IEEE Access
Multidisciplinary ⋮ Rapid Review ⋮ Open Access Journal

Received January 25, 2021, accepted February 6, 2021, date of publication February 19, 2021, date of current version March 2, 2021.

Digital Object Identifier 10.1109/ACCESS.2021.3060447

Automatic Classification of Cervical Cells Using Deep Learning Method

SUXIANG YU[1], XINXING FENG[2], BIN WANG[1], HUA DUN[1], SHUAI ZHANG[3], RUIHONG ZHANG[4], AND XIN HUANG[5]

[1]Department of Pathology, The Fourth Central Hospital of Baoding City, Baoding 072350, China
[2]Endocrinology and Cardiovascular Disease Centre, Fuwai Hospital, National Center for Cardiovascular Diseases, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing 100037, China
[3]Department of Computer Science, The University of Manchester, Manchester M13 9PL, U.K.
[4]Department of Science and Teaching, The Fourth Central Hospital of Baoding City, Baoding 072350, China
[5]Solar Activity Prediction Center, National Astronomical Observatories, Chinese Academy of Sciences, Beijing 100012, China

Corresponding authors: Ruihong Zhang (13931391449@163.com) and Xin Huang (xhuang@bao.ac.cn)

ABSTRACT Cervical cancer is the fourth most prevalent disease among women. Prompt diagnosis and its management can significantly improve patients' survival rates. Therefore, routine screening for cervical cancer is of paramount importance. Herein, we explore the potential of a deep learning model to automatically distinguish abnormal cells from normal cells. The ThinPrep cytologic test dataset was collected from the fourth central hospital of Baoding city, China. Based on the dataset, four classification models were developed. The first model was a 10-layer convolutional neural network (CNN). The second model was an advancement of the first model equipped with a spatial pyramid pooling (SPP) layer (CNN + SPP) to treat cell images based on their sizes. Based on the first model, the third model replaced the CNN layers with the inception module (CNN + Inception). However, the fourth model incorporated both the SPP layer and the inception module into the first model (CNN + inception + SPP). The performances of the four models are estimated and compared by using the same testing data and evaluation index. The testing results demonstrated that the fourth model yields the best performance. Moreover, the area under the curve (AUC) for module four was 0.997.

INDEX TERMS Cell classification, deep learning, neural networks, cervical cytology.

I. INTRODUCTION

Cervical cancer refers to some cervix cells rapidly becoming malignant [1]. Besides, it is among the prime reasons for cancer death in women [2]. However, cervical cancer can be effectively treated at an early stage. Therefore, routine screening for cervical cancer is of paramount importance.

The screening process involves either Papanicolaou smear or ThinPrep cytologic tests (TCTs) and subsequent examination under a microscope by a pathologist for the presence of abnormal cells. There are thousands of cells per the testing result, hence the pathologist carefully scans and makes a judgment. This is a time-consuming process with subjective or biased experiences. With advances in image processing and machine learning technologies, computer-assisted cervical screening methods are proposed to examine the cells in the whole image and categorizes them as normal and abnormal [3].

The core of the automatic screening system is to develop classification models using the machine learning method [4]. Traditional machine learning manually extracts features from the images of cells before establishing a relationship between features and classes. Besides, hand-crafted features limit the performance of the model. Nevertheless, deep learning [5], [6] integrates feature extraction and classification into one optimized process. There is no need to design hand-crafted features because it can learn effective features and yield satisfactory performance.

Deep learning requires a large number of labeled cell images with fixed size to develop a classification model. It is time-consuming to label the cervical data because the size of cervical cells is not fixed.

Herein, we adopt the inception module [7], [8] following its potential in increasing the depth and width of the network with a slight increase in the number of network

The associate editor coordinating the review of this manuscript and approving it for publication was Massimo Cafaro.

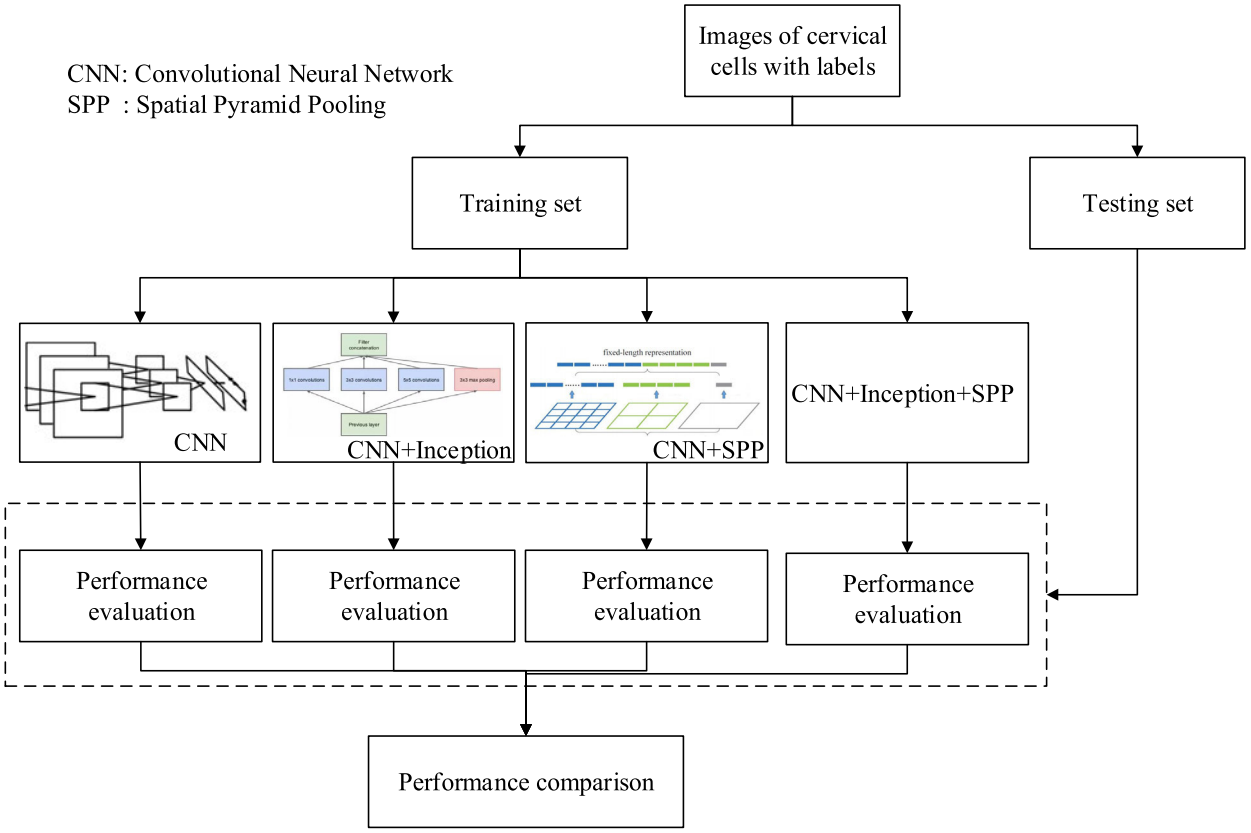


FIGURE 1. The flow chart of the proposed models.

parameters. Elsewhere, the spatial pyramid pooling (SPP) layer [9] was used to treat images with different cell sizes.

Four deep learning models (convolutional neural network (CNN), a CNN with inception module, a CNN with SPP layer, a CNN with inception module and SPP layer) were developed on the training set with both their estimated performances compared during the testing set (Figure 1). Finally, the best model was selected to distinguish abnormal cells from normal cells.

To the best of our knowledge, this is the first work to adopt a model with both the inception module and SPP layer to automatically classify cervical cells.

The structure of this paper is as follows:

Sec. II includes related works on automatic classification of the cervical cell. Sec. III specifies the modeling methods. Sec. IV has experiments and results. Sec. V provides discussions of our model. Finally, Sec. VI has a brief conclusion of the work.

II. RELATED WORKS

Manually distinguishing abnormal cells from normal cells is time-consuming, subjective to bias and prone to errors. Therefore, machine learning can be applied to develop an automatic classification model to improve the screening system performance. A machine learning system should include data acquisition, feature extraction and modeling method. Related works are summarized in Table 1.

Based on the dataset, the Herlev pap smear dataset was the frequently used public data [12]–[17], [32]. Notably, UCI (digitized cervical cancer data set) was among the popular datasets in the cervical cancer dataset. However, the original images were excluded, only extracted features were included in these datasets [34], [35]. Apart from public data, some private datasets were also collected. For example, pap smear dataset was collected from Fortis Hospital Mohali, India [27], liquid-based cytology datasets from People's Hospital of Nanshan District, China [10] and Alzahra Hospital of Tabriz, Iran [18] and pathological images stained with hematoxylin and eosin from Tianjin Tumor Hospital, China [19] and first Affiliated Hospital of Xinjiang Medical University, China [29].

Regarding features, morphometric [11], [27], [28], [31]–[33], textual [11], [19], [21], [23], [31]–[33], color histogram [19], [21], [24], geometric features [26], [32] as well as local binary patterns [16] were extracted from the nucleus and cytoplasm. Features are not only extracted from a single cell but also from blocks of cells in whole slide cervical cell images to reduce the computational complexity [19]. Although many features can be extracted, not all are useful. Feature selection methods such as particle swarm optimization-based feature selection [14] and genetic

TABLE 1. Related works of automatic cervical cell classification.

Num.	Data	Features	Methods	Ref.
1	Liquid-based cytology data collected from People's Hospital of Nanshan District, China	Shape, size and texture of the nuclei	Neural networks, Ensemble learning, Support vector machine, Random forest	[10]
2	Pap smears dataset	Morphometric and textual features of the cells	Support vector machine	[11]
3	3 Pap smear dataset (ERUDIT, LCH, Herlev)	Features calculated from nucleus and cytoplasm	Bayesian classifier, Linear discriminant analysis, K-nearest neighbor, Neural networks, Support vector machine	[12]
4	Herlev Pap smear dataset	20 features for nucleus and cytoplasm	Neural network	[13]
5	Herlev Pap smear dataset	20 features for nucleus and cytoplasm	Ensemble learning	[14]
6	Herlev Pap smear dataset	20 features for nucleus and cytoplasm	Ensemble learning	[15]
7	Herlev Pap smear dataset	Local binary patterns	Support vector machine	[16]
8	Herlev Pap smear dataset	Discriminative feature extraction method	K nearest neighbor	[17]
9	Liquid-based cytology dataset collected from ALZAHRAHOSPITAL of Tabriz, Iran	Linear plot (linear transformation on specially customized axis)	Neural network	[18]
10	Pathological images stained with hematoxylin and eosin collected from TianjinTumor Hospital, China	Texture and color histogram features extracted from blocks of cells in whole slide cervical cell image	Support vector machine	[19]
11	Herlev Pap smear dataset and liquid-based cytology datasets	Deep leaning features	Convolutional neural networks	[20]
12	2 pap smear datasets (SIPaKMeD and Herlev datasets)	Texture, shape and color features extracted from the regions of segmented nuclei and cytoplasm	Ensemble learning	[21]
13	Herlev Pap Smear dataset.	Deep learning features	Convolutional neural networks	[22]
14	Histology images of hematoxylin and eosinophil	Texture, Cellular Features, Nuclei Features	Ensemble learning	[23]
15	6 histopathological image datasets (AQP1, AQP2, HIF1, HIF2, VEGF1 and VEGF2 datasets)	Color, texture and deep learning features	Multilayer hidden conditional random fields	[24]
16	Herlev Pap Smear dataset.	Deep learning features	Convolutional neural networks and extreme learning machine	[25]
17	Pap smear dataset	Geometric and texture features	Support vector machine	[26]
18	Pap smear dataset collected from Fortis Hospital Mohali, India	Morphological features	K nearest neighbor	[27]
19	Pap smear datasets (DTU dataset and Herlev dataset)	29 morphology features	fuzzy c-means algorithm to classify	[28]
20	Pathological images stained with hematoxylin and eosin collected from the First Affiliated Hospital of Xinjiang Medical University, China	Deep learning features	Convolutional neural network	[29]
21	Liquid-based cytology slides	28 features including 20morphological and 8texture features	C4.5 and LogicalRegression	[31]
22	3 Pap smear dataset (Herlev, Norup, MRRH)	29 features including 20 morphological features, 3 geometric features and 6 texture features	Trainable Weka Segmentation, sequential elimination, simulated annealing, fuzzy C-means	[32]
23	Pap smear dataset collected from Rajah Muthiah Medical College, Annamalainagar	44 features including 14 texture features and 30 shape features	SVM	[33]
24	UCI (digitized cervical cancer data set)	30 features such as age, smokes, HIV, HPV, number of sexual partners	Softmax classification with stacked autoencoder model	[34]
25	UCI (digitized cervical cancer data set)	30 features such as age, smokes, HIV, HPV, number of sexual partners	Random forest	[35]

algorithm-based feature selection [15] are used to discard redundant features.

With modeling algorithms, several machine learning algorithms have been adopted in developing classification models for cervical cell, for example, linear discriminant analysis [12], K-nearest neighbor [12], [17], [27], neural networks [10], [12], [13], [18], Bayesian classifier [12] and support vector machine [10]–[12], [16], [19]. To improve the single classification model performance, ensemble learning that incorporates multiple models to solve problems was used in developing the classification model [10], [14], [15], [21].

In traditional machine learning methods, feature extraction and modeling algorithm are two separate processes. Classification model performances are difficult to improve with hand-crafted features whose discriminative ability is limited. However, deep learning potentially comprehends features from input images before integrating feature extraction and model development into a unified framework. CNN [20], [22], [25], [29], a popular deep learning method in treating images, has been applied in distinguishing abnormal cervical cells from normal cells.

In this paper, we improve the automatic cervical cell classification model performance by incorporating both the inception module and the SPP layer into the CNN. Incorporating the inception module facilitates faster training in the classification model with fewer data and higher performance.

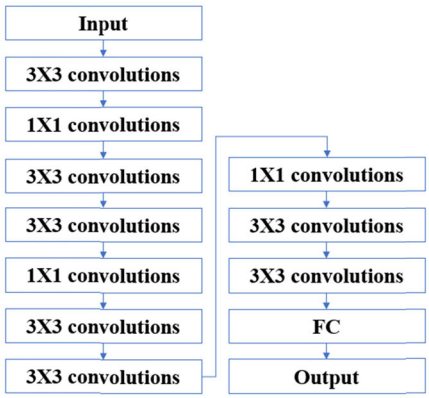


FIGURE 2. The structure of Model A.

However, the SPP layer enhances the processing of input images of any size in the classification model.

III. METHOD

A. DATASET

The dataset of 2504 cell samples (1202 abnormal and 1302 normal samples) were collected from the fourth central hospital of Baoding city, China. Pathologists scanned whole images of TCT using a digital camera mounted on a microscope and manually cutout single cells and categorized them as normal and abnormal. Each cell was double-checked by pathologists. The dataset was categorized into the training set and the testing set as ratio of 8:2.

Generalization of the final model was ascertained using the 5-fold cross-validation.

B. MODELING METHOD

Here, we developed a method to classify normal and abnormal cells using four related models. Model A was a basic model and both Model B and C were improved based on model A, respectively. Model D combined the advantages of the aforementioned models.

Model A was a simple CNN. This model had different parts such as convolutional (conv), non-linearity, pooling (pool) layers, and fully connected (FC) layers. The input of Model A was a 128p × 128p image. The structure of Model A is shown in Figure 2. There are pooling layers after the 4^{th}, 7^{th} and 10^{th} convolutional layer.

To avoid the impact of the variable size for cell images, Model B adds the SPP layer before the FC layers that made the model adaptable to different input sizes.

Unlike the traditional pooling layer, SPP [9] used a fixed number of pooling windows to generate feature maps. By automatically adjusting the size and pooling stride of pooling windows, the size of pooling was common on different sizes of input. Therefore, by combining every pooling result, the model will have a fixed size of result without a limitation of input size. The structure of the SPP layer is shown in Figure 3.

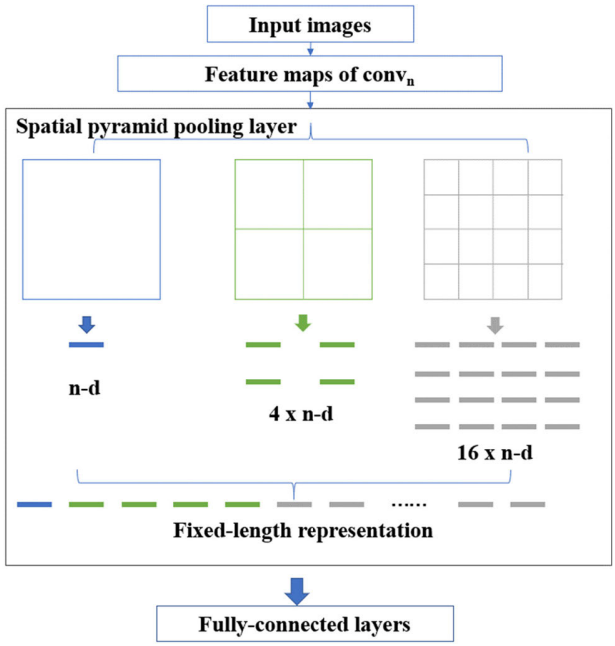


FIGURE 3. The structure of SPP.

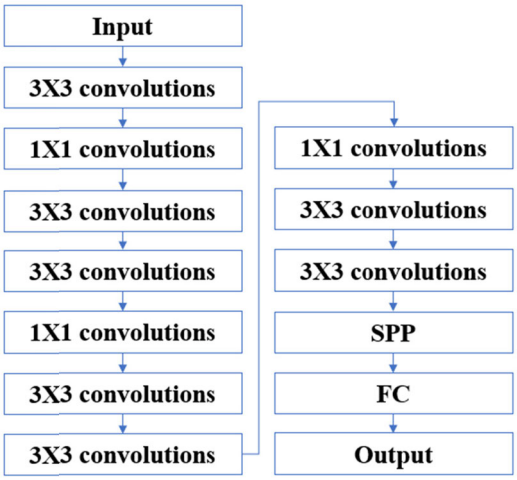


FIGURE 4. The structure of Model B.

The structure of Model B incorporated with SPP before the FC layer (Figure 4).

To improve performance of Model A, Model C replaced CNN layers with the inception module.

Based on previous studies, the inception module, as a network, contains several branches that increase the width of the network [7], [8]. The structure of the inception module is shown in Figure 5. The inception module adds some branches that differ from basic layers and combines them. This strategy can improve the fitting ability of models. The structure of Model C is displayed in Figure 6.

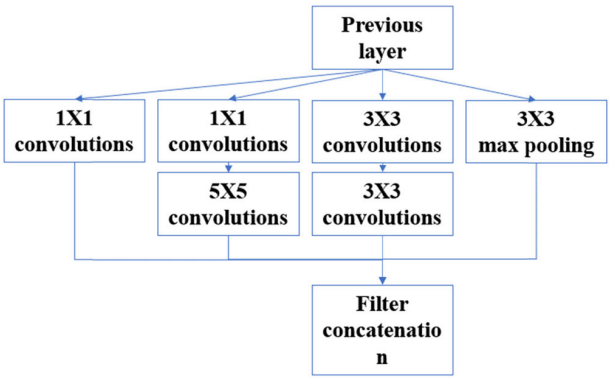


FIGURE 5. The structure of the inception module.

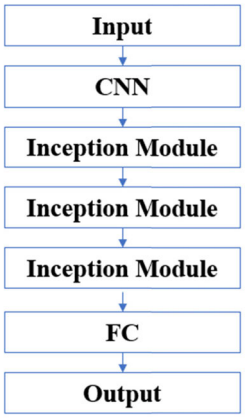


FIGURE 6. The structure of Model C.

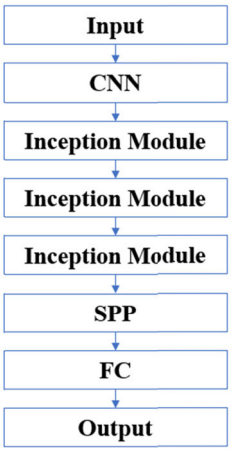


FIGURE 7. The structure of Model D.

Briefly, Model D combined SPP and the inception module to develop a more flexible model with high accuracy. The structure of Model D is shown in Figure 7.

C. DATA PREPROCESSING

Both Model A and C are designed to deal with the fixed size without SPP. Following variations on image sizes in our dataset from 951p × 580p to 41p × 34p, we elected the 128p × 128p as the formal input size.

IV. RESULTS

This work summarizes model performance based on precision, sensitivity, specificity, accuracy, F1 score and area under the curve (AUC).

Precision and sensitivity showed the exactness and completeness of classifiers, respectively. Besides, specificity showed the potential of a classifier to correctly classify normal data. Accuracy showed that a classifier can correctly categorize the two-class task. Considering both recall and precision, the F1 score and AUC were defined to evaluate performances of the classification model. The equations of performance indices are as follows.

$$precision = \frac{TP}{TP + FP} \tag{1}$$

$$sensitivity = \frac{TP}{TP + FN} \tag{2}$$

$$specificity = \frac{TN}{TN + FP} \tag{3}$$

$$accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{4}$$

$$F1_{score} = \frac{2 * TP}{2 * TP + FP + FN} \tag{5}$$

$$H_{mean} = \frac{2 * sensitivity * specificity}{sensitivity + specificity} \tag{6}$$

A. TRAINING RESULTS

We programmed the algorithm in Python to conduct the experiments using NVIDIA GeForce RTX 2070 8G, Windows operating system, Intel® Core™ i7-9700K CPU @ 3.60GHz and 16 GB RAM. Additionally, we used PyTorch-1.2.0 to develop a basic framework for the classification model of cervical cells.

NNI (Neural Network Intelligence), an open-source AutoML toolkit from Microsoft, was used to determine the best combination of hyperparameters (including learning momentum, learning rate and dropout rate). By using the SPP Module for the model to manage different input sizes, the batch size can only be 1.

The NNI results are shown in Figure 8. These results are based on Model D to identify the best combination of the learning rate, learning momentum and dropout rate. Metis-Tuner was used as an optimization strategy. From the NNI final results, the best combination of the aforementioned hyperparameters had a learning momentum, learning rate and dropout rate of 0.9, 0.0001 and 0.5, respectively.

We trained Model A for 400 epochs using a learning momentum, learning rate and a batch size of 0.9, 0.0001 and 1, respectively. However, Models B, C and D were trained for 450, 600 and 600 epochs, respectively. We use random flipping online to augment the training set.

Figure 9 shows the training results at every phase and the training accuracy and loss in Model A-D.

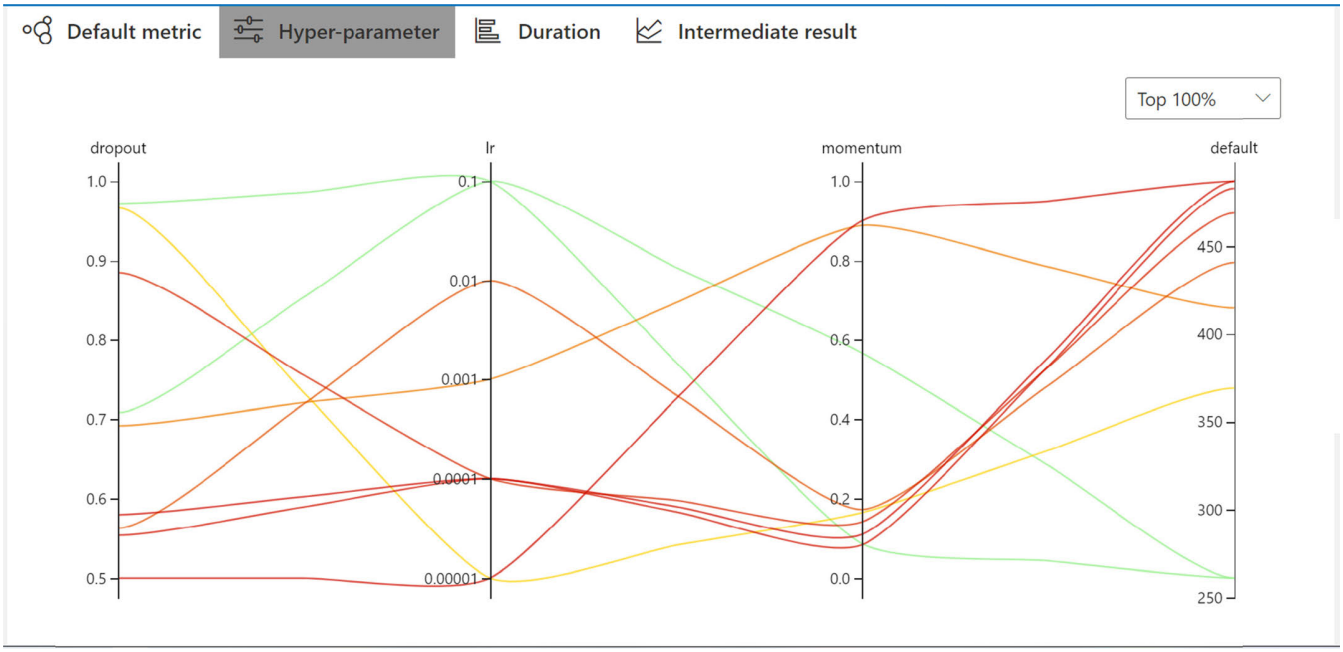


FIGURE 8. Hyper-parameter of NNI results.

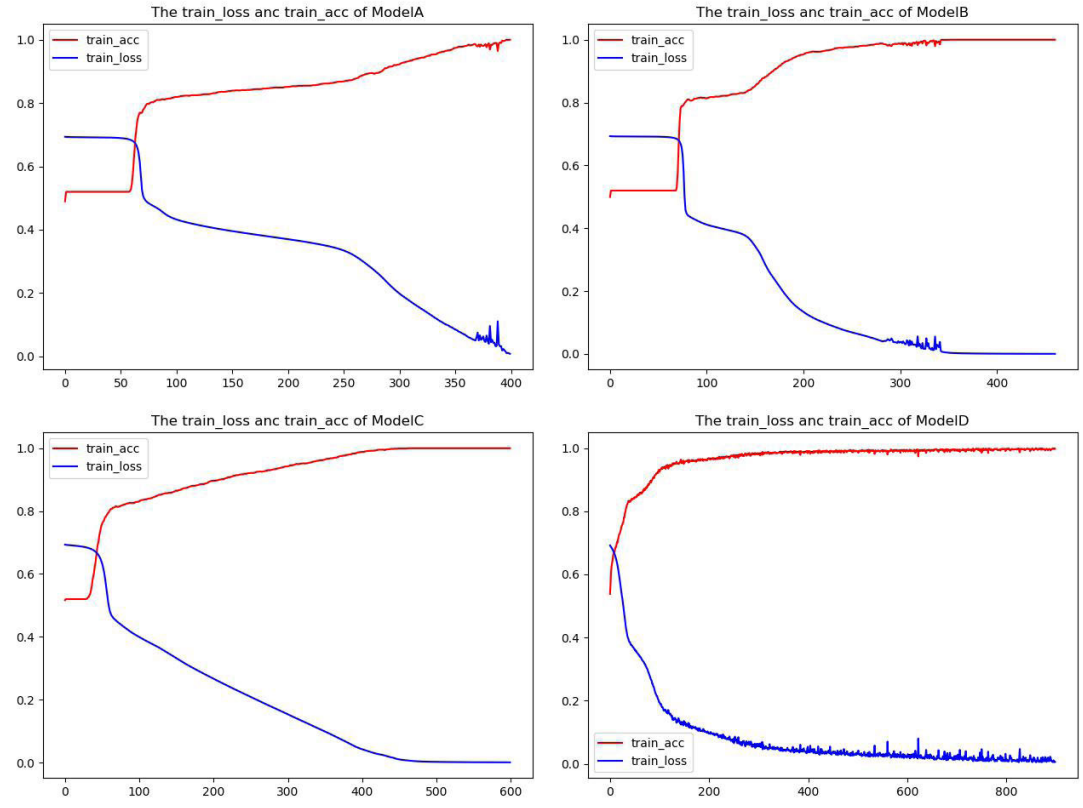


FIGURE 9. Training accuracy and loss of Model A-D.

The receiver operating characteristic (ROC) curves of Model A-D are shown in Figure10. The inception module and the SPP significantly improved the performance of the model. Details of test results are shown in Table 2. Models

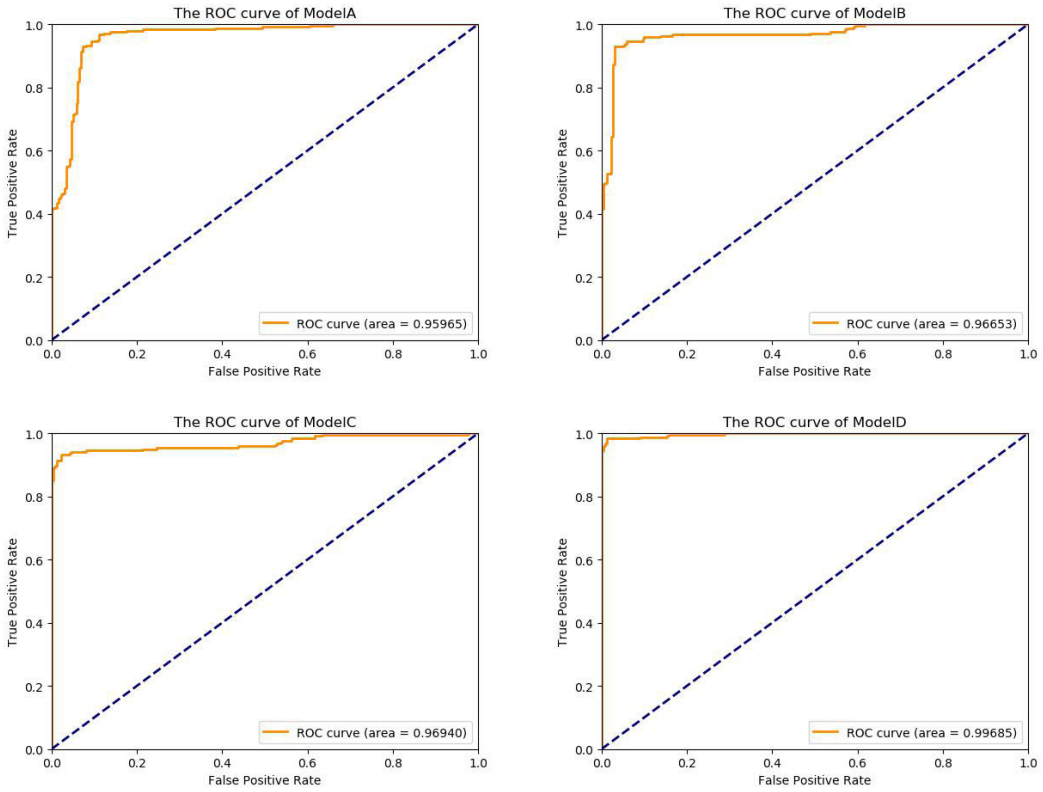


FIGURE 10. Testing ROC curves of Model A-D.

TABLE 2. Testing results of four models.

Model	precision (%)	sensitivity (%)	specificity (%)	accuracy (%)	F1 score (%)	H-mean (%)	AUC
A	87.6	97.1	87.4	92.0	92.1	92.0	0.953
B	93.5	95.9	93.9	94.8	94.7	94.8	0.967
C	93.4	94.6	93.9	94.2	94.0	94.2	0.966
D	**97.5**	**98.3**	**97.7**	**98.0**	**97.9**	**98.0**	**0.997**

TABLE 3. 5-FOLD cross-validation of Model D.

Fold	precision (%)	sensitivity (%)	specificity (%)	accuracy (%)	F1 score (%)	H-mean (%)	AUC
1	97.53	98.34	97.70	98.01	97.93	98.02	0.9969
2	100.00	96.27	100.00	98.21	98.10	98.10	0.9966
3	97.91	97.10	98.08	97.61	97.50	97.59	0.9957
4	98.35	99.17	98.47	98.81	98.76	98.82	0.9970
5	100.00	97.48	100.00	98.79	98.72	98.72	0.9991
Final	**98.76 ± 1.10**	**97.67 ± 1.01**	**98.85 ± 0.94**	**98.28 ± 0.21**	**98.20 ± 0.23**	**98.25 ± 0.21**	**0.9971 ± 0.000001**

C and B achieved similar performance. The performances of Models B and C were better than that of Model A, and Model D achieved the best performance (Table 2). These results demonstrate that both the inception module and the SPP can improve the performances for the classification of cervical cells. Furthermore, a combination of the inception module and the SPP can achieve the best performance.

We used 5-fold cross-validation to test the generalization of Model D. The testing results are shown in Table 3. Consequently, Model D resulted (5-fold cross-validation) in a precision, sensitivity, specificity, accuracy, F1, H-mean and an AUC score of 98.76 ± 1.10%, 97.67 ± 1.01%, 98.85 ± 0.94%, 98.28 ± 0.21%, 98.20 ± 0.23%, 98.25 ± 0.21% and 0.9971 ± 0.000001, respectively. These results indicated that Model D is stable.

TABLE 4. Performance comparison of different cervical cell classification models.

Model	AUC
ENS [16]	0.884
Dis(S+M) [17]	0.964
Ensemble [36]	0.97
RegressionConstraint [37]	0.94
AlexN-3C [38]	0.962±0.008
GoogLeNet-3C [38]	0.979±0.005
ResNet-3C [38]	0.978±0.018
DenseNet-3C [38]	0.970±0.013
The proposed model	**0.975**

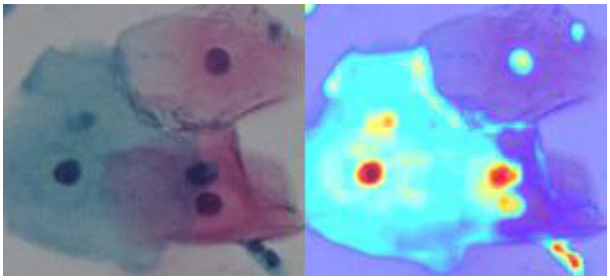


FIGURE 11. Original image and the heat map of Model D.

To compare the performance of our model with related works, we used the popular Papanicolaou smear dataset-Herlev dataset to test the performance of the proposed Model D. The comparison is given in Table 4. We achieved an AUC of 0.975, which is better than ENS [16], Dis(S+M) [17], Ensemble [36] and RegressionConstraint[37] and close to AlexN-3C, GoogLeNet-3C, ResNet-3C and DenseNet-3C, respectively [38]. Hence, our model performed well on the famous cervical cancer classification dataset-Herlev dataset.

V. DISCUSSION

The original image and the heat map from Model D are shown in Figure 11. In the heat map, the highlighted parts are considered areas of importance in classification. Notably, the deep learning model extract features are mostly from the cell nucleus and partly from the cytoplasm. Coincidentally, these parts are also crucial in traditional feature extraction methods [11], [19], [21]. This implies that features extracted by the deep learning method are reasonable and reliable to some degree.

VI. CONCLUSION

In this paper, four deep learning models (CNN, CNN + SPP, CNN + Inception, CNN + SPP + Inception) were built to automatically distinguish abnormal cervical cells from normal cells. By comparing the performances of these models, the best model (CNN + SPP + Inception) was determined with an AUC value of 0.997. This model can input cell images with arbitrary size. From the analysis of feature maps, the best model extracts features from the nucleus, cytoplasm and their boundary, respectively. These results were consistent with the understanding of pathologists. Recently most models are developed to treat cell images from the Papanicolaou smear test, we learned the classification mode from cell images of TCT. It is noteworthy that the TCT is more sensitive than the Papanicolaou smear test in screening of cervical cancer. The performance of our model was tested by using images of the Papanicolaou smear test. We found that the proposed model was effective not only for TCT, but also for the Papanicolaou smear test.

The volume of data, especially the abnormal cells, was limited. Thus, adequate data should be collected and labeled or the image generation technology should be used to improve the classification model performance in the future.

ACKNOWLEDGMENT

The authors would like to thank anonymous reviewers for their valuable suggestions. *(Xinxing Feng is the first author.)*

REFERENCES

[1] The American Cancer Society Medical and Editorial Content Team. (Jul. 2020). *What is Cervical Cancer?* Accessed: Feb. 20, 2021. [Online]. Available: https://www.cancer.org/cancer/cervical-cancer/about/what-is-cervical-cancer.html

[2] F. Bray, J. Ferlay, I. Soerjomataram, R. L. Siegel, L. A. Torre, and A. Jemal, "Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries," *CA, Cancer J. Clinicians*, vol. 68, no. 6, pp. 394–424, Nov. 2018.

[3] H. C. Kitchener, R. Blanks, G. Dunn, L. Gunn, M. Desai, R. Albrow, J. Mather, D. N. Rana, H. Cubie, C. Moore, R. Legood, A. Gray, and S. Moss, "Automation-assisted versus manual reading of cervical cytology (MAVARIC): A randomised controlled trial," *Lancet Oncol.*, vol. 12, no. 1, pp. 56–64, Jan. 2011.

[4] C. Li, H. Chen, X. Li, N. Xu, Z. Hu, D. Xue, S. Qi, H. Ma, L. Zhang, and H. Sun, "A review for cervical histopathology image analysis using machine vision approaches," *Artif. Intell. Rev.*, vol. 53, no. 7, pp. 4821–4862, Oct. 2020, doi: 10.1007/s10462-020-09808-7.

[5] A. Krizhevsky, I. Sutskever, and G. E. Hinton, "ImageNet classification with deep convolutional neural networks," in *Proc. Adv. Neural Inf. Process. Syst. (NIPS)*, 2012, pp. 1097–1105.

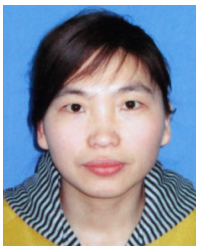
[6] Y. LeCun, Y. Bengio, and G. Hinton, "Deep learning," *Nature*, vol. 521, pp. 436–444, May 2015.

[7] C. Szegedy, W. Liu, Y. Jia, P. Sermanet, S. Reed, D. Anguelov, D. Erhan, V. Vanhoucke, and A. Rabinovich, "Going deeper with convolutions," in *Proc. IEEE Conf. Comput. Vis. Pattern Recognit.*, Jun. 2015, pp. 1–9.

[8] C. Szegedy, S. Ioffe, V. Vanhoucke, and A. Alemi, "Inception-v4, inception-resnet and the impact of residual connections on learning," in *Proc. 31st AAAI Conf. Artif. Intell.*, 2017, pp. 1–7.

[9] K. He, X. Zhang, S. Ren, and J. Sun, "Spatial pyramid pooling in deep convolutional networks for visual recognition," *IEEE Trans. Pattern Anal. Mach. Intell.*, vol. 37, no. 9, pp. 1904–1916, Sep. 2015.

[10] L. Zhang, H. Kong, C. Ting Chin, S. Liu, X. Fan, T. Wang, and S. Chen, "Automation-assisted cervical cancer screening in manual liquid-based cytology with hematoxylin and eosin staining," *Cytometry A*, vol. 85, no. 3, pp. 214–230, Mar. 2014.
[11] Y.-F. Chen, P.-C. Huang, K.-C. Lin, H.-H. Lin, L.-E. Wang, C.-C. Cheng, T.-P. Chen, Y.-K. Chan, and J. Y. Chiang, "Semi-automatic segmentation and classification of Pap smear cells," *IEEE J. Biomed. Health Inform.*, vol. 18, no. 1, pp. 94–108, Jan. 2014.
[12] T. Chankong, N. Theera-Umpon, and S. Auephanwiriyakul, "Automatic cervical cell segmentation and classification in Pap smears," *Comput. Meth. Programs Biomed.*, vol. 113, no. 2, pp. 539–556, 2014.
[13] J. Jantzen, J. Norup, G. Dounias, and B. Bjerregaard, "Pap-smear benchmark data for pattern classification," in *Proc. Nature-Inspired Smart Inf. Syst. (NiSIS)*, 2005, pp. 1–9.
[14] Y. Marinakis, M. Marinaki, and G. Dounias, "Particle swarm optimization for pap-smear diagnosis," *Expert Syst. Appl.*, vol. 35, no. 4, pp. 1645–1656, Nov. 2008.
[15] Y. Marinakis, G. Dounias, and J. Jantzen, "Pap smear diagnosis using a hybrid intelligent scheme focusing on genetic algorithm based feature selection and nearest neighbor classification," *Comput. Biol. Med.*, vol. 39, no. 1, pp. 69–78, Jan. 2009.
[16] L. Nanni, A. Lumini, and S. Brahnam, "Local binary patterns variants as texture descriptors for medical image analysis," *Artif. Intell. Med.*, vol. 49, no. 2, pp. 117–125, Jun. 2010.
[17] Y. Guo, G. Zhao, and M. Pietikäinen, "Discriminative features for texture description," *Pattern Recognit.*, vol. 45, no. 10, pp. 3834–3843, Oct. 2012.
[18] B. Sokouti, S. Haghipour, and A. D. Tabrizi, "A framework for diagnosing cervical cancer disease based on feedforward MLP neural network and ThinPrep histopathological cell image features," *Neural Comput. Appl.*, vol. 24, no. 1, pp. 221–232, Jan. 2014.
[19] M. Zhao, A. Wu, J. Song, X. Sun, and N. Dong, "Automatic screening of cervical cells using block image processing," *Biomed. Eng. OnLine*, vol. 15, no. 1, p. 14, Dec. 2016.
[20] L. Zhang, L. Lu, I. Nogues, R. M. Summers, S. Liu, and J. Yao, "DeepPap: Deep convolutional networks for cervical cell classification," *IEEE J. Biomed. Health Inform.*, vol. 21, no. 6, pp. 1633–1643, Nov. 2017.
[21] K. P. Win, Y. Kitjaidure, K. Hamamoto, and T. M. Aung, "Computer-assisted screening for cervical cancer using digital image processing of Pap smear images," *Appl. Sci.*, vol. 10, no. 5, p. 1800, Mar. 2020.
[22] Kurnianingsih, K. H. S. Allehaibi, L. E. Nugroho, Widyawan, L. Lazuardi, A. S. Prabuwono, and T. Mantoro, "Segmentation and classification of cervical cells using deep learning," *IEEE Access*, vol. 7, pp. 116925–116941, 2019.
[23] P. Guo, K. Banerjee, R. Joe Stanley, R. Long, S. Antani, G. Thoma, R. Zuna, S. R. Frazier, R. H. Moss, and W. V. Stoecker, "Nuclei-based features for uterine cervical cancer histology image analysis with fusion-based classification," *IEEE J. Biomed. Health Inform.*, vol. 20, no. 6, pp. 1595–1607, Nov. 2016.
[24] C. Li, H. Chen, L. Zhang, N. Xu, D. Xue, Z. Hu, H. Ma, and H. Sun, "Cervical histopathology image classification using multilayer hidden conditional random fields and weakly supervised learning," *IEEE Access*, vol. 7, pp. 90378–90397, 2019.
[25] A. Ghoneim, G. Muhammad, and M. S. Hossain, "Cervical cancer classification using convolutional neural networks and extreme learning machines," *Future Gener. Comput. Syst.*, vol. 102, pp. 643–649, Jan. 2020.
[26] D. Kashyap, A. Somani, J. Shekhar, A. Bhan, M. K. Dutta, R. Burget, and K. Riha, "Cervical cancer detection and classification using independent level sets and multi SVMs," in *Proc. 39th Int. Conf. Telecommun. Signal Process. (TSP)*, Jun. 2016, pp. 523–528.
[27] M. Sharma, S. Kumar Singh, P. Agrawal, and V. Madaan, "Classification of clinical dataset of cervical cancer using KNN," *Indian J. Sci. Technol.*, vol. 9, no. 28, pp. 1–5, Jul. 2016.
[28] W. William, A. Ware, A. H. Basaza-Ejiri, and J. Obungoloch, "Cervical cancer classification from Pap-smears using an enhanced fuzzy C-means algorithm," *Informat. Med. Unlocked*, vol. 14, pp. 23–33, Feb. 2019.
[29] M. Wu, C. Yan, H. Liu, Q. Liu, and Y. Yin, "Automatic classification of cervical cancer from cytological images by using convolutional neural network," *Biosci. Rep.*, vol. 38, no. 6, Dec. 2018, Art. no. BSR20181769.
[30] K. Bora, M. Chowdhury, L. B. Mahanta, M. K. Kundu, and A. K. Das, "Automated classification of Pap smear images to detect cervical dysplasia," *Comput. Methods Programs Biomed.*, vol. 138, pp. 31–47, Jan. 2017.
[31] J. Su, X. Xu, Y. He, and J. Song, "Automatic detection of cervical cancer cells by a two-level cascade classification system," *Anal. Cellular Pathol.*, vol. 2016, pp. 1–11, May 2016.
[32] W. William, A. Ware, A. H. Basaza-Ejiri, and J. Obungoloch, "A pap-smear analysis tool (PAT) for detection of cervical cancer from pap-smear images," *Biomed. Eng. OnLine*, vol. 18, no. 1, pp. 1–22, Dec. 2019.
[33] B. Ashok and P. Aruna, "Comparison of feature selection methods for diagnosis of cervical cancer using SVM classifier," *Int. J. Eng. Res. Appl.*, vol. 6, pp. 94–99, Jan. 2016.
[34] K. Adem, S. Kiliçarslan, and O. Cömert, "Classification and diagnosis of cervical cancer with stacked autoencoder and softmax classification," *Expert Syst. Appl.*, vol. 115, pp. 557–564, Jan. 2019.
[35] S. F. Abdoh, M. A. Rizka, and F. A. Maghraby, "Cervical cancer diagnosis using random forest classifier with SMOTE and feature reduction techniques," *IEEE Access*, vol. 6, pp. 59475–59485, 2018.
[36] E. Hussain, L. B. Mahanta, C. R. Das, and R. K. Talukdar, "A comprehensive study on the multi-class cervical cancer diagnostic prediction on pap smear images using a fusion-based decision from ensemble deep convolutional neural network," *Tissue Cell*, vol. 65, Aug. 2020, Art. no. 101347.
[37] A. Pirovano, L. G. Almeida, and S. Ladjal, "Regression constraint for an explainable cervical cancer classifier," 2019, *arXiv:1908.02650*. [Online]. Available: http://arxiv.org/abs/1908.02650
[38] H. Lin, Y. Hu, S. Chen, J. Yao, and L. Zhang, "Fine-grained classification of cervical cells using morphological and appearance based convolutional neural networks," *IEEE Access*, vol. 7, pp. 71541–71549, 2019.

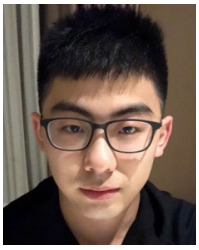


SUXIANG YU graduated in clinical medicine from Hebei Medical University, in June 1996. She received the master's degree in anatomy and histology and embryology from Chengde Medical College, in 2009. From August 2016 to August 2017, she studied for half a year with the Department of Pathology, China-Japan Friendship Hospital. She is currently the Deputy Director of the Baoding Center for Quality Control in Pathology. She currently works with the Department of Pathology, The Fourth Central Hospital of Baoding City. Her current research interests include early diagnosis and prevention of tumor. She was also appointed as a member of the Hebei Anti-Cancer Association and the Hebei Maternal and Child Health Association, in 2016.

XINXING FENG received the M.D. degree from the Peking Union Medical College. He is currently an Associate Professor with the Fuwai Hospital, National Center for Cardiovascular Diseases, Chinese Academy of Medical Sciences and Peking Union Medical College. His research interest includes the field of combining medicine with artificial intelligence.

BIN WANG received the bachelor's degree in clinical medicine from Hebei Medical University, in 2007, and the master's degree in pathology and pathophysiology from Shanxi Medical University, in 2010. Since July 2010, he has been working with the Department of Pathology, The Fourth Central Hospital of Baoding City, Hebei, China.

HUA DUN received the bachelor's degree in clinical medicine from Hebei North University, in June 2007. From August 2014 to August 2015, she studied for one year with the Department of Pathology, Peking University Third Hospital, and obtained the certificate of completion. Since 2008, she has been working with the Department of Pathology, Tang County People's Hospital.



SHUAI ZHANG received the B.Eng. degree in software engineering from the Beijing University of Posts and Telecommunications. He is currently pursuing the master's degree in artificial intelligence with The University of Manchester. His current research interests include machine learning, computer vision, and software engineering.

RUIHONG ZHANG received the master's degree from Shanxi Medical University, in 2009. In April 2003, she worked with The Fourth Central Hospital of Baoding City. From February to May 2017, she passed the selection examination of the Talent Exchange Center of the National Health and Family Planning Commission, went to Davis Medical Center attached to the University of California to study, participated in wound management and health leadership training programs, and was highly praised by an American medical staff. She is currently the President Assistant with the hospital, the Chief of Science and Education, and a Chief Nurse. She is also a member of the Hebei Nursing Association and the third-level talent of Hebei Province. She is also the Deputy Chairman of the Baoding Nursing Research Working Committee and the Baoding Youth Talent Committee.

XIN HUANG received the B.S., M.S., and Ph.D. degrees from the Harbin Institute of Technology, Harbin, China, in 2004, 2006, and 2010, respectively. From 2010 to 2012, he worked as a Postdoctoral Fellow with the Solar Activity Prediction Center, National Astronomical Observatories, Chinese Academy of Sciences (NAOC). In 2012, he joined the Solar Activity Prediction Center, NAOC. He is currently an Associate Professor. His research interests include solar activity prediction and medical data mining.