

XIU HUANG

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SUMMARY OF SPECIALTIES

Cancer Genomics, Human Genetics, Next-Generation Sequencing Analysis, Omics Data Integration, ctDNA Mutation Calling, Microarray Data Analysis, Biomarker Identification, Pathway Analysis, Statistical Modeling, Machine Learning, Natural Language Processing, Network Analysis

EDUCATION

YALE UNIVERSITY

Expected May, 2016

Ph.D., *Program in Computational Biology and Bioinformatics*

New Haven, CT

- Advisor: Prof. Hongyu Zhao
- Thesis Title: Novel Statistical Methods for Identification and Interpretation of cancer biomarkers

HUAZHONG UNIVERSITY OF SCIENCE AND TECHNOLOGY (HUST)

June, 2010

B.E., *Bioinformatics*

Wuhan, China

- Graduate with Honors

RESEARCH EXPERIENCE

Yale Center for Statistical Genomics and Proteomics

Aug 2011 - Present

Research Assistant

New Haven, CT

- **Patient stratification:** Integratively analyzed the transcriptomic data from solid tumor and adjacent normal samples to identify biomarker signals that can stratify tumor patients, which led to the surprising discovery that adjacent normal samples contained novel biomarker signals.
- **Mutation calling:** Developed a novel statistical methodology to refine somatic mutation calls and recalibrate mutation rate calculations for circulating tumor DNA Next Generation Sequencing data.

Department of Pharmacology, Yale University School of Medicine

Aug 2012 - Present

Research Assistant

New Haven, CT

- **Biomarker identification:** Designed experiments and methodologies to analyze both in vivo and in vitro gene expression profiles to monitor PHY906's effectiveness as an adjuvant cancer treatment.
- **Biostatistical consulting:** Provided consulting services to biologists and clinicians and communicated/discussed results and follow-up experiments on a weekly basis.

Shanghai Center for Bioinformation Technology

July 2009 - May 2010

Research Intern

Shanghai, China

- **Database construction:** Collected mass spectrometry protein data and constructed databases for the Chinese Government National 973 Project

TEACHING EXPERIENCE

- MCDB 261 Introduction to Dynamical Systems in Biology (Spring, 2015)
- CBB 752 Bioinformatics: Practical Application of Data Mining & Simulation (Spring, 2016)

HONORS AND AWARDS

- Awardee of AAAS/Science Program for Excellence in Science (YALE), 2016
- Fellowship from the CSC-Yale World Scholars Program (YALE), 2010-2012
- Title of Outstanding Graduate from university (HUST), 2010
- Title of National Youth Ambassador (Jiangsu Province), 2009
- Scholarship for Self-reliance from university (HUST), 2009
- Title of Outstanding Student from university (HUST), 2007-2008
- Scholarship for Outstanding Study Performance from department (HUST), 2007-2008
- Scholarship for Outstanding Student Leader from department (HUST), 2006-2007

TECHNICAL STRENGTHS

Computer Languages	Proficient in R, C/C++, Perl, Unix shell script, Python; familiar with Matlab, Java and HTML
Databases	MySQL
Tools	Git, Vim, Emacs, Markdown, Jekyll and L ^A T _E X
Language	English (fluent) and Chinese (native)

PUBLICATIONS

8. **Xiu Huang**, Wing Lam, Jiehuan Sun, Yung-Chi Cheng, Hongyu Zhao. 2016. SoMctDNA: Somatic Mutation Calling Method Specifically Tailored for Sequencing Data of Circulating Tumor DNAs (ctDNAs).
7. Jiehuan Sun, Jose Herazo-Maya, **Xiu Huang**, Naftali Kaminski, Hongyu Zhao. 2016. Distance-correlation based Gene Set Analysis in Longitudinal Studies. Submitted to the Bioinformatics.
6. **Xiu Huang**, David Stern, Hongyu Zhao. 2016. Transcriptional Profiles from Paired Normal Samples Offer Complementary Information on Cancer Patient Survival Evidence from TCGA Pan-Cancer Data. Scientific Reports 6:20567.
5. Lam Wing, Zaoli Jiang, Fulan Guan, **Xiu Huang**, Rong Hu, Jing Wang, Scott Bussom, et al. 2015. PHY906(KD018), an Adjuvant Based on a 1800-Year-Old Chinese Medicine, Enhanced the Anti-Tumor Activity of Sorafenib by Changing the Tumor Microenvironment. Scientific Reports 5: 9384.
4. Zhang Jing, Xiang Li, Cong Li, Zhichao Lian, **Xiu Huang**, Guocheng Zhong, Dajiang Zhu, et al. 2014. Inferring Functional Interaction and Transition Patterns via Dynamic Bayesian Variable Partition Models. Human Brain Mapping 35 (7): 331431.
3. Sun Jiehuan, Xintao Hu, **Xiu Huang**, Yang Liu, Kaiming Li, Xiang Li, Junwei Han, Lei Guo, Tianming Liu, and Jing Zhang. 2012. Inferring Consistent Functional Interaction Patterns From Natural Stimulus fMRI Data. NeuroImage, March.
2. Xing Xiao-Bin, Qing-Run Li, Han Sun, Xing Fu, Fei Zhan, **Xiu Huang**, Jing Li, et al. 2011. The Discovery of Novel Protein-Coding Features in Mouse Genome Based on Mass Spectrometry Data. Genomics 98 (5): 34351.
1. Jiang Xiao, Wu Yuan-xi, Liu Xing-fu, **Xiu Huang**, and Yuan Jiao. 2009. Designing Open Experiments, Improving Comprehensive Abilities. Experiment Science & Technology 7 (2).

PROFESSIONAL ACTIVITY

Reviewer for peer-reviewed journals

- Including BMC Bioinformatics, BioMed Research International, and Human Genomics

Academic presentations

- Xiu Huang, Ena Wang, Scott Bussom, Wing Lam, Zaoli Jiang, Francesco M Marincola, Yung-Chi Cheng and Hongyu Zhao. Individual Based Pathway Analysis (IBPA) and Its Application in Assessing PHY906s Adjuvant Anti-cancer Effect with CPT-11. 12th Meeting of Consortium for Globalization of Chinese Medicine (CGCM), 2013. Graz, Austria
- Xiu Huang. SoMctDNA: Somatic Mutation Calling for ctDNA Sequencing Data. CBB Research in Progress Talk, 2015. New Haven, CT
- Xiu Huang. Novel Statistical Methods for Identification and Interpretation of Cancer Biomarkers. Bina Technologies Invited Talk, 2016. San Francisco, CA

REFERENCES

Hongyu Zhao

- Ira V. Hiscock Professor of Biostatistics and Professor of Statistics and Genetics, Chair of the Biostatistics Department and the Co-Director of Graduate Studies of the Inter-Departmental Program in Computational Biology and Bioinformatics

Yale School of Public Health

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- Henry Bronson Professor of Pharmacology; Chairman, Consortium for the Globalization of Chinese Medicine (CGCM)

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Mark B Gerstein

- Albert L. Williams Professor of Molecular Biophysics and Biochemistry and Professor of Computer Science; Co-Director, Yale Computational Biology and Bioinformatics Program

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