Huwenbo Shi

CONTACT INFORMATION	Apt. 201, 925 Weyburn Place Los Angeles, CA, 90024	310-994-3519 shihuwenbo@ucla.edu

RESEARCH INTERESTS

Bioinformatics, statistical genetics, machine learning

EDUCATION

University of California Los Angeles, Los Angeles, CA

Ph.D., Bioinformatics Interdepartmental Program, *Expected:* June 2018
- Tentative Thesis Topic: *Modeling linkage disequilibrium in large-scale genetic studies of complex human traits*
- Advisor: Bogdan Pasaniuc, Ph.D.

University of California Los Angeles, Los Angeles, CA

B.S., Computer Science, June 2013
- Advisor: Richard Korf, Ph.D.

ACADEMIC EXPERIENCE

Graduate Student Researcher   June 2014 to present
Bioinformatics Interdepartmental Program,
University of California Los Angeles, Los Angeles, CA
Supervisor: Bogdan Pasaniuc, Ph.D.

Summer Research Student   July 2013 to Sept 2013
Pathology Department,
University of California Los Angeles, Los Angeles, CA
Supervisor: Bogdan Pasaniuc, Ph.D.

Undergraduate Student Researcher   Sept 2010 to June 2012
Computer Science Department,
University of California Los Angeles, Los Angeles, CA
Supervisor: Glenn Reinman, Ph.D.

INDUSTRY EXPERIENCE

Software Development Engineer Intern   June 2012 to Sept 2012
Supply Chain Optimization Team,
Amazon.com, Seattle, Washington
Supervisor: Timothy Tien

REFEREED JOURNAL PUBLICATIONS

1. **Shi, H.**, Pasaniuc, B., Lange, K. "A multivariate Bernoulli model to predict DNaseI hypersensitivity status from haplotype data." *Bioinformatics 2015*.

2. Pasaniuc B., Zaitlen N., **Shi H.**, Bhatia G., Gusev A., Pickrell J., Hirschhorn J., Strachan D.P., Patterson N., Price A.L. "Fast and accurate imputation of summary statistics enhances evidence of functional enrichment." *Bioinformatics 2014*

3. Orozco L.D., Morselli M., Rubbi L., Guo W., Go J., **Shi H.**, Lopez D., Furlotte N.A., Bennett B.J., Farber C.R., Ghazalpour A., Zhang M.Q., Bahous R., Rozen R., Lusis A.J., Pellegrini M. "Epigenome-wide association of liver methylation patterns and complex metabolic traits in mice." *Cell Metabolism 2015*

4. Gusev A., Ko Arthur., **Shi H.**, Bhatia G., Price A., Pajukanta P., Pasaniuc B., et al. "Integrative approaches for large-scale transcriptome-wide association studies." *Nature Genetics 2016.*

5. Gusev A., **Shi H.**, Kichaev G., Price A., Pasaniuc B., et al. "Genomic functional atlas of prostate cancer heritability in European and African Americans reveals extensive tissue-specific regulation."
Nature Communication (in press).

SUBMITTED JOURNAL PUBLICATIONS

1. **Shi, H.**, Kichaev, G., Pasaniuc B. "Contrasting the genetic architecture of 30 complex traits from summary association data." *American Journal of Human Genetics (in revision)*

PROJECTS IN PROGRESS

1. **Shi, H.**, et al. "Estimating genetic correlation between gene expression and complex trait from summary association data."

2. Mancuso, N., **Shi, H.**, Gusev A., Pasaniuc B. "Transcriptome-wide association study of 30 complex traits."

POSTERS

1. **Shi, H.**, Kichaev, G., Pasaniuc B. "Fine-scale mapping of genomic heritability using summary association statistics." *ASHG 2015*

2. Kichaev, G., **Shi, H.**, Roytman M., Pasaniuc B. "Large scale integrative fine mapping over 20 complex traits spanning 2.2 million phenotypic measurements." *ASHG 2015*

3. Mancuso, N., **Shi, H.**, Gusev A., Pasaniuc B. "Enhanced methods for gene expression imputation from genetic variation data." *ASHG 2015*

PRESENTATIONS
- Bioinformatics IDP Retreat, Los Angeles, CA   May 2015

SOFTWARE

1. ImpG-Summary – Imputation from summary statistics

AWARDS AND FELLOWSHIPS
- 1st year Bioinformatics IDP Fellowship, UCLA   2013-2014

SERVICES	• Reviewer for the journal *Bioinformatics*	January 2015
	• Reviewer for the conference *ISBRA 2015*	March 2015
	• Reviewer for the journal *Bioinformatics*	March 2016

HARDWARE AND SOFTWARE SKILLS

Computer Programming:
- C, C++, Java, CUDA, Matlab, Python, R, Unix shell script

Hardware and Systems:
- Graphics Processing Unit, Distributed Computing System

COURSES TAKEN

- Linear Programming, Convex Optimization, Optimization Methods for Large-Scale Systems, Monte Carlo Methods for Optimization, Optimization Methods in Biology, Matrix Algebra and Optimization
- Applied Probability, Bayesian Statistics, Theoretical Statistics, Statistical Methods in Computational Biology, Multivariate Analysis, Machine Learning and Pattern Recognition

LANGUAGES

- Chinese, English