Shicheng Guo, Ph.D. candidate(2009-2014), School of Life Sciences, Fudan University. His supervisors are Li Jin, Jiucun Wang and Momiao Xiong (Uthealth, Houston). The realm which he focus on now is computational biology and medical statistics including: manifold kinds of microarray analysis, meta-analysis, genome-wide SNP, RNA, Methylation, CNV analysis based on next generation sequencing technology. In the past three years, he had participated in series of attractive research( Yan-Huang methylome project et.al), and participated in publishing several interesting papers( Nature Biotechnology, Plos Biology et al) and two Chinese patents. Specially, in clinical field, he want to explore some high sensitive and specific diagnosis and prognosis biomarkers for some complex disease such as immune diseases, cancer. And then establish some high accuracy disease prediction models so that doctors can make more felicitous decision to his/her patients. 5 years Perl, R usage exprience under Ubuntu system and skilled text minning operation ensure that he can make deeply data or text analysis in biology or medical family or disease data.

As the development of sequencing technology, more and more sequence data will be come out in the few years, especially with the stimulation of 1000 Genome, TCGA Project,10000 UK Project, HEP Project. So utilizing large-scale complex data sets in recent genomic and familial studies and by important biological questions that emerges from the analysis of these data. my current interests can be divided into two parts: 1) Development of biomarkers for early dectect/screening of complex disease, such as cancers, diabetes, or multiple systemic immune diseases which based on DNA methylation, gene expression, miRNA in the context of genetic variations, such as SNP, CNV. 2) Develop effective risk models for health surveillance so that provide early warning for some disease which are difficult to cure. 3) Explore the mechanism of the aging and the corresponding pathogenic risk. 4) Association study related SNP-SNP interaction