

## EXPERIENCE

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

- 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** 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  
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

**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

## 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

## PUBLICATIONS

1. Huang, K.-I. *et al.* Spatially interacting phosphorylation sites and mutations in cancer. *Nature Communications* **12**, 2313. doi:10.1038/s41467-021-22481-w (2021).
2. **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).
3. 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).

4. Dou, Y. *et al.* Proteogenomic Characterization of Endometrial Carcinoma. *Cell* **180**, 729–748.e26. doi:10.1016/j.cell.2020.01.026 (2020).
5. 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).
6. 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).
7. 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).
8. 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).
9. 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).
10. 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*).
11. 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).
12. 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).
13. 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).
14. Lai, Y.-P. <sup>\*</sup>, **Wang, L.-B.** <sup>\*</sup>, Wang, W.-A. <sup>\*</sup>, 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).
15. 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).
16. **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).
17. Lee, C.-Y. <sup>\*</sup>, Chiu, Y.-C. <sup>\*</sup>, **Wang, L.-B.** <sup>\*</sup>, Kuo, Y.-L. <sup>\*</sup>, 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).
18. 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 <sup>st</sup> 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"> <li>• <b>Programming:</b> Python, R, SQL, C</li> <li>• <b>Tools:</b> conda, Snakemake</li> <li>• <b>Database:</b> PostgreSQL, SQLite</li> </ul> | <ul style="list-style-type: none"> <li>• <b>Web backend:</b> Django, Flask, SQLAlchemy</li> <li>• <b>Web frontend:</b> HTML, CSS, JavaScript</li> </ul> |
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## COMMUNITY ENGAGEMENT

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### 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](http://blog.liang2.tw/talks)