

# Rachael M. Cox

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## SUMMARY

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Interdisciplinary computational biochemist with a passion for chemistry, systems biology, machine learning and large-scale data science; aspires to leverage integrative and comparative multi-omic frameworks to inform technology development, with previous projects having applications to agricultural engineering and human health.

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## EDUCATION

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### **Doctor of Philosophy, Biochemistry**

*The University of Texas at Austin, Austin, Texas*

**Jun. 2018 – Dec. 2023**

### **Bachelor of Science, Chemistry**

*Texas A&M University, College Station, Texas*

**Aug. 2009 – Dec. 2013**

## RESEARCH EXPERIENCE

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### **AI Computational Biology Intern**

*Invitae Corporation*

**Jun. 2022 – Aug. 2022**

- Built a model for evaluating genetic similarity across thousands of patients given their sequencing data; stratifying patients by genetic similarity empowers causal variant analysis for genotype-to-phenotype research
- Built a pipeline that, given filters of interest (e.g. whole exome data and/or probands with sequenced family members), queries a Snowflake SQL warehouse and then an API for downloading patient sequencing data and meta data
- Led another intern who was moved onto my project halfway through the summer; we worked together to use my genetic similarity metrics as input to multiple machine learning algorithms to predict  $n$ th degree relationships (e.g. a second cousin would be a 6<sup>th</sup> degree relationship)

### **Graduate Research Assistant**

*Prof. Edward Marcotte, The University of Texas at Austin*

**Jun. 2018 – present**

- Engineered a machine learning pipeline for the comparative evolution of protein organization using co-fractionation mass spectrometry data across the tree of life as input; disruption of highly conserved molecular systems play a significant role human disease, and this work seeks to characterize those systems
- 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 to inform synthetic biology strategies
- 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 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-ISC11-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**

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- **Computational:** Python (numpy, pandas, sklearn, networkx, matplotlib), R (tidyverse, ggplot2, igraph), SQL (Snowflake), Bash; proficient in high-performance computing/cloud-based Linux environments
- **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
- **Instrumentation:** Mass spectrometry, NMR ( $^1\text{H}/^{13}\text{C}/^{32}\text{P}$ ), FTIR spectrometry, UV-Vis and fluorescence spectroscopy

## PUBLICATIONS

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- **Cox, R. M.**; Papoulas, O.; Lee, C.; Battenhouse, A.; Yang, D.; Drew, K.; McWhite, C. M.; Wallingford, J. B.; Marcotte, E. M.; The conserved eukaryotic interactome reveals mechanisms of modern genetic disorders. (2023, *in prep*)
- Huebner, R. J.; Weng, S.; Lee, C.; Sarikaya, S.; Papoulas, O.; **Cox, R. M.**; Marcotte, E. M.; Wallingford, J. B. “ARVCF catenin controls force production during vertebrate convergent extension.” *Dev. Cell.* **57(9)**, 1119-1131.e5 (2022).
- Devitt, C. C.; Lee, C.; **Cox, R. M.**; O. Papoulas; Alvarado, J.; Marcotte, E. M.; Wallingford, J. B. “Twintilin1 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

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- **Cox, R. M.**; Papoulas, O.; McWhite, C. D.; Battenhouse, A.; Marcotte, E. M. “Leveraging comparative proteomics across the tree of life to improve human disease mapping.” US Human Proteomics (HUPO) Conference 2022 (March 2022 – Invited talk)
- **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](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

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- Lead instructor **Summer 2020 - present**
  - **Introduction to R for Biologists** (UT Austin, Big Data in Biology Summer School)
  - **General Introduction to R** (UT Austin, Center for Biomedical Research Support)
- Teaching Assistant **Spring 2020**
  - **Computational Biology and Bioinformatics** (UT Austin, Department of Statistics and Data Science)

## ORGANIZATIONS & OUTREACH

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- **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 – May 2023**
  - 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”
  - Raised more than \$10,000 towards filling “School Break” food boxes for children who usually depend on school-provided meals; we 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

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Graduate Dean’s Prestigious Fellowship Award (2023)  
 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

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- Dr. Edward Marcotte (**email:** [edward.marcotte@gmail.com](mailto:edward.marcotte@gmail.com))
- Dr. Andrew Ellington (**email:** [ellingtonlab@gmail.com](mailto:ellingtonlab@gmail.com))
- Dr. John Wallingford (**email:** [wallingford@austin.utexas.edu](mailto:wallingford@austin.utexas.edu))
- Dr. Alix Lacoste (**email:** [alix.lacoste@invitae.com](mailto:alix.lacoste@invitae.com))
- Dr. Damon Billodeaux (**email:** [dbillodeaux@eastman.com](mailto:dbillodeaux@eastman.com))