Jing Xu

+86 156-2094-6366 | joy1314bubian@gmail.com
github.com/joy1314
Birthday: 1995/7 | Female

EDUCATION

Nankai University *Sep 2017 - Jun 2020*

Master Student Computer Science and Technoledgy College of Computer Science *Tianjin, China*

Advisor: Han Zhang

Nankai University *Aug 2013 - Jun 2017*

B.S. Automation College of Computer and Control Engineering *Tianjin, China*

GPA: 88.7 / 100

PROJECTS

an Elderly Smart Home Robot Design *May 2015 - May 2017*

Project Leader

- We designed an elderly smart home robot based on ROS system. The robot could perform a series of simple actions such as automatic obstacle avoidance, grabbing and recognizing objects.

Enzyme Annotation *Sep 2017 - Sep 2019*

Project Leader

- We developed a new amino acid k-mer based CAZyme classification, motif identification, and genome annotation tool using a bipartite network algorithm.
- We developed a Python package named "eCAMI"

Huntington's Disease-Associated Genes Identification *Mar 2018 - Jun 2018*

Project Participant

- We proposed an ensemble method based on consensus-guided unsupervised feature selection (CGUFS) in order to further improve the accuracy and the stability of disease-associated genes identification.
- We also proposed a bagging integration strategy to integrate the results of CGUFS.

Antimicrobial Peptides Identification *Oct 2018 - Jul 2019*

Project Participant

- We proposed a deep learning structure named "multi-scale convolutional network" to identify antimicrobial peptide sequences. The multi-scale convolutional network, which contains multiple convolutional layers of various filter lengths, could utilize all latent features captured by the multiple convolutional layers.
- We incorporated redundant information into the designed model and proposed a fusion model to further improve the performance.
- We developed a Python package named "APIN".

Motif Occupancy Analysis *May 2019 - Aug 2019*

Project Participant

- We designed a multi-scale CNN, which employed convolutional filters of different scales to extract all latent features of DNA sequence, for the motif occupancy task.
- We used different methods to encode DNA sequence, which grouped two or three adjacent nucleotides in turn and encoded them together, to further improve the performance.

PAPERS

- **Jing Xu** †, Han Zhang †, Jinfang Zheng, Philippe Dovoedo, Yanbin Yin. eCAMI: simultaneous classification and motif identification for enzyme annotation. Bioinformatics, btz908.
- Xin Su †, **Jing Xu** †, Yanbin Yin, Xiongwen Quan, Han Zhang. Antimicrobial Peptide Identification Using Multi-scale Convolutional Network. BMC Bioinformatics 20, 730 (2019).

- Wei Li, **Jing Xu**, Yanbin Yin, Han Zhang. Multi-scale Convolutional Neural Network for Improved Motif Occupancy Analysis. In preparation.
- Xia Guo, Xue Jiang, **Jing Xu**, Xiongwen Quan, Min Wu, Han Zhang. Ensemble Consensus-Guided Unsupervised Feature Selection to Identify Huntington's Disease-Associated Genes. Genes 2018, 9(7), 350.

HONORS & AWARDS

- "Mingshanyunneng" Scholarship *Nankai University, 2017*
- "Excellent Graduation Thesis for Undergraduates" Award *Nankai University, 2017*
- 2nd Prize for "National Undergraduate Training Program for Innovation and Entrepreneurship" *Nankai University, 2017*
- "Gongneng" Scholarship *Nankai University, 2016*
- Comprehensive 2nd Scholarship *Nankai University, 2015*
- Comprehensive 2nd Scholarship *Nankai University, 2014*

MISCELLANEOUS

- **Skills:** C++, Python
- **Platforms:** Windows/Linux
- **Languages:** Toefl:85(L:19 S:19 R:25 W:22)