

# Hanyu Wang

Homepage | GitHub

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## OVERVIEW

I am an incoming M.S. student in Epidemiology of Infectious Diseases (Quantitative Specialization) at Yale University, with a B.Sc. in Statistics and Quantitative Biology from the University of Toronto. My research interest is Environmental Epidemiology (especially in infectious disease). During my undergraduate studies, I have focused on theoretical foundations and applications of Gaussian Processes and Machine Learning, with an emphasis on probabilistic modeling and data-driven prediction. I have an ultimate goal of providing actionable insights for disease prevention and risk mitigation by integrating epidemiological modeling, environmental data analysis, and advanced statistics.

## EDUCATION

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|---|--|
| <ul style="list-style-type: none"><li>• <b>Yale University   Master of Science</b></li><li>• <i>Epidemiology of Infectious Diseases - Quantitative Specialization</i></li></ul>               | New Haven, America<br><i>Start in Sep 2025</i> |
| <ul style="list-style-type: none"><li>• <b>University of Toronto   Honours Bachelor of Science</b></li><li>• <i>Statistics Major, Quantitative Biology Major, Mathematics Minor</i></li></ul> | Toronto, Canada<br><i>Sep 2022 - Jun 2025</i>  |
| <i>Courses: Machine Learning (R &amp; Python), Time Series Analysis (R), Multivariate Data Building (R), Experimental Analysis (R), Population Ecology (R), Computer Programming (Python)</i> |  |

## SKILLS SUMMARY

- **Technical Skills:** R (Seurat, custom pipelines), Python (Scanpy, scikit-learn)
- **Data Analysis:** Machine Learning (Logistic Regression, Random Forest, LDA), Statistical Modeling (PCA, UMAP, GMM), Data Visualization (t-SNE, UMAP)
- **Domains:** Epidemiological Modeling, Biomedical Informatics, Public Health Analytics

## WORK EXPERIENCE

- |  |                     |
|--|---------------------|
| <b>Single-Cell Transcriptome Sequencing Data Analysis</b>  | Sep 2024 - Dec 2024 |
| • <i>Remote research project conducted in the Biological Diagnosis and Treatment Center@Xibei Hospital</i>   |                     |
| ○ Analyzed single-cell transcriptome data to study gene expression in enteritis, identifying 10 cell subtypes from 19 clusters for downstream therapeutic insights.                |                     |
| ○ Built R pipelines using PCA, Louvain/Leiden clustering, and Scanpy/Seurat libraries; visualized results with t-SNE and UMAP.   |                     |
| ○ Strengthened skills in biomedical data analysis and machine learning, supporting health informatics applications.  |                     |
| <b>Multifactorial Compartmental Model for Infectious Disease Dynamics</b>  | May 2024 - Aug 2024 |
| • <i>Research project conducted under the supervision of Prof. Jianhong Wu@York University</i>   |                     |
| ○ Developed an optimized SEIRS compartmental model with birth, death, and immune decay factors, incorporating stochasticity and spatial dynamics to simulate disease transmission. |                     |
| ○ Enhanced expertise in mathematical modeling and computational simulations, contributing to public health informatics research.   |                     |
| ○ Collaborated with a team of four to refine model accuracy, improving technical communication skills.   |                     |

## ACADEMIC PROJECT

- **Identifying Autism-Specific Brain Connectivity Patterns | University of Toronto | Jan - Apr 2025 [view]**
  - Built a predictive model for autism diagnosis with 92.5% accuracy, analyzing ABIDE fMRI data using PCA, UMAP, and Gaussian Mixture Models.
  - Uncovered distinct connectivity patterns, advancing knowledge in computational neuroscience and health informatics.
  - Presented findings to peers, enhancing scientific communication skills.
- **Prediction for Alzheimer's Disease Risk and Progression | University of Toronto | Sep – Dec 2024 [view]**
  - Designed a machine learning diagnostics model that achieved 94.59% accuracy using Logistic Regression, Random Forest, and Naïve Bayes.
  - Improved model performance with hyperparameter tuning (grid search), k-fold cross-validation, and SMOTE for data balancing.
  - Gained proficiency in feature engineering and optimization, applicable to biomedical data challenges.

## PUBLICATIONS

- **Reactivating T cell immunity in Wnt-hyperactivated non-small cell lung cancer through a supramolecular droplet of carnosic acid and peptide**

Na Liu, Y. Tu, Hanyu Wang, X. Zheng, F. Ji, M. Geng, X. Wei, J. Xin, W. He, Q. Zhao, T. Liu.

*Journal of Pharmaceutical Analysis*, DOI: 10.1016/j.jpha.2025.101309, 2025