Alexander L. Cope, PhD
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Department of Genetics, Robert Wood Johnson Medical School
Rutgers University, Piscataway, NJ

Professional Appointments

Postdoctoral Researcher   July 2020 – present
Rutgers University, Piscataway, NJ
Advisor: Dr. Premal Shah, Dr. Matthew Pennell (co-advisor since August 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   Aug. 2015 – May 2020
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.

Grants/Fellowships/Awards

Blavatnik Regional Awards for Young Scientists (Nominated)   Jan. 2022
- 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   Sep 2021 – present
- 3-year postdoctoral fellowship at Rutgers University
- 30% of time dedicated to developing skills as a teacher and mentor, including teaching at minority-serving institutions

$2,500 NIMBioS Graduate Student Award   Apr. 2019
- 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   Aug. 2011 – May 2015
- 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

1. V. Jain and **A.L. Cope.** Determining the effects of temperature on the evolution of bacterial tRNA pools, bioRxiv, September 2023, https://doi.org/10.1101/2023.09.26.559538

2. 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, https://doi.org/10.1093/molbev/msad169

3. O.J. Akeju and **A.L. Cope**. Re-examining supposed correlations between synonymous codon usage and protein bond angles in E. coli. bioRxiv, June 2023, https://doi.org/10.1101/2022.10.26.513858 (in review, *Genome Biology and Evolution*)

4. 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

5. **A.L. Cope**, P. Shah. Intragenomic variation in mutation 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

6. **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

7. 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

8. **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, 15 April 2022, Pages 2358–2360, doi: https://doi.org/10.1093/bioinformatics/btac093

9. **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

10. 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

11. 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

12. **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

13. **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

14. 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: https://doi.org/10.1093/bioinformatics/bty138

Presentations/Posters

1. **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

2. **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.

3. **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.

4. **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.

5. **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, United Kingdom. April 2022.

6. 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, United Kingdom. April 2022. Presented by E.W.J. Wallace.

7. **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.

8. **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.

9. **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).

10. **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.

11. **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.

12. 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.

13. **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.

14. **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.

Teaching Experience

Guest Lecturer   Mar. – Apr. 2023
William-Patterson University
Instructor: Dr. Emily Monroe
  • Guest lectured 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   Mar. – Apr. 2022
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   July 2021
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)

Guest Lecturer   Oct. 2018
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)

Workshop Instructor   Apr. 2018
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   Aug. 2016 – Dec. 2017
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   Feb. 2014 – May 2015
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
  ◦ Taught scientific writing, successfully drafted a first-author manuscript (see Publications/Manuscripts section)
- Vatsal Jain, Biotechnology High School   July 2021 – present
  ◦ Examining evolution of tRNA pool across microbial species
  ◦ Taught how to implement mathematical models described in primary literature from scratch
  ◦ Taught basic programming in R
  ◦ Taught scientific writing, successfully drafted a first-author manuscript (see Publications/Manuscripts section)
  ◦ Summer 2022 internship: Memorial-Sloan Kettering Cancer Center
- Alan Ho, Undergraduate Student, Rutgers University   July 2021 – Jan. 2022

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

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*
- **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)

Education

Ph.D. Graduate School of Genome Science and Technology   Aug. 2015 – May 2020
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   Aug. 2011 – May 2015
Centre College, Danville, KY
Advisors: Dr. Ellen Swanson (Mathematics), Dr. Christine Shannon (Computer Science)
GPA: 3.738 (*Magna Cum Laude*)

Software Packages

- riboviz 2.0 (GitHub: https://github.com/riboviz)
  - 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: https://github.com/acope3/RibModelFramework)
  - Current maintainer
  - Responsible for model implementation, debugging, and documentation of code.

Skills and Certifications

- Proficient in programming with Python, R, C/C++
- Strong expertise with frequentist and Bayesian statistical inference
- Expert with phylogenetic methods and software
- Expert working with high-throughput omics data such as RNA-seq and tandem mass spectrometry data
- Center for the Integration of Research Teaching and Learning (CIRTL) Practitioner Level of Certification

References

Premal Shah
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Matthew W. Pennell
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University of Southern California, Los Angeles, CA
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Michael A. Gilchrist
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University of Tennessee, Knoxville, TN
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