

# Mo Huang, Ph.D.

Senior Scientist, Biostatistics  
Merck

Email: mohuangx@gmail.com

Website: mohuangx.github.io

Last Updated: December 2021

## Education

- **Ph.D. Statistics**, The Wharton School, University of Pennsylvania, 2020  
Advisor: Nancy R. Zhang
- **B.A. Mathematics**, Washington University in St. Louis, 2015

## Experience

- **Senior Scientist, Biostatistics**  
Merck  
*2020 -- Present*
- **PhD Candidate**  
Department of Statistics, The Wharton School, University of Pennsylvania  
*2015 -- 2020*
- **Biostatistics Summer Intern**  
Genentech  
*Summer 2018*
- **Undergraduate Researcher/Amgen Scholar**  
McDonnell Genome Institute at Washington University  
*2013 -- 2015*
- **Summer Intern**  
National Institutes of Health  
*Summers 2012 -- 2013*

## Honors and Awards

- Donald S. Murray Prize for Excellence in Teaching, 2019
- NSF Graduate Fellowship, 2016 -- 2019
- Judith & William Bollinger Fellowship, 2018
- Florence Moog Fellowship in Biological Sciences, 2011 -- 2015

## Publications

- Reeder J., **Huang, M.**, Kamingker, J.S., Paulson, J.N. (2021). *MicrobiomeExplorer*: an R package for the analysis and visualization of microbial communities. *Bioinformatics*, 37 (9), 1317-1318.
- **Huang, M.** (2020). A Statistical Framework for Denoising Single-cell RNA Sequencing Data

(Dissertation). *PQDT-UK & Ireland*.

- **Huang, M.**, Zhang, Z., Zhang, N.R. (2020). Dimension reduction and denoising of single-cell RNA sequencing data in the presence of observed confounding variables. *bioRxiv*.
- Wang, J., Agarwal, D., **Huang, M.**, Hu, G., Zhou, Z., Ye, C., Zhang, N.R. (2019). Data Denoising with transfer learning in single-cell transcriptomics. *Nature Methods*, 16(9), 875-878.
- **Huang, M.**, Wang, J., Torre, E., Dueck, H., Shaffer, S., Bonasio, R., ... Zhang, N. R. (2018). SAVER: Gene expression recovery for single-cell RNA sequencing. *Nature Methods*, 15(7), 539–542.
- Wang, J., **Huang, M.**, Torre, E., Dueck, H., Shaffer, S., Murray, J., ... Zhang, N. R. (2018). Gene Expression Distribution Deconvolution in Single Cell RNA Sequencing. *Proceedings of the National Academy of Sciences of the United States of America*, 115(28), E6437-E6446.
- Jayasinghe, R. G., Cao, S., Gao, Q., Wendl, M. C., Vo, N. S., Reynolds, S. M., ... Ding, L. (2018). Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, 23(1), 270–281.e3.
- Jin, T., **Huang, M.**, Jiang, J., Smith, P., & Xiao, T. S. (2018). Crystal structure of human NLRP12 PYD domain and implication in homotypic interaction. *PLOS ONE*, 13(1), e0190547.
- Wyczalkowski, M. A., Wylie, K. M., Cao, S., Mclellan, M. D., Flynn, J., **Huang, M.**, ... Ding, L. (2017). BreakPoint Surveyor: A pipeline for structural variant visualization. *Bioinformatics*, 33(19), 3121–3122.
- Jin, T., Chuenchor, W., Jiang, J., Cheng, J., Li, Y., Fang, K., ... Xiao, T. S. (2017). Design of an expression system to enhance MBP-mediated crystallization. *Scientific Reports*, 7(January), 40991.
- Jin, T., **Huang, M.**, Smith, P., Jiang, J., & Xiao, T. S. (2013). Structure of the caspase-recruitment domain from a zebrafish guanylate-binding protein. *Acta Crystallographica Section F Structural Biology and Crystallization Communications*, 69(8), 855–860.
- Jin, T., **Huang, M.**, Smith, P., Jiang, J., & Xiao, T. S. (2013). The structure of the CARD8 caspase-recruitment domain suggests its association with the FIIND domain and procaspases through adjacent surfaces. *Acta Crystallographica Section F Structural Biology and Crystallization Communications*, 69(5), 482–487.

## **Presentations**

- Joint Statistical Meetings, July 2019
- Joint Statistical Meetings, July 2018
- American Society of Human Genetics Meeting, October 2017

## **Programming Languages**

- R (expert)
- Python, Keras, PyTorch (proficient)
- Bash (proficient)
- SQL (competent)