Liang-Bo Wang

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EDUCATION

Washington University in St. Louis   St. Louis, USA
Ph.D. in Computational and Systems Biology   2016–2021

National Taiwan University   Taipei, Taiwan
M.S. in Biomedical Electronics and Bioinformatics   2014–2016
B.S. in Electrical Engineering and minor in Economics   2009–2014

EXPERIENCE

Mandatory National Service   Taipei, Taiwan
Substitute Services Draftee   Mar 2022–Mar 2023

Washington University in St. Louis   St. Louis, USA
PhD Research, Li Ding Lab   May 2017–Dec 2021

- Thesis: Building a toolbox and insights toward proteogenomic characterization of glioblastoma
- Characterized human tumor using mass spectrometry, single cell sequencing, spatial transcriptomics, multiplexed imaging, and other high-throughput technologies.
- 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)
- Led the data analysis team of CPTAC glioblastoma study, coordinating collaboration across institutions nationwide
- Developed tools and databases (PTMcosmos, CharGer) to analyze large-scale multi-modal datasets

Open Source Software Contributor   2015–Present

- Contributed to tools and projects including conda-forge, bioconda, and cyvcf2
- Familiar with R & Python software development process (testing, packaging, CI/CD, and documentation)

Pinkoi   Taipei, Taiwan
Internship on search improvement   Summer 2015

- Pinkoi is an online marketplace for unique and original design goods in Asia
- 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
Research 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
- Developed a cloud platform to process and analyze sequencing data, including a web portal, a data processing job queue scheduler, and a database to track data and visualize results

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

SKILLS

Programming languages: Python (general purpose), R (data analysis, statistics, visualization), SQL

Analysis tools: (bio)conda, Snakemake, tidyverse, Bioconductor genomics-related tool stack

Databases: PostgreSQL, SQLite, DuckDB

Web development: Django, Flask, basic frontend knowledge

Tool development: Python (pytest, Sphinx), GitHub Actions/Workflow

LEADERSHIP EXPERIENCE

Tech communities   2013–Present

Speaker at PyCon APAC & Taiwan & China and Taiwan & China R conferences, Taipei Bioinformatics Omnibus and other R and Python local meetups

- Presented technical topics including Snakemake, genomic analysis, visualization, text search, statistics, convolutional neural network, HDF5, and parallel computing
- Past presentations available at blog.liang2.tw/talks

PyCon Taiwan   2016

Program Committee Chair

- Oversaw the main theme and agenda planning of the 3-day conference with 50 talks and 700+ attendees
- Headed the talk proposal review process and keynote speaker invitations
- Introduced a new double blind multi-stage peer review system

PyCon APAC   2015

Public Relations Manager

Taiwan R User Group   2013–2016

Organizer and Host

SCHOLARSHIPS & AWARDS

- 1st 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

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. Dou, Y. *et al.* Proteogenomic characterization of endometrial carcinoma. *Cell* 180, 729–748.e26. doi:10.1016/j.cell.2020.01.026 (2020).

7. 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).

8. 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).

9. 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).

10. 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).

11. 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).

12. 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)*.

13. 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).

14. Huang, K.-l. *et al.* Pathogenic germline variants in 10,389 adult cancers. *Cell* 173, 355–370.e14. doi:10.1016/j.cell.2018.03.039 (2018).

15. 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).

16. 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).

17. 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).

18. **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).

19. 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).

20. 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.