Xiangchun Li (李祥春)

+86 150-1261-9467 lixiangchun2014@foxmail.com Tianjin Medical University Cancer Institute & Hospital Huanhu Xi Road, Tiyuan Bei, Hexi District, Tianjin, China 300060
Personal website: https://lixiangchun.github.io

Profile

I obtained Bachelor of Engineering in Bioinformatics from Huazhong University of Science & Technology (HUST) in 2010 and Ph.D in Medical Sciences from The Chinese University of Hong Kong, Hong Kong (CUHK). I joined in BGI since 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

Senior Bioinformatics Analyst, BGI-Tech; Shenzhen, China – 2009/10~2017/01

I have been working as a bioinformatics analyst in BGI since 2009/10/20, where devoting myself 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, mainly 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 in Medical Sciences, 2012/8~2016/7

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 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. William K.K. Wu, **Xiangchun Li***, Xiansong Wang, Rudin Z.W. Dai, Alfred S.L. Cheng, Maggie H.T. Wang, Thomas Kwong, Tai C. Chow, Jun Yu, Matthew T.V. Chan, S. H. W. Oncogenes without a neighboring tumor-suppressor gene are more prone to amplification. *Mol Biol Evol*. (2017). doi:10.1093 (IF: 13)

2. **Li, Xiangchun***, Wu, W. K. K., Xing, R., Wong, S. H., & Liu, Y. (2016). Distinct subtypes of gastric cancer defined by molecular characterization include novel mutational signatures with prognostic capability, *Cancer Research*, *76*(7), 1724–1733. doi:10.1158/0008-5472.CAN-15-2443 (IF: 9.329)

3. Nakatsu, G., **Li, Xiangchun***, Zhou, H., Sheng, J., Wong, S. H., Wu, W. K. K., ... Sung, J. J. Y. (2015). Gut mucosal microbiome across stages of colorectal carcinogenesis. *Nature Communications*, *6*, 8727. doi: 10.1038/ncomms9727 (IF: 11.47)

4. Chen, K., Yang, D., **Li, Xiangchun***, Sun, B., Song, F., Cao, W., ... Gao, Z. (2015). Mutational landscape of gastric adenocarcinoma in Chinese : Implications for prognosis and therapy. *Proceedings of the National Academy of Sciences*, *6*(1), 1–6. doi:10.1073/pnas.1422640112 (IF: 9.674)

5. Song, Y., Li, L., Ou, Y., Gao, Z., Li, E., **Li, Xiangchun***, ... Zhan, Q. (2014). Identification of genomic alterations in oesophageal squamous cell cancer. *Nature*, *509*(7498), 91–5. doi:10.1038/nature13176 (IF: 41.456)

6. Yu, J., Wu, W. K. K., **Li, Xiangchun***, X. X., He, J., Li, X.-X. X., Ng, S. S. M., ... Sung, J. J. Y. (2015). Novel recurrently mutated genes and a prognostic mutation signature in colorectal cancer. *Gut*, *64*(4), 636–45. doi:10.1136/gutjnl- 2013-306620 (IF: 14.66)

7. Song, F., **Li, Xiangchun***, Song, F., Zhao, Y., & Li, H. (2015). Comparative genomic analysis reveals bilateral breast cancers are genetically independent. *Oncotarget*. doi:10.18632/oncotarget.5569 (IF: 6.359)

8. Li, C., Gao, Z., Li, F., **Li, Xiangchun***, Sun, Y., Wang, M. M., ... Wei, Q. (2015). Whole Exome Sequencing Identifies Frequent Somatic Mutations in Cell-Cell Adhesion Genes in Chinese Patients with Lung Squamous Cell Carcinoma. *Scientific Reports*, *5*(August), 14237. doi:10.1038/srep14237 (IF: 5.578)

9. Cao, Y., He, M., Gao, Z., Peng, Y., ... **Li, Xiangchun**, ... Ning, G. (2014). Activating hotspot L205R mutation in PRKACA and adrenal Cushing's syndrome. *Science*, *344*(6186), 913–7. doi:10.1126/science.1249480 (IF: 33.611)

10. Zhang, L., Zhou, Y., Cheng, C., Cui, H., Cheng, ... **Li, Xiangchun**, ... Cui, Y. (2015). Genomic analyses reveal mutational signatures and frequently altered genes in esophageal squamous cell carcinoma. *American Journal of Human Genetics*, *96*(4), 597–611. doi:10.1016/j.ajhg.2015.02.017 (IF: 10.931)

11. Yu, C., Yu, J., Yao, X., Wu, W. K. K., Lu, Y., ... **Li, Xiangchun**, ... Wang, J. J. (2014). Discovery of biclonal origin and a novel oncogene SLC12A5 in colon cancer by single-cell sequencing. *Cell Research*, *24*(6), 701–12. doi:10.1038/cr.2014.43 (IF: 12.413)

12. Zhao, Y., Yang, J., Chen, Z., Gao, Z., Zhou, F., **Li, Xiangchun**, ... He, J. (2014). Identification of somatic alterations in stage I lung adenocarcinomas by next- generation sequencing. *Genes Chromosomes and Cancer*, *53*(4), 289–298. doi:10.1002/gcc.22138 (IF: 4.041)

13. Xu, L., Li, X. X., Cai, M., Chen, J., Li, X. X., Wu, W. K. K., ... **Li, Xiangchun** ... Yu, J. (2015). 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. doi: 10.1136/gutjnl-2014-308257 (IF: 14.66)

14. Liu, L., Xu, Y., He, M., Zhang, M., Cui, F., Lu, L., ... **Li, Xiangchun**, ... Esteban, M. A. (2014). Transcriptional pause release is a rate-limiting step for somatic cell reprogramming. *Cell Stem Cell*, *15*(5), 574–588. doi: 10.1016/j.stem.2014.09.018 (IF: 22.268)

15. Cheng, C., Zhou, Y., Li, H., Xiong, T., Li, S., Bi, Y., ... **Li, Xiangchun**, ... Cui, 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 (IF: 10.931)

16. Tsang, D. P. F., Wu, W. K. K., Kang, W., Lee, Y.-Y., Wu, F., Yu, Z., ... **Li, Xiangchun**, ... Cheng, A. S. L. (2016). Yin Yang 1-mediated epigenetic silencing of tumour-suppressive microRNAs activates Nuclear Factor-κB in hepatocellular carcinoma. *The Journal of Pathology*. doi:10.1002/path.4688 (IF: 7.429)

17. Tang, S., Wu, W. K. K., **Li, Xiangchun**, Wong, S. H., Wong, N., Chan, M. T. V., ... Yu, J. (2016). Stratification of Digestive Cancers with Different Pathological Features and Survival Outcomes by MicroRNA Expression. *Scientific Reports*, *6*(4), 24466. doi:10.1038/srep24466 (IF: 5.578)

18. My publication collection: http://www.ncbi.nlm.nih.gov/sites/myncbi/1L_7fz6vO8TAC/bibliography/48607824/public/?sort=date&direction=ascending