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# Research on fine-tuning CNN for cancer diagnosis with gene expression data

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Convolutional neural networks have been used for cancer type prediction with gene expression data. However, its success is impeded by the lack of large labeled datasets in gene expression data. The class imbalance problem leads to that the model ignores the performance of the minority class. To handle the small sample size problem, fine-tuning CNN is used to transfer the knowledge of pre-trained model for cancer type predicting. The dataset with one cancer is used for training a model. The pre-model is fine-tuned with the training set of a new cancer type, and the fine-tuned model could be used for identifying the new cancer type. And the SMOTE resampling method is used for handling the class imbalance problem. We carried out experiments on The TCGA datasets with 1D-CNN and 2D-CNN models. The fine-tuned 1D-CNN obtains 97.5% accuracy, 98.6% Fscore of cancer type and 78.1% Fscore of normal type on average, and fine-tuned 2D-CNN obtains 97.4% accuracy, 98.5% Fscore of cancer type and 77.4% of normal type on average. Using fine-tuned CNN with SMOTE, the accuracy, Fscore of cancer type and the one of normal type are respectively increased about 1.5%, 0.5% and 21.5% on average.

**CCS CONCEPTS** • Computing methodologies • Machine learning • Machine learning approaches

**Additional Keywords and Phrases:** Convolutional neural network, gene expression data, cancer diagnosis, class imbalance

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## 1 INTRODUCTION

Intense interest in applying convolutional neural networks (CNNs) in cancer diagnosis is wide spread[1][2], but its success is impeded by the lack of labeled datasets in gene expression data. Labeling gene expression data is not only tedious and time consuming, but also demanding of costly domain knowledge and skills, which are not easily

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accessible[3]. In addition, the class imbalance problem in gene expression data also decrease the performance of correctly identifying the minority class. To handle these problems, fine-tuning CNN is used in cancer diagnosis with gene expression data. Transfer learning aims at transferring the model of source domain to the target domain[4]. This paper aims at transferring the model trained on the data of one cancer to predict another cancer by fine-tuning the pre-trained models. So that the existing models could be used to predict other cancers without retraining the whole deep learning model. It is able to leverage the knowledge of pre-trained model and reduce the time consumption on training the CNN model, and decrease the overfitting for predicting new cancer type. The contributions of this paper mainly include:

1) To handle the small sample size problem, we research the fine-tuning CNN method for transferring the CNN model trained on a tumor data to classify another cancer from the normal data.

2) The experiments are carried out on the TCGA datasets. The 1D-CNN and 2D-CNN architectures are evaluated in our experiments. The results show that the fine-tuned 1D-CNN obtains 97.5% accuracy, 98.6% Fscore of cancer type and 78.1% Fscore of normal type on average. The fine-tuned 2D-CNN obtains 97.4% accuracy, 98.5% Fscore of cancer type and 77.4% of normal type on average.

3) The data resampling method SMOTE(Synthetic Minority Oversampling Technique) is used to handle the class imbalance problem in cancer diagnosis with gene expression data. The results show that the fine-tuned CNN is improved about 1.5% accuracy, 0.5% Fscore of cancer type and 21.5% of normal type on average.

The rest of this paper is organized as follows. The related works are overviewed in Section 2. Our devised method is introduced in Section 3. Experimental datasets and performance evaluation metrics are introduced in Section 4. The experimental results are discussed in Section 5. The conclusion of this paper is shown in Section 6.

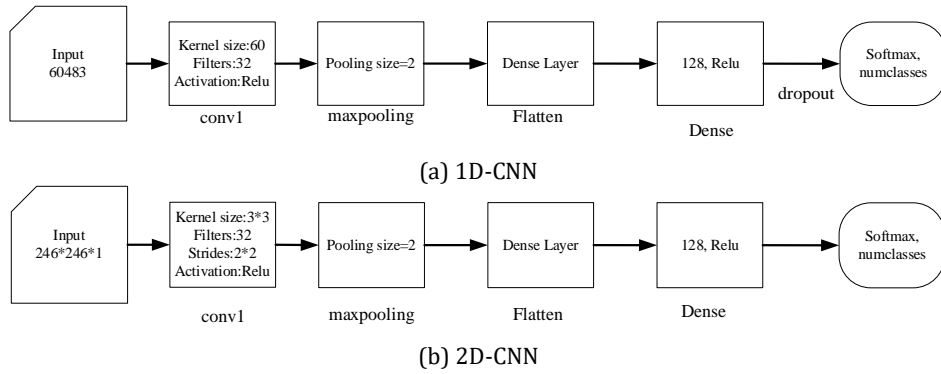
## 2 RELATED WORK

A variety of machine learning methods[5] have been used for cancer diagnosis based on microarray gene expression data, such as SVM[6], SVM-RFE with random value-based oversampling[7], active learning with rough-fuzzy classifier[8], complex network [9] and modified k-nearest neighbor[10]. Recently, deep learning algorithms also applied in the cancer classification with gene expression data[11][12]. Khorshed et al. [3] research on the deep learning for cancer classification. They proposed a method named Deep Learning for Multi-Tissue Cancer Classification of Gene Expressions (GeneXNet). It includes convolution layer, L GeneXNet Block and a GAP layer and a Softmax layer. In a GeneXNet Block, it a kind of the combination of DenseNet and ResNet. The output of the DenseNet is used as the input of the ResNet. The transfer learning is used to build binary classifiers for organ sites that did not have sufficient data to be trained independently. However, the transfer learning method show that the transfer learning is worse than the full learning on most datasets. On few datasets, it obtains better accuracy than full learning method. And the training data of transfer learning is the same as that used in pre-trained model. Only the classes are different, in the training set of the pre-trained model, there are 33 classes, and the training set of transfer learning is two classes. Sevakula et al. [4] presented a transfer learning procedure for cancer classification. It uses feature selection and normalization techniques in conjunction with sparse autoencoders on gene expression data. Mostavi et al [13] introduced several CNN models for cancer classification. Based on different designs of gene embeddings and convolution schemes, they implemented three CNN models: 1D-CNN, 2D-Vanilla-CNN, and 2D-Hybrid-CNN. However, these models can only be used to classify the specific cancer types. When classifying new type of cancers, the model is required to be re-trained. This paper is based on the work in [13], and utilize the transfer learning to improve the performance of different CNN models.

### 3 PROPOSED METHOD

#### 3.1 CNN

1D-CNN and 2D-CNN are used in this paper. The structures of the two kinds of models are shown in Fig.1. Fig.1(a) shows the 1D-CNN architecture. The vectors are the input of the conv1d layer without any resizing and reshape processing. The shape of the output of the conv1d layer is reduced by max-pooling. And then all units are flattened and are as the input of densely layer with 128 units. Then the 128 units are fully connected with the output units. The detail of the 1D-CNN layers, output size and the number of parameters is shown in Table 1. Fig.2(b) shows the structure of 2D-CNN. The input vectors are all resized into 60516 firstly. And then each vector is reshaped into 246\*246\*1 and they are as the input of conv2d. And the max-pooling follows the convolutional layer. And then all units are flattened and fully connected with a dense layer. The dense layer is fully connected with the output layer. The detail of the 2D-CNN is shown in Table 2. In Tables 1 and 2, the number of output units(#classes) is 2.



**Fig.1** the structure of 1D-CNN and 2D-CNN

**Table 1** the detail of 1D-CNN

Layer type(hyperparameters)	Output Shape	#Param
Conv1D(Filters=32,Kernel size=60,Activation=Relu)	(#samples, 60420,32)	2080
Maxpooling1D(Pool_size=2)	(#samples, 60420,32)	0
Flatten	(#samples, 966720)	0
Dense(Units=128, Activation=Relu)	(#samples,128)	123740288
Dense(Units=2, Activation=Softmax)	(#samples,2)	258

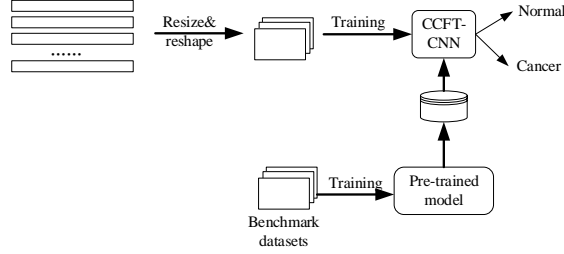
**Table 2** the detail of 2D-CN

Layer type(hyperparameters)	Output Shape	#Param
Conv1D(Filters=32, Kernel size=246, Activation=Relu)	(#samples, 122, 122, 32)	320
Maxpooling1D(Pool_size=(2,2))	(#samples, 62, 62, 32)	0
Flatten	(#samples, 119072)	0
Dense(Units=128, Activation=Relu)	(#samples, 128)	15241344
Dense(Units=2, Activation=Softmax)	(#samples, 2)	258

#### 3.2 Fine-tuning CNN

To handle the small sample size problem, the basic CNN model is improved using the fine-tune techniques. The flow chart of the Cancer Classification method with fine-tuning CNN(named CCFT-CNN in short) is shown in Fig.2. Based on the pre-trained CNN model, the model could be fine-tuned to identify the other cancers. The pre-trained

model is finetuned by freezing the first 2 layers and training the last 3 layers with new training set. And the number of units of the last layer is changed into the number of classes in the new training set. This means that only the parameters of the last 3 layers are adjusted, so as to save the time consuming on training. The comparison of the number of parameters between the full training and the finetuning is shown in Table 3. The number of parameters of fine-tuned model is less than that of the full-trained model.



**Fig.2** the flowchart of CCFT-CNN

**Table 3** the number of parameters in full-training model and fine-tuning model

CNN type	#Parameters in full-training model	#Parameters in fine-tuning model
1D-CNN	123,742,626	123,740,546
2D-CNN	15,241,922	15,241,602

#### 4 DATASETS AND PERFORMANCE EVALUATION METRICS

In TCGA datasets[15], there are 11,093 human samples for mRNA gene expression quantification, which were collected from 26 different human anatomical organ sites and covering 33 different Cancer tumor types. Each individual human sample represents the whole transcriptome and includes a total of 60,483 genes annotated against a reference genome. In this paper, mRNA-seq data from the TCGA public dataset were downloaded from UCSC Xena. The data is in the Illumina HiSeq 2000 log2(fpkm+1) scaled. Due to the lack of samples in most cancer types, we considered 15 datasets. The number of cancer and normal samples in each dataset is shown in Table 4.

**Table 4** TCGA datasets

Datasets	Normal	Cancer	Datasets	Normal	Cancer
BRCA	113	1104	ESCA	11	162
LUAD	59	526	HNSC	24	65
LUSC	49	501	LIHC	50	374
KICH	24	65	PRAD	52	499
KIRC	72	535	STAD	32	375
KIRP	32	289	THCA	58	510
BLCA	19	411	UCEC	35	548
COAD	41	471			

The classification performance evaluation metrics are also calculated to evaluate the performance of feature reduction algorithm. The *Acc* and *Fscore* of cancer data are used as evaluation metrics. The *Acc* is defined as

$$Acc = \frac{TP + TN}{n} \quad (1)$$

The *Fscore* is the composite evaluation of *recall* (*R*) and *precision* (*P*). If *recall* is improved but *precision* drops significantly, and the *Fscore* could not be improved.

$$Fscore = \frac{2RP}{R + P} \quad (2)$$

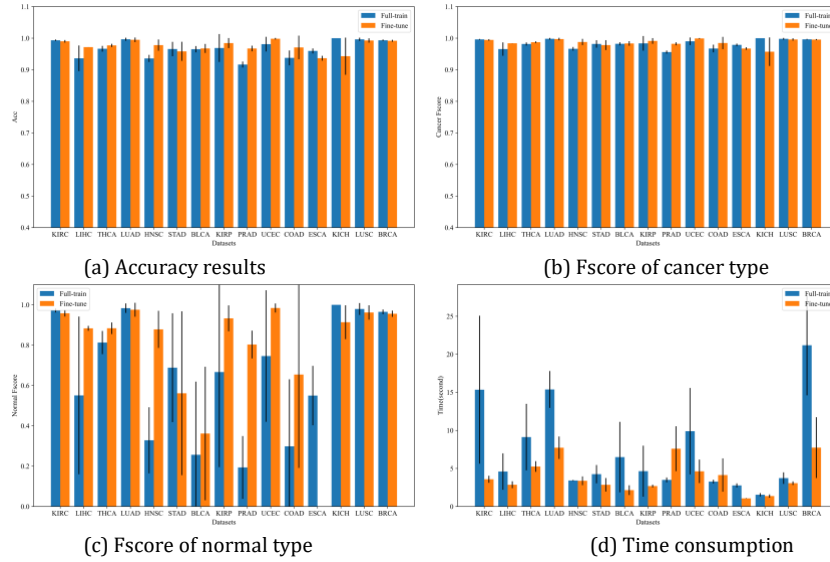
The recall is the ratio between the number of correctly classified positive samples and the total number of positive samples. The precision is the ratio between the number of correctly classified positive samples and the number of samples predicted as positive class.

## 5 RESULTS ANALYSIS

In this section, we carried out our experiments from the following three aspects. 1) We evaluate the cross validation on each dataset. 2) We evaluate the performance of the model with data resampling for handling the class imbalance problem. 3) We evaluate the performance of the model in the case of cross-cancer classification.

### 5.1 Cross validation results

In this section, we carry out experiments to evaluate the performance of CCFT-CNN. And the experiments are performed on TCGA datasets. When testing on one dataset (e.g. D1), all other datasets (e.g. D2~D15) are used to pre-train a model and the output layer size of the pre-trained model is 14. The pre-trained model is finetuned with the training set in D1 and evaluated on the testing set in D1. And the 1D-CNN and 2D-CNN models are also fully trained (full-train in short) to compare with the results of fine-tuned model. And each dataset shown in Table 4 is used for fine-tuning in turn. The 3-cross validation evaluation is carried out on each dataset. The results on the 1D-CNN and 2D-CNN are respectively shown in Figs.3 and 4.

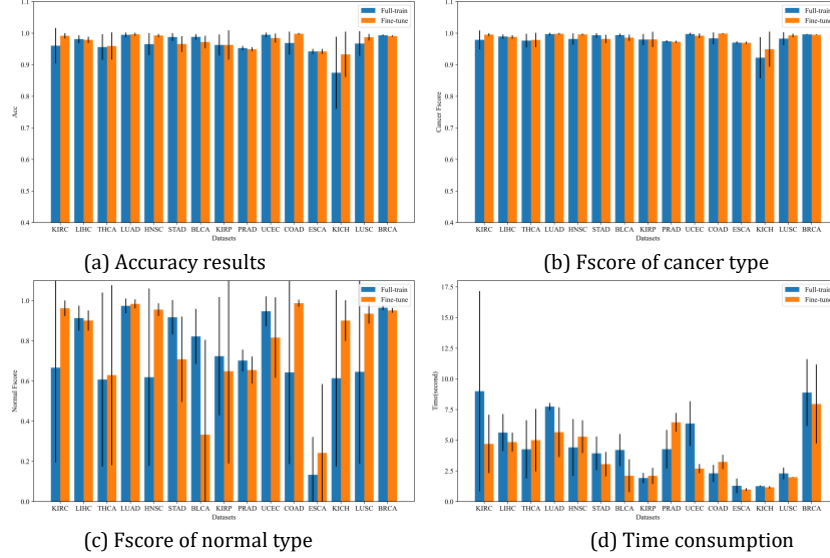


**Fig.3** the Accuracy and F1-score in 1D-CNN with 3 cross validation

The x-axis denotes the dataset used for fine-tuning and fully training, and y-axis denotes the classification performance or time consuming. Results show that fine-tune model outperforms the full-train model 8 out of 15 datasets in terms of Acc, Fscore of Cancer class and Fscore of normal class when using the 1D-CNN architecture. Fine-tune model consumes less time on 13 datasets than full-train model when using the 1D-CNN architecture. When 2D-CNN is used, results show that fine-tune model also outperforms full-train model on 8 out of 15 datasets in terms of Acc and Fscore. And the fin-tune model consumes less time than full-train model on 10 out of 15 datasets.

The fine-tune model obtains much worse Fscore of normal class on some datasets such as BLCA, STAC and UCUE. This may be resulted by the class imbalance problem.

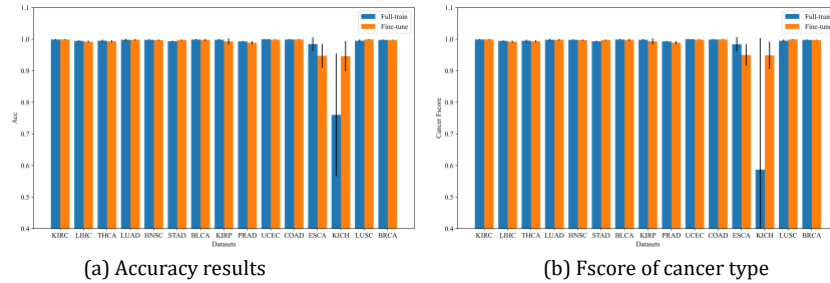
On average, the fine-tuned 1D-CNN obtains 97.5% accuracy, 98.6% Fscore of cancer type and 78.1% Fscore of normal type; fine-tuned 2D-CNN obtains 97.4% accuracy, 98.5% Fscore of cancer type and 77.4%; the full-trained 1D-CNN obtains 96.7% accuracy, 98.3% Fscore of cancer type and 66.6% Fscore of normal type; and fine-tuned 2D-CNN obtains 96.6% accuracy, 98.1% Fscore of cancer type and 72.6% Fscore of normal type. This shows that the 2D-CNN model performs better than the 1D-CNN model. As the length limit of this paper, only the 2D-CNN architecture is applied in the following experiments.

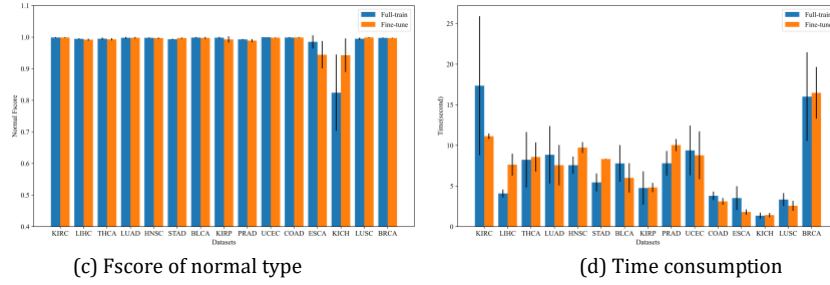


**Fig.4** the Accuracy and F1-score in 2D-CNN with 3 cross validation

## 5.2 Results with data resampling

As the class imbalance exist in the TCGA datasets, SMOTE[14] resampling is used to increase the number of samples of the minority class in the training set. The results with data resampling are shown in Fig.5. The training sets of the full-train and fine-tune models are all imbalance by SMOTE method. Results show that the performance of the fine-tuning method on those above-mentioned datasets is improved. The accuracy, Fscore of cancer type and the one of normal type are respectively increased about 1.5%, 0.5% and 21.5% on average.

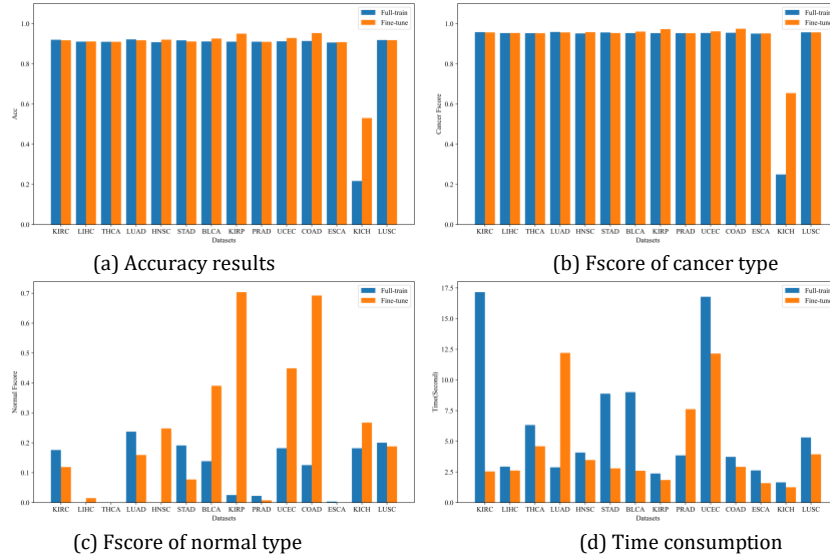




**Fig.5** results with data resampling

### 5.3 Cross-cancer classification results

On the above experiments, the rest of 14 datasets are all used to pre-train a model when one dataset is used to evaluate the performance of fine-tune model. And cross valuation is evaluated on each dataset. In this section, we take the cross-cancer classification experiments. This means that the model trained on a specific cancer and tested on the dataset with other cancer types. The data set BRCA with the largest number of samples is used to build the pre-trained model. Then, the pre-trained model is finetuned on a dataset and evaluated on the rest of 13 datasets (all other datasets removing BRCA dataset).



**Fig.6** cross-cancer classification results

The results are shown in Fig.6, where the axis denotes the datasets used for finetuning the pre-trained model. Full-train denotes the model with the same 2D-CNN architecture shown as Table 2 is retrained with the datasets in x-axis. And the y-axis denotes the classification performance evaluated on all samples of the rest 13 datasets. Results show that the fine-tuning method outperforms full-train method in terms of Acc and Fscore. When compared with full-train method, the fine tune method improves the Acc, Cancer Fscore and Normal Fscore about 3.0%, 3.3% and 13.1% respectively. This further demonstrates that the good performance of fine-tune method on cross-cancer classification situation.



## 6 CONCLUSIONS

This paper researches on the fine-tuning CNN method in the cancer classification. The 1D-CNN and 2D-CNN architecture are researched and evaluated on the TCGA datasets. The cross validation and cross-cancer datasets show that fine-tuning method performance better than full-train method, especially in the case of cross-cancer classification. In addition, on handling the class imbalance in TCGA datasets, we used SMOTE for increasing the number of minority class samples. And the results show that this method could improve the fine-tuning method on classifying the minority class. In future, we will further research the method on adaptively handling the class imbalance combining with the fine-tuning method.

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## REFERENCES

- [1] Abder-Rahman Ali. Deep Learning in Oncology – Applications in Fighting Cancer, <https://emerj.com/ai-sector-overviews/deep-learning-in-oncology/>, Last access: 2021.8.28
- [2] C. Gunavathi, K. Sivasubramanian, P. Keerthik and C. Paramasivam. A review on convolutional neural network based deep learning methods in gene expression data for disease diagnosis. *Materials Today: Proceedings*, 45(2), 2021: 2282-2285.
- [3] Tarek Khorshed, Mohamed N Moustafa and Ahmed Rafea. Deep Learning for Multi-Tissue Cancer Classification of Gene Expressions (GeneXNet). *IEEE Access*, 2020(99): 90615 - 90629.
- [4] Rahul K Sevakula, Vikas Singh, Nishchal K Verma, Chandan Kumar and Yan Cui. Transfer Learning for Molecular Cancer classification using Deep Neural Networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2018: 2089 - 2100.
- [5] Kubra Tuncal, Boran Sekeroglu, and Cagri Ozkan, Lung Cancer Incidence Prediction Using Machine Learning Algorithms, *Journal of Advances in Information Technology*, 11(2): 91-96
- [6] Terrence S. Furey, Nello Cristianini, Nigel Duffy, David W. Bednarski, Michèl Schummer and David Haussler, Support vector machine classification and validation of cancer tissue samples using microarray expression data, *Bioinf.*, 2000, 16(10): 906–920.
- [7] Muhammed Abd-Elnaby, Marco Alfonse and Mohamed Roushdy. Classification of Breast Cancer Using Microarray Gene Expression Data: A Survey. *Journal of Biomedical Informatics*, 2021: 103764.
- [8] Anindya Halder and Ansuman Kumar. Active learning using rough fuzzy classifier for cancer prediction from microarray gene expression data. *Journal of Biomedical Informatics*, 92, 2019: 103136.
- [9] Peng Wu and Wang Dong. Classification of a DNA Microarray for Diagnosing Cancer Using a Complex Network Based Method. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2018: 801-808.
- [10] Sarah M Ayyad, Ahmed I Saleh and Labib M Labib. Gene expression cancer classification using modified K-Nearest Neighbors technique. *Biosystems*, 2019, 176:41-51.
- [11] Rasool Fakoor, Faisal Ladhak, Azade Nazi and Manfred Huber. Using deep learning to enhance cancer diagnosis and classification, *The 30th International Conference on Machine Learning (ICML 2013), WHEALTH workshop*. 2013.
- [12] Qing Liao, Ye Ding, Zoe L. Jiang, XuanWang, Chunkai Zhang and Qian Zhang. Multi-task deep convolutional neural network for cancer diagnosis. *Neurocomputing*, 2019, 348:66-73.
- [13] Milad Mostavi, Yu-Chiao Chiu, Yufei Huang and Yidong Chen. Convolutional neural network models for cancer type prediction based on gene expression. *BMC Med Genomics*, 2023, 13(Suppl 5): 44.
- [14] Nitesh V. Chawla, Kevin W. Bowyer, Lawrence O. Hall and W. Philip Kegelmeyer. SMOTE: Synthetic Minority Over-sampling Technique. *Journal of Artificial Intelligence Research*, 2002, 16(1):321-357.
- [15] The Cancer Genome Atlas (TCGA) Research Network. Available: <https://www.cancer.gov/tcga>. Last access: 2021.9.8.
- [16] Wenbin Zhang and Eirini Ntoutsi. Faht: an adaptive fairness-aware decision tree classifier. In *International Joint Conference on Artificial Intelligence (IJCAI)*, pages 1480–1486, 2019.
- [17] Wenbin Zhang, Xuejiao Tang, and Jianwu Wang. On fairness-aware learning for non-discriminative decision-making. In *International Conference on Data Mining Workshops (ICDMW)*, pages 1072–1079, 2019.

- [18] Wenbin Zhang and Albert Bifet. Feat: A fairness-enhancing and concept-adapting decision tree classifier. In International Conference on Discovery Science, pages 175–189. Springer, 2020.
- [19] Wenbin Zhang et al. Flexible and adaptive fairness-aware learning in non-stationary data streams. In IEEE 32nd International Conference on Tools with Artificial Intelligence (ICTAI), pages 399–406, 2020.
- [20] Wenbin Zhang and Liang Zhao. Online decision trees with fairness. arXiv preprint arXiv:2010.08146, 2020.
- [21] Wenbin Zhang. Learning fairness and graph deep generation in dynamic environments. 2020.
- [22] Wenbin Zhang, Albert Bifet, Xiangliang Zhang, Jeremy C Weiss, and Wolfgang Nejdl. Farf: A fair and adaptive random forests classifier. In Pacific-Asia Conference on Knowledge Discovery and Data Mining, pages 245–256. Springer, 2021.
- [23] Wenbin Zhang and Jeremy Weiss. Fair decision-making under uncertainty. In 2021 IEEE International Conference on Data Mining (ICDM). IEEE, 2021.
- [24] Wenbin Zhang and Jeremy C Weiss. Longitudinal fairness with censorship. In Proceedings of the AAAI Conference on Artificial Intelligence, volume 36, pages 12235–12243, 2022.
- [25] Wenbin Zhang, Shimei Pan, Shuigeng Zhou, Toby Walsh, and Jeremy C Weiss. Fairness amidst non-iid graph data: Current achievements and future directions. arXiv preprint arXiv:2202.07170, 2022.
- [26] Wenbin Zhang, Tina Hernandez-Boussard, and Jeremy C Weiss. Censored fairness through awareness. In Proceedings of the AAAI Conference on Artificial Intelligence, 2023.
- [27] Wenbin Zhang and Jeremy Weiss. Fairness with censorship and group constraints. Knowledge and Information Systems, 2022.
- [28] Wenbin Zhang and Jianwu Wang. A hybrid learning framework for imbalanced stream classification. In IEEE International Congress on Big Data (BigData Congress), pages 480–487, 2017.
- [29] Wenbin Zhang, Jian Tang, and Nuo Wang. Using the machine learning approach to predict patient survival from high-dimensional survival data. In IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2016.
- [30] Wenbin Zhang and Jianwu Wang. Content-bootstrapped collaborative filtering for medical article recommendations. In IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2018.
- [31] Xuejiao Tang, Lihua Zhang, et al. Using machine learning to automate mammogram images analysis. In IEEE International Conference on Bioinformatics and Biomedicine (BIBM), pages 757–764, 2020.
- [32] Lihua Zhang et al. A comparison of different pattern recognition methods with entropy based feature reduction in early breast cancer classification. European Scientific Journal, 3:303–312, 2014.
- [33] Mingli Zhang, Xin Zhao, et al. Deep discriminative learning for autism spectrum disorder classification. In International Conference on Database and Expert Systems Applications, pages 435–443. Springer, 2020.
- [34] Xuejian Wang, Wenbin Zhang, Aishwarya Jadhav, and Jeremy Weiss. Harmonic-mean cox models: A ruler for equal attention to risk. In Survival Prediction-Algorithms, Challenges and Applications, pages 171–183. PMLR, 2021.
- [35] Wenbin Zhang, Jianwu Wang, Daeho Jin, Lazaros Oreopoulos, and Zhibo Zhang. A deterministic self-organizing map approach and its application on satellite data based cloud type classification. In IEEE International Conference on Big Data (Big Data), 2018..
- [36] Xuejiao Tang, Xin Huang, et al. Cognitive visual commonsense reasoning using dynamic working memory. In International Conference on Big Data Analytics and Knowledge Discovery. Springer, 2021.
- [37] Wenbin Zhang, Liming Zhang, Dieter Pfoser, and Liang Zhao. Disentangled dynamic graph deep generation. In Proceedings of the SIAM International Conference on Data Mining (SDM), pages 738–746, 2021.
- [38] Zhen Liu, Ruoyu Wang, Nathalie Japkowicz, Deyu Tang, Wenbin Zhang, and Jie Zhao. Research on unsupervised feature learning for android malware detection based on restricted boltzmann machines. Future Generation Computer Systems, 120:91–108, 2021.
- [39] Thomas Guyet, Wenbin Zhang, and Albert Bifet. Incremental mining of frequent serial episodes considering multiple occurrences. In 22nd International Conference on Computational Science, pages 460–472. Springer, 2022.