# Ziqi (Amber) Tang

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One Bungtown Road, Cold Spring Harbor, NY

# Education \_\_\_\_

# **Cold Spring Harbor Laboratory**

Ph.D. Candidate in Biology

Fall 2019 - Current

Expected graduation May 2024

# 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

- · Assessed transfer learning with transformer-based language models for various RNA regulation prediction tasks
- Prototyped a multi-task convolutional network that predicts various RNA regulatory functions from primary sequence
- 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

# **Camford Capital**

Venture Fellow July 2023 - Oct 2023

- Prototyped algorithms for Deep Learning guided sequence design
- · Participated in internal venture initiatives at the interface of Computation, Artificial Intelligence and Biomedicine

# 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., EvoAug: improving generalization and interpretability of genomic deep neural networks with evolution-inspired data augmentations, Genome Biology, May 2023. [link]
- Tang, Z., Toneyan, S., Koo, P., Current approaches to genomic deep learning struggle to fully capture human genetic variation, Nature Genetics, News & Views, Dec 2023. [link]

• Tang, Z., Koo, P., Evaluating the representational power of pre-trainedDNA language models for regulatory genomics, BioRxiv, Mar 2024. [link]

# **Conferences and Presentations**

Poster presenter

- Building foundation models for regulatory genomics requires rethinking large language models; International Conference on Machine Learning Computational Biology Workshop 2023
- Benchmarking Binary and Quantitative Genomic Models; Biology of Genomes 2022
- Evaluating deep learning for predicting epigenomic profiles; Intelligent Systems for Molecular Biology 2022
- Evaluating deep learning for predicting epigenomic profiles; American Society of Human Genomics 2022

# **Professional Service** \_\_\_\_\_

# Diversity Initiative for the Advancement of STEM at CSHL

E-board member

Spring 2022 - Current

· Organized seminars and discussions to support and increase the presence of underrepresented minorities in STEM fields

#### Reviewer

Nature Genetics, Nature Methods, Bioinformatics, Machine Learning in Structural Biology workshop, NeurIPS 2022, International Conference on Research in Computational Molecular Biology 2024

# **Program Committee**

• Machine Learning in Computational Biology 2022

# Additional Experience \_\_\_\_\_\_

# **CSHL Post-baccalaureate Research Education Program**

Mentor

Summer 2023 - Current

• Mentored a PREP scholar, guiding their research project and supporting the preparation of graduate school applications.

### **CSHL Undergraduate Research Program**

Mentor

Summer 2021-2023

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

# CIFAR Deep Learning + Reinforcement learning Summer School

Participant

July 2021

• Participated in lecture and discussions about cutting-edge topics in machine learning

# 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)

# References \_

Dr. Peter Koo

Assistant Professor, Cold Spring Harbor Laboratory, Ph.D. Advisor ☑ koo@cshl.edu

• Dr. Justin Kinney

Associate Professor, Cold Spring Harbor Laboratory, Thesis Committee Member 

☑ jkinney@cshl.edu

· Dr. Jesse Gillis

Associate Professor, University of Toronto, Thesis Committee Chair

☑ jesse.gillis@utoronto.ca