

WENTING LUO

(+1) 5203316829 | wentingluo@arizona.edu | <http://linkedin.com/in/wenting-luo-296890180>

TECHNICAL SKILLS

Programming: R, SQL, Python, SAS, Linux, L^AT_EX, Git

Machine Learning and Data Modeling: Machine Learning (supervised, unsupervised), Deep Learning (TensorFlow, PyTorch), Big Data Technologies, Model Deployment

Statistical Analysis and Communication: Statistical Modeling and Analysis, Experimental Design, A/B Testing, Data Cleaning and Preprocessing, Data Visualization, Data Management and Communication, Data Ethics, Effective Communication and Collaboration

PROFESSIONAL EXPERIENCE

University of Arizona

Research assistant

Aug 2019 - Present

Tucson, AZ

· **Saguaro Cacti Detection and Counting with Deep Learning**

- Developed an efficient system for the detection and counting of saguaro cacti utilizing deep learning techniques.
- Solved challenges related to computing resources and data processing by applying Roboflow and Detectron2.
- Optimized training datasets considering sensor heights, resolutions, and angles, achieving accurate and automated saguaro cacti detection.

· **Survival Analysis of COVID-19 and Specific Cancer Types**

- Conducted a comprehensive survival analysis using a multivariate Cox proportional hazard model.
- Investigated the hazard ratio by comparing COVID-19 positive to negative patients among 13 specific cancer types, utilizing data from the UK Biobank.
- This analysis provided valuable insights into the impact of COVID-19 on cancer patients.

· **Case-Control Study on Housing Environments and COVID-19**

- Executed logistic regression models for a case-control study to examine the effects of housing environments on COVID-19 transmission, anxiety, and stress.
- Leveraged data from the COVID-19 Participant Experience dataset to draw correlations between housing conditions and health outcomes, contributing to the understanding of pandemic-related challenges.

· **SEMFA - Multi-Omics Fusion and Analysis Software**

- Developed SEMFA, an innovative multi-omics fusion and analysis software. SEMFA is equipped to perform general parametric tests for the Mahalanobis Similarity of samples based on factor scores generated by an extended version of conventional Multiple Factor Analysis (MFA).
- This tool enhanced the analysis of complex multi-omics datasets, and facilitated insights into biological systems.

· **Longitudinal Analysis of Cuticular Waxes in Lettuce Growth**

- Applied a linear mixed model to analyze longitudinal data collected through High-Throughput Phenotyping (HTP) techniques. Investigated the variation in cuticular waxes during growth, considering genetic traits of lettuce and surrounding environmental factors.
- This research shed light on the dynamics of cuticular wax production and its correlation with genetics and environmental conditions in lettuce.

Zhejiang University

Research assistant

Sep 2016 - Jun 2019

Hangzhou, China

- Investigated the expression of Porcine delta coronavirus (PDCoV) NS6 protein during infection *in vivo* and its incorporation into PDCoV virions.
- Explored the effect of HEV non-structural proteins on Sendai virus (SEV)-activated type I interferon pathway.

EDUCATION

University of Arizona, Tucson, AZ

Aug 2019 - expected May 2025

Ph.D. Student in Statistics & Data Science, Minor in Information

M.S. of Biosystems Analytics & Technologies

Aug 2019 - May 2023

Relevant Courses:

Statistical Machine Learning, Fundamentals of Optimization, Neural Networks, Artificial Intelligence

Zhejiang University, Hangzhou, China

Sep 2016 - Jun 2019

M.S. of Science in Preventive Veterinary Medicine

Northeast Agricultural University, Harbin, China

Sep 2011 - Jun 2016

B.A. of Science in Veterinary Medicine

CONFERENCE

Oral presentation at The Southwest Data Science Conference (Best Paper Award), 2023

Oral presentation at The Southwest Data Science Conference, 2022

Attended The AMIA Virtual Informatics Summit, 2021

PUBLICATIONS

1. **Luo, W. T.**, Emmanuel G., Ariyan Z., Sebastian C., Bruno R., Jeffrey D., ... Duke P. (n.d.). Leaf Cuticular Wax Composition of a Genetically Diverse Collection of Lettuce (*Lactuca sativa* L.) Cultivars Evaluated Under Field Conditions. *Heliyon* (2024).
2. **Luo, W. T.**, Baldwin, E., Jiang, A. Y., Li, S., Yang, B., Li, H. (2022). Effects of housing environments on COVID-19 transmission and mental health revealed by COVID-19 Participant Experience data from the All of Us Research Program in the USA: a case-control study. *BMJ Open*, 12(12), e063714.
3. Xu, L. D., Zhang, F., Chen, C., Peng, L., **Luo, W. T.**, Chen, R., ... Huang, Y. W. (2022). Revisiting the Mongolian Gerbil Model for Hepatitis E Virus by Reverse Genetics. *Microbiology Spectrum*, 10(2), e02193-21.
4. Li, H., Baldwin, E., Zhang, X., Kenost, C., **Luo, W.**, Calhoun, E. A., ... Lussier, Y. A. (2021). Comparison and impact of COVID-19 for patients with cancer: a survival analysis of fatality rate controlling for age, sex and cancer type. *BMJ Health & Care Informatics*, 28(1).
5. Qin, P., **Luo, W. T.**, Su, Q., Zhao, P., Zhang, Y., Wang, B., Yang, Y. L., Huang, Y. W. (2021). The porcine delta-coronavirus accessory protein NS6 is expressed in vivo and incorporated into virions. *Virology*, 556, 1-8.
6. Baldwin, E., Han, J., **Luo, W.**, Zhou, J., An, L., Liu, J., Zhang, H., Li, H. (2020). On fusion methods for knowledge discovery from multi-omics datasets. *Computational and Structural Biotechnology Journal*, 18, 509-517.
7. Xu, L. D., Zhang, F., Peng, L., **Luo, W. T.**, Chen, C., Xu, P., Huang, Y. W. (2020). Stable expression of a hepatitis E virus (HEV) RNA replicon in two mammalian cell lines to assess mechanism of innate immunity and antiviral response. *Frontiers in Microbiology*, 11.
8. Qin, P., Du, E. Z., **Luo, W. T.**, Yang, Y. L., Zhang, Y. Q., Wang, B., Huang, Y. W. (2019). Characteristics of the life cycle of porcine deltacoronavirus (PDCoV) in vitro: replication kinetics, cellular ultrastructure and virion morphology, and evidence of inducing autophagy. *Viruses*, 11(5), 455.
9. Wang, B., Liu, Y., Ji, C. M., Yang, Y. L., Liang, Q. Z., Zhao, P., Xu, L. D., Lei, X. M., **Luo, W. T.**, Huang, Y. W. (2018). Porcine deltacoronavirus engages the transmissible gastroenteritis virus functional receptor porcine aminopeptidase N for infectious cellular entry. *Journal of Virology*, 92(12).