# Liang-Bo Wang

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## 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. *(co-first author)*.

[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. *(co-first author)*.

[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