



# The University of Georgia

Institute of Bioinformatics

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Dear Dr. Brun:

I am writing to give my strongest recommendation to Dr. Zhengchang Su, a research assistant scientist in my lab, for an assistant professor position in your organization. I have known Zhengchang since late 2002 when he joined my group at Oak Ridge National Laboratory (ORNL) as a postdoctoral research fellow. He came to my lab with strong recommendation from his Ph.D. thesis advisor and his then postdoctoral advisor Dr. Steve Harvey for who Zhengchang worked for a few months. He decided to leave Harvey Lab because Steve was recruited to Georgia Tech as an eminent scholar from UAB and Zhengchang did not want to live in a big city like Atlanta. When our lab moved from ORNL to the University of Georgia, Zhengchang moved with me.

Zhengchang was recruited to our lab to develop computational techniques for inferring wiring diagrams of regulatory, signaling and metabolic networks in microbial organisms, as part of the DOE GTL project. At that time, nobody in my group had a clear idea about how to do this as this problem represents a very challenging problem which many bioinformaticians and computational biologists have been working hard trying to figure out effective ways to tackle. For about six months, Zhengchang, another postdoc in the group and I myself struggled together trying to make headways in tackling this very difficult problem. The first breakthrough came when Zhengchang developed a sophisticated computational pipeline for integrating multiple pieces of information, including protein functions, protein-protein interactions, protein-DNA interactions, which can piece together network diagrams. He then quickly predicted a network model, using this pipeline, for the phosphorus assimilation process in *Synechococcus sp* WH8102, which led to the first publication by our group in this area. The unique feature of this computational pipeline is its powerful capability in fusing multiple sources of information, derived through comparative genome analysis and analysis of microarray and proteomic data, for inference of network topologies of biological systems and processes. This work laid the foundation of our work in this whole area, which has further led to the formation of our Pathway/Network Inference and Modeling group in our lab. Zhengchang is the leader of this group now with five Ph.D. level scientists.

Zhengchang's second major work is in the prediction of *ntcA* regulon, the core group of genes involved in nitrogen assimilation, in the 11 sequenced *cyanobacterial* genomes. In this work, he first developed a highly novel and very effective method for prediction of transcriptional regulatory binding motifs at a genome scale, and then applied this technique to successfully identify a substantial subset of genes regulated by the *ntcA* regulator, many of which were later

validated by microarray and proteomic data. This work has been published in *Nucleic Acids Research*, one of the top journals in the field. I expect that this work could become a highly cited work as it provides a powerful way, mainly through comparative genome analysis, to make computational prediction of component genes involved in a complex biological system or process, before much is known about the target system/process. Such a prediction could provide highly useful guidance for further experimental design.

Zhengchang's recent work on prediction of the cross-talk network between nitrogen assimilation and photosynthesis in *cyanobacteria* could represent a milestone type of work as it for the first time proposed a detailed molecular model for how the nitrogen assimilation process and the photosynthesis process coordinate with each other, based on comparative genome analysis and microarray data analysis. While researchers have previously suspected that these two important biological processes may work together through some unknown mechanism, Zhengchang's computational prediction has provided a working model for this complex interaction process, which could guide experimental design for investigating these two highly important biological processes. The significance of this work is in that it demonstrates that through computational prediction, network models could be developed for very complex biological processes before experimental investigation. While such a model might not be 100 % accurate, it can provide highly useful guidance to experimentalists in their experimental investigation.

In addition to his own research work, Zhengchang has been playing key roles in guiding other members' research in his group, which has led to multiple joint publications, including new methods for operon prediction, methods for pathway mapping, methods for identification of functional modules and prediction of various biological networks.

One of the most amazing things about Zhengchang is that his biological knowledge, ranging from human physiology to environmental effects on microbial organisms, is unbelievably good. In our lab with over 20 people with trainings in different areas of biology, he is by far the most knowledgeable person about biology in general. His understanding about biology seems to be always deeper than other members of our lab and often than our experimental collaborators. I am always amazed by his level of understanding about the microbial systems we have been investigating.

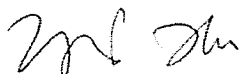
Because of his knowledge and understanding about biology, he always knows the right biological problems to tackle, which makes him a natural leader for a scientific group. Technically, Zhengchang is very strong in computer algorithm design, statistical analysis and method develop and computer programming, making him a highly skillful bioinformatician. I consider him as a first-rate bioinformatician/computational biologist and one of the best postdocs among the 20+ postdocs I have supervised since 1997, some of whom have gone on to take faculty positions in different universities.

I have to say that I have a mixed feeling about him leaving as he is one of the most valuable people in my lab. Late last year, I promoted him to be an assistant research scientist (or called assistant research professor) and hope that he will stay here for a couple of more years. But I respect his decision to look for a more independent position such as a staff scientist position in a national lab or a faculty position in a university. I believe that he will be highly successful anywhere he goes.

On a personal level, Zhengchang is a wonderful person to work with – he is an ideal person to collaborate with as he is always easy to work with, willing to help and good to have a scientific discussion with. Hate to lose him but wish him most successful in his new career. Please let me

know if I can be of any further assistance in your evaluation of Zhengchang's credential and suitability for the position you are trying to fill.

Sincerely yours,

A handwritten signature in black ink, appearing to read 'Ying Xu', written in a cursive style.

Ying Xu, Ph.D.  
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