

# Ji-Gang Zhang, Ph.D

---

## Education

- Ph.D.** in Statistical genetics, China Agricultural University, Beijing, P.R. China, 2002- 2005
- M.S.** in Animal Genetics, Shanxi Agricultural University, Taigu, Shanxi, P.R. China, 1999- 2002
- B.S.** in Animal Husbandry, Shanxi Agricultural University, Taigu, Shanxi, P.R. China, 1995- 1999
- 

## Experience

- Jan. 2011- 2017 Senior Research Scientist, Department of Global Biostatistics and Data Science, School of Public Health & Tropical Medicine, Tulane University
- Dec. 2005-Jan.2011 Research associate, Department of Basic Medical Science, School of Medicine, University of Missouri-Kansas City
- 

## Peer reviewed research articles:

- 1) Fang J, **Zhang JG**, , Deng HW, Wang YP. Joint Detection of Associations between DNA Methylation and Gene Expression from Multiple Cancers. *IEEE Journal of Biomedical and Health Informatics*, 2017, 99.
- 2) Xu C, **Zhang JG**, Lin DD, Zhang L, Shen H, Deng HW. A Systemic Analysis of Transcriptomic and Epigenomic Data to Reveal Regulation Patterns for Complex Disease. *G3*, 2017.
- 3) He H, Lin DD, **Zhang JG**, Wang YP, Deng HW. Comparison of statistical methods for subnetwork detection in the integration of gene expression and protein interaction network. *BMC bioinformatics*, 2017, 18 (1):149.
- 4) Greenbaum J, ,..., **Zhang JG**,..., Deng HW. Increased detection of genetic loci associated with risk predictors of osteoporotic fracture using a pleiotropic cFDR method. *Bone*, 2017, 99: 62–68.
- 5) Zhang M,..., **Zhang JG**,..., Deng HW. SNP rs11185644 of RXRA gene is identified for dose-response variability to vitamin D3 supplementation: a randomized clinical trial. *Sci Rep*, 2017, doi: 10.1038/srep40593.
- 6) Zhu W,..., **Zhang JG**,..., Deng HW. Cytosolic proteome profiling of monocytes for male osteoporosis. *Osteoporosis International*, 2016, doi:10.1007/s00198-016-3825-y.
- 7) Zeng Y,..., **Zhang JG**,..., Deng HW. Mass spectrometry based proteomics profiling of human monocytes. *Protein & Cell*, 2016, doi:10.1007/s13238-016-0342-x.
- 8) Xu C, Wu KH, **Zhang JG**,..., Deng HW. Low-, high-coverage and two-stage DNA sequencing in the design of the genetic association study. *Genetic Epidemiology*, 2016, doi:10.1002/gepi.22015.
- 9) Lin DD, **Zhang JG**,..., Wang YP. An integrative imputation method based on multi-omics datasets. *BMC Bioinformatics*, 2016, 17:247.
- 10) Zeng Y,..., **Zhang JG**,..., Deng HW. Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis. *Journal of proteomics*. 2016, 142, 45-52.
- 11) Zhang L,..., **Zhang JG**,..., Deng HW. NETWORK-BASED PROTEOMIC ANALYSIS FOR POSTMENOPAUSAL OSTEOPOROSIS IN CAUCASIAN FEMALES, *Proteomics*. 2016, 16(1):12-28. doi: 10.1002/pmic.201500005.
- 12) Yang TL, Guo Y, **Zhang JG**, Xu C, Tian Q, Deng HW. Genome-wide Survey of Runs of Homozygosity Identifies Recessive Loci for Bone Mineral Density in Caucasian and Chinese Populations. *The Journal of Bone and Mineral Research*. 2015, 30(11):2119-26. doi: 10.1002/jbmr.2558.
- 13) **Zhang JG**,..., Deng HW. Integrative Analysis of Transcriptomic and Epigenomic Data to Reveal Regulation Patterns for BMD Variation. *PLoS One*. 2015, 10(9):e0138524. doi: 10.1371/journal.pone.0138524.
- 14) Tang WL,...**Zhang JG**, MicroRNA-mRNA interaction analysis to detect potential dysregulation in complex diseases. *Network Modeling Analysis in Health Informatics and Bioinformatics*. 2015, 4:1. **Note: Zhang JG is the corresponding author.**
- 15) Liu YZ,..., **Zhang JG**, Deng HW. Attenuated Monocyte Apoptosis, A New Mechanism For Osteoporosis Suggested By A Transcriptome-Wide Expression Study Of Monocytes. *PLoS One*. 2015, 10(2):e0116792. doi: 10.1371/journal.pone.0116792

- 16) Xu C, **Zhang JG**, Wang YP, Deng HW, Li J. Characterization of human chromosomal material exchange with regard to the chromosome translocations using next-generation sequencing data. *Genome Biol Evol.* 2014, 6(11):3015-24
- 17) Tang WL, **Zhang JG**, Lin DD. Pleiotropic Enrichment Analysis with Diverse Omics Data. *Adv Genet Eng.* 2014, 3: e106
- 18) Lin DD, **Zhang JG**, ..., Wang YP, Integrative analysis of multiple diverse omics datasets by sparse group multitask regression, *Frontiers in Cell and Developmental Biology*, section Systems Biology. 2014, 2: 62, doi: 10.3389/fcell.2014.00062.
- 19) Tan LJ, ..., **Zhang JG**, ..., Deng HW. Replication of 6 obesity genes in a meta-analysis of genome-wide association studies from diverse ancestries. *PLoS One.* 2014, 30;9(5):e96149.
- 20) Duan J, **Zhang JG**, Wan MX, Deng HW, Wang YP. Population clustering based on copy number variations detected from next generation sequencing data. *Journal of bioinformatics and computational biology.* 2014, 12(4):1450021.
- 21) He H, ..., **Zhang JG**, ..., Deng HW. Integrative analysis of GWASs, human protein interaction and gene expression identified gene modules associated with BMDs. *J Clin Endocrinol Metab.* 2014, 99(11):E2392-9. doi: 10.1210/jc.2014-2563.
- 22) Deng FY, ..., **Zhang JG**, ..., Deng HW. Is GSN significant for hip BMD in female Caucasians? *Bone.* 2014, 63:69-75.
- 23) Zhang L, ..., **Zhang JG**, ..., Deng HW. Multi-stage genome-wide association meta-analyses identified two new loci for bone mineral density. *Hum. Mol. Genet.* 2013, 23(7):1923-33. doi: 10.1093/hmg/ddt575.
- 24) Duan J, **Zhang JG**, Deng HW, Wang YP. CNV-TV: A robust method to discover copy number variation from short sequencing reads. *BMC Bioinformatics.* 2013, 14:150
- 25) Lin DD, **Zhang JG**, ..., Wang YP. Group Sparse Canonical Correlation Analysis for Genomic Data Integration. *BMC Bioinformatics*, 2013, 14:245
- 26) Chen J, **Zhang JG**, Li J, Pei YF, Deng HW. On combining reference data to improve imputation accuracy. *PLoS One.* 2013, 8(1):e55600.
- 27) Shen H, Li J, **Zhang JG**, Xu C, Jiang Y, Wu ZK, Zhao FP, Liao L, Chen J, Lin Y, Tian Q, Papasian CJ, Deng HW, Comprehensive Characterization of Human Genome Variation by High Coverage Whole-Genome Sequencing of Forty Four Caucasians. *PLoS One*, 2013, 8(4): e59494.
- 28) Tang W, Duan J, **Zhang JG**, Wang Y-P. Subtyping glioblastoma by combining miRNA and mRNA expression data using compressed sensing-based approach, *EURASIP Journal on Bioinformatics and Systems Biology.* 2013(1):2.
- 29) Duan J, **Zhang JG**, Deng HW, Wang YP. Comparative studies of copy number variation detection methods for next-generation sequencing technologies. *PLoS One.* 2013;8(3):e59128
- 30) **Zhang JG**, Li J., Tang W., Deng HW., Fusing Gene Interaction to Improve Disease Discrimination on Classification Analysis. *Advancements in Genetic Engineering.* 2012; 1:102.
- 31) Tang W, Cao H, **Zhang JG**, Duan J, Lin D, Wang YP. Subtyping of glioma by combining gene expression and CNVs data based on a compressive sensing approach. *Advancements in Genetic Engineering.* 2012, 1:101.
- 32) Li H, Wu G, **Zhang JG**, Yang N. Identification of the heart-type fatty acid-binding protein as a major gene for chicken fatty acid metabolism by Bayesian network analysis. *Poult. Sci.* 2010, 89: 1825-1833.
- 33) **Zhang JG**, Li J, Deng HW. Identifying Gene Interaction Enrichment for Gene Expression Data. *PLoS One.* 2009, 4(11): e8064.
- 34) **Zhang JG**, Li J, Deng HW. Class-specific correlations of gene expressions: identification and their effects on clustering analyses. *American Journal of Human Genetics.* 2008, 83(2), 269-277.
- 35) **Zhang JG**, Deng HW. Gene selection for classification of microarray data based on the Bayes error. *BMC Bioinformatics.* 2007, 8:370.
- 36) **Zhang JG**, Zhang Q, Yin ZJ. Study on normalization method for cDNA microarray data. *Journal of Agricultural Biotechnology.* 2006, 14(3): 356-359.
- 37) **Zhang JG**, Yin ZJ, Zhang Q. A non-transformation method for identifying differentially expressed genes from cDNA microarrays. *ACTA GENETICA SINICA (Journal of Genetics and Genomics).* 2006, 33(1):80-88.
- 38) Yin ZJ, Zhang Q, **Zhang JG**, Liu JF. Methodology of Predicting Additive Polygene Effect for Hereditary Resistance Using Generalized Linear Method. *ACTA VETERINARIA ET ZOOTECHNICA SINICA.* 2006, 37(4): 313-316.
- 39) Liu JF, ..., **Zhang JG**. Study on mapping Quantitative Trait Loci for animal complex binary traits using Bayesian-Markov chain Monte Carlo approach. *Science in China Series C-Life Sciences.* 2006, 49(6): 552-559.
- 40) Yin ZJ, Zhang Q, **Zhang JG**, Ding XD. Methodology of mapping quantitative trait loci for ordinal traits of disease resistance in livestock. *ACTA GENETICA SINICA (Journal of Genetics and Genomics).* 2005, 32(11):1147-1155.

- 41) Yin ZJ, Zhang Q, Chen H, **Zhang JG**, Ding XD, Wang CK. Methodology of mapping quantitative trait loci for discrete traits using maximum likelihood, ACTA GENETICA SINICA (Journal of Genetics and Genomics). 2005, 32(9):923-929.
- 42) Yin ZJ, Zhang Q, **Zhang JG**, Ding XD. Mapping Quantitative Trait Loci for Ordinal Traits of Disease Resistance Using Generalized Linear Method. ACTA VETERINARIA ET ZOOTECHNICA SINICA. 2005, 36(12):1241-1246.
- 43) Du MH, Li BG, **Zhang JG**, Wang X, Zhou ZX. Analysis of Application and Prospects for Boer Goat in China, GRASS-FEEDING LIVESTOCK. 2002,2:23-25.
- 44) Zhu WJ, Cao RQ, **Zhang JG**, Wang X, Du MH, Guo CJ. The Molecular Marker-AFLP and Its Application in Genetic Analysis, ANIMAL SCIENCE & VETERINARY MEDICINE, 2001, 19(5):21-23.
- 45) **Zhang JG**, Zhu WJ, Wang X, Zhou ZX, Microsatellite Markers and Its Application in Genetics and Breeding. SWINE PRODUCTION. 2001, 2:34-35.
- 46) Du MH, **Zhang JG**,..., Zhou ZX. Modern Biotechnology and Animal Breeding, ANIMAL SCIENCE & VETERINARY MEDICINE. 2001, 18(6):14-16.
- 47) **Zhang JG**, Wang X, Du MH, Zhou ZX. Species Diversity and the Way to Protect MA SHEN ZHU. JOURNAL OF SHANXI AGRICULTURAL UNIVERSITY (NATURAL SCIENCE EDITION), 2001,21(2):188-191.

## Conference Papers:

- 1) Lin DD, **Zhang JG**, Li JY, Calhoun V, Wang YP, Detection of genetic factors associated with multiple correlated imaging phenotypes by a sparse regression model, International Symposium on Biomedical Imaging (ISBI 2015), New York City, USA, April 16-19, 2015
- 2) Lin DD, **Zhang JG**, Li JY, Calhoun V, Wang YP. Identifying Genetic Connections with Brain Functions in Schizophrenia Using Group Sparse Canonical Correlation Analysis. The International Symposium on BIOMEDICAL IMAGING: From Nano to Macro (ISBI) 2013: 278 - 281
- 3) Duan JB, **Zhang JG**, Deng HW, Wang YP., Detection of common copy number variation with application to population clustering from next generation sequencing data. Conf Proc IEEE Eng Med Biol Soc. 2012:1246-9. doi: 10.1109/EMBC.2012.6346163
- 4) Duan JB, **Zhang JG**, Cao HB, Deng HW, Wang YP, Copy number variation estimation from multiple next-generation sequencing samples, Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine, 2012, pp 555-557
- 5) Duan JB; **Zhang JG**; Lefante, J.; Deng HW; Wang YP, Detection of copy number variation from next generation sequencing data with total variation penalized least square optimization. Bioinformatics and Biomedicine Workshops (BIBMW), 2011 Nov: 3 - 12
- 6) Tang WL., Cao HB., **Zhang JG**, Duan JB, Lin DD, Wang YP, Classifying Six Glioma Subtypes from Combined Gene Expression and CNVs Data Based on Compressive Sensing Approach. Workshop on Cancer Informatics, BIBM, 2011, Nov 12-15.

## Book Chapters:

- **Application of Clinical Bioinformatics.** 2016. Springer Netherlands.
  - i. Biostatistics, Data Mining and Computational Modeling.
  - ii. Gene Expression and Profiling.
  - iii. The Next Generation Sequencing and Applications in Clinical Research.
  - iv. Proteomic Profiling: Data Mining and Analyses.
  - v. Metagenomic Profiling, Interaction of Genomics with Meta-genomics.
- **Multi-omic Data Integration.** 2015. Frontiers Media SA.
  - i. Integrative analysis of multiple diverse omics datasets by sparse group multitask regression.
- **Beef Production and Management Decisions** (Fourth Edition). By Thomas G. Field and Robert E. Talor. 1996. Translation into Chinese (Dr. Qingxiang Meng). 2005. China Agricultural University Press, Beijing, China.

## Honors and awards:

- Semifinalist for Trainee Research Award in the “12th International Congress of Human Genetics”, Oct 11-15, 2011, Montreal, Canada, \$500 (selected as one of 79 out of nearly 450 trainee submissions)
- Outstanding Postdoctoral Research Award from “Association of Chinese Geneticists in America”, 2011, \$200
- Travel Award to “12th Summer Institute in Statistical Genetics”, 2007, University of Washington, Seattle, WA. Waive of registration fee +\$200

## **Professional Services:**

- **Review Editor** of Statistical Genetics and Methodology of Frontiers in Genetics
- **Associate Editor** of Journal of Medical Science
- **Associate Editor** of International Journal of Medical Biotechnology & Genetics
- Serve as a **Judge** for Annual DNA Day Essay Contest sponsored by The American Society of Human Genetics.

## **Professional Societies:**

- American Society of Human Genetics
- Association of Chinese Geneticists in America

## **Professional meeting attended:**

- 64th Annual Meeting of the American Society of Human Genetics, San Diego, California, from Oct 18 – 22, 2014
- 62th Annual Meeting of American Society of Human Genetics, San Francisco, USA, November 6-10, 2012
- 12th International Congress of Human Genetics, Montreal, Canada, October 11-15, 2011
- 61th Annual Meeting of American Society of Human Genetics, Montreal, Canada, October 11-15, 2011
- 60th Annual Meeting of American Society of Human Genetics, Washington D.C., USA, November 2-6, 2010
- Evolution of Next Generation Sequencing, Providence, RI September 27– 29, 2010
- Complete Genomics Incorporation (CGI) 1st User Conference. October 12-13, San Francisco, 2010
- 58th Annual Meeting of American Society of Human Genetics, Philadelphia, PA. USA, November 11-15, 2008
- 57th Annual Meeting of American Society of Human Genetics, San Diego, CA. USA, October 23-27, 2007
- 56th Annual Meeting of American Society of Human Genetics, New Orleans, LA. USA, October 10-13, 2006

## **Paper Review Activities for Journals**

- PLOS ONE
- Genetica
- BMC Bioinformatics
- Bioinformatics
- Network Modeling Analysis in Health Informatics and Bioinformatics
- Statistical Genetics and Methodology of Frontiers in Genetics
- IEEE Gensips
- American Journal of Physical Anthropology

## **Selected Presentation and Posters presented:**

- Genome-Wide Runs of Homozygosity Analyses Identified Recessive Loci for Osteoporosis, 97th Annual Meeting of the Endocrine Society, San Diego, California, from Mar 5 – 8, 2015.
- Integrative Analysis of Transcriptomic and Epigenomic Data to Reveal Regulation Patterns for Osteoporosis, 64th Annual Meeting of the American Society of Human Genetics, San Diego, California, from Oct 18 – 22, 2014
- Integrative analysis of GWASs, human protein interaction and gene expression identified gene modules associated with BMD, 142nd AHA Annual Meeting and Exposition, 2014
- Pathway-based analysis of gene-gene interactions for complex diseases, 62nd Annual Meeting of the American Society of Human Genetics, 2012.

- On Combining Reference Data to Improve Imputation Accuracy, 62nd Annual Meeting of the American Society of Human Genetics, 2012.
- Multi-stage genome-wide association meta-analyses identified two new loci for bone mineral density, 2012, 62nd Annual Meeting of the American Society of Human Genetics.
- Oral Presentation (the 12th International Congress of Human Genetics) –Presentation #118 “Comprehensive characterization of human genome variation by high coverage whole-genome sequencing of forty-four Caucasians”, Montréal, Canada, from Oct 10 – 15, 2011.
- Attenuated monocyte apoptosis, a new mechanism for osteoporosis suggested by a transcriptome-wide expression study of monocytes, Annual Meeting of The American Society for Bone and Mineral Research (ASBMR), 2013.
- Pathway Analysis for Multiple Traits in Genome-Wide Association Studies, 60th Annual Meeting of the American Society of Human Genetics, 2010.
- Gene Set Analysis based on Gene Interactions for Microarray Expression Data. 59th Annual Meeting of the American Society of Human Genetics, 2009.
- Gene Selection for Classification of Microarray Data Based on the Bayes Error, 57th Annual Meeting of the American Society of Human Genetics, 2007.
- Sample size estimation under fixed statistical power and FDR (false discovery rate) control in microarray experiments using a nonparametric test, 56th Annual Meeting of the American Society of Human Genetics, 2006.
- Incorporating single locus tests into haplotype cladistic analysis in case control studies. 56th Annual Meeting of the American Society of Human Genetics, 2006.