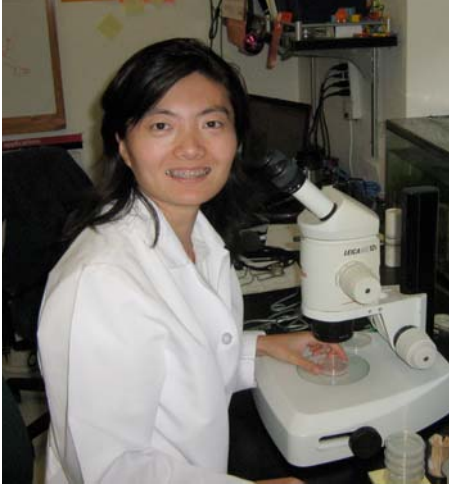


# New Faculty in Rice Biochemistry & Cell Biology



## Weiwei Zhong

Assistant Professor of Biochemistry & Cell Biology

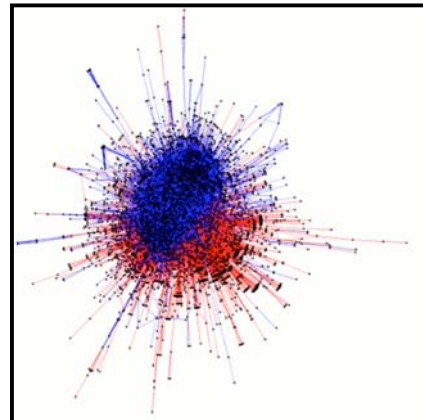
B.S. Biology (1997) University of Science and Technology of China

Ph.D. Cellular Biology (2002) University of Georgia

M.S. Computer Science (2003) University of Georgia

How does a genome specify the properties of an organism? One approach to answer this question is to inactivate a single gene and study the defects. As our knowledge deepens, we wish to identify the regulators and targets of each gene, and to study

complex traits and diseases that are controlled by multiple genes and pathways. The one-gene approach becomes inadequate for these purposes and a network view of gene function becomes essential. Our goal is to achieve a system-level understanding of genetic interaction networks. We are using both computational and experimental approaches to reach this goal.



### 1. Computational prediction of genetic

**interactions.** How to extract reliable genetic interaction predictions from genomic data that are often incomplete and of heterogeneous quality?

Taking a bioinformatic approach, we are developing data mining systems that apply machine-learning algorithms to statistically integrate these genomic data.

**2. Experimental identification of genetic interactions.** Using the nematode *C. elegans* as a model system, we are conducting large-scale, quantitative screens to reveal the genetic interaction networks that regulate development, behavior, and physiology. We are also developing automated systems that employ computer vision and robotics to facilitate such high-throughput screens.

Reliable computational prediction of genetic interactions can help prioritize candidates for experimental testing. In return, large-scale experimental results can provide an invaluable resource for further data mining. With the systems biology approach, we expect to bring new insights into the classical quest for underlying mechanisms of genome function.

### **Selected Publications:**

Zhong, W. and Sternberg, P.W. "Automated data integration for developmental biological research." *Development*, 134 (2007): 3227-3238.

Zhong, W. and Sternberg, P.W. "Genome-wide prediction of *C. elegans* genetic interactions." *Science*, 311 (2006): 1481-1484.

Zhong, W., Feng, H., Santiago, F.E., and Kipreos, E.T. "CUL-4 ubiquitin ligase maintains genome stability by restraining DNA replication licensing." *Nature*, 423 (2003): 885-889.

Feng, H.\*, Zhong, W.\*, Punkosdy, G., Gu, S., Zhou, L., Seabolt, E.K., and Kipreos, E.T. "CUL-2 is required for the G1-to-S-phase transition and mitotic chromosome condensation in *Caenorhabditis elegans*." *Nature Cell Biology*, 1 (1999): 486-491.

\* equal contribution