Liang-Bo Wang

Email: liang-bo.wang@wustl.edu
Mobile: +1 (314) 285-8111
Website: blog.liang2.tw
GitHub: ccwang002

EDUCATION

Washington University in St. Louis   St. Louis, USA
Ph.D. candidate in Computational and Systems Biology   2016–Present

National Taiwan University   Taipei, Taiwan
M.S. in Biomedical Electronics and Bioinformatics   2014–2016
B.S. in Electrical Engineering and minor in Economics   2019–2014

EXPERIENCE

Washington University in St. Louis   St. Louis, USA
PhD Research, Li Ding Lab   2017–Present

- Thesis: Proteogenomic and spatial characterization of glioblastoma tumors at bulk and single cell Level
- Human tumor characterization using mass spectrometry, single cell sequencing, spatial transcriptomics, and multiplexed imaging
- Member of large-scale cancer research communities including The Cancer Genome Atlas (TCGA), Clinical Proteogenomic Tumor Analysis Consortium (CPTAC), and Human Tumor Atlas Network (HTAN)
- Data analysis lead of CPTAC glioblastoma study, coordinating collaboration across institutions nationwide
- Developed tools and databases to analyze large-scale multi-modal datasets

Pinkoi   Taipei, Taiwan
Internship on search improvement   Summer 2015

- Improved e-commerce product search by improving Mandarin/Chinese text segmentation on ElasticSearch and implementing a Word2Vec-based semantic search

Microsoft Research Asia   Beijing, China
Reasearch Internship, Eric Chang Group   2014–2015

- Deep learning based cancer image and pathway analysis
- Applied convolutional neural network to histopathology image analysis

National Taiwan University   Taipei, Taiwan
Master's Research, Eric Y. Chuang Lab   2014–2016

- Thesis: BioCloud: an online sequencing analysis platform

National Taiwan University   Taipei, Taiwan
Undergraduate Research on genomic data analysis, Eric Y. Chuang Lab   2012–2014
Undergraduate Research on Bio-MEMS sensor design, Wei-Cheng Tian Lab   2011-2012

PUBLICATIONS

[1] Kuan-lin Huang et al. "Spatially interacting phosphorylation sites and mutations in cancer". In: *Nature Communications* 12.1 (2021), p. 2313. DOI: 10.1038/s41467-021-22481-w.

[2] **Liang-Bo Wang**[*] et al. "Proteogenomic and metabolomic characterization of human glioblastoma". In: *Cancer Cell* 39.4 (2021), 509–528.e20. DOI: 10.1016/j.ccell.2021.01.006.

[3] Matthew H. Bailey et al. "Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples". In: *Nature Communications* 11.1 (2020), p. 4748. DOI: 10.1038/s41467-020-18151-y.

[4] Yongchao Dou et al. "Proteogenomic Characterization of Endometrial Carcinoma". In: *Cell* 180.4 (2020), 729–748.e26. DOI: 10.1016/j.cell.2020.01.026.

[5] Michael A. Gillette et al. "Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma". In: *Cell* 182.1 (2020), 200–225.e35. DOI: 10.1016/j.cell.2020.06.013.

[6] Jason E. McDermott et al. "Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability". In: *Cell Reports Medicine* 1.1 (2020), p. 100004. DOI: 10.1016/j.xcrm.2020.100004.

[7] Francesca Petralia et al. "Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer". In: *Cell* (2020). DOI: 10.1016/j.cell.2020.10.044.

[8] Orit Rozenblatt-Rosen et al. "The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution". In: *Cell* 181.2 (2020), pp. 236–249. DOI: 10.1016/j.cell.2020.03.053.

[9] David J. Clark et al. "Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma". In: *Cell* 179.4 (2019), 964–983.e31. DOI: 10.1016/j.cell.2019.10.007.

[10] Galen F. Gao[*] et al. "Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons' Data". In: *Cell Systems* 9.1 (2019), 24–34.e10. DOI: 10.1016/j.cels.2019.06.006. *(co-first author)*.

[11] Kuan-lin Huang et al. "Pathogenic Germline Variants in 10,389 Adult Cancers". In: *Cell* 173.2 (2018), 355–370.e14. DOI: 10.1016/j.cell.2018.03.039.

[12] Sam Q. Sun, R. Jay Mashl, Sohini Sengupta, Adam D. Scott, Weihua Wang, Prag Batra, **Liang-Bo Wang**, Matthew A. Wyczalkowski, and Li Ding. "Database of evidence for precision oncology portal". In: *Bioinformatics* 34.24 (2018), pp. 4315–4317. DOI: 10.1093/bioinformatics/bty531.

[13] The Bioconda Team, Björn Grüning, Ryan Dale, Andreas Sjödin, Brad A. Chapman, Jillian Rowe, Christopher H. Tomkins-Tinch, Renan Valieris, and Johannes Köster. "Bioconda: sustainable and comprehensive software distribution for the life sciences". In: *Nature Methods* 15.7 (2018), pp. 475–476. DOI: 10.1038/s41592-018-0046-7.

[14] Yi-Pin Lai[*], **Liang-Bo Wang**[*], Wei-An Wang[*], Liang-Chuan Lai, Mong-Hsun Tsai, Tzu-Pin Lu, and Eric Y. Chuang. "iGC—an integrated analysis package of gene expression and copy number alteration". In: *BMC Bioinformatics* 18 (2017), p. 35. DOI: 10.1186/s12859-016-1438-2.

[15] Yan Xu, Zhipeng Jia, **Liang-Bo Wang**, Yuqing Ai, Fang Zhang, Maode Lai, and Eric I-Chao Chang. "Large scale tissue histopathology image classification, segmentation, and visualization via deep convolutional activation features". In: *BMC Bioinformatics* 18 (2017), p. 281. DOI: 10.1186/s12859-017-1685-x.

[16] **Liang-Bo Wang**, Eric Y. Chuang, and Tzu-Pin Lu. "Identification of predictive biomarkers for ZD-6474 in lung cancer". In: *Translational Cancer Research* 4.4 (2015), pp. 324–331. DOI: 10.3978/j.issn.2218-676X.2015.08.10.

[17] Chien-Yueh Lee[*], Yu-Chiao Chiu[*], **Liang-Bo Wang**[*], Yu-Lun Kuo[*], Eric Y. Chuang, Liang-Chuan Lai, and Mong-Hsun Tsai. "Common applications of next-generation sequencing technologies in genomic research". In: *Translational Cancer Research* 2.1 (2013), pp. 33–45. DOI: 10.3978/j.issn.2218-676X.2013.02.09.

[18] C.-T. Sun, Y.-C. Lin, C.-J. Hsieh, J.-C. Liou, **L.-B. Wang**, and W.-C. Tian. "A linear-response CMOS-MEMS capacitive tactile sensor". In: *2012 IEEE SENSORS*. 2012 IEEE SENSORS. 2012, pp. 1–4. DOI: 10.1109/ICSENS.2012.6411545.

Scholarships & Awards

• 1st place in 3-minute thesis competition at McDonnell Academy	2021
• McDonnell International Scholars Academy, WUSTL	2016–2021
• Taiwan Ministry of Education WUSTL Scholarship	2016–2021
• Outstanding Summer Research Award, Center of Genomic Medicine, NTU	2012

Skills

- **Programming:** Python, R, SQL, C
- **Tools:** conda, Snakemake
- **Database:** PostgreSQL, SQLite
- **Web backend:** Django, Flask, SQLAlchemy
- **Web frontend:** HTML, CSS, JavaScript

Community Engagement

PyCon Taiwan & APAC Organizing Committee   Taipei, Taiwan
Program Committee Chair of PyCon Taiwan 2016   2015–2016
Public Relations Manager of PyCon APAC 2015   2014–2015

Open Source Software Communities   Taipei, Taiwan
Speaker & Organizer   2013–2016

- Speaker at PyCon Taiwan, Taipei.py, Taiwan R User Group, and PyCon China
- Gave technical talks over convolutional neural network, text search, genomic data processing, HDF5, parallel computing, and R ggplot2 plotting
- Past presentations available at blog.liang2.tw/talks