T. Jeffrey Cole

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Education

☑ **Ph.D. in Biological Sciences**   May 2021

East Carolina University, Greenville NC

- Dissertation title: *Molecular evolution of venom proteins in Ctenidae spiders*

☑ **B.S. in Biology,** *magna cum laude*   May 2016

Samford University, Birmingham AL

- **GPA:** 3.88
- **Honors**
  - ◇ Beta Beta Beta National Biology Honors Society (2013-2015)
    - · Vice President (2015)
  - ◇ Alpha Lambda Delta Honors Society (2013-2015)

Experience

☑ **Senior Bioinformatics Engineer**   Feb 2022 - present

ExosomeDx (Bio-Techne), Austin TX

- **Multi-omic liquid biopsy bioinformatics platform**
  - ◇ Lead developer of bioinformatics pipelines for RNA fusions and splice variants in RNAseq datasets
  - ◇ Lead coordinator of AWS infrastructure and pipeline management through Seqera platform
  - ◇ Contributor to nextflow pipelines for RNAseq gene quantification, differential gene expression, and cfDNA methylation analysis
- **Biomarker discovery machine learning platform**
  - ◇ Project coordinator for interdivisional machine learning competition for biomarker discovery using TCGA data
  - ◇ Lead developer of machine learning models and algorithms for biomarker discovery using multi-omic liquid biopsy data

☑ **Postdoctoral Research Fellow**   Jan 2021 - Jan 2022

University of Texas at Austin, Austin TX

- **Discovery of antimicrobial peptides in bacterial genomic datasets**
  - ◇ Developer of bioinformatics pipeline to identify small novel antimicrobial peptides in bacterial genome assemblies
- **Design of antimicrobial peptides with protein language deep learning models**

◇ Lead contributor of analysis to combine libraries of synthetic peptides with machine learning models to inform design of peptides with optimal antimicrobial properties
 – **Integration of deep protein language models with 3D structural models**
     ◇ Project coordinator for the development of machine learning models that aggregate information from sequence based models and structure based models to improve protein function prediction

Publications

Full list here: `https://scholar.google.com/citations?user=MbxmQhcAAAAJ&hl=en`

Tutrone R, Lowentritt B, Neuman B, Donovan MJ, Hallmark E, **Cole TJ**, Yao Y, Biesecker C, Kumar S, Verma V, Sant GR. (2023). *Prostate Cancer and Prostatic Diseases*, 26(3), 596-601.

Randall JR, DuPai CD, **Cole TJ**, Davidson G, Groover KE, Slater SL, Mavridou DA, Wilke CO, Davies BW. (2023). Designing and identifying β-hairpin peptide macrocycles with antibiotic potential. *Science Advances*, 9 (2), eade0008.

Kulikova AV, Diaz DJ, Chen T, **Cole TJ**, Ellington AD, Wilke CO. (2023). Two sequence-and two structure-based ML models have learned different aspects of protein biochemistry. *Scientific Reports*, 13 (1), 13280.

Cole TJ, Parker JK , Feller AL, Wilke CO, Davies BW. (2022). Evidence for Widespread Class II Microcins in Enterobacterales Genomes. *Applied and Environmental Microbiology* 88 (23), e01486-22.

Randall JR, Davidson G, Fleeman RM, Acosta SA, Riddington IM, **Cole TJ**, DuPai CD, Davies BW. (2022). Synthetic antibacterial discovery of symbah-1, a macrocyclic β-hairpin peptide antibiotic. *IScience*, 25 (1).

Brewer MS, **Cole TJ**. (2023). Killer knots: Molecular evolution of inhibitor cystine knot toxins in Wandering spiders (Araneae: Ctenidae). Toxins 15 (2), 112.

Cole TJ, Brewer MS. (2019). toxify: a deep learning approach for classifying animal venom proteins. *PeerJ*, 7, p.e7200.

Cole TJ, Brewer MS. (2018) FUSTr: A tool for finding gene Families Under Selection in Transcriptome databases. *PeerJ*, 6, e4234.

Skills

Bioinformatics Pipelines: Nextflow, nf-core tools, Snakemake

Machine Learning: scikit-learn, TensorFlow, PyTorch

Data Visualization: tidyverse, ggplot2, plotly

Cloud Computing: AWS (S3, EC2, Batch), Seqera Platform

Reproducible Analysis: Conda, Docker

Programming Languages: Python, R, BASH, Go