

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
- Combine 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

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>

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*)

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 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>

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, 15 April 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>

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>

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>

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

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. Los Angeles, CA. May 19th, 2022.

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 10th, 2022.

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 10th, 2022. Presented by E.W.J. Wallace.

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 29th, 2021.

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 29th, 2020.

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 1st, 2020 (Canceled due to COVID-19 pandemic).

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. 19th, 2020.

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.

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.

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.

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

- Guest lectured 3 class periods (2.75 hours each)
- Developed class lectures and activities using backwards design
- Introduced students to programming in R for biological data analysis

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
 - 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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Michael A. Gilchrist

Associate Professor, Department of Ecology and Evolutionary Biology
University of Tennessee, Knoxville, TN
Phone: (865) 974 - 6453
Email: mikeg@utk.edu

Robert L. Hettich

Distinguished Research Staff Member
Oak Ridge National Laboratory, Oak Ridge, TN
Phone: (865) 574 - 4968
Email: hettichrl@ornl.gov

Matthew W. Pennell

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University of Southern California, Los Angeles, CA
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