# **PEIYU LIU**

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#### **SUMMARY**

- **Biostatistics Ph.D. Student** at University of Florida with 7+ years' experience in statistical modelling.
- Proficient in multiple coding languages including R/Rshiny, SAS, Python, Maple, SQL, Matlab, C++ etc.
- Specialized in Mathematical modelling, Machine learning, Biostatistics computing, and Clinical trial analysis.

#### **EXPERIENCES**

Biostatistician Gainesville, U.S.

Emerging Pathogens Institute | University of Florida

05/2025-present

- Designed and executed an **RSV** severity analysis using **CoxPh and logistic regression** to study age, gender, birth history, and comorbidities against length of stay, ICU admission, oxygen, ventilation, and inpatient status.
- Conducted analysis of Florida kindergarten measles **vaccine coverage**, quantifying **outbreak probabilities** and expected **outbreak sizes** under varying coverage scenarios.
- Developed the **open-source R package vaxineR**, standardizing outbreak risk modeling with functions for Re estimation, vaccination scenario simulations, and county-level **vaccination data visualization**.
- Provided outbreak risk plots and quantitative summaries cited in a *Science* news article on vaccination coverage decline, and produced RSV analytic figures for a manuscript submission to *Nature Communications*.
- Provide pre-proposal study design guidance: perform power analyses, calculate appropriate sample size for testing intervention effects such as vector control, vaccination etc.

Research Assistant Gainesville, U.S.

Biostatistics Department | University of Florida

08/2023-present

- Developed **3 R Shiny** apps: a dengue trial simulator (serological vs. clinical endpoints), a SIR model estimator (**LS**, **bootstrap**, **MCMC**), and a US weather app (**ggplot2 visualization**, **K-means**, **Machine learning forecasting**).
- Taught Kaplan–Meier and Nelson–Aalen survival curve estimation (4–8 hrs) as a guest lecturer.
- Innovated a unified **trial evaluation** framework by integrating a stochastic antibody kinetics model (ANPP) with temperature-driven SEIR-SIR model, comparing the **novel serological vs traditional clinical endpoints**.
- Formulated mosquito bite—driven **antibody dynamics** into closed-form moment equations, validated with large-scale **Monte Carlo** simulations, and derived standardized **sample size formulas** for trial design.
- Synthesized quantitative evidence demonstrating that serological endpoints reduce vector-control trial sample sizes by several orders of magnitude, linking different interventions to endpoint choices and follow-up timing.
- Led statistical analyses in a pediatric clinical-genomic RSV study, integrating **CoxPh** and **regression models** with viral **genotype data** to examine **genotype-phenotype associations** and their impact on disease severity.

### **Research Fellow and Lecturer**

Changsha, China.

Math Department | Hunan Institute of Science and Technology

06/2021-08/2023

- Taught **Probability Theory** and **Mathematical Statistics** to 200+ students, 243 class hours each year.
- Mentored a student team to a second prize in the National Mathematical Modeling Contest in China.
- Formulated a three-dimensional **pulsed differential equation** model capturing interactions among **tumor cells**, **effector cells**, and **helper T cells**, and proved the existence and **stability of tumor-free periodic solutions**.
- Performed bifurcation analysis on therapy intensity, effector-cell activation, and birth rates to evaluate how radioimmunotherapy strategies shift thresholds for tumor-free dynamics.
- Completed multinational weather datasets via spline interpolation and led spatial analytics using bivariate choropleth mapping to explore environmental determinants of disease transmission across 10 countries.
- Directed a 50,000 CNY municipal-funded project to build a **COVID-19 visualization platform** integrating statistical and mathematical models for epidemic monitoring.

Researcher Xian, China.

School of Mathematics and Statistics | Shaanxi Normal University

07/2018-06/2022

- Built SEIAR compartmental models, applying Nonlinear Least Squares, Bootstrap, and MCMC with sensitivity and threshold analyses to quantitatively evaluate and inform vaccination and NPI strategies.
- Supported a data-driven COVID-19 forecasting and **visualization platform** by designing and maintaining **compartmental modeling** components.
- Applied machine learning techniques including Expectation Maximization (EM), Lasso regression, and Generalized Additive Models (GAM) to model meteorological impacts on air pollution across Xi'an districts.

• Developed and analyzed a nonlinear predator—prey differential system with **saturation effects**, proving **equilibrium coexistence** and **stability** under **stochastic** noise through bifurcation and Poincaré map analyses.

#### **EDUCATION**

**Ph.D.** (Biostatistics, GPA: 3.9/4)

08/2023 - present

School of Public Health & Health Professions, University of Florida

Gainesville, U.S.

• Coursework: Biostatistics Methods and Computing, Statistical Machine Learning, Survival Analysis, Casual Inference, Data visualization, Longitudinal Analysis, Analytical methods for Infectious Diseases

M.S. (Computational Mathematics, top 5%)

05/2021

School of Mathematics and Statistics, Shaaxi Normal University

Xian, China

• Coursework: Advanced Biomathematics, Stochastic Process, Stability, Qualitative Theory of Differential Equations

**B.S.** (Statistics, top 5%)

05/2017

School of Mathematics and Statistics, Shaaxi Normal University

Xian, China

• Coursework: Probability Theory, Statistical Analysis and R, Mathematical Modeling, Practical Regression Analysis, Multivariate Statistical Analysis, Statistical Computing, Time Series Analysis

### **SELECTED PUBLICATIONS**

- Liu, P., Hitchings, M., Rong, L., & Cummings, D. (2025). Serological markers as efficient endpoints for vector control trials: A mechanistic modeling framework for comparative evaluation with clinical and entomological endpoints. Under review.
- Santos, L. A., Castillo, A., Gustani-Buss, E., Hitchings, M. D. T., & Liu, P. (2025). Increased genomic diversification frequency of respiratory syncytial virus (RSV) types A and B in pediatric cohort in the United States after the onset of the COVID-19 pandemic. Under review at *Nature Communications*.
- Yan, Q., & Liu, P. (2023). Effects of climatic factors and control measures on the spread of COVID-19. Journal of Zhejiang University (Science Edition), 50(2). (https://doi.org/10.3785/j.issn.1008-9497.2023.02.003)
- Wang G., Ding W., Zhang Z., **Liu, P**.. (2022) Qualitative analysis of a tumor-immune model with impulsive control strategies at fixed time. Journal of Hunan Institute of Science and Technology, 35(3): 1-6. (doi: 10.16740/j.cnki.cn43-1421/n.2022.03.017)
- Liu, P., He S., Rong L., and Tang S.. (2020) The effect of control measures on COVID-19 transmission in Italy: Comparison with Guangdong province in China. *Infectious Diseases of Poverty*, 9(130):1-13. (https://doi.org/10.1186/s40249-020-00730-2)
- Xia F., Xiao Y., **Liu, P.**, Cheke R.. (2020) Differences in how interventions coupled with effective reproduction numbers account for marked variations in COVID-19 epidemic outcomes. Mathematical Biosciences and Engineering, 17:85-98. (<a href="http://dx.doi.org/10.3934/mbe.2020274">http://dx.doi.org/10.3934/mbe.2020274</a>)

## **HONORS**

- **Invited speaker**: Stochastic Epidemic Models with Inference, Rollins School of Public Health, Emory University (SISMID) 2025.
- Coach & Judge: ASA DataFest, University of Florida (American Statistical Association) 2025.
- Mentored undergraduate students win second prize in China Mathematical Contest in Modeling 2022.
- National Scholarship by Ministry of Education (Top 1% nationwide) in China 2021.
- Second Prize in China Mathematical Contest in Modeling 2016.

## APPLICATIONS/PACKAGES

Developed R Package

• Peiyu Liu, Matt Hitchings, Ira Longini. Package "vaxineR" A Statistical Tools for Vaccine coverage analysis and outbreak risk assessment. <a href="https://cran.r-project.org/web/packages/vaxineR/">https://cran.r-project.org/web/packages/vaxineR/</a>

Developed Online Tools/Webpages (R-shiny):

- Dengue Clinical Trial (serological vs. clinical endpoints): https://peiyuliu.shinyapps.io/anpp-trial-comparison/
- US Weather Analyses (ggplot2 visualization, K-means clustering, Machine Learning forecasting): https://peiyuliu.shinyapps.io/us-weather-analysis/
- SIR Model Estimation (Least Squares, Bootstrap, MCMC): https://peiyuliu.shinyapps.io/sir-estimation-comparison/

## GOOGLE SCHOLAR

Available at: <a href="https://scholar.google.com/citations?user=O6KFoOUAAAAJ&hl=en&oi=ao">https://scholar.google.com/citations?user=O6KFoOUAAAAJ&hl=en&oi=ao</a>