Artificial Intelligence and Neutrosophic Machine learning in the Diagnosis and Detection of COVID 19

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Abstract

The world has always suffered and from diseases and epidemics, and the coronavirus is one of the most dangerous viruses that threatened human life that requires the use of all scientific methods and means to respond to it and reduce its spread by early detection of infections and taking necessary measures In view of the significant role that artificial intelligence plays in most fields of science, it has become one of the most important scientific methods used to resolve complex issues and has been harnessed in medical diagnosis, one of the most complex areas. Many AI and machine learning algorithms have been used to diagnose and detect diseases in general and coronavirus in particular. The support vector machine (svm) machine algorithm was one of the most important algorithms in this area and is one of the most effective compilations used in the knowledge extraction process In spite of all this, the results they present remain incomplete because classification issues do not deal with cognitive uncertainties such as ambiguity, neutrality and inconsistency associated with perception of human thinking, This adversely affects the work of a classic support vector machine and affects the accurate diagnosis of the disease To solve this problem, we have done this research using a Neutrosophic Support Vector Machine because it takes into account all possible cases during the study of the sample and it reduces the impact of extreme values. This increases the accuracy of the results when diagnosing coronavirus symptoms. The study was conducted according to the following steps:

1. We extract features from chest radiographs based on GLCM
2. We form a neutrosophic dataset.
3. We train Neutrosophic Support Machine N-SVM on new data.
4. We record the results.

Comparing the results, we got using the upgraded N-SVM algorithm with the classic SVM algorithm results we found that it gives a more accurate diagnosis of the disease.

Keywords: Corona virus; Gray-level Co-Occurrence matrix; Neutrosophic Support Vector Machine algorithm.

Studies by the World Health Organization show that the coronavirus targets the most vulnerable groups (the elderly, chronically ill, immunocompromised, cardiac and diabetic) [1.2]. coronavirus belongs to a large family of viruses (HCoV-229E, HCoV-OC43, HCoV-NL63, HKU1-CoV) [3]. More than 7.5 million cases have been diagnosed in more than 200 countries as of 11 June 2020, including some 421,000 deaths, 3.8 million recoveries, 3.2 million mild cases and 54,000 critical cases [4.5]. The high speed of the spread of the virus, the lack of testing centers and delays in showing the result of testing make many countries in the world unable to cope with the risk of these viruses and reduce their spread and unable to count positive cases of coronavirus [6]. CXR images help in early detection of infection, but cannot be relied upon because they are similar to different images of pneumonia, viral infections, infectious lung diseases and other infections, leaving radiologists unable to distinguish between COVID-19 and other viral infections.

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Misdiagnosis of the disease increases the numbers of positive cases of the COVID-19 virus accelerate [7.8]. Therefore, other methods of early detection of positive cases have to be used, and due to the great success of AI across the board in the health field, where many AI algorithms have been used in diagnosis and disease detection, researchers interested in the coronavirus pandemic have used classic AI and machine learning algorithms. Classification issues are known not to deal with cognitive uncertainties such as ambiguity, neutrality and inconsistency associated with perception of human thinking. s learning algorithms because they cannot handle non-assignments. So we need a logic that takes into account all the data and addresses cases of indefinition to get the desired results. In this research, we used the concepts of neutrosophic logic that is the new vision of modeling and designed to effectively address the uncertainties inherent in the real world. and replaced the bilateral logic recognizing right and wrong by introducing a third neutral case that could be interpreted as undefined or uncertain. Founded by American mathematic philosopher Florentin Smarandache in 1995 [9,10,11,12,13], neutrosophy logic has grown considerably in recent years and its domains have diversified through research and studies by researchers and those interested in research and scientific development [13,14,15,16,17,18,19,20,21,22,23], and has been used in the medical field, especially in virus detection through the use of neutrosophic support vector machine to detect positive cases.

The main reason why we used a neutrosophic support vector machine is to know before that the most common problems affecting the decision-making process are the problem of outliers because of its negative role reflected in the accuracy of the model. we used a neutrosophic SVM in order to reduce the impact of outliers and also because it can handle data located on it.

It takes into account all possible situations and deals with cognitive uncertainties such as in contrast to the classic support vector machine, it is weaker than the neutrosophic support vector machine algorithm in reducing the impact of outliers. It is also worth noting that the classic support vector machine algorithm cannot classify the outliers data. It is unable to handle the undetermined elements. Therefore, the classic SVM does not study all possible cases, making it unable to reach the optimal decision accurately.

Discussion: There are several studies in which the classic support vector machine algorithm has been used in diagnosis and detection of COVID-19 using chest radiographs but all of them reach high accuracy.

The large number of training samples, which increases the learning of the algorithm, but in case of a problem of a very small number of data (i.e., we did not have enough data for any reason) Ref [31] made the support vector machine algorithm learn from only 30 radiographic images also based on GLCM technology in critical features where it reached resolution 57.1. In this research we applied the neutrosophic vector machine algorithm to the same few data used in [31] and compared it in accuracy. First, we configure the data we want to work on, which are chest radiographs made up of 30 images 15 including COVID19, as well as 15 images intact, and the data format is jpg and the size of the image is 25 * 25.

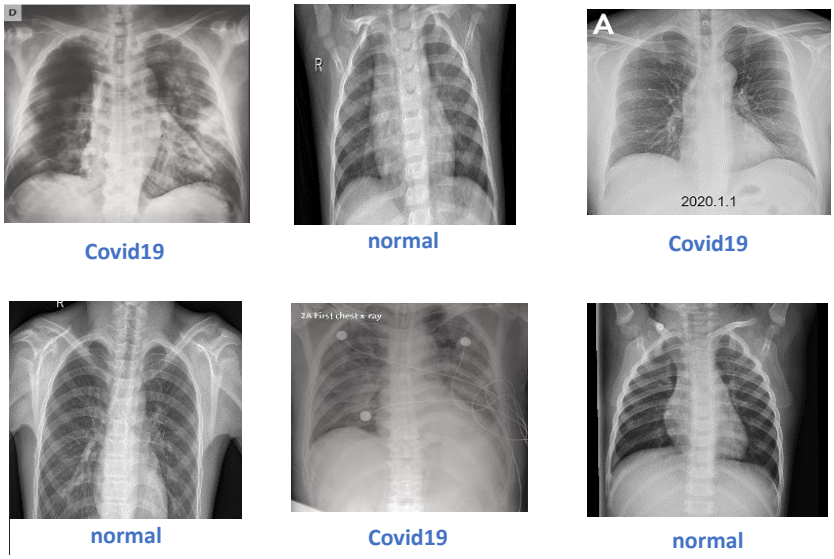

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Figure1: Samples of two different dataset cases: patient suffering from covid-19 ,and normal healthy person

After the data is configured, the training of the model is carried out in accordance with the following stages:

1. We enter an image of the data to be processed.
2. We extract features based on GLCM technology.
3. We form a neutrosophic dataset..
4. Then we make the vector machine algorithm support neutrosophic learn from the training data.

We represent these stages with the following diagram:

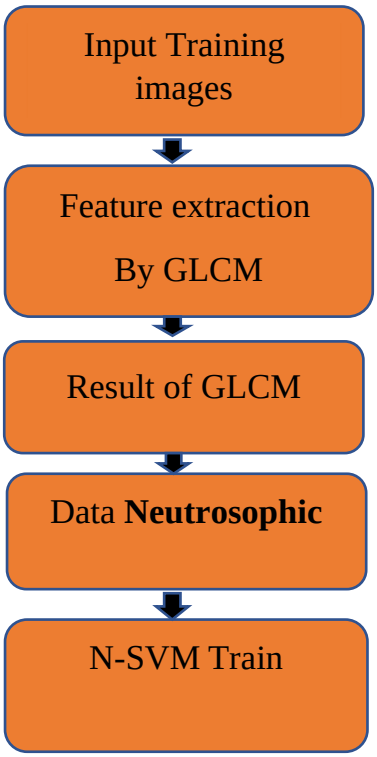

Figure 2: Training N-SVM Model

1.The stage of entering a picture of the data to be processed is illustrated by the following diagram:

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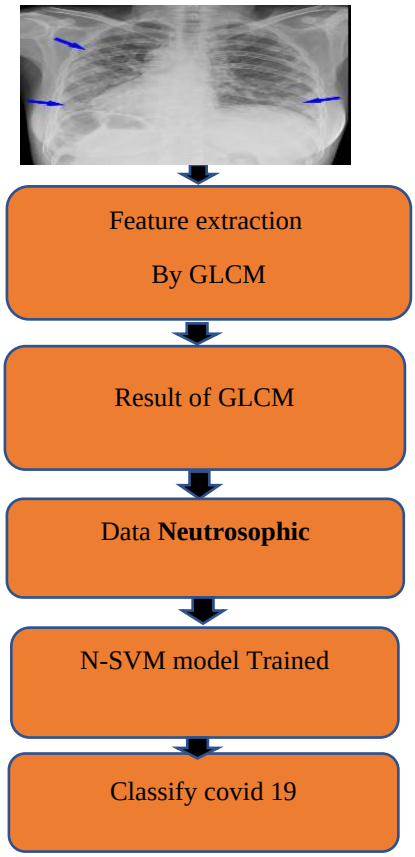

Figure 4: Classification Flow Diagram

2.Extract features from x-ray radiographs , representing energy, contrast and homogeneity we follow the next steps:[24.25.26]

a) We enter the x-ray image that we want to process.
b) We make the picture with a gray gradient.
0.299R+0.587G+0.114B

c) Convert greyscale image from field 0-255 to new scale representing greyscale.

d)In this study we used the scale 0-9, i.e. we have reduced the pixel value making it easier for us to calculate GLCM.

e) we Convert the pixel value in the new scale into a matrix.

f) We compute the GLCM element that represents the appearance of gray value pairs of reference pixels, pixels and adjacent units in the distance and directions specified in the study using proximity 1 pixel and 0 direction.

g) We get the new matrix based on the account results.

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h) We calculate GLCM parameters according to the relationships described in the table below:

Table1: shows the parameters of GLCM

Parameter GLCM	**Arithmetic relationship**
Contrast	$\sum_j \sum_i (j-i)^2 N[I,J]$
Energy	$\sum_j \sum_i N^2[I,J]$
Homogeneity	$\sum_j \sum_i \frac{N[I,J]}{1+[i-j]}$

N: GLCM matrix

i: the row number in N, the column number in N

So after we configured the data of 30 chest radiographs, we extracted the features from these images. Depending on parameters of Gray-level Co-Occurrence matrix represented by (Energy, Contrast, Homogeneity) As shown in Tables 2 and 3.

Table2: features extracted

N.	Energy	Cont	Hom.
1	0.0023	123.693	0.0178
2	0.0015	121.084	0.1849
3	0.0015	121.118	0.188
4	0.0016	112.858	0.1941
5	0.0015	108.897	0.1985
6	0.0027	142.454	0.1628
7	0.0025	130.193	0.1804
8	0.0019	103.057	0.1911
9	0.0019	103.710	0.2084
10	0.0017	111.213	0.1907
11	0.0015	101.739	0.2009
12	0.0018	122.323	0.1823
13	0.0021	114.802	0.1984
14	0.002	142.613	0.1669
15	0.0017	99.8898	0.1986

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Table3: features extracted**.**

N.	Energy	Cont	Hom
1	0.0016	118.582	0.1881
2	0.0016	113.954	0.191
3	0.0017	118.268	0.1839
4	0.0015	125.244	0.1869
5	0.0016	113.045	0.1932
6	0.0015	113.794	0.1944
7	0.0016	124.162	0.1863
8	0.0017	112.098	0.2007
9	0.0016	100.961	0.196
10	0.0016	116.398	0.1903
11	0.0016	108.578	0.2026
12	0.0015	119.241	0.1894
13	0.0016	112.839	0.1905
14	0.0017	127.526	0.1791
15	0.0017	118.506	0.1893

3**. Formation of Neutrosophic Dataset:**

$\forall\, X = (x_1, x_2, x_3, \dots, x_n)^T$ set of features for binary classification data extracted using GLCM technology, but these features in this form reflect classic data and are not without cognitive uncertainties. In order to solve the problem of decisive data, we form a neutrosophic data set, which is a generalization of the classical and hazardous groups. The degree of neutrality has been introduced and added to the neutrosophic group and therefore the neutrosophic group has been defined as < T, I, F > where each element of the previous set is symbolized as [27]:

$$\forall x(t, i, f) \in < \mathrm{T}, \mathrm{I}, \mathrm{F} >$$

i: represents neutrality, t: represents membership, f: represents Non-membership, t, i, f are real numbers of T, I, F respectively.

We also know that one of the disadvantages of the SVM algorithm that it is very sensitive to outliers, values, and to solve this problem we have reformulated the neutrosophic group of input samples based on the distances between the sample.

Neutrosophic group helps solve the problem of outlier values when combined with reformulated SVM.

Using the same preceding symbols that reflect data representation, we can know the input samples associated with the neutrosophic group by a set of points as follows:

$$(x_j, y_j, t_j, i_j, f_j); j = 1,2,3, \dots, n$$

$$g_j = t_j + i_j - f_j$$

For the set of points that fall on the line y = 1

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$$t_j = 1 - \frac{\|x_j - \rho^+\|}{max_{x_{k\epsilon N}}\|x_k - \rho^+\|}$$

$$i_j = 1 - \frac{\|x_j - \rho^{all}\|}{max_{x_{k\epsilon N}}\|x_k - \rho^{all}\|}$$

$$f_j = 1 - \frac{\|x_j - \rho^-\|}{max_{x_{k\epsilon N}}\|x_k - \rho^-\|}$$

For the set of points that fall on the line y is equal to -1.

$$t_j = 1 - \frac{\|x_j - \rho^-\|}{max_{x_{k\epsilon N}}\|x_k - \rho^-\|}$$

$$i_j = 1 - \frac{\|x_j - \rho^{all}\|}{max_{x_{k\epsilon N}}\|x_k - \rho^{all}\|}$$

$$f_j = 1 - \frac{\|x_j - \rho^+\|}{max_{x_{k\epsilon N}}\|x_k - \rho^+\|}$$

where ρ+ represents the average of the data set on the line y = 1.

Where ρ - the average of the data set on theliney is equal to minus 1.

Where ρ^{all} represents the mean of the entire dataset.

The ρ is calculated in the form

$$\rho^{all} = \frac{1}{n}\sum_{k=1}^{n^{all}} x_k \qquad \rho^+ = \frac{1}{n^+}\sum_{k=1}^{n^+} x_k \quad \rho^+ = \frac{1}{n^+}\sum_{k=1}^{n^+} x_k$$

n^+ :the number positive s, n^- : the number negative .

We formed the neutrosophic components by calculating the g elements that represent three components of Membership degree and symbolize them with T and non-membership and symbolize them with F and neutrality and symbolize it with I, we showed the neutrosophic dataset according to the chart shown in the format fig3 where the blue line expresses Membership (T) and the orange line of Indeterminacy (I) and the gray line (Non-membership (F) as shown in figure 3.

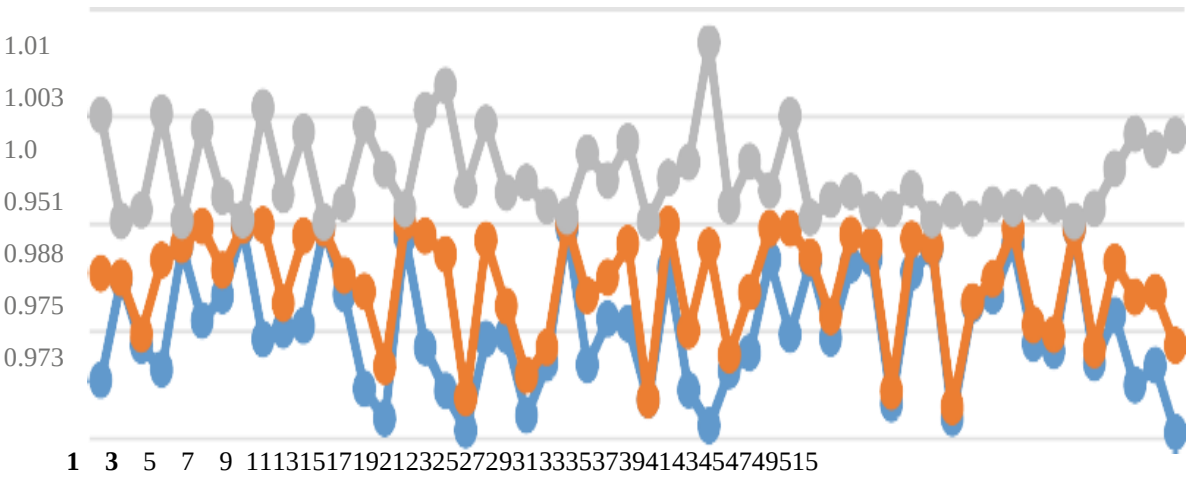

Fig3: some Neutrosophic features

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4. The Machine Algorithm Vector Support Neutrosophic N-SVM:

In this research, we classified the points that are regularly distributed in the field [-1.1]. We added a neutrosophic value to determine the degree of affiliation of each entry to the intended category, and based on the fact that the training data is not linearly separable and almost not devoid of outliers, which makes the algorithm tolerate errors in classification, which requires a solution to this problem by applying the linear kernel function Φ:x→Φ(x) to the training data, so the set of training points became as follows [27,28,29]:

$$(\Phi(x_1), y_1, g_1), (\Phi(x_2), y_2, g_2), \dots, (\Phi(x_n)\ , y_n, g_n)$$

We look for the best super surface that categorizes points for two categories. The problem is a nonlinear programming problem with an objective function as follows:

$$f(x) = \min \frac{1}{2}\|w\|^2 + C\sum_{i=1}^{n} g_i\ \epsilon_i \qquad \dots (1)$$

$$Subject\ to\ \ y_i(w.\Phi(x_i) + b) \geq 1 - \ \epsilon_i \quad ;\ i = 1, \dots, n$$

$$\epsilon_i \geq 0$$

Where $\Phi(x_i) = x_i x_i^t, i = 1,2,3, \dots, n$

g_i: Represents neutrosophic data and is formed in phase 3

C: a qualitative constant associated with g .

ϵ_i: mistakes committed by the decision limit through limitations

The Lagrange equation becomes:

$$L(w, b, \epsilon, \alpha, \beta) = \frac{1}{2}\|w\|^2 + C\sum_{i=1}^{n} g_i\ \epsilon_i$$

$$-\sum_{i=1}^{n} \alpha_i(y_i(w.\Phi(x_i) + b) - 1 + \epsilon_i) - \sum_{i=1}^{n} \beta_i\ \epsilon_i$$

w and b: are input arguments that the algorithm sets and any change in them affects the algorithm's output.

α, β: Lagrange factors.

To find the perfect solution we derive with respect to w,b,ϵ_i

$$\frac{\partial L(w, b, \epsilon, \alpha, \beta)}{\partial w} = w - \sum_{i=1}^{n} \alpha_i\ y_i\ \Phi(x_i) = 0 \qquad \dots (2)$$

$$\frac{\partial L(w, b, \epsilon, \alpha, \beta)}{\partial b} = -\sum_{i=1}^{n} \alpha_i y_i = 0 \qquad \dots (3)$$

$$\frac{\partial L(w, b, \epsilon, \alpha, \beta)}{\partial \epsilon_i} = g_i C - \alpha_i - \beta_i = 0 \qquad \dots (4)$$

Substituting relationships (4), (3) and (2) into relationship (1), we find the optimality problem:

$$\max W(\alpha) = \sum_{i=1}^{n} \alpha_i - \frac{1}{2}\sum_{i=1}^{n}\sum_{j=1}^{n} \alpha_i\ \alpha_j y_i\ y_j\ x_i x_i^t$$

within the terms $\sum_{i=1}^{l} y_i \alpha_i = 0$

$$0 \leq \alpha_i \leq g_i C \quad , i = 1, \dots, n \qquad \dots (5)$$

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Choosing an inappropriate value for α makes the algorithm go to unsatisfactory results, , which means that we have to search for an optimal value for α, so we need the error expression ϵ, and to apply the Kuhn-Tucker conditions.

1. Error ε: the difference between the calculated output (6) and the actual output (y) in absolute terms is calculated as follows:

$$\epsilon = |(w.\Phi(x) + b) - y| \qquad \dots (6)$$

The relationship (2) shall be replaced by (6) and the following phrase shall constitute the error:

$$\epsilon_i = \left| \left(\sum_{i=1}^{n} \alpha_i \, y_i \, \Phi(x_i) \, . \Phi(x_i) + b \right) - y_i \right|$$

Kuhn-Tucker Terms: can be written as [30]:

$$(g\ C - \alpha)\ \epsilon = 0 \text{ :and from it } \epsilon \geq 0 \text{ and } g\ C - \alpha \geq 0$$

Here we distinguish two situations:

Either C 0<α<g any ε=0 there is no error in classifying the support beam.

or g C-α=0 any g C=α ε>0 and there is a classification error or point located on the margin line. Where α are associated with g and C.

After we finish the algorithm training phase any new income is tested by applying the following sign function:

$$sign(w\Phi(x) + b) = \begin{cases} \text{output} \geq 0 \Rightarrow y = +1 \text{ Belonging to the first class} \\ \text{output} < 0 \Rightarrow y = -1 \text{ belonging to the second class} \end{cases}$$

Thus, any new income is classified to the appropriate output.

4. Conclusion and Results:

Initially, we extracted features using Grey-level Co-Occurrence matrix Technology because if the algorithm's income (image x-ray) is too large, it will form a surplus of data that results in the high cost of computation, processing and useless consumption of computer memory, so we converted the data into a simpler form representing the original data and this is known as feature extraction.

The advantages that we obtained are almost not devoid of outliers and vertices that fall on the decision boundary (unconfirmed values), so we used a neutrosophic support machine model in order to address the outliers and take into account the undefined values, where we trained the model on a small number of data which are 30 chest radiographs divided into 15 images for positive cases and 15 images for negative cases. We obtained a classification accuracy result of 63.8%, meaning that we obtained this accuracy after extracting the features using GLCM and training N-SVM on the extracted data. Thus, our proposed model outperforms the classic support vector machine algorithm in terms of classification accuracy as shown in Table4:

Table 4*:* Comparison of accuracy between SVM and N-SVM

Accuracy	
SVM Classic [31]	57.1%
N-SVM	63.8%

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