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# Breast cancer detection via wavelet energy and support vector machine

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***Abstract*—**Breast cancer as one of the most feared killers of women, there are still no effective means of prevention and treatment on it. However, the popularity of its research continues to rise in academic field. The traditional medical diagnosis is mainly by observing the patient's symptoms to confirm the variety of diseases, but the efficiency is undesirable, and the scientific contribution is poor. At present, due to the dramatical development of the application of machine learning in data detection, the application of computer technology in disease diagnosis has become a new and effective means. This paper used the wavelet energy to extract features of breast cancer, then established a breast cancer predicting model, while re-use data grouping function of support vector machine (SVM), then algorithm would accurately distinguish the characteristics of the data among benign malignant tumors. So, the accuracy of intelligent diagnosis in breast cancer has be improved, and proven to be better than two state-of-the-art approaches.

***Keyword*—**disease diagnosis; machine learning; wavelet energy; SVM

## I. Introduction

Among all breast cancer patients, the number of Women constituting 99 percent. The disease has become one of the biggest risks to women's health [1]. At present, there is still no effective way to prevent the occurrence of breast cancer [2-5]. However, early diagnosis plays a key role in the follow-up treatment.

On the other hand, Machine learning, predictive analysis and pattern recognition have achieved remarkable results in breast cancer diagnosis, which are far more accurate than the diagnostic accuracy of human pathologists and are more efficient. The methods of the Machine Learning based on Wavelet Energy applied successfully in the prediction model of breast cancer [6], but the computational efficiency of different algorithms is different. Therefore, the optimization of prediction algorithm is of great significance.

Ting and Sim [7] formulated two steps to deal with breast cancer dataset and categorized samples into three classes: (i) preprocess samples, the noise is filtered to obtain high quality images and used them as input; (ii) classify samples, applied self-regulated ML-NN to recognize benign, malignant and normal patients. Aličković and Subasi [8] considered a novel diagnostic system for breast cancer includes genetic algorithm and rotation forest. Firstly, using GA to eliminate redundancy features and improve work efficiency. Using Rotation Forest to calculate and evaluate fitness value, so experts can achieve the most useful features. Then detecting input samples by Rotation Forest and the correct rate of the proposed method is 99.48%. Tan, et al. [9] described a deep learning method, Convolutional Neural Network (CNN), to develop the technology for breast cancer and improve 10%~20% accuracy compared to previous methods. The researchers augmented the dataset by using rotational operation and then entered the samples into CNN (two convolution layers, two pooling layers, one fully connected layer). Monica Jenefer and Cyrilraj [10] have helped medical staff diagnose breast cancer cells and further classified the growth stages of cancer cells so that experts can take the most effective treatment. They established a hybrid mathematical hierarchical regression model (HMHR) which combined with linear and nonlinear model. According to the domain approximation, HMHR categorized the cell growth stages. Padmavathy, et al. [11] implemented an effective method, NSST+ANFIS, for distinguishing normal and abnormal breast cells. Using NSST to decompose the source images in multiscale and multiple directions and using adaptive clustering with ANFIS to classify input images. Compared with active contour with ANFIS, the method has better performance in sensitivity, accuracy and specificity. All above methods used neural network which had a simple structure and strong problem-solving ability. However, there were also several major shortcomings. Its troubles of algorithm can be listed as follows: local optimization, poor convergence, long training time and easy over-fitting. On the other hand, Milosevic, et al. [12] used graylevel cooccurrence matrix (GLCM) and naïve Bayesian classifier (NBC). Zhu, et al. [13] proposed a Parameter-Constrained Generalized Hough Transform (PCGHT) approach for detect occluded object, which is the situation of our task. However, the accuracy of both two methods was unsatisfactory.

Our contribution is to propose a novel automatic breast cancer detection method, which is based on the mixture of wavelet energy and support vector machine [14-18]. The former one can extract efficient features, and the latter one is commonly-used as a powerful classifier. The results showed the effectiveness of our method.

## II. Method

### *A. Dataset*

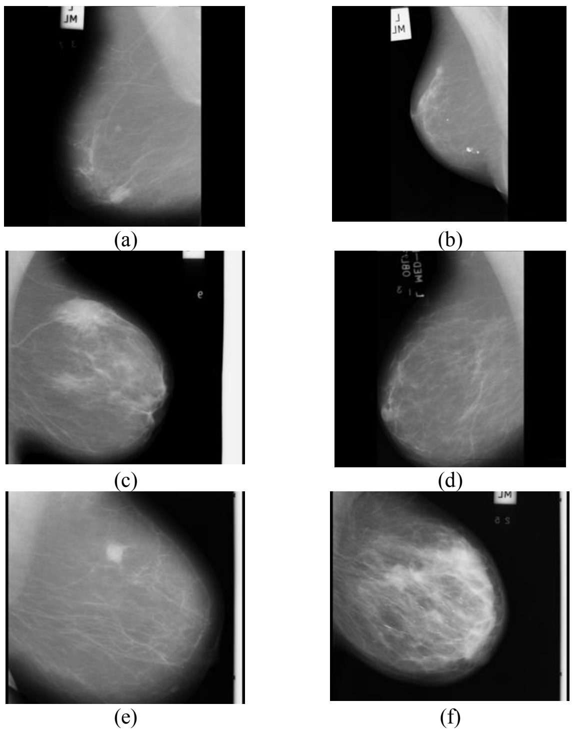


**FIGURE 1** six abnormal breast types: (a) Circumscribed Mass; (b) Asymmetry; (c) Architectural distortion; (d) Calcification; (e) Ill-defined masses; (f) Spiculated masses

The mini-MIAS database [19] was used, which contains 322 single-breast mammogram images with sizes of 1024x1024. Figure 1 shows the six types of abnormal breasts. Our task is to identify abnormal breasts from healthy breasts in this study, which is a preliminary work. In the future, we aimed to identify each abnormal type. Now we randomly select 50 abnormal breast images, and 50 normal breast images.

### *B. Wavelet Energy*

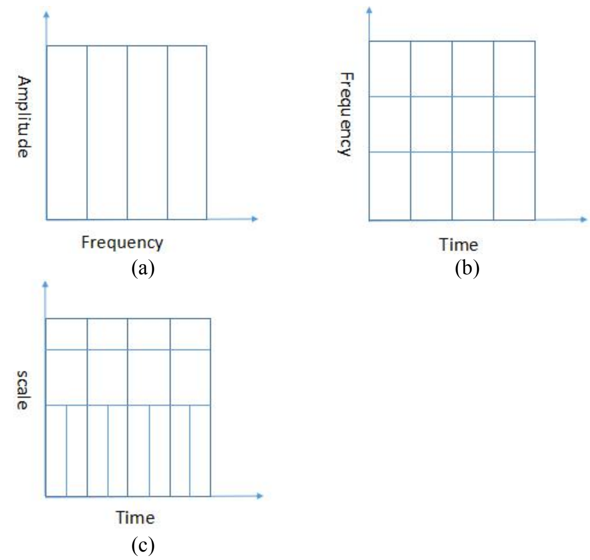


**FIGURE 2** Three different signal processing methods

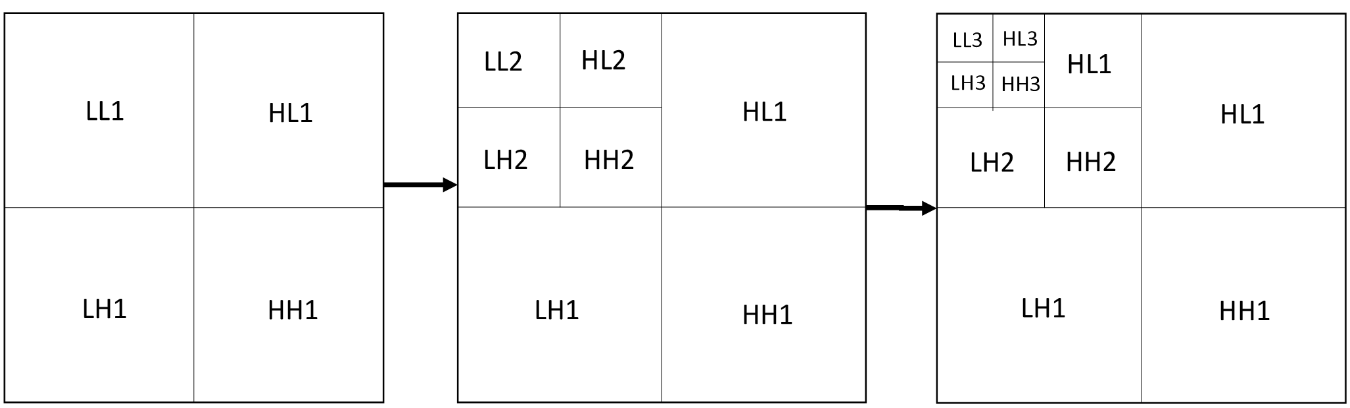


**FIGURE 3** Three-level decomposition

**FIGURE 2** shows three typical signal processing methods. The first is Fourier transform (FT), where the user decomposes signal into frequency spectrum. The next generation used short-time Fourier transform, and divide the signal into small pieces along time axis, and perform FT on each piece. Nowadays, the wavelet is more powerful than former two methods. It can directly decompose signal into time-and-scale plot.

Wavelets Energy are a kind of wave oscillation, the amplitude starts from zero, increases, and then decreases to zero. It is often intentionally designed to have specific properties that will make them useful for signal processing [20].

The Wavelet Energy (abbreviated as WG, since WE was commonly used to denote wavelet entropy) can be combined with the known damage signal to extract information from the unknown part [21-25]. As a mathematical tool, it can be used to obtain information from many different kinds of data, including – but certainly not limited to – audio signals and images.

The wavelet energy (WG) in horizontal, vertical and diagonal directions at $i$ -th level is, respectively defined as:

$$E_i^h = \sum_{x=1}^{M}\sum_{y=1}^{N}(H_i(x,y))^2 \tag{1}$$

$$E_i^v = \sum_{x=1}^{M}\sum_{y=1}^{N}(V_i(x,y))^2 \tag{2}$$

$$E_i^d = \sum_{x=1}^{M}\sum_{y=1}^{N}(D_i(x,y))^2 \tag{3}$$

These energies reflect the strength of the images' details in different direction at the $i$ -th level decompose level. Nowadays, Wavelet Energy has become a successful tool to extract features， while it achieved great applications in many fields. **FIGURE 3** shows an illustration of three-level decomposition, where LL, HL, LH, and HH are four subbands of each decomposition.

Wavelet energy analysis as a new method of signal analysis, performing well in time domain and frequency domain with ability of denoting local signal characteristics. Since then it has been widely applied in in many disciplines, such as signal and image processing , pattern recognition, speech recognition, seismic exploration. This paper applied the noise elimination function of wavelet energy to remove the subtle fluctuation in the prediction model, and only the general trend was considered, so as to smooth the algorithm. What's more, the data were optimized to further improve the accuracy of SVM in breast cancer prediction.

### *C. Support Vector Machine*

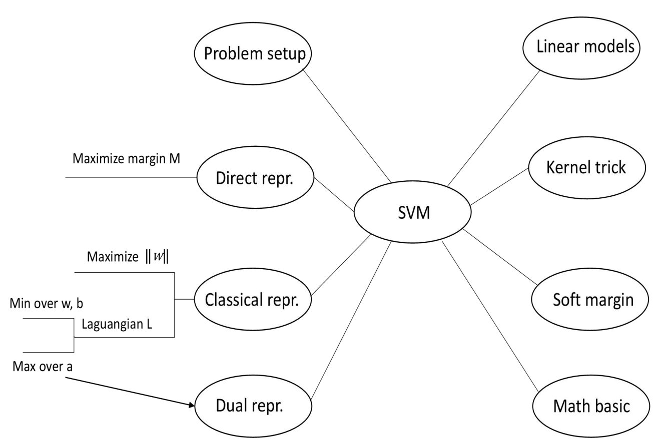


**FIGURE 4** Models and variants of SVM (repr. refers to representation)

In 1995, Corinna Cortes and Vapnik proposed Support Vector Machine (SVM, or Support Vector Networks). Their achievement was successively applied in many other studies, It performed well in solving small sample, nonlinear and even in high dimensional pattern recognition. What' more, it has been successfully applied in medical diagnosis and other study areas. [26-30].

In machine learning theory, SVM is an effective method for establishing classification model. It has many applications, such as data analysis, data classification, regression analysis etc. [31], SVM training algorithm firstly establish a classification model, which is in order to find a hyperplane, which can let the closest point of all to it has the largest spacing, so that the classification can be more accurate. **FIGURE 4** shows the common models and variants of SVM.

A basic theory of SVM is the Maximum Marginal, which means that the larger the gap is, the better it will be. Same to two categories separated by the line. The closest point to the separation line is called the support vector. As shown in **FIGURE 5**, the lines at both ends are called plus plane and minus plane, which is the surface of the support vector. The gap between the two lines is called Margin Width, and the middle line is Classifier Boundary, which is also Best Decision Boundary. [32-36]. Both red line and green line definately can seperate the classes, but all of them just exist with small margins. The middle black line is the Best Decision Boundary with the maximum margin.

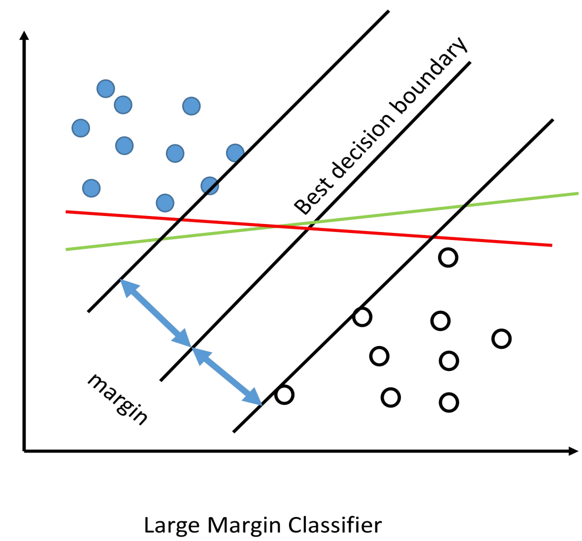


**FIGURE 5** Illustration of SVM

From the above analysis, it can be seen that constructions of hyperplane or hyperplane sets by support vector machines in high dimensional space can be used for classification, regression or other tasks. From the intuitive point of view, a good separation is a hyperplane, of which maximum distance is the closest point of training data in any class (the so-called function boundary). In general, the smaller the classifier's generalization error is, the larger its edges are [37].

At first, in a linear space, the question is to distinguish whether a set of linear spaces could be separated. When a space is transformed from the original linear space into a higher dimensional space, it is divided by a hyperplane. The advantage of this is that the two groups of similar data can be distinguished by adding dimensions. In order to make the computation load reasonable, SVM uses a mapping to map to a larger space, so that cross-products can be easily calculated in a variable in the original space. Cross-products in larger Spaces are defined as a kernel function $K(x, y)$ that can be selected to accommodate the problems. The vectors defining the hyperplanes can be selected to be linear combinations with parameters $\alpha_i$ of images of feature vectors $x_i$ which occur in the data base. With this choice of a hyperplane, the point $x$ in the feature space is mapped to hyperplane are defined by the relation:

$$\sum_i \alpha_i k(x_i, x) = constant \tag{4}$$

The function of the kernel is to map the low dimension to the higher dimension, which is easy to classify. The kernel includes Linear kernel, Gaussian kernel. The Gaussian kernel even maps the original space to infinite dimensional space, and the kernel function has some good properties, for example, it will not increase the amount of extra computation under linear conditions, etc. [38-40]. The hyperplane in the higher-dimensional space is defined as the set of points whose cross product with a vector in that space is constant.

If $K(x, y)$ becomes small as $y$ increases further from $x$, each element in the sum would measure the proximity of the test point $x$ to the corresponding point $x_i$ in database. In this way, the kernel on the sum of each test point can be used to measure the relative distance of the data points which are identified in one or another group. Note that a collection of points mapped to any fixed pointing hyperplane can complicatedly allow more complex discrimination between the results set apart from convex of original space.

## III. Experiments and Results

### *A. Statistical Analysis*

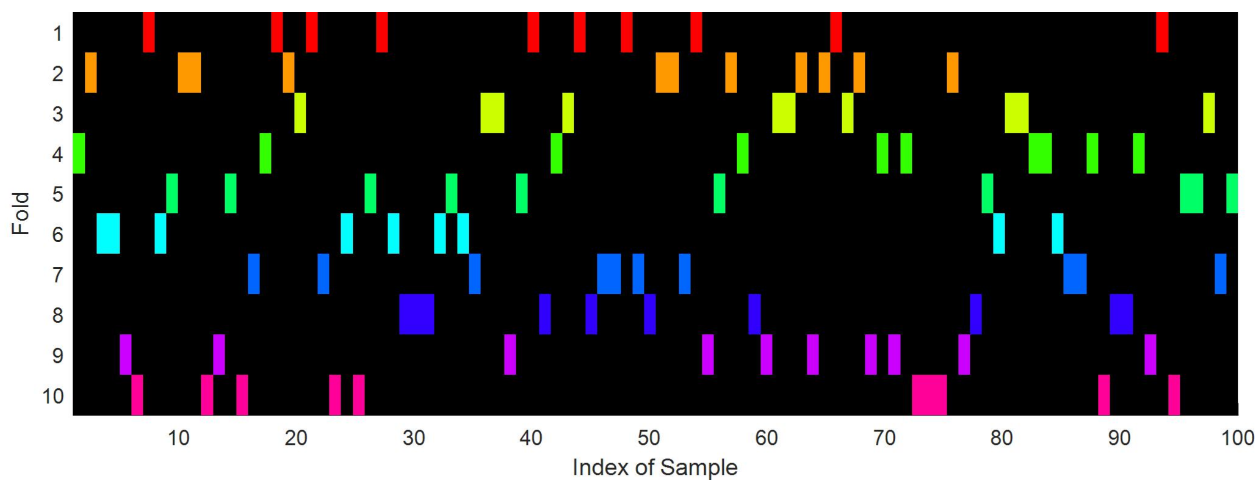


**FIGURE 6** Index of segmentation of 10 folds

The 10x10-fold cross validation was used to report the out-of-sample error. We used db2 wavelet and the decomposition level was 3. The WG features were then submitted to SVM. **FIGURE 6** shows the segmentation of 10 folds. The results of each run and each fold are listed in Table 1. Here $(c+d) = g$ means $c$ abnormal breasts and $d$ healthy breasts were correctly identified; thus, altogether $g$ images were identified correctly.

Table 1 Result of correct identification (Tk means the test at k-th fold)

| Run | T1 | T2 | T3 | T4 | T5 | T6 | T7 | T8 | T9 | T10 | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|
| R1 | 5+2 =7 | 5+5 =10 | 5+3 =8 | 5+4 =9 | 4+5 =9 | 4+3 =7 | 4+3 =7 | 5+3 =8 | 4+5 =9 | 3+5 =8 | 44+38 =82 |
| R2 | 5+4 =9 | 4+3 =7 | 5+5 =10 | 3+3 =6 | 3+4 =7 | 5+4 =9 | 5+2 =7 | 5+5 =10 | 2+5 =7 | 4+5 =9 | 41+40 =81 |
| R3 | 4+4 =8 | 3+5 =8 | 3+5 =8 | 4+5 =9 | 4+4 =8 | 4+4 =8 | 2+4 =6 | 5+4 =9 | 4+5 =9 | 4+3 =7 | 37+43 =80 |
| R4 | 5+4 =9 | 2+5 =7 | 5+4 =9 | 2+5 =7 | 5+4 =9 | 5+4 =9 | 5+4 =9 | 4+4 =8 | 4+4 =8 | 5+3 =8 | 42+41 =83 |
| R5 | 4+5 =9 | 4+5 =9 | 4+4 =8 | 2+4 =6 | 5+3 =8 | 5+4 =9 | 4+5 =9 | 4+4 =8 | 4+4 =8 | 5+4 =9 | 41+42 =83 |
| R6 | 3+2 =5 | 4+4 =8 | 5+2 =7 | 3+5 =8 | 5+5 =10 | 5+5 =10 | 5+4 =9 | 4+5 =9 | 4+4 =8 | 4+4 =8 | 42+40 =82 |
| R7 | 4+5 =9 | 4+5 =9 | 4+5 =9 | 3+5 =8 | 4+4 =8 | 5+5 =10 | 4+4 =8 | 4+3 =7 | 5+2 =7 | 3+4 =7 | 40+42 =82 |
| R8 | 4+3 =7 | 5+4 =9 | 4+5 =9 | 4+5 =9 | 5+5 =10 | 4+4 =8 | 5+2 =7 | 3+5 =8 | 4+4 =8 | 3+4 =7 | 41+41 =82 |
| R9 | 5+1 =6 | 3+5 =8 | 5+2 =7 | 5+5 =10 | 5+5 =10 | 3+4 =7 | 3+4 =7 | 5+3 =8 | 4+5 =9 | 5+5 =10 | 43+39 =82 |
| R10 | 5+3 =8 | 5+4 =9 | 5+5 =10 | 4+3 =7 | 3+4 =7 | 4+4 =8 | 5+3 =8 | 4+5 =9 | 3+3 =6 | 4+5 =9 | 42+39 =81 |

Three measures were used, including sensitivity, specificity, and accuracy. Their results were listed below in Table 2. Our "WG+SVM" method achieved a sensitivity of 82.60± 3.78%, a specificity of 81.00± 3.16%, and an accuracy of 81.80± 0.92%.

Table 2 Statistical performance over 10x10-fold cross validation

| Run | Sen | Spc | Acc |
|---|---|---|---|
| 1 | 88 | 76 | 82 |
| 2 | 82 | 80 | 81 |
| 3 | 74 | 86 | 80 |
| 4 | 84 | 82 | 83 |
| 5 | 82 | 84 | 83 |
| 6 | 84 | 80 | 82 |
| 7 | 80 | 84 | 82 |
| 8 | 82 | 82 | 82 |
| 9 | 86 | 78 | 82 |
| 10 | 84 | 78 | 81 |
| Average | 82.60± 3.78 | 81.00± 3.16 | 81.80± 0.92 |

### *B. Hyperparameter Decomposition Level*

Table 3 Optimal decomposition level

| Decomposition level | Sen | Spc | Acc |
|---|---|---|---|
| 1 | 70.20± 5.77 | 70.80± 6.34 | 70.50± 0.71 |
| 2 | 76.60± 4.62 | 76.20± 4.76 | 76.40± 0.97 |
| 3 | 82.60± 3.78 | 81.00± 3.16 | 81.80± 0.92 |

| | | | |
|---|---|---|---|
| 4 | 79.20± 3.16 | 78.60± 2.50 | 78.90± 0.99 |

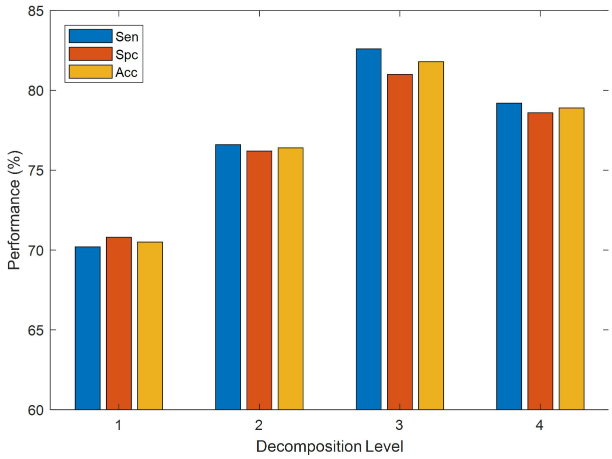

**FIGURE 7** Determine the optimal decomposition level

In this experiment, we helped to find the optimal decomposition level of WG. In previous experiment, we assigned the decomposition level as 3. Now we changed the decomposition level from 1 to 4, and recorded the corresponding classification performances as shown in Table 3. The corresponding plot was shown in **FIGURE 7**.

We can observe that the WG with decomposition level of 1 and 2 achieved performances less than 80%. The performances of level 3 yield the highest result. Afterwards, the level 4 decreased the performance slightly.

### *C. State-of-the-art Comparison*

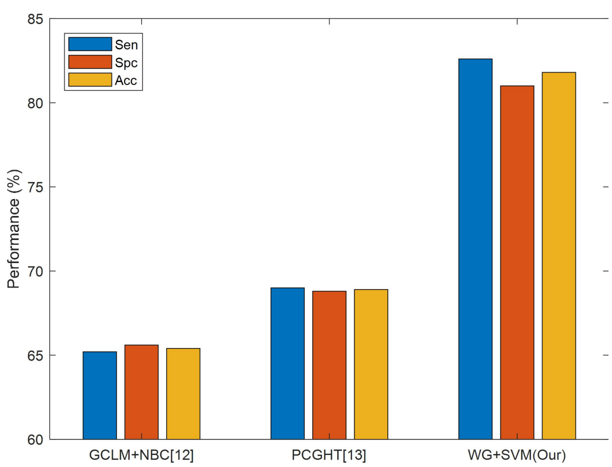

**FIGURE 8** Comparison to state-of-the-art approaches

Finally, we compared our method with state-of-the-art approaches, including GCLM+NBC [12], PCGHT [13]. The results were listed in Table 4. The GCLM+NBC [12] method yields a sensitivity of 65.20± 4.02%, a specificity of 65.60± 4.50%, and an accuracy of 65.40± 1.17%. The PCGHT [13] method yields a sensitivity 69.00± 3.68%, a specificity of 68.80± 4.24%, and an accuracy of 68.90± 1.10%. The performances of both methods are lower than 70%, while our proposed WG+SVM method yields a result greater than 80%. For clear view, **FIGURE 8** plots the comparison.

Table 4 Comparison to State-of-the-art Approaches

| Method | Sen | Spc | Acc |
|---|---|---|---|
| GCLM+NBC [12] | 65.20± 4.02 | 65.60± 4.50 | 65.40± 1.17 |
| PCGHT [13] | 69.00± 3.68 | 68.80± 4.24 | 68.90± 1.10 |
| WG+SVM (Our) | 82.60± 3.78 | 81.00± 3.16 | 81.80± 0.92 |

## IV. Conclusions

This article is based on the principle of support vector machine, and we proposed a new intelligent algorithm "WG+SVM" for breast cancer diagnosis. Through using wavelet energy as an activation function to extract features of breast cancer, it improved the accuracy of intelligent diagnosis in breast cancer so that it would accurately distinguish benign and malignant tumors. In the end, the validity of this method is verified by numerical experiments. Three measures were used, including sensitivity, specificity, and accuracy. Their results were compared to prove the performance of the method that put forward in the article. In contain, WG+SVM has been proved to be effective in the diagnosis of breast cancer.

Support Vector Machine (SVM) technology has been widely applied in the classification, feature extraction and so on. In medicine, the application of its advantage in disease diagnosis classification is very huge, and its accuracy and efficiency on diagnosis were superior to the traditional diagnosis methods. However, large data of sample will cause the training speed quite slow, this is a major defect of the SVM method. Though most existing literatures paid more attention to improve the diagnostic accuracy of SVM method, the future research direction would be carried out in the optimization of algorithm and the parallelization of algorithm.

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