Shicheng Guo
Ph. D Student
MOE Key Laboratory of Contemporary Anthropology
School of Life Sciences
Fudan University
Shanghai, China
June 9, 2012

Dear Mr. Guo:

I am glad that you will have opportunity to study abroad by financial support from Fudan University, China. I invite you to study and to do research work in the Human Genetics Center and Division of Biostatistics in the School of Public Health at the University of Texas Health Science Center at Houston to pursue your continuous graduate study for Ph. D degree and research under my advise for four months from September 15, 2012 to January 15, 2013.

My research areas are to develop methods and algorithms in biostatistics and computational systems biology. Your background in statistics, bioinformatics and genetics will match our research interests in general statistic genetics, population genetics and computational systems biology.

Computational systems biology and biostatistics are the frontier in the research of biomedicine. Recently, I and my colleagues in Medical School at University of Texas at Houston and Baylor College of Medicine are carrying out several projects for investigation of population genomics, cancer genomics and mechanism of complex diseases and drug target discovery. These projects are financially sponsored by NIH in the U. S. A.

Diseases are caused by dynamic interaction among many genes and many environmental exposures through regulation and metabolism. Biological phenomena of the entire organism are not only determined by steady-state characteristics of the biological systems, but also by intrinsic dynamic properties of biological systems, including stability, transient-response, and controllability, which determine how the systems maintain their functions and performance under a broad range of random internal and external perturbations. Pending conceptual and statistical challenges are (1) how to identify and construct multi-level networks which are complex organization of the genetic, epigenetic, biochemical and physiological subsystems and

the interactions of these with a lifetime of environmental exposures and involved in endpoint clinical phenotypes under perturbation of environments, (2) how to develop mathematical models for complex networks that determine the health status of individuals and statistical methods for estimation parameters in the network, (3) how to develop statistics to test for differential methylation in a genomic region, (5) to identify mEQTL, and (6) how to connect genetic and epigenetic variations to disease outcomes through cellular intermediate traits.

One of our project is to develop novel analytic strategies for analyzing the large data sets that come from next-generation sequencing technologies, jointly testing association of the entire spectrum of genomic and epigenomic variations , which will finally lead to deciphering path from genomic information to complex diseases.

If you come here you will take part in this project. I am sure that the accomplishment of this project will have broad impact in biomedical research and deep implication on your career development.

Since you will visit University of Texas School of Public Health as a visiting scholar you do not need to pay tuition fees for registering courses.

I am glad that your English is excellent and have thorough knowledge in statistics, bioinformatics, and genetics. Computational biology is an interdisciplinary research area. Your knowledge and skills will be very valuable to the analysis of next-generation sequencing data.

As you know that I have collaborated with Professor and Vice President Li Jin at Fudan University in China, working on projects involving statistical genetics, population genetics and computational systems biology. I am sure that you will go back to China to continuously pursue Ph. D degree after you finish study in U. S.

Sincerely,

Momiao Xiong
Professor
Human Genetics Center
Division of Biostatistics
School of Public Health
University of Texas Health Science Center at Houston