

Wei Zhang

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EDUCATION

University of Miami

Ph.D student in Biostatistics, 3.96/4.00

The George Washington University

MS in Statistics, 3.76/4.00

State University of New York (SUNY) at Binghamton

BS in Economics Analysis & Double Majors: Actuarial Math, 3.70/4.00

Miami, FL

2019–Present

Washington, DC

2017–2019

Binghamton, NY

2014–2017

RESEARCH EXPERIENCE

Research Interests

Statistical and machine learning methods in dimensional reduction and data integration of high-dimensional multi-omics data.

Graduate Research Assistant

Miami, FL

Translational Statistical Bioinformatics Lab

08/2020–Present

Projects

Random Forest Data Integration on Multi-omics Data

01/22–Present

TNBC Neoadjuvant Chemotherapy Signature

08/20–12/21

- Assisted in developing machine learning regularization methods to discover the triple negative breast cancer (TNBC) chemotherapy resistant biomarkers by integrative genomic approaches;
- Conducted ensemble survival random forest model to improve the prediction accuracy of survival rate and pathologic complete response in patients with neoadjuvant chemotherapy;
- Discovered signature genes that related to both chemotherapy results and survival status with differential expression and meta analysis on multiple data sources.

ACADEMIC PROJECT

G-priors Bayesian Model Average on Microarray Data

Bayesian Analysis, Advisor: Ishwaran, Hement

Spring/2021

- Analyzed the variable selection and prediction performance on different g-priors in Bayesian model average method on high-dimensional microarray data;
- Discussed the model properties and its competitive to regularization methods;
- Paper link: <https://noblegasss.github.io/stats/BMA/>

Skin Data HAM10000

Deep Learning and Neural Networks, Advisor: Sarkar, Dilip

Fall/2020

- Built convolutional neural network models and transfer learning models to the benchmark seven-class skin data HAM10000;
- Explored the effects of different data balancing methods and increased the accuracy rate of classification with a modified DenseNet model to 0.92;
- Implemented deep learning models with keras and tensorflow in python.

Beat AML DREAM Challenge

DREAM Challenge, Advisor: Chen, Xi (Steven)

Spring/2020

- Explored and visualized the high dimensional RNA-seq data of acute myeloid leukemia (AML) patients for two challenges provided by DREAM Challenge organization;
- Applied dimension reduction methods (sparse PCA), and selected signature genes by variable selection methods such as elastic net and random forest backward selection with R;
- Predicted ex-vivo drug sensitivity using clinical and selected genes of tumors to predict and gathered all information to predict clinical response of AML patients;
- Achieved top 1% in the leaderboard phase for both challenges.

SKILLS

Computer Languages: R, Python, SAS, SQL, LaTeX, STATA, SPSS

Libraries: caret, tidyverse, R-shiny, keras, tensorflow, pandas, NumPy, Matplotlib