

# Hao He

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## CONTACT

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## EDUCATION

### Ph.D in Biostatistics and Bioinformatics

**Aug 2011 — Present**

School of Public Health and Tropical Medicine, Tulane University

Advisor: Hong-Wen Deng, Ph.D.

Research Areas: Network Analysis in Systems Biology, Multi-Omics data, Bioinformatics, Next Generation Sequencing, Data Integration

Thesis title: *Integrative Network Analysis of High-Dimensional Biological Data in Complex Disease for Module Detection and Biomarker Discovery*

### M.Sc

**Aug 2008 — Jun 2011**

Hunan Normal University, China

### B.Sc

**Aug 2004 — Jun 2008**

Hunan Normal University, China

## WORK EXPERIENCE

### Center for Bioinformatics and Genomics, Tulane University

**Aug 2011 — Present**

Research Assistant

### Ochsner Health System

**Jun 2016 — Present**

Intern: Assistant Biostatistician

### Laboratory of Molecular and Statistical Genetics, College of Life Sciences, Hunan Normal University

**Aug 2008 — Jun 2011**

Research Assistant

## RESEARCH BACKGROUND

**Computational Methods:** Machine learning, Gaussian graphical models, generalized linear models, parametric and nonparametric testing

**Programming Skills:** R/Bioconductor, SAS, Python, Awk, Shell

### Research Experience:

- Genome-wide association studies (Plink/seq, GCTA) and Next-Generation Sequencing (eg, bwa, samtools, GATK etc.);
- RNA-seq and Microarray;
- Post-transcriptional regulation by microRNAs;
- Epigenetics in complex diseases such as obesity, osteoporosis, schizophrenia and cancer;
- Pathway and network analysis of biological “omics” data, such as genomics, transcriptomics, proteomics, methylomics, *etc*;

- Develop and apply computational and statistical approaches to integrate and interpret large-scale biological “omics” data, with the goal of identifying disease mechanisms, biomarkers and treatment targets.

## SELECTED HONORS AND REWARD

- Webster Jee Travel Award, 5<sup>th</sup> International Conference on Osteoporosis and Bone Research (ICOBR), Shenzhen, China, 2010
- Scholarship and Travel Award from Summer Institute in Statistical Genetics, Seattle, University of Washington, 2013

## BOOK CHAPTERS

**H He, D Lin, J Zhang, Y Wang, HW Deng: Biostatistics, Data Mining and Computational Modeling.** *Application of Clinical Bioinformatics*, Springer 2016:23-57

## JOURNAL PUBLICATION

1. **He, H.**, Zhang, L., Li, J., Wang, Y.P., Zhang, J.G., Shen, J., Guo, Y.F., and Deng, H.W. (2014). **Integrative analysis of GWASs, human protein interaction, and gene expression identified gene modules associated with BMDs.** *The Journal of clinical endocrinology and metabolism* 99, E2392-2399.
2. **He, H.**, Liu, Y., Tian, Q., Papasian, C.J., Hu, T., and Deng, H.W. (2016). **Relationship of sarcopenia and body composition with osteoporosis.** *Osteoporosis international* 27, 473-482.
3. **He, H.**, Cao, S., Niu, T., Zhou, Y., Zhang, L., Zeng, Y., Zhu, W., Wang, Y.P., and Deng, H.W. (2016). **Network-Based Meta-Analyses of Associations of Multiple Gene Expression Profiles with Bone Mineral Density Variations in Women.** *PloS one* 11, e0147475.
4. Chen, Y.C., Guo, Y.F., **He, H.**, Lin, X., Wang, X.F., Zhou, R., Li, W.T., Pan, D.Y., Shen, J., and Deng, H.W. (2016). **Integrative Analysis of Genomics and Transcriptome Data to Identify Potential Functional Genes of BMDs in Females.** *Journal of bone and mineral research : the official journal of the American Society for Bone and Mineral Research* 31, 1041-1049.
5. **He, H.**, Lei, S.-f., Zhang, F., Li, J., Liu, Y.-j., Tian, Q., and Deng, H.-w. (2010). **Pathway-based genome-wide association analysis identified the biological importance of pyrimidine metabolism pathway contributing to osteoporosis.** *Bone* 47, S365-S366.
6. Lin, D., **He, H.**, Li, J., Deng, H.-W., Calhoun, V.D., and Wang, Y.-P. (2013). **Network-based investigation of genetic modules associated with functional brain networks in schizophrenia.** In *Bioinformatics and Biomedicine (BIBM)*, 2013 IEEE International Conference on. (IEEE), pp 9-16.
7. Lin, D., Zhang, J., Li, J., **He, H.**, Deng, H.W., and Wang, Y.P. (2014). **Integrative analysis of multiple diverse omics datasets by sparse group multitask regression.** *Frontiers in cell and developmental biology* 2, 62.
8. Niu, T., Liu, N., Yu, X., Zhao, M., Choi, H.J., Leo, P.J., Brown, M.A., Zhang, L., Pei, Y.F., Shen, H., **He, H.**, Fu, X., Lu, S., Chen, X.D., Tan, L.J., Yang, T.L., Guo, Y., Cho, N.H., Shen, J., Guo, Y.F., Nicholson, G.C., Prince, R.L., Eisman, J.A., Jones, G., Sambrook, P.N., Tian, Q., Zhu, X.Z., Papasian, C.J., Duncan, E.L., Uitterlinden, A.G., Shin, C.S., Xiang, S., and Deng, H.W. (2016). **Identification of IDUA and WNT16 Phosphorylation-Related Non-Synonymous Polymorphisms for Bone Mineral Density in Meta-Analyses of Genome-Wide Association Studies.** *Journal of bone and mineral research : the official journal of the American Society for Bone and Mineral Research* 31, 358-368.
9. Niu, T., Liu, N., Zhao, M., Xie, G., Zhang, L., Li, J., Pei, Y.F., Shen, H., Fu, X., **He,**

H., Lu, S., Chen, X.D., Tan, L.J., Yang, T.L., Guo, Y., Leo, P.J., Duncan, E.L., Shen, J., Guo, Y.F., Nicholson, G.C., Prince, R.L., Eisman, J.A., Jones, G., Sambrook, P.N., Hu, X., Das, P.M., Tian, Q., Zhu, X.Z., Papasian, C.J., Brown, M.A., Uitterlinden, A.G., Wang, Y.P., Xiang, S., and Deng, H.W. (2015). **Identification of a novel FGFRL1 MicroRNA target site polymorphism for bone mineral density in meta-analyses of genome-wide association studies.** *Human molecular genetics* 24, 4710-4727.

10. Pei, Y.F., Zhang, L., Liu, Y., Li, J., Shen, H., Liu, Y.Z., Tian, Q., He, H., Wu, S., Ran, S., Han, Y., Hai, R., Lin, Y., Zhu, J., Zhu, X.Z., Papasian, C.J., and Deng, H.W. (2014). **Meta-analysis of genome-wide association data identifies novel susceptibility loci for obesity.** *Human molecular genetics* 23, 820-830.

11. Quillen, E.E., Chen, X.D., Almasy, L., Yang, F., He, H., Li, X., Wang, X.Y., Liu, T.Q., Hao, W., Deng, H.W., Kranzler, H.R., and Gelernter, J. (2014). **ALDH2 is associated to alcohol dependence and is the major genetic determinant of "daily maximum drinks" in a GWAS study of an isolated rural Chinese sample.** *American journal of medical genetics Part B, Neuropsychiatric genetics : the official publication of the International Society of Psychiatric Genetics* 165B, 103-110.

12. Tan, L.J., Zhu, H., He, H., Wu, K.H., Li, J., Chen, X.D., Zhang, J.G., Shen, H., Tian, Q., Krousel-Wood, M., Papasian, C.J., Bouchard, C., Perusse, L., and Deng, H.W. (2014). **Replication of 6 obesity genes in a meta-analysis of genome-wide association studies from diverse ancestries.** *PloS one* 9, e96149.

13. Zeng, Y., Zhang, L., Zhu, W., Xu, C., He, H., Zhou, Y., Liu, Y.Z., Tian, Q., Zhang, J.G., Deng, F.Y., Hu, H.G., Zhang, L.S., and Deng, H.W. (2016). **Quantitative proteomics and integrative network analysis identified novel genes and pathways related to osteoporosis.** *Journal of proteomics* 142, 45-52.

14. Zhang, J.G., Tan, L.J., Xu, C., He, H., Tian, Q., Zhou, Y., Qiu, C., Chen, X.D., and Deng, H.W. (2015). **Integrative Analysis of Transcriptomic and Epigenomic Data to Reveal Regulation Patterns for BMD Variation.** *PloS one* 10, e0138524.

15. Zhang, L., Liu, Y.Z., Zeng, Y., Zhu, W., Zhao, Y.C., Zhang, J.G., Zhu, J.Q., He, H., Shen, H., Tian, Q., Deng, F.Y., Papasian, C.J., and Deng, H.W. (2016). **Network-based proteomic analysis for postmenopausal osteoporosis in Caucasian females.** *Proteomics* 16, 12-28.

## SUBMITTED MANUSCRIPT

1. He, H., Cao, S.L., Zhang, J.G., Shen, H., Wang, Y.P., Deng, H.W. **A Statistical Test for Differential Network Analysis Based on Inference of Gaussian Graphical Model.** 2016

2. He, H., Sun, D., Zeng, Y., Wang, R.F., Cao, S.L., Bray, A.G., Chen, W., Shen, H., Sacks, M. F., Qi, L., Deng, H.W. **A Systems Genetics Approach Identified GPD1L and its Molecular Mechanism for Obesity in Human Adipose Tissue.** *Under review*, 2016

3. Han, Y.Y., Zhao, L.J., Yang T.L., Lin, Y., He, H., Tian, Q., Shen, H., Chen, X.D., Deng, H.W. **Multiple Analysis Indicate That NR1I3 Regulating C6 and TNN May Be Involved in Hip BMD Regulation.** *Under review*, 2016

## PRESENTATION

1. Network-based meta-analyses of multiple gene expression profiles with BMD variations in females, *ASHG 2015 Annual Meeting, Baltimore, Oct 6-10 (Poster)*

2. Integrative Analysis of GWASs, Human Protein Interaction and Gene Expression Identified Gene Modules Associated with BMDs, *ASBMR 2014 Annual Meeting, Houston, Sep 12- 15 (Poster)*

3. Pathway-based genome-wide association analysis identified the biological importance of pyrimidine metabolism pathway contributing to osteoporosis, *2010 5<sup>th</sup> International Conference on Osteoporosis and Bone Research (ICOBR), Shenzhen, China, Oct 28-31(Oral Presentation)*

**MENTOR  
EXPERIENCE**

- 05/14/2015–05/27/2015 Mentor of high school student Fahrawn Gill from Metairie park country day school.
- 03/08/2014–06/01/2014 Mentor of visiting scholar Tarneem Mahmoud from Egypt.
- 03/10/2014–07/01/2014 Mentor of graduate students Shanshan Lu and Yuancheng Chen from Hunan Normal University and China Southern Medical University, respectively. Publish a paper in JBMR.