

Shicheng Guo

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Education

2009-2015 Ph.D. School of Life Sciences, Fudan University, Shanghai, China
2005-2009 B.S. School of Life Sciences, Northeast Agricultural University, Harbin, China

Present Position

2020-Pres Assistant Scientist, Department of Medical Genetics, School of Medicine and Public Health, University of Wisconsin-Madison, Madison, WI, USA
2020-Pres Associate Research Scientist, Center for Precision Medicine Research, Marshfield Clinic Research Institute, Marshfield, WI

Experience

2017-2019 Postdoctoral Research Fellow, Center for Precision Medicine Research, Marshfield Clinic Research
2015-2017 Postdoctoral Research Fellow, Department of Bioengineering, University of California, San Diego, CA
2013-2015 Research Assistant/Postdoc, University of Texas Health Science Center at Houston, Houston, TX
2012-2013 Visiting Scholar, University of Texas Health Science Center at Houston, Houston, TX
2012-2013 Internship, CAS-MPG Partner Institute for Computational Biology, Shanghai, China
2011-2014 Internship, Institute of Rheumatology, Immunology and Allergy, Shanghai, China

Patents

Methods and kits for the diagnosis of bladder cancer with urine exfoliated cell
Methods and kits for the prognosis of bladder cancer after surgery with exfoliated cell in urine

Awards and Honors

2019 Computation and Informatics in Biology and Medicine Training Program, UW-Madison/NLM
2014 First Place Poster, 17th Annual Human and Molecular Genetics Symposium, GSBS, Houston, TX
2012 Silver award of "Cup of Challenge" for College Students' Innovative 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

Ph.D. Dissertation

Cancer Biomarker Research Based on Genome-wide DNA methylation Profile: Diagnosis and Prognosis, 2015.
Supervisor: Dr. Li Jin, MOE Key Laboratory of Contemporary Anthropology, Fudan University

Manuscripts in preparation and submitted

1. Zhang H.*, P Dong*, **S Guo***, C. Tao, W Zhao, J Wang, Ramsey Cheung, Augusto Villanueva, H. Ding, Steven J. Schrod†, D. Zhang#, C. Zeng#. Circulating cell-free DNA based low-pass genome-wide bisulfite sequencing aids non-invasive surveillance to Hepatocellular carcinoma. *Science Advances* (submitted)

2. Liu Y., Zhang Z., Kang Z., Zhou X. Wang S., Liu S., Jin Q., **Guo S.**, Nath Swapan., Steven J. Schrodi, Chen W., Liu Y., and Xu H., Interleukin 4 Reverses B cell Anergy by Upregulating Surface IgM on Anergic B Cells and Contributes to the Pathogenesis of Systemic Lupus Erythematosus. (in progress: 90% completed)
3. He D.*, Guo Q.*, Zhu Q.*, Shen J., Jiang T., Tang X., Cheng P., Wang R., Ding Q., Steven J. Schrodi#, **Guo S#.**, Bao C#. Triple Therapy of cDMARDs in Patients with Rheumatoid Arthritis: Results of a double-blind randomized controlled study. (In progress: 80% completed)

Publications

4. **Guo, S.***, J. Liu*, T. Jiang, D. Lee, R. Wang, X. Zhou, Y. Jin, Y. Shen, Y. Wang, F. Bai, Q. Ding, Grace. Wang, J. Zhang, X. Zhou, S.J. Schrodi, D. He (2019). (5R)-5-Hydroxytryptolide (LLDT-8) induces substantial epigenetic mediated immune response network changes in fibroblast-like synoviocytes from rheumatoid arthritis patients. *Scientific Reports*. 9, 11155.
5. Chen S, Pu W, **S. Guo**, Jin L, He D, Wang J (2019). Genome-Wide DNA Methylation Profiles Reveal Common Epigenetic Patterns of Interferon-Related Genes in Multiple Autoimmune Diseases. *Front Genet*. 10: 223.
6. **Guo, S*.**, S. Jiang*, N. Epperla, Y. Ma, M. Maadooliat, Z. Ye, B. Olson, M. Wang, T. Kitchner, J. Joyce, R. Stenn, J.J. Mazza, J.K. Meece, W. Wu, L. Jin, J.A. Smith, J. Wang, S.J. Schrodi (2019). A Gene-Based Recessive Diplotype Exome Scan Discovers FGF6, a Novel Hepcidin-Regulating Iron Metabolism Gene. *Blood*, 133 (88-98)
7. D Jiang., Z He., Y Zhou., F Li., W Pu., X Zhang., X Feng., M Zhang., X Yuecheng., Y Xu., L Jin., **S. Guo#.**, J Wang#, M. Wang# (2018). Epigenetic silencing of ZNF132 mediated by methylation-sensitive Sp1 binding promotes cancer progression in esophageal squamous cell carcinoma. *Cell Death & Disease*, 10, (1).
8. Xu, X.-H., Y. Bao, X. Wang, F. Yan, **S. Guo**, Y. Ma, D. Xu, L. Jin, J. Xu, J. Wang (2018) Hypoxic-Stabilized Epas1 Proteins Transactivate Dnmt1 and Cause Promoter Hypermethylation and Transcription Inhibition of Epas1 in Non-Small Cell Lung Cancer. *The FASEB Journal*, 2018.
9. Wang, C., W. Pu, D. Zhao, Y. Zhou, T. Lu, S. Chen, Z. He, X. Feng, Y. Wang, C. Li, S. Li, **S. Guo#**, J Wang#, M Wang#. (2018) Identification of Hyper-Methylated Tumor Suppressor Genes-Based Diagnostic Panel for Esophageal Squamous Cell Carcinoma (ESCC) in a Chinese Han Population. *Front Genet*, 9:356.
10. Pu, W., C. Wang, S. Chen, D. Zhao, Y. Zhou, Y. Ma, Y. Wang, C. Li, Z. Huang, L. Jin, **S. Guo#**, J. Wang#, M. Wang# (2017) Targeted Bisulfite Sequencing Identified a Panel of DNA Methylation-Based Biomarkers for Esophageal Squamous Cell Carcinoma (ESCC). *Clinical Epigenetics*, 9:129.
11. Lei, Y., L. Liu, S. Zhang, **S. Guo**, X. Li, J. Wang, B. Su, Y. Fang, X. Chen, H. Ke (2017) HDAC7 Promotes Lung Tumorigenesis by Inhibiting STAT3 Activation. *Molecular cancer*, 16(1):170.
12. He, D., J. Liu, Y. Hai, Q. Zhu, Y. Shen, **S. Guo**, W. Zhang, X. Zhou (2017) Increased Dot1l in Synovial Biopsies of Patients with OA and RA. *Clin Rheumatol*, 37:1327-1332
13. **Guo, S*.**, Q. Zhu*, T. Jiang, R. Wang, Y. Shen, X. Zhu, Y. Wang, F. Bai, Q. Ding, X. Zhou (2017) Genome-Wide DNA Methylation Patterns in Cd4+ T Cells from Chinese Han Patients with Rheumatoid Arthritis. *Mod Rheumatol*, 27:441-447.
14. **Guo, S*.**, D. Diep*, N. Plongthongkum, H.-L. Fung, K. Zhang, K. Zhang (2017) Identification of Methylation Haplotype Blocks Aids in Deconvolution of Heterogeneous Tissue Samples and Tumor Tissue-of-Origin Mapping from Plasma DNA. *Nature Genetics*, 49(4):635-642.
15. Geng, X., W. Pu, Y. Tan, Z. Lu, A. Wang, L. Tan, S. Chen, **S. Guo#**, J. Wang#, X. Chen# (2017) Quantitative Assessment of the Diagnostic Role of Fhit Promoter Methylation in Non-Small Cell Lung Cancer. *Oncotarget*, 8(4):6845.
16. Fan, L., L. Chen, X. Ni, **S. Guo**, Y. Zhou, C. Wang, Y. Zheng, F. Shen, V.K. Kolluri, M. Muktiali (2017) Genetic Variant of Mir-4293 Rs12220909 Is Associated with Susceptibility to Non-Small Cell Lung Cancer in a Chinese Han Population. *PLoS One*, 12(4):e0175666.
17. Ding, W., W. Pu, L. Wang, S. Jiang, X. Zhou, W. Tu, L. Yu, J. Zhang, **S. Guo**, Q. Liu (2017) Genome-Wide DNA Methylation Analysis in Systemic Sclerosis Reveals Hypomethylation of IFN-Associated Genes in Cd4+ and Cd8+ T Cells. *Journal of Investigative Dermatology*, 138:1069-1077.

18. Zhang, X., J. Zhang, R. Wang, **S. Guo**, H. Zhang, Y. Ma, Q. Liu, H. Chu, X. Xu, Y. Zhang (2016) Hypermethylation Reduces the Expression of Pnpla7 in Hepatocellular Carcinoma. *Oncology letters*, 12(1):670-674.
19. Suzuki, K., Y. Tsunekawa, R. Hernandez-Benitez, J. Wu, ..., **S. Guo**, ...K. Zhang, J.C. Belmonte (2016) In Vivo Genome Editing Via Crispr/Cas9 Mediated Homology-Independent Targeted Integration. *Nature*, 540(7631):144-149.
20. Shen, F., J. Chen, **S. Guo**, Y. Zhou, Y. Zheng, Y. Yang, J. Zhang, X. Wang, C. Wang, D. Zhao (2016) Genetic Variants in Mir-196a2 and Mir-499 Are Associated with Susceptibility to Esophageal Squamous Cell Carcinoma in Chinese Han Population. *Tumor Biology*, 37(4):4777-4784.
21. Pu, W., X. Geng, S. Chen, L. Tan, Y. Tan, A. Wang, Z. Lu, **S. Guo**[#], X. Chen[#], J. Wang[#] (2016) Aberrant Methylation of Cdh13 Can Be a Diagnostic Biomarker for Lung Adenocarcinoma. *J Cancer*, 7(15):2280.
22. **Guo, S.**, Y. Li, Y. Wang, H. Chu, Y. Chen, Q. Liu, G. Guo, W. Tu, W. Wu, H. Zou (2016) Copy Number Variation of Hla-Dqa1 and Apobec3a/3b Contribute to the Susceptibility of Systemic Sclerosis in the Chinese Han Population. *J Rheumatol*, 43(5):880-886.
23. Zhang, P., J. Wang, T. Lu, X. Wang, Y. Zheng, **S. Guo**, Y. Yang, M. Wang, V.K. Kolluri, L. Qiu (2015) Mir-449b Rs10061133 and Mir-4293 Rs12220909 Polymorphisms Are Associated with Decreased Esophageal Squamous Cell Carcinoma in a Chinese Population. *Tumor Biology*, 36(11):8789-8795.
24. Wang, J., J. Li, J. Gu, J. Yu, **S. Guo**, Y. Zhu, D. Ye (2015) Abnormal Methylation Status of Fbxw10 and Smpd3, and Associations with Clinical Characteristics in Clear Cell Renal Cell Carcinoma. *Oncology letters*, 10(5):3073-3080.
25. Pan, L.I., Y.M. Huang, M. Wang, X.E. Zhuang, D.F. Luo, **S. Guo**, Z.S. Zhang, Q. Huang, S.L. Lin, and S.Y. Wang (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(2):218-223.
26. Lin, N., J. Jiang, **S. Guo**, M. Xiong (2015) Functional Principal Component Analysis and Randomized Sparse Clustering Algorithm for Medical Image Analysis. *PLoS One*, 10(7):e0132945.
27. Jiang, J., N. Lin, **S. Guo**, J. Chen, M. Xiong (2015) Multiple Functional Linear Model for Association Analysis of Rna-Seq with Imaging. *Quantitative biology* (Beijing, China), 3(2):90.
28. **Guo, S.**, F. Yan, J. Xu, Y. Bao, J. Zhu, X. Wang, J. Wu, Y. Li, W. Pu, Y. Liu (2015) Identification and Validation of the Methylation Biomarkers of Non-Small Cell Lung Cancer (NSCLC). *Clinical Epigenetics*, 7(1):3.
29. **Guo, S.**, T. Jiang, R. Wang, Y. Shen, X. Zhu, F. Bai, Q. Ding, G. Chen, D. He (2105) Genome-Wide Dna Methylation Patterns in Cd4+ T Reveal Significant Contribution of Dna Methylation to Rheumatoid Arthritis. *Arthritis & Rheumatology*, 67:1596-1597.
30. Dong, Z., **S. Guo**, Y. Yang, J. Wu, M. Guan, H. Zou, L. Jin, J. Wang (2015) Association between Abcg2 Q141k Polymorphism and Gout Risk Affected by Ethnicity and Gender: A Systematic Review and Meta-Analysis. *Int J Rheum Dis*, 18(4):382-391.
31. Zhao, Y., F. Xue, J. Sun, **S. Guo**, H. Zhang, B. Qiu, J. Geng, J. Gu, X. Zhou, W. Wang (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. *Clinical Epigenetics*, 6(1):30.
32. Zhao, Y., J. Sun, H. Zhang, **S. Guo**, J. Gu, W. Wang, N. Tang, X. Zhou, J. Yu (2014) High-Frequency Aberrantly Methylated Targets in Pancreatic Adenocarcinoma Identified Via Global DNA Methylation Analysis Using Methylcap-Seq. *Clinical Epigenetics*, 6(1):18.
33. Xiao, Q., S. Gao, H. Luo, W. Fan, **S. Guo**, H. Yao, S. Leng, Z. Xu, T. Tao, X. Liu (2014) 9q33.3, a Stress-Related Chromosome Region, Contributes to Reducing Lung Squamous Cell Carcinoma Risk. *Journal of Thoracic Oncology*, 9(7):1041-1047.
34. Wang, R., J. Zhang, Y. Ma, L. Chen, **S. Guo**, X. Zhang, Y. Ma, L. Wu, X. Pei, S. Liu (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(5):2736-2744.

35. Song, X., **S. Guo**, Y. Chen, C. Yang, H. Ji, F. Zhang, Z. Jiang, Y. Ma, Y. Li, L. Jin (2014) Association between Hla-Dqa1 Gene Copy Number Polymorphisms and Susceptibility to Rheumatoid Arthritis in Chinese Han Population. *Journal of Genetics*, 93(1): 215-218.
36. Huang, L*, Y. Li*, **S. Guo***, Y. Sun, C. Zhang, Y. Bai, S. Li, F. Yang, M. Zhao, B. Wang (2014) Different Hereditary Contribution of the Cfh Gene between Polypoidal Choroidal Vasculopathy and Age-Related Macular Degeneration in Chinese Han People. *Investigative Ophthalmology & Visual Science*, 55(4):2534-2538.
37. He, D., J. Wang, L. Yi, X. Guo, **S. Guo**, G. Guo, W. Tu, W. Wu, L. Yang, R. Xiao (2014) Association of the Hla-Drb1 with Scleroderma in Chinese Population. *PLoS One*, 9(9):e106939.
38. **Guo, S.**, Y.L. Wang, Y. Li, L. Jin, M. Xiong, Q.H. Ji, J. Wang (2014) Significant Snps Have Limited Prediction Ability for Thyroid Cancer. *Cancer Med*, 3(3):731-735.
39. **Guo, S.**, L. Tan, W. Pu, J. Wu, K. Xu, J. Wu, Q. Li, Y. Ma, J. Xu, L. Jin (2014) Quantitative Assessment of the Diagnostic Role of Apc Promoter Methylation in Non-Small Cell Lung Cancer. *Clinical Epigenetics*, 6(1):5.
40. Zhao, Y., H. Zhou, K. Ma, J. Sun, X. Feng, J. Geng, J. Gu, W. Wang, H. Zhang, Y. He, **S. Guo**, X. Zhou, J. Yu, Q. Lin (2013) Abnormal Methylation of Seven Genes and Their Associations with Clinical Characteristics in Early Stage Non-Small Cell Lung Cancer. *Oncology Letters*, 5(4):1211-1218.
41. Wu, L., **S. Guo**, D. Yang, Y. Ma, H. Ji, Y. Chen, J. Zhang, Y. Wang, L. Jin, and J. Wang (2013) Copy Number Variations of Hla-Drb5 Is Associated with Systemic Lupus Erythematosus Risk in Chinese Han Population. *Acta Biochim Biophys Sin*, 46(2):155-160.
42. Wang, Y.L. *, S.H. Feng*, **S. Guo***, W.J. Wei, D.S. Li, Y. Wang, X. Wang, Z.Y. Wang, Y.Y. Ma, L. Jin (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. *J Med Genet*, p. jmedgenet-2013-101687.
43. Wang, X., L. Wang, **S. Guo**, Y. Bao, Y. Ma, F. Yan, K. Xu, Z. Xu, L. Jin, D. Lu (2013) Hypermethylation Reduces Expression of Tumor-Suppressor Plzf and Regulates Proliferation and Apoptosis in Non-Small-Cell Lung Cancers. *The FASEB Journal*, 27(10):4194-4203.
44. Wang, J., Y. Yang, **S. Guo**, Y. Chen, C. Yang, H. Ji, X. Song, F. Zhang, Z. Jiang, Y. Ma (2013) Association between Copy Number Variations of Hla-Dqa1 and Ankylosing Spondylitis in the Chinese Han Population. *Genes Immun*, 14(8):500-503.
45. Lin, S., L. Pan, **S. Guo**, J. Wu, L. Jin, J.C. Wang, S. Wang (2013) Prognostic Role of Microrna-181a/B in Hematological Malignancies: A Meta-Analysis. *PLoS One*, 8(3):e59532.
46. Zhao, Y.*, **S. Guo***, J. Sun*, Z. Huang, T. Zhu, H. Zhang, J. Gu, Y. He, W. Wang, K. Ma (2012) Methylcap-Seq Reveals Novel DNA Methylation Markers for the Diagnosis and Recurrence Prediction of Bladder Cancer in a Chinese Population. *PLoS One*, 7(4):e35175.
47. Wu, J., J. Liu, Y. Zhou, J. Ying, H. Zou, **S. Guo**, L. Wang, N. Zhao, J. Hu, D. Lu (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(14):3972-3981.
48. Wu, J., J. Wu, Y. Zhou, H. Zou, **S. Guo**, J. Liu, L. Lu, H. Xu (2011) Quantitative Assessment of the Variation in Igf2bp2 Gene and Type 2 Diabetes Risk. *Acta Diabetologica*, 49 Suppl 1:S87-97.
49. He, Y., Y. Cui, W. Wang, J. Gu, **S. Guo**, K. Ma, X. Luo (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(9):841-853.
50. Zhou, X., J. Sun, Y. He, H. Zhang, J. Yu, **S. Guo**, Y. Cai, X. Hu, J. Zhu (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 [Chinese journal of oncology]*, 32(5):328.
51. Xiang, H., J. Zhu, Q. Chen, F. Dai, X. Li, M. Li, H. Zhang, G. Zhang, D. Li, Y. Dong, L. Zhao, Y. Lin, D. Cheong, J. Yu, J. Sun, X. Zhou, K. Ma, Y. He, Y. Zhao, **S. Guo**, M. Ye, G. Guo, Y. Li, R. Li, X. Zhang, L. Ma, K. Kristiansen, Q. Guo, J. Jiang, S. Beck, Q. Xia, W. Wang, J. Wang (2010) Single Base-Resolution Methylome of the Silkworm Reveals a Sparse Epigenomic Map. *Nature Biotechnology*, 28(5):516-520.

52. Li, Y., J. Zhu, G. Tian, N. Li, Q. Li, M. Ye, H. Zheng, J. Yu, H. Wu, J. Sun, H. Zhang, Q. Chen, R. Luo, M. Chen, Y. He, X. Jin, Q. Zhang, C. Yu, G. Zhou, J. Sun, Y. Huang, H. Zheng, H. Cao, X. Zhou, **S. Guo**, X. Hu, X. Li, K. Kristiansen, L. Bolund, J. Xu, W. Wang, R. Li, S. Beck, J. Wang, X. Zhang (2010) The DNA Methylome of Human Peripheral Blood Mononuclear Cells. *PLoS Biol*, 8(11):e1000533.
53. Ao, J.X., X.J. Gao, Y.B. Yu, B. Qu, X.H. Yuan, Y. Liu, **S. Guo** (2009) Construction of a General Standard Molecule for the Qualitative Detection in Different Transgenic Foodcrops. *Journal of Northeast Agricultural University* (English Edition), 16(2):37-41.
54. Ao, J., X. Gao, Y. Qiu, **S. Guo** (2009) Real-Time Quantitative PCR and the Application in the Detection of Genetically Modified Plants [J]. *Journal of Northeast Agricultural University*, 6:033.
55. Ao, J.X., X.J. Gao, B. Qu, X.H. Yuan, Y. Liu, Y.W. Qiu, **S. Guo** (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.

Books and book Chapters

Tumor suppressor genes mediated by DNA hypermethylation, Tumor Suppressor Genes, IntechOpen (in preparation)

Presentations

Invited Talks

1. **Guo S** (2019), Gene based Genome-wide association study with next-generation data to identify novel disease and pharmaceutical targets. Spring House, PA, US. 12/09/2019
2. **Guo S** (2019), Weill Cornell Medicine. NY, US. 11/30/2019
3. **Guo S** (2019) Genome-wide cell-free DNA fragmentation in patients with cancer and cell-free DNA based cancer diagnosis, MCRI, Postdoc Journal Club. 08/19/2019
4. **Guo S**, Schrodi S (2019). Mapping Hemochromatosis Genes using a Novel Recessive Diplotype Approach in the Marshfield Clinic Personalized Medicine Research Project (PMRP), MCRI Scientific Seminar, 03/13/2019
5. **Guo S**, Schrodi S (2019). Identification of novel Hemochromatosis genes using Recessive Diplotype Approach in the Marshfield Clinic Personalized Medicine Research Project (PMRP), MCRI scientist meeting, 04/15/2019
6. **Guo S**, Schrodi S (2018). DNA Methylation Research in Rheumatology Arthritis: Promising and Challenging, AMRBSA, 2018, Shanghai

Poster Presentations

7. **Guo S**, Schrodi Steven (2019). Deep learning prediction of chemotherapy response using multi-omics features, ASHG 2019, id: 1920576, Houston, Texas
8. **Guo S**, Li L, Jiang J, Lin N., Chen M. Jin L, Xiong M. (2014) A novel approach to MBD-seq data analysis based on functional principal component analysis (FPCA) 2014, ASHG
9. **Guo S**, Xiong M, Jin L, Wang J. (2014). Epigenetic Approaches for non-small cell lung cancer diagnosis based on DNA methylation, HGV2014, Sep 17- Sep 19, Belfast, Northern Ireland, UK
10. Lin N, Jiang J, Guan X, Yu X, **Guo S** and Xiong MM. (2014). A novel method for ultrasound image analysis. NCI-NIBIB Point of Care Technologies for Cancer Conference. January 8-10, 2014, Natcher Center, NIH campus- Building 45, Bethesda, Maryland.
11. Lin N, Jiang J, **Guo S**, Yu X, Ma L and Xiong MM. (2014). Classification Analysis of Big Image Data. Statistical and Computational Theory and Methodology for Big Data Analysis. Feb 9-Feb 14, 2014, Calgary, AB Canada.
12. Yu J, Lin N, Ma L, **Guo S** and Xiong MM. (2014). Cloud computing for joint big genetic, epigenetic and image data analysis. Keystone Symposia: Big Data in Biology, March 23-25, 2014. Fairmont San Francisco, San Francisco, California.
13. **Guo S**, Wang J, Li Jin. (2012) A Panel of Epigenetic Biomarkers of NSCLC identified by genome-wide DNA methylation microarray, 2012, ASHG

Journal Service

Conferences Reviewer	BIBM 2014: Bioinformatics and Biomedicine ASHG 2017: Genetics and Epigenetics
Editorial Board Member	Journal of Clinical Epigenetics Austin Journal of Lung Cancer Research Jacobs Journal of Biomarkers SM Journal of Pulmonary Medicine SRL Oncology & Hematology

Ad hoc Reviewer

Journals: *Journal of Thoracic Oncology* (IF=12.5)
Clinical Cancer Research (IF=8.9)
Cancer Letter (IF=6.5)
Cancer (IF=6.2)
Brain Behavior and Immunity (IF=6.1)
Clinical Epigenetics (IF=5.5)
PLoS Genetics (IF=5.2)
Frontiers in Cell and Developmental Biology (IF=5.2)
Epigenetics (IF=5.0)
Journal of Genetics and Genomics (IF=4.6)
Epigenomics (IF=4.4)
Scientific Reports (IF=4.0)
Frontiers in Oncology (4.1)
Frontiers in Genetics (IF=4)
Journal of Cancer (IF=3.18)
PLoS One (IF=3)
Functional & Integrative Genomics (IF=2.7)
Genes and Immunity (IF=2.6)
BMC Genetics (IF=2.5)
Molecular Genetics & Genomic Medicine (IF=2.4)
Cancer investigation (IF=1.9)
Medicine (IF=1.8)
Biomarker (IF=1.7)

Ongoing Research

CIBM: Phenome-wide association study maps genetic variation in epigenetic factors with human complex diseases.
Role: CIBM training grant for Dr. Guo

Genome-wide DNA methylation Patterns of Atrial Fibrillation Patients derived from Marshfield Clinic PMRP cohort
Role: Co-Investigator in collaboration with Dr. Ingrid Glurich and Dr. Michael Caldwell (PI)

Detecting shared chromosomal regions and compound heterozygous effects for diseases within PMRP
Role: Co-Investigator with Dr. Steven Schrodi

Sparse conditional generate adversarial networks for personalized biomarker selection and treatment effect estimation
Role: Co-Investigator with Dr. Momiao Xiong

Genome-wide DNA methylation profiling for a novel identified COL2A1 caused synovial chondromatosis pedigree
Role: Co-Investigator in collaboration with Dr. Steven Schrodi and Dr. Dongyi He

Genome-wide association study to identify novel susceptibility genes for rheumatoid arthritis
Role: Co-Investigator in collaboration with Dr. Steven Schrodi and Dr. Dongyi He

Genome-wide association study to identify novel pharmacogenomics genes for triple-therapy in rheumatoid arthritis
Role: Co-Investigator in collaboration with Dr. Steven Schrodi and Dr. Dongyi He

Deep Learning Prediction of Chemotherapy Response using Multi-Omics Features
Role: Principal Investigator, funded by MCRI.

Completed Research

Unified Statistical Methods for Sequence-Based Association Studies. NIGMS
Role: Co-Investigator (2012-2015) in collaboration with Dr. Momiao Xiong (PI)

Statistical Methods for Finding Missing Heritability NHLBI
Role: Co-Investigator (2012-2014) in collaboration with Dr. Momiao Xiong (PI)

Understanding the genetic architecture of schizophrenia in Chinese population NIMH
Role: Co-Investigator (2013-2014) in collaboration with Dr. Momiao Xiong (PI)

Programming Language and High Performance Computing

Linux/Ubuntu with 10 years experiences

Perl with 10 years experiences.

R with 8 years experiences.

PBS/ TORQUE with 7-year experiences.

MYSQL with 4-year experiences.

Python with 3-year experiences.

Madison/HT-condor with 2-year experiences

More information: please check my website: <https://shicheng-guo.github.io>