Ziqi (Amber) Tang

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One Bungtown Road, Cold Spring Harbor, NY

Education

Cold Spring Harbor Laboratory

Ph.D. Candidate in Biology — Current

University of North Carolina at Chapel Hill

BS. in Biology; BS. in Computer Science — Fall 2015 - Spring 2019

Graduated with Distinction and Highest Honors

Research Experience

Peter Koo Lab at Cold Spring Harbor Laboratory

Ph.D. candidate — April 2020 - Current

- Prototyped a multi-task convolutional network that predicts various RNA regulatory functions from primary sequence
- Developed a transformer-based language model for RNA sequences and assessed transfer learning on various RNA regulation prediction tasks
- Developed a framework to comprehensively evaluate the generalization and interpretability of convolutional networks for predicting epigenomics data
- Deployed a deep convolutional network to model single-cell ATAC-seq data and performed model interpretability methods to uncover learned cell-type specific features

Terry Furey Lab at Department of Genetics, UNC Chapel-Hill

Research Assistant — Fall 2017 - Spring 2019

- Analyzed ATAC-seq data from patients with Crohn’s disease
- Investigated the role of allelic imbalance expression in inflammatory tissue

Dayan Network Neuroscience Lab at Department of Radiology, UNC Chapel-Hill

Research Assistant — Fall 2017 - Spring 2019

- Differentiated prodromal Parkinson’s disease patients from healthy individuals fMRI images using SVM
- Generated brain connectivity matrix for Parkinson’s Disease patients

Publications and Conferences

Publications

- Toneyan, S.*, **Tang, Z.***, Koo, P., *Evaluating deep learning for predicting epigenomic profiles*, Nature Machine Intelligence, Dec 2022. [Link]
- Kawaguchi,R., **Tang, Z.**, Fischer, S., Rajesh, C., Tripathy, R., Koo, P., Gillis, J., *Learning single-cell chromatin accessibility profiles using meta-analytic marker genes*, Briefings in Bioinformatics, Dec 2022. [Link]
- Majdandzic, A., Rajesh, C., **Tang, Z.**, Toneyan, S., Labelson, E., Tripathy, R., Koo, P., *Selecting deep neural networks that yield consistent attribution-based interpretations for genomics*, Proceedings of the 17th Machine Learning in Computational Biology meeting, Dec 2022. [Link]
- Lee, N., **Tang, Z.**, Toneyan, S., Koo, P., *Evolution-inspired augmentations improve deep learning for regulatory genomics*, BioRxiv, Dec 2022. [link]

Conferences and Other

- Poster presentation at Biology of Genomes 2022, Intelligent Systems for Molecular Biology 2022, and American Society of Human Genomics 2022
- Participant. CIFAR Deep Learning + Reinforcement Learning Summer School 2021
- Reviewer, Machine Learning in Structural Biology workshop, NeurIPS 2022
- Program Committee member, Machine Learning in Computational Biology 2022

Extracurricular Experience

Diversity Initiative for the Advancement of STEM at CSHL

E-board member — Current

- Organized seminar and discussions to support and increase the presence of underrepresented minorities in STEM fields

CSHL Undergraduate Research Program

Mentor — Summer 2021-2022

- Lead lectures in Programming Course, introducing methods in biological data analysis for 20+ students

Computer Science department, UNC Chapel-Hill

Teaching Assistant — Fall 2017 - Fall 2018

- Assisted teaching in Data Structure and Introduction to Algorithm for 100+ students

Technical Skills

- Coding in Python, C, java, SQL
- Frameworks including TensorFlow, PyTorch and git
- Experience with developing machine learning models, evaluating their performance, and model interpretation for scientific discovery on high performance computing clusters (UGE, Slurm)