Patrick Wu, PhD

contact.patrickwu@gmail.com • https://github.com/pwatrick

Professional Summary

Bioinformatics physician-scientist with strong statistical/computational skills and experience in genotype-phenotype association analyses of complex traits

- Developed and applied statistical genetics approaches to predict complex disease conditions using genomics and clinical data
- Over 5 years of experience with approaches for marker-trait and gene-trait association (GWAS, PheWAS, and TWAS)
- Analyzed large data sets using Python/Jupyter notebooks and R
- Ability to communicate insights and presenting concepts to a diverse audience

Education

2022 MD (expected May 2022), Vanderbilt University School of Medicine, Nashville, TN
2021 PhD in Biomedical Informatics, Vanderbilt University School of Medicine, Nashville, TN
2020 MS in Biomedical Informatics, Vanderbilt University School of Medicine, Nashville, TN
2011 BS in Biological Sciences, Cornell University, Ithaca, NY

Skills and Techniques

Experience with communicating effectively and collaborating within diverse teams

- Led and collaborated with others on projects with 5 publications, 2 awards, and 1 invited presentation

Domain expertise

- Developed and applied statistical genetic analysis methods to generate insights about human disease and diverse complex traits
- Conducted genotype-phenotype association analyses of complex traits: GWAS, PheWAS, and TWAS
- Mined modern, large-scale genetic databases: UK Biobank and EBI GWAS Catalog

Math & statistics

- Experience in applying linear/non-linear regression models, dimensionality reduction and clustering methods

Coding skills

- Python, R, SQL

Experience

MD/PhD Student 2014 - present
MD/PhD program, Vanderbilt University School of Medicine

Graduate Student in Biomedical Informatics 2017 - 2021
Vanderbilt University School of Medicine (Nashville, TN) Advisor: Wei-Qi Wei, MD, PhD

- Worked collaboratively with a diverse team of clinicians, data scientists, and statisticians to improve cardiovascular event prediction using machine learning
- Pioneered a computational approach integrating diverse datasets, including genetic data, to generate drug repurposing hypotheses
- Developed a method using external and internal data sources to detect potential complications due to drug interactions
- Created and evaluated a resource to transform ICD-10 billing codes to computable phenotypes for genotype-phenotype association analyses in large biobanks

Postbaccalaureate Fellow 2012 - 2014
National Institutes of Health (Bethesda, MD) Advisor: Dorian McGavern, PhD

- Identified novel immunotherapies to promote the clearance of chronic viral infections using flow cytometry, immunohistochemistry, and two-photon microscopy

Undergraduate Researcher 2008 - 2011
Cornell University (Ithaca, NY) Advisor: Tim Huffaker, PhD

- Examined interactions between microtubule-associated proteins involved in cell division

Service

Representative of the Student Advisory Committee 2021 - present
MD/PhD program, Vanderbilt University School of Medicine

- Partnered with 3 faculty members and 23 classmates to resolve arising problems, address important questions, and facilitate programming in the MD/PhD program

President 2018 - 2020
American Physician Scientists Association, Vanderbilt Chapter

- Invited and planned visits for 4 physician-scientist speakers
- Reviewed and submitted applications from 8 students for the national physician-scientist conference

Co-chair of Website Committee 2017 - 2018
MD/PhD program, Vanderbilt University School of Medicine

- Mobilized a team of 5 individuals to overhaul the directory page for 111 students: https://medschool.vanderbilt.edu/mstp/current-students/

Publications

Wu P, Feng Q, Kerchberger VE, Nelson SD, Chen Q, Li B, Edwards TL, Cox NJ, Phillips EJ, Stein CM, Roden DM, Denny JC, Wei W-Q. Integrating Gene Expression and Clinical Data to Identify Drug Repurposing Candidates for Hyperlipidemia and Hypertension. (under review).

Wu P, Nelson SD, Zhao J, Stone CA Jr, Feng Q, Chen Q, et al. DDIWAS: High-throughput electronic health record-based screening of drug-drug interactions. J Am Med Inform Assoc. 2021;28: 1421–1430.

Zhao J, Feng Q, **Wu P**, Lupu RA, Wilke RA, Wells QS, et al. Learning from Longitudinal Data in Electronic Health Record and Genetic Data to Improve Cardiovascular Event Prediction. Sci Rep. 2019;9: 717.

Zhao J, Zhang Y, Schlueter DJ, **Wu P**, Eric Kerchberger V, Trent Rosenbloom S, et al. Detecting time-evolving phenotypic topics via tensor factorization on electronic health records: Cardiovascular disease case study. J Biomed Inform. 2019;98: 103270.

Wu P, Gifford A, Meng X, Li X, Campbell H, Varley T, et al. Mapping ICD-10 and ICD-10-CM Codes to Phecodes: Workflow Development and Initial Evaluation. JMIR Med Inform. 2019;7: e14325.

Zhao J, Feng Q, **Wu P**, Warner JL, Denny JC, Wei W-Q. Using topic modeling via non-negative matrix factorization to identify relationships between genetic variants and disease phenotypes: A case study of Lipoprotein(a) (LPA). PLoS One. 2019;14: e0212112.