

Kangcheng Hou

kangchenghou@gmail.com kangchenghou.github.io (424)407-5507

RESEARCH INTERESTS

Leveraging population-scale data and developing data-driven statistical methods around two major topics:

- (1) Predicting disease combining both genetic and non-genetic factors across individuals of diverse contexts, e.g., implementing calibrated and accurate risk prediction for all individuals across genetic and socio-environmental backgrounds in future healthcare systems.
- (2) Prioritizing disease-critical variants / genes and understanding their mechanisms impacting complex diseases, e.g., leveraging genetic and functional genomic data to determine the pathogenicity of genetic variants and their cascading effects to downstream genes, cell types and functional pathways.

EDUCATION

PhD in Bioinformatics

2019-2024 (expected)

UCLA, Los Angeles, CA

Bachelor in Computer Science

2015-2019

Zhejiang University, Hangzhou, China

SELECTED PUBLICATIONS

* denotes equal contribution.

- [1] Kangcheng Hou, Ziqi Xu, Yi Ding, Arbel Harpak, and Bogdan Pasaniuc. **Calibrated prediction intervals for polygenic scores across diverse contexts.** *medRxiv*, 2023.
- [2] Kangcheng Hou, Yi Ding, Ziqi Xu, Yue Wu, Arjun Bhattacharya, Rachel Mester, Gillian M Belbin, Steve Buyske, David V Conti, Burcu F Darst, Myriam Fornage, Chris Gignoux, Xiuqing Guo, Christopher Haiman, Eimear E Kenny, Michelle Kim, Charles Kooperberg, Leslie Lange, Ani Manichaikul, Kari E North, Ulrike Peters, Laura J Rasmussen-Torvik, Stephen S Rich, Jerome I Rotter, Heather E Wheeler, Genevieve L Wojcik, Ying Zhou, Sriram Sankararaman, and Bogdan Pasaniuc. **Causal effects on complex traits are similar for common variants across segments of different continental ancestries within admixed individuals.** *Nature Genetics*, 2023.
- [3] Yi Ding, Kangcheng Hou, Ziqi Xu, Aditya Pimplaskar, Ella Petter, Kristin Boulier, Florian Privé, Bjarni J Vilhjálmsson, Loes M Olde Loohuis, and Bogdan Pasaniuc. **Polygenic scoring accuracy varies across the genetic ancestry continuum.** *Nature*, 2023.
- [4] Martin JinYE Zhang*, Kangcheng Hou*, Kushal K Dey, Saori Sakaue, Karthik A Jagadeesh, Kathryn Weinand, Aris Taychameekitchai, Poorvi Rao, Angela Oliveira Pisco, James Zou, Bruce Wang, Michael Gandal, Soumya Raychaudhuri, Bogdan Pasaniuc, and Alkes L Price. **Polygenic enrichment distinguishes disease associations of individual cells in single-cell RNA-seq data.** *Nature Genetics*, 2022.
- [5] Yi Ding*, Kangcheng Hou*, Kathryn S Burch, Sandra Lapinska, Florian Privé, Bjarni Vilhjálmsson, Sriram Sankararaman, and Bogdan Pasaniuc. **Large uncertainty in individual polygenic risk score estimation impacts PRS-based risk stratification.** *Nature Genetics*, 2022.
- [6] Kathryn S Burch*, Kangcheng Hou*, Yi Ding, Yifei Wang, Steven Gazal, Huwenbo Shi, and Bogdan Pasaniuc. **Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes.** *The American Journal of Human Genetics*, 2022.
- [7] Kangcheng Hou, Arjun Bhattacharya, Rachel Mester, Kathryn S Burch, and Bogdan Pasaniuc. **On powerful GWAS in admixed populations.** *Nature Genetics*, 2021.
- [8] Kangcheng Hou*, Kathryn S Burch*, Arunabha Majumdar, Huwenbo Shi, Nicholas Mancuso, Yue Wu, Sriram Sankararaman, and Bogdan Pasaniuc. **Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture.** *Nature Genetics*, 2019.

OTHER PUBLICATIONS

- [9] Kangcheng Hou, Stephanie Gogarten, Joohyun Kim, Xing Hua, Julie-Alexia Dias, Quan Sun, Ying Wang, Taotao Tan, Elizabeth G Atkinson, Alicia Martin, Jonathan Shortt, Jibril Hirbo, Yun Li, Bogdan Pasaniuc, and Haoyu Zhang. **Admix-kit: an integrated toolkit and pipeline for genetic analyses of admixed populations.** *Bioinformatics*, 2024.
- [10] Toni Boltz, Tommer Schwarz, Merel Bot, Kangcheng Hou, Christa Caggiano, Sandra Lapinska, Chenda Duan, Marco P Boks, Rene S Kahn, Noah Zaitlen, Bogdan Pasaniuc, and Roel Ophoff. **Cell-type deconvolution of bulk-blood RNA-seq reveals biological insights into neuropsychiatric disorders.** *The American Journal of Human Genetics*, 2024.

- [11] Rachel Mester, Kangcheng Hou, Yi Ding, Gillian Meeks, Kathryn S Burch, Arjun Bhattacharya, Brenna M Henn, and Bogdan Pasaniuc. **Impact of cross-ancestry genetic architecture on GWASs in admixed populations.** *The American Journal of Human Genetics*, 2023.
- [12] Ashok Patowary, Pan Zhang, Connor Jops, Celine K Vuong, Xinzhu Ge, Kangcheng Hou, Minsoo Kim, Naihua Gong, Michael Margolis, Daniel Vo, Xusheng Wang, Chunyu Liu, Bogdan Pasaniuc, Jingyi Jessica Li, Michael J Gandal, and Luis de la Torre-Ubieta. **Developmental isoform diversity in the human neocortex informs neuropsychiatric risk mechanisms.** *bioRxiv*, 2023.
- [13] Ella Petter, Yi Ding, Kangcheng Hou, Arjun Bhattacharya, Alexander Gusev, Noah Zaitlen, and Bogdan Pasaniuc. **Genotype error due to low-coverage sequencing induces uncertainty in polygenic scoring.** *The American Journal of Human Genetics*, 2023.
- [14] Hanbin Lee, Moo-Hyuk Lee, Kangcheng Hou, Bogdan Pasaniuc, and Buhm Han. **Single locus theory of admixture is insufficient for the study of complex traits in admixed populations.** *medRxiv*, 2023.
- [15] Xihao Li, Godwin Yung, Hufeng Zhou, Ryan Sun, Zilin Li, Kangcheng Hou, Martin JinYE Zhang, Yaowu Liu, Theodore Arapoglou, Chen Wang, Iuliana Ionita-Laza, and Xihong Lin. **A multi-dimensional integrative scoring framework for predicting functional variants in the human genome.** *The American Journal of Human Genetics*, 2022.
- [16] Tommer Schwarz, Toni Boltz, Kangcheng Hou, Merel Bot, Chenda Duan, Loes Olde Loohuis, Marco P Boks, René S Kahn, Roel A Ophoff, and Bogdan Pasaniuc. **Powerful eQTL mapping through low-coverage RNA sequencing.** *Human Genetics and Genomics Advances*, 2022.
- [17] Matthew G Heffel, Jingtian Zhou, Yi Zhang, Dong-Sung Lee, Kangcheng Hou, Oier Pastor Alonso, Kevin Abuhanna, Anthony D Schmitt, Terence Li, Maximilian Haeussler, Brittney Wick, Martin JinYE Zhang, Fangming Xie, Ryan S Ziffra, Eran A Mukamel, Eleazar Eskin, Bogdan Pasaniuc, Joseph R Ecker, Jesse Dixon, Tomasz J Nowakowski, Mercedes F Paredes, and Chongyuan Luo. **Epigenomic and chromosomal architectural reconfiguration in developing human frontal cortex and hippocampus.** *bioRxiv*, 2022.
- [18] Gita A Pathak, Kritika Singh, Tyne W Miller-Fleming, Frank R Wendt, Nava Ehsan, Kangcheng Hou, Ruth Johnson, Zeyun Lu, Shyamalika Gopalan, Loic Yengo, Pejman Mohammadi, Bogdan Pasaniuc, Renato Polimanti, Lea K Davis, and Nicholas Mancuso. **Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization.** *Nature communications*, 2021.
- [19] Ruth Johnson, Kathryn S Burch, Kangcheng Hou, Mario Paciuc, Bogdan Pasaniuc, and Sriram Sankararaman. **Estimation of regional polygenicity from GWAS provides insights into the genetic architecture of complex traits.** *PLoS computational biology*, 2021.
- [20] Ali Pazokitoroudi, Yue Wu, Kathryn S Burch, Kangcheng Hou, Aaron Zhou, Bogdan Pasaniuc, and Sriram Sankararaman. **Efficient variance components analysis across millions of genomes.** *Nature communications*, 2020.
- [21] Igor Mandric, Tommer Schwarz, Arunabha Majumdar, Kangcheng Hou, Leah Briscoe, Richard Perez, Meena Subramaniam, Christoph Hafemeister, Rahul Satija, Chun Jimmie Ye, Bogdan Pasaniuc, and Eran Halperin. **Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis.** *Nature communications*, 2020.
- [22] Simon S Du, Kangcheng Hou, Barnabás Póczos, Ruslan Salakhutdinov, Ruosong Wang, and Keyulu Xu. **Graph Neural Tangent Kernel: Fusing Graph Neural Networks with Graph Kernels.** *Advances in Neural Information Processing Systems*, 2019.
- [23] Xiaoguang Han, Kangcheng Hou, Dong Du, Yuda Qiu, Shuguang Cui, Kun Zhou, and Yizhou Yu. **Caricatureshop: Personalized and photorealistic caricature sketching.** *IEEE transactions on visualization and computer graphics*, 2018.

TALKS

- [1] **Calibrated prediction intervals for polygenic scores across diverse contexts.**
Talk at Annual UCLA QCBio Retreat, 2023
- [2] **Admix-kit: an integrated toolkit and pipeline for genetic analyses of admixed populations.**
Invited talk at PRIMED Consortium, 2023
- [3] **Causal effects on complex traits are similar across segments of different continental ancestries within admixed individuals.**
Platform talk at ASHG, 2022