CURRICULUM VITAE
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Education

2009-2015	Ph.D Candidate	School of life sciences, Fudan University, **Shanghai**, China
2005-2009	Bachelor of Science	School of life sciences, Northeast Agricultural University, **Harbin**, China

Experience

2015.04-present,   Postdoc scholar at the Department of Bioengineering, University of California, San Diego, CA
2013.05-2015.04,   Research scholar at the University of Texas Health Science Center at Houston, Houston, TX
2012.12-2013.04,   Visiting Student at the University of Texas Health Science Center at Houston, Houston, TX
2012.01-2013.12,   Internship in the CAS-MPG Partner Institute for Computational Biology, Shanghai, China
2011.12-2014.09,   Internship in the institute of Rheumatology, Immunology and Allergy, Shanghai, China

Key Skills

Programming Language: Five years' experience in R, Perl, awk, sed, bash, Linux
Software: Matlab, SPSS, Graphpad, Original, Photoshop and Illustrator, IGV, SeqMonk
Supercomputer Calculation: Ubuntu and Portable Batch System (torque)
Comprehensive analysis experiences in NGS data including: BS-seq, RRBS, RNA-seq, ChIP-seq, MBD-seq

Ph.D. Dissertation

Cancer Biomarker Research Based on Genome-wide DNA methylation Profile: Diagnosis and Prognosis, 2015, Fudan University. Supervisor: Dr. Li Jin (Fudan University), Dr. Jingde Zhu (Fudan University) , Dr. Jiucun Wang (Fudan University) and Dr. Momiao Xiong (Uthealth).

Awards and Honors

2014, First Place Poster, 17th Annual Human and Molecular Genetics Program Symposium, GSBS, Houston, TX
2012, Silver award of "Cup of Challenge" for College Students' Innovative Undertaking Contest in Shanghai, China
2009-2013, Model Student of Academic Records (2009, 2012, 2013, Fudan University), Shanghai, China
2007, Second prize of National Mathematical Modeling Contest in Heilongjiang province, Harbin, China
2007, Social practice scholarship (NEAU), Harbin, China
2006, National Encouragement Scholarship, Harbin, China
2005-2007, Model Student of Academic Records (NEAU), Harbin, China
2005, National Scholarship (NEAU), Harbin, China

Project Details:

MONOD Project: Methylation Haplotyping for Non-invasive Diagnosis
Role: Bioinformatics Analysis including: Bisulfite-sequencing data alignment, methylation status calling, haplotype calling, and deconvolution analysis (tissue-of-origin prediction)

QAMC Project: Quantitative assessment of methylation biomarker for non-small cell lung cancer
Role: Public data collection, data integration, batch effect elimination, meta-analysis, association study.

NSCLC-MethBio project: Methylation Diagnostic panel for Non-small cell lung cancer based on DNA methylation
Role: Public data collection, data integration, machine learning, feature selection, diagnostic model training and validation, manuscript writing.

AMLMS Project: acute myeloid leukaemia mutation screening based on Chinese pedigree
Role: Bioinformatics and linkage analysis including: DNA-sequencing analysis, SNP variation calling and linkage analysis to identify disease related mutations.

Personal Statement

My research interests and activities mainly centered around the following areas: 1) Susceptibility or heritability components of cancer derived from genetic (SNP, CNV) and epigenetic variation (DNA methylation). 2) Screening, early diagnosis and prognosis model for cancer identification or surveillance. 3) Cancer biomarker research strategy leveraged by high dimensional genome-wide genetic or epigenetic dataset based on microarray or next generation sequencing. 4) Novel cancer related DNA methylation aberrant detection methods develop (bisulfite free detection) and analysis method

(Functional based analysis method). 5) Relationship between elements of genome and epigenome and the interaction routine among environment factors with genetic and epigenetic variations in cancer.

<u>Selective Publications (1-33)</u>

1.	Guo, S., Li, Y., Wang, Y., Chu, H., Chen, Y., Liu, Q., Guo, G., Tu, W., Wu, W., Zou, H. *et al.* (2016) Copy Number Variation of HLA-DQA1 and APOBEC3A/3B Contribute to the Susceptibility of Systemic Sclerosis in the Chinese Han Population. *The Journal of rheumatology*, **43**, 880-886.
2.	Zhang, P., Wang, J., Lu, T., Wang, X., Zheng, Y., Guo, S., Yang, Y., Wang, M., Kolluri, V.K. and Qiu, L. (2015) miR-449b rs10061133 and miR-4293 rs12220909 polymorphisms are associated with decreased esophageal squamous cell carcinoma in a Chinese population. *Tumor Biology*, **36**, 8789-8795.
3.	Wang, J., Li, J., Gu, J., Yu, J., Guo, S., Zhu, Y. and Ye, D. (2015) Abnormal methylation status of FBXW10 and SMPD3, and associations with clinical characteristics in clear cell renal cell carcinoma. *Oncol Lett*, **10**, 3073-3080.
4.	Shen, F., Chen, J., Guo, S., Zhou, Y., Zheng, Y., Yang, Y., Zhang, J., Wang, X., Wang, C. and Zhao, D. (2015) Genetic variants in miR-196a2 and miR-499 are associated with susceptibility to esophageal squamous cell carcinoma in Chinese Han population. *Tumor Biology*, 1-8.
5.	Pan, L.-l., Huang, Y.-m., Wang, M., Zhuang, X.-e., Luo, D.-f., Guo, S.-c., Zhang, Z.-s., Huang, Q., Lin, S.-l. and Wang, S.-y. (2015) Positional cloning and next-generation sequencing identified a TGM6 mutation in a large Chinese pedigree with acute myeloid leukaemia. *European Journal of Human Genetics*, **23**, 218-223.
6.	Lin, N., Jiang, J., Guo, S. and Xiong, M. (2015) Functional Principal Component Analysis and Randomized Sparse Clustering Algorithm for Medical Image Analysis. *PLoS One*, **10**, e0132945.
7.	Jiang, J., Lin, N., Guo, S., Chen, J. and Xiong, M. (2015) Multiple functional linear model for association analysis of RNA-seq with imaging. *Quantitative Biology*, **3**, 90-102.
8.	Guo, S., Yan, F., Xu, J., Bao, Y., Zhu, J., Wang, X., Wu, J., Li, Y., Pu, W. and Liu, Y. (2015) Identification and validation of the methylation biomarkers of non-small cell lung cancer (NSCLC). *Clin Epigenetics*, **7**, 1-10.
9.	Dong, Z., Guo, S., Yang, Y., Wu, J., Guan, M., Zou, H., Jin, L. and Wang, J. (2015) Association between ABCG2 Q141K polymorphism and gout risk affected by ethnicity and gender: a systematic review and meta‐analysis. *International journal of rheumatic diseases*, **18**, 382-391.
10.	Zhao, Y., Xue, F., Sun, J., Guo, S., Zhang, H., Qiu, B., Geng, J., Gu, J., Zhou, X. and Wang, W. (2014) Genome-wide methylation profiling of the different stages of hepatitis B virus-related hepatocellular carcinoma development in plasma cell-free DNA reveals potential biomarkers for early detection and high-risk monitoring of hepatocellular carcinoma. *Clin Epigenetics*, **6**, 1-18.
11.	Zhao, Y., Sun, J., Zhang, H., Guo, S., Gu, J., Wang, W., Tang, N., Zhou, X. and Yu, J. (2014) High-frequency aberrantly methylated targets in pancreatic adenocarcinoma identified via global DNA methylation analysis using methylCap-seq. *Clin Epigenetics*, **6**, 18.
12.	Xiao, Q., Gao, S., Luo, H., Fan, W., Guo, S., Yao, H., Leng, S., Xu, Z., Tao, T. and Liu, X. (2014) 9q33. 3, a stress-related chromosome region, contributes to reducing lung squamous cell carcinoma risk. *Journal of Thoracic Oncology*, **9**, 1041-1047.
13.	Wang, R., Zhang, J., Ma, Y., Chen, L., Guo, S., Zhang, X., Ma, Y., Wu, L., Pei, X. and Liu, S. (2014) Association study of miR-149 rs2292832 and miR-608 rs4919510 and the risk of hepatocellular carcinoma in a large-scale population. *Molecular medicine reports*, **10**, 2736-2744.
14.	Song, X., Guo, S., Chen, Y., Yang, C., Ji, H., Zhang, F., Jiang, Z., Ma, Y., Li, Y. and Jin, L. (2014) Association between HLA-DQA1 gene copy number polymorphisms and susceptibility to rheumatoid arthritis in Chinese Han population. *Journal of genetics*, **93**, 215.
15.	Huang, L., Li, Y., Guo, S., Sun, Y., Zhang, C., Bai, Y., Li, S., Yang, F., Zhao, M. and Wang, B. (2014) Different Hereditary Contribution of the CFH Gene Between Polypoidal Choroidal Vasculopathy and Age-Related Macular Degeneration in Chinese Han PeopleHereditary Contribution of CFH in PCV and AMD. *Investigative ophthalmology & visual science*, **55**, 2534-2538.
16.	He, D., Wang, J., Yi, L., Guo, X., Guo, S., Guo, G., Tu, W., Wu, W., Yang, L. and Xiao, R. (2014) Association of the HLA-DRB1 with Scleroderma in Chinese Population. *PLoS One*, **9**, e106939.
17.	Guo, S., Wang, Y.L., Li, Y., Jin, L., Xiong, M., Ji, Q.H. and Wang, J. (2014) Significant SNPs have limited prediction ability for thyroid cancer. *CANCER MEDICINE*, **3**, 731-735.
18.	Guo, S., Tan, L., Pu, W., Wu, J., Xu, K., Wu, J., Li, Q., Ma, Y., Xu, J. and Jin, L. (2014) Quantitative assessment of the diagnostic role of APC promoter methylation in non-small cell lung cancer. *Clin Epigenetics*, **6**, 1.
19.	Zhao, Y., Zhou, H., Ma, K., Sun, J., Feng, X., Geng, J., Gu, J., Wang, W., Zhang, H. and He, Y. (2013) Abnormal methylation of seven genes and their associations with clinical characteristics in early stage non-small cell lung cancer. *Oncol Lett*, **5**, 1211-1218.

20.   Wu, L., Guo, S., Yang, D., Ma, Y., Ji, H., Chen, Y., Zhang, J., Wang, Y., Jin, L. and Wang, J. (2013) Copy number variations of HLA-DRB5 is associated with systemic lupus erythematosus risk in Chinese Han population. *Acta biochimica et biophysica Sinica*, gmt137.

21.   Wang, Y.-L., Feng, S.-H., Guo, S.-C., Wei, W.-J., Li, D.-S., Wang, Y., Wang, X., Wang, Z.-Y., Ma, Y.-Y. and Jin, L. (2013) Confirmation of papillary thyroid cancer susceptibility loci identified by genome-wide association studies of chromosomes 14q13, 9q22, 2q35 and 8p12 in a Chinese population. *Journal of medical genetics*, **50**, 689-695.

22.   Wang, X., Wang, L., Guo, S., Bao, Y., Ma, Y., Yan, F., Xu, K., Xu, Z., Jin, L. and Lu, D. (2013) Hypermethylation reduces expression of tumor-suppressor PLZF and regulates proliferation and apoptosis in non-small-cell lung cancers. *The FASEB Journal*, **27**, 4194-4203.

23.   Wang, J., Yang, Y., Guo, S., Chen, Y., Yang, C., Ji, H., Song, X., Zhang, F., Jiang, Z. and Ma, Y. (2013) Association between copy number variations of HLA-DQA1 and ankylosing spondylitis in the Chinese Han population. *Genes and immunity*, **14**, 500-503.

24.   Lin, S., Pan, L., Guo, S., Wu, J., Jin, L., Wang, J.-C. and Wang, S. (2013) Prognostic role of microRNA-181a/b in hematological malignancies: a meta-analysis. *PLoS One*, **8**, e59532.

25.   Zhao, Y., Guo, S., Sun, J., Huang, Z., Zhu, T., Zhang, H., Gu, J., He, Y., Wang, W. and Ma, K. (2012) Methylcap-seq reveals novel DNA methylation markers for the diagnosis and recurrence prediction of bladder cancer in a Chinese population. *PLoS One*, **7**, e35175.

26.   Wu, J., Liu, J., Zhou, Y., Ying, J., Zou, H., Guo, S., Wang, L., Zhao, N., Hu, J. and Lu, D. (2012) Predictive value of XRCC1 gene polymorphisms on platinum-based chemotherapy in advanced non–small cell lung cancer patients: a systematic review and meta-analysis. *Clinical Cancer Research*, **18**, 3972-3981.

27.   Wu, J., Wu, J., Zhou, Y., Zou, H., Guo, S., Liu, J., Lu, L. and Xu, H. (2011) Quantitative assessment of the variation in IGF2BP2 gene and type 2 diabetes risk. *Acta Diabetologica*, 1-11.

28.   He, Y., Cui, Y., Wang, W., Gu, J., Guo, S., Ma, K. and Luo, X. (2011) Hypomethylation of the hsa-miR-191 locus causes high expression of hsa-mir-191 and promotes the epithelial-to-mesenchymal transition in hepatocellular carcinoma. *Neoplasia*, **13**, 841-IN823.

29.   Zhou, X., Sun, J., He, Y., Zhang, H., Yu, J., Guo, S., Cai, Y., Hu, X. and Zhu, J. (2010) Correlation of the methylation status of CpG islands in the promoter region of 10 genes with the 5-Fu chemosensitivity in 3 breast cancer cell lines]. *Zhonghua Zhong Liu Za Zhi*, **32**, 328.

30.   Xiang, H., Zhu, J., Chen, Q., Dai, F., Li, X., Li, M., Zhang, H., Zhang, G., Li, D. and Dong, Y. (2010) Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. *Nat Biotechnol*, **28**, 516-520.

31.   Li, Y., Zhu, J., Tian, G., Li, N., Li, Q., Ye, M., Zheng, H., Yu, J., Wu, H. and Sun, J. (2010) The DNA methylome of human peripheral blood mononuclear cells. *PLoS Biol*, **8**, e1000533.

32.   AO, J., GAO, X., QIU, Y. and GUO, S. (2009) Real-time quantitative PCR and the application in the detection of genetically modified plants [J]. *Journal of Northeast Agricultural University*, **6**, 033.

33.   AO, J.-x., GAO, X.-j., QU, B., YUAN, X.-h., LIU, Y., QIU, Y.-w. and GUO, S.-c. (2008) Construction of a standard reference plasmid for detecting exogenous genes in transgenic soybean, maize and rice [J]. *Journal of China Agricultural University*, **6**, 005.