**Haotian Teng**

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**EDUCATION**

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

*Doctor of Philosophy, 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 2016 - 2018

**Peking University**, Beijing, China

Bachelor of Science, Physics 2011 - 2015

**RESEARCH EXPERIENCE**

**Ph.D. Research Assistant, Advised by Prof. Carl Kingsford and Prof. Ziv Bar-Joseph, Carnegie Mellon University**

**Target-based drug generation using graph neural networks with probabilistic diffusion model.** Nov 2022 – present

* Designed an E(*3*) equivalent graph neural network with probabilistic diffusion model to generate small molecules with high binding affinity to given target protein pocket.

**Clustering the single-cell spatial transcriptomics data with novel probabilistic graphical model.** Aug2019 - Feb 2022

* Developed a novel probabilistic graphical model [FICT](https://academic.oup.com/bioinformatics/article/38/4/997/6384569) that clusters the cell for spatial transcriptomics data. By simultaneously modelling the spatial distribution and the gene expression, FICT can discover spatial pattern.
* Identified genes related to neuron differentiation by DGE analysis on spatial sub-clusters identified by FICT in the MERFISH dataset.

**Detecting N6-methyladenosine (m6A) modification in RNA using long read sequencing**  Sept 2019 – Jan 2023

* Introduced *Xron*, an interpretable hybrid deep learning model combining *non-homogeneous Hidden Markov Model* (NHMM) and *Convolutional-Recurrent Neural Network* (CRNN) that achieve accurate detection of m6A in RNA. Obtained a 22% and 7% relative improvement of AUC-ROC on Yeast and human HEK293T cell lines compared to state-of-the-art.
* Obtained model parameters of nanopore from the hybrid model. Constructed pore models based on the parameters and completed accurate signal segmentation in an unsupervised manner.

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

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

**PROFESSIONAL EXPERIENCE**

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

* Optimized the human resequencing and laboratory automation pipeline cooperatively in a medium size group with 7 people, achieved 50% faster processing speed.
* Initiated the first long-read sequencing cloud platform, achieved real-time online basecalling and metagenomics analysis.

**SELECTED PUBLICATIONS**

* **Teng, H.**, Yuan, Y., & Bar-Joseph, Z. (2021). Clustering Spatial Transcriptomics Data. *Bioinformatics*, *38*(4), 997-1004. (**Citation 21)**
* **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 135)**
* 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 70)**
* **Teng, H.** “A neuron-muscle circuit model of C.elegans’s locomotion.” *Bachelor of Science Thesis: Peking University, 2015*

**SKILLS**

* Programming: Python, C++, Bash, MATLAB, R, PHP, CSS
* Selected Packages&Platforms: Tensorflow, PyTorch, Linux, OpenGL, BWA, SAMtools, Velvet.
* General Machine Learning: Linear Regression, Logistic Regression, SVM, Decision Tree, Random Forest, Probabilistic Graphical Models, RBM, GMM, KNN, K-Means, PCA, t-SNE, UMAP, Bagging, AdaBoost, Gradient Boosting.
* Deep Learning: CNN, RNN, LSTM, GNN, Diffusion model, GAN, VAE, BERT, Transformer, deep Q-learning, Active Learning.