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**BIOGRAPHICAL SKETCH**

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NAME		POSITION TITLE	
Zhao, Jing Hua / 赵京华		Genetic Analyst / Senior Research Associate	
EDUCATION/TRAINING ( <i>Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.</i> )			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
Shandong (Medical) University, China	Bachelor	1980-1985	Public Health
Fudan (Shanghai Medical) University, China	Master	1985-1988	Medical Statistics
King's College London, UK	PhD	1996-2002 (part-time)	Statistical Genetics

**A. Positions and employment**

1988.9-1994.8	Research associate, Division of Sampling Survey, Center for Health Statistics Information, Ministry of Health
1994.8-1996.5	Visiting scientist, Department of Environmental Science, School of Public Health & Channing Laboratory, Medical School, Harvard University
1996.5-2002.8	PostDoc & Lecturer (2001.3-2002.8), Section of Genetic Epidemiology and Biostatistics, Division of Psychological Medicine, Institute of Psychiatry, King's College London
2002.9-2005.9	Statistician, Social and Genetic Epidemiology, Department of Epidemiology and Public Health, University College London
2005.9-2018.7	Investigator scientist in Genetics, MRC Epidemiology Unit
2018.8-	Genetic Analyst / Senior Research Associate, Cardiovascular Epidemiology Unit, Department of Public Health and Primary Care, University of Cambridge

**B. Research interests**

My work relates to methods and applications in epidemiology/public health with a current focus on proteogenomics. Following earlier efforts on candidate genes and genomewide association studies (GWASs), I have contributed to consortium work including recently the Host Genetics Initiatives on COVID-19 through the INTERVAL study. I am interested in predictive modeling involving polygenic effects, gene-environment interactions and web technologies. I have striven for reproducible research by distributing R packages at the comprehensive R Archive network (CRAN), <https://cran.r-project.org>, and giving tutorials at UseR! Conferences and a Henry-Stewart talk. My pipelines for large-scale genomic data have been made available through GitHub, <https://github.com/jinghuazhao>. At CEU, I have created GitHub repositories linking through website <https://cambridge-ceu.github.io>. I have a personal page: <https://jinghuazhao.github.io>.

**C. Favorite publications**

COVID-19 Host Genetics Initiative. Mapping the human genetic architecture of COVID-19. *Nature* 2021. doi: 10.1038/s41586-021-03767-x.

**Zhao JH**, Luan JA, Congdon P. Bayesian linear mixed model of polygenic effects. *J Stat Soft.* 2018, 85(6):1-27. doi: 10.18637/jss.v085.i06

**Zhao JH**, Luan JA. Mixed modeling with whole genome data. *J Prob Stat.* 2012. doi: 10.1155/2012.485174.

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Xue F, Li S, Luan J, Yuan Z, Luben RN, Khaw K-T, Wareham NJ, Loos RJF, **Zhao JH**. A latent variable partial least squares path modeling approach to regional association and polygenic effect with applications to a human obesity study. *PLoS ONE* 2012, 7(2): e31927

Loos RJ, *et al*. Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nat Genet* 2008; 40(6):768-75

**Zhao JH**. gap: genetic analysis package. *J Stat Soft* 2007, 23 (8):1-18. doi: 10.18637/jss.v023.i08.

**Zhao JH**, Brunner EJ, Kumari M, Singh-Manoux A, Hawe E, Talmud PJ, Marmot MG, Humphries SE. *APOE* polymorphism, socioeconomic status and cognitive function in later mid-life: The Whitehall II longitudinal study. *Soc Psychiatr and Psychiatr Epidemiol* 2005, 40:557-563

**Zhao JH**, D Curtis, PC Sham. Model-free and permutation tests for allelic associations. *Hum Hered* 2000, 50(2), 133-139.

#### D. Peer-reviewed publications (in chronological order)

1. **Zhao JH**. Computer software for secondary analysis of statistical data. *Chin J Health Stat* 1990, 7:9-10.
2. **Zhao JH**. Some perspectives of SAS/STAT 6.03 on personal computers. *Chin J Health Stat* 1990, 7:49-51.
3. Li NH, **Zhao JH**. Principal component analysis of factors affecting diabetes of the old people. *Chin J Gerontol* 1991, 11(6): 333-334.
4. **Zhao JH**. Computer data processing for survey of total health expenditure. in Du, LX *et al*. eds. *The Survey of Total Health Expenditure*. Also in *The Survey of Total Health Expenditure* edited by Center for Health Statistics Information, 1993.
5. **Zhao JH**. A quick method to produce frequency table using Foxbase+. *J China Computer Users Group*. 1993 Supplement.
6. **Zhao JH**. A BASIC program for debugging Fortran code. *China Computers* 1991 Jan, and also in *Digest of Personal Computer Applications*, Kehai Hi-tech Co.
7. **Zhao JH**. A simple method to identify your type of personal computer. *China Computers* 1991 Jun.
8. **Zhao JH**, Tan Q. Trend analysis of fertility data in Shandong province. *Chin J Health Stat* 1994, 11 (supplement).
9. **Zhao JH**, Wang CY. Internet and health statistics. *Med Info Proc Res* (Chinese). 1996. 4(1):35-38
10. Xu X, **JH Zhao**. Ecogenetics I. *J Environ Health* 1996, 1:43-46.
11. **Zhao JH**, Niu T. Ecogenetics II. *J Environ Health* 1996, 3:139-144.
12. **Zhao JH**, Niu T. Ecogenetics III. *J Environ Health* 1996, 4:189-190.
13. Sham PC, **JH Zhao**, D. Curtis. Optimal weighting scheme for affected sib-pair analysis of sibship data. *Ann Hum Genet* 1997, 61:61-69.
14. Li T, K Xu, H Deng, G Cai, J Liu, X Liu, RA Wang, XY Xiang, **JH Zhao**, RM Murray, PC Sham, DA Collier. Association analysis of the dopamine D4 gene exon III VNTR and heroin abuse in Chinese subjects. *Mol Psychiatr* 1997, 2:413-416.
15. Li T, HP Vallada, X Liu, T Xie, XD Tang, **JH Zhao**, MC O'Donovan, RM Murray, PC Sham, DA Collier. Analysis of CAG/CTG repeat size in Chinese subjects with schizophrenia and bipolar affective disorder using the repeat expansion detection method. *Biol Psychiatr* 1998, 44(11):1160-5.

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16. Arranz MJ, J Munro, MJ Owen, G Spurlock, PC Sham, **J Zhao**, G Kirov, DA Collier, RW Kerwin. Evidence for association between polymorphisms in the promoter and coding regions of the 5-HT<sub>2A</sub> receptor gene and response to clozapine. *Mol Psychiatr* 1998, **3**:61-66.
17. Niu T, X Xu, J Rogus, Y Zhou, C Chen, J Yang, Z Fang, C Schmitz, **J Zhao**, VS Rao, K Lindpainter. Angiotensinogen gene and hypertension in Chinese. *J Clin Invest* 1998, **101**(1): 188-194.
18. **Zhao JH**, PC Sham. A method for calculating probability convolution using ternary numbers with application in the determination of twin zygosity. *Comp Stat Data Anal* 1998, **28**(2): 225-232.
19. Vallada H, D Curtis, P Sham, H Kunugi, **J Zhao**, R Murray, P McGuffin et al. A transmission disequilibrium and linkage analysis of D22S278 marker alleles in 574 families: further support for a susceptibility locus for schizophrenia at 22q12. *Schizophr Res* 1998, **32**:115-121.
20. Wright P, E Dawson, PT Donaldson, JA Underhill, PC Sham, **JH Zhao**, M Gill, S Nanko, MJ Owen, P McGuffin, RM Murray. A transmission/disequilibrium study of the DRB1\*04 gene locus on chromosome 6p21.3 with schizophrenia. *Schizophr Res* 1998, **32**:75-80.
21. Ohadi M, MRA Laloz, P Sham, **J Zhao**, AM Dearlove, C Shiach, S Kinsey, M Rhodes, DM Layton. Localization of a Gene for Familial Hemophagocytic Lymphohistiocytosis at Chromosome 9q21.3-22 by Homozygosity Mapping. *Am J Hum Genet* 1999, **64**(1):165-171.
22. Abusaad I, D Mackay, **J Zhao**, P Stanford, DA Collier, IP Everall. Stereological estimation of the total number of neurons in the murine hippocampus using the optical disector. *Am J Med Genet (Neuropsychiatric Genet)* 1998, **81**(6):483, *The J Comparat Neurol* 1999, **408**:560-566.
23. **Zhao JH**, PC Sham, D Curtis. Letter to the Editor: A program for the Monte Carlo evaluation of significance of the extended TDT (ETDT). *Am J Hum Genet* 1999, **64**(5):1484-1485.
24. Curtis D, **JH Zhao**, PC Sham. Comparison of GENEHUNTER and MFLINK for analysis of COGA linkage data. *Genet Epidemiol* 1999, **17** (suppl 1):115-120.
25. **Zhao JH**, D Curtis, PC Sham. Model-free and permutation tests for allelic associations. *Hum Hered* 2000, **50**(2):133-139.
26. Li T, ZH Zhu, XH Liu, X Hu, **JH Zhao**, PC Sham, DA Collier. Association analysis of polymorphisms in the DRD4 gene and heroin in Chinese subjects. *Am J Med Genet* 2000, **96**:616-621.
27. Sham PC, MW Lin, **JH Zhao**, D Curtis. Power comparison of parametric and nonparametric linkage tests in small pedigrees. *Am J Hum Genet* 2000, **66**(5):1661-1668.
28. Sham PC, **JH Zhao**, D Curtis. The effect of marker polymorphism on the power to detect linkage disequilibrium due to single or multiple ancestral mutations. *Ann Hum Genet* 2000, **64**, 161-169.
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31. Li T, X Liu, Z Hong, **J Zhao**, X Hu, P Sham, D Collier. Association analysis of polymorphisms in the *mu* opiod gene and heroin abuse in Chinese subjects. *Addict Biol*, 2000, **5**:181-186.
32. Li T, X Liu, ZH Zhu, **J Zhao**, X Hu, DM Ball, PC Sham, DA Collier. No association between (AAT)<sub>n</sub> repeats in the cannabinoid receptor gene (CNR1) and heroin abuse in a Chinese population. *Mol Psychiatr*, 2000 **5**, 128-130.
33. Li T, D Ball, **J Zhao**, RM Murray, X Liu, PC Sham, DA Collier. Family-based linkage disequilibrium mapping using SNP marker haplotypes: application to a potential locus for schizophrenia at chromosome 22q11. *Mol Psychiatr*, 2000, **5**, 77-84.
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35. Sham PC, **JH Zhao**. The power of genome-wide sib pair linkage scans for quantitative trait loci using the new Haseman-Elston regression method, *GeneScreen* 2000, **1**:103-106.
36. Koch HG, J McClay, EW Loh, S Higuchi, **JH Zhao**, P Sham, D Ball and IW Craig. Allele association studies with SSR and SNP markers at known physical distances within a 1MB region embracing from the ALDH2 locus in the Japanese. *Hum Mol Genet*, 2000, **9**:2993-2999
37. Sham PC, **JH Zhao**, I Waldman, D Curtis. Should ambiguous trios for {TDT} be discarded? *Ann Hum Genet* 2000, **64**:575-576.
38. Karwautz A, S Rabe-Hesketh, X Hu, **J Zhao**, P Sham, DA Collier, JL Treasure. Individual-specific risk factors for anorexia nervosa: a pilot study using a discordant sister-pair design. *Psych Med* 2001, **31**(2):317-329.
39. Meira-Lima IV, **JH Zhao**, P Sham, AC Pereira, JE Krieger and H Vallada. Association and linkage studies between bipolar affective disorder and the polymorphic CAG/CTG repeat loci ERDA1, SEF2-1B, MAB21L and KCNN3, *Mol Psych* 2001, **6**(5):565-569.
40. Mill J, S Curran, L Kent, S Richards, A Gould, V Virdee, L Hockett, J Sharp, C Batten, S Fernando, E Simanoff, M Thompson, **J Zhao**, P Sham, E Taylor, P Asherson. Attention deficit hyperactivity disorder (ADHD) and the dopamine D4 receptor gene: evidence of association but no linkage in a UK sample. *Mol Psych* 2001, **6**(4): 440-444.
41. Cai G, T Li, H Deng, **J Zhao**, X Hu, RM Murray, X Liu, PC Sham, DA Collier. Affected sibling pair linkage analysis of qualitative and quantitative traits for schizophrenia on chromosome 22 in a Chinese population. *Am J Med Genet* 2001, **105**(4):321-327.
42. Russ C, JF Powerll, **J Zhao**, M Baker, M Hutton, F Crawford, M Mullan, G Roks, M Cruets, S Lovestone. The microtubule associated protein Tau gene and Alzheimer's disease - an association study and meta-analysis. *Neurosci Lett* 2001, **314**(1-2):92-96.
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44. **Zhao JH**, PC Sham. Faster allelic association using unrelated individuals. *Hum Hered* 2002, **53**: 36-41.
45. Li T, X Liu, **J Zhao**, X Hu, DM Ball, E-W Loh PC Sham and DA Collier. Allelic association analysis of the dopamine D2, D3, 5-HT(2A) and GABA(A)gamma2 receptors and the serotonin transporter genes with heroin abuse in Chinese subjects. *Am J Med Genet* 2002, **114**: 329-334.
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47. **Zhao JH**, S Lissarrague, L Essioux, PC Sham. GENECOUNTING: haplotype analysis with missing genotypes. *Bioinformatics* 2002, **18**: 1694-1695.
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51. Shi J, S Zhang, C Ma, X Liu, T Li, M Tang, H Han, Y Guo, **JH Zhao**, K Zheng, X Kong, K Zhang, Z Su, Z Zhao. Association between apolipoprotein CI HpaI polymorphism and sporadic Alzheimer's disease in Chinese. *Acta Neurol Scan* 2004, **109**:140-145.

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56. Parsian A, R Sinha, B Racette, **JH Zhao**, JS Perlmutter. Association of a variation in the promotor of the brain-derived neurotrophic factor gene with familial parkinson's disease. *Parkinsonism and Related Disorders* 2004, **10**:213-219.
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58. Shi J, S Zhang, M Tang, C Ma, **J Zhao**, T Li, X Liu, Y Sun, Y Guo, H Han, Y Ma, Z Zhao. Mutation screening and association study of the neprilysin gene in sporadic Alzheimer's disease in Chinese persons. *J Gerontology Bio Sci* 2005, **60A**: 301-306.
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62. **Zhao JH**. Mixed-effects Cox models of alcohol dependence in extended families. *BMC Genetics* 2005, (Suppl) **6**:127.
63. Tan Q, K Christensen, L Christiansen, L Bathum, S Li, **JH Zhao**, TK Kruse. Haplotype association analysis of human disease traits using multi-locus genotype data of unrelated subjects. *Genetical Res* 2005, **86**: 223-231.
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71. **Zhao JH**, J Luan, F Baksh, Q Tan. Mining gene networks with application to GAW15 problem 1. *BMC Proc* 2007, **1** (Suppl 1):S52

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74. Tan Q, M Thomassen, KM Jochumsen, **JH Zhao**, K Christensen, TA Kruse. Evolutionary Algorithm for Feature Subset Selection in Predicting Tumor Outcomes Using Microarray Data. I. Măndoiu, R. Sunderraman, and A. Zelikovsky (Eds.): ISBRA 2008, LNBI 4983, pp. 426–433, 2008. © Springer-Verlag Berlin Heidelberg 2008
75. Weedon MN, et al. Genome-wide association analysis identifies 20 loci that influence adult height. *Nat Genet* 2008, **40**:575-583.
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100. Yang Q, et al. Racial/Ethnic Differences in Association of Fasting Glucose–Associated Genomic Loci With Fasting Glucose, HOMA-B, and Impaired Fasting Glucose in the U.S. Adult population *Diabetes Care* 2010, **33**:2370-2377.
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