BIOGRAPHICAL SKETCH

NAME	POSITION TITLE
Zhao, Jing Hua / 赵京华	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, 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 recent focus on proteogenomics. Following earlier efforts on familial aggregation, segregation analysis, candidate genes and genomewide association studies (GWASs, my current work is capitalised on the meta-analysis at the Cardiovascular Epidemiology Unit (CEU) and within the SCALLOP consortium using the Olink inflammation panel as well as other proteomic panels measured for the INTEVAL samples. I have also led analyses contributed to collaborative projects such as the Host Genetics Initiative, the SCALLOP-Seq(uence) consortium and other ongoing projects. I have actively promoted reproducible research through distribution of software on CRAN (https://cran.r-project.org) and GitHub (https://github.com) and through web-based materials from my personal page, https://jinghuazhao.github.io/ and CEU page, https://cambridge-ceu.github.io/.

I have been open to new challenges. Among other subjects, my self-taught and formal training into mathematics and statistics started from middle school throughout undergraduate studies and in my postgraduate training I took postgraduate courses and exams in mathetical statistics, optimization methods, and numerical methods at Shanghai Jiaotong University. At the Ministry of Health, I was involved in statistical and IT support across departments (while formally working on a World Bank project for integrated regional health information systems) and compiled *Practical Guides to Statistical Packages*. Through research projects, I picked up Fortran, C/C++ (and then developed one of the earliest R packages for genetic data analysis and most recently pQTLtools), Bayesian computation and web technologies. From postgraduate years, I have followed closely the development of computational statistics, artificial intelligence and machine learning, in particular implementations in Lisp and R/Python.

C. Favorite 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.
46. Mallett R, J Leff, D Bhugra, D Pang, **JH Zhao**. Social environment, ethnicity and schizophrenia: a case-control study. *Social Psychiatr and Psychiatric Epidemiol* 2002, **37**: 329-335.
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.
65. **Zhao JH**, Drawing pedigree diagrams with R and graphviz, R News 6:38-41, 2006

66. **Zhao JH**. Pedigree-drawing with R and graphviz. *Bioinformatics* **22**(8):1013-1014.
67. **Zhao JH**, Q Tan. Genetic dissection of complex traits *in silico*: approaches, problems and solutions. *Curr Bioinformatics* 2006, **1**:359-369.
68. **Zhao JH**, Luan JA, Tan Q, Loos R, Wareham NJ. Analysis of large genomic data *in silico*: the EPIC-Norfolk study of obesity. In DS Huang, L Heutte, and M Loog (Eds). Advanced Intelligent Computing Theories and Applications with Aspects of Contemporary Intelligent Computing Techniques, Third International Conference on Intelligent Computing (ICIC) 2007: 781-790.
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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.
77. Tan Q, **J Zhao**, S Li, L Christiansen, TA Kruse, K Christensen. Differential and correlation analyses of microarray gene expression data in the CEPH Utah families. *Genomics* 2008, **92**:94-100.
78. Tan Q, **JH Zhao**, TA Kruse, K Christiensen. Power for genetic association study of human longevity using the case-control design. *Am J Epidemiol* 2008, **168**:890-896.
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82. Prokopenko I, et al. Variants in MTNR1B influence fasting glucose levels. *Nat Genet*, 2009, **41**:77-81.
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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.
86. Lindgren CM, et al. Genome wide association scan meta-analysis identifies three loci influencing adiposity and fat distribution, *PLoS Genetics.* 2009, **5**(6):e1000508.
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88. Beardsal K, Ong KK, Murphy N, Ahmed ML, **Zhao JH**, Peeters M, Dunger DB. Heritability of **c**hildhood weight gain from birth and risk markers for adult disease in prepubertal twins. *JCEM.* 2009, **94**:3708-3713.
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91. Repapi E, et al. Genome-wide association study identifies five loci associated with lung function. *Nat Genet.*2010, **42**(1):36-44.
92. 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
93. 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
94. Peng Q, **Zhao JH**, Xue F. PCA-based bootstrap confidence interval tests for gene-disease association involving multiple SNPs. *BMC Genet* 2010, **11**:6
95. Peng Q, **Zhao JH**, Xue F. A gene-based method for detecting gene-gene co-association in a case-control association study. *Eur J Hum Genet* 2010, **18**:582-587
96. Liu JZ, et al. Meta-analysis and imputation refines the association of 15q25 with smoking quantity. *Nat Genet* 2010, **42**(5):436-40
97. Teslovich et al. Biological, clinical, and population relevance of 95 loci mapped for serum lipid concentrations. *Nature* 2010, **466**:707-13
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99. Tan Q, **Zhao JH**, Li S, Kruse TA, Christensen K. Power assessment for genetic association study of human longevity using offspring of long-lived families. *Eur J Epidemiol* **21**:501-506, 2010.
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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health-related phenotypes in a large population-based cohort. *Int J Obe* (*Lond*). 2010; **34**(6):1028-33.
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