

# Tongxin Wang

tw11@iu.edu | 614-886-9177  
714 Blake St Apt D, Indianapolis, IN 46202

## EDUCATION

### Indiana University Bloomington

PhD Candidate in Computer Science, Minor in Bioinformatics; GPA: 4.00/4.0

Bloomington, IN  
Aug. 2017 - Jun. 2021 (Expected)

### The Ohio State University

PhD Student in Electrical and Computer Engineering; GPA: 4.00/4.0

Columbus, OH  
Aug. 2016 - Aug. 2017

### Fudan University

Bachelor of Science in Physics; GPA: 3.64/4.0

Shanghai, China  
Aug. 2011 - Jul. 2016

## INDUSTRY EXPERIENCE

### Facebook, Inc.

Software Engineer Intern (Machine Learning)

Menlo Park, CA  
May 2020 - Aug. 2020

- Developed machine learning models for feed ranking projects to improve the newsfeed experience for Facebook App users.

### Tencent AI Lab

Algorithm Research Intern

Shenzhen, China  
May 2019 - Aug. 2019

- Developed a pipeline to predict microsatellite instability status of patients from H&E histological whole-slide images using deep residual neural networks implemented by Python and PyTorch.
- Co-first-author paper accepted by *IEEE International Symposium on Biomedical Imaging (ISBI) 2020*.

### Bosch IoT Research Group

Research Assistant Intern

Shanghai, China  
Jul. 2015 - Sep. 2015

- Developed a product registration and validation system using physical unclonable functions technologies and error correction algorithms implemented by C++, Matlab, and OpenCV.
- Tested the robustness and feasibility of the aforementioned system on various packaging materials.

## RESEARCH EXPERIENCE

### Regenstrief Institute, Indiana University

Research Assistant

Adviser: Dr. Kun Huang  
Aug. 2017 - Present

- **Deep Transfer Learning for Single-cell RNA Sequencing Batch Correction**
  - \* Developed BERMUDA, an innovative method to integrate multiple single-cell RNA sequencing datasets and remove batch effects based on deep neural networks with maximum mean discrepancy loss using Python and PyTorch.
  - \* First-author paper accepted by *Genome Biology*.
- **Topological Methods for Analysis of Single-cell RNA Sequencing Data**
  - \* Developed a novel method to combine topological data analysis techniques with gene co-expression network analysis for single-cell RNA sequencing data visualization using Python.
  - \* First-author paper accepted by *Pacific Symposium on Biocomputing (PSB) 2019* with oral presentation.
- **Generalized Gene Co-expression Analysis via Subspace Clustering Using Low-rank Representation**
  - \* Developed a new, generalized gene co-expression network analysis method based on low-rank representation and a quasi-clique detection algorithm using Matlab and R.
  - \* First-author paper accepted by *BMC Bioinformatics*.

### Department of ECE, The Ohio State University

Research Assistant, University Fellowship

Adviser: Dr. Kun Huang  
Apr. 2017 - Aug. 2017

- **Diagnosing Effusion Fluid Cytology Using Whole Slide Imaging and Multiple Instance Learning**
  - \* Developed an algorithm to identify patches with malignant cells in effusion fluid cytology whole slide images based on multiple clustered instance learning using Matlab.

## TECHNICAL SKILLS

- **Programming Languages:** Python, R, Matlab, Java, SQL
- **Algorithm Design:** Machine Learning, Data Mining, Biomedical Informatics

## COURSEWORK & TRAINING

Machine Learning, Deep Learning, Artificial Intelligence, Data Mining, Data Visualization, Database Concepts, Computer Vision, Image Processing, Data Structure, Algorithms, Bioinformatics

**Tongxin Wang**, Wei Shao, Zhi Huang, Haixu Tang, Jie Zhang, Zhengming Ding, Kun Huang. MORONET: multi-omics integration via graph convolutional networks for biomedical data classification. *bioRxiv*.

Travis S Johnson, Y Yu Christina, Zhi Huang, Siwen Xu, **Tongxin Wang**, Chuanpeng Dong, Wei Shao, Mohammed Abu Zaid, Yijie Wang, Christopher Bartlett *et al.* Diagnostic Evidence GAUGE of Single cells (DEGAS): A transfer learning framework to infer impressions of cellular and patient phenotypes between patients and single cells. *bioRxiv*.

---

## PUBLICATIONS

**Tongxin Wang**, Zhengming Ding, Wei Shao, Haixu Tang, and Kun Huang. Towards fair cross-domain adaptation via generative learning. *IEEE/CVF Winter Conference on Applications of Computer Vision (WACV)*, 2021.

Rui Cao, Fan Yang, Si-Cong Ma, Li Liu, Yu Zhao, Yan Li, De-Hua Wu, **Tongxin Wang**, Wei-Jia Lu, Wei-Jing Cai *et al.* Development and interpretation of a pathomics-based model for the prediction of microsatellite instability in colorectal cancer. *Theranostics* (IF = 8.6), 2020.

Wei Shao, **Tongxin Wang**, Liang Sun, Tianhan Dong, Zhi Han, Zhi Huang, Jie Zhang, Daoqiang Zhang, and Kun Huang. Multi-task multi-modal learning for joint diagnosis and prognosis of human cancers. *Medical Image Analysis* (IF = 11.1), 2020.

**Tongxin Wang\***, Weijia Lu\*, Fan Yang\*, Li Liu, Zhongyi Dong, Weimin Tang, Jia Chang, Wenjing Huan, Kun Huang, and Jianhua Yao. *IEEE International Symposium on Biomedical Imaging (ISBI)*, 2020, Iowa City, USA.

**Tongxin Wang**, Travis S Johnson, Wei Shao, Zixiao Lu, Bryan R Helm, Jie Zhang, and Kun Huang. BERMUDA: a novel deep transfer learning method for single-cell RNA sequencing batch correction reveals hidden high-resolution cellular subtypes. *Genome Biology* (IF = 14.0), 2019.

**Tongxin Wang**, Jie Zhang, and Kun Huang. Generalized gene co-expression analysis via subspace clustering using low-rank representation. *BMC Bioinformatics*, 2019.

**Tongxin Wang**, Travis Johnson, Jie Zhang, and Kun Huang. Topological methods for visualization and analysis of high dimensional single-cell RNA sequencing data. *Pacific Symposium on Biocomputing (PSB)*, 2019, Big Island, HI.

Travis S Johnson, **Tongxin Wang**, Zhi Huang, Christina Y Yu, Yi Wu, Yatong Han, Yan Zhang, Kun Huang, and Jie Zhang. LAMBDA: label ambiguous domain adaptation dataset integration reduces batch effects and improves subtype detection. *Bioinformatics*, 2019.

Wei Shao, **Tongxin Wang**, Zhi Huang, Jun Cheng, Zhi Han, Daoqiang Zhang, and Kun Huang. Diagnosis-guided multi-modal feature selection for prognosis prediction of lung squamous cell carcinoma. *International Conference on Medical Image Computing and Computer Assisted Intervention (MICCAI)*, 2019, Shenzhen, China.

Zhi Huang, Zhi Han, **Tongxin Wang**, Wei Shao, Shunian Xiang, Paul Salama, Maher Rizkalla, Kun Huang, and Jie Zhang. TSUNAMI: translational bioinformatics tool suite for network analysis and mining. *Genomics, Proteomics & Bioinformatics*, (accepted) 2019.

Wei Shao, Zhi Han, Jun Cheng, Liang Cheng, **Tongxin Wang**, Liang Sun, Zixiao Lu, Jie Zhang, Daoqiang Zhang, and Kun Huang. Integrative analysis of pathological images and multi-dimensional genomic data for early-stage cancer prognosis. *IEEE Transactions on Medical Imaging*, 2019.

(\* denotes equal contribution)