

# Michelle Jonika

BIOINFORMATICIAN · COMPUTATIONAL BIOLOGIST · MOLECULAR GENETICIST

4225 Pendleton Dr. Apt. 7104 Bryan, TX, 77802, USA

☎ (281)-825-9621 | ✉ michellemjonika@gmail.com | 🏠 michellejonika@github.io | 📷 michellejonika | 📺 michellejonika

## Summary

As a computational biologist, I enjoy the puzzle-like nature of coding genetics and genomics problems, specifically bringing this approach to the evolution of genomic content and sex chromosomes. Detail-oriented planning, project management, experimental design, and clear communication are important to my critical thinking and problem solving strategies for research. I am pursuing a Ph.D. in Genetics and Genomics at Texas A&M University, and I defended my dissertation in January 2023 with a graduation date of May 2023. I am interested in career paths in industry intersecting bioinformatics, computational biology, genetics, genomics, and molecular biology.

## Expertise

<b>Genomics:</b>	NGS Analysis and Pipeline Development (SRA, Trimmomatic, bwa, samtools, GATK), Genome Assembly (HiFiiasm, QUAST, BUSCO, BlobToolKit), RNASeq (FastQC, bowtie2, DESeq2), GWAS (PLINK, GEMMA), Genomic Prediction (rrBLUP)
<b>Genetics:</b>	Evolutionary Biology (Genome structure evolution, Mammalian Sex chromosome evolution, Morphometrics), Veterinary Medicine (Clinical Data Evaluation, Cancer Prediction), Crop Science (Epistasis, Introgression)
<b>Molecular Biology:</b>	Primer optimization, gDNA/DNA extraction, RNA extraction, PCR, qPCR, Gel visualization/imaging, Flow Cytometry
<b>Chemistry:</b>	GC-MS, DART-MS, Drug Database Design, LC-MS
<b>Programming:</b>	R, Linux/Unix, tidyverse, Python, LaTeX, HTML/CSS, R Shiny
<b>Code Management:</b>	Git/GitHub, VSCode, BitBucket, Docker, JIRA, conda
<b>Data Science:</b>	Large dataset management (>20Gb), Machine Learning, Bayesian statistics, Phylogenetics, Simulations, Data Visualization, Software Development, Amazon Web Services (AWS)/Cloud Computing, HPC Cluster Computing
<b>Soft Skills:</b>	Project management, Public Speaking and Communication, Leadership, Multi-disciplinary Collaboration, Adaptive problem solving, Multi-tasking, Self-Motivated, Time Management, Strategic Planning

## Education

### Ph.D. in Genetics and Genomics

TEXAS A&M UNIVERSITY | ADVISOR: HEATH BLACKMON

- Dissertation: Patterns and Processes in the Evolution of Sequence Classes and Genomic Compartments

College Station, Texas

Aug. 2018 - May 2023

### B.S. in Forensic and Investigative Science

TEXAS A&M UNIVERSITY | ADVISOR: AARON M. TARONE

- Thesis: Genes as Markers of Sex for Forensic Entomology

College Station, Texas

Aug. 2014 - May 2018

## Experience

### PetDx

BIOINFORMATICS INTERN | BIOINFORMATICS AND DATA SCIENCE TEAM

- Leveraged high-complexity data set to predict canine cancer types
- Used machine learning (Random Forest) approaches to train and evaluate different models
- Performed extensive data evaluation to curate sample metrics, obtain balanced training and testing sets and identify meaningful model parameters

San Diego, California

June 2022 - Aug. 2022

### Bayer Crop Science

DATA SCIENCE INTERN | GENOMICS DISCOVERY AND APPLICATION TEAM

- Identifying historic data to test for epistasis and designing a follow-up experiment to test for epistasis
- Developing a statistical testing framework to identify interactions between introgressed loci
- Three-month, full-time position exposure in an industry setting
- Establishing multi-disciplinary connections with teams with expertise in data science, genomics, and precision breeding

St. Louis, Missouri

May 2021 - Aug. 2021

### Ph.D. Research | Advisor: Dr. Heath Blackmon

TEXAS A&M INTERDISCIPLINARY PROGRAM IN GENETICS AND GENOMICS | TEXAS A&M DEPARTMENT OF BIOLOGY

- Developing an R package (Lo et al. 2019) to characterize microsatellite evolution and applying this package to characterize microsatellite evolution across 300 million years of insect evolution (Jonika et al. 2020)
- Elucidating the role of centromere type in insect chromosome evolution (Ruckman et al. 2020) and effective population size in carnivore chromosome evolution (Jonika et al. In Prep)
- Designing an automated genomic pipeline and TensorFlow based machine learning application to categorize genomic characteristics for 100s of mammalian species totaling 1000s of TB of genomic data

College Station, Texas

Aug. 2018 - May 2023

- Completed additional experimentation and formal writing from undergraduate thesis project (**Jonika et al. 2020**)
- Applied new sex determination methodology and primer optimization to additional applications in forensic entomology (**Pimsler et al. 2021**) and stem cell research (**Pitonak et al. 2022**)

## Teaching & Mentorship

### Teaching Assistant

DEPARTMENT OF BIOLOGY | DEPARTMENT OF GENETICS

- Python for Biologists | Spring 2023 | Texas A&M
- Anatomy and Physiology | Spring 2022 | Texas A&M
- Critical Writing in Biology | Fall 2020, Spring 2021 | Texas A&M
- Introduction to Genetics Laboratory | Spring 2019, Spring 2023 | Texas A&M
- Guest Lecture - Forensic Genetics | Topic: Genetic Testing | Sep. 2022 | Texas A&M
- Guest Lecture - Bioinformatics | Topic: Genetic Privacy | Nov. 2021 | Utah Valley University

### Graduate Student Mentor

UNDERGRADUATE RESEARCH ASSISTANTS

- Mentee: Johnathan Lo | Topic: Microsatellite Characterization and Evolution
- Mentee: Abhi Arekere | Topic: Carnivore Chromosome Number Evolution
- Mentee: Ragan Miller, Joseph Ward, Leen Fardoun | Topic: Chrysina Morphometrics

## Leadership & Outreach

### Genetics Graduate Student Association

PRESIDENT | VICE PRESIDENT | GRADUATE STUDENT REPRESENTATIVE | SEMINAR COMMITTEE

May 2019 - Current

- Facilitate monthly graduate student association meetings
- Oversee communication between current graduate students, genetics faculty, and the program executive committee

### Texas A&M College of Science

OUTREACH COMMITTEE | WOMEN IN SCIENCE AND ENGINEERING

Jan. 2019 - Current

- Participated in various outreach activities important to the mission of the College of Science and Women in Science and Engineering
- Served on the Women in Science and Engineering outreach committee and organized school STEM nights

### Genetics Society of America

EARLY CAREER LEADERSHIP PROGRAM - CAREER DEVELOPMENT SUBCOMMITTEE

Jan. 2020 - Dec. 2022

- Contribute career development blog pieces for Genes to Genomes blog
- Curate resources contributing to a career development toolkit and early career researcher newsletters
- Organize career development workshops for bimonthly workshop series and TAGC conference

## Awards & Grants

- 2023 **Texas A&M Distinguished Graduate Student Award**, Texas A&M University
- 2023 **Montgomery Award**, Texas A&M University Graduate and Professional School
- 2023 **Outstanding Ph.D. Student Presentation**, Biology Department, Student PostDoc Research Conference
- 2022 **Texas A&M Data Science Ambassador**, Texas A&M University
- 2022 **Research Excellence Award**, Interdisciplinary Genetics and Genomics Program

## Selected Publications

\*Please see Google Scholar for a full publications list

M. Pitonak, M. Aceves, P.A. Kumar, G. Dampf, P. Green, A. Tucker, V. Dietz, D. Miranda, S. Letchuman, **M.M. Jonika**, D. Bautista, H. Blackmon, J.N. Dulin. 2022. Effects of Biological Sex Mismatch on Neural Progenitor Cell Transplantation for Spinal Cord Injury in Mice. *Nature Communications*. 13(1):1-12.

**M.M. Jonika**, J.M. Alfieri, T. Sylvester, A.R. Buhrow, H. Blackmon. 2022. Why Not Y Naught. *Heredity*. 129. 75-78.

S. Ruckman\*(Co-first author), **M.M. Jonika\*(Co-first author)**, C. Casola, H. Blackmon. 2020. Chromosome Number Evolves at Equal Rates in Holo-centric and Monocentric Clades. *PLOS Genetics* 16(10):e1009076.

**M.M. Jonika**, C.E. Hjelmén, A.M. Faris, A.S. McGuane, A.M. Tarone. 2020. An Evaluation of Differentially Spliced Genes as Markers of Sex for Forensic Entomology. *J. of Forensic Science* 65(5): 1579-1587

J. Lo, **M.M. Jonika**, H. Blackmon. 2019. micRocounter: Microsatellite Characterization in Genome Assemblies. *G3* 9(10): 3101-3104

J.M. Alfieri, G. Wang, **M.M. Jonika**, C.A. Gill, G.N. Athrey, H. Blackmon. 2022. A Primer for Single-Cell Sequencing in Non-Model Organisms. *Genes* 13(2).