

## RESEARCH ARTICLE

# Prediction of Complex Acute Appendicitis Based on HGS-MSVM

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**ABSTRACT** In this paper, we propose an effective and intelligent prediction model that can well distinguish complex acute appendicitis from uncomplicated acute appendicitis. In this study, 358 patients admitted to the First Hospital of Jilin University in Changchun for acute appendicitis in the past 5 years were included, and the data panel was constructed based on 32 factors collected. The framework comprised mainly of a Principal Component Analysis (PCA) algorithm and a Support Vector Machine (SVM) with new kernel function named the Mercer Support Vector Machine (MSVM) model and optimized by a Hunger Game Search (HGS) algorithm. First, the PCA was used to reduce the dimension of the data. Second, the HGS integrated into the MSVM was employed to train the parameter of the classification model MSVM to obtain the optimal model—Hunger Game Search (HGS-MSVM). Finally, based on the acute appendicitis data, comparative experiments were conducted between HGS-MSVM and five well-known machine-learning models, namely the Random Forest (RF), K-Nearest Neighbor (KNN), MSVM, Logistic Regression (LR) and Discriminant Analysis (DA). The experimental data shows that the proposed model can achieve the best prediction performance, with a sensitivity, specificity, Matthews correlation coefficient (MCC), and accuracy (ACC) of 87.5%, 71.95%, 60.43%, and 81.65%, respectively. The experimental data proved that the HGS-MSVM model can be used for clinical auxiliary diagnosis of complex acute appendicitis.

**INDEX TERMS** Complex acute appendicitis, support vector machine, hunger game search algorithm, disease diagnosis, machine-learning model.

## I. INTRODUCTION

Acute appendicitis is one of the most common abdominal emergencies [1], [2], [3], and the risk of suffering from acute appendicitis is approximately 7% [4]. Acute appendicitis develops rapidly, and if it is not diagnosed and treated in time, it is likely to develop into complex acute appendicitis with gangrene, perforation, and other serious complications. The most common treatment for acute appendicitis is surgical resection; hence, surgery for acute appendicitis is one of the most commonly carried out operations [5], [6], [7]. However, a large number of experiments have proved that

conservative antibiotic treatment is effective for simple acute appendicitis [8], [9], [10], [11]. Therefore, making an accurate prediction of complex acute appendicitis can not only reduce the likelihood of patients progressing to complex acute appendicitis but also reduce the probability of patients undergoing unnecessary surgery and hospitalization, which can help with the current shortage of hospital bed resources in China. Moreover, surgical treatment requires more medical resources than antibiotic treatment, so accurate prediction of complex acute appendicitis can also save more medical resources.

Computed tomography (CT) is an effective imaging tool to improve the diagnostic accuracy of acute appendicitis and complex acute appendicitis [12]. However, the long CT

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imaging time and demand rate is much higher than the supply rate, often resulting in long waiting times. At the same time, CT examination is also highly dependent on the operator, as the technique used will affect the imaging quality. In addition, some tests have shown that CT scans with radiation increase the risk of cancer [13], [14].

In order to effectively avoid the disadvantages of CT examination, many components in blood examination have been proved to be markers of complex acute appendicitis [15], [16]. Hajibandeh et al. presented that the ratio of neutrophils to lymphocytes (NLR) could be used as a marker to distinguish simple acute appendicitis from complex acute appendicitis [17]. Symeonidis et al. reported that serum sodium level is a routine low-cost test that can be used as an auxiliary marker to help surgeons identify complex acute appendicitis in the early stage [18]. Ribeiro et al. found that C-reactive protein can be a good predictor of complex acute appendicitis [19]. Antić et al. found that white blood cells could be an important independent predictor of complex acute appendicitis by performing logistic regression analysis on the collected biomarkers [20]. Poudel et al. performing multivariate regression analysis on 73 patients and found that an increased total white blood cell count could be a good marker for complex appendicitis [21]. Kang et al. found that white blood cell count had the highest correlation by using univariate regression analysis of factors that may be related to the severity of acute appendicitis patients, such as abdominal pain score, duration of abdominal pain, maximum body temperature, tenderness range, and other factors [22].

The prediction performance of a single marker is limited, and the combination of multiple markers will achieve better results. Many scoring systems are built around these markers and other signs [23], [24], [25], [26]. Jose et al. verified that the Appendicitis Inflammatory Response (AIR) score can effectively reduce the probability of negative appendectomy by using comparative tests. In addition, some experiments show that the performance of the AIR score is better than that of the Alvarado scoring system. Although the scoring system has a relatively ideal accuracy, there are still controversial conclusions concerning its sensitivity and specificity [27].

With the recent advances in machine learning, various machine-learning methods have been applied to the field of medical prediction [28], [29], [30], [31]. Ahmed et al. integrated support vector machine (SVM) with artificial neural network (ANN) to diagnose whether diabetic patients are negative or positive [32]. Li et al. created an online application based on an extreme gradient Boosting (XGBoost) model for early warning work of acute renal failure (ARF) [33]. Yuan et al. designed a fusion algorithm based on fuzzy logic and gradient boosting decision tree (GBDT), and improved the algorithm to form the Bagging-Fuzzy-GBDT algorithm, which finally confirmed that the algorithm had good performance in the field of heart disease prediction. Based on the comparison of the articles, it can be seen that it is valuable to apply machine learning to the field of medical prediction... [34].

By comparing 48 articles on medical disease prediction, Uddin et al. found that SVM had the highest utilization rate [35]. SVM is a kind of generalized linear classifier that performs binary classification on data by supervised learning, and its decision boundary is the maximum margin hyperplane solved on the learning samples. Optimizing the parameter of SVM kernel function can effectively improve the classification performance of the SVM. However, it is a complex task to optimize the penalty factor and kernel function parameters of SVM, so it is still considered an arduous task. Swarm intelligence algorithm is widely used in various complex problems. Ant Colony Optimization (ACO) is applied to path optimization [36], [37] and virtual machine deployment... [38]. Harris Hawk Optimization (HHO) is applied to image segmentation, model parameter optimization, and feature selection [39], [40], [41]. Whale Optimization Algorithm (WOA) is applied to hyperparameter optimization, resource scheduling, and power distribution fault solving [42], [43], [44].

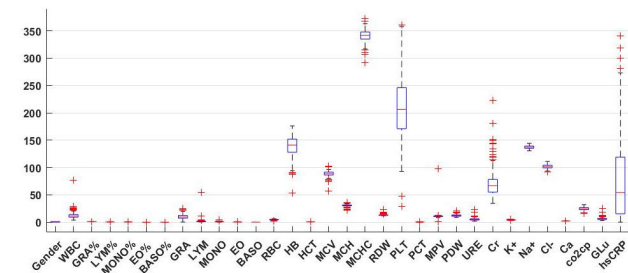
In this paper, to optimize the sum function parameters of SVM, the Hunger Games Search (HGS) was selected. HGS was proposed by Yang et al. in 2021, which was a relatively new algorithm. HGS has been experimentally compared with 15 other basic optimization algorithms such as Particle Swarm Optimization (PSO), Firefly Algorithm (FA), WOA, and Grey Wolf Algorithm (GWO). Compared with 10 state-of-the-art advanced optimization algorithms such as IWOA and DBWOA, it was confirmed that the optimization performance of HGS was better than these algorithms... [45]. At present, HGS has been applied in many fields and shows excellent performance [46], [47], [48]. In this study, HGS was mainly applied to optimize the parameters in SVM to improve its prediction performance.

The remainder of this paper is structured as follows. Section II analyzes the collected patient information data in detail, and introduces the experimental method. Section III introduces the specific settings involved in the experiment. In Section IV, the experimental results are presented and analyzed. Finally, the results are summarized in Section 5.

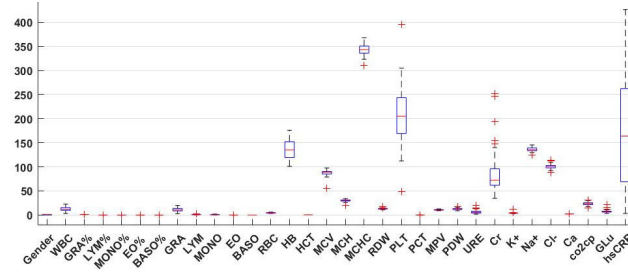
## II. MATERIALS AND METHODS

### A. DATA COLLECTION

In this experiment, the data of 358 patients admitted to the First Hospital of Jilin University in Changchun due to acute appendicitis in the past 5 years (171 cases of complex acute appendicitis group [CAP] and 187 cases of uncomplicated acute appendicitis group [UAP]) were collected. Pathological reports and surgical results were used as the gold standard. The ethics committee of the institution approved the study, and informed consent was obtained from all patients. Data regarding the patient's sex and the results of blood routine, biochemical, and high-sensitivity C-reactive protein tests were mainly collected. Blood routine included 22 indicators such as white blood cell, neutrophil percentage, and lymphocyte percentage. Biochemical tests included urea, creatinine, potassium and other eight indicators. The specific normal value range of each index is shown in Table 1. The patients



A. Box diagram of UAP



B. Box diagram of CAP

FIGURE 1. Box diagram(A and B).

were divided into two groups, namely CAP and UAP. The classification was based on whether the patients had obvious complications such as gangrene, perforation, and peritonitis. The patients with obvious complications were classified as CAP, while those with other types of complications were classified as UAP. Figure 1 shows the box diagram of each group.

SPSS 16.0 was used for all statistical analyses. Student’s t-test was used to analyze measurement data, and Fisher’s exact test was used to analyze classification variables. A value of  $p \leq 0.05$  was considered statistically significant. The detailed statistical analysis results are shown in Table 2. Table 2 shows that muscle tension, rebound tenderness, white blood cells, neutrophils, lymphocytes, basophils, monocytes, platelets, and high-sensitivity C-reactive protein showed significant differences between the two groups.

**B. OVERALL MODEL**

**1) DATA DIMENSION REDUCTION BASED ON PCA**

Data dimensionality reduction can achieve the purpose of reducing unimportant features by processing high-dimensional data such as denoising. In this experiment, Principal Component Analysis (PCA) was selected to reduce the dimension of the data, and the flow chart of PCA is shown in Figure 2. PCA was first introduced by Karl Pearson in 1901 and later developed by Hotelling in 1933. PCA is an unsupervised learning method. The core principle of PCA is to apply orthogonal transformation to transform a set of variables that may be correlated into a set of linearly uncorrelated variables. The transformed variables are called principal components, where each principal component is a linear combination of the original variables, and each principal component is uncorrelated with each other. In this way, when studying more complex problems, only a few

TABLE 1. Normal value range of each index.

rade	G	Index abbreviation	Normal value range	
			Female	Male
1	F	Sex		
2	F	WBC	(4.0–	(4.0–
3	F	GRA%	$10.0) \times 10^9$	$10.0) \times 10^9$
4	F	LYM%	50–70%	70%
5	F	MONO%	20–40%	20–
6	F	EO%	3–8%	3–8%
7	F	BASO%	0.5–5%	0.5–
8	F	GRA	0–1%	0–1%
9	F	LYM	(1.8–	(1.8–
10	F	MONO	$6.3) \times 10^9$	$6.3) \times 10^9$
11	F	EO	(0.8–	(0.8–
12	F	BASO	$4) \times 10^9$	$4) \times 10^9$
13	F	RBC	(0.1–0.6	(0.1–
14	F	HCT	$) \times 10^9$	$0.6) \times 10^9$
15	F	MCV	(0.005–	(
16	F	MCH	$0.05) \times 10^9$	$0.005–0.05) \times 10^9$
17	F	MCHC	(0–	(0–
18	F	RDW	$0.1) \times 10^9$	$0.1) \times 10^9$
19	F	PLT	(3.5–	(4–
20	F	PCT	$5.0) \times 10^{12}$	$5.5) \times 10^{12}$
21	F	MPV	110–150g	120–
22	F	PDW	160g	160g
23	F	URE	37–43%	42–
24	F	Cr	49%	49%
25	F	K+	82–100	82–100
26	F	Na+	26–32	26–32
27	F	Cl-	(pg)	(pg)
28	F	Ca	320–360	320–
29	F	co2cp	360	360
30	F	GLU	11–15%	11–
31	F	hsCRP	(100–	(100–
32	F	hsCRP	$300) \times 10^9$	$300) \times 10^9$

principal components can be studied without losing a lot of information. Furthermore, it is not only easier to grasp the main contradiction and reveal the regularity between the internal variables of things but also simplify the problem and improve the analysis efficiency. PCA has been widely used

TABLE 2. Statistical analysis results of various indicators.

Index	Uncomplex acute appendicitis	Complex acute appendicitis	P-value
Gender	0.56	0.59	0.67
WBC	10.49±3.99	12.86±6.	0.00
GRA%	0.79±0.12	0.84±0.0	0.00
LYM%	0.15±0.10	0.10±0.0	0.00
MONO	0.05±0.03	0.05±0.0	0.96
EO%	0.01±0.01	0.00±0.0	0.05
BASO%	0.00±0.00	0.01±0.0	0.00
GRA	0.00±3.72	0.00±3.8	0.00
LYM	1.38±1.32	1.44±4.0	0.87
MONO	0.55±0.35	0.68±0.4	0.01
EO	0.04±0.05	0.03±0.0	0.79
BASO	0.02±0.02	0.02±0.0	0.69
RBC	4.53±0.55	4.60±0.6	0.42
HB	137.72±18.6	139.37±1	0.53
HCT	0.40±0.05	0.41±0.0	0.77
MCV	88.84±5.50	88.35±4.	0.48
MCH	30.39±1.88	30.29±1.	0.69
MCHC	340.47±10.4	342.86±1	0.11
RDW	13.01±1.11	12.85±1.	0.33
PLT	223.49±58.2	204.22±5	0.02
PCT	0.23±0.06	0.21±0.0	0.02
MPV	10.32±1.39	10.99±6.	0.20
PDW	12.10±1.95	12.19±1.	0.74
VRE	5.23±2.39	5.62±2.8	0.29
Cr	70.24±30.14	75.10±30	0.25
K+	3.8±0.46	3.96±0.7	0.17
Na+	136.94±3.10	136.82±3	0.77
Cl-	101.59±3.72	101.27±3	0.24
Ca	2.25±0.13	2.25±0.1	0.96
Co2cp	24.08±3.39	24.30±3.	0.61
GLU	6.22±3.05	6.54±2.1	0.40
hsCRP	68.32±80.31	113.97±9	0.00

in various fields and has achieved excellent results. However, it is worth noting that before using PCA, it is necessary to conduct a fitness test, that is, a KMO statistic test. Only when the result of the KMO statistic is, can the collected data be suitable for PCA.

2) HUNGER GAME SEARCH (HGS)

In recent years, the advantages of swarm intelligence optimization algorithms have become increasingly obvious, and their application fields have begun to expand year by year. Among them, swarm intelligence optimization algorithms

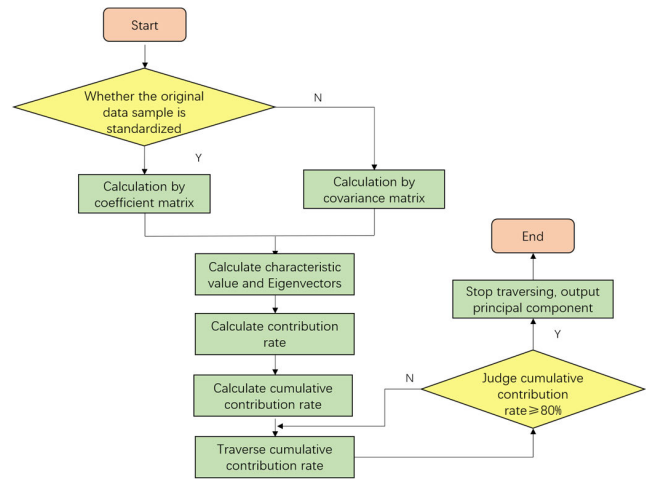


FIGURE 2. Flow chart of PCA.

such as ACO, GWA, and WOA have been widely used to solve various optimization problems. However, it has been noted that the performance of many swarm optimization algorithms is controversial for practical application, because of immature exploration and development skills, which has led to an imbalance between exploration and development when swarm optimization is applied to solve practical problems, further causing underfitting or local optimum. Therefore, to obtain better performance of swarm intelligence optimization algorithms, users begin to study the improvement of existing swarm optimization algorithms.

Hunger Game Search(HGS) is an original algorithm. Its core idea is based on the thinking logic that animals in nature make decisions, search dynamically, and take actions based on the feeling of “hunger,” in which the feeling of “hunger” is the key for animals to maintain their balance in nature. From the perspective of a mathematical theory, hunger search means to apply the adaptive weight design method to construct the steps of decision-making, search and action of animals in nature based on the sense of “hunger”. Different “hunger” weights represent different effects of different hunger on animal decision-making, search, and action. Figure 3 represents the logic diagram of the starvation search algorithm. In the original paper, the performance of the hungry search algorithm has been explained, and it is verified that the hungry search algorithm can better solve constrained and unconstrained problems.

The mathematical model of HGS is as follows:

$$\vec{X}(t+1) = \begin{cases} \vec{X}(t) (1 + randn(1)), & r_1 < l \\ \vec{W}_1 \times \vec{X}_b + \vec{R} \times \vec{W}_2 \left| \vec{X}_b - \vec{X}(t) \right|, & r_1 > l, r_2 > E \\ \vec{W}_1 \times \vec{X}_b - \vec{R} \times \vec{W}_2 \left| \vec{X}_b - \vec{X}(t) \right|, & r_1 > l, r_2 < E \end{cases} \quad (2.1)$$

The upper limit and lower limit of the search will be set according to the actual problem. To control the search activity within the set range, the parameter  $\vec{R}$  is set, and the

calculation formula is as follows:

$$\vec{R} = (2 \times rand - 1) \times a \tag{2.2}$$

$$a = 2 \times \left(1 - \frac{t}{Max_{iter}}\right) \tag{2.3}$$

where rand is a random number between [0, 1], so the range of  $\vec{R}$  is  $[-a, 0]$ .

$r_1, r_2$  are random numbers between [0, 1], rand (1) is a random number that satisfies the standard normal distribution,  $t$  is the current iteration number of the overall algorithm.  $\vec{X}_b$  is the position of the best individual in the current iteration,  $\vec{X}(t)$  is each individual location. Set constant  $l$  for improving algorithm performance. To control the change of all positions, set parameters  $E$ , the calculation formula is as follows:

$$E = \text{sech}(|F(i) - BF|) \tag{2.4}$$

where  $i \in (1, 2, \dots, n)$ ,  $F(i)$  is the fitness value of each individual, BF is the best fitness in the current iteration and the best fitness in all iterations so far. sech is a hyperbolic function which is calculated as follows:

$$\text{sech}(x) = \frac{2}{e^x + e^{-x}} \tag{2.5}$$

HGS is constructed based on the principle of hung-driven behavior activity, so two parameters representing hunger are constructed, which are  $\vec{W}_1$  and  $\vec{W}_2$ ,  $\vec{W}_1$  specifically representing the weight of hunger. The expression of  $\vec{W}_1$  is as follows:

$$\vec{W}_1(t) = \begin{cases} \text{hungry}(i) \times \frac{N}{SHungry} \times r_4, & r_3 < l \\ 1, & r_3 > l \end{cases} \tag{2.6}$$

The expression of  $\vec{W}_2$  is as follows:

$$\vec{W}_2(t) = (1 - \exp(-|\text{hungry}(i) - SHungry|)) \times r_5 \times 2 \tag{2.7}$$

where hungry is the hunger level of each individual,  $N$  is the total number of all individuals, SHungry is the sum of the hunger levels of all individuals,  $r_3, r_4, r_5$  are random numbers between [0, 1]. The expression of hungry ( $i$ ) is as follows:

$$\text{hungry}(i) = \begin{cases} 0, & \text{AllFitness}(i) = BF \\ \text{hungry}(i) + H, & \text{else} \end{cases} \tag{2.8}$$

where ALLFitness ( $i$ ) save the fitness of each individual, the expression of  $H$  is as follows:

$$TH = \frac{F(i) - BF}{WF - BF} \times r_6 \times 2 \times (UB - LB) \tag{2.9}$$

$$H = \begin{cases} LH \times (1 + r), & TH < LH \\ TH, & \text{else} \end{cases} \tag{2.10}$$

where  $r_6$  is a random number between [0, 1], BF is the current optimal fitness, WF is the current worst fitness, UB and LB are the upper and lower limit of search respectively, LH is a fixed parameters the lower bound of  $H$ .

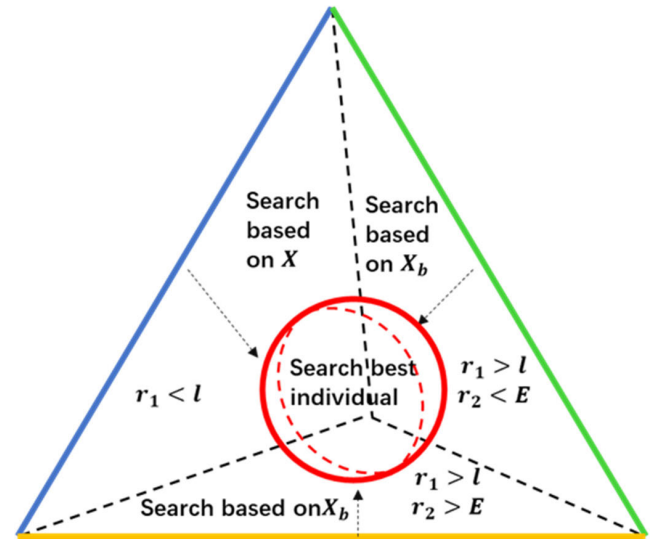


FIGURE 3. Logic diagram of HGS.

### 3) MERCER SUPPORT VECTOR MACHINE

Support Vector Machine (SVM) is a kind of generalized linear classifier for binary classification of data in a semi-supervised learning mode. Its decision boundary is the maximum margin hyperplane to solve for the learning sample, which can be transformed into a convex quadratic programming problem. SVM can be used to solve linear problems as well as nonlinear problems. Compared with logistic regression and neural network, support vector machine provides a clearer solution to nonlinear problems, and has high classification performance. Specifically, when solving linearly separable problems, an SVM constructs a line or a hyperplane in the original space for problem classification. The larger the distance between the training point and the line or hyperplane, the better the performance of the SVM. When solving the problem of linear non-separability, SVM introduces kernel function and uses nonlinear mapping to map samples from low-dimensional input space to high-dimensional space to make them linearly separable, so that the optimal classification hyperplane can be found in the feature space.

The sample matrix is denoted by  $D$ .  $D = \{x_i, y_i\}$  ( $i = 1, 2, \dots, s$ ), where  $x_i$  is a vector composed of all features of a sample,  $y_i$  is the output of the sample.  $n$  is the total number of data samples.

When mapping  $x_i$  to a high-dimensional space, the following functions are used:

$$y = w \times \varphi(x) + b \tag{2.11}$$

where  $w$  is the weight,  $b$  is the intercept,  $y$  and  $x$  are the feature vectors and corresponding outputs mentioned above respectively.

It can be known from Eq 11 that  $w$  and  $b$  are the main parameters that determine the mapping results, and the mapping results will affect the performance of SVM classification, so it is equivalent to the value of  $w$  and  $b$  will affect



the performance of SVM classification, so the optimization of SVM performance can be transformed into the optimization of parameters  $w$  and  $b$ .

$$\min \frac{1}{2} \|w\|^2 + C \sum_{i=1}^n (\xi_i + \xi_i^*) \quad (2.12)$$

However, the Eq2.12 should be used within the following constraints:

$$\begin{cases} w \times \varphi(x_i) - y_i + b \leq \varepsilon + \xi_i^* \\ y_i - w \times \varphi(x_i) - b \leq \varepsilon + \xi_i \\ \xi_i^* \geq 0, \xi_i \geq 0, i = 1, 2, \dots, s \end{cases} \quad (2.13)$$

In Eq2.12  $C$  is the penalty factor,  $\xi_i^*$  and  $\xi_i$  forms a relaxation interval  $[\xi_i, \xi_i^*]$  ( $\xi_i < \xi_i^*$ ), which can be understood as error range.  $\varepsilon$  is the maximum error.

The Eq2.12 is relatively complex, so in order to improve the efficiency of optimization, the Lagrange multiplier method is applied to transform it into a dual problem. After the transformation, the following formula is applied:

$$\begin{aligned} \min \frac{1}{2} \sum_{i,j=1}^n (a_i^* - a_i) (a_j^* - a_j) G(x_i, x_j) \\ + \varepsilon \sum_{i=1}^n (a_i^* + a_i) - \sum_{i=1}^n y_i (a_i^* - a_i) \end{aligned} \quad (2.14)$$

The constraints are as follows:

$$\begin{cases} \sum_{i=1}^N (a_i - a_i^*) = 0 \\ 0 \leq a_i, a_i^* \leq C, i = 1, 2, \dots, s \end{cases} \quad (2.15)$$

where  $a_i^*$  and  $a_i$  are the Lagrange coefficient,  $G(x_i, x_j)$  is the kernel function of SVM.

There are four kinds of kernel functions in traditional SVM, which are linear kernel function, polynomial kernel function, Gaussian kernel function and Sigmoid kernel function. In the process of using these kernel functions, it is found that SVM can not achieve high prediction accuracy, which leads to the limitations of SVM. In order to solve this phenomenon, Lin Peng constructed a new kernel function based on Mercer's theorem and created a new SVM, named Mercer Support Vector Machine(MSVM.) Experiments in the original paper showed that the performance of MSVM was better than traditional SVM. Therefore, this paper chooses MSVM as the basic prediction model, and the kernel function expression is as follows:

$$\begin{aligned} G(x_i, x_j) = w_1 M_{LMNN} M_{LMNN}^T + w_2 M_{NCA} M_{NCA}^T \\ + w_3 M_{MLKR} M_{MLKR}^T \end{aligned} \quad (2.16)$$

where  $M_{LMNN}$ ,  $M_{NCA}$ ,  $M_{MLKR}$  are the matrix transformed by metric functions LMNN, NCA and MLKR, metric functions LMNN, NCA and MLKR are defined according to the original paper,  $w_1, w_2, w_3$  are the weights of  $M_{LMNN}$ ,  $M_{NCA}$  and  $M_{MLKR}$ .

TABLE 3. Running time of each model on different input.

Model	Raw data as input	Data processed by PCA as input
HGS-MSVM	4.0595	3.9794
MSVM	1.3117	1.2499
RF	1.2857	1.2182
DA	0.3021	0.2557
KNN	0.3094	0.2361
LR	0.5963	0.5937

Finally, after integration, the following nonlinear functions can be obtained:

$$y = \sum_{i=1}^n (a_i - a_i^*) G(x_i, x_j) + b \quad (2.17)$$

It can be known from the above formula that the values of penalty factor  $C$  and weight factors  $w_1, w_2, w_3$  are uncertain, and different values of the two will have different effects on the operation process of MSVM, which will change the output results of MSVM. Among them, the penalty factor  $C$  affects the error interval of MSVM. If the value of  $C$  is small, the error interval of the whole MSVM will be small, which may lead to certain limitations of MSVM and can not be widely summarized. If  $C$  is large, MSVM will not have a high recognition ability, which will reduce the applicability of MSVM. Weight factors  $w_1, w_2$  and  $w_3$  affect the performance of the kernel function in MSVM. The performance of the kernel function determines the ability of MSVM to map data from low-dimensional space to high-dimensional space. Therefore, selecting appropriate penalty factor  $C$  and weight factors  $w_1, w_2, w_3$  are absolutely helpful to improve the performance of MSVM.

In this study, HGS is introduced that in order to find out the optimal parameters  $C, w_1, w_2, w_3$  to improve the performance of MSVM. HGS is a swarm intelligence algorithm that can find the optimal parameters automatically. The new model is hence named HGS-MSVM. To verify the performance of the proposed model, HGS-MSVM was applied to the actual prediction field to predict CAP.

#### 4) HGS-MSVM PROPOSED IN THIS PAPER

The performance of MSVM is mainly determined by penalty factor and weight factors. HGS can find the optimal solution by calculating the fitness of the search solution according to the fitness function. Therefore, the core principle of HGS-MSVM is to construct a fitness function according to MSVM, and then HGS can search for the optimal solution according to the fitness function, and assign the optimal solution to the parameters of MSVM. Algorithm 1 shows the pseudo-code of the proposed HGS.

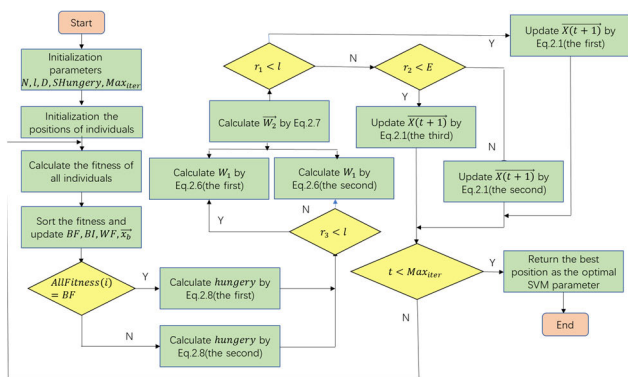
The HGS-MSVM flowchart is shown in Figure 4.

The fitness function constructed based on MSVM is as follows:

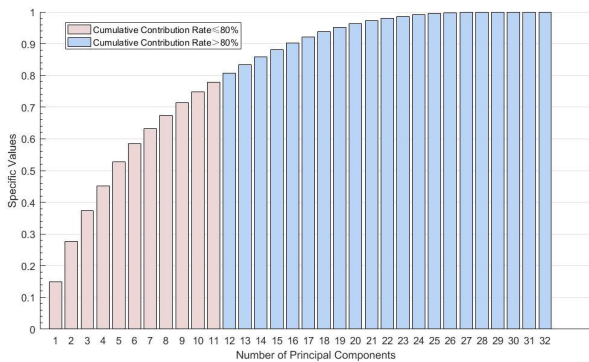
$$Fitness = \frac{\sum_{i=1}^G acc_i}{G} \quad (2.18)$$

**Algorithm 1** Pseudo-Code of HGS-MSVM

Initialize the parameters  $N, T, l, D, SHungry$   
 Tent map initialize the positions of Individuals  $X_i (i = 1, 2, \dots, N)$   
 While( $t \leq T$ )  
   Calculate the fitness of all Individuals  
   Update  $BF, WF, X_b, BI$   
   Calculate the Hungry by Eq.2.8  
   Calculate the  $\bar{W}_1$  by Eq.2.6  
   Calculate the  $\bar{W}_2$  by Eq.2.7  
   For each Individuals  
     Calculate  $E$  by Eq.2.4  
     Update  $R$  by Eq.2.2  
     Update positions by Eq.2.12  
 End for  
 $t = t + 1$   
 End While  
 Return the best positions to MSVM



**FIGURE 4.** HGS-SVM Flow Chart.

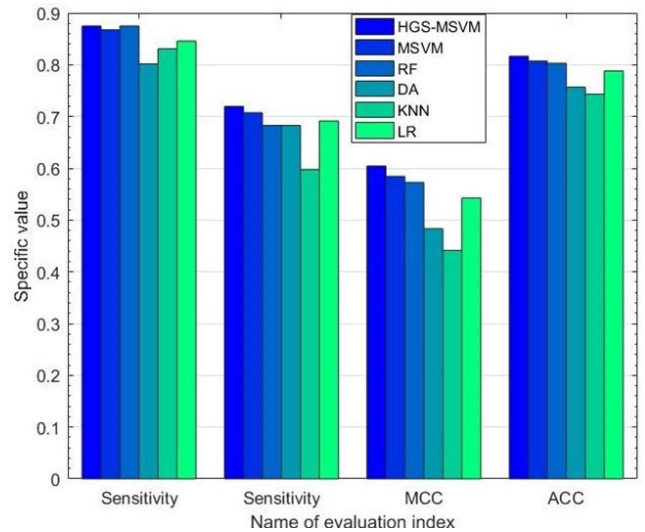


**FIGURE 5.** Results of PCA.

**III. EXPERIMENTAL SETUP AND RESULTS**

**A. EXPERIMENTAL ENVIRONMENT**

All the experiments were carried out in the laboratory, and the prediction system was implemented based on MATLAB. To verify the effectiveness of the prediction system, HGS-MSVM was developed in this experiment and compared with other five prediction systems, namely Random Forest (RF), K-Nearest Neighbor (KNN), MSVM, Logistic Regression (LR), and Discriminant Analysis (DA). RF was implemented using the RF toolbox, and HGS used the code on <https://aliasgharheidari.com/HGS.html>. The codes on HGS, MSVM, KNN, LR, DA, and PCA were implemented by



**FIGURE 6.** Comparison of ACC, MCC, sensitivity, and specificity of each model.

MATLAB. The parameter was set according to the original text or the default settings were retained. The maximum number of iterations was set to 50, and the search range of MSVM parameters was set to  $[2^{-5}, 2^5]$ . The experiment was performed 10 times, and the average value was taken as the final result. To verify the performance of the prediction model in this study, four common performance indicators were selected as evaluation indicators, namely ACC, MCC, specificity, and sensitivity.

**B. EXPERIMENTAL RESULT**

The result of the KMO statistic calculated before the application of PCA was, indicating that the data collected were applicable to PCA. The results of PCA are shown in Figure 5. PCA usually considers the principal components whose cumulative contribution rate reaches 80%, and it can be seen from Figure 5 that the cumulative contribution rate of the first 11 principal components can reach 80%. Therefore, in this experiment, the first 11 principal components are used to replace the 32 features in the original data as the new feature input, and the results show that the data achieves the effect of dimensionality reduction. Table 3 presents the comparison of the running times of the models HGS-MSVM, KNN, MSVM, RF, LR, and DA upon selecting different data as the input. As shown in Table 3, taking the data after PCA dimensionality reduction as the input reduces the running time of the model compared to taking the original data as the input.

In this research model, MSVM was used as the main prediction model, and HGS was used as the optimization algorithm to optimize the parameters of SVM. Therefore, the parameters of MSVM could be automatically determined by HGS, and MSVM could also achieve the best prediction performance. To verify the performance of the prediction model in this study, five other prediction models, namely MSVM, RF, DA, KNN, and LR were selected to compare with four evaluation indicators that were sensitivity, specificity, MCC,

and ACC. The experimental results are shown in Figure 6. For the sensitivity evaluation index, HGS-MSVM had the best performance (87.50%). RF was the same as HGS-MSVM, followed by MSVM (86.76%). HGS-MSVM was 0.75% points higher than MSVM. KNN and LR showed a significant decline, which were 83.09% and 84.56%, respectively. DA ranked last, and the decline was also relatively large, which was 7.35% points lower than HGS-MSVM. This indicates that compared with the other five models, only RF had the same sensitivity as HGS-MSVM, and the sensitivity of other models was lower than HGS-MSVM, especially DA. Even for the specificity evaluation index, HGS-MSVM achieved the best performance that reached 71.95%, which was 1.22% points higher than the second place MSVM. The specificity differences of RF, DA, and LR were small, indicating that the three models had similar intentional performance, while the specificity of KNN only reached 59.76%. Compared with HGS-MSVM, the difference was 12.19% points. This indicated that the specificity of the other five models was lower than that of HGS-MSVM, especially KNN, whose specificity was much lower than that of HGS-MSVM. For the MCC evaluation index, HGS-MSVM outperformed the other five models that reached 60.43%, and RF and MSVM ranked second and third that reached 57.27% and 58.43%, respectively, with a difference of 3.16% points and 2% points compared with HGS-MSVM, followed by LR. The last two were KNN and DA, which only reached 44.13% and 48.33%, with poor MCC. This showed that compared with the other five models, the difference between HGS-MSVM and MSVM and between RF and LR was relatively small, and the performance of DA and KNN was much lower than that of HGS-MSVM. For the ACC evaluation index, HGS-MSVM had the best performance (81.65), which was 0.92% points higher than MSVM, 1.37% points higher than RF, and 2.85% points higher than LR; DA and KNN had the worst accuracy at 75.69% and 74.31%, respectively. This showed that HGS-MSVM had the highest ACC. The sensitivity evaluation index evaluates the performance of the prediction model to correctly predict the positive data. The specificity evaluation index evaluates how well the prediction model predicted the negative data correctly. MCC evaluates the correlation between the predicted results and the real results of the prediction model. The higher the correlation, the better the model performance, and the worse the model performance. ACC evaluates how well the prediction model correctly predicts the overall data. The above experimental results could fully verify that the HGS-MSVM model proposed in this study had the best performance in the four indicators, which, in turn, showed that HGS-MSVM was the most comprehensive. Although Table 3 shows that HGS-MSVM runs the longest, this seems insignificant compared to its superior performance in other aspects.

#### IV. CONCLUSION AND FUTURE WORK

In this paper, the PCA method was used to reduce the data dimension, and the experimental results showed that the

application of PCA could indeed achieve the purpose of data dimensionality reduction. Furthermore, by constructing the fitness function, the hunger search algorithm was used to adaptively identify the optimal parameters of MSVM, to improve the prediction performance of the MSVM; this newly proposed model was named the HGS-MSVM. Finally, the data after dimensionality reduction was used as the input of the model to predict complex acute appendicitis. At the same time, the model proposed in this study was compared with other five widely used traditional prediction models for four evaluation indices. The accuracy rate was as high as 81.65%, which could make an accurate prediction for CAP.

In this study, the basic demographic information of patients and the results of blood routine tests, biochemical tests, and high-sensitivity C-reactive protein test were used as the input, and CT and other imaging predictors were discarded, which not only reduced the cost of examination for patients but also reduced the time and complexity of the examination. It is well known that the examination time and complexity of CT and other imaging modalities are much higher than those of routine blood tests. Especially in some economically backward areas, many patients find it difficult to bear the high cost of imaging examinations. In certain remote areas, imaging is not available at all, which makes having such a prediction system crucial. At the same time, this study also rejected all subjective predictors such as the presence of abdominal tenderness and abdominal rebound pain and other widely used scoring systems, along with the predictors of other prediction systems. All predictors in this study were either accurately measured by medical instruments or objective facts. This makes the prediction system proposed in this study have absolute objectivity, and, to our knowledge, there is no phenomenon that affects the prediction results because of the deviation of subjective judgment.

This study has some limitations. First, the samples in this study were all from one hospital, so the sample size was not large enough. Second, there was no combination of imaging predictors. Although there are many drawbacks in the use of imaging predictors, and they may not be applicable in some remote areas, imaging still has high value in the prediction of CAP, and the combination of imaging predictors can likely enhance the application performance of the model in developed areas. Finally, some studies have shown that heart rate can be used as a predictor of CAP; thus, in future studies, heart rate should be tried as a predictor to input into the model for prediction and verify its effectiveness.

In future work, first, data from more hospitals should be collected to optimize the performance of the model. The imaging detection results should be included in the study to enhance the diagnostic effect of the model on individual cases and improve the performance of the clinical application of the model. Finally, we hope to conduct further research on the applicability of HGS-SVM in other diseases and other fields such as the identification of crops in agriculture and prediction of stock prices in the financial market.



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