

# Peiyu Liu

Biostatistician | Ph.D. Student in Biostatistics, University of Florida

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## Summary

- 3rd year Biostatistics Ph.D student at University of Florida with 8+ years' experience in statistical modelling.
- Proficient in multiple coding languages including R/Rshiny, Matlab, SAS, Python, C++, etc.
- Specialized in statistical models, differential equations, and Bayesian estimation.

## Skills

Mathematical modelling • Biostatistics computing • Machine learning • Clinical trial analysis • R • Matlab • SAS

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## Positions and Experiences

### Biostatistician (Consulting Core&CSQUID)

University of Florida | Emerging Pathogens Institute

- 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

University of Florida | Biostatistics Department | Aug 2023 - Current

- 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 can reduce 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

Hunan Institute of Science and Technology | Math Department | Aug 2021 - Aug 2023

- Taught Probability Theory and Mathematical Statistics to 200+ students, 243 class hours each year.
- Mentored undergraduate team to a second prize in the National Mathematical Modeling Contest.
- 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.
- Applied spline interpolation to complete multinational weather datasets (10 countries) and performed descriptive and spatial analyses, including bivariate choropleth mapping.
- Directed a 50,000 CNY municipal-funded project to build a COVID-19 visualization platform integrating statistical and mathematical models for epidemic monitoring. Mentored undergraduate team to a second prize in the National Mathematical Modeling Contest.

### Researcher

Shaanxi Normal University | School of Mathematics and Statistics | Aug 2017 - Aug 2021

- Built continuous and discrete SEIAR compartmental model, 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 data imputation (interpolation, EM), variable selection (Lasso regression, Spearman analysis), Generalized additive model, and spatial econometric models (Moran's I, Spatial Lag Models) to quantify meteorological impacts on air pollution across Xi'an districts.
- Developed and analyzed a nonlinear dynamical system (Riker model) with saturation effects, proving equilibrium coexistence, conducting bifurcation analysis under stochastic disturbances, and validating dynamics through Poincaré map simulations.

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## Projects

### Public Health Outbreak Risk Modeling & vaxineR Package

Lead Statistician

Center of Statistics and Quantative Infectious Dieases | Sep 2025 - Present

- Led rapid-response analyses of kindergarten vaccine coverage under new government policies, coordinating a 12-member cross-functional team to align methodologies and deliver reproducible findings within days.
- Communicated epidemiological insights to high-profile media (e.g., Science, CNN), with analytical visuals cited.
- Directed the full development lifecycle of the open-source vaxineR R package and its companion RShiny dashboard

### AI-Powered Identification of Pediatric Crohn's Disease from Medical Imaging

Lead Statistician

Department of Pediatrics | Ongoing

- Defining the statistical and machine learning strategy for classifying active vs. inactive Crohn's disease, including data preprocessing to validation.
- Establishing the evaluation framework for performance, bias assessment, and interpretability.

### Large-Scale Application and Inferential Extension of the ANPP Model

Lead Methodologist & Analyst

Department of Biostatistics | Aug 2025 - Present

- Developing a moment-based estimation framework as a computationally efficient alternative to likelihood-based methods for fitting complex stochastic antibody models to cross-sectional data.
- Leading the application across 20+ serological studies, conducting inverse inference to estimate parameters such as mosquito biting intensity and antibody boosting/waning rates.
- Characterizing geographic variation in vector exposure and immune responses.

### Statistical Modeling of Arbovirus Transmission Drivers in Puerto Rico

Lead Methodologist & Analyst

Centers for Disease Control and Prevention | Sep 2025 - Present

- Building a household-level transmission model (chain-binomial) for dozens of families, estimating secondary attack rates and within- vs. between-household spread. .
- Applying multilevel regression with geospatial random effects and lagged climate inputs to test drivers (location, demographics, rainfall/temperature); quantify effect sizes with CIs..
- Characterizing policy simulations to compare targeted interventions (e.g., focused vector control or prophylaxis when available) and prioritize high-risk households/areas.

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## Education

### Ph.D. in Biostatistics

College of Public Health & Health Professions, University of Florida

Aug 2023 - Current

### M.S. in Computational Mathematics

School of Mathematics and Statistics , Shaaxi Normal University

Aug 2018 - May 2021

### B.S. in Statistics

School of Mathematics and Statistics , Shaaxi Normal University

Aug 2013 - May 2017

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