Tongxin Wang

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EDUCATION

Indiana University Bloomington   Bloomington, IN
PhD Candidate in Computer Science, Minor in Bioinformatics; GPA: 4.00/4.0   *Aug. 2017 - May 2021 (Expected)*

The Ohio State University   Columbus, OH
PhD Student in Electrical and Computer Engineering; GPA: 4.00/4.0   *Aug. 2016 - Aug. 2017*

Fudan University   Shanghai, China
Bachelor of Science in Physics; GPA: 3.64/4.0   *Aug. 2011 - Jul. 2016*

INDUSTY EXPERIENCE

Facebook, Inc.   Menlo Park, CA
Software Engineer Intern (Machine Learning)   *May 2019 - Aug. 2019*

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

Tencent AI Lab   Shenzhen, China
Algorithm Research Intern   *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   Shanghai, China
Research Assistant Intern   *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   Adviser: Dr. Kun Huang
Research Assistant   *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   Adviser: Dr. Kun Huang
Research Assistant, University Fellowship   *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   Adviser: Dr. Haipeng Wang
Undergraduate Thesis Project   *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

PREPRINTS

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

Tongxin Wang, Zhengming Ding, Wei Shao, Haixu Tang, and Kun Huang. Towards fair cross-domain adaptation via generative learning. *arXiv*.

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

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* (accepted, 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 = 10.8), 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)