杨海

所属学院 信息科学与工程学院

学科领域 Computer application technology

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个人简介

Educational experience:

(1) 2008/08-2013/07, University of Chinese Academy of Sciences, Signal and Information Processing, PhD

(2) 2004/08-2008/07, Xi'an Jiaotong University, software engineering, bachelor

Research and academic work experience:

(1) 2019/01-present, East China University of Science and Technology, Department of Computer Science and Engineering, Distinguished associate research professor

(2) 2014/12-2018/12, Vanderbilt University, Bioinformatics, postdoctoral researcher

(3) 2013/08-2014/12, Assistant Researcher, Institute of Acoustics, Chinese Academy of Sciences

研究方向

Artificial intelligence, machine learning, big data, bioinformatics

研究成果及主要发表文章

Dr. Yang is currently focusing on studying complex disease genomes based on artificial intelligence and machine learning. The cancer driver gene discovery tool, iDriver are developed to explore driver genes in many different cancers. For the first time, iDriver integrates multiple omics data such as somatic mutation, copy number variation, gene expression differences, methylation differences, and protein expression differences. It uses a multivariate nonparametric statistical model to perform pattern recognition on nearly 20,000 genes in the entire genome. Almost 50 new driver genes have been found in many different cancers. The research results of iDriver have been reported by many media such as "Sina Technology" and "Sina Medicine". The non-coding region functional mutation research tool DVAR is developed to found no less than five distinct mutation patterns in the whole genome. A unified framework was developed to evaluate the functional impact of mutations in the 3 billion base pairs of the human genome based on a detailed analysis of its functions. The DVAR research results were introduced and recommended by more than 20 research institutions such as Ensemble. Currently, more than ten papers are published in academic journals and conferences. Several articles were published in the "Bioinformatics," "PLoS computational biology." As the sixth author, he published an article in Nature Neuroscience (a well-known sub-journal of Nature) that integrates multi-omics data to study schizophrenia genes. The research results of this article were reported by Xinhuanet (Xinhua News Agency website) and other well-known institutions and websites and served as reviewers for journals such as "Bioinformatics", "Briefings in Bioinformatics", "BMC genomics", "BIOMED RES INT", etc. In terms of international communication, he won the ASHG (2017) Excellent Article Award of the Genomics Conference and participated in the Harvard University Quantitative Genome Project Conference (2016).