SIYUAN FENG

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- **Computational Biologist** highly skilled in **population genomics** and **functional multi-omics**, with 13 peer-reviewed papers published in five years.
- Experienced in building and executing both **computational** and **wet-lab multi-omic pipelines**, able to solve complex biological questions using samples or public datasets.
- Interdisciplinary **problem-solver** and **collaborator** applying **statistical modeling** to real-world challenges in **public health** and **athletic training**, with 11 additional peer-reviewed papers published in three years.
- **Product developer** who has promoted innovations in molecular cancer diagnostics.

EDUCATION

University of Wisconsin - Madison Madison, US
PhD candidate & MS, **Genetics** (GPA: 4.0/4.0) 9/2020 - 8/2026
PhD thesis: Decode the regulatory blueprint of adaptive evolution using multi-omics
Advisor: Prof. John Pool

Sichuan Agricultural University Chengdu, China
BS & MS, **Animal Genetics, Breeding and Reproduction** (GPA: 3.9/4.0) 9/2013 - 6/2019
Advisor: Prof. Qianzi Tang

SKILLSETS

- **Cancer genomics & molecular diagnostics**: variant DB integration, oncogenicity prediction & classification
- **Large-scale multi-omic analyses & experiments:** WGS, ATAC-seq, transcriptomics, proteomics, metabolome
- **Profiling of gene-regulatory traits**: chromatin accessibility, transcriptional factor binding, RNA expression, alternative splicing, RNA editing, small RNA regulation, protein expression, post-translational modifications
- **Population genomic analyses:** detection of SNPs and CNV, summary statistics, demographic inference, detection of population structure, introgression, and selection, genome-environment association
- **Statistical analyses & experiment design:** Mendelian randomization, structural equation modeling, hypothesis testing, linear and logistic regression, ANOVA, factorial structure, RCBD, mixed models
- **Large language models (LLM):** RAG, API integration, prompt engineering, structured output
- **Programming & version control & reproducibility**: Python, R, Bash, Git, GitHub, Docker, nextflow
- **Backend development**: Djangle, SQL, cloud computing (AWS)

RELATED EXPERIENCE

Computational oncology research intern - BillionToOne, Inc., CA 2025.06.12 - 2025.08.22

- Built an LLM-powered tumor-variant annotation and interpretation system to deliver higher-quality diagnostic reports while reducing cost.
- Built a web app and database to visualize and curate variant annotations and experimental evidence.
- Collaborated with clinical genomics scientists to de-risk the project.

PhD research assistant - Laboratory of Genetics, University of Wisconsin-Madison, WI 2020 - present

- Decoded the regulatory blueprint of adaptive evolution using multi-omics and Bayesian statistical modeling.
- Developed multi-omic computational and wet-lab workflows for WGS, ATAC-seq, RNA-seq, and proteomics.
- Developed a novel statistical framework to identify adaptive multi-omic traits.
- Uncovered the genomic basis of the invasion success of an agricultural pest that causes $1 billion loss per year.
- Collaborated with human geneticists to examine the effects of scaling in population genetic simulations.
- Discovered causal effects of physical activity intensity on COVID-19 outcomes by performing mendelian randomization on GWAS (UK biobank) and COVID-19 Host Genetics Initiative datasets.
- Invited to present genomic research at seven international conference and university departments.

Bioinformatician & Master 's research assistant– Sichuan Agricultural University, China 2013-2019

- Published 11 peer-reviewed papers as the lead bioinformatician on a 30-people research team.
- Collaborated with wet-lab scientists in over 20 research projects involving transcriptomics of over 20 species from plants to animals.

AWARDS

- Louis and Elsa Thomsen Wisconsin Distinguished Graduate Fellowship (for research excellence, $50000)
- Marie Christine Kohler Fellowship at Wisconsin Institute of Discovery (for art & science fusion, $6000)

PEER-REVIEWED PUBLICATIONS

24 Peer-reviewed research papers # of citations: 737

Population genomics & evolution

1. Ferrari T, **Feng S**, Zhang X, Mooney J. Parameter Scaling in Population Genetics Simulations May Introduce Unintended Background Selection: Considerations for Scaled Simulation Design. *Genome Biology and Evolution*. 2025 May 23;evaf097.
2. **Feng S,** DeGrey SP, Guédot C, Schoville SD, Pool JE. Genomic Diversity Illuminates the Environmental Adaptation of *Drosophila suzukii. Genome Biology and Evolution*. 2024 Sep;16(9):evae195.

Meta-analysis of public health & athletic training

3. Jiang C, Zhang X, **Feng S**, Li H. Engaging in Physical Activity in Green Spaces at Night Is Associated with Mental Well-Being and Happiness. *Behavioral Sciences*. 2025; 15(3):313.
4. Luo H, Zhang X, Su S, Zhang M, Yin M, **Feng S**, Peng R, Li H. Using structural equation modeling to explore the influences of physical activity, mental health, well-being, and loneliness on Douyin usage at bedtime. *Frontiers in Public Health*. 2024 Jan 5;11:1306206.
5. Yang T, Bi S, Zhang X, Yin M, **Feng S**, Li H. The Impact of Different Intensities of Physical Activity on Serum Urate and Gout: A Mendelian Randomization Study. *Metabolites*. 2024 Jan 19;14(1):66.
6. Zhang X, Li H, **Feng S**, Su S. The Effect of Various Training Variables on Developing Muscle Strength in Velocity-based Training: A Systematic Review and Meta-analysis. *International Journal of Sports Medicine*. 2023 Aug 15.
7. Zhang X, Zhang X, **Feng S**, Li H. The causal effect of physical activity intensity on COVID-19 susceptibility, hospitalization, and severity: Evidence from a mendelian randomization study. *Frontiers in Physiology*. 2023 Mar 8;14:1089637.
8. Li H, Zhang X, Zhang X, Wang Z, **Feng S**, Zhang G. Can Intelligence Affect Alcohol-, Smoking-, and Physical Activity-Related Behaviors? A Mendelian Randomization Study. *Journal of Intelligence*. 2023 Jan 31;11(2):29.
9. Zhang X, **Feng S**, Li H. The Effect of Velocity Loss on Strength Development and Related Training Efficiency: A Dose–Response Meta–Analysis. *Healthcare*. 2023 Jan;11(3):337.
10. Tian H, Li H, Liu H, Huang L, Wang Z, **Feng S**, Peng L. Can Blood Flow Restriction Training Benefit Post-Activation Potentiation? A Systematic Review of Controlled Trials. *International Journal of Environmental Research and Public Health.* 2022 Sep 21;19(19):11954.
11. Zhang X, **Feng S**, Peng R, Li H. Using Structural Equation Modeling to Examine Pathways between Physical Activity and Sleep Quality among Chinese TikTok Users. *International Journal of Environmental Research and Public Health*. 2022 Apr 23;19(9):5142.
12. Zhang X, **Feng S**, Peng R, Li H. The Role of Velocity-Based Training (VBT) in Enhancing Athletic Performance in Trained Individuals: A Meta-Analysis of Controlled Trials. *International Journal of Environmental Research and Public Health*. 2022 Jan;19(15):9252.
13. Chen H, Zhang G, Wang Z, **Feng S**, Li H. The Associations between Daytime Physical Activity, While-in-Bed Smartphone Use, Sleep Delay, and Sleep Quality: A 24-h Investigation among Chinese College Students. *International Journal of Environmental Research and Public Health*. 2022 Jan;19(15):9693.

Functional genomics (* equal contributions)

14. Wang X*, Yan P*, **Feng S**, et al. Identification and expression pattern analysis of miRNAs in pectoral muscle during pigeon (Columba livia) development. *PeerJ*. 2021 Jun 23;9:e11438.
15. Fu Y, Fan P, Wang L, Shu Z, Zhu S, **Feng S**, et al. Improvement, identification, and target prediction for miRNAs in the porcine genome by using massive, public high-throughput sequencing data. *Journal of Animal Science*. 2021 Feb;99(2):skab018.
16. **Feng S***, Ma J*, Long K*, Zhang J, Qiu W, et al. Comparative microRNA transcriptomes in domestic goats reveal acclimatization to high altitude. *Frontiers in Genetics.* 2020 Jul 31;11:809.
17. Wang X*, Lin Z*, **Feng S,** Liu L, Zhao L, et al. MicroRNA expression profile analysis during myogenic differentiation in pigeon (Columba livia) skeletal muscle satellite cells. *International Journal of Agriculture and Biology.* 2020;24(5):7.
18. Long K*, **Feng S***, Ma J*, Zhang J, Jin L, et al. Small non-coding RNA transcriptome of four high-altitude vertebrates and their low-altitude relatives. *Scientific Data.* 2019 Oct 4;6(1):192.
19. Zhou J, Zhao H, Zhang L, Liu C, **Feng S**, et al. Integrated analysis of RNA-seq and microRNA-seq depicts miRNA–mRNA networks involved in stripe patterns of Botia superciliaris skin. *Functional & integrative genomics.* 2019 Sep;19(5):827-38.
20. Ma Y*, **Feng S***, Wang X, Qazi IH, Long K, et al. Exploration of exosomal microRNA expression profiles in pigeon 'Milk' during the lactation period. *BMC Genomics*. 2018 Dec;19:1-2.
21. Wang Y*, Ma J*, Qiu W*, Zhang J, **Feng S**, et al. Guanidinoacetic acid regulates myogenic differentiation and muscle growth through miR-133a-3p and miR-1a-3p Co-mediated Akt/mTOR/S6K signaling pathway. *International Journal of Molecular Sciences*. 2018 Sep 19;19(9):2837.
22. Xiao J*, **Feng S***, Wang X, Long K, Luo Y, et al. Identification of exosome-like nanoparticle-derived microRNAs from 11 edible fruits and vegetables. *PeerJ.* 2018 Jul 31;6:e5186.
23. Ma J *, Fu Y*, Zhang J*, **Feng S**, et al. Testosterone-Dependent miR-26a-5p and let-7g-5p Act as Signaling Mediators to Regulate Sperm Apoptosis via Targeting PTEN and PMAIP1. *International Journal of Molecular Sciences*. 2018 Apr 18;19(4):1233.
24. Li X*, **Feng S***, Luo Y, Long K, et al. Expression profiles of microRNAs in oxidized low-density lipoprotein-stimulated RAW 264.7 cells. *In Vitro Cellular & Developmental Biology – Animal*. 2018 Feb;54(2):99–110.