

# XIU HUANG

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## EDUCATION

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### YALE UNIVERSITY

Expected May, 2016

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

*New Haven, CT*

- Thesis: Statistical modeling of gene expression and next generation sequencing data towards understanding and identifying cancer biomarkers
- Advisors: Prof. Hongyu Zhao

**HUAZHONG UNIVERSITY OF SCIENCE AND TECHNOLOGY (HUST)** June, 2010

**B.E**, *Bioinformatics*

*Wuhan, China*

- Thesis: Analysis of massive protein mass spectrometry data and its application in human genome annotation.

## RESEARCH EXPERIENCE

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### Yale Center for Statistical Genomics and Proteomics

Aug 2011 - Present

*Research Assistant*

*New Haven, CT*

- Statistical modeling of gene expression data to assess PHY906 as an adjuvant drug in treating cancer
- Statistical assessment of transcriptional profiles from paired normal samples of cancer patients to identify new biomarkers to better predict cancer survival
- Statistical method to call somatic mutations specifically designed for sequencing data of circulating tumor DNAs

### Department of Pharmacology, Yale University School of Medicine

Aug 2012 - Present

*Research Assistant*

*New Haven, CT*

- Assess PHY906 as an adjuvant cancer treatment to induce gene expression changes in different tissues of genetically engineered mouse model and xenograft mouse models carrying colon cancer
- Assess PHY906 induced circulating DNAs mutation profile changes in clinical trials colon cancer patients

### Shanghai Center for Bioinformation Technology

July 2009 - May 2010

*Research Intern*

*Shanghai, China*

- Collection of mass spectrometry protein data and construction of databases for the Chinese Government National 973 Project

## TEACHING EXPERIENCE

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

## HONORS AND AWARDS

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- 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

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<b>Computer Languages</b>	Proficient in R, C/C++, Perl, Unix shell script; familiar with Matlab, Python and Java
<b>Databases</b>	MySQL
<b>Tools</b>	Git, Vim, Emacs, RMarkdown
<b>Language</b>	English (fluent) and Chinese (native)

## PUBLICATIONS

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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).

## MANUSCRIPTS

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2. **Xiu Huang**, Wing Lam, Jiehuan Sun, Yung-Chi Cheng, Hongyu Zhao. Somatic Mutation Calling for Sequencing Data of Circulating Tumor DNAs. 2016. Submitted to *BMC Bioinformatics*
1. **Xiu Huang**, David Stern, Hongyu Zhao. Transcriptional Profiles from Paired Normal Samples Offer Complementary Information on Cancer Patient Survival – Evidence from TCGA Pan-Cancer Data. 2016. Accepted by *Scientific Reports*

## PROFESSIONAL ACTIVITY

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### 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