Randy Parrish

Atlanta, GA | randy.parrish@emory.edu | GitHub

EDUCATION

PhD, Biostatistics — August 2022–Present
Rollins School of Public Health (RSPH), Emory University | Atlanta, GA

MSPH, Biostatistics — May 2021
Rollins School of Public Health (RSPH), Emory University | Atlanta, GA
Thesis: *"TIGAR-V2 with nonparametric Bayesian eQTL weights estimated from GTEx V8 & Leveraging multiple reference panels to improve TWAS power by ensemble machine learning"*

BS, Biology–Cellular/Physiology Track — May 2019
BA, Mathematics — May 2019
University of Louisville (UofL) | Louisville, KY
Minor: Global Public Health | *Cum Laude*

RESEARCH OUTCOMES

Parrish, R. L., Buchman, A. S., Tasaki, S., Wang, Y., Avey, D., Xu, J., De Jager, P. L., Bennett, D. A., Epstein, M. P., Yang, J. SR-TWAS: Leveraging Multiple Reference Panels to Improve Transcriptome-Wide Association Study Power by Ensemble Machine Learning. (August, 2024). *Nature Communications*, **15** (6646). `https://doi.org/10.1038/s41467-024-50983-w`

Robinson K., **Parrish R.**, Adeyemo W.L., Beaty T.H., Butali A., Buxó C.J., Gowans L.J.J., Hecht J.T., Moreno Uribe L., Murray J.C., Shaw G.M., Weinberg S.M., Brand H., Marazita M.L., Cutler D.J., Epstein M.P., Yang J., Leslie E.J. Genome-wide study of gene-by-sex interactions identifies risks for cleft palate. (November, 2024). *Human Genetics*, **143** (11). `https://doi.org/10.1007/s00439-024-02704-y`

Hu T., **Parrish R.L.**, Dai Q., Buchman A.S., Tasaki S., Bennett D.A., Seyfried N.T., Epstein M.P., Yang J. Omnibus proteome-wide association study identifies 43 risk genes for Alzheimer disease dementia. (September 2024). *American Journal of Human Genetics*, **111** (9). `https://doi.org/10.1016/j.ajhg.2024.07.001`

Parrish, R., Gibson, G., Epstein, M. P., Yang, J. TIGAR-V2: Efficient TWAS Tool with Nonparametric Bayesian eQTL Weights of 49 Tissue Types from GTEx V8. (November, 2021). *HGG Advances*, **3** (1). `https://doi.org/10.1016/j.xhgg.2021.100068`

Yang, J., **Parrish, R.**, Gibson, G., Epstein, M. P. (October, 2021). TIGAR-V2: Efficient TWAS Tool with Nonparametric Bayesian eQTL Weights of 49 Tissue Types from GTEx V8 [Poster]. ASHG Virtual Meeting 2021.

Tang, S., **Parrish, R.**, Buchman, A. S., De Jager, P. L., Bennett, D. A., Epstein, M. P., Yang, J. (October, 2020). Powerful variance-component method for TWAS identifies novel and known risk genes for Alzheimer's dementia [Poster Presentation]. ASHG Virtual Meeting 2020.

Staples, A. K., King, R. A., Doughty, M. A., **Parrish, M. L.**, Klann, J. K., Rinehart, C. A., ... Hatfull, G. F. (2017). Mycobacterium phage TinaFeyge, complete genome [Direct Submission]. GenBank: KY471266.1.

PRESENTATIONS

SR-TWAS: Leveraging multiple reference panels to improve TWAS power by ensemble machine learning [Platform Presentation] — October 2021
ASHG 2021 Virtual Meeting | Website

Correlation of geographical distribution of mycobacteriophages with genomic clusters and genome distance [Poster] — May 2013
12th Annual UT-ORNL-KBRIN Bioinformatics Summit | Buchanan, TN | Abstract

Mycobacteriophage sub-cluster distribution and correlation to hydrologic regions [Poster] November 2012
BISC and HPCC Research Symposium, WKU | Bowling Green, KY

Research Experience

Stacked Regression-Transcriptome-Wide Association Study (SR-TWAS) January 2021–Present
Dr. Jingjing Yang | *Emory University School of Medicine* | Atlanta, GA

- wrote SR-TWAS code which can optimize linear combinations of multiple user-input trained models
- applying SR-TWAS tool to GTEx V8, ROS/MAP data
- conducting simulation studies under different proportion of causal SNPs and expression heritability

Transcriptome-Integrated Genetic Association Resource (TIGAR) February 2020–Present
Dr. Jingjing Yang | *Emory University School of Medicine* | Atlanta, GA

- preparing/analyzing large multi-omics data in HPC cluster environment
- applying TIGAR tool to GTEx V8 data
- optimizing code to reduce memory consumption and execution time in all TIGAR Python scripts
  - gene expression model training time for TIGAR example data on 1 core reduced from 17+ minutes to <4 for all models

Modeling qPCR Curves August 2018–May 2019
Dr. Gary Cobbs | *UofL* | Louisville, KY

- modified and developed R code to model qPCR curves in order to predict initial absolute concentration of template DNA from raw fluorescence values
- investigated kinetics of primer/probe annealing, processivity in literature
- generated visualizations from model output using ggplot2

Mycobacteriophage Sub-Cluster Distribution & Correlations August 2012–May 2013
Dr. Claire Rinehart | *Western Kentucky University (WKU)* | Bowling Green, KY

- used Mathematica to analyze geographic distribution of phages and to generate visualizations
- assessed distribution of phage clusters and examined correlation between geographic distance and genetic distance within each cluster

Mycobacteriophage Isolation & Genome Annotation August 2011–May 2012
Dr. Rodney King & Dr. Claire Rinehart | *SEA-PHAGES & WKU* | Bowling Green, KY

Technical Skills

- R, Python, Bash, AWK, SAS 9.4
- Linux, HPC Cluster, Sun Grid Engine, Slurm, parallel computing in R/Python, Docker, AWS
- MS Office, Zotero reference manager, LaTeX, BibTeX

Employment

Research Specialist June 2021–August 2022
Research Assistant February 2020–June 2021
YangLab, Center for Computational and Quantitative Genetics,
Emory University School of Medicine | Atlanta, GA

Small Group Tutor for Biostatistics & Microbiology October 2016–April 2018
REACH Learning Resource Center, UofL | Louisville, KY

Honors

- Women in Natural Science (WinS) Fellowship 2022
- ASHG 2021 Charles J. Epstein Trainee Awards Semifinalist 2021
- NCWIT Aspirations in Computing Kentucky Affiliate 2013
- Carol Martin Gatton Academy of Mathematics and Science in Kentucky 2011–2013