

# Hua Chai

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1607014/publications.pdf>

Version: 2024-02-01

25  
papers

331  
citations

933447

10  
h-index

888059

17  
g-index

28  
all docs

28  
docs citations

28  
times ranked

339  
citing authors

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Integrating multi-omics data through deep learning for accurate cancer prognosis prediction. <i>Computers in Biology and Medicine</i> , 2021, 134, 104481.   | 7.0 | 68        |
| 2  | Imputing missing RNA-sequencing data from DNA methylation by using a transfer learning-based neural network. <i>GigaScience</i> , 2020, 9, .   | 6.4 | 33        |
| 3  | Deep learning-based ovarian cancer subtypes identification using multi-omics data. <i>BioData Mining</i> , 2020, 13, 10.   | 4.0 | 30        |
| 4  | Cancer survival analysis using semi-supervised learning method based on Cox and AFT models with L1/2 regularization. <i>BMC Medical Genomics</i> , 2016, 9, 11.  | 1.5 | 26        |
| 5  | Robust Sparse Logistic Regression With the $L_{1+q}$ Regularization for Feature Selection Using Gene Expression Data. <i>IEEE Access</i> , 2018, 6, 68586-68595.   | 4.2 | 22        |
| 6  | A new semi-supervised learning model combined with Cox and SP-AFT models in cancer survival analysis. <i>Scientific Reports</i> , 2017, 7, 13053.  | 3.3 | 18        |
| 7  | A novel logistic regression model combining semi-supervised learning and active learning for disease classification. <i>Scientific Reports</i> , 2018, 8, 13009.   | 3.3 | 15        |
| 8  | Descriptor Selection via Log-Sum Regularization for the Biological Activities of Chemical Structure. <i>International Journal of Molecular Sciences</i> , 2018, 19, 30.  | 4.1 | 15        |
| 9  | scAdapt: virtual adversarial domain adaptation network for single cell RNA-seq data classification across platforms and species. <i>Briefings in Bioinformatics</i> , 2021, 22, .  | 6.5 | 13        |
| 10 | Identification of 13 blood-based gene expression signatures to accurately distinguish tuberculosis from other pulmonary diseases and healthy controls. <i>Bio-Medical Materials and Engineering</i> , 2015, 26, S1837-S1843. | 0.6 | 11        |
| 11 | The L1/2 regularization approach for survival analysis in the accelerated failure time model. <i>Computers in Biology and Medicine</i> , 2015, 64, 283-290.  | 7.0 | 11        |
| 12 | Cancer survival prognosis with Deep Bayesian Perturbation Cox Network. <i>Computers in Biology and Medicine</i> , 2022, 141, 105012.   | 7.0 | 9         |
| 13 | Application of L1/2 regularization logistic method in heart disease diagnosis. <i>Bio-Medical Materials and Engineering</i> , 2014, 24, 3447-3454.   | 0.6 | 7         |
| 14 | An Adaptive Transfer-Learning-Based Deep Cox Neural Network for Hepatocellular Carcinoma Prognosis Prediction. <i>Frontiers in Oncology</i> , 2021, 11, 692774.  | 2.8 | 7         |
| 15 | Complex harmonic regularization with differential evolution in a memetic framework for biomarker selection. <i>PLoS ONE</i> , 2019, 14, e0210786.  | 2.5 | 6         |
| 16 | Detecting lncRNA-Cancer Associations by Combining miRNAs, Genes, and Prognosis With Matrix Factorization. <i>Frontiers in Genetics</i> , 2021, 12, 639872.   | 2.3 | 6         |
| 17 | Predicting bladder cancer prognosis by integrating multi-omics data through a transfer learning-based Cox proportional hazards network. <i>CCF Transactions on High Performance Computing</i> , 2021, 3, 311-319.            | 1.7 | 6         |
| 18 | Semi-Supervised Learning with Ensemble Self-Training for Cancer Classification. , 2018, , .  |     | 5         |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 19 | Multi-omics Cancer Prognosis Analysis Based on Graph Convolution Network. , 2021, , .  |     | 5         |
| 20 | Robust sparse accelerated failure time model for survival analysis. Technology and Health Care, 2018, 26, 55-63.                                 | 1.2 | 2         |
| 21 | A novel Log penalty in a path seeking scheme for biomarker selection. Technology and Health Care, 2019, 27, 85-93.                               | 1.2 | 2         |
| 22 | Low-rank and sparse matrix decomposition based on $S_{1/2}$ and $L_{1/2}$ regularizations in dynamic MRI. , 2016, , .                            |     | 1         |
| 23 | A greedy screening test strategy to accelerate solving LASSO problems with small regularization parameters. Soft Computing, 2020, 24, 5245-5253. | 3.6 | 1         |
| 24 | Image Super-Resolution Reconstruction via $L_{1/2}$ and $S_{1/2}$ Regularizations. , 2016, , .   |     | 0         |
| 25 | A Genotype-Based Ensemble Classifier System for Non-Small-Cell Lung Cancer. IEEE Access, 2020, 8, 128509-128518.                                 | 4.2 | 0         |