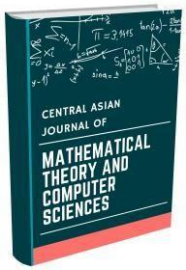

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Article

Using Sport Vector Machine for to Distinguish Between Benign and Malignant Brain Tumors

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Abstract: In light of the advancement of artificial intelligence (AI) tools, which now have widespread applications across various fields such as medicine, engineering, biology, and beyond, there is an urgent need to leverage AI tools in statistical applications. In the study under consideration, one of the AI techniques, Support Vector Machine (SVM), will be utilized to perform classification tasks, return elements to their original population, and provide accurate predictions for future observations. This method will be applied to a complex medical phenomenon: distinguishing between benign and malignant brain tumors. This represents a valuable study in utilizing AI tools for classification purposes.This effort marks a significant step in the medical field, as it aims to spare patients from undergoing biopsies, which could potentially worsen their condition due to side effects. Data has been collected from two groups: Patients with benign brain tumors and Patients with malignant brain tumors. The SVM method will be employed to build a predictive model with high accuracy in classifying observations into their respective categories.

Keywords: Support Vector Machine (SVM), Misclassification ,malignant brain tumors, malignant brain tumors

1. Introduction

Support Vector Machines (SVM) are an efficient and robust machine learning algorithm that falls under the concept of supervised machine . SVM has become a widely popular tool for classification tasks. It was proposed by (vapnik(1992)), focusing on the idea of finding the optimal hyperplane(A decision boundary that divides the data into distinct classes is called a hyperplane. It is just a line in a two-dimensional environment, but it becomes a plane or a higher-dimensional surface in a three-dimensional space. Finding the best hyperplane to separate the data into distinct classes is the aim of SVM.)(Yeom, H. G (2009)) that separates data points into different categories with the maximum possible margin.The main concept of SVM focuses on support vectors, which are the data points closest to the hyperplane. These vectors play a critical role in defining the classification boundaries and generalizing the classification model. This feature has made SVM preferable to many other algorithms. The SVM algorithm emphasizes minimizing classification errors as much as possible while simultaneously maximizing the margin, which enhances performance on unseen data. The origin of the discovery of the Support Vector Machine (SVM) technique lies in finding the optimal solution to the problem of pattern recognition by selecting the separating hyperplane for the data(Nilsson, R.,(2007)).

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This technique revolves around a primary goal: identifying the optimal separating hyperplane for the studied data, which is to be classified and divided into two categories.SVM has a significant capability to handle both linear and non-linear classification problems by relying on linear classifiers(SVM looks for a linear hyperplane that separates the data into classes when the data is linearly separable. When a straight line or hyperplane can be used to divide classes, a linear decision boundary performs well.(Ghosh, S.,(2019)) and non-linear classifiers(When the data is not linearly separable, SVM maps the data into higher dimensions where a linear separating hyperplane can be found using kernel functions. The kernel trick is the name given to this technique. Typical kernel capabilities consist of). In some classification problems, there may not be a simple separating hyperplane that can act as a criterion for separation. To address this, the concept of the non-linear classifier was introduced, enabling the identification of a simple separating hyperplane through the use of kernels(Suykens, J. A. (2001, May)).

2.Linear Support Vector Machine

With liner support vector machine the mathematical formulation can defined as following(Zhou, Z. H., & Zhou, Z. H. (2021)):

$$\{x_i, y_i\} \text{ where } i = 1,2, \ldots . L \ , y_i \ \in \{-1, +1\}, x \in R^D$$

where

L is be all of the training data points.

x_iis a D-dimensional space, each data point is represented as a feature vector.

y_i is every data point has a class identifier label, where y_i is either +1 or -1. The two groups to which the data points may fall are represented by these values. Learning a decision boundary (hyperplane) that divides these two classes is the SVM's objective.

Training Data: Each data point x_i has a corresponding label y_i. The training data set is made up of pairs $\{xi, yi\}$. SVM uses the training data to identify the best hyperplane dividing the class +1 data points from class −1 data points ((Zhou, Z. H., & Zhou, Z. H. (2021)):).

The value of D-dimensional space is very important for choose hyperplane if the value of D=2

With regard to the characteristics x_1 and x_2, the separating line can be drawn on the graph when D=2. In this case, the data points are shown in two dimensions, and a linear classifier can be used to draw a straight line that divides the two classes. The data points on either side of this line are classified into separate classifications. This dividing line's 2D equation is expressed as follows:

$$w_1 x_1 + w_2 x_2 + b = o$$

The equation (2) is a straight line in D=2 for feature space ,where(w_i,i=1,2) are the weights linked with 〖(x)〗 ᵢ,i=1,2) ,b is the bias term (Hearst, M. A.,1998).

We can explain the equation (2) , When we wish to divide the data into two groups (for example, +1 and -1), we search for the line that divides them.

If the point lies on the line: when the equation equals zero, w_1 x+w_2 x_2+b=o then the point (x_1,x_2)lies exactly on the separating line(Tax, D. M., & Duin, R. P. (1999,)).

If the point lies on the positive side of the line $w_1 x_1 + w_2 x_2 + b = o$: if the value w_1 $w_1 x_1 + w_2 x_2 + b > o$ then the point lies in the positive class (class +1).

If the point lies on the negative side of the line: if the value $w_1 x_1 + w_2 x_2 + b < o$ then the point lies in the negative class (class -1).

The clustered points close to the hyperplane are called support vectors, and their values range between (+1 and -1), where a value of +1 represents the first group and -1 represents the second group. Finally, The process of classifying observations is carried out according to the following two formulas

$$w_i^T x_i + b \leq -1 \quad \rightarrow y_i = -1 \qquad or\ w_i^T x_i + b \geq 1 \quad \rightarrow y_i = 1 \qquad (3)$$

The Support Vector Machine (SVM) margin is the separation between the hyperplane and the support vectors. The SVM margin must be maximized in order to guarantee that the hyperplane is as far away from the support vectors as feasible. The mathematical expressions you provided are part of the optimization process in Support Vector Machines (SVM). First , maximizing the margin The norm of the weight vector $\|w\| = \sum_{i=1}^{L} {w_i}^2$ is inversely proportional to the margin. In particular:

$$Margin = \frac{2}{\sum_{i=1}^{L} {w_i}^2}$$

when maximize of the margin ,the our aim minimize of $\sum_{i=1}^{L} {w_i}^2$,we can introduced simplest form to a Minimization Problem, the minimizing ‖w‖^2/2 is equivalent maximizing 2/‖w‖ . It is simpler to use in optimization techniques and has mathematical equivalents (Steinwart, I. (2008))

$$min\frac{\|w\|}{2} = min\frac{w^T w}{2} \ (5)$$

Therefore, maximizing the objective function

$$min\frac{w^T w}{2},\ \text{s.t}\ y_i w^T w + y_i b \geq 1 = y_i(w^T w + b) \geq 1 \qquad (6)$$

The term of $min\frac{w^T w}{2}$is equivalent of Min Min $\frac{\|w\|^2}{2}$,therefore to solve this amount we can use the Lagrange multipliers, from the objective function and restrictions of the objective function(Schölkopf, B.,2000)

$$\text{Min}\ \frac{\|w\|^2}{2}\ \text{s.t}\ y_i w^T w + y_i b - 1 \geq 0 \quad (7)$$

To solve the equation (7),we can used Lagrange multipliers as following

$$L_p(w, b, \theta) = \frac{w^T w}{2} - y_i w^T w + \theta_i[\{(w^T x_i + b) - 1\}] \ (8)$$

From the objective function and constraints, we can minimize the function in the initial formula and maximize the function in the second formula to determine the values of w and b. As a result, w and b will be calculated first using the formula (8). Via a set of Partial derivatives by w and b(Burges, C. J. (1998).).

$$\underset{\theta}{\text{Max}}\left[\sum_{i=1}^{L} \theta_i - \frac{1}{2}\sum_{i=1}^{L} \theta' w\, \theta\right] \text{s.t}\ \theta_i \geq 0\ \forall i\ ,\ \sum_{i=1}^{L} \theta_i y_i = 0 \ldots\ldots (9)$$

This optimization issue looks to be the dual form of a Support Vector Machine (SVM), specifically for a binary classification task. Via using Quaratic programming we obtained the value of θ_i and from the value of θ_i we obtained the value w_i . From this information we obtained support vector (Campbell, C., & Ying, Y. (2022)). The equation $y_s(x_s w + b) = 1$, is main concept in svm describe the limitations associated with support vectors in the more optimal hyperplane formulation. The value of

$w = \sum_{i=1}^{L} \theta_i y_i x_i$. Therefore , the concept of $y_s(x_s w + z) = 1$ is become $y_s(x_s \sum_{d\in s} \theta_d y_d x_d + z) = 1$. The value of mount b is become $b = y_s - {y_s}^2(x_s \sum_{d\in s} \theta_d y_d x_d)$under assume $b = y_s - (x_s \sum_{d\in s} \theta_d y_d x_d)$. from all information the value of z is become .

$$b = \frac{1}{Ns}\sum_{m\in s}(\ y_s - \sum_{m\in s} \theta_d y_d x_d\ .x_s \ (10)$$

where,

Ns: is represent of Number of support vectors. 〖 y〗 _s: is represent of a support vector Label ,and the amount of 〖 y〗 _s is belong to the interval (1,-1).b is the l expression for the bias. After obtaining the parameters estimated of the Support Vector Machine

(SVM) method, intelligent classification can be achieved via back new observation to their original group(Tian, Y., (2012)).as following equation. $y_{i(new)} = w_i^T x_i + b \leq -1$

2.1Misclassification

Misclassification in the context of Support Vector Machine (SVM) refers to situations in which the model predicts the wrong class for a data item. Misclassification happens when the expected and true class labels do not match. From general formula with slack variables ξ_i(Burges, C. J., & Schölkopf, B. (1996)).we will obtained the following formula:

$w^T xi + b - 1 + \xi_i \geq 0$ (11)

$\hat{y} = sign(f(x)) = sign(w^T xi + b - 1 + \xi_i \geq 0)$ (12)

Where y is new predicted of observation, in this case we have two probability as following :

ξ_i=0 if the point is correctly classified

ξ_i>0 If the point is incorrectly classified or breaches the margin

Misclassification occurs when the anticipated class label fails to match the true class label, therefore, we can summarize the role of classification as the below table

Table 1 show the role classification

$\hat{y}$	Type 1	Type 2
Type 1	Correct classification	Wrong classification
Type 2	Wrong classification	Correct classification

The classification of observations into their original groups can be performed using the Support Vector Machine (SVM) technique through the (e1071) package available in the statistical program R.

2. Materials and Methods

The method used focuses on how to classify observations into their original groups with very minimal misclassification error and on building a predictive function with high capability in classifying the original observations.

3.The Study Sample and Variables

In the current study, focus will be placed on a random sample consisting of two groups. The first group represents patients diagnosed with malignant brain tumors, comprising 30 individuals. The second group represents patients diagnosed with benign brain tumors, comprising 43 individuals. These data were collected from the Oncology Hospital affiliated with Al-Diwaniyah General Hospital over the past five years (2019–2024).

The study focused on six variables, and data for these variables were collected for both groups. These variables are listed below:

X_1:WBC(White Blood Cells Test)

X_2:ESR(Erythrocyte Sedimentation Rate Test)

X_3:LDH (Lactate Dehydrogenase Test)

X_4:CSF(Cerebrospinal Fluid Analysis)

X_5:MGMT Analysis(O6-methylguanine-DNA methyltransferase)

X_6:MGMT Analysis(AFP (Alpha-fetoprotein)

After collecting data related to the variables for both groups and inputting this data into the code designed for building predictive classification models, the following results were obtained:

$\hat{y}$	malignant brain tumors	benign brain tumors	Sum
malignant brain tumors	27	3	30
benign brain tumors	4	39	43
Sum	31	42	73

Table 2 show confusion matrix for Correct and Incorrect Classification SVM

From the results shown in the table above, which correspond to the classification model based on the Support Vector Machine (SVM), the outcomes are summarized into two groups: the malignant brain tumors group and the benign brain tumors group, as follows:

Out of 27 malignant brain tumor cases, 27 were correctly classified into their group (the malignant tumor group), achieving a classification accuracy of (27/30)*100%=90%.The remaining 3 cases of malignant brain tumors were misclassified into the second group (the benign tumor group), resulting in a misclassification rate of(3/30)*100%=10%.Similarly, out of 43 benign brain tumor cases, 39 were correctly classified into their group (the benign tumor group), achieving a classification accuracy of (39/43)*100%=91%.The remaining 4 cases of benign brain tumors were misclassified into the second group (the malignant tumor group), resulting in a misclassification rate of(4/43)*100%=9%.However, it is observed that the general classification accuracy of the Support Vector Machine (SVM) function for both groups, malignant and benign brain tumors, reached (27+39/73)*100%=91%, but general misclassification rate of(4+3/73)*100%=9%.

3.1 Support Vectors

3.1.1-Results of Support Vectors of malignant brain tumors set

Table -3- show the Support Vectors of malignant brain tumors

Support Vectors of malignant brain tumors						
obvs	X_1	X_2	X_3	X_4	X_5	X_6
1	-0.719	1.003	0. 585	0.795	-1.266	1.542
7	0.535	1.634	-1.169	-1.276	0.4327	1.738
9	-0.926	0.142	-0.788	-1.266	-1.053	0.418
10	1.003	0.542	-0.813	-0.389	0.875	0.324
11	-1.250	-0.692	0.775	0.149	0.679	-0.549
12	0.195	-0.853	-0.718	-0.539	-0.303	-0.348
13	0.141	1.095	-1.643	-0.194	-0.058	-0.342
14	-0.528	0.795	-0.289	0.045	-0.539	-0.842
16	-1.604	-0.146	-0.711	0.734	-1.268	-1.672
19	1.634	1.208	-1.266	-0.745	0.875	-0.983
29	1.634	-1.604	-0.711	0.689	0.928	-1.210
32	0.097	-0.1454	-1.687	1. 566	0.0145	-1.942
35	-1.250	-1.072	-1.961	-1.532	1.622	0.864
46	0.333	0.097	0.014	1.2581	-1.623	-1.201
51	-0.336	0.048	-0.486	0.5241	1.615	-1.864
52	1.071	0.795	0.539	0.0195	-1.543	-0.467
56	-0.145	-0.692	0.614	0.095	1. 422	0.374
58	0. 589	-1.498	-1. 443	0.0125	-0. 255	-0.545
59	-0.934	-0.854	0.578	-1. 443	-0.278	-0.864

62	1. 581	1.162	2.529	-1.943	-0.612	0.487
64	-1.256	-0.161	-0. 268	1.964	1.809	0.648
69	0.198	0. 381	-0.144	1.693	-0. 367	-0.641

From the results listed in table (3),the number of important Support Vectors of malignant brain is (22), the observation column shown in first column of the above table , It is the one that serves as the support vectors of malignant brain via used the Support Vector Machine (SVM) method . In this support vectors the active observations that are((1,7,9,10,11,12,13,14,16,19,29,32,35,46,51.52,56,58,59,62,64,and 69) respectively

3.1.2-Result of Support Vectors of benign brain tumors set

Table -4- show the Support Vectors of benign brain tumors

Support Vectors of benign brain tumors						
obvs	X_1	X_2	X_3	X_4	X_5	X_6
4	-0.298	-0.256	0.539	2.638	0.695	0.162
5	2.006	1.795	-0.324	-0.718	1.682	0.795
8	-0.370	-0.256	0.695	2.698	0.015	1.642
15	-0.513	0.795	-0.669	-0.5239	0.239	0.845
18	-0.817	-1.256	-0.149	0.6209	0.595	-1.931
24	0.112	0.795	0.4307	1.769	0.093	0.821
25	0.518	-1.256	-1.1006	-1. 461	0.0165	-1.232
27	-1.652	0.735	-0.567	-1.162	-1.647	0.342
34	-0.202	0.772	-0.362	-0.813	-1.543	1.544
38	-0.288	0. 5875	-1.567	-0.664	1.634	-0.626
41	-0.055	0. 875	-0.811	-0.728	0.075	1.295
46	-0.751	-1.166	-0.495	0.805	-1.646	0.595
49	-0.761	-1.266	-0.4671	0.815	-1.607	0.664
53	-0.857	-1.356	-0.046	-0.434	0. 955	-0. 253
56	-0.278	0.185	-1.196	-0.614	1.567	-0.244
58	-0.615	0.772	-1.126	-0.718	0.0621	-1. 563
61	-0.771	-1.367	-0.476	0.825	-1.971	2.536
64	-1.652	0.785	-1.667	-1.162	-1.734	-0.191
68	-0.202	0.755	-1.319	-0.863	-1.127	1.331
72	-0.288	0.165	-1.169	-0.668	1.626	-0.294

From the results listed in table (4),the number of important Support Vectors of benign brain is (20), the observation column shown in first column of the above table , It is the one that serves as the support vectors of benign brain via used the Support Vector Machine (SVM) method . In this support vectors the active observations that are(((4,5,8,15,18,24,25,27,34,38,41,46,49,53,56.58,61,64,68, and 72)) respectively

3.2observations classification

The observations can be classified into their original group or the other group by using the objective function associated with the Support Vector Machine (SVM) method. The patient can be classified into the group they belong to according to the following:

Table 5 Classifying the observations of the malignant brain tumors via (SVM) method.

Observations	Value
1	1. 248
4	0. 292
6	0.538
7	0.524
9	1.006
10	-0.486
11	0.945
12	1.192
13	1.276
14	0.989
15	1.175
16	1. 952
19	0.455
22	0.542
26	0.857
27	1. 564
29	-0.090
32	1.213
35	1.724
46	-0. 967
49	0.548
50	0.437
51	0.225
52	0.5110
53	0. 754
56	0.978
58	1.568
59	-0. 672
62	0.634
64	0.382
73	0.978

The results in the table above represent the correct classification of the malignant brain tumor group, as well as the incorrect classification of the malignant brain tumor group. The first column in the table represents the observations, while the second column represents the estimated values of those observations using the SVM method. According to the results shown in the table, 27 observations from the malignant brain tumor group were correctly classified by assigning them to their appropriate group. Conversely, 4 observations from the malignant brain tumor group were incorrectly classified by assigning them to the benign brain tumor group. This is evident from the estimated values, where the number of observations correctly classified is 27, and their estimated values were positive. Meanwhile, the 4 incorrectly classified observations had negative estimated values, namely (59, 46, 29, 10) (misclassification).

Table 6 Classifying the observations of the benign brain tumors via (SVM) method

Observations	Value
2	-0.951
3	-1.505
5	0.468
8	-1.707
17	-1.835
18	-1.268
20	-1.918
21	-1.175
23	-1.459
24	-2.143
25	-2.0285
28	-1.813
30	-1.524
31	-0.562
33	-0.215
34	-1.627
36	-1.348
37	-1.134
38	-0.534
39	-1.537
40	-1.854
41	-0.674
42	-0.348
43	-0.428
44	-0.524
45	-0.824
47	1.0054
48	-1.654
54	-1.829
55	-1.854
57	-0.754
60	-1.512
61	-2.152
63	-1.086
65	-2.252
66	1. 095
67	-1.082
68	-1.546
69	-0.641
70	-0.675
71	-0.584
72	-0.237

The results in the table above represent the correct classification of the benign brain tumor group, as well as the incorrect classification of the benign brain tumor group. The first column in the table represents the observations, while the second column represents the estimated values of those observations using the SVM method.According to the results shown in the table, 39 observations from the benign brain tumor group were correctly classified by assigning them to their appropriate group. Conversely, 3 observations from the benign brain tumor group were incorrectly classified by assigning them to the malignant brain tumor group. This is evident from the estimated values, where the number of correctly classified observations is 39, and their estimated values were negative. Meanwhile, the 3 incorrectly classified observations had positive estimated values, namely (66, 47, 5) (misclassification).

3.3.Weight support vector values

Table 7 show Weight support vector values

X_1	X_2	X_3	X_4	X_5
-12. 184	14.528	-8.325	10.204	-5.652

From the results presented in Table 7, it is observed that there is a variation in the relative importance among the variables used in the classification for both groups.

3. Results

Out of 27 malignant brain tumor cases, 27 were correctly classified into their group (the malignant tumor group), achieving a classification accuracy of (27/30)*100%=90%.The remaining 3 cases of malignant brain tumors were misclassified into the second group (the benign tumor group), resulting in a misclassification rate of(3/30)*100%=10%.Similarly, out of 43 benign brain tumor cases, 39 were correctly classified into their group (the benign tumor group), achieving a classification accuracy of (39/43)*100%=91%.The remaining 4 cases of benign brain tumors were misclassified into the second group (the malignant tumor group), resulting in a misclassification rate of(4/43)*100%=9%.However, it is observed that the general classification accuracy of the Support Vector Machine (SVM) function for both groups, malignant and benign brain tumors, reached (27+39/73)*100%=91%, but general misclassification rate of(4+3/73)*100%=9%.

4. Discussion

The results in the table above represent the correct classification of the malignant brain tumor group, as well as the incorrect classification of the malignant brain tumor group. The first column in the table represents the observations, while the second column represents the estimated values of those observations using the SVM method. According to the results shown in the table, 27 observations from the malignant brain tumor group were correctly classified by assigning them to their appropriate group. Conversely, 4 observations from the malignant brain tumor group were incorrectly classified by assigning them to the benign brain tumor group. This is evident from the estimated values, where the number of observations correctly classified is 27, and their estimated values were positive. Meanwhile, the 4 incorrectly classified observations had negative estimated values, namely (59, 46, 29, 10) (misclassification).

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malignant brain tumor group. This is evident from the estimated values, where the number of correctly classified observations is 39, and their estimated values were negative. Meanwhile, the 3 incorrectly classified observations had positive estimated values, namely (66, 47, 5) (misclassification).

5. Conclusion

Based on the results shown in the current study, it is observed that the classification accuracy was very high. Consequently, the classification process using the Support Vector Machine (SVM) method proved to be highly effective in categorizing items into their original groups. Given this data, the predictive classification using the SVM method is highly efficient in distinguishing categories. For instance, out of 31 observations, 27 were correctly classified, which pertains to the group of malignant brain tumors. Similarly, out of 42 observations, 39 were correctly classified, which pertains to the group of benign brain tumors. Therefore, the classification error in the current study was minimal, reflecting positively on prediction accuracy.The results also indicate that the six study variables had different relative importance levels. Notably, the variable x2x_2x2: ESR (Erythrocyte Sedimentation Rate Test) had the highest significance among the study variables for both groups.

We recommend using the Support Vector Machine (SVM) method for binary or multi-class classification, as this method possesses specialized tools in artificial intelligence. Consequently, the estimation accuracy with this method will be very high, while classification errors will be significantly low. Additionally, we suggest applying the SVM method in various applied sciences due to its high capability in estimating the parameters of predictive models. For critical medical conditions, we recommend utilizing classification and discrimination tools to ensure accurate diagnosis of complex medical cases. Furthermore, we encourage researchers in the field of classification to consider using or integrating regularization methods with the SVM approach to enhance their outcomes.

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