

Tongxin Wang

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EDUCATION

Indiana University Bloomington

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

Bloomington, IN

Aug. 2017 - May 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

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* (IF = 14).
- 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.

School of Information Science, Fudan University

Undergraduate Thesis Project

Adviser: Dr. Haipeng Wang

Jan. 2016 - Jun. 2016

- SAR Image Automatic Target Recognition Based on Deep Learning**
 - Developed an algorithm based on convolutional neural networks to classify SAR images in MSTAR dataset with both amplitude and phase information using Caffe.

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

PUBLICATIONS

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*, 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.