

Binbin Wang

School of life Sciences and Technology
Tongji University, 1239 Siping Road
Shanghai, P.R. China

Email: wangbinbintj@gmail.com
Tel: +86-18018587332

Education

- | | |
|-----------|--|
| 2017-2018 | Visiting scholar, Dana Farber Cancer Institute, Harvard Medical School, Boston, US |
| 2014-2019 | Ph.D., Bioinformatics, Tongji University, Shanghai, China |
| 2008-2012 | B.A, Biotechnology, Northeast Agriculture University, Harbin, China |

Research Experience

2014.07- Graduate Research
Pres. Advisor: Dr. Xiaole Shirley Liu

Algorithm development of CRISPR screen data analysis

- Developed the MAGeCKFlute algorithm to process, analyze and visualize CRISPR/Cas9 knockout screening. MAGeCKFlute can be applied to remove batch effects, correct copy-number bias, identify screening hits and perform downstream functional analysis for various CRISPR screens. For CRISPR screening samples that treated with a drug, MAGeCKFlute can also be used to identify drug-associated genes.
- Optimized gRNA pair design and analysis for knockout of druggable genes. A paired gRNA library was designed to target druggable genes to identify synergy gene pairs. Designed several customized sgRNA libraries in various systems.
- Developed machine learning algorithms to predict gene essentiality. Applied this model to cell surface genes to identify essential cell-surface genes in cancer cells.
- Used genome-wide CRISPR screens to identify candidate therapeutic targets for BRAFi-resistant melanoma. Integration of expression data, ATAC-seq, and CRISPR screen results identified key transcription factors that enabled resistance to BRAFi in melanoma cells (collaboration).
- Designed a large-scale murine CRISPR knockout library ("MusCK") and conducted an in vivo screen in two murine triple-negative breast cancer (TNBC) models to identify genetic factors that regulate TNBC progression and response to PD-1 immune checkpoint blockade (in collaboration with Myles Brown lab at DFCI). Integrated

RNA-seq data, ATAC-seq, mass spectrometry, and CRISPR screen data to identify novel regulators in the TNBC tumor immune microenvironment.

- Identify synthetic lethal interactions with BET bromodomain inhibitors (BBDI) using CRISPR and small-molecule inhibitor screens combined with comprehensive molecular profiling of BBDI response and resistance (in collaboration with Kornelia Polyak lab at DFCI). In the project, I was responsible for analyzing and integrating CRISPR screen, ATAC-seq, and Chip-seq data.

Computational characterization of T cell and B cell repertoire and cancer immunology

- Developed an algorithm to Identify neo-antigens using mutation and expression data to Identify and characterize neo-antigens of TCGA patients.
- Developed a novel computational method, TRUST, for de novo assembly of CDR3 regions using RNA-seq data, and applied it on samples from the TCGA. We observed exciting interactions between the tumor and the host immune system and identified potential therapeutic targets that might be useful for multiple immunotherapies. In this project, I was responsible for analyzing the RNAseq data of TCGA samples with TRUST, and performing the downstream analysis with the distinct CDR3 sequences.
- Enhanced our previous computational algorithm TRUST to extract the B cell immunoglobulin hypervariable regions from bulk tumor RNA-sequencing data. TRUST assembled more than 30 million CDR3 sequences of the B cell heavy chain (IgH) from TCGA. Widespread B cell clonal expansions and immunoglobulin subclass switch events were observed in diverse human cancers. In this project, I was responsible for optimizing and testing the algorithm.
- Developed the Tumor Immune Estimation Resource (TIMER; cistrome.shinyapps.io/timer) to comprehensively investigate the molecular characterization of tumor-immune interactions. TIMER provides six major analytic modules that allow users to interactively explore the associations between immune infiltrates and a wide spectrum of factors, including clinical outcomes, somatic mutations, and somatic copy number alterations. In this project, I was in charge of the gene expression part and data preprocessing of other parts.

Protein degradation and Ubiquitin-Proteasome System in Cancer

- Developed an algorithm to integrate mass spectrometry data and other multi-omics data. Revealed that a significant fraction of cancer driver genes impacts the function of the UPS, and degron loss leads to up-regulated protein abundance.

Work Experience

- 2013-2014 Bioinformatics counsellors
Representatives products of high throughput sequences, such as RNA-seq, Chip-seq, to customers, and interrupt the sequencing and analysis results
- 2012-2013 Purchasing Agent, Yurun Group
Obtains the equipment and raw material by verifying, preparing, and forwarding purchase orders; verifies receipt of items; authorizes payment

Academic Conference Attended

- 2019 Scientific and Technical Advances in Cancer Immunology, Suzhou, China
- 2018 The 8th National Conference on Bioinformatics and Systems Biology of China and the 1st (Macao) International Bioinformatics Symposium, Macao, China. **(Poster)**
- 2018 Computational analysis of single-cell data and cell-type heterogeneity: the next frontier, Shanghai, China
- 2018 Mathematics, computer and life sciences cross research young scholars Forum, Beijing, China
- 2017 Harvard Chinese Life Science Annual Research Symposium, Boston, USA
- 2016 Systems Biology of Gene Regulation & Genome Editing Cold Spring Harbor Asia, Suzhou, China
- 2016 The 7th Bioinformatics and systems biology conference, Chengdu, China
- 2015 The 12th International Bioinformatics Workshop, IBW2015, Harbin, China
- 2015 Statistical Genomic Workshop, Shanghai, China

Honors and Awards

- 2018 National scholarship for doctoral students
- 2010 Outstanding student Cadres
- 2009 Student Award for Research and Innovation

Teaching Experience

- | | |
|------|---|
| 2018 | Bioinformatics course, CRISPR screen and cancer immunology.
Tongji University. Teaching Assistant |
| 2016 | Bioinformatics course, Analysis of microarray and RNASeq data.
Tongji University. Teaching Assistant |
| 2015 | Dragon Star course, Integrated analysis of TCGA data. Harbin,
China. Teaching Assistant |

Posters

CCBCB 2018 (Macao): “Integrative analysis of pooled CRISPR genetic screens using MAGeCKFlute”

Technical Skills

1. Next generation sequencing data analysis and integrated analysis of RNA-seq, Chip-seq, CRISPR and mass spectra data
2. Data processing and analysis pipelines development and deploy for a variety of NGS protocols and related methods
3. Bioinformatics tool and algorithm development
4. Machine learning and statistical modeling
5. Programming languages: python, R, shell, html
6. High performance computing: work flow management (snakemake)
7. Code version control system: git, bitbucket

Montee/Montor undergrad students

- Yaru Song, PhD candidate at Tongji University (2015 - 2016)
- Jingxin Fu, PhD candidate at Tongji University (2016 - 2017)
- Jin Wang, PhD candidate at Tongji University (2016 - 2017)
- Wubing Zhang, PhD candidate at Tongji University (2017 - 2018)
- Hantong, PhD candidate at Tongji University (2017 - 2018)
- Xiaoying Shi, PhD candidate at Tongji University (2018 - 2019)
- Dongqing Sun, PhD candidate at Tongji University (2018 - 2019)
- Ya Han, PhD candidate at, 2018 to 2019, Tongji University (2018 - 2019)
- LiangDong Sun, Master student at Shanghai Pulmonary Hospital Tongji University (2018 – present)
- Jun Ge, Master student at Tongji University (2019 – present)

Publications

1. Binbin Wang*, Mei Wang*, Wubing Zhang*, Tengfei Xiao, Chen-Hao Chen, Alexander Wu, Feizhen Wu, Nicole Traugh, Xiaoqing Wang, Ziyi Li, Shenglin Mei, Yingbo Cui, Sailing Shi, Jesse Jonathan Lipp, Matthias Hinterndorfer, Johannes Zuber, Myles Brown, Wei Li#, Xiaole Shirley Liu#. *Integrative analysis of pooled CRISPR genetic screens using MAGeCKFlute. Natue Protocol*

14(3):756-780 (2019)

2. Ziyi Li*, Binbin Wang*, Shengqing Gu, Peng Jiang, Avinash Sahu, Chen-Hao Chen, Tong Han, Sailing Shi, Xiaoqing Wang, Nicole Traugh, Hailing Liu, Yin Liu, Qiu Wu, Myles Brown, Tengfei Xiao, Genevieve M. Boland, X. Shirley Liu. *CRISPR Screens Identify Essential Cell Growth Mediators in BRAF Inhibitor-resistant Melanoma*. **Genomics Proteomics Bioinformatics**, 18(1) (2020)
3. Xiaoqing Wang*, Binbin Wang*, Shengqing Gu, Collin Tokheim, Qin Tang, Yihao Li, Nicole Traugh, Ziyi Li, Tengfei Xiao, Wei Li, Cliff Meyer, Jingyu Peng, Yi Zhang, Blair Stewig, Paloma Cejas, Klothilda Lim, Henry Long, Myles Brown, X. Shirley Liu. *In vivo CRISPR screening identifies Cop1 as a triple-negative breast cancer immunotherapy target via suppressing macrophage infiltration*. (Manuscript in preparation)
4. Collin Tokheim, Binbin Wang, Jun Ge, Wubing Zhang, X. Shirley Liu. Genomic Landscape of the Ubiquitin-Proteasome System in Human Cancers. (Submitted to Cell)
5. Shaokun Shu, Hua-Jun Wu, Jennifer Y. Ge, Rhamy Zeid, Isaac S. Harris, Bojana Jovanovic, Katherine Murphy, Binbin Wang, Xintao Qiu, Jennifer E. Endress, Jaime Reyes, Klothilda Lim, Alba Font-Tello, Sudeepa Syamala, Tengfei Xiao, Chandra Sekhar Reddy Chilamakuri, Evangelia K. Papachristou, Clive D'Santos, Jayati Anand, Kunihiro Hinohara, Wei Li, Thomas. McDonald, Adrienne Luoma, Rebecca J. Modiste, Quang-De Nguyen, Brittany Michel, Paloma Cejas, Cigall Kadoch, Jacob D. Jaffe, Kai W. Wucherpfennig, Jun Qi, X. Shirley Liu, Henry Long, Myles Brown, Jason S. Carroll, Joan S. Brugge, James Bradner, Franziska Michor, Kornelia Polyak. *Synthetic lethal and resistance interactions with BET bromodomain inhibitors in triple-negative breast cancer*. **Molecular Cell**, (Available online 15 May 2020)
6. Xihao Hu, Jian Zhang, Jin Wang, Jingxin Fu, Taiwen Li, Xiaoqi Zheng, Binbin Wang, Shengqing Gu, Peng Jiang, Jingyu Fan, Xiaomin Ying, Jing Zhang, Michael C. Carroll, Kai W. Wucherpfennig, Nir Hacohen, Fan Zhang, Peng Zhang, Jun S. Liu#, BoLi# & X. Shirley Liu#. *Landscape of B cell immunity and related immune evasion in human cancers*. **Nature Genetics**, 51: 560–567 (2019) (2018)
7. Shenglin Mei, Clifford A Meyer, Rongbin Zheng, Qian Qin, Qiu Wu, Peng Jiang, Bo Li, Xiaohui Shi, Binbin Wang, Jingyu Fan, Celina Shih, Myles Brown, Chongzhi Zang, Liu XS#. *Cistrome Cancer: a web resource for integrative gene regulation modeling in cancer*, **Cancer research**, 77 (21), e19-e22 (2017).
8. Bo Li, Taiwen Li, Binbin Wang, Ruoxu Dou, Jian Zhang, Jun S Liu, X Shirley Liu. *Ultrasensitive detection of TCR hypervariable-region sequences in solid-tissue RNA-seq data*. **Nature Genetics**, 49(4):482-3 (2017).
9. Taiwen Li, Jingyu Fan, Binbin Wang, Qianming Chen, Jun S Liu, Bo Li# and X. Shirley Liu. *TIMER: A web server for comprehensive analysis of tumor-*

infiltrating immune cells. Cancer research, 77 (21), e108-e110 (2017).

10. Bo Li*, Taiwen Li*, Jean-Christophe Pignon, Binbin Wang, Jinzeng Wang, Sachet Shukla, Ruoxu Dou, Qianming Chen, F. Stephen Hodi, Toni K. Choueiri, Catherine Wu, Nir Hacohen, Sabina Signoretti, Jun S. Liu# and X. Shirley Liu#. *Landscape of tumor-infiltrating T cell repertoire of human cancers. Nature Genetics*; 48(7):725-32 (2016).

Peer Review

1. *Cellular Physiology and Biochemistry*, 2018
2. *Bioinformatics*, 2018
3. *Cell*, 2017

Presentation

Synthetic lethal and resistance interactions with BET bromodomain inhibitors in triple-negative breast cancer. Center for Functional Cancer Epigenetics Seminar, Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Nov 2017.

Grant

Applications that I helped preparing:

- National Natural Science Foundation of China (General Program), 81872290, Molecular characteristics of microinvasive adenocarcinoma, January 2019
- Science Foundation for The Excellent Youth Scholars of Ministry of Education of China, 31801110, Identify cancer cell essential genes via multi-omics data integration analysis
- Key (Key grant) Project of Chinese Ministry of Education, 2017YFC0908500, Personalized drug evaluation of head and neck malignant tumors and establishment of clinical transformation system