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Research Interests	My academic pursuits are centered in the realm of computational biology and bioinformatics. With a background in Animal Sciences, my PhD work has involved using omics techniques to assess the impact of environmental factors on the animal epigenome and transcriptome. In my latest professional endeavor, I have been utilizing computational methods to analyze multi-omics data with the aim to decipher the changes in the tissue microenvironment that potentially elevate cancer risks.	
Education	<b>University of Wisconsin-Madison</b> , Madison, Wisconsin USA Ph.D., Animal Sciences, 09/2020 - 12/2023 <ul style="list-style-type: none"><li>Dissertation: <a href="#">Revealing the Impact of Environmental Perturbations on the Bovine Epigenome</a></li></ul>	
	<b>University of Wisconsin-Madison</b> , Madison, Wisconsin USA M.S., Computer Sciences, 09/2021 - 05/2023	
	<b>University of Florida</b> , Gainesville, Florida USA M.S., Animal Sciences, 08/2018 - 08/2020 <ul style="list-style-type: none"><li>Thesis: <a href="#">Deciphering Complex Biological Processes Using Gene Coexpression Networks</a></li></ul>	
	<b>Huazhong Agricultural University</b> , Wuhan, P.R. China B.S., Animal Sciences, 09/2014 - 07/2018	
Professional Positions	<b>Sanford Burnham Prebys Medical Discovery Institute</b> , La Jolla, California USA <ul style="list-style-type: none"><li>Postdoctoral Computational Biologist</li></ul> <b>01/2024 - Present</b>	
	Department of Animal and Dairy Sciences <b>University of Wisconsin-Madison</b> , Madison, Wisconsin USA <ul style="list-style-type: none"><li>Graduate Research Assistant</li></ul> <b>09/2020 - 12/2023</b>	
	Department of Animal Sciences <b>University of Florida</b> , Gainesville, Florida USA <ul style="list-style-type: none"><li>Graduate Research Assistant</li><li>Graduate Teaching Assistant</li></ul> <b>09/2018 - 08/2020</b> <b>Fall 2019</b>	

Draft Manuscripts

2024	5. S Sinha; N Sinha; M P. Garcia; A V. Tarrab; T Nyugen; <b><u>L Liu</u></b> ; T Cantore; S Patiyal; S Mukherjee; S Madan; K Tharp; J Zhao; G Flanigan; D Meerzaman; U Ben-David; A J. Deshpande; E
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Ruppín (2024) *DeepTarget Predicts Primary and Secondary Targets of Cancer Drugs by integrating large-scale genetic and drug screens.* (Under review)

4. A Gonella-Díaz, M Sponchiado, M França, **L Liu**, G Pugliesi, E Turco, F Peñagaricano, M Binelli (2024) *The metabolomic composition of the oviductal fluid is controlled by the size of the peri-ovulatory follicle in beef cows.* (Under review)
3. **L Liu** & F Peñagaricano (2024) *EnrichKit: A Multi-Omics Tool for Livestock Research.* (Biorxiv; [codes](#))
2. **L Liu**, J Laporta, F Peñagaricano (2024) *Dry period heat stress alters the mammary gland transcriptome in the subsequent lactation of dairy cows.*
1. M Guenther, B Dado-Senn, **L Liu**, F Peñagaricano, G Dahl, J. Laporta (2024) *Fetal exposure to heat stress impacts the mammary gland epigenome at birth.*

#### Peer Reviewed Journal Articles

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| 2023 | 8. R Amorín*, <b>L Liu</b> *, P Moriel, N DiLorenzo, PA Lancaster, F Peñagaricano (2023) <i>Maternal diet induces persistent DNA methylation changes in the muscle of beef calves.</i> <i>Scientific Reports</i> . 13, 1587. doi: <a href="https://doi.org/10.1038/s41598-023-28896-3">10.1038/s41598-023-28896-3</a>   |
| 2022 | 7. CM Sheftel, <b>L Liu</b> , SL Field, SR Weaver, CM Vezina, F Peñagaricano and LL Hernandez(2022) <i>Impact of Fluoxetine Treatment and Folic Acid Supplementation on the Mammary Gland Transcriptome During Peak Lactation.</i> <i>Frontiers in Pharmacology</i> . 13:828735. doi: <a href="https://doi.org/10.3389/fphar.2022.828735">10.3389/fphar.2022.828735</a> |
| 2021 | 6. <b>L Liu</b> , R Amorín, P Moriel, N DiLorenzo, PA Lancaster, F Peñagaricano (2021) <i>Maternal methionine supplementation during gestation alters alternative splicing and DNA methylation in bovine skeletal muscle.</i> <i>BMC Genomics</i> . 22, 780. doi: <a href="https://doi.org/10.1186/s12864-021-08065-4">10.1186/s12864-021-08065-4</a>                   |
|      | 5. MA Mezera, W Li, <b>L Liu</b> , R Meidan, F Peñagaricano, MC Wiltbank (2021) <i>Effect of natural pre-luteolytic prostaglandin F2α pulses on the bovine luteal transcriptome during spontaneous luteal regression.</i> <i>Biology of Reproduction</i> . 105 (4), 1016-1029. doi: <a href="https://doi.org/10.1093/biolre/iaob123">10.1093/biolre/iaob123</a>         |
|      | 4. SL Field, MG Marrero, <b>L Liu</b> , F Peñagaricano, J Laporta (2021) <i>Histological and transcriptomic analysis of adipose and muscle of dairy calves supplemented with 5-hydroxytryptophan.</i> <i>Scientific Reports</i> . 11.1: 1-10. doi: <a href="https://doi.org/10.1038/s41598-021-88443-w">10.1038/s41598-021-88443-w</a>                                  |
| 2020 | 3. <b>L Liu</b> , R Amorín, P Moriel, N DiLorenzo, PA Lancaster, F Peñagaricano (2020) <i>Differential network analysis of bovine muscle reveals changes in gene coexpression patterns in response to changes in maternal nutrition.</i> <i>BMC genomics</i> . 21.1: 1-12. doi: <a href="https://doi.org/10.1186/s12864-020-07068-x">10.1186/s12864-020-07068-x</a>     |
|      | 2. H Louvandini, PS Corrêa, R Amorín, <b>L Liu</b> , EH Ieda, CR Jimenez, SM Tsai, CM McManus, F Peñagaricano (2020) <i>Gestational and lactational exposure to gossypol alters the testis transcriptome.</i> <i>BMC genomics</i> . 21(1), 1-11. doi: <a href="https://doi.org/10.1186/s12864-020-6487-2">10.1186/s12864-020-6487-2</a>                                 |
|      | 1. A Sigdel, <b>L Liu</b> , R Abdollahi-Arpanahi, I Aguilar, F Peñagaricano (2020) <i>Genetic dissection of reproductive performance of dairy cows under heat stress.</i> <i>Animal Genetics</i> . 51(4), 511-520. doi: <a href="https://doi.org/10.1111/age.12943">10.1111/age.12943</a>   |

## Editorial Activities

### Ad Hoc Reviewer

- Number of articles reviewed in total: **26** (not counting revisions) / **30** (counting revisions):  
BMC Genomics (1), Frontiers in Genetics (1), Gene(2), Epigenomes (1),  
International Journal of Molecular Sciences(2), Cancers (3), Genome (1), Genes (4),  
Biology (3), Animal Genetics (1), Animal Gene (1), Animals (4), Gene Reprots(1),  
Contrast Media Molecular Imaging (1)

## Software Development

### **R package/ Full-stack Web**

- [EnrichKit](#): a toolkit for omics data analysis in animal species. ([Web](#) / [Python](#) / [R](#))

## Technical Skills

### BIOINFORMATICS & DATA ANALYSIS

- RNA-seq, WGB-Seq, Bioconductor, Pandas/NumPy/SciPy, scikit-learn, TensorFlow

### PROGRAMMING LANGUAGES

- Python, Java, R, Shell (Bash), SQL (MySQL), C++, JavaScript/HTML/CSS, MATLAB

### FRAMEWORK

- Django, Spring Boot, ReactJS, NodeJS, JUnit, CUDA, OpenMP

### DEVELOPER TOOL

- Git, Docker, Conda, Nextflow, Slurm, GCP, AWS (EC2, RDS, S3), Elasticsearch, Jira

## Honors/Awards

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| 2022      | • <b><i>Neal A. Jorgensen Genome Travel Awards</i></b>   PAG Conference 30 (San Diego, CA) |
| 2019      | • <b><i>Top-up Award</i></b>   University of Florida, ANS Department                       |
| 2017      | • <b><i>Study Abroad Scholarship</i></b>   China Scholarship Council (CSC)                 |
| 2016      | • <b><i>National Scholarship of P.R.China (Undergraduate)</i></b>   Ministry of Education  |
| 2014-2015 | • <b><i>Outstanding Undergraduate Award</i></b>   Huazhong Agricultural University, China  |