T. Jeffrey Cole

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Education

May 2021

East Carolina University, Greenville NC

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

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 Segera 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

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

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- ♦ 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,

Machine Learning: scikit-learn, TensorFlow, **PyTorch**

Data Visualization: tidyverse, ggplot2, plotly

Snakemake

Cloud Computing: AWS (S3, EC2, Batch), Segera **Platform**

Reproducible Analysis: Conda, Docker

Programming Languages: Python, R, BASH, Go

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