Alexander L. Cope

Phone: (502) 542-9807
E-mail: acope3@vols.utk.edu
Graduate School of Genome Science and Technology
University of Tennessee, Knoxville, TN

Education:

University of Tennessee, Knoxville, TN
5th year doctoral candidate (GPA: 3.910), Graduate School of Genome Science and Technology, Expected Graduate Date: May 2020

Centre College, Danville, KY
B.Sc, *Magna Cum Laude* (GPA: 3.738), Mathematics and Computer Science, May 2015

Research/Teaching Experience:

University of Tennessee, Knoxville, TN
Ph.D candidate, Graduate Research Assistant
Aug. 2015 – present
Advisors: Dr. Michael A. Gilchrist, Dr. Robert L. Hettich
Evolutionary bioinformatician employing mathematical models and evolutionary theory (eg. population genetics, phylogenetics) to study omics-scale data. Projects include examining codon usage bias as it relates to protein biogenesis and detecting co-evolution of gene expression using phylogenetic comparative methods. Other work includes co-expression network analysis of quantitative proteomics data to determine possible functions of proteins of unknown function in cellulolytic bacteria. Also assistant software developer and a maintainer of the AnaCoDa CRAN package.

University of Tennessee, Knoxville, TN
Guest Lecturer
Oct. 2018
Instructor: Dr. Brian O'Meara, BIO 464: Macroevolution
Led two class sessions on the topic of genome evolution. Students were mostly junior and senior Ecology and Evolutionary Biology majors. The first day was a traditional lecture class in which students were introduced to some of the major hypotheses on the topic genome evolution (e.g. the mutational hazard hypothesis). The other portion was a journal club-style class, in which groups of students each read a different paper on the topic of genome evolution and summarized the papers to the class, applying the knowledge they gained from the lecture. Students had to explain which hypotheses were supported by the paper and justify their conclusions. I received a Practitioner Level of Certification from the Center for the Integration of Research Teaching and Learning (CIRTL) for this guest lecture.

University of Tennessee, Knoxville, TN
Workshop Instructor
April 2018
As part of the 2018 Genome Science and Technology Colloquium, I helped lead a workshop introducing researchers to various machine learning methods with Python using the scikit and

TensorFlow packages. This included creating lecture slides developing the background of decision trees, as well as creating code examples which could be run easily by all attending the lecture.

University of Tennessee, Knoxville, TN
Graduate Teaching Assistant
Aug. 2016 – Dec. 2017
Instructor: Dr. Tamah Fridman, LFSC 507: Programming for Biological Data Analysis
Reconstructed the course to make use of the Python programming language. This included the development of new programming lab assignments. Responsibilities also included weekly lectures covering programming principles, techniques, basic statistical analysis, and a brief introduction to machine learning.

Publications/Manuscripts:

Alexander L. Cope, Brian O'Meara, Michael 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, 2020, doi: https://doi.org/10.1186/s12864-020-6761-3

Suresh Poudel, **Alexander L. Cope (Co-first author),** Kaela O'Dell, Adam M. Guss, Robert L. Hettich; An integrated approach to characterize proteins of unknown function (PUFs) in *Clostridium thermocellum* DSM 1313 as potential genetic engineering targets, *mSystems* (In Review)

Alexander L. Cope, Robert L. Hettich, Michael 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

Cedric Landerer, **Alexander Cope**, Russell Zaretzki, Michael 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:

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

Alexander 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, Feb. 19th, 2020

Alexander L. Cope, Robert L. Hettich, Michael A. Gilchrist; Quantifying Codon Usage Bias in Signal Peptides Amino Acid Usage and Gene Expression Explain Apparent Selection for

Inefficient Codons in E. coli, Society of Molecular Biology and Evolution, Manchester, UK, July 2019 (Poster)

Suresh Poudel, **Alexander L. Cope**, Kaela O'Dell, Adam M. Guss, Robert L. Hettich; An integrated experimental and computational approach for the characterization of proteins of unknown function (PUFs) in *Clostridium thermocellum* DSM 1313, American Society of Mass Spectrometry, Atlanta, GA, June 2019 (Poster, Presenter: Suresh Poudel)

Alexander L. Cope, Robert L. Hettich, Michael A. Gilchrist; Quantifying selection on codon usage in the signal peptides of *E. coli*. Society of Molecular Biology and Evolution, Austin, TX, July 2017 (Poster)

Alexander L. Cope, Michael A. Gilchrist, Robert L. Hettich; Examining Codon Usage as Bias as a Potential Marker of Extracellular Proteins. American Society of Mass Spectrometry, Indianapolis, IN, June 2017 (Poster)

Grants, Honors and Awards:

- 2019 NIMBioS Graduate Student Award
- Lead Bioinformatician on NSF Grant #1846245 (PI: Tessa Burch-Smith)
- *Magna Cum Laude,* Centre College (Overall GPA: 3.738)
- James Graham Brown Colonel Scholar (undergraduate merit scholarship)
- Combs Achievement Scholar (undergraduate merit scholarship)

Skills and Certifications:

- Programming Languages: Python, R, C/C++, Java
- Center for the Integration of Research Teaching and Learning (CIRTL) Practitioner Level of Certification
- Familiar with Frequentist and Bayesian statistical inference
- Experience with phylogenetic analysis methods and software
- Experience working with high-throughput omics data, including raw tandem mass spectrometry and RNA-Seq data

Professional Affiliations:

- Pi Mu Epsilon (Mathematical Honors Society)
- Omicron Delta Kappa (Leadership Honors Society)

References:

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

Brian C. O'Meara
Professor and Associate Head, Department of Ecology and Evolutionary Biology
University of Tennessee, Knoxville, TN
Phone: (865) 974 - 2804
Email: bomeara@utk.edu

Jeff Heath
Associate Professor, Department of Mathematics
Centre College, Danville, KY
Phone: (859) 238 - 5407
Email: jeffrey.heath@centre.edu