

Kangcheng Hou

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EDUCATION

Postdoc	2024-Present
Broad Institute, Cambridge, MA	
Postdoc	2024-Present
Harvard School of Public Health, Boston, MA	
PhD in Bioinformatics	2019-2024
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, Ravi Mandla, Zhuozheng Shi, Kristin Boulter, Arbel Harpak, and Bogdan Pasaniuc. **Calibrated prediction intervals for polygenic scores across diverse contexts.** *Nature Genetics*, 2024.
- [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 Boulter, 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] Ashok Patowary, Pan Zhang, Connor Jops, Celine K Vuong, Xinzhou 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.** *Science*, 2024.
- [10] 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.
- [11] 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.

- [12] 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.
- [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