Xuran Wang (Ph.D.)

Carnegie Mellon University

Department of Statistics and Data Science

Baker Hall 129D, Pittsburgh, PA 15213

xuranw@andrew.cmu.edu

(215)-512-9968

https://xuranw.github.io/personalwebsite

EDUCATION

- **University of Pennsylvania** — Philadelphia, PA
  Ph.D. in Applied Mathematics and Computational Science — *05/2019*
  - **Thesis topic**: Mendelian Randomization and Single Cell Deconvolution, Two Problems in Statistical Genetics

- **University of Science and Technology of China** — Hefei, China
  B.S. of Statistics — *06/2014*

ACADEMIC APPOINTMENT

- **Carnegie Mellon University** — Pittsburgh, PA
  Postdoctoral fellow — *07/2019 – Present*

RESEARCH EXPERIENCE

- **Cell type specific eQTL combining bulk and single cell RNA-seq data**
  Advisor: Kathryn Roeder, Yuting Wei — *02/2021 - Present*

- **Cell Specific Networks Analysis on Brain Single-cell Data**
  Advisors: Kathryn Roeder, Dave Choi — *07/2019 - 02/2021*

- **Bulk Tissue Cell Type Deconvolution with Multi-subject Single-cell Reference**
  Advisors: Nancy R. Zhang, Mingyao Li — *03/2017 - 07/2018*

- **Sensitivity Analysis and Power for Instrumental Variable Studies**
  Advisors: Dylan S. Small, Nancy R. Zhang — *10/2016 - 12/2017*

- **Allele Specific Information in Mendelian Randomization**
  Advisors: Dylan S. Small, Nancy R. Zhang, Mingyao Li — *09/2015 - 2017*

PUBLICATIONS

- **Wang, X.**, Jiang, Y., Zhang, N. R., & Small, D. S. (2018). Sensitivity analysis and power for instrumental variable studies. *Biometrics.* doi:10.1111/biom.12873.

- **Wang, X.**, Park, J., Susztak, K., Zhang, N., & Li, M. (2019). Bulk Tissue Cell Type Deconvolution with Multi-Subject Single-Cell Expression Reference. *Nature Communications.* doi:10.1038/s41467-018-08023-x.

- Fan, J.**Wang, X**, Xiao, R., Li, M. (2021). Detecting cell-type-specific allelic expression imbalance by integrative analysis of bulk and single-cell RNA sequencing data. *PLOS Genetics.* doi:https://doi.org/10.1101/2020.08.26.267815

- Nguyen, A.T., Wang, K., Hu, G., **Wang, X.**, Miao, Z., Azevedo, J.A., Suh, E., Van Deerlin, V.M., Choi, D., Roeder, K. and Li, M.(2020). APOE and TREM2 regulate amyloid-responsive microglia in Alzheimer's disease. *Acta Neuropathologica.* doi:10.1007/s00401-020-02200-3.

- **Wang, X.**, Choi, D., Roeder, K.(2021). Constructing local cell specific networks from single cell data. *Proceedings of the National Academy of Sciences.* https://doi.org/10.1073/pnas.2113178118

- Barry, T., **Wang, X.**, Morris, J.A., Roeder, K., Katsevich, E.(2021). SCEPTRE improves calibration and sensitivity in single-cell CRISPR screen analysis, *Genome Biology.* doi: https://doi.org/10.1186/s13059-021-02545-2

- **Wang, X.**, Peng, M., Hoffman, G., Roussos, P. , Wei, Y., Roeder, K. (2021+). Cell type specific eQTL combing bulk and single cell RNA-seq data, (In progress)

- Fan, J., Lyu, Y., Zhang, Q., **Wang, X.**, Li, M., Xiao, R. (2021+). MuSiC2: cell type deconvolution for multi-condition bulk RNA-seq data (In progress)

- Shen, M., **Wang, X.**, Devlin, B,, Roeder, K. (2021+), Integrative functional genomic analyses and Schizophrenia Risk genes, (In progress)

SOFTWARE

- **locCSN**: Matlab and Python package: Local Cell Specific Networks   https://github.com/xuranw/locCSN
- **MuSiC**: R package: Multi-subject Single-cell deconvolution   https://github.com/xuranw/MuSiC
- **AllelicMR**: R package: Allele specific Mendelian Randomization   https://github.com/xuranw/AllelicMR

PRESENTATIONS

INVITED SEMINARS AND CONFERENCE PRESENTATIONS

- **University of Pennsylvania**: The Penn Institute for Computational Science (PICS)   2021
- **University of Chicago**: Human Genetics Seminar   2021
- **Carnegie Mellon University**: Networkshop, Department of Statistics and Data Science   2020
- **University of Science and Technology of China**: Mathematical Science Department   2019

CONTRIBUTED CONFERENCE PRESENTATIONS AND POSTERS

- **ASHG (10/2017)**: Allele Specific Information in Mendelian Randomization (Poster)
- **JSM (08/2018)**: Bulk Tissue Deconvolution with Multi-subject Single-cell Expression Reference (Poster)
- **ASHG (10/2018)**: Bulk Tissue Deconvolution with Multi-subject Single-cell Expression Reference (Poster)
- **JSM (08/2020)**: Constructing local cell specific networks from single cell data (Poster)
- **ASHG (10/2020)**: Constructing local cell specific networks from single cell data (Poster)

PROGRAMMING SKILLS

- **Languages**: R, Python, Matlab, LaTeX

ACADEMIC SERVICES

- **Referee**: Nature Communitications; PLOS Computational Biology; Bioinformatics; Statistics in Biosciences.

- **Topic Editor**: Frontiers.

TEACHING EXPERIENCES

- **Statistical Genomics and High Dimensional Inference**   Carnegie Mellon University
  Co-instructor, Department of Statistics and Data Science   *Fall 2021*

- **Statistical Methods for Gene Expression Analysis**   University of North Carolina at Chapel Hill
  Guest Lecturer, Department of Human Genetics   *Fall 2020*

- **Advanced Calculus II**   University of Pennsylvania
  Recitation Instructor, Mathematics Department   *Fall 2015*

- **Linear Algebra II**   University of Pennsylvania
  Teaching Assistant, Mathematics Department   *Spring 2016*

- **Introductory of Statistics**   University of Pennsylvania
  Recitation Instructor, Statistics Department   *Spring 2017*

MENTORSHIP

- **Academic Advisor**: Maya Shen, Doctoral Student at CMU Statistics and Data Science Department   2021 - Present

LEARDERSHIP

- **SASgov**: Finance committee member of the Penn graduate student government of the school of arts & sciences   *2018-2019*