THE FACULTY OF MEDICINE
Harvard University

Curriculum Vitae

Date Prepared:	June 16, 2019
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Place of Birth:	Nanjing, China

Education

06/2003	B.S. *Highest Honors*	Physics	Nanjing University
05/2005	M.A.	Physics	Johns Hopkins University
03/2012	Ph.D.	Biomedical Engineering (Advisor: Dr. Joel Bader)	Johns Hopkins School of Medicine

Postdoctoral Training

03/12 - 01/17	Research Fellow	Analytic and Translational Genetics Unit (Advisor: Dr. Mark Daly)	Massachusetts General Hospital

Faculty Academic Appointments

05/17 - present	Instructor in Medicine	Department of Medicine	Harvard Medical School

Appointments at Hospitals/Affiliated Institutions

Current

01/17 - present	Research Staff	Analytic and Translational Genetics Unit	Massachusetts General Hospital

07/17 - present	Associated Scientist	Stanley Center for Psychiatric Research	Broad Institute of MIT and Harvard

Other Professional Positions

Past

2007	Intern	Systems Toxicology, Merck & Co., Inc.
2011	Intern	Healthcare Informatics, IBM Research

Major Administrative Leadership Positions

Local

2017 - present	Director, Stanley Center Asia Initiatives	Broad Institute of MIT and Harvard

Committee Service

Local

2017-	Steering Committee, Medical and Population Genetics	Broad Institute of MIT and Harvard

International

2018	Program Committee	1st Pan Asia Symposium on the Genetics of Brain Disorders (Shanghai, China)
2021	Program Committee	2nd Pan Asia Symposium on the Genetics of Brain Disorders (Singapore)

Professional Societies

2010 - present	American Society of Human Genetics (ASHG)	Member
	2017, 2018	Abstract Reviewer, ASHG Annual Meeting
2017 - present	International Society of Psychiatric Genetics	Member

Grant Review Activities

2017	Fellows Award	The MQ Foundation
	2017	Ad hoc Reviewer

Editorial Activities

Ad hoc Reviewer

Nature Genetics

PLoS Computational Biology

PLoS Genetics

PLoS ONE

PMC Genetics

JAMA Psychiatry

Translational Psychiatry

Biological Psychiatry

The Pharmacogenomics Journal

Bioinformatics

Journal of Medical Genetics

Human Molecular Genetics

Nucleic Acid Research

Clinical Epigenetics

Inflammatory Bowel Diseases

The British Journal of Psychiatry

Neuropsychopharmacology

Cancer Informatics

Cancer Medicine

Journal of Cardiovascular Disease Research

Genetics

Hereditas

Pacific Symposium on Biocomputing 2013

Honors and Prizes

2003	3rd place, National Challenge Cup award	Ministry of Education, China	Research
2006	Travel award	DIMACS (Center for Discrete Mathematics and Theoretical Computer Science) Workshop	Research
2006	Travel award	RECOMB (Research in Computational Molecular Biology) Satellite Conference on Systems Biology	Research
2012	Award for Outstanding Self-financed Students Abroad	China Scholarship Council	Research
2013	Bristol-Myers Squibb Scholar-in-Training Award	The American Association for Cancer Research	Research

2013	Magna Cum Laude	International Society for Magnetic Resonance in Medicine	Research
2015	Charles J. Epstein Trainee Award for Excellence in Human Genetics Research – Semifinalist	American Society of Human Genetics	Research
2017	Harvard Chinese Life Sciences Yongjin Distinguished Research Award	Harvard Medical School Chinese Scientists and Scholars Association	Research

Report of Funded and Unfunded Projects

Funding Information

Past

Current

2017 - 2021 Genetics and Gene Regulation in the Inflammatory Bowel Diseases
NIH K01 DK114379
PI (total direct costs - $579,413)
This grant proposes to investigate the regulatory functions of non-coding causal variants for the inflammatory bowel diseases and how they contribute to the disease etiology.

2018 - 2020 Mitochondrial-Nuclear Genetic Interactions in Spontaneous HCV Clearance
NIH R21 AI139012
Co-Investigator (PI: Todd Hulgan)
The goal of this project is to investigate the connection between mitochondrial genetic factors and the spontaneous HCV clearance

2020 - 2021 Contribution of major histocompatibility complex locus to schizophrenia in the East Asian populations
NARSAD Young Investigator Grant, Brain and Behaviors Research Foundation
PI (total direct costs - $100,000)
The goal of this project is to investigate the contribution of major histocompatibility complex to schizophrenia in the East Asian populations.

2020 Finding rare protective variants for the inflammatory bowel diseases using polygenic signatures in large population controls
Center for the study of IBD (MGH) -- Pilot/Feasibility Study
PI (total direct costs - $50,000)
The goal of this project is to develop and implement a novel test using population controls and known genetic risk profiles to identify rare protective variants for IBD.

2018 - Philanthropic Gift
Zhengxu & Ying He Foundation
Recipient (total direct + indirect - $150,000)
This gift supported my psychiatric genetics studies in China and East Asia.

Projects submitted for Funding

2020 Genetic correlation across ancestrally diverse populations for human complex disorders and traits
Eleanor and Miles Shore Faculty Development Award

PI (total direct costs - $30,000)
This proposed project will design a cross-ancestry genetic correlation test and use it to evaluate the landscape of disease-genetic mechanism shared across diverse populations. Review date: May 2020

2020 Novel fine-mapping methods to improve causal variant detection in genetic loci associated with serious mental illness
NIMH R01
MPI with Hilary Finucane (total direct costs - $2,400,000)
This proposed project will develop and apply novel statistical methods that will greatly increase the reliability and resolution with which we can pinpoint putatively causal variants for psychiatric disease, furthering our understanding of the biological basis of these disorders. Review date: July 2020

Training Grants and Mentored Trainee Grants

2016 - 2017 A novel trans-ethnicity fine-mapping method for complex traits in human and animal
China Scholarship Council
Co-mentor of Ruize Liu
The major goal is to design a novel fine-mapping algorithm that leverages the genetic diversity to improve the resolution to isolate the causal allele for the complex diseases and traits.

2019 - 2020 A study of the genetic association between schizophrenia and immune response of gluten or casein
China Scholarship Council
Mentor of Baijia Li
The goal of this study is to elucidate the connection between genetic factors, immune response to gluten and casein and schizophrenia

2020 - 2021 The genetics of complex disorders
China Scholarship Council
Mentor of Dadong Deng
Dadong's research activities will focus on developing novel statistical genetics methods to elucidate the genetics of human complex disorders, including inflammatory and psychiatric disorders

Report of Local Teaching and Training

Formal Teaching of Residents, Clinical Fellows and Research Fellows (post-docs)

2016	Statistical Genetics workshop / BroadE series	Broad Institute
	Trainees in the Harvard-MIT community	One-hour lecture
2017 - 2019	Global Initiative for Neuropsychiatric Genetics Education in Research	Harvard T.H. Chan School of Public Health
	Fellows in the program	2017, four one-hour lectures 2018, two one-hour lectures 2019, two one-hour course videos
2019	A practical introduction to statistical genetics	Massachusetts General Hospital
	Residents, Clinical Fellows, and Research Fellows	Two lectures, each 1.5 hour

Research Supervisory and Training Responsibilities

2016 - 2017	Supervision of a visiting graduate student	Analytic and Translational Genetics Unit, MGH 1:1 supervision two hours per week
2017 - present	Advisor to a research fellow	Brigham and Women's Hospital 1:1 supervision one hour per week
2018 - present	Supervision of research fellows	Stanley Center for Psychiatric Research at the Broad Institute 1:1 supervision 4.5 hours per week
2018 - present	Supervision of research fellows	Massachusetts General Hospital 1:1 supervision 2.5 hours per week
2019 - present	Supervision of a visiting graduate student	Xi'an JiaoTong University 1:1 supervision one hour per week

Mentored Trainees and Faculty

2017-present	Wenyu Song, Ph.D. / Research Fellow, Brigham and Women's Hospital Career stage: fellow. Mentoring role: research advisor. Accomplishments: manuscript and grants in review.
2018-present	Max Lam, Ph.D. / Research Fellow, Massachusetts General Hospital Career stage: fellow. Mentoring role: research mentor. Accomplishments: manuscripts published and in review.

Local Invited Presentations

No presentations below were sponsored by outside entities.

2009	HistoneHits-A database for histone mutations and their phenotypes / Monthly Colloquium Department of Molecular Biology & Genetics, Johns Hopkins School of Medicine
2011	GWiS: a novel gene-based test of association for the identification of multiple independent effects / Monthly Colloquium High-Throughput Biology Center, Johns Hopkins School of Medicine
2013	Fine-mapping of inflammatory bowel disease risk loci using immunochip / Seminar Series Center for Human Genetics Research, Massachusetts General Hospital
2015	Fine-mapping genome-wide association loci / Program Meeting Medical and Population Genetics, Broad Institute
2015	Association mapping of inflammatory bowel disease loci to single variant resolution / Seminar Series Center for Human Genetics Research, Massachusetts General Hospital
2017	Fine-mapping genetic risk loci to single-variant resolution / Invited presentation Chinese Scientists and Scholars Association, Harvard Medical School

2018	Fine-mapping genetic associations to single-variant resolution / Seminar Series Channing Division of Network Medicine, Brigham and Women's Hospital
2018	Fine-mapping genetic associations to single-variant resolution / Seminar Series Program in Genetic Epidemiology and Statistical Genetics, Harvard T.H. Chan School of Public Health
2019	Fine-mapping genetic loci associated with human complex disorders / Primer Series Stanley Center for Psychiatric Research, the Broad Institute of MIT and Harvard

Report of Regional, National and International Invited Teaching and Presentations

No presentations below were sponsored by outside entities.

Regional

2016	Genomics and Human diseases / Invited lecture Longwood Translational Medicine China Initiative, Boston, MA
2018	Fine-map genetic risk loci to single-variant resolution / Invited talk Yale School of Medicine Genetics Department Seminar Series

National

2006	Group tests for protein interactions / Selected oral abstract DIMACS workshop, Piscataway, NJ
2010	GWiS: a novel gene-based test of association for the identification of multiple independent effects / Selected oral abstract American Society of Human Genetics annual meeting, Washington DC
2014	Fine mapping of inflammatory bowel disease risk loci using immunochip / Selected oral abstract The Biology of Genome, Cold Spring Harbor, NY
2015	Single variant resolution association mapping of inflammatory bowel disease loci / Selected oral abstract American Society of Human Genetics annual meeting, Baltimore, MD
2018	Comparative genetic architectures of schizophrenia in East Asian and European populations. / Selected oral abstract American Society of Human Genetics annual meeting, San Diego, CA

International

2006	Probabilistic paths for protein complex inference / Selected oral abstract RECOMB Satellite Conference on Systems Biology, San Diego, CA
2008	Biological network and regulation / Invited presentation Nanjing University, Jiangsu, China

2013	Using Paired Tissue and Serum Samples to Characterize Human Lung Cancer Metabolomics with ex vivo 1H HRMAS MRS / Selected oral abstract International Society for Magnetic Resonance in Medicine annual meeting, Salt Lake City, UT
2013	Computational Approaches to Study the Relation Between Genomic Variations and Phenotypes / Invited presentation Chinese Academy of Science, Beijing, China
2014	Fine-mapping of the genetic risk loci underlying human disorders / Selected oral abstract The Sixth National Conference on Bioinformatics and Systems Biology, Jiangsu, China
2015	Fine mapping of inflammatory bowel disease risk loci using immunochip / Invited presentation Gordon conference on Quantitative Genetics & Genomics, Lucca (Barga), Italy
2015	Statistical Genomics Workshop / Invited lectures Shanghai Jiaotong University, Shanghai, China
2016	Fine-mapping of disease associated loci / Invited presentation Shanghai Jiaotong University, Shanghai, China
2017	Fine-mapping of genetic loci underlying human complex disorders / Invited presentation Advanced Technologies in Precision Medicine, Shanghai, China
2018	The 5th Summit on Chinese Psychiatric Genetics / Invited lectures The affiliated Guangji Hospital of Soochow University, Suzhou, China
2018	Diversity and psychiatric genetics: why do genetics in a global setting / invited presentation Pan-Asia Symposium on the Genetics of Brain Disorders, Shanghai, China
2017-2018	Statistical Genomics Workshop / Invited lectures Beijing Computing Center, Beijing, China
2015-2019	Annual Genetic Epidemiology Workshop / Invited lectures Academia Sinica, Taipei, ROC
2019	Fine-mapping genetic risk loci to single variant resolution/ Invited presentation Symposium on Precision Medicine and Mental Health**,** Hong Kong SAR, China
2019	Fine-map genetic loci associated with human complex disorders to single-variant resolution / Invited presentation The 4th Global Conference of Chinese Geneticists, Shanghai, China
2019	Comparative genetic architectures of schizophrenia in East Asian and European populations / Invited presentation Asian College of Neuropsychopharmacology, Fukuoka, Japan
2019	Increasing ancestry diversity in psychiatric genomics research / Plenary talk

World Congress of Psychiatric Genetics, Anaheim, CA

Report of Technological and Other Scientific Innovations

Gene-wide significance (GWiS) test: novel gene-based methods for the identification of genetic associations having multiple independent effects	US Patent Application, 13/953,403, filed July 29, 2013 Under the supervision of my Ph.D. advisor, I developed GWiS, a novel gene-based method. Using Bayesian regularized regression, this method combined multiple independent associations within a gene and had greater power than all other existing methods. The improvements in power identified additional associations from existing dataset, saving considerable resources to recruit and genotype more samples. An implementation of this method that only requires summary data is being used in consortia of psychiatric, autoimmune, and cardiovascular diseases.

Report of Education of Patients and Service to the Community

No activities below were sponsored by outside entities.

Activities

2016	MIT-China Innovation and Entrepreneurship Forum / Panelist, Healthcare Panel An annual forum to address key issues in technology, innovation, and entrepreneurship in China and US, providing a platform upon which high-impact discussions and collaborations can take place.
2017	STEP Forum / Invited Speaker A platform for young elites across the world to exchange ideas
2018 - 2019	Broad Institute outreaching activities Speak at various outreaching activities to introduce psychiatric genetics

Report of Scholarship

Peer-Reviewed Scholarship in print or other media

Research Investigations

1. Stuart LM, Boulais J, Charriere GM, Hennessy EJ, Brunet S, Jutras I, Goyette G, Rondeau C, Letarte S, **Huang H**, Ye P, Morales F, Kocks C, Bader JS, Desjardins M, Ezekowitz RAB. A systems biology analysis of the Drosophila phagosome. Nature. 2007; 445(7123): 95-101. PMID: 17151602.

2. **Huang H**, Jedynak BM, Bader JS. Where have all the interactions gone? Estimating the coverage of two-hybrid protein interaction maps. PLoS Comput Biol. 2007 Nov;3(11):e214. PMID: 18039026.

3. Dai J, Hyland EM, Yuan DS, **Huang H**, Bader JS, Boeke JD. Probing nucleosome function: a highly versatile library of synthetic histone H3 and H4 mutants. Cell. 2008 Sep 19;134(6):1066-1078. PMID: 18805098.

4. **Huang H**, Bader JS. Precision and recall estimates for two-hybrid screens. Bioinformatics. 2009 Feb 1;25(3):372-378. PMID: 19091773.

5. **Huang H**, Maertens AM, Hyland EM, Dai J, Norris A, Boeke JD, Bader JS. HistoneHits: a database for histone mutations and their phenotypes. Genome Res. 2009 Apr;19(4):674-681. PMID: 19218532.

6. Zhong J, Krawczyk SA, Chaerkady R, **Huang H**, Goel R, Bader JS, Wong GW, Corkey BE, Pandey A. Temporal profiling of the secretome during adipogenesis in humans. J Proteome Res. 2010 Oct 1;9(10):5228-5238. PMID: 20707391.

7. **Huang H**, Chanda P, Alonso A, Bader JS, Arking DE. Gene-based tests of association. PLoS Genet. 2011 Jul;7(7):e1002177. PMID: 21829371.

8. Early RJ, Yu H, Mu XP, Xu H, Guo L, Kong Q, Zhou J, He B, Yang X, **Huang H**, Hu E, Jiang Y. Repeat oral dose toxicity studies of melamine in rats and monkeys. Arch Toxicol. 2013 Mar;87(3):517-527. PMID: 23052191.

9. **Huang H**, Tata S, Prill RJ. BlueSNP: R package for highly scalable genome-wide association studies using Hadoop clusters. Bioinformatics. 2013 Jan 1;29(1):135-136. PMID: 23202745.

10. Chanda P, **Huang H**, Arking DE, Bader JS. Fast association tests for genes with FAST. PLoS One. 2013 Jul 23;8(7):e68585. PMID: 23935874.

11. Chiu YL, Shan L, **Huang H**, Haupt C, Bessell C, Canaday DH, Zhang H, Ho YC, Powell JD, Oelke M, Margolick JB, Blankson JN, Griffin DE, Schneck JP. Sprouty-2 regulates HIV-specific T cell polyfunctionality. J Clin Invest. 2014 Jan;124(1):198-208. PMID: 24292711.

12. Ananthakrishnan AN, **Huang H**, Nguyen DD, Sauk J, Yajnik V, Xavier RJ. Differential effect of genetic burden on disease phenotypes in Crohn's disease and ulcerative colitis: analysis of a North American cohort. Am J Gastroenterol. 2014 Mar;109(3):395-400. PMID: 24419484.

13. Goldstein JI, Jarskog LF, Hilliard C, Alfirevic A, Duncan L, Fourches D, **Huang H**, Lek M, Neale BM, Ripke S, Shianna K, Szatkiewicz JP, Tropsha A, van den Oord EJ, Cascorbi I, Dettling M, Gazit E, Goff DC, Holden AL, Kelly DL, Malhotra AK, Nielsen J, Pirmohamed M, Rujescu D, Werge T, Levy DL, Josiassen RC, Kennedy JL, Lieberman JA, Daly MJ, Sullivan PF. Clozapine-induced agranulocytosis is associated with rare HLA-DQB1 and HLA-B alleles. Nat Commun. 2014 Sep 4;5:4757. PMID: 25187353.

14. Li X, Yang H, **Huang H**, Zhu T. CELLCOUNTER: novel open-source software for counting cell migration and invasion in vitro. Biomed Res Int. 2014;2014:863564. PMID: 25054152.

15. Arking DE, Pulit SL, Crotti L, van der Harst P, Munroe PB, Koopmann TT, Sotoodehnia N, Rossin EJ, Morley M, Wang X, Johnson AD, Lundby A, Gudbjartsson DF, Noseworthy PA, Eijgelsheim M, Bradford Y, Tarasov KV, Dörr M, Müller-Nurasyid M, Lahtinen AM, Nolte IM, Smith AV, Bis JC, Isaacs A, Newhouse SJ, Evans DS, Post WS, Waggott D, Lyytikäinen LP, Hicks AA, Eisele L, Ellinghaus D, Hayward C, Navarro P, Ulivi S, Tanaka T, Tester DJ, Chatel S, Gustafsson S, Kumari M, Morris RW, Naluai ÅT, Padmanabhan S, Kluttig A, Strohmer B, Panayiotou AG, Torres M, Knoflach M, Hubacek JA, Slowikowski K, Raychaudhuri S, Kumar RD, Harris TB, Launer LJ, Shuldiner AR, Alonso A, Bader JS, Ehret G, **Huang H**, Kao WH, Strait JB, Macfarlane PW, Brown M, Caulfield MJ, Samani NJ, Kronenberg F, Willeit J; CARe Consortium; COGENT Consortium, Smith JG, Greiser KH, Meyer Zu Schwabedissen H, Werdan K, Carella M, Zelante L, Heckbert SR, Psaty BM, Rotter JI, Kolcic I, Polašek O, Wright AF, Griffin M, Daly MJ; DCCT/EDIC, Arnar DO, Hólm H, Thorsteinsdottir U; eMERGE Consortium, Denny JC, Roden DM, Zuvich RL, Emilsson V, Plump AS, Larson MG, O'Donnell CJ, Yin X, Bobbo M, D'Adamo AP, Iorio A, Sinagra G, Carracedo A, Cummings SR, Nalls

MA, Jula A, Kontula KK, Marjamaa A, Oikarinen L, Perola M, Porthan K, Erbel R, Hoffmann P, Jöckel KH, Kälsch H, Nöthen MM; HRGEN Consortium, den Hoed M, Loos RJ, Thelle DS, Gieger C, Meitinger T, Perz S, Peters A, Prucha H, Sinner MF, Waldenberger M, de Boer RA, Franke L, van der Vleuten PA, Beckmann BM, Martens E, Bardai A, Hofman N, Wilde AA, Behr ER, Dalageorgou C, Giudicessi JR, Medeiros-Domingo A, Barc J, Kyndt F, Probst V, Ghidoni A, Insolia R, Hamilton RM, Scherer SW, Brandimarto J, Margulies K, Moravec CE, del Greco M F, Fuchsberger C, O'Connell JR, Lee WK, Watt GC, Campbell H, Wild SH, El Mokhtari NE, Frey N, Asselbergs FW, Mateo Leach I, Navis G, van den Berg MP, van Veldhuisen DJ, Kellis M, Krijthe BP, Franco OH, Hofman A, Kors JA, Uitterlinden AG, Witteman JC, Kedenko L, Lamina C, Oostra BA, Abecasis GR, Lakatta EG, Mulas A, Orrú M, Schlessinger D, Uda M, Markus MR, Völker U, Snieder H, Spector TD, Ärnlöv J, Lind L, Sundström J, Syvänen AC, Kivimaki M, Kähönen M, Mononen N, Raitakari OT, Viikari JS, Adamkova V, Kiechl S, Brion M, Nicolaides AN, Paulweber B, Haerting J, Dominiczak AF, Nyberg F, Whincup PH, Hingorani AD, Schott JJ, Bezzina CR, Ingelsson E, Ferrucci L, Gasparini P, Wilson JF, Rudan I, Franke A, Mühleisen TW, Pramstaller PP, Lehtimäki TJ, Paterson AD, Parsa A, Liu Y, van Duijn CM, Siscovick DS, Gudnason V, Jamshidi Y, Salomaa V, Felix SB, Sanna S, Ritchie MD, Stricker BH, Stefansson K, Boyer LA, Cappola TP, Olsen JV, Lage K, Schwartz PJ, Kääb S, Chakravarti A, Ackerman MJ, Pfeufer A, de Bakker PI, Newton-Cheh C. Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nat Genet. 2014 Aug;46(8):826-836. PMID: 24952745.

16. Betz RC, Petukhova L, Ripke S, **Huang H**, Menelaou A, Redler S, Becker T, Heilmann S, Yamany T, Duvic M, Hordinsky M, Norris D, Price VH, Mackay-Wiggan J, de Jong A, DeStefano GM, Moebus S, Böhm M, Blume-Peytavi U, Wolff H, Lutz G, Kruse R, Bian L, Amos CI, Lee A, Gregersen PK, Blaumeiser B, Altshuler D, Clynes R, de Bakker PI, Nöthen MM, Daly MJ, Christiano AM. Genome-wide meta-analysis in alopecia areata resolves HLA associations and reveals two new susceptibility loci. Nat Commun. 2015 Jan 22;6:5966. PMID: 25608926.

17. Knights D, Silverberg MS, Weersma RK, Gevers D, Dijkstra G, **Huang H**, Tyler AD, van Sommeren S, Imhann F, Stempak JM, Huang H, Vangay P, Al-Ghalith GA, Russell C, Sauk J, Knight J, Daly MJ, Huttenhower C, Xavier RJ. Complex host genetics influence the microbiome in inflammatory bowel disease. Genome Med. 2014 Dec 2;6(12):107. PMID: 25587358.

18. Goyette P, Boucher G, Mallon D, Ellinghaus E, Jostins L, **Huang H**, Ripke S, Gusareva ES, Annese V, Hauser SL, Oksenberg JR, Thomsen I, Leslie S; International Inflammatory Bowel Disease Genetics Consortium; Australia and New Zealand IBDGC; Belgium IBD Genetics Consortium; Italian Group for IBD Genetic Consortium; NIDDK Inflammatory Bowel Disease Genetics Consortium; United Kingdom IBDGC; Wellcome Trust Case Control Consortium; Quebec IBD Genetics Consortium, Daly MJ, Van Steen K, Duerr RH, Barrett JC, McGovern DP, Schumm LP, Traherne JA, Carrington MN, Kosmoliaptsis V, Karlsen TH, Franke A, Rioux JD. High-density mapping of the MHC identifies a shared role for HLA-DRB1*01:03 in inflammatory bowel diseases and heterozygous advantage in ulcerative colitis. Nat Genet. 2015 Feb;47(2):172-179. PMID: 25559196.

19. Goldstein JI, Jarskog LF, Hilliard C, Alfirevic A, Duncan L, Fourches D, **Huang H**, Lek M, Neale BM, Ripke S, Shianna K, Szatkiewicz JP, Tropsha A, van den Oord EJ, Cascorbi I, Dettling M, Gazit E, Goff DC, Holden AL, Kelly DL, Malhotra AK, Nielsen J, Pirmohamed M, Rujescu D, Werge T, Levy DL, Josiassen RC, Kennedy JL, Lieberman JA, Daly MJ, Sullivan PF. Clozapine-induced agranulocytosis is associated with rare HLA-DQB1 and HLA-B alleles. Nat Commun. 2014 Sep 4;5:4757. PMID: 25187353.

20. Knights D, Silverberg MS, Weersma RK, Gevers D, Dijkstra G, Huang H, Tyler AD, van Sommeren S, Imhann F, Stempak JM, **Huang H**, Vangay P, Al-Ghalith GA, Russell C, Sauk J, Knight J, Daly MJ,

Huttenhower C, Xavier RJ. Complex host genetics influence the microbiome in inflammatory bowel disease. Genome Med. 2014 Dec 2;6(12):107. PMID: 25587358.

21. Betz RC, Petukhova L, Ripke S, **Huang H**, Menelaou A, Redler S, Becker T, Heilmann S, Yamany T, Duvic M, Hordinsky M, Norris D, Price VH, Mackay-Wiggan J, de Jong A, DeStefano GM, Moebus S, Böhm M, Blume-Peytavi U, Wolff H, Lutz G, Kruse R, Bian L, Amos CI, Lee A, Gregersen PK, Blaumeiser B, Altshuler D, Clynes R, de Bakker PI, Nöthen MM, Daly MJ, Christiano AM. Genome-wide meta-analysis in alopecia areata resolves HLA associations and reveals two new susceptibility loci. Nat Commun. 2015 Jan 22;6:5966. PMID: 25608926.

22. Goyette P, Boucher G, Mallon D, Ellinghaus E, Jostins L, **Huang H**, Ripke S, Gusareva ES, Annese V, Hauser SL, Oksenberg JR, Thomsen I, Leslie S; International Inflammatory Bowel Disease Genetics Consortium; Australia and New Zealand IBDGC; Belgium IBD Genetics Consortium; Italian Group for IBD Genetic Consortium; NIDDK Inflammatory Bowel Disease Genetics Consortium; United Kingdom IBDGC; Wellcome Trust Case Control Consortium; Quebec IBD Genetics Consortium, Daly MJ, Van Steen K, Duerr RH, Barrett JC, McGovern DP, Schumm LP, Traherne JA, Carrington MN, Kosmoliaptsis V, Karlsen TH, Franke A, Rioux JD. High-density mapping of the MHC identifies a shared role for HLA-DRB1*01:03 in inflammatory bowel diseases and heterozygous advantage in ulcerative colitis. Nat Genet. 2015 Feb;47(2):172-179. PMID: 25559196.

23. Liu JZ, van Sommeren S, **Huang H**, Ng SC, Alberts R, Takahashi A, Ripke S, Lee JC, Jostins L, Shah T, Abedian S, Cheon JH, Cho J, Daryani NE, Franke L, Fuyuno Y, Hart A, Juyal RC, Juyal G, Kim WH, Morris AP, Poustchi H, Newman WG, Midha V, Orchard TR, Vahedi H, Sood A, Sung JJ, Malekzadeh R, Westra HJ, Yamazaki K, Yang SK; International Multiple Sclerosis Genetics Consortium; International IBD Genetics Consortium, Barrett JC, Franke A, Alizadeh BZ, Parkes M, B K T, Daly MJ, Kubo M, Anderson CA, Weersma RK. Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nat Genet. 2015 Sep;47(9):979-986. PMID: 26192919.

24. Cao Z, Conway KL, Heath RJ, Rush JS, Leshchiner ES, Ramirez-Ortiz ZG, Nedelsky NB, **Huang H**, Ng A, Gardet A, Cheng SC, Shamji AF, Rioux JD, Wijmenga C, Netea MG, Means TK, Daly MJ, Xavier RJ. Ubiquitin Ligase TRIM62 Regulates CARD9-Mediated Anti-fungal Immunity and Intestinal Inflammation. Immunity. 2015 Oct 20;43(4):715-726. PMID: 26488816.

25. Cleynen I, Boucher G, Jostins L, Schumm LP, Zeissig S, Ahmad T, Andersen V, Andrews JM, Annese V, Brand S, Brant SR, Cho JH, Daly MJ, Dubinsky M, Duerr RH, Ferguson LR, Franke A, Gearry RB, Goyette P, Hakonarson H, Halfvarson J, Hov JR, **Huang H**, Kennedy NA, Kupcinskas L, Lawrance IC, Lee JC, Satsangi J, Schreiber S, Théâtre E, van der Meulen-de Jong AE, Weersma RK, Wilson DC; International Inflammatory Bowel Disease Genetics Consortium, Parkes M, Vermeire S, Rioux JD, Mansfield J, Silverberg MS, Radford-Smith G, McGovern DP, Barrett JC, Lees CW. Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. Lancet. 2016 Jan 9;387(10014):156-167. PMID: 26490195.

26. Ruan Y, Jiang J, Guo L, Li Y, **Huang H**, Shen L, Luan M, Li M, Du H, Ma C, He L, Zhang X, Qin S. Genetic Association of Curative and Adverse Reactions to Tyrosine Kinase Inhibitors in Chinese advanced Non-Small Cell Lung Cancer patients. Sci Rep. 2016 Mar 18;6:23368. PMID: 26988277.

27. Ji Z, Song R, **Huang H**, Regev A, Struhl K. Transcriptome-scale RNase-footprinting of RNA-protein complexes. Nat Biotechnol. 2016 Apr;34(4):410-413. PMID: 26900662.

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Other peer-reviewed scholarship

1. **Huang H**, Zhang LV, Roth FP, Bader JS. Probabilistic paths for protein complex inference. In: Ideker T, Bafna V, editors. Systems Biology and Computational Proteomics: Joint RECOMB 2006 Satellite Workshops on Systems Biology and on Computational Proteomics, San Diego, CA, USA, December 1-3, 2006, Revised Selected Papers. New York: Springer; 2007. p. 14-28.

Scholarship without named authorship

1. **Schizophrenia Working Group of the Psychiatric Genomics Consortium***. Biological insights from 108 schizophrenia-associated genetic loci. Nature. 2014 Jul 24;511(7510):421-427. PMID: 25056061.
   *I am an analyst in this project responsible for fine-mapping and the co-localization analysis with brain eQTL.

2. **Autism Spectrum Disorders Working Group of The Psychiatric Genomics Consortium***. Meta-analysis of GWAS of over 16,000 individuals with autism spectrum disorder highlights a novel locus at 10q24.32 and a significant overlap with schizophrenia. Mol Autism. 2017 May 22;8:21. PMID: 28540026.
   *I am an analyst in this project responsible for the gene-based tests.

3. **CNV and Schizophrenia Working Groups of the Psychiatric Genomics Consortium.** Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nat Genet. 2017 Jan;49(1):27-35. PMID: 27869829;
   *I am an analyst in this project responsible for performing quality control on a subset of the data.

4. **The Brainstorm Consortium***. Analysis of shared heritability in common disorders of the brain. Science. 2018 Jun 22;360(6395).
   *I am an analyst in this project responsible for performing analyses on a subset of the data.

5. **ADHD Working Group of the Psychiatric Genomics Consortium (PGC).** Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nat Genet. 2019 Jan;51(1):63-75.
   *I am an analyst in this project responsible for performing analyses on a subset of the data.

6. **Cross-Disorder Group of the Psychiatric Genomics Consortium.** Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell. 2019 Dec 12;179(7):1469-1482.e11.
   *I am an analyst in this project responsible for performing analyses on a subset of the data.

Non-Peer Reviewed scientific or medical scholarship/materials in print or other media

Reviews, chapters, monographs and editorials

1. Aleixo Muise and **Hailiang Huang**. Sequencing and Mapping IBD Genes to Individual Causative Variants and Their Clinical Relevance. Molecular Genetics of Inflammatory Bowel Disease 2019 (Editor: Mauro D'Amato)

Professional Educational Materials or Reports in print or other media

1. Post-GWAS analyses: heritability, genetic correlation and annotation

   Type: Course video recording
   I created and used this video to teach a course for the “Global Initiative for Neuropsychiatric Genetics Education in Research” at the Harvard T.H. Chan School of Public Health. (2019)

2. Population structure in genetic association studies

   Type: Course video recording
   I created and used this video to teach a course for the “Global Initiative for Neuropsychiatric Genetics Education in Research” at the Harvard T.H. Chan School of Public Health. (2019)

Thesis

Huang, Hailiang. "Computational Approaches to Study the Relation Between Genomic Variations and Phenotypes". Ph.D. dissertation, Johns Hopkins University, 2012.

Abstracts, Poster Presentations and Exhibits Presented at Professional Meetings

1. **Huang H**, Rivas M, Genovese G, Singh T, Howrigan D, Satterstrom FK, McCarroll S, Neale BM, Daly MJ. A comprehensive survey of protein truncating variants in schizophrenia. American Society of Human Genetics annual meeting, Vancouver, Canada. 2016.

2. Lam M* and **Huang H** on behalf of the Psychiatric Genomics Consortium (PGC) Schizophrenia Asia working group, Psychiatric Genomics Consortium – Genetic architecture of schizophrenia in Asian populations, World Congress of Psychiatric Genetics, Jerusalem, Israel. 2016.
   (*selected oral abstract presented by Max Lam)

3. Ajmera V, **Huang H**, Daly M, Lee WM, Chun R. CXCL16 polymorphism is associated with Acute Liver Failure from Hepatitis B Virus. American Association for the Study of Liver Diseases, Boston MA. 2016.

4. **Huang H** and Lam M*, Chen C, Martin A, Li Z, Ripke S, O'Donovan M, Daly M, and PGC Schizophrenia Asia Initiative, Using Genetic Diversity From East Asia to Improve the Biological Insight Into Schizophrenia, World Congress of Psychiatric Genetics, Orlando, FL. 2017.
   (*selected oral abstract presented by Max Lam)

5. **Huang H**, Lam M, Chen C, Martin A, Li Z, Ripke S, O'Donovan M, Daly M, and PGC Schizophrenia Asia Initiative, Using Genetic Diversity from East Asia to Improve the Biological Insight into Schizophrenia, American Society of Human Genetics annual meeting, Orlando, FL. 2017.

Narrative Report

I am a statistical geneticist with special interests in the genetics of human complex disorders. I received my Ph.D. training in Dr. Joel Bader's lab at the Johns Hopkins School of Medicine, with focuses on biological pathways and networks, statistical genetics and bioinformatics. One major component in my dissertation was the development of a new gene-based method for genome-wide association studies that combined multiple independent associations within a gene and had greater power than all other existing methods. This method has been used widely in consortia of psychiatric, autoimmune, and cardiovascular diseases. Due to the burgeoning commercial interests in this method, a U.S. patent (pending) was filed, and I was also hired by the IBM Healthcare Informatics group as a summer intern to extend this method in their parallel computing environment.

After receiving my Ph.D., I joined Dr. Mark J. Daly's lab at the Massachusetts General Hospital. I focused on developing methods and analyses to investigate the genetics of common disorders, especially the inflammatory bowel diseases (IBD) and schizophrenia. I have been heavily involved in international IBD genetics consortia and contributed to several major studies. I led the fine-mapping project and developed a Bayesian approach to resolve known genetic associations to much smaller sets of variants with high causal probabilities. This project mapped IBD associations down to a single variant and significantly advanced our knowledge of IBD genetics. Moreover, a simplified implementation of this method that only requires summary data has been widely used for other disorders including schizophrenia and migraines. In addition to this fine-mapping project, I have led or participated in the study design, method development, or analysis of other IBD studies covering a broad range of topics, including IBD genetic associations, clinical sub-phenotyping, functional studies of *CARD9* and *GPR65*, and the interaction between the microbiome and host genetics in IBD.

In addition to IBD genetics, I have led a workgroup in Psychiatric Genomics Consortium (PGC) to understand the genetic contributions to schizophrenia in Asian populations. Working with over 40 participants across 10 countries, I have built a large Asian schizophrenia cohort. Together, we are working to identify new schizophrenia genetic loci, evaluate the genetic correlations between Asian and European populations, and understand whether or how the schizophrenia genetic effects differ between the two populations. With support from the Stanley Center at the Broad Institute, I am also spearheading new major research collaborations with institutes and hospital networks in East Asia and the Broad Institute to expand our psychiatric genetics initiatives in Asia. As part of this, I am organizing and teaching an annual statistical genetics workshop series in Shanghai (2015), Beijing (2017 and 2018) and Taipei (2015-2019). These workshops have been attended by over 600 participants from more than 70 institutions and helped to build global genetics research capacity.

In parallel with my research activities, I am committed to teaching and mentoring. I am one of the teaching fellows for the Harvard T.H. Chan School of Public Health (HSPH) *Global Initiative for Neuropsychiatric Genetics Education in Research*, a training program that aims to boost global capacity to conduct neuropsychiatric genetics research. I participated in the initial curriculum design in 2017, and since then taught annually in person (Boston and London), in virtual classroom and as recorded course lectures. My lectures have covered genome-wide association studies, population structure, genetic correlations, career development and grant writing. In 2019, I co-taught a new MGH course with Dr. Tian Ge (Assistant Professor, HMS and MGH) entitled *A Practical Introduction to Statistical Genetics*. Over 50 participants with Harvard affiliations attended this course. I taught sessions in the genome-wide association studies and fine-mapping studies. Lastly, I have mentored or co-mentored 6 research fellows and 3 visiting fellows from Harvard affiliated hospitals and institutions (MGH, BWH and the Broad Institute). I met with them regularly, worked closely with them on statistical genetics, psychiatric genetics, or computational biology projects, and assisted them in career development and grant writing. Our work together has led to manuscripts in publication and in preparation and grant in review.