Power, J.D. Walsh, J.S. Akella, P. Shah, M.M. Barr. Isolation, profiling, and tracking of extracellular vesicle cargo in *Caenorhabditis elegans*, *Current Biology*, Volume 32, Issue 9, May 2022, Pages 1924 -- 1936, doi: https://doi.org/10.1016/j.cub.2022.03.005
- A.L. Cope, F. Anderson, J.S. Favate, M. Jackson, A. Mok, A. Kurowska, E. MacKenzie, V. Shivakumar, P. Tilton^{*}, S.M. Winterbourne, S. Xue, K. Kavoussanakis, L.F. Lareau, P. Shah, E.W.J. Wallace. riboviz 2.0: A flexible and robust ribosome profiling data analysis and visualization workflow, *Bioinformatics*, Volume 38, Issue 8, March 2022, Pages 2358–2360, doi: https://doi.org/10.1093/bioinformatics/btac093
- A.L. Cope, S. Vellappan, J.S. Favate, K.S. Skalenko, S.S. Yadavalli, P. Shah. Exploring Ribosome-Positioning on Translating Transcripts with Ribosome Profiling. In: Dassi E. (eds) *Post-Transcriptional Gene Regulation. Methods in Molecular Biology*, vol 2404. Humana, New York, NY, 2022, doi: https://doi.org/10.1007/978-1-0716-1851-6_5
- K.S. Skalenko, L. Li, Y. Zhang, I.O. Vvedenskaya, J.T. Winkelman, A.L. Cope, D.M. Taylor, P. Shah, R.H. Ebright, J.B. Kinney, Y. Zhang, B.E. Nickels. Promoter-sequence determinants and structural basis of primer-dependent transcription initiation in *Escherichia coli*, *PNAS*, Volume 118, Issue 27, June 2021, doi: https://doi.org/10.1073/pnas.2106388118
- 14. S. Poudel, A.L. Cope (Co-first author), K. O'Dell, A.M. Guss, H. Seo, C.T. Trinh, R.L. Hettich. An integrated approach to characterize proteins of unknown function (PUFs) in *Clostridium thermocellum* DSM 1313 as potential genetic engineering targets, *Biotechnology for Biofuels*, Volume 14, Issue 116, May 2021. doi: https://doi.org/10.1186/s13068-021-01964-4
- A.L. Cope, B.C. O'Meara, M.A. Gilchrist. Gene Expression of Functionally-Related Genes Coevolves Across Fungal Species: Detecting Coevolution of Gene Expression Using Phylogenetic Comparative Methods, *BMC Genomics*, Volume 21, Issue 370, May 2020, doi: https://doi.org/10.1186/s12864-020-6761-3
- 16. A.L. Cope, R.L. Hettich, M.A. Gilchrist. Quantifying codon usage in signal peptides: Gene expression and amino acid usage explain apparent selection for inefficient codons, *Biochimica et Biophysica Acta – Biomembranes*, Volume 1860, Issue 12, December 2018, Pages 2479 – 2485, doi: https://doi.org/10.1016/j.bbamem.2018.09.010

Apr. 2024

 C. Landerer, A. Cope, R. Zaretzki, M.A. Gilchrist; AnaCoDa: analyzing codon data with Bayesian mixture models, *Bioinformatics*, Volume 34, Issue 14, 15 July 2018, Pages 2496–2498, doi: <u>https://doi.org/10.1093/bioinformatics/bty138</u>

Teaching Experience

Co-instructor

William-Patterson University Instructor: Dr. Emily Monroe, Dr. Carey Waldburger

- Taught 4 class periods (2.75 hours each) of R programming for biological data analysis
- Taught 2 class periods (2.5 hours each) on next-generation sequencing transcriptomics technology (e.g., RNA-seq)
- Employed active learning teaching methods, e.g. flipped classroom
- Activities were designed using backwards design principle

Co-instructor

William-Patterson University Instructor: Dr. Emily Monroe

- Taught 3 class periods (2.75 hours each)
- Employed active learning teaching methods
- Activities were designed using backwards design principle
- Introduced students to programming in R for biological data analysis using guided R notebooks

Guest Lecturer

William-Patterson University and New Jersey City University INSPIRE-related visit to program sister schools

- Guest lecture describing my research on codon usage bias (approx. 20 minutes)
- Students were primarily undergraduate biology majors attending minority-serving institutions
- Developed R Shiny application to allow students to analyze real biological data (https://acope3.shinyapps.io/codon_usage)

Workshop Instructor

Workshop on Ribosome Profiling (Virtual) Biochemical Society (United Kingdom)

- Provided overview of analysis tools for Ribo-seq data
- Included breakdown of basic steps (pre-processing to visualization) in analysis of Ribo-seq data
- Specifically emphasized use of riboviz 2 (see Publications/Manuscripts section)

Co-instructor

University of Tennessee, Knoxville, TN BIO 464: Macroevolution Instructor: Dr. Brian O'Meara

- Led two class sessions on the topic of genome evolution
- 14 students mostly junior and senior Ecology and Evolutionary Biology majors
- Combined traditional lecture with active learning activities, including flipped classroom
- Introduced students to primary literature
- Received Practitioner Level of Certification from the Center for the Integration of Research Teaching and Learning (CIRTL)

Mar. – Apr. 2023

Mar. – Apr. 2022

July 2021

Oct. 2018

Workshop Instructor

University of Tennessee, Knoxville, TN Genome Science and Technology Colloquium

- Public workshop introducing University of Tennessee faculty and graduate students to various machine learning methods
- Introduced Python, and the scikit and TensorFlow packages
- Focused on implementing and interpreting supervised machine learning methods (e.g. decision trees)

Graduate Teaching Assistant

University of Tennessee, Knoxville, TN LFSC 507: Programming for Biological Data Analysis Instructor: Dr. Tamah Fridman

- Reconstructed course syllabus to better emphasize general programming skills
- Developed new lab assignments designed to use the Python programming language (previously had used FORTRAN)
- Gave weekly lectures covering programming principles, techniques, and statistical analysis

Mathematics Tutor

Centre College, Danville, KY MAT 130: Introduction to Statistics; MAT 145: Applied Calculus and Mathematical Modeling

• Tutored students in introductory-level mathematics courses

Mentoring Experience

- Opetunde Akeju, Summer Intern, New Jersey City University June 2022 – Aug. 2022
 - 10-week internship as part of the Research-intensive Summer Experience (RiSE) for diverse undergraduates
 - Re-examined recent findings of a correlation between synonymous codon usage and protein bond angles
 - Taught basic R programming, data visualization, and working with AnaCoDa R package 0
 - Taught scientific writing, successfully publisheda first-author manuscript (see Publications/Manuscripts section)
- Vatsal Jain, Biotechnology High School
 - Current: Duke University (early decision)
 - Examining evolution of tRNA pool across microbial species 0
 - 0 Taught how to implement mathematical models described in primary literature from scratch
 - Taught basic programming in R 0
 - Taught scientific writing, successfully published first-author manuscript а (see Publications/Manuscripts section)
 - Summer 2022 internship: Memorial-Sloan Kettering Cancer Center
 - Alan Ho, Undergraduate Student, Rutgers University
 - Current: Miller School of Medicine, University of Miami
 - Undergraduate Major: Biomathematics, Cognitive Science
 - Examined the effects of selection on codon usage on evolutionary rate estimation

Aug. 2016 - Dec. 2017

Feb. 2014 – May 2015

July 2021 – present

July 2021 – Jan. 2022

	0	Basics of model comparison (likelihood ratio tests, information criterion)
	o	Taught how to use tools for quantifying natural selection from coding-sequence alignments (HyPHY)
	o	Taught how to use tools for identifying orthologous proteins (OrthoFinder)
•	Pe	ter Tilton, Undergraduate Student, Rutgers University May 2021 – Mar. 2022
	0	Undergraduate Major: Computer Science, Cognitive Science
	0	Implemented Shiny R application for visualizing data from Nikinorova et al. (see Publications/Manuscripts section)
	0	Developed communication skills by working with empiricists
	o	Taught to evaluate implementation requests from client as essential or non-essential
•	Ał	nmed Abdellatif, Undergraduate Student, Rutgers University Jan. 2021 – Dec. 2021
	0	Undergraduate Major: Genetics
	0	Studied evolution of codon usage bias in cellulolytic thermophile
	0	Learned to apply Bayesian methods (e.g. Markov Chain Monte Carlo simulations)
•	Al	exandra Logerfo, PhD candidate, Rutgers University Sep. 2020 – May 2021
	0	Current: PhD candidate in Molecular Biosciences
	o	Helped develop approach for quantifying isoform-specific translation
	o	Taught maximum likelihood estimation and model validation
•	De	enizhan Pak, Undergraduate Student, University of Tennessee Knoxville. May 2017 – June 2019
	o	Current: PhD candidate at Indiana University
	o	Undergraduate Major: Computer Science

• Advised on software development for AnaCoDa

Presentations/Posters

* indicates mentored undergraduate

- 1. A.L. Cope. Integrating population genetic models with emerging functional genomic technologies to reveal the rules of proteome evolution. Invited Seminar (Host: Dr. Antonis Rokas, Department of Biological Sciences). Vanderbilt University. Nashville, TN. June 2024.
- 2. A.L. Cope, J. Schraiber, M. Pennell, Phylogenetic analysis reveals how selection and mutation shape the coevolution of mRNA and protein abundances. Poster Presentation. Society of Molecular Biology and Evolution. Puerto Vallerta, Mexico. July 2024.
- 3. A.L. Cope, J. Schraiber, M. Pennell, Phylogenetic analysis reveals how selection and mutation shape the coevolution of mRNA and protein abundances. Poster Presentation. IRACDA 2024. Chapel Hill, NC. June 2024
- 4. A.L. Cope, M.A. Gilchrist, P. Shah, E.W.J. Wallace. Molecular Spandrels and codon usage: Why evolutionary models are needed to understand the patterns, functions, and mechanisms, of codon usage. Poster Presentation. 2nd Workshop on Codon Usage: Function, Mechanism, and Evolution, Edinburgh, U.K. May 2024. (Received travel award to attend conference)
- 5. M.A. Gilchrist, D. Pak*, A. Cope, Quantifying and Contextualizing the Importance of Nonsense Errors on the Evolution of Codon Usage Bias. Oral Presentation. 2nd Workshop on Codon Usage: Function,

Mechanism, and Evolution, Edinburgh, U.K., May 2024. Presented by M.A. Gilchrist. (Received travel award to attend conference)

- 6. A.L. Cope. Integrating population genetic models with emerging functional genomic technologies to reveal the rules of proteome evolution. Invited Seminar (Host: Dr. David Lambert, Department of Biology). University of Rochester. Rochester, NY. Mar. 2024.
- 7. A.L. Cope, J. Schraiber, F. Machado, J. Uyeda, P. Shah, M. Pennell, Coevolution between mRNA and protein abundances: resolving the direction of causality in gene expression evolution using phylogenetic comparative methods. Poster Presentation. Society of Molecular Biology and Evolution. Ferrara, Italy. July 2023
- 8. A.L. Cope, J. Schraiber, D. Jiang, P. Shah, M. Pennell, Coevolution between mRNA and protein abundances: resolving the direction of causality in gene expression evolution using phylogenetic comparative methods. Poster Presentation. IRACDA 2023. San Antonio, TX. June 2023.
- 9. A.L. Cope and P. Shah. Evolution of codon usage bias: using population genetics models to quantify variation in codon usage across the Saccharomycotina subphylum. Poster Presentation. IRACDA 2022. Albuquerque, NM. July 2022.
- 10. A.L. Cope and P. Shah. Evolution of codon usage bias: using population genetics models to quantify variation in codon usage across the Saccharomycotina subphylum. Poster Presentation. USC Computational Biology Symposium. Los Angeles, CA. May 2022.
- 11. A.L. Cope and P. Shah. Evolution of codon usage bias: using population genetics models to quantify variation in codon usage across the Saccharomycotina subphylum. Poster Presentation. EMBL Workshop Codon Usage: Function, mechanism, and evolution. Edinburgh, U.K. April 2022.
- 12. E.W.J. Wallace, A.L. Cope, M.A. Gilchrist, P. Shah. Molecular spandrels and codon usage: why evolutionary models are needed to understand the patterns, functions, and mechanisms of codon usage. Oral Presentation. EMBL Workshop Codon Usage: Function, mechanism, and evolution. Edinburgh, U.K. April 2022. Presented by E.W.J. Wallace.
- 13. A.L. Cope. Signals of selection on codon usage can be obscured by intragenomic variation in mutation biases. Oral Communication. Biochemical Society Translation UK 2021, Virtual Conference. June 2021.
- 14. A.L. Cope. Analyzing codon usage patterns with population genetics-based models. Invited Virtual Seminar (Host: Dr. Ellen Swanson, Department of Mathematics). Centre College. Danville, KY. July 2020.
- 15. A.L. Cope. Quantifying variation in codon usage: using a mechanistic model to detect signatures of natural selection on codon usage related to protein biogenesis. Invited Seminar (Host: Dr. Jeff Heath, Department of Mathematics), Centre College. Danville, KY. April 2020 (Canceled due to COVID-19 pandemic).
- 16. A.L. Cope. Quantifying variation in codon usage: using a mechanistic model to detect signatures of natural selection on codon usage related to protein biogenesis. Invited Seminar (Host: Dr. Premal Shah, Department of Genetics). Rutgers University. Piscataway, NJ. Feb. 2020.
- 17. A.L. Cope, R.L. Hettich, M.A. Gilchrist. Quantifying Codon Usage Bias in Signal Peptides Amino Acid Usage and Gene Expression Explain Apparent Selection for Inefficient Codons in *E. coli*. Poster Presentation. Society of Molecular Biology and Evolution. Manchester, UK. July 2019.

- 18. S. Poudel, A.L. Cope, K. O'Dell, A.M. Guss, R.L. Hettich; An integrated experimental and computational approach for the characterization of proteins of unknown function (PUFs) in *Clostridium thermocellum*, DSM 1313. Poster Presentation. American Society of Mass Spectrometry, Atlanta, GA. June 2019. Presented by S. Poudel.
- 19. A.L. Cope, R.L. Hettich, M.A. Gilchrist. Quantifying selection on codon usage in the signal peptides of *E. coli.* Poster Presentation. Society of Molecular Biology and Evolution. Austin, TX. July 2017.
- 20. A.L. Cope, M.A. Gilchrist, R.L. Hettich. Examining Codon Usage as Bias as a Potential Marker of Extracellular Proteins. Poster Presentation. American Society of Mass Spectrometry, Indianapolis, IN. June 2017.

Professional Services/Outreach

- Summer Undergraduate Research Mentor Research-intensive Summer Experience (RiSE) for diverse undergraduates
- **Reviewer** *PLOS Biology, Molecular Biology and Evolution, BMC Bioinformatics, Biochemical Society Transactions, Environmental and Molecular Mutagenesis, Frontiers in Microbiology, Computational and Structural Biotechnology Journal, BMC Plant Biology, eLife, Genome Biology and Evolution*
- Judge 14th Molecular Biosciences Graduate Student Organization Research Symposium (Mar. 26, 2021, Rutgers University)
- Guest teacher Developed and taught lesson on collecting and analyzing data to 6th grade students (Greenback School, Greenback, TN, 2016)

Software Packages

- <u>r</u>iboviz 2.0 (GitHub: <u>https://github.com/riboviz</u>)
 - Current developer
 - Key contributions include adding new functionality, debugging, and improving code readability
 - Have added numerous example analyses to assist researchers with running riboviz 2.0.
- AnaCoDa (GitHub: <u>https://github.com/acope3/RibModelFramework</u>)
 - Current maintainer
 - Responsible for model implementation, debugging, and documentation of code.

Skills and Certifications

- Proficient in programming with Python, R, C/C++
- Analysis of next-generation sequencing data (RNA-seq, Ribo-seq) and proteomics data
- Comfortable working with many popular bioinformatics tools (e.g., kallisto, FASTQC, cutadapt)
- Comfortable with frequentist and Bayesian statistical inference
- Expert with phylogenetic methods and software
- Center for the Integration of Research Teaching and Learning (CIRTL) Practitioner Level of Certification

References

Matthew W. Pennell

Associate Professor of Quantitative and Computational Biology and Biological Sciences University of Southern California, Los Angeles, CA Email: mpennell@usc.edu

Michael A. Gilchrist

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