A Suggested Diagnostic System of Corona Virus based on the Neutrosophic Systems and Deep Learning

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Abstract

The idea for this paper is based on the use of a computer-connected microscope associated with Deep Learning, using Convolutional Neural Network (CNN). CNN is a mathematical type of Deep Learning used to recognize and diagnose images. After that, we photograph blood samples, as well as samples, were taken from the mouth and nose, as well as it is possible to photograph the throat from the inside of a large number of injured and uninfected people as well as suspected of infection and provide a large number of references for this program for each type of those different samples. It is possible to perform this process in few minutes, save time and money, make analyzes for the largest possible number of people, and provide results in an accurate and documented manner, which is through the Neutrosophic time series. The basis and analysis of dealing with all data, whether specific or not, that can be taken by time series values, then we present the linear model for the neutrosophic time series, and we test the significance of its coefficient based on patients distribution. Finally, from the above, we can provide a patient neutrosophic time series according to the linear model through which we can accurately predict the program will give degrees of verification and degrees of the uncertainty of the data.

Keywords: COVID-19, Corona Virus, Neutrosophic Systems, Neutrosophic Domain, Deep Learning, Convolutional Neural Network

Background: Coronavirus disease has widely spread all over the world since the beginning of 2020. It is desirable to develop automatic and accurate detection of COVID-19 using chest CT.

1. Introduction

Medical workers deal with a vast amount of information, which has arisen from the womb of laboratory tests and clinical and physiological observations. As doctors began a shift in clinical practice from an accidental analysis to relying on the accuracy of their observation to analyzing different evidence and structured algorithms, relying on groups of constantly updated to improve the ability to diagnose a disease or predict patient outcomes. From this standpoint, that study, which relies on the use of artificial intelligence and Neutrosophic data to identify people with this virus in degrees of certainty, uncertainty, impartiality, and to exploit this in the medical aspect to provide the greatest amount of time and money. Coronavirus, also known as COVID-19, which is among the viruses is a large series of viruses that cause many diseases ranging from the common cold and acute respiratory diseases, and the disease was first discovered in 2012 [10], who are infected with children and the elderly, the cause of their immunodeficiency and those who have heart diseases are more vulnerable to this virus. This virus has invaded many countries in the world now, caused a recession in the world economy, left many deaths, and injured. Neutrosophic is a new view of modeling, designed to effectively deal with underlying doubts in the real world, as it came to replace binary logic that recognized right and wrong by introducing a third neutral case which
could be interpreted as non-specific or uncertain. Founded by Florentin Smarandache in 1999 \[2,3\], as a 
generalization of fuzzy logic. As an extension of this, A. A. Salama introduced the neutrosophic crisp sets Theory 
as a generalization of crisp sets \[1\] and developed, inserted and formulated new concepts in the fields of 
mathematics, statistics, computer science and information systems \[4-9\]. Neutrosophic has grown significantly in 
recent years through its application in measurement, sets and graphs and in many scientific and practical fields.

2. **Scientific Experiment:**

   The first step of the experiment is defining the pre-dataset of images of the available samples about 
people who are infected with the Coronavirus, to make image references for comparison with modern intraoral 
pictures. There is four sections of data set are used, as follows:

   - The first section is images of blood samples.
   - The second section is images of saliva samples.
   - The third section is images of nose samples.
   - The fourth section is images of nose samples.

   The system needs a microscope imaging connected to a computer as well as a photographic camera connected 
to the same device and a computer device that uses CNN to match and identify similarities of images with the pre-
dataset of images that were previously placed on the program, by enlarging the modern images that are pulled 
from the microscope and the camera. The pre-dataset of images is the reference to diagnose each section separately 
so that the system gives an expectation to each section through analyzing and processing data and images as well 
as determining the probability of a person being injured or not, as well as the risk of injury.

The following experiment package:

![Experiment Tools](image1)

**Fig.1. Experiment Tools**

Below are the stages and mechanism for implementing the idea and requirements:

1- **Stages:**

   ![Stage 1](image2)

   ![Stage 2](image3)

   ![Stage 3](image4)

   ![Stage 4](image5)
Fig. 2. Implementation stages (1, 2, 3 and 4)
In the last step of the system, the principles of neutrosophic computing useful to system implementation for a large plethora of applications.

The following figure represents the Neutrosophic COVID-19 image classifier Architecture

The algorithm for the proposed system is given below which presented in Figure 4:

1. Convert each image in the database from the spatial domain to the neutrosophic domain.
2. Create a database containing various COVID-19.
4. Construct a combined feature vector for T, I, F and Stored in another database called Featured Database.
5. Find the distance between feature vectors of query COVID-19 and that of featured databases.
6. Sort the distance and Retrieve the N-top most similar.

The RNN structure replaces the traditional neuron by two neurons (lower neuron, upper neuron) to represent lower and upper approximations of each attribute in the CTG data set, its structure formed from 4 layers input, 2 hidden and output layers. The hidden layers have rough neurons, which overlap and exchange information between each other, While the input and output layers consist of traditional neurons.
The following figure gives an example of a patient’s neutrosophic time series

![Neutrosophic componant](image)

**Fig.5. Patient neutrosophic time series**

**Recommendations:**

**The implementation steps require:**

1) Providing modern computers inside the isolation hospitals equipped with a program for matching pictures, processing data, and issuing expectations and recommendations.

2) Provide a special microscope for imaging samples connected to a computer, as well as a high-quality camera connected to the computer as well.

3) Place blood samples, as well as samples, were taken from the mouth and nose, on the microscope, take pictures and place them on the aforementioned program.

4) Take pictures of patients' mouths from the inside (the beginning of the throat) and put them on the program.

5) Use all images for samples and mouth and put them as references for the system and divide the pictures into patterns and each reference pattern is different.

6) Determine the different virus patterns from the pictures and put all the data related to that pattern of symptoms, health status, and development in the case.

7) Take samples from the persons suspected of being infected, as well as those in contact with patients, and provide them with the program.

8) The start of applying this system in hospitals to identify the injured and the savings of time, effort and money.

**Conclusion and Future Works**

The idea for this study is based on the use of a computer-connected microscope associated with Deep Learning, using Convolutional Neural Network. The basis and analysis of dealing with all data, whether specific or not, that can be taken by time series values, then we present the linear model for the neutrosophic time series, and we test the significance of its coefficient based on patients distribution. Finally, from the above, we can provide a patient neutrosophic time series according to the linear model through which we can accurately predict the program will give degrees of verification and degrees of the uncertainty of the data. Furthermore, the proposed framework can also be extended towards other important domains of healthcare such as diabetes, cancer, and hepatitis, which can provide efficient services to corresponding patients.

**References**

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