

# Xiangchun Li

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## Profile

I obtained Bachelor of Engineering in Bioinformatics from HUST in 2010 and formally participated in BGI (actually, I joined BGI in 2009/10), where I have been dedicated myself to next-generation sequencing (NGS) data analyses and successfully provided new insights into tumourigenesis of several human cancer types.

## Experience

### **Bioinformatics Analyst, BGI-Tech; Shenzhen, China – 2009/10~Present**

I have been working as a bioinformatics analyst in BGI since 2009/10/20, devoting to deciphering NGS data from multiple human cancer genomes. I'm primarily carrying out bioinformatics analyses on multi-omics data from different platforms, such as whole-exome sequencing (WES), whole-genome sequencing (WGS), whole-genome bisulfite sequencing (WGBS) and RNA-seq, as well as MeDIP-seq and ChIP-seq etc.

The cancer genome projects, of which I have been in charge, primarily encompass a variety of different human cancer types, such as oesophageal squamous cell carcinoma, colorectal cancer, lung squamous cell carcinoma, breast cancer, diffused large B-cell lymphoma and gastric adenocarcinoma. These involve the applications of systems biology, bioinformatics and data mining strategies to search for new cancer genes, key signalling pathways frequently altered, defining genomic alteration landscapes and discovering novel prognostic biomarkers.

## Education

Huazhong University of Science & Technology, Wuhan, China – Bachelor of Engineering in Bioinformatics, 2006/9~2010/7

The Chinese University of Hong Kong, Hong Kong, China – Ph.D. Candidate in Medical Sciences, 2012~Present

## Skills

Apart from comprehensive skills I earn from analysing multi-omics NGS data. I'm especially experienced in dissecting cancer genomes, including the following areas but not limited to:

1. Basic data analyses, such as identifying somatic mutations, detecting copy number changes and characterising structural variations etc.
2. Identification of significantly mutated genes and/or altered cell signalling pathways that are conferring selective and proliferative advantages on neoplastic cells.
3. Clonality analyses for deep sequencing to determine clonal complexity and identify clonal and subclonal mutations that may drive tumour initiation and progression.
4. Phylogenetic tree reconstruction for tumour with multi-region sampling or cancer patient with multiple tumour samples sequenced to determine evolution paths.
5. Deciphering signatures of mutational processes that are operative in human cancer to explore mutagenic processes and defective in DNA repair mechanisms.

6. Kaplan-Meier survival and univariate/multivariate Cox regression analyses to identify prognostic factors that can be exploited to stratify tumours into distinct groups.
7. Hypothesis-driven data mining and cross-validation analyses based on The Cancer Genome Atlas (TCGA) data sets.
8. Deep convolutional neural network for multiple human cancer type classification.

Besides, I'm an excellent team-player. I have excellent command of both spoken and written English. I am working with unix-like operating systems and proficient at programming with several computer languages, namely Python, R, Bash. I'm also familiar with other computer languages, such C/C++, Java and Matlab, as well as many Bioinformatics Databases.

## Publications

1. Kexin Chen, Da Yang, **Xiangchun Li (co-first author)**, Baocun Sun, Fengju Song, Wenfeng Cao, Daniel Brat, Zhibo Gao, Haixin Li, Han Liang, Yanrui Zhao, Hong Zheng, Miao Li, Jan Buckner, Scott D. Patterson, Xiang Ye, Christoph Reinhard, Anahita Bhathena, Deepa Joshi, Paul S. Mischel, Carlo Croce, Yi Michael Wang, Sreekumar Kaimal, Hui Li, Xin Lu, Yang Pan, Han Chang, Sujuan Ba, Longhai Luo, Webster Cavenee, Wei Zhang, Xishan Hao ***Mutational Landscape of Gastric Adenocarcinoma in Chinese: Implications for Prognosis and Therapy*** *PNAS* 1-6 (2015) doi:10.1073/pnas.1422640112.
2. Nakatsu G, **Xiangchun Li (co-first author)**, Zhou H, et al: Gut mucosal microbiome across stages of colorectal carcinogenesis. *Nature Communication* 6:1-9, 2015
3. **Xiangchun Li**, Wu WKK, Xing R, et al: ***Distinct subtypes of gastric cancer defined by molecular characterization include novel mutational signatures with prognostic capability*** (Accepted by *Cancer Research*)
4. Yongmei Song, Lin Li, Yunwei Ou, Zhibo Gao, Enmin Li, **Xiangchun Li (co-first author)**, Weimin Zhang, Jiaqian Wang, Liyan Xu, Yong Zhou, Xiaojuan Ma, Lingyan Liu, Zitong Zhao, Xuanlin Huang, Jing Fan, Lijia Dong, Gang Chen, Liying Ma, Jie Yang, Longyun Chen, Minghui He, Miao Li, Xuehan Zhuang, Kai Huang, Kunlong Qiu, Guangliang Yin, Guangwu Guo, Qiang Feng, Peishan Chen, Zhiyong Wu, Jianyi Wu, Ling Ma, Jinyang Zhao, Longhai Luo, Ming Fu, Bainan Xu, Bo Chen, Yingrui Li, Tong Tong, Mingrong Wang, Zhihua Liu, Dongxin Lin, Xiuqing Zhang, Huanming Yang, Jun Wang, Qimin Zhan ***Identification of genomic alterations in oesophageal squamous cell cancer.*** *Nature* **509**, 91-95 (2014).
5. Jun Yu, William K K Wu, **Xiangchun Li (co-first author)**, Jun He, Xiao-Xing Li, Simon S M Ng, Chang Yu, Zhibo Gao, Jie Yang, Miao Li, Qiaoxiu Wang, Qiaoyi Liang, Yi Pan, Joanna H Tong, Ka F To, Nathalie Wong, Ning Zhang, Jie Chen, Youyong Lu, Paul B S Lai, Francis K L Chan, Yingrui Li, Hsiang-Fu Kung, Huanming Yang, Jun Wang, Joseph J Y Sung ***Novel recurrently mutated genes and a prognostic mutation signature in colorectal cancer.*** *Gut*. **0**,1-10 (2014).
6. Fangfang Song, **Xiangchun Li (co-first author)**, Fengju Song et al. ***Comparative Genomic Analysis Reveals Bilateral Breast Cancers are Genetically Independent*** *Oncotarget* (2015).
7. Li C, Gao Z, Li F, **Xiangchun Li (co-first author)** et al: Whole Exome Sequencing Identifies Frequent Somatic Mutations in Cell-Cell Adhesion Genes in Chinese Patients with Lung Squamous Cell Carcinoma. *Sci Rep* 5:14237, 2015
8. Yanan Cao, Minghui He, Zhibo Gao, Ying Peng, Yanli Li, Lin Li, Weiwei Zhou, **Xiangchun Li**, Xu Zhong, Yiming Lei, Tingwei Su, Hang Wang, Yiran Jiang, Lin Yang, Wei Wei, Xu Yang, Xiuli Jiang, Li Liu, Juan He, Junna Ye, Qing Wei, Yingrui Li, Weiqing Wang, Jun Wang, Guang Ning ***Activating Hotspot L205R Mutation in PRKACA and Adrenal Cushing's Syndrome.*** *Science* **344**, 913-917 (2014).

9. Zhang L, Zhou Y, Cheng C, ..., Xiangchun Li, ... et al: ***Genomic Analyses Reveal Mutational Signatures and Frequently Altered Genes in Esophageal Squamous Cell Carcinoma***. *Am J Hum Genet* 96:597-611, 2015
10. Chang Yu, Jun Yu, Xiaotian Yao, William KK Wu, Youyong Lu, Senwei Tang, Xiangchun Li, Li Bao, Xiaoxing Li, Yong Hou, Renhua Wu, Min Jian, Ruoyan Chen, Fan Zhang, Lixia Xu, Fan Fan, Jun He, Qiaoyi Liang, Hongyi Wang, Xueda Hu, Minghui He, Xiang Zhang, Hancheng Zheng, Qibin Li, Hanjie Wu, Yan Chen, Xu Yang, Shida Zhu, Xun Xu, Huanming Yang, Jian Wang, Xiuqing Zhang, Joseph Jy Sung, Yingrui Li, Jun Wang ***Discovery of biclonal origin and a novel oncogene SLC12A5 in colon cancer by single-cell sequencing***. *Cell Research* 24:701-712 (2014).
11. Yuda Zhao, Jie Yang, Zhaoli Chen, Zhibo Gao, Fang Zhou, Xiangchun Li, Jiagen Li, Susheng Shi, Xiaoli Feng, Nan Sun, Ran Yao, Chengcheng Zhou, Sheng Chang, Miao Li, Yong Zhou, Lin Li, Xiuqing Zhang, Jie He ***Identification of somatic alterations in stage I lung adenocarcinomas by next-generation sequencing***. *Genes Chromosomes and Cancer* 53, 289-298 (2014).
12. Xu L, Li X, Cai M, ... Xiangchun Li ... et al: ***Increased expression of Solute carrier family 12 member 5 via gene amplification contributes to tumour progression and metastasis and associates with poor survival in colorectal cancer***. *Gut* 1-12, 2015
13. Longqi Liu, Yan Xu, Minghui He, ... Xiangchun Li ... et al. ***Transcriptional Pause Release Is a Rate-Limiting Step for Somatic Cell Reprogramming***. *Cell Stem Cell* 574-588, 2014.
14. Cheng, C., Zhou, Y., Li, H., Xiong, T., Li, S., Bi, Y., ... Li, Y. (2016). Whole-Genome Sequencing Reveals Diverse Models of Structural Variations in Esophageal Squamous Cell Carcinoma. *The American Journal of Human Genetics*, 1-19. doi:10.1016/j.ajhg.2015.12.013
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