

# Hanyu Wang

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## OVERVIEW

Highly quantitative MSc student in **Epidemiology of Infectious Diseases (Quantitative Specialization)** at Yale University, with a strong background in Statistics and Quantitative Biology. Research focuses on **applying advanced statistical modeling and machine learning** to understand how environmental factors influence infectious disease dynamics and public health outcomes. Seeking a PhD position to integrate **epidemiological modeling, environmental data, and advanced computation** for actionable disease prevention and risk mitigation.

## EDUCATION

- **Yale University | Master of Science** New Haven, CT, USA  
Expected May 2026
  - *Epidemiology of Infectious Diseases - Quantitative Specialization*
  - **Relevant Coursework:** Quantitative Methods for Infectious Disease (R), Global Change and Infectious Disease, Advanced Regression Model (R), Transmission Dynamic Models for Infectious Diseases (R), Machine Learning & Causal Inference (R)
- **University of Toronto | Honours Bachelor of Science** Toronto, Canada  
Jun 2025
  - *Statistics Major, Quantitative Biology Major*
  - **Relevant Coursework:** Time Series Analysis (R), Methods for Multivariate Data (R), Machine Learning (R & Python), Experimental Analysis (R), Population Ecology (R), Computer Programming (Python)

## WORK EXPERIENCE

- **Multifactorial Compartmental Model for Infectious Disease Dynamics** York University  
May 2024 - Aug 2024
  - *Research Project (Supervisor: Prof. Jianhong Wu)*
    - Developed an optimized **SEIRS compartmental model** to simulate infectious disease transmission, incorporating demographic and biological factors.
    - Integrated **stochasticity and spatial dynamics**, explicitly modeling birth, death, and immune decay via computational simulations.
    - Collaborated with a team of four to refine model accuracy; enhanced expertise in **mathematical modeling and public health informatics**.
- **Single-Cell Transcriptome Sequencing Data Analysis** Xibei Hospital  
Sep 2024 - Dec 2024
  - *Research Project*
    - Analyzed scRNA-seq data from enteritis patients to study gene expression heterogeneity and identify therapeutic cell populations.
    - Built **R pipelines** using **Seurat**, implementing PCA, Louvain/Leiden clustering, and visualization (t-SNE, UMAP).
    - Identified **10 cell subtypes from 19 clusters**, advancing skills in biomedical data analysis and machine learning.

## ACADEMIC PROJECT

- **Identifying Autism-Specific Brain Connectivity Patterns** | University of Toronto | Jan - Apr 2025 [view]
  - Analyzed ABIDE fMRI data using multivariate statistical methods including **correlation matrices, permutation testing, effect-size estimation, and FDR correction** to identify ASD-related connectivity differences.
  - Found robust hyperconnectivity centered on the Left Middle Temporal Gyrus (posterior division), refining understanding of ASD neural mechanisms.
- **Prediction for Alzheimer's Disease Risk and Progression** | University of Toronto | Sep – Dec 2024 [view]
  - Designed and compared **Logistic Regression, Random Forest, and Naive Bayes** models, achieving **94.33% accuracy**.
  - Enhanced robustness via **grid search hyperparameter tuning, k-fold cross-validation, and SMOTE** for data balancing.

## TECHNICAL & RESEARCH SKILLS

### Programming & Software

R (Expert): Custom pipelines, **Seurat**, time series, multivariate analysis, experimental design

Python (Proficient): **scikit-learn**, Scanpy, machine learning

### Statistical Modeling & Machine Learning

Probabilistic Modeling: **Gaussian Processes** (self-study/projects), **Gaussian Mixture Models**

Algorithms: Logistic Regression, Random Forest, LDA, Naive Bayes, PCA, UMAP, t-SNE

Techniques: Grid search, k-fold CV, SMOTE

### Research Domains

Epidemiology: **SEIRS modeling**, infectious disease dynamics, public health analytics

Biomedical Informatics: scRNA-seq, gene expression, computational neuroscience