

Rachael M. Cox

2500 Speedway, MBB 3.128B, Austin, TX 78705

email: rachaelcox@utexas.edu

website: <https://rachaelcox.github.io/>

SUMMARY

Highly interdisciplinary and well-rounded computational biochemist with a passion for chemistry, systems biology, machine learning and large-scale data analyses; aspires to leverage comparative evolutionary frameworks to inform technology development, with current projects having applications to agricultural engineering and human health.

EDUCATION

Doctor of Philosophy, Biochemistry

Jun. 2018 – present

The University of Texas at Austin, Austin, Texas

Bachelor of Science, Chemistry

Aug. 2009 – Dec. 2013

Texas A&M University, College Station, Texas

RESEARCH EXPERIENCE

Graduate Research Assistant

Jun. 2018 – present

Prof. Edward Marcotte, The University of Texas at Austin

- Use machine learning and statistical models for comparative evolution of protein organization across multicellular organisms in the context of human disease
- Validate machine learning predictions for protein complexes using gene knock-out and “guilt-by-association” phenotype predictions
- Lead bioinformatician for engineering non-model plants (e.g., dandelions) to elicit a specific response, given a specific input, by integrating comparative proteomic and transcriptomic approaches
- Developed a novel de Bruijn graph-based algorithm for multiple sequence alignment; the algorithm scales linearly with input size and detects evolutionarily conserved sequence motifs and clusters

Research Technician

Mar. 2015 – Jun. 2018

Eastman Chemical Company

- Evaluated new inorganic catalysts to make a process more efficient or environmentally friendly using reaction kinetics and yield as metrics
- Researched new chemistry to anticipate market demands (e.g., designing a less volatile solvent that functions as well as existing products), while working in conjunction with plant engineers to tune reaction conditions to ensure new products are realistic given existing manufacturing infrastructure
- Designed and constructed continuous reaction systems at various scales (i.e., 1g/min to 1kg/min process rates) that model existing industrial-scale processes to generate reliable data for commercialization of new processes

RESEARCH EXPERIENCE (cont.)

Research Technician

Sept. 2014 – Mar. 2015

Prof. Deepak Nijhawan, University of Texas Southwestern Medical Center

- Pursued drug discovery and characterization using mammalian cell tissue culture techniques in conjunction with bio-orthogonal click chemistry and immunohistochemical experiments
- Identified drug targets using streptavidin-biotin affinity purification, immunoprecipitation, silver staining and LCMS
- Evaluated synthetic lethality with drug titrations and luminescent cell viability assays to generate dose-response curves

Research Technician (Undergraduate)

May 2013 - Jun. 2014

Prof. David Barondeau, Texas A&M University

- Evaluated mechanistically significant residues on the surface of the human iron-sulfur cluster protein frataxin
- Helped design, optimize, and perform fluorescence anisotropy experiments for characterizing binding kinetics associated with FXN and the NFS1-ISD11-ISCU2 complex in the human ISC system
- Processed kinetic data and computed binding constants
- Trained in biosynthetic protocols such as recombinant protein expression (DNA transfection, PCR cloning and sequencing) and purification (FPLC affinity chromatography, aerobic and anaerobic)

SKILLS

- **Computational:** Python for scripting and machine learning; R for statistical analysis and data visualization; Bash for scripting, string manipulation and large-scale data management; proficient in a Linux environment
- **Organic and biochemistry:** Organic synthesis and inorganic catalysis; small and large molecule chromatography (i.e., gas and liquid chromatography); recombinant protein expression and purification; gel electrophoresis
- **Molecular and synthetic biology:** Mammalian, yeast and microbial tissue culture; plasmid engineering, Sanger and Illumina sequencing and analysis
- **Instrumentation:** Mass spectrometry, NMR ($^1\text{H}/^{13}\text{C}/^{32}\text{P}$), FTIR spectrometry, UV-Vis and fluorescence spectroscopy

PUBLICATIONS

- Huebner, R. J.; Weng, S.; Lee, C.; Sarikaya, S.; Papoulas, O.; **Cox, R. M.**; Marcotte, E. M.; Wallingford, J. B. "Cell adhesions link subcellular actomyosin dynamics to tissue scale force production during vertebrate convergent extension." <https://www.biorxiv.org/content/10.1101/2021.06.21.449290v1> (2021).
- Devitt, C. C.; Lee, C.; **Cox, R. M.**; O. Papoulas; Alvarado, J.; Marcotte, E. M.; Wallingford, J. B. "Twinfilin1 controls lamellipodial protrusive activity and actin turnover during vertebrate gastrulation." *J. Cell. Sci.* 134 14:jcs254011 (2021).

- Lee, C.; **Cox, R. M.**; Papoulas, O.; Horani, A.; Drew, K.; Devitt, C. C.; Brody, S. L.; Marcotte, E. M.; Wallingford, J. B. “Functional partitioning of a liquid-like organelle during assembly of axonemal dyneins.” *eLife* 9:e58662 (2020)
- Drew, K.*; Lee, C.*; **Cox, R. M.**; Dang, V.; Devitt, C. C.; Papoulas, O.; Huizar, R. L.; Marcotte, E. M.; Wallingford, J. B. “A systematic label-free method for identifying RNA-associated proteins *in vivo* provides insights into vertebrate ciliary beating.” *Dev. Biol.* **467**, 108-117 (2020).
- McWhite, C. D.*; Papoulas, O.*; Drew, K.; **Cox, R. M.**; Oldfield-June, V.; Dong, O. X.; Kwon, T.; Wan, C.; Salmi, M. L.; Emili, A.; Roux, S. J.; Chen, J. Z.; Browning, K. S.; Ronald, P. C.; Marcotte, E. M. “Deep conservation and interaction-to-phenotype in a pan-plant protein complex map” *Cell* **181**, 460-474.e14 (2020).
- Vranish, J.; Russell, W.; Yu, L. E.; **Cox, R. M.**; Russell, D. H.; Barondeau, D. P. “Fluorescent probes for Tracking metal the Transfer of Iron-Sulfur Cluster and other Metal Cofactors in Biosynthetic Reaction Pathways” *J. Am. Chem. Soc.* **137**, 390–398 (2015).

TALKS & PRESENTATIONS

- **Cox, R. M.**; Papoulas, O.; McWhite, C. D.; Battenhouse, A.; Marcotte, E. M. “Leveraging comparative proteomics to improve human disease models.” HUPO ReCONNECT 2021 World Congress (November 2021 – Poster)
- **Cox, R. M.**; Papoulas, O.; McWhite, C. D.; Battenhouse, A.; Marcotte, E. M. “Orthology models enable large-scale comparative proteomics.” Quest for Orthologs Consortium (July 2021 – Poster)
- **Cox, R. M.** “Conserved systems intermediate organism-specific genotype and phenotype.” Invited talk, Durand Lab meeting (July 2021).
- **Cox, R. M.** “Engineering endogenous promoters for non-model plant species.” Biology Talks About Computers, Organisms and Systems (BioTACOS) **(February 2020)**
- **Cox, R. M.** “Predicting Legendary Pokemon Using a Random Forest Algorithm (a Machine Learning Demo)” UT Austin Open Coding Hour, Special Edition (December 2019, https://github.com/rachaelcox/pokemon_machine_learning_demo)
- **Cox, R. M.** “Falling Forward: Lessons in Failure” UT Austin Chips and Dip Seminar Series (December 2019)
- **Cox, R. M.** “Leveraging comparative proteomics for health and engineering” UT Austin Chips and Dip Seminar Series (November 2019)
- **Cox, R. M.** “The role of systems biology in health and engineering” They Blinded Me With Science Radio Show 91.7HD2 (October 2019)
- **Cox, R. M.** “Protein lightning: multi-species sequence alignments visualized via de Bruijn graphs” UT Austin College of Natural Science’s Art in Science Event (October 2019 – Poster)
- **Cox, R. M.**; McWhite, C. D.; Dinkeloo, K. D.; Tran, J.; Lloyd, A.; Qiao, H.; Ellington, A.; Marcotte, E. M. “Leveraging orthology and systems biology for engineering in non-model organisms” UT Austin Institute for Cell and Molecular Biology Annual Retreat (September 2019 – Poster)
- **Cox, R. M.**; McWhite, C. D.; Dinkeloo, K. D.; Tran, J.; Lloyd, A.; Qiao, H.; Ellington, A.; Marcotte, E. M. “Leveraging orthology and systems biology for engineering in non-model organisms” UT Austin Synthetic Biology Symposium (August 2019 – Poster)

TEACHING

- Lead instructor
 - **Introduction to R**; Fall Short Courses, Center for Biomedical Research Support (Fall 2021)
 - **Introduction to R for Biologists**; Big Data in Biology Summer School, Center for Biomedical Research Support (Summer 2021)
 - **Practical Approaches to Analyzing Biological Data in R**; Big Data in Biology Summer School, Center for Biomedical Research Support (Summer 2020)
- Teaching Assistant
 - **Computational Biology and Bioinformatics**; UT Austin (Spring 2020)

ORGANIZATIONS & OUTREACH

Open Coding Hour Jan. 2019 – present

- In charge of organizing and scheduling a weekly help session designed to help students with data science and programming-related problems
- Spearheaded a new monthly program where computational scientists demo a useful programming skill (e.g., programmatic figure making, machine learning models)

Graduate Student Association Jun. 2019 – present

- Vice President (2020-present)
- First Year Student Liaison (2019-2020)

Junior League of Longview Dec. 2016 – Jun. 2018

- Project coordinator for the program “Buy a Box, Feed a Child”
- This project raised more than \$10,000 towards filling “School Break” boxes with food for children who usually depend on school-provided meals; my group converted that money to food supplies and delivered the organized boxes to East Texas schools
- Awarded “Provisional of the Year” for this effort

AWARDS & HONORS

NIH F31 Ruth L. Kirschstein Predoctoral Individual NRSA (2021-present)

Honorable Mention, NSF Graduate Research Fellowship Competition (2020)

Provisional of the Year, Junior League of Longview (2018)

REFERENCES

- Dr. Edward Marcotte (**email**: edward.marcotte@gmail.com)
- Dr. Andrew Ellington (**email**: ellingtonlab@gmail.com)
- Dr. John Wallingford (**email**: wallingford@austin.utexas.edu)
- Dr. Claus Wilke (**email**: wilke@austin.utexas.edu)
- Dr. Damon Billodeaux (**email**: dbillodeaux@eastman.com)