# Erika Schwarz Taylor

Kyle, TX 78640 • (512) 348-0265 • enstaylor@gmail.com

## EDUCATION

M.Jur. Business Risk, Ethics, and Compliance, 2022 St. Mary's University School of Law, San Antonio
Ph.D. Plant Biology, 2016 University of Texas at Austin
M.S. Marine Biology, 2011 University of North Carolina, Wilmington
B.S. Biology, 2009 University of North Carolina, Wilmington

## CERTIFICATIONS

Certified Compliance & Ethics Professional (CCEP)®, Credential ID 110278

## TEACHING EXPERIENCE

**Texas State University, San Marcos, TX**

*Assistant Faculty of Instruction, Department of Biology* *2026 - present*

- Design and deliver course curriculum for freshmen majors introductory biology, Functional Biology (BIO1330) and Genetics (BIO2316)
- Coordinate Genetics lab (BIO2116) across 20+ sections including hiring Instructional Assistants, ordering supplies, and iterating on curriculum to ensure students are gaining valuable skills applicable to the job market.
- Facilitate active problem-solving sessions that build quantitative reasoning and improve performance on applied assessments
- Translate complex concepts for diverse learners using digital tools, visual aids, and real world case studies
- Continuously iterate on course materials based on student feedback and student performance data

*Lecturer, Department of Biology* *2025-2026*

- Design and deliver instruction for non-majors biology (BIO 1320) and genetics (BIO 2450), reaching a broad range of student backgrounds and learning goals.
- Facilitate active problem-solving sessions that build quantitative reasoning and improve performance on applied assessments
- Translate complex concepts for diverse learners using digital tools, visual aids, and scaffolded case studies
- Continuously iterate on course materials based on student feedback and student performance data

**St. Mary's University, San Antonio, Texas** **2020 – 2022**

*Assistant Professor of Biological Sciences and Bioinformatics Specialist*

- Developed a four-year Bioinformatics degree program, including cross-departmental collaboration to ensure graduates received well-rounded training in biology, computer science, and statistics.
- Designed, piloted, and iteratively refined the core curriculum, including: Genes, Genomes, and Genomics; Transcriptomics, Proteomics, and Metabolomics; Algorithms for Bioinformatics; Big Data Concepts; Programming in R, and Bioinformatics Research/Internship.
- Trained students on next-generation sequencing platforms, including the Ion Torrent S5 and Applied Biosystems SeqStudio
- Mentored research students in genome annotation and evidence-based curation as an active member of the Genomics Education Partnership (GEP)

**St. Edward's University, Austin, Texas** **2016 – 2019**

*Visiting Assistant Professor and Interim Laboratory Coordinator, Biological Sciences*

- Organized course material, materials, meetings, faculty, etc. for 9-12 lab sections per semester - Collaborated with colleagues in implementing active learning into Freshman Biology for Majors lecture courses (BIOL1307/1308)
- Designed and implemented a semester-long bioinformatics project for Freshman Biology lecture (BIOL1307) to

parallel molecular biology lecture topics
- Designed and implemented course curriculum for the Course-based Undergraduate Research Experience (CURE) model used in laboratory courses
- Worked closely with colleagues designing and implementing assessment measures and materials in both lecture and laboratory courses

**Austin Community College, Austin, TX** **2014 - present**

*Adjunct Associate Professor, Biology*
- Implementation of active learning in Biology courses for both non-majors and majors.
- Implemented Bioinformatics course curriculum using materials from the Genomics in Education Partnership (GEP) in the Biotechnology Department workforce program
- Collaborated on designing course curriculum for an algae biotechnology track with UTEX Algae - Collection through the Algae Technology Educational Consortium (ATEC) for the Biotechnology Department workforce program

## OTHER EXPERIENCE

**Sequencing.com** **2025 - 2026**

*Sequencing Coach*
- Helped customers understand their whole genome sequencing information and what it can and cannot tell them in one-on-one Zoom calls
- Included education regarding interpretation of information associated with clinical variants from resources such as ClinVar and the GWAS Catalog.
- Provided relevant materials to customers to support their ability to be their own advocate and have conversations with their healthcare provider(s).

**GenRAIT, Inc.** **2024 - 2025**

*Head of Science*
- Acted as a product manager for the genomics platform, driving UI/UX initiatives aligned with the co-founders' strategic vision. Provided roadmap guidance from a subject matter expert perspective grounded in -omics and bioinformatics.
- Led decisions on feature inclusion, tool selection, and platform functionalities to support SME workflows.
- Partnered closely with the Head of Engineering and development teams to deliver user-centered feedback, recommending feature enhancements, design improvements, and documentation updates.
- Delivered user stories and identified key pain points to guide AI integration, streamlining workflows for bioinformaticians and laboratory scientists.
- Validated scientific workflows deployed on the platform using SEQC2 data and Genome in a Bottle benchmarking datasets to ensure reliability and accuracy.
- Provided technical customer support and served as a scientific liaison between clients and Engineering, translating feature requests and bug reports into actionable updates.

**Form Bio, Remote**

*Manager, Computational Biology* **2023 - 2024**
- Mentored my team on how to protect their time so they could work most efficiently, how to approach prioritization when goal posts moved often, and how to prioritize when everything is deemed “high priority”. - Developed, planned, and rolled out a compliance framework for SOC2 compliance to the entire company. - Worked closely with the CTO and Director of Engineering to draft and enforce 21 new company policies for data privacy, governance, and regulation for SOC2 compliance with overlapping implications for ISO and HIPAA compliance.
- Conducted a Risk Assessment that covered all major business units including Information Security, HR, Sales,

Financial, and Legal.

- Interacted with auditors to complete a SOC2 Type I audit and developed the framework for the Type II audit. - Worked closely with legal counsel to edit policies, such as the Privacy Policy, that encompassed requirements for auditors.
- Maintained office hours and utilized company-wide events, such as Lunch & Learns and All Hands meetings, to provide education on the compliance framework and importance of the undertaking.
- Provided bioinformatics professional services for wet lab biologists focusing on de-extinction of the Dodo by performing Avian comparative genomics, processing -omics data from various samples and synthesizing the information to limit the search space for genomic editing.
- Built genomic resources for others to use by pulling publicly available genomes and annotations, where available, to build a wide variety of file types for easy access such as new annotations using Form Bio's FLAG workflow, building index files needed by bwa, salmon, variant call files, etc.
- Worked closely with my team to benefit from our collective genius for brainstorming sessions, troubleshooting, and generating ways to work more efficiently.
- Acted as a beta user of the Form Bio bioinformatics platform and provided guidance to the Engineering team for improvements or bug fixes.

**Bioinformatics CRO, Remote** **2022 – 2024**

*Contractor*

- Designed and implemented a custom pipeline integrating Illumina and PacBio HiFi sequencing data to generate a high-quality hybrid assembly of a potato cultivar, enabling targeted promoter extraction based on client specifications.
- Evaluated and compared multiple genome assembly tools to optimize accuracy, coverage, and performance.
- Conducted repeat analysis on a red algae genome; produced data visualizations and contributed a curated repeat family annotation track for interactive browsing via JBrowse.
- Collaborated cross-functionally with bioinformaticians and proteomics experts to perform transcriptome- and proteome-informed genome annotation, improving functional insight and data usability for downstream applications.

**EQO, Austin, Texas** **2016 – 2023**

*Co-founder, Chief Scientific Officer*

- Launched two main product lines: 1) Osprey handheld eRNA-capture collection system, and 2) Calypso permanent installation 12-sample eRNA-capture collection system.
- Managed an SBIR Phase I grant for proof-of-concept for a third product line, a therapeutic that targeted invasive zebra mussels.
- Played an active role in managing employees, prioritization of projects, invoicing, prioritization of time, and pursuing funding opportunities.
- Communicated with a wide variety of clients from large government organizations to small, private companies.
- Created organizational structure using principles from EOS.
- Provided guidance and support for research and development endeavors related to next generation sequences, bioinformatics, and invasive, toxic, and nuisance aquatic species

## PUBLICATIONS


Stanek, TJ., Leung, W., Shaffer, CD., **The Genomics Education Partnership**, *et al*. 2025. Recombination Suppression Drives Expansion of the *Drosophila* Dot Chromosome. Molecular Biology and Evolution. 42(12):1537-1719

Alexandre, N., Balacco, J., Tilley, T., Abueg, L., Brajukaz, N., Moreira, L., Whelan, C., **Schwarz Taylor, E.**, Jarvis, E.D., Fedrigo, O., Shapiro, B., Keyte, A.L. 2025. A Chromosome-level genome of the Nicobar pigeon, *Caloenas*

*nicobarica*. Journal of Heredity. https://doi.org/10.1093/jhered/esaf031

Choi, I-S., **Schwarz, E.N**., Ruhlman, T.A, Khiyami, M.A., Sabir, J.S.M., Hajarah, N.H., Sabir, M.J., Rabah, S.O. Jansen, R.K. 2019. Fluctuations in Fabaceae mitochondrial genome size and content are both ancient and recent. BMC Plant Biology. 19(1):448.

**Schwarz, E.N.**, Ruhlman, T.A., Weng, M.-L., Khiyami, M.A., Sabir, J.S.M., Hajarah, N.H., Alharbi, N.S., Rabah, S.O., and Jansen, R.K. 2017. Plastome-wide nucleotide substitution rates reveal accelerated rates in Papilionoideae and correlations with genome features across legume subfamilies. Journal of Molecular Evolution. 84(4):187-203.

Dugas, DV, Hernandez, D., Koenen, E., **Schwarz, E.**, Straub S., Hughes, CE., Jansen, RK., Nageswara-Rao, M., Staats, M., Trujillo, J., Hajrah, NH., Alharbi, NS., Al-Malki, AL., Sabir, JSM., Bailey, CD. 2015. Mimosoid legume plastome evolution: IR expansion, tandem repeat expansions, and accelerated rate of evolution in clpP. Scientific Reports. 5:16958.

**Schwarz, E.N.**, Ruhlman, T., Sabir, JSM., Hajrah, NH., Alharbi, NS., Al-Malki, AL., Bailey, CD and Jansen, R.K. 2015. Plastid genomes reveal parallel inversions and multiple losses of rps16 in papilionoids. Journal of Systematics and Evolution. 53(5): 458-468.

Bahieldin, A., Al-Kordy, M., Shokry, M., Gadalla, N., Al-Hejin, A., Sabir, J., Al-Ahmadi, A., **Schwarz, E.**, El-Domyati, F. and Jansen, R. 2014. Short communication: corrected sequence of the wheat plastid genome. C R Biologies 337: 727-731.

Sabir, J., **Schwarz, E. N.**, Ellison, N., Zhang, J., Baeshen, N.A., Mutwakil, M., Jansen, R. and Ruhlman, T. 2014. Evolutionary and biotechnology implications of plastid genome variation in the IR loss clade of legumes. Plant Biotechnology Journal 12: 743-754.

Borkman, D.G., Smayda, T.J., **Schwarz, E.N.**, Flewelling, L.J. and Tomas, C.R. 2014. Recurrent vernal presence of the toxic Alexandrium tamarense/Alexandrium fundyense (Dinoflagellata) species complex in Narragansett Bay, USA. Harmful Algae. 32:73-80.