

# Zhenyuan (Jerry) Lu

## Curriculum Vitae

Doreen Ware Lab  
Cold Spring Harbor Laboratory  
Cold Spring Harbor, NY 11724

Phone: (636)-288-4160  
Email: luj@cshl.edu

### **Education:**

MS, Computer Science, University of Oklahoma, Norman, OK, 2004

MS, Biochemistry, University of Oklahoma, Norman, OK, 2001

BS, Biochemistry, East China University of Science and Technology, Shanghai, China, 1997

### **Research Interests:**

Large-scale data integration and numeric simulation

Scientific visualization

Biological applications development

### **Professional Experience:**

CSHL, Cold Spring Harbor, NY, Scientific Informatics Developer, 09/2007 – present

- Designed and performed analysis pipeline for the phase of Craig Venter's genome on Linux cluster.
- Maintained and enhanced the Hapmap website content and software infrastructure, designed GBrowser plugin for genotype imputation and various glyphs for visualization.

Monsanto Co., St. Louis, MO, Bioinformaticist, 09/2004 – 08/2007

- Developed web applications to support Marker Assisted Selection in three commercial pig lines; implemented a streamlined process to manage marker nomination, animal selection, and genotype data QC using Model-View-Control framework (Maypole and Catalyst) and AJAX technology
- Designed and implemented a scheme for selecting informative SNP markers with high assay conversion rate by using Perl and BioPerl, which led to the construction of most comprehensive porcine genetic map with close to 6000 SNP markers
  - 1) Ranked each marker by an index of multiple factors (including polymorphism, location, and breed specificity) to identify most appropriate markers to nominate
- Implemented CMAP in-house and built comprehensive human-porcine comparative map
- Served as web chair for annual company-wide scientific conference
  - 1) Revamped the website to better fit company needs
  - 2) Responsible for maintaining and curating scheduling information for each mini-symposia

Monsanto Co., St. Louis, MO, Research Intern, 06/2003 – 09/2004

- Designed and implemented a streamlined process for targeted SNP discovery by using Perl and bioinformatics software
  - 1) Performed DNA sequence processing, screening, and primer design
  - 2) Performed linkage disequilibrium based SNP marker clustering

Georgetown University, Washington, DC, Data Specialist, 06/2004 – 09/2004

- Designed and implemented a software by using Bioperl package to analyze sequence data and generate report for the studies of the effect of polymorphism in KIR receptor in human immune system
- Built a system by using Perl and Bioperl to automate the process of retrieving data from public database server through Internet, transforming data, and updating local database