

# Mingsi Liao

Blacksburg, VA 24060, USA

☎ +1 (571)224-5227 | ✉ msliao@vt.edu | 🏠 mingsiliao.github.io/mingsi.github.io//

## Summary

---

Ph.D. student in Genetics, Bioinformatics, and Computational Biology at Virginia Tech School of Animal Sciences. My research focuses on leveraging machine learning, bioinformatics, computer vision, and whole genome sequencing to advance precision livestock farming and agricultural innovation.

## Professional Skills & Cetificates

---

1. **Lab skills & animal handling (dairy calf):** DNA extraction, serum spinning, fecal/oral/blood sample collection (jugular venipuncture)
2. **Bioinformatics & genomic analysis:** NGS (FastQC, MultiQC, Trimmomatic, STAR, BWA, FeatureCounts, vcftools, bcftools, samtools), GWAS (PLINK, Beagle, GEMMA), Variants calling and annotation (GATK, freeBayes, delly, SnpEFF, VEP), Metatranscriptome (SortMeRNA, MEGAHIT, Kraken)
3. **Computational skills:** Operating Systems (Linux, Windows, macOS), Computer vVision (OpenCV), Deep Learning/Machine Learning (YOLOv8, CNNs, Transfer Learning, Regression Models, Clustering), Programming & Scripting (Python-pandas, numpy, os, matplotlib, R, Bash/Shell, LaTeX, Jupyter Notebooks)
4. **Soft skills:** Leadership, teamwork, problem-solving, willingness to learn
5. **Certifications:** Graduate Certificate in Data Analytics, Institutional Animal Care and Use Committee (IACUC) Training Certificate, Public Nutritionist (Level Three)

## Education

---

<b>Virginia Tech</b>	<b>GPA: 3.78/4.00</b>
Ph.D., Genetics, Bioinformatics and Computational Biology, Animal Sciences	2022 - present
<b>George Mason University</b>	<b>GPA: 3.71/4.00</b>
M.S. (non-thesis), Bioinformatics and Computational Biology	2019 - 2021

## Research Projects and Publications

---

1. **Whole Genome Sequencing (WGS) Analysis for Breed Differentiation (Royal White vs. White Dorper)**
  - Identification of breed-specific genetic variation by analyzing high-quality SNPs and indels, assessing population structure, and revealing key genetic differentiation between Royal White and White Dorper breeds.
  - Publication (manuscript in preparation):
    - **Liao, M.**, Kravitz, A., R., Cockrum, R. and Sriranganathan, N., 2025. Whole Genome Sequencing Analysis for Breed Differentiation between Royal White and White Dorper.
2. **Automatically Videos Collection and Prediction of Calf Body Weight using a Depth Camera**
  - Creation of an automated system for predicting dairy calf weights, combining top-view video recordings from a depth camera, electronic weighing scales, and contour extraction to measure

calf dimensions, with a machine learning model that utilizes video-derived measurements and weight data.

- Publication (manuscript under review):
  - **Liao, M.**, Morota, G., Bi Y., Cockrum, R. (2024). Comparison of Deep Learning (YOLOv8) and Threshold-Based Methods for Depth Image Segmentation using Extreme Gradient Boosting to Predict Dairy Calf Body Weight. *Animals*

### 3. Metatranscriptomics Reveals Functional Profiles of Rumen Microbial Ecosystem in Dairy Cows

- Characterization of rumen microbiome by aligning RNA reads to the NCBI-nr database, revealing the abundance and functional roles of bacteria, fungi, archaea, and protozoa.
- Publication (manuscript in preparation):
  - **Liao, M.**, Ramirez, A. M., Duncan, J., Alward, K., Owens, C., Campos, L. M., Hanigan, M. D., Cockrum, R. (2024). Effect of Dietary Crude Protein on Lactation, Feed Efficiency, and Rumen Microbial Ecological Dynamics in Holstein Cows: A Shotgun Metatranscriptome Analysis. *FEMS*

### 4. Genetic Association Analysis in Ovine Johne's Disease

- Investigation of SNP associations with disease phenotypes in sheep using genotypic data from the Ovine SNP50 BeadChip, with quality control to exclude low-call-rate SNPs and individuals, imputation of missing genotypes via Beagle, and logistic regression analysis to identify disease-associated genetic variants.
- Publication
  - Kravitz, A., **Liao, M.**, Morota, G., Tyler, R., Cockrum, R., Manohar, B.M., Ronald, B.S.M., Collins, M.T. and Sriranganathan, N., 2024. Retrospective Single Nucleotide Polymorphism Analysis of Host Resistance and Susceptibility to Ovine Johne's Disease Using Restored FFPE DNA. *International Journal of Molecular Sciences*, 25(14), p.7748.

### 5. Diarrhea Identification in Dairy Holstein Calves using Machine Learning Model

- Development of a predictive machine learning model for diarrhea detection through image processing techniques.
- Status: Data collection

### 6. Investigating the Impact of Early Lactose Exposure on Dairy Calf Development

- Analysis of growth, health, and metabolic differences in dairy calves resulting from early lactose exposure, comparing calves fed with and without lactose during the first 3 days and monitored from day 0 to weaning.
- Status: Data collection

## Selected Courses

---

Machine Learning II, Deep learning, Computer Vision, Data Analytics, Statistics in Research, Bioinformatics Methods, Molecular Cell Biology, Molecular Biotechnology, Bioinformatics Programming, Systems Biology, Biological Data Analysis, Protein Structure Analysis, Next Generation Sequencing, Comp Analysis Viral Genomes

## Honors and Awards

---

2024 **2<sup>nd</sup> Place Award in Poster Presentation (GPSS Research Symposium)**  
22-24 **John Lee Pratt Animal Nutrition Scholarship**  
2016 **2<sup>nd</sup> Place Institutional Scholarship**  
2015 **1<sup>st</sup> Place Institutional Scholarship**  
2014 **Food Safety Publicity Competition**