**Haotian Teng**

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Personal Website: <https://haotianteng.github.io/>

**EDUCATION**

**Carnegie Mellon University (CMU)**,Pittsburgh, PA, United States

*Doctor of Philosophy, Computational Biology, School of Computer Science (SCS)*

Advisor: Ziv Bar-Joseph, Machine Learning and Computational Biology department, SCS, CMU. 2019 - present

**Core Courses**: Machine Learning 10-701, Deep Reinforcement Learning 10-703, Probabilistic Graphical Models 10-708, Convex Optimization 10-725, Advanced Natural Language Processing 11-711, Computational Genomics 02-710

**University of Queensland**, Brisbane, Queensland, Australia

*Master of Bioinformatics, Queensland Brain Institute* 2016 - 2018

**Peking University**, Beijing, China

Bachelor of Science, Physics 2011 - 2015

**RESEARCH EXPERIENCE**

**Ph.D. Candidate, Carnegie Mellon University**, Pittsburgh, PA

**Target-based drug generation using E(3) equivalent graph neural network and diffusion model** Dec 2022 - Present

* Implemented an **E**(3)-equivalent graph neural network combined with a probabilistic diffusion model to generate small molecules with both high binding affinity to target protein pockets and enhanced druggability.

**Clustering single-cell spatial transcriptomics data using hybrid model.** Aug2019 - Feb 2022

* Introduced FICT, a Gaussian-Multinomial probabilistic graphical model, to cluster cells from single-molecule spatial transcriptomics data, discovering six novel neuron development-related genes based on spatially-aware clusters.
* Developed a general gene embedding algorithm using a denoising autoencoder, achieving a 17.3X speed increase compared to UMAP.
* Created a simulation pipeline based on Metropolis-Hastings sampling to validate spatial transcriptomics clustering results.

**Detecting N6-methyladenosine (m6A) modification in RNA using long read sequencing**  Jan 2021 – Jan 2023

* Developed a hybrid PyTorch model that combines Non-Homogeneous Hidden Markov Model (NHMM) and Convolutional-Recurrent Neural Network (CRNN) for semi-supervised training on time-series signals to detect m6A modifications in RNA sequencing.
* Achieved state-of-art accuracy in RNA methylation detection, obtain a 22% and 7% relative improvement on yeast and human HEK293T cell lines.

**Neural architecture search using deep reinforcement learning** Jan2021 – Jul 2021

* Identified 3 novel convolutional neural layer structures using neural architecture search and achieved better performance than the usual residual connection layer on several common tasks in the OpenAI gym library with 20% fewer parameters.

**WORK EXPERIENCE**

**Bioinformatics Engineer @ Novogene Europe** Sep2018 - Feb 2019

* Optimized the human resequencing and laboratory automation pipeline cooperatively in a group with 7 people.
* Designed and developed the long-read sequencing platform as group leader with 3 group members.

**Research Scientist Intern @ Digitalgene.AI** Jun 2021 – Sep 2021

 Developed a comprehensive ligand-protein virtual screening cloud platform, which included automated protein binding pocket recognition, ligand structure refinement, docking, and protein-ligand interaction profiling. This resulted in an 87.2% success redocking rate for 282 known PDB drug complexes, representing a 31% improvement.

 Conducted virtual screening of over 1 million molecules from Topscience's natural product library in just one day using our cloud platform, successfully identifying 119 molecules with high binding affinity.

**SELECTED PUBLICATIONS**

* **Teng, H.**, et al. (2022). Clustering Spatial Transcriptomics Data. *Bioinformatics*, *38*(4), 997-1004. (**Citation 19)**
* **Teng, H.**, Cao, M. D., Hall, M. B., Duarte, T., Wang, S., & Coin, L. J. (2018). Chiron: translating nanopore raw signal directly into nucleotide sequence using deep learning. *GigaScience, 7(5), giy037.* (**Citation 137)**
* Avitan, L., Pujic, Z., Mölter, J., Van De Poll, M., Sun, B., **Teng, H.**, Amor, R., Scott, E.K. and Goodhill, G.J., 2017. Spontaneous activity in the zebrafish tectum reorganizes over development and is influenced by visual experience. *Current Biology, 27(16), pp.2407-2419.* (**Citation 73)**

**SKILLS**

* Programming: Python, C++, Bash, MATLAB, R
* Packages&Platforms: Tensorflow, PyTorch, OpenGL, BWA, SAMtools, Velvet.
* Deep Learning: CNN, RNN, LSTM, GNN, Diffusion model, GAN, VAE, BERT, Transformer, deep Q-learning