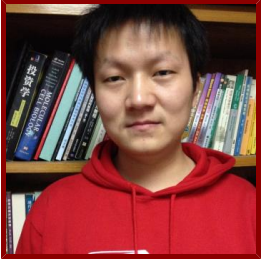


# Stanford

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## Huaying Fang

Postdoctoral Research Fellow, Genetics

### Bio

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#### PROFESSIONAL EDUCATION

- Doctor of Philosophy, Peking University (2016)
- Bachelor of Science, Wuhan University (2011)

#### STANFORD ADVISORS

- Hua Tang, Postdoctoral Faculty Sponsor

#### LINKS

- Github: <https://github.com/huayingfang>
- Facebook: <https://www.facebook.com/huaying.fang.37>
- Twitter: [https://twitter.com/Huaying\\_Fang](https://twitter.com/Huaying_Fang)

### Research & Scholarship

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#### CURRENT RESEARCH AND SCHOLARLY INTERESTS

My research aims to develop efficient computational approaches for constructing meaningful networks using multi-omics data. The rapid development of sequencing technologies produces a lot of multi-omics data. We could construct much more stable and accurate biological networks from these multi-omics data than only one-omic data. Then we can make further analysis on the association between networks and diseases from the system views.

#### LAB AFFILIATIONS

- Hua Tang, Tang Lab (8/4/2016 - - 8/3/2019)

### Publications

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#### PUBLICATIONS

- **Association of APOL1 Risk Alleles with Cardiovascular Disease in African Americans in the Million Veteran Program.** *Circulation*  
Bick, A. G., Akwo, E., Robinson-Cohen, C., Lee, K., Lynch, J., Assimes, T. L., DuVall, S., Edwards, T., Fang, H., Freiberg, S. M., Giri, A., Huffman, J. E., Huang, et al  
2019
- **Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies.** *American journal of human genetics*  
Fang, H., Hui, Q., Lynch, J., Honerlaw, J., Assimes, T. L., Huang, J., Vujkovic, M., Damrauer, S. M., Pyarajan, S., Gaziano, J. M., DuVall, S. L., O'Donnell, C. J., Cho, et al  
2019

- **Case-cohort design for accelerated hazards model** *Statistics and Its Interface*  
Ding, J., Chen, X., Fang, H., Liu, Y.  
2018; 11: 657-668
- **VCNet: Vector based gene Co-expression Network construction and its application to RNA-seq data.** *Bioinformatics*  
Wang, Z., Fang, H., Tang, N. L., Deng, M.  
2017
- **gCoda: Conditional Dependence Network Inference for Compositional Data.** *Journal of computational biology : a journal of computational molecular cell biology*  
Fang, H., Huang, C., Zhao, H., Deng, M.  
2017
- **Graphical model selection with latent variables** *Electronic Journal of Statistics*  
Wu, C., Zhao, H., Fang, H., Deng, M.  
2017; 11 (2): 3485-3521
- **Network clustering analysis using mixture exponential-family random graph models and its application in genetic interaction data.** *IEEE/ACM transactions on computational biology and bioinformatics*  
Wang, Y., Zhao, H., Deng, M., Fang, H., Yang, D.  
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- **Leveraging Multi-ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations.** *American journal of human genetics*  
Coram, M. A., Fang, H., Candille, S. I., Assimes, T. L., Tang, H.  
2017; 101 (2): 218–26
- **Localized high abundance of Marine group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation** *Environmental Microbiology*  
Xie, W., Luo, H., Murugapiran, S. K., Dodsworth, J. A., Chen, S., Sun, Y., Hedlund, B. P., Wang, P., Fang, H., Deng, M., Zhang, C.  
2017
- **CCLasso: correlation inference for compositional data through Lasso** *BIOINFORMATICS*  
Fang, H., Huang, C., Zhao, H., Deng, M.  
2015; 31 (19): 3172-3180
- **RNA Editome in Rhesus Macaque Shaped by Purifying Selection** *PLOS GENETICS*  
Chen, J., Peng, Z., Zhang, R., Yang, X., Tan, B. C., Fang, H., Liu, C., Shi, M., Ye, Z., Zhang, Y. E., Deng, M., Zhang, X., Li, et al  
2014; 10 (4)