Hai-tao **Li**

Ph.D. candidate · BIOINFORMATICS, SEU

**Profile**

|  |  |  |
| --- | --- | --- |
| **Hometown** | Jining City, Shandong Province, China |  |
| **Laboratory** | State Key Laboratory of Bioelectronics,  School of Biological Science and Medical Engineering,  Southeast University |  |
| **Birth** | 1989.02 |  |
| **Gender** | Male |  |
| **Working Mail** | leehightall@seu.edu.cn |  |
| **Personal Website** | https://leehightall.github.io |  |

**Education**

|  |  |
| --- | --- |
| **Ph.D. Candidate of Engineering (Supervisor: Prof. Xiao Sun)** | ***2016-now*** |
| Department of Bioinformatics and System Biology  State Key Laboratory of Bioelectronics  School of Biological Science and Medical Engineering  Southeast University |  |
| **Bachelor of Science (Supervisor: Prof. Chun-Hou Zheng)** | **2013-2016** |
| Department of Bioinformatics  School of Biomedical Engineering and Informatics  School of Basic Medical Sciences  Qufu Normal University |  |

**Skills**

|  |
| --- |
| Programming; R, Matlab, Python et al. |
| Machine learning, Data mining and statistical analysis |
| Working in Linux environment |
| Proficiency in using common bioinformatics software or databases |
| Proficiency in English academic writing and communication |
| Sequencing data analysis; RNA-seq, ChIP-seq, Hi-C et al. |

**Research Interests**

|  |
| --- |
| Machine Learning Tasks in Bioinformatics or Medical Informatics |
| Bioinformatics Software & Database Development |
| Cancer Driver Gene Identification and Imaging Genomics Analysis |
| Multi-omics data fusion analysis |

**Research Experience**

|  |
| --- |
| Identified subtypes of MCI based on genetic polymorphism and gene expression |
|  |
| Annotation for human genomic variation during the BMP4-induced conversion from embryonic stem cells to trophoblast |

Present a network method named DriverFinder to identify driver genes

by integrating multi-omics data of cancer

**Publications**

[1] **Hai-Tao Li**, Shao-Xun Yuan, Jian-Sheng Wu, Xiao-Zhu Zhang, Yun Liu, Xiao Sun. (2021) Molecular Subtyping of Mild Cognitive Impairment based on Genetic Polymorphism and Gene Expression. *The Journal of Prevention of Alzheimer's Disease* 8.2 (2021): 224-233. (PDF)

[2] **Hai-Tao Li**,Ya-Jun Liu, Hong-De Liu, Xiao Sun. (2020). Effect for Human Genomic Variation During the BMP4-Induced Conversion From Pluripotent Stem Cells to Trophoblast. *Frontiers in genetics*, *11*, 230. (PDF)

**[3] Hai-Tao Li**, Yu-Lang Zhang, Chun-Hou Zheng, and Hong-Qiang Wang (2014). Simulated Annealing Based Algorithm for Identifying Mutated Driver Pathways in Cancer. *Biomed Res Int*, ID 375980. (PDF)

**[4] Hai-Tao Li**, Jun Zhang, Jun-Feng Xia, Chun-Hou Zheng (2016).Identification of Driver Pathways in Cancer Based on Combinatorial Patterns of Somatic Gene Mutations. *Neoplasma* 63,1,2016:57-63. (PDF)

[5] Shao-Xun Yuan, **Hai-Tao Li**, Jian-Sheng Wu, Xiao Sun. (2021). Classification of Mild Cognitive Impairment with Multimodal Data using both Labeled and Unlabeled Samples. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. (PDF)

[6] Shao-Xun Yuan, **Hai-Tao Li**, Jian-Ming Xie, Xiao Sun. (2019). Quantitative Trait Module-Based Genetic Analysis of Alzheimer’s Disease. *International journal of molecular sciences*, *20*(23), 5912. (PDF)

[7] Yue-Zhen Yu, **Hai-Tao Li**, Ya-bing Yang, Hussain Sajidakbar, Chun-Hou Zheng, Jun-Feng Xia, Yan Chen (2016) Identification of breast cancer candidate genes using gene co-expression and protein-protein interaction information. *Oncotarget*, *7*(24), 36092. (PDF)

[8] Pi-Jing Wei, Di Zhang, **Hai-Tao Li**, Jun-Feng Xia, Chun-Hou Zheng. (2017). DriverFinder: a gene length-based network method to identify Cancer driver genes. *Complexity*, 2017. (PDF)