Liang-Bo Wang

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Computational biologist proficient in multi-omics/single-cell analysis and tool/pipeline development

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

- Optimized the user experience of Taiwan's national long-term care system by contributing to a Data for Social Good project in partnership with Taiwan's Ministry of Health and Welfare
- Improved the call center operations of the national long-term care system by designing a data-driven staffing system and updating standard operating protocols by analyzing call transcriptions and service applications

Washington University in St. Louis — St. Louis, USA
PhD Research, Li Ding Lab — Sep 2016–Dec 2021

- Collaborated with leading 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 efforts across multiple institution, to identify different patient stratifications and druggable targets in signaling pathways using multi-omics analysis with multiplexed mass spectrometry and bulk genomics
- Investigated tumor heterogeneity and microenvironment using single cell sequencing, spatial transcriptomics and multiplexed imaging (Hyperion, CODEX)
- Developed tools, processing pipelines, and databases (PTMcosmos, CharGer) to analyze multi-modal datasets
- Conducted quality control analysis on different versions of the mutation calling pipeline on the NCI Genomics Data Commons, a platform hosting and reprocessing data of multiple cancer genome programs

Open Source Software — Online
Contributor — 2015–Present

- Contributed to the development of open source tools and projects including conda-forge, bioconda, and cyvcf2
- Demonstrated proficiency in the software development workflow, including testing, packaging, CI/CD, issue triaging, and documentation

Pinkoi — Taipei, Taiwan
Internship on search improvement — Summer 2015

- Enhanced the search functionality on Pinkoi, Asia's leading online marketplace for original design goods
- Investigated various Mandarin/Chinese text segmentation methods in ElasticSearch
- Developed a product recommendation system when user's search query failed to match any exact product by implementing a Word2Vec-based semantic search

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

- Investigated the use of deep learning for histopathology image and pathway analysis in the brain and colon cancer
- Achieved highly accurate histopathology image classification and segmentation using convolutional neural network (CNN) based models
- Analyzed the CNN activation features and discovered that the model was able to accurately identify key morphological features and ignore irrelevant background noise as identified by pathologists

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

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 packaging (pytest, Sphinx), GitHub Actions/Workflow

Cloud/HPC computing: GCP, AWS, Azure, LSF, Docker

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 a team of 11 volunteers
- Coordinated 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.