

Liang-Bo Wang

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EDUCATION

Washington University in St. Louis Ph.D. in Computational and Systems Biology	St. Louis, USA 2016–2021
National Taiwan University M.S. in Biomedical Electronics and Bioinformatics B.S. in Electrical Engineering and minor in Economics	Taipei, Taiwan 2014–2016 2009–2014

EXPERIENCE

Washington University in St. Louis PhD Research, Li Ding Lab	St. Louis, USA 2017–2021
<ul style="list-style-type: none">• Thesis: Building a toolbox and insights toward proteogenomic characterization of glioblastoma• 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 Internship on search improvement	Taipei, Taiwan Summer 2015
<ul style="list-style-type: none">• Improved e-commerce product search by improving Mandarin/Chinese text segmentation on Elasticsearch and implementing a Word2Vec-based semantic search	
Microsoft Research Asia Research Internship, Eric Chang Group	Beijing, China 2014–2015
<ul style="list-style-type: none">• Deep learning based cancer image and pathway analysis• Applied convolutional neural network to histopathology image analysis	
National Taiwan University Master's Research, Eric Y. Chuang Lab	Taipei, Taiwan 2014–2016
<ul style="list-style-type: none">• Thesis: BioCloud: an online sequencing analysis platform	
National Taiwan University Undergraduate Research on genomic data analysis, Eric Y. Chuang Lab Undergraduate Research on Bio-MEMS sensor design, Wei-Cheng Tian Lab	Taipei, Taiwan 2012–2014 2011–2012

PUBLICATIONS

1. Cui Zhou, D. *et al.* Spatially restricted drivers and transitional cell populations cooperate with the microenvironment in untreated and chemo-resistant pancreatic cancer. *Nature genetics* 54, 1390–1405. doi:10.1038/s41588-022-01157-1 (2022).
2. Storrs, E. P. *et al.* Pollock: fishing for cell states. *Bioinformatics advances* 2, vbac028. doi:10.1093/bioadv/vbac028 (2022).
3. Huang, K.-l. *et al.* Spatially interacting phosphorylation sites and mutations in cancer. *Nature communications* 12, 2313. doi:10.1038/s41467-021-22481-w (2021).

4. **Wang, L.-B.** *et al.* Proteogenomic and metabolomic characterization of human glioblastoma. *Cancer cell* 39, 509–528.e20. doi:10.1016/j.ccell.2021.01.006 (2021).
5. Bailey, M. H. *et al.* Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature communications* 11, 4748. doi:10.1038/s41467-020-18151-y (2020).
6. Gillette, M. A. *et al.* Proteogenomic characterization reveals therapeutic vulnerabilities in lung adenocarcinoma. *Cell* 182, 200–225.e35. doi:10.1016/j.cell.2020.06.013 (2020).
7. McDermott, J. E. *et al.* Proteogenomic characterization of ovarian HGSC implicates mitotic kinases, replication stress in observed chromosomal instability. *Cell reports medicine* 1, 100004. doi:10.1016/j.xcrm.2020.100004 (2020).
8. Petralia, F. *et al.* Integrated proteogenomic characterization across major histological types of pediatric brain cancer. *Cell* 183, 1962–1985.e31. doi:10.1016/j.cell.2020.10.044 (2020).
9. Rozenblatt-Rosen, O. *et al.* The Human Tumor Atlas Network: charting tumor transitions across space and time at single-cell resolution. *Cell* 181, 236–249. doi:10.1016/j.cell.2020.03.053 (2020).
10. Clark, D. J. *et al.* Integrated proteogenomic characterization of clear cell renal cell carcinoma. *Cell* 179, 964–983.e31. doi:10.1016/j.cell.2019.10.007 (2019).
11. Gao, G. F. *et al.* Before and after: comparison of legacy and harmonized TCGA genomic data commons' data. *Cell systems* 9, 24–34.e10. doi:10.1016/j.cels.2019.06.006 (2019). (*co-first author*).
12. Grüning, B., Dale, R., Sjödin, A., Chapman, B. A., Rowe, J., Tomkins-Tinch, C. H., Valieris, R., Köster, J. & **The Bioconda Team**. Bioconda: sustainable and comprehensive software distribution for the life sciences. *Nature methods* 15, 475–476. doi:10.1038/s41592-018-0046-7 (2018).
13. Huang, K.-I. *et al.* Pathogenic germline variants in 10,389 adult cancers. *Cell* 173, 355–370.e14. doi:10.1016/j.cell.2018.03.039 (2018).
14. Sun, S. Q., Mashl, R. J., Sengupta, S., Scott, A. D., Wang, W., Batra, P., **Wang, L.-B.**, Wyczalkowski, M. A. & Ding, L. Database of evidence for precision oncology portal. *Bioinformatics* 34, 4315–4317. doi:10.1093/bioinformatics/bty531 (2018).
15. Lai, Y.-P. ^{*}, **Wang, L.-B.** ^{*}, Wang, W.-A. ^{*}, Lai, L.-C., Tsai, M.-H., Lu, T.-P. & Chuang, E. Y. iGC—an integrated analysis package of gene expression and copy number alteration. *BMC bioinformatics* 18, 35. doi:10.1186/s12859-016-1438-2 (2017).
16. Xu, Y., Jia, Z., **Wang, L.-B.**, Ai, Y., Zhang, F., Lai, M. & Chang, E. I.-C. Large scale tissue histopathology image classification, segmentation, and visualization via deep convolutional activation features. *BMC bioinformatics* 18, 281. doi:10.1186/s12859-017-1685-x (2017).
17. **Wang, L.-B.**, Chuang, E. Y. & Lu, T.-P. Identification of predictive biomarkers for ZD-6474 in lung cancer. *Translational cancer research* 4, 324–331. doi:10.3978/j.issn.2218-676X.2015.08.10 (2015).
18. Lee, C.-Y. ^{*}, Chiu, Y.-C. ^{*}, **Wang, L.-B.** ^{*}, Kuo, Y.-L. ^{*}, Chuang, E. Y., Lai, L.-C. & Tsai, M.-H. Common applications of next-generation sequencing technologies in genomic research. *Translational cancer research* 2, 33–45. doi:10.3978/j.issn.2218-676X.2013.02.09 (2013).
19. Sun, C.-T., Lin, Y.-C., Hsieh, C.-J., Liou, J.-C., **Wang, L.-B.** & Tian, W.-C. A linear-response CMOS-MEMS capacitive tactile sensor in. 2012 IEEE SENSORS (2012), 1–4. doi:10.1109/ICSENS.2012.6411545.

SCHOLARSHIPS & AWARDS

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|---|-----------|
| • 1 st place in Three-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

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| <ul style="list-style-type: none"> • Programming languages: Python (general purpose), R (data analysis, visualization), SQL • Analysis tools: (bio)conda, Snakemake, tidyverse, | <ul style="list-style-type: none"> Bioconductor genomics-related tool stack • Databases: PostgreSQL, SQLite, DuckDB • Web: Django, Flask, basic frontend skill |
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COMMUNITY ENGAGEMENT

Open Source Projects

2015–Present

Contributor of conda-forge, bioconda, cyvcf2 and other open-source projects (see my GitHub).

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