# BIOGRAPHICAL SKETCH

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

My master courses include Linear Algebra/Design of Experiment/Medical Statistics/Multivariate Aanalysis/Epidemiology at Fudan, and Mathematical Statistics/Optimization Methods/Numerical Methods at Shanghai Jiaotong Universities.

## A. Positions and employment

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|---|---|
| 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 is human health-related research which over years includes familial aggregation, segregation, linkage, candidate genes and genomewide association studies (GWASs). The most recent is proteogenomics within the SCALLOP consortium using the Olink and mass spectrometry (MS) panels measured for the INTERVAL samples. I have also led collaborative analysis to the SCALLOP-Seq(uence, both WES and NGS) consortium and Host Genetics Initiative.

I have promoted reproducible research through CRAN (https://cran.r-project.org), GitHub (https://github.com) and websites. I developed genetic analysis package (gap), protein quantitative trait tools (pQTLtools) and curated https://jinghuazhao.github.io/Computational-Statistics/, https://jinghuazhao.github.io/software-notes/ and https://jinghuazhao.github.io/Omics-analysis/. By closely following up developments in computational statistics, machine learning and artificial intelligence, I have made computing and omics analysis tools available from the University HPC, https://cambridge-ceu.github.io/csd3/, whose components include AI with BitNet, GeminiCLI, Ollama, llama.cpp, llm, featuring AI for MS data with InstaNovo & DIA-NN, molecule optimization with DrugAssist, single-cell omics with Seurat, scp, scanpy, scvi-tools, scGPT, C2S-Scale, mtDNA analysis with MToolBox, fNUMT, haplogrep as well as long-read sequencing analysis with SVanalyzer, hap.py, sniffles, truvari. Explorations in population genetics include selscan, angsd, relate, clues2 and fastsimcoal2. These are coupled with extensive experiments on various models, architectures, platforms as with libraries such as TensorFlow, PyTorch, scikit-llm, LangChain.

## C. Key publications

**Zhao JH**, et al. Mapping pQTLs of circulating inflammatory proteins identifies drivers of immune-mediated disease risk and novel therapeutic targets. *Nat Immunol* 2023, **24**(9):1540-1551, 10.1038/s41590-023-01588-w, https://www.nature.com/articles/s41590-023-01588-w.

COVID-19 Host Genetics Initiative. Mapping the human genetic architecture of COVID-19. *Nature* **600**:472–477 (2021); Pathak, G.A. et al. A first update on mapping the human genetic architecture of COVID-19. *Nature* **608**:E1-E10 (2022); The Host Genetics Initiative. A second update on mapping the human genetic architecture of COVID-19. *Nature* **621**:E7–E26 (2023).

**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.

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, 2**3** (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**. Ecogentics 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.
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$_{2A}$ 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 Lalloz, 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 allellic 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.

29. Aitchison KJ, JG Frank, LC Quattrochi, A Sapone, **JH Zhao**, H Zaher, G Elizondo, C Bryant, JM, DA Collier, AJ Makoff, RW Kerwin. Identification of novel polymorphisms in the 5' flanking region of CYP1A2, characterization of interethnic variability, and investigation of their functional significance. *Pharmacogenet*, 2000, **10**:695-704.

30. Aitchison KJ, MW Jann, **JH Zhao**, T Sakai, H Zaher, K Wolff, AJ Makoff, DA Collier, RW Kerwin, FJ Gonzalez. Clozapine pharmacokinetics and Pharmacogenetics studied with CYP1A2-null mice. *J Psychopharmacol*, 2000, **14**, 353-359.

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)n 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.

34. Sham P, **JH Zhao**, SS Cherny, JK Hewitt. Variance components QTL linkage analysis of selected and non-normal samples: conditioning on trait values. *Genet Epidemiol*, 2000, **19**, (suppl 1), 22-28

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 Huckett, 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 Cruts, 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.

43. RYL Chen, P Sham, EYH Chen, T Li, EFC Cheung, TCK Hui, CL Kwok, F Lieh-Mak, **JH Zhao**, D Collier, R Murray. No association between T102C polymorphism of serotonin-2A receptor gene and clinical phenotypes of Chinese schizophrenic patients. *Psychitr Res* 2001, **105**: 175-185

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.

48. **Zhao JH**, PC Sham. Generic number system and haplotype analysis. *Comp Meth Prog Biomed* 2003, **70**: 1-9.

49. Gabrovsek M, M Brecelj-Anderluh, L Bellodi, E Cellini, D Di Bella, X Estivill, F Fernandez-Aranda, B Freeman, F Geller, M Gratacos, R Haigh, J Hebebrand, A Hinney, J Holliday, X Hu, A Karwautz, B Nacmias, M Ribases, H Remschmidt, R Komel, S Sorbi, M Tomori, J Treasure, G Wagner, **J Zhao**, DA Collier. Combined family trio and case-control analysis of the COMT val158met polymorphism in European patients with anorexia nervosa *Am J Med Genet B (Neuropsychiatric Genet)* 2004, **124B**:68–72

50. Huang Y, T Li, Y Wang, J Ansar, G Lanting, X Liu, **JH Zhao**, X Hu, PC Sham, D Collier. Linkage disequilibrium analysis of polymorphisms in the gene for myelin oligodendrocyte glycoprotein in Tourette's syndrome patients from a Chinese sample. *Am J Med Genet. (Neuropsychiatric Genet)* 2004, **124B**:76-80.

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.

52. Shi J, S Zhang, M Tang, X Liu, T Li, H Han, Y Wang, Y Guo, **J Zhao**, H Li, C Ma. Possible association between Cys311Ser polymorphism of paraoxonase 2 gene and late-onset Alzheimer's disease in Chinese. *Mol Brain Res* 2004, **120**:201–204.

53. Tan Q, **JH Zhao**, I Iachine, J Hjelmborg, W Vach, JW Vaupel, Christensen K, TA Kruse. Power of non-parametric linkage analysis in mapping genes contributing to human longevity *Genet Epidemiol* 2004, **26**:245-253.

54. **Zhao JH**. 2LD, GENECOUNTING and HAP: Computer programs for linkage disequilibrium analysis. *Bioinformatics* 2004, **20**:1325-1326.

55. **Zhao JH**, Book review: Lachin JM (2000): Biostatistical methods: the assessment of relative risks. New York: John Wiley. Stat Methods Med Res 2004; 13: 414-415.

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.

57. Walshe M, C McDonald, M Taylor, **J Zhao**, P Sham, A Grech, K Schulze, E Bramon, R Murray. Obstetric complications in patients with Schizophrenia and their unaffected siblings *European Psychiatr* 2005, **20**:28-34.

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.

59. Tan Q, L Christiansen, L Bathum, **JH Zhao**, AI Yashin, JW Vaupel, K Chritensen, TA Kruse. Estimating haplotype relative risks on human survival in population-based association studies. *Hum Hered 2005,* **59**:88-97.

60. Tan Q, L Christiansen, L Bathum, **JH Zhao**, W Vach, JW Vaupel, K Christensen, TA Kruse. Haplotype effects on human survival: logistic regression models applied to unphased genotype data. *Ann Hum Genet 2005*, **69**: 168-175.

61. **Zhao JH**, EJ Brunner, M Kumari, A Singh-Manoux, E Hawe, PJ Talmud, MG Marmot, SE Humphries. *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.

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.

64. **Zhao JH**, Q Tan. Integrated analysis of genetic data with R. *Hum Genomics* 2006, **2**(4):258-265.
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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
72. **Zhao JH**. gap: genetic analysis package. *J Stat Soft* 2007, **23** (8):1-18.
73. Sandhu MS, et al. LDL-cholesterol concentrations: a genome-wide association study. *Lancet* 2008, **371**:483-491.
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.
76. Loos R, et al. Common variants near *MC4R* are associated with fat mass, weight and risk of obesity. *Nat Genet* 2008, **40**:768-775.
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McGeehin MA, Ness AR, Northstone K, Ring SM, Rubin C, Sims MA, Song K, Strachan DP, Vollenweider P, Waeber G, Waterworth DM, Wong A, Deloukas P, Barroso I, Mooser V, Loos RJ, Wareham NJ. Genetic variation in *LIN28B* is associated with the timing of puberty. *Nat Genet* 2009, **41**:729-733.

85. Newton-Cheh C, et al. Genome-wide association study identifies eight loci associated with blood pressure. *Nat Genet* 2009, **41**:666-676.

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91. Zhao, J. H. Genetic association analysis with R. *The Biomedical & Life Sciences Collection* **2009**, e1002430 (2009), https://doi.org/10.69645/DCRY5578.

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93. Dupuis J, et al. Novel genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nat Genet.* 2010, **42**:105-116

94. Saxena R, et al. Genetic variation in *GIPR* influences the glucose and insulin responses to an oral glucose challenge. *Nat Genet* 2010, **42**:142-148

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