Serum Tumor Markers Detection Based on Data Mining Technology for Assisted Diagnosis and Therapeutic Evaluation of Lung Cancer

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Abstract
In recent years, the diagnosis and treatment of lung cancer has been rapidly improved, but there is no specific clinical symptoms in the early stage of lung cancer. Therefore, to explore and develop effective methods of early detection and early diagnosis is of great significance to improve the treatment and prognosis of lung cancer patients, as well as the health and quality of life of patients. The clinical data of 99 patients with lung cancer admitted to the Anhui provincial Hospital were retrospectively analyzed. Patients with advanced lung cancer were diagnosed for the first time. Serum tumor markers and clinical features were recorded before initial treatment. To analyze the relationship between changes in serum tumor markers and short-term therapeutic effects. The level of serum tumor markers in lung cancer is significantly higher than that in patients with benign diseases. There were no significant differences in CEA levels between patients with different types of lung cancer. This indicates that the combined detection of serum tumor markers can improve the accuracy and sensitivity, and is of great significance for the diagnosis and treatment of lung cancer.

Key words: Data mining; Serum Tumor Markers; Assisted Diagnosis of Lung Cancer.

1. Introduction
Lung cancer, one of the most common malignant tumors in the world, is the leading cause of cancer-related death in the world. At present, the incidence of lung cancer in most countries is still increasing year by year, occupying the first place in male common malignant tumors, is a serious threat to people's health [1]. In China,
In recent decades, lung cancer has become the most common malignant tumor and the leading cause of death among all cancers [1]. According to statistics from the World Health Organization, lung cancer ranks first among the most common malignant tumors and herps in cities, while 84% of newly diagnosed lung cancer patients are diagnosed with non-small cell lung cancer every year. According to the data published by the World Health Organization, lung cancer is the second leading cause of death after cardiovascular and cerebrovascular diseases, ranking first among all kinds of malignant tumors. Lung cancer has a high mortality rate and poor prognosis. The 5-year survival rate is only 9% and the early stage is mostly asymptomatic. The patients are in advanced stage and lose the opportunity of operation and the best treatment [2]. Therefore, early diagnosis and early treatment are important measures to improve the cure rate and reduce the mortality rate. Although lung cancer responds very well to the effects of chemotherapy and radiotherapy, the clinical exploration of different treatment modes in the past decade or two has not been able to find a treatment that significantly improves the prognosis of lung cancer or clinical cure [3]. Almost all patients can achieve remission after active first-line treatment, but after a certain period of treatment, the tumor recurs, local recurrence or distant tissue and organ metastasis. Therefore, the effective diagnosis of lung cancer to improve the treatment of lung cancer and improve the quality of life of patients has become the focus of current research [4].

At present, disease stage is still the most important prognostic indicator for small cell lung cancer. The key to the prevention and treatment of lung cancer is still the early diagnosis and the combined application of various treatment measures [5, 6]. At present, the main treatment method is comprehensive treatment. It has been controversial about the feasibility of limited-stage small cell lung cancer. There is no unified understanding of the value of surgical treatment. At the same time, there is no new means for the diagnosis of early small cell lung cancer. There are few studies on serum tumor markers [7]. In 2015, researchers proposed a study of the relationship between Glasgow's prognosis score and serum tumor markers in patients with advanced non-small cell lung cancer [8]. Later in 2016, research on the clinical evaluation and therapeutic monitoring value of serum tumor markers in lung cancer patients was proposed [9]. Tumor markers are a class of chemical substances that are produced and secreted by tumor cells and released into blood, body fluids, and tissues to reflect tumorogenesis and development during tumorigenesis and development, or that host cells are overexcited by tumor cell signal stimulation. The normal cellular components produced. Detection of serum tumor markers in patients with lung cancer can assist in early diagnosis, judgment of pathological type and efficacy, monitoring of tumor recurrence, metastasis, and prognosis [10]. Some patients have had brain metastases when they diagnosed the primary tumor, and some patients have neurological symptoms as the first symptom. Brain metastases can be single or multiple. The metastatic site of tumor cells is often proportional to local blood flow [11].

Normal tumor markers in patients with lung cancer usually occur in the early stage of disease or after effective control of disease, and the increase of tumor markers often indicates the progress of disease. However, according to clinical observation, some patients’ serum tumor markers are always normal in the course of disease occurrence and development [12]. Whether the patients with normal serum tumor markers (hereinafter referred to as normal serum tumor markers) have different clinical characteristics and prognosis from those with abnormal serum tumor markers, literature retrieval lacks systematic analysis results. Through retrospective investigation and analysis, this paper evaluates the value of surgical treatment in the comprehensive treatment of early lung cancer, understands the characteristics of serum tumor markers of lung cancer, and evaluates the value of neuroenolase, carcinoembryonic antigen and cytokeratin 19 fragment in the auxiliary diagnosis of lung cancer [13, 14]. And combined detection to achieve the auxiliary diagnosis of lung cancer. On this basis, the tumor markers detected by protein chips are extracted using traditional statistical classification techniques and data mining techniques to extract effective features for lung cancer diagnosis [15]. Two models of decision tree and discriminant analysis were established to explore the value of each model combined with tumor markers in the diagnosis of lung cancer, in order to find the optimal model to improve the accuracy and clinical applicability of tumor marker-assisted lung cancer diagnosis [16]. At the same time, the clinical and survival prognosis of patients with normal non-small cell lung cancer and small cell lung cancer serum tumor markers were explored to deepen the understanding of patients with normal lung cancer with serum tumor markers [17, 18].

### 2. Methodology

Patients with lung cancer were followed up by telephone enquiry and medical records. The follow-up content was mainly the survival of lung cancer patients and the time of death due to lung cancer [19]. The defined survival time is the time from the diagnosis of lung cancer to the time of death due to lung cancer or the deadline for follow-up. The time is calculated in units of “months”. The initial event was all pathologically confirmed lung cancer patients, and the termination event was the truncated value of all patients who died of lung cancer, who survived the follow-up or follow-up deadline, or died of other events other than lung cancer [20]. The patients were selected from the lung cancer patients who were newly diagnosed in the Anhui provincial hospital. 99 patients were enrolled in the study. 70 patients were lost to follow-up during the follow-
up. The follow-up data of 29 patients were basically perfect. All patients were confirmed to be small cell lung cancer by surgical resection of pathology or lung biopsy biopsy. There are complete head and chest enhancement CT, neck and abdomen B ultrasound, whole body bone scan or whole body PET-CT and other imaging data. The clinical diagnosis of all cancer patients was confirmed by pathology or cytology. Patients with benign pulmonary diseases were also confirmed not to have lung or other organ tumors. Tumor marker protein chip detection was approved by patients and the results were recorded in detail.

The gender of lung cancer and benign lung cancer patients and the general characteristics of the subjects in this study are shown in Table 1 and Figure 1 below. Gender and the general characteristics of the subjects have statistical significance.

| Table 1. General characteristics of subjects in lung cancer group and control group |
|-----------------------------------------------|--------------|--------------|
| Gender variable | Standard deviation | Variance |
| Male | 0.68 | 0.65 |
| Female | 0.72 | .81 |

![Figure 1. General characteristics of subjects in lung cancer group and control group](image1)

The P value and the positive rate of the two serum tumor markers in the two groups are shown in Table 2 and Figure 2. According to the reference value provided by the kit as a positive criterion, the cross-four-square chi-square test table is used and then the positive detection rate of the three indicators can be obtained. The difference in expression rates between the two groups was statistically significant.

| Table 2. Positive rate of detection of two tumor markers in two groups of patients |
|-----------------------------------------------|----------------|------------|
| Group | P value | Positive rate (%) |
| Lung cancer group | 36.45 | 45.66 |
| Control group | 29.84 | 54.71 |

![Figure 2. Positive rate of detection of two tumor markers in two groups of patients](image2)
Of the 25 patients in the surgical intervention group, 10 patients were confirmed as SCLC by histological examination and histopathological biopsy before operation. The remaining 15 patients did not get a definite preoperative pathological diagnosis or the type of preoperative pathological diagnosis was not clear. Finally, the pathological diagnosis was confirmed by surgery. In the non-operative group, 74 patients were diagnosed by fibrobronchoscope biopsy or exfoliated cells. The remaining 29 patients were diagnosed as SCLC by puncture of pulmonary masses. For the diagnosis of brain metastasis, the patient had one or more of the symptoms of intramedullary hypertension, dyskinesia, sensory impairment, focal weakness, language loss, visual impairment, epilepsy, cognitive change and attention loss. Head anesthesia magnetic resonance imaging or computed tomography imaging suggests brain metastases, some asymptomatic patients combined or need to be confirmed by a tumor specialist above the name. It has played a certain role in the rescue and treatment of other acute and critical illnesses. The treatment of patients with chronic renal failure complicated with other organ failure, severe trauma, shock, acute necrotizing pancreatitis and electrolyte imbalance is closely observed. It can be seen from the test data that the clearance of serum urea nitrogen and creatinine can be better by CRRT treatment. The analysis results are shown in Table 3 and Figure 3. From the results, the predicted values of 54 predicted samples are consistent with the actual values, and the 35 predicted samples do not match the actual ones. Of the 22 mispredicted samples, the actual value was 3 but there were 10 samples predicted.

Table 3. Decision tree model prediction results

<table>
<thead>
<tr>
<th>Group</th>
<th>Predicted value</th>
<th>Actual value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lung cancer group</td>
<td>54</td>
<td>22</td>
</tr>
<tr>
<td>Control group</td>
<td>35</td>
<td>10</td>
</tr>
</tbody>
</table>

Figure 3. Decision tree model prediction results

The comparison of decision tree and data mining model according to the evaluation index of screening experiment can be seen in Table 4 and Figure 4. It can be seen that each index of decision tree model is the highest. Data mining model is in the middle. The predicted values of regression sensitivity and accuracy are low.

Table 4. Comparisons of classification results of forecasting sets by different models

<table>
<thead>
<tr>
<th>Evaluating indicator</th>
<th>Sensitivity (%)</th>
<th>Accuracy (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Decision tree</td>
<td>90.36</td>
<td>98.85</td>
</tr>
<tr>
<td>Data Mining Model</td>
<td>94.67</td>
<td>95.22</td>
</tr>
</tbody>
</table>

Statistical analysis was carried out with statistical software, and the counting data were tested. The similarities and differences in age, sex, family history, smoking history, clinical stage, primary lesion location and metastasis location between normal group and elevated group were analyzed. Methods Survival curves were drawn to estimate the survival rates of patients with normal serum tumor markers and those with ascending pupils. The differences of survival rates between normal and ascending pupils were examined and analyzed. Through thoracic and abdominal CT, brain CT, isotope whole body bone imaging and hematological examination including tumor markers, 99 patients with advanced non-small cell lung cancer were recorded before treatment. Their general physical condition, level of tumor markers, age, sex, histological type and smoking history were observed and analyzed. Treatment with CRRT can effectively regulate some inflammatory factors in the body, while maintaining the stability of the body environment, reducing the pain caused by the inflammatory reaction, thereby facilitating the recovery of the disease. With the updating and
development of medical technology and equipment, the application and prognosis of CRRT treatment have received more and more clinical attention. Only medical personnel with proficiency in professional knowledge can ensure the smooth progress and curative effect of patients, and alleviate the pain for patients. The data sets actually collected by the clinic are often noisy data, incomplete data, and inconsistent data. If processed directly, sometimes it does not meet the model requirements, so preprocessing is often required to improve the quality of the original data.

![Figure 4. Comparisons of classification results of forecasting sets by different models](image)

Comparing the results of serum tumor markers in lung cancer patients and healthy volunteers, the patients in the lung cancer group were significantly higher than those in healthy volunteers, and there were statistical differences. The sensitivity of the three serum tumor markers combined with diagnosis of lung cancer was 98.36% and the specificity was 99.68%, which was higher than the results of individual indicators. In particular, the sensitivity is greatly improved, and there is a statistical difference from the comparison of the individual detection results. See Table 5.

**Table 5. Comparison of the results of three serum tumor markers in each group**

<table>
<thead>
<tr>
<th>Diagnostic project</th>
<th>Lung cancer group</th>
<th>Healthy control group</th>
</tr>
</thead>
<tbody>
<tr>
<td>CEA</td>
<td>35.69</td>
<td>98.36</td>
</tr>
<tr>
<td>CA125</td>
<td>56.14</td>
<td>99.68</td>
</tr>
<tr>
<td>CA19-9</td>
<td>40.18</td>
<td>56.63</td>
</tr>
</tbody>
</table>

The relative expression level of genes in non-small cell lung cancer was systematically evaluated by querying the database. We compared the expression of PTGR-1 in cancer with that in normal tissues and different cancer subtypes. Differential expression analysis of CEA in non-small cell lung cancer tissues and normal tissues showed that the results of the four data sets showed significant differences in gene expression values in the database. As shown in Figure 5 below.

![Figure 5. Through data mining of tumor database, it was found that CEA was over expressed in non-small cell lung cancer](image)
The positive rate of serum NSE in early SCLC patients was significantly higher than that in early lung squamous cell carcinoma and adenocarcinoma patients, with statistical difference. The serum NSE level of early SCLC patients was significantly higher than that of early squamous cell lung cancer and adenocarcinoma patients. The positive rate of serum CYFRA21-1 in early SCLC was lower than that in early lung squamous cell carcinoma. The results are shown in Table 6 below.

**Table 6.** Comparison of three tumor marker concentrations in early SCLC and early lung squamous cell carcinoma and early lung adenocarcinoma

<table>
<thead>
<tr>
<th>Group</th>
<th>CEA</th>
<th>CYFRA21-1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Early SCLC</td>
<td>1.78</td>
<td>3.34</td>
</tr>
<tr>
<td>Early squamous cell lung cancer</td>
<td>8.96</td>
<td>4.17</td>
</tr>
<tr>
<td>Early adenocarcinoma of lung</td>
<td>3.14</td>
<td>5.69</td>
</tr>
</tbody>
</table>

The data we synthesized included gene expression data from micro RNA networks in non-small cell lung cancer and adenocarcinoma. We need to first collect data, reconstruct the specific network of NSCLC adenocarcinoma, and then identify possible micro RNA biomarkers based on the network structure and biological function. The flow of the whole process can be seen in Figure 6.

**Figure 6.** Data collection process, comprehensive analysis and identification of micro RNA biomarkers and verification of micro RNA biomarkers

The time of occurrence and development of brain lesions was observed and the changes of serum were recorded. Therapeutic efficacy evaluation criteria were based on short-term efficacy evaluation criteria of solid tumors. The effective treatment group was defined as imaging showing disappearance or shrinkage of brain metastases, no new lesions, disappearance of neurological symptoms or significant relief after systematic treatment. The progressive group was defined as imaging showing increase of brain metastases for at least two weeks. New lesions and neurological symptoms persisted or aggravated. The stable group was defined as having no significant changes in brain imaging and neurological symptoms. Sensitivity, specificity, positive predictive value, negative predictive value, and model prediction accuracy of the evaluation index of the screening test. The curve is used as an evaluation index for the model. According to whether there was surgical involvement in the comprehensive treatment, all the patients enrolled were labeled as 38 patients in the S group and 61 patients in the W group. Group A (surgery combined with chemotherapy or and radiotherapy) and group B (chemotherapy combined with radiotherapy). Patients in group A and group B received systemic intravenous chemotherapy. The number of chemotherapy cycles was 8-12, and the median chemotherapy cycle was 3 cycles. The systemic chemotherapy regimen selected standard platinum-containing and/or anthracycline-containing regimens.

3. Result Analysis and Discussion

Currently, small cell lung cancer-associated tumor markers are mainly neuron-specific dilute alcohoholase and gastrin-releasing peptide precursors. NSE is a tumor marker present in neuroendocrine cells. It has a better
diagnostic effect on patients with extensive disease, and it also has a suggestive effect on its treatment and prognosis. In patients who underwent chemotherapy, patients with elevated NSE levels had significantly lower CR rates than normal patients and showed a poor prognosis. In this study, we found that brain metastases differed between different histological types. Of the 99 adenocarcinoma patients, 55 had brain metastases, and 44 had squamous cell carcinoma and other types of non-small cell lung cancer. Of these, only 16 cases had brain metastases and there was a difference between the two. At the same time, the study found a significant association between high serum CEA levels and adenocarcinoma in comparison with other tissue types of lung cancer. The long-term survival rate of the operation-involved group was significantly better than that of the non-operation-involved group. The 1-year, 2-year and 3-year progression-free survival rates in the early SCLC group were 75.36%, 64.18% and 50.03% respectively, while those in the non-surgical group were 74.22%, 29.64% and 21.34% respectively. Compared with the PFS of the two groups, the PFS of the patients in the surgical intervention group was significantly higher than that in the non-surgical intervention group. The above results show that surgical treatment plays a positive role in the prognosis of patients with early stage small cell lung cancer, and significantly prolongs the long-term survival of patients.

The serum CEA positive rate and concentration of early SCLC were lower than those of early lung adenocarcinoma, with statistical difference. The sensitivity of neuroenolase to early SCLC detection was significantly higher than that of cytokerin 19 fragment and carinoembryonic antigen (CEA). See Table 7 and Figure 7 below.

Table 7. Comparison of positive rates of three tumor markers in early SCLC, squamous cell carcinoma and adenocarcinoma of lung

<table>
<thead>
<tr>
<th>Group</th>
<th>CEA positive rate(%)</th>
<th>NSE positive rate(%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Early SCLC</td>
<td>14.3</td>
<td>46.97</td>
</tr>
<tr>
<td>Early squamous cell lung cancer</td>
<td>40.14</td>
<td>13.65</td>
</tr>
<tr>
<td>Early adenocarcinoma of lung</td>
<td>55.36</td>
<td>33.45</td>
</tr>
</tbody>
</table>

There were significant differences in serum concentration and positive rate of NSE between early SCLC and late SCLC. See Table 8 and Figure 8.

Table 8. Comparison of serum tumor marker concentration and NSE positive rate in early and late SCLC

<table>
<thead>
<tr>
<th>Group</th>
<th>NSE positive rate(%)</th>
<th>Serum concentration</th>
</tr>
</thead>
<tbody>
<tr>
<td>Early SCLC</td>
<td>40.36</td>
<td>1.36</td>
</tr>
<tr>
<td>Late SCLC</td>
<td>76.35</td>
<td>2.17</td>
</tr>
</tbody>
</table>
Figure 8. Comparison of serum tumor marker concentration and NSE positive rate in early and late SCLC

In practical application, the choice of step size $q$ is very important. If the step size $q$ is large, the convergence rate will be fast, but if the step size $q$ is too large, it may cause instability. The simplest way to solve this contradiction is to add a momentum term, that is, to modify the weight formula as follows:

$$ M(q) = R_0 - \eta \frac{\Delta R q}{Q_0} $$

(1)

In general, the fitness function is transformed from the objective function. A certain mapping transformation to the objective function range is called scale transformation of fitness. There are three commonly used scale transformations. Linear transformation method. Assuming that the original fitness function is $M$ and the transformed fitness function is $u$, the linear transformation can be expressed as:

$$ M(t) = u(t) / i(t) = R_0 \sqrt{1 - 2\eta R \Phi(t) / Q_0 R_0^2} $$

(2)

Power function transformation method. The transformation formula is:

$$ M(t) = u / i = R_0 \sqrt{1 - 2\eta R U t / Q_0 R_0^2} $$

(3)

The power exponent $t$ is related to the optimal relationship. Exponential transformation method. The transformation formula is as follows:

$$ M(t) = R_0 (1 + \frac{2\Delta R U}{Q_0 R_0^2} t_0^{0.5}) $$

(4)

The fitness allocation population based on ranking is ranked according to the target value. The fitness depends only on the individual's order in the population, not the actual target value. Define the selection probability formula for linear ranking:

$$ M(t_0) = R_0 (1 + \frac{2\Delta R U}{Q_0 R_0^2} t_0^{0.5}) $$

(5)

Proportional fitness allocation, using the probability of proportion to individual fitness to determine its possibility of leaving or leaving. The formula is expressed as:

$$ \Delta y = M(t_0 + \Delta t) - M(t_0) $$

(6)

The decision tree and data mining model are used to analyze the discriminant results of the prediction set, and the diagnostic value of the model for lung cancer is compared. The results show that the decision tree has higher prediction accuracy and better accuracy. The data mining model is better than the diagnostic value of the decision tree. As shown in Figure 9.
Clinically, a tumor marker can appear or increase in a variety of tumors. At the same time, the occurrence and development of a certain tumor can also have the appearance or elevation of multiple tumor markers, but there is no specific marker. How to review these tumor markers has become a key issue to be solved when the clinical diagnosis needs are well met. At present, several markers with better sensitivity and specificity are combined clinically or one or more are established. Classification models to improve their clinical diagnostic value for tumors. Lung cancer is the most common type of malignant tumor in the world today, and its number of cases and deaths rank first among all types of tumors. In recent years, the number of lung cancer patients in China is gradually increasing every year, and now it has become the highest proportion of malignant tumors. Male malignant tumors accounted for the first and female malignant tumors accounted for the second. SCLC is a special type of lung cancer pathology. The number of patients with SCLC increases with the increase of lung cancer incidence. High serum levels were correlated with primary lung adenocarcinoma. Among the 55 patients with brain metastases, most of them were adenocarcinomas. Related analysis suggests that in locally advanced non-small cell lung cancer patients, adenocarcinoma often indicates a higher risk of brain metastasis, and for peripherally advanced adenocarcinoma, special analysis and observation are needed to confirm the clinical factors predicting brain metastasis.

At temperature $x$, a new state $y$ is generated from the current state. The energy of the two states is $P$ and $T$, respectively. The transition probability corresponding to the acceptance criterion is:

$$D_k(x,y) = \begin{cases} 
255 & |P_k(x,y) - B_k(x,y)| > T_h \\
0 & \text{else} \end{cases}$$

To improve the competitiveness between individuals. After improvement, the fitness of the $x$th individual is:

$$I_k(x,y) = |P_k(x,y) - P_{k-1}(x,y)|$$

In order to enable the data mining algorithm to perform a local search on a certain key area, a simulated annealing operator is applied to the group after the mutation, that is, the retention probability of $D$ is determined as:

$$D_k(x,y) = |f_{k-1}(x,y) - f_k(x,y)|$$

Because the network with too many nodes tends to memorize all the training data, it will reduce the generalization ability of the network. Therefore, we should follow the principle of achieving the best generalization approximation ability with as few nodes as possible. This paper uses the following empirical formulas to determine a rough number.
\[ B_k(x, y) = \left| f_k(x, y) - B(x, y) \right| \]  

(10)

In the later stage of operation, it should be prevented that the genetic algorithm can not search the key areas because of the non-competition of evolution process. Let the output error of the network be:

\[ T_k(x, y) = D_k(x, y) + B_k(x, y) \]  

(11)

At the same time, the fitness function is defined as:

\[ K(X, Y) = K(U_x, U_y) \]  

(12)

Here, the choice of inheritance and elite selection strategies are introduced. The classic choice inheritance is determined by the following formula:

\[ r_i(i) = P(q_i = s_i | y) \]  

(13)

The worst members of fitness function are eliminated. This competition mechanism can solve this problem better. The process of selecting inheritance is as follows.

\[ R = \sum_{i=1}^{N} r_i c_i \]  

(14)

The diagnostic model results show that the area under the curve of decision tree discriminant analysis is less than 0.5, and the accuracy is low. The prediction accuracy of data mining model and decision tree is greater than 0.8, and the accuracy is medium, which is better than the diagnostic value of discriminant analysis. The result is shown in Figure 10 below.

**Figure 10.** Curves of two models for classification of prediction sets

CEA is a class of non-specific tumor markers originally identified as a class of acidic glycoproteins with embryonic antigenic determinants secreted by gastrointestinal cells. The increase is mainly seen in digestive system tumors, and later found in breast cancer, liver cancer, lung cancer, etc. Patient serum CEA can also be elevated. Compared with non-small cell lung cancer, SCLC cells have special biological characteristics. SCLC has the characteristics of poor cell differentiation, rapid growth of multiple times, short reproductive cycle, early regional lymph node metastasis, and rapid spread of distant organs. Even though the molecular molecular basis of SCLC has not been overcome, molecular targeted therapy has been increasingly applied to the clinic, but further breakthroughs in SCLC treatment are still very difficult, mainly due to unclear pathogenesis and targeted therapy. Failure to make a breakthrough. The expression in normal tissues is very little, which is related to the immune response of tumor cells or surrounding host. If the immune suppression is more obvious, the higher the content of serum is. It has great clinical significance for gastrointestinal malignant tumors such as pancreatic cancer and colorectal cancer. Basically, all patients can achieve remission after active first-line treatment, but after a certain period of treatment, the tumor resurgence, local recurrence or distant tissue and organ metastasis occur. At present, the key to the prevention and treatment of SCLC still lies in the early diagnosis and the combined and orderly application of various therapeutic measures.

In addition, bone metastasis and brain metastasis are the most common distant metastasis sites in lung cancer patients. The results of this study show that bone metastasis and brain metastasis in non-small cell lung cancer patients are significantly correlated with the elevation of serum tumor markers. Prospective randomized
trials have shown that although patients cannot benefit from survival, prophylactic brain irradiation can significantly reduce brain metastasis in locally advanced non-small cell lung cancer patients receiving chemoradiotherapy. Therefore, it is very necessary to analyze the possibility of brain metastasis and give appropriate treatment in time by taking various clinical characteristics of patients as part of the reference. SCLC is a systemic disease. There may be distant metastasis objectively regardless of the presence of distant metastasis or examination of metastases. The efficacy of chemotherapy for small cell lung cancer is highly sensitive; the tumor tissue is treated during surgery. Squeeze and hemorrhage can cause dissemination and undetectable metastases in organs. In addition, surgery can block sequential chemotherapy, which can lead to accelerated growth of cancer cells. Unpredictable organ damage is present during and after surgery. Therefore, CEA single detection has limited value in the diagnosis of lung cancer, and should be combined with the smoking status of patients and other tumor markers to comprehensively analyze the possibility of lung cancer.

4. Conclusions

The model established by using data mining technology combined with tumor marker protein chip can quickly identify and diagnose lung cancer and benign lung disease. Decision tree and neural network model are superior to discriminant analysis model in differential diagnosis of lung cancer and benign lung disease. Through this retrospective study, the changes of serum tumor markers in the serum of early small cell lung cancer were very intuitively counted, and the specific changes in the positive rate were also compared with those of non-small cell lung cancer. Our conclusion is that NSE can still provide a reference for the early clinical diagnosis of SCLC, which is helpful for early diagnosis of early SCLC and avoid delay in diagnosis and treatment. The serum tumor markers of non-small cell lung cancer (NSCLC) from diagnosis to death are always normal and related to the biological characteristics of tumor cells. The biological behavior of tumor cells is less invasive, migratory and signal stimulation to normal cells. Therefore, the normal serum tumor markers of lung cancer can indicate early stage of disease, low incidence of metastasis and longer survival period. Serum levels before initial treatment were correlated with brain metastasis in patients with advanced non-small cell lung cancer. The detection of serum level is valuable for the evaluation of curative effect and prognosis of patients with brain metastasis. Many studies have shown that the elevated serum carcinoembryonic antigen (CEA) concentration corresponds to the types of cell carcinogenesis in lung cancer. The serum CEA concentration in lung adenocarcinoma patients is significantly higher than that in squamous cell carcinoma and SCLC patients. Although the serum levels of lung squamous cell carcinoma and SCLC patients also increased to some extent, their positive rates were far lower than those of adenocarcinoma.

References


