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Convolution neural network based infection transmission analysis on Covid-19 using GIS and Covid data materials

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ABSTRACT

Towards the improvement of predicting and analyzing the infection transmission, a novel CNN (Convolution Neural Network) based Covid Infection Transmission Analysis (CNN-CITA) is presented in this article. The method works based on both GIS data set and the Covid data set. The method reads all the data from the data sets. From the remote sensing data, the method extracts different climate conditions like temperature, humidity, and rainfall. Similarly from Global Information System data set, the locations of the peoples are fetched and merged. The merged data has been split into number of time frame, at each condition, the data sets are merged. Such merged data has been trained with deep learning networks which support the search of person location and mobility. Based on the result and the data set maintained by the governments, the infection transmission rate has been measured on region basis. In each region of movement performed by any person, the method computes the infection Transmission Rate (ITR) in two time window as before and after. According to the infection rate and ITR value of different region, a subset of sources are selected as vulnerable sources. The method produces higher performance in predicting the vulnerable sources and supports the reduction of infection rate.

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1. Introduction

In the recent times, the novel Corona virus has been identified as the most threatening disease which has been affected by huge world population. The virus has been mentioned as spread from china as it has been first identified in Wugan a city in China. As it spreads from the fish market in that city, and continuous to spread to many countries. The human society facing huge challenge from novel corona virus which is being spread throughout the world more than 230 countries. Still there is no solution has been identified for the problem of Covid-19. As the virus is pandemic which is capable of getting transmitted to person to person in higher rate, containing the rate of infection has become a huge challenge.

According to the media information, the most world countries has enforced lock down to block their people mobility due to the reason that the virus spreads between human to human either by contact or through some water particles expose through the mouth of the human. Due to the infection, there mortality rate has been hiked in Europe countries like Germany, Brazil and many more. The USA (united states of America) has been identified as the

most hit country by the Covid-19 virus. To secure the people from the virus various activities has been taken by different countries but still its rate of infection is getting increased every day. The government of any country is maintaining the details of infected peoples and their location with their mobility. By pinpointing the remote sense data with GIS data set at current time frame, their mobility of different infected peoples who supports the spread of pandemic can be analyzed. According to the data available in both remote sensing and GIS, both can be merged to analyze the transition of infection to different geographic region. This would support the detection of serious carriers and would help to block such serious carriers. Because not all the infected human is capable of transmitting to all others but by identifying the serious carriers, the rate of pandemic can be reduced.

Towards the scope, a CNN based infection transmission analysis model is presented. The method uses both geologic and pandemic data in the transmission analysis. The model split the geographic area into number of regions and measure infection rate on various areas at different time stamp. According to the GIS data and mobility of users, the method computes the infection transmission support (ITS) to find the vulnerable users. Similarly, the CNN is

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adapted for various problems of prediction and the same can be used towards transmission analysis. The data belongs to GIS can be trained and according to the presence of particular person in particular region, the infection induction rate (IIR) can be measured to compute the ITS. To support this, the remote sensing data has been used with the GIS data. The detailed approach is presented in detail in the next sections.

2. Related works

There are a variety of methods explored in the literature to classify susceptible sources for different diseases. This section outlines the collection of strategies associated with the problem.

Remote Sensing in Human Health: A 10-Year Bibliometric Analysis [1] offers an overview of the state of science on the use of remote sensing evidence in human health and highlights the most involved partners, e.g. writers and organisations in the area, to advise future new collaborative research groups. The goal of this research is to analyse, track, map, schedule, distribute and locate government PHCCs in the selected study area in order to incorporate remote sensing and GIS to manage primary health care centers [2]. The paper also focuses on the follow-up of supply and demand in PHCCs; maintaining various health care (HC) facilities in compliance with the requirements and expectations of the Ministry of Health and Population (MOHP) for the incorporation of remote sensing data and geographic information system GIS from a regional and HC viewpoint for the best treatment facility.

Geographical Information Systems (GIS) should be used as a means of preparing for health care providers to reduce the backlog of patients waiting to be seen. In order to determine how useful the associations between Kano Metropolis neurons can be, 6 central blue E-type neurons and 6 central yellow N-type neurons have been picked. The report was performed with ArcView GIS 3.2a for the ArcView GIS analysis and the findings of the research reveal that most health facilities are concentrated between Kano Municipal and Nassarawa and Tarauni. Remote-Sensing Systems for Environmental Health Research [3], address that the International Space Station would acquire three new devices, one that will monitor how winds work across the planet, one that will quantify clouds and aerosols (particles floating throughout the atmosphere)—two factors that remain challenging to forecast in climate change models—and one that will take worldwide, long-term action. With respect to temperatures in a wide range of climate zones across Africa, the best data shows that short-term temperature variations can have a direct effect on pathogen transmission.

Climate Information for Public Health: the role of the IRI Climate Data Library in an Interconnected Knowledge System [4], discuss that the Climate Information for Public Health Initiative of the International Research Institute for Climate and Society (IRI) aims to improve the capacity of the public health sector to recognise, use and demand relevant climate data and climate information. The use of remote sensing as a monitoring instrument for endemic diseases in Brazil [5] poses the characteristics and potentialities of remote sensing as a valuable environmental observation method for applied endemic management research in Brazil. [5] On-board satellite sensors allow a comprehensive study of a given territory, delivering in-depth spatial and temporal information on an extremely broad scale and at a regional level. When [6] the point estimation of SARS-CoV-2 seroprevalence in asymptomatic individuals over time was reviewed [7], two cohort studies were reviewed.

The author discusses two separate aspects in which the hygiene effect could have an influence on our bodies. In the one hand, this will allow our body to remain safe and even develop, but on the other hand, it may also create other issues. Here, it is proposed that the disruption of microbial sharing associated with dysbiosis (loss

of bacterial diversity associated with a microbiota imbalance with deleterious consequences for the host) can worsen the prognosis of COVID-19 disease. In Article [8], the author addresses that the virus has spread around the globe and caused millions of confirmed infections and hundreds of thousands of deaths. To help explain the essence of the pandemic and the emergence and distribution of the virus in Arizona, we sequenced viral genomes from clinical samples examined at the TGen North Clinical Laboratory, the Arizona Department of Health Services, and obtained as part of community monitoring programmes at Arizona State University and the University of Arizona.

In the previous article, [9] the author explains and describes in detail the different clinical dimensions of the Covid pandemic that are spread by inhalation or interaction with infectious droplets and, for example, the incubation time is between 2 and 14 days. Diseases that also contain these symptoms are generally fever, cough, sore throat, shortness of breath, weakness, malaise, among others. The most prevalent cause of disease is cold and mild influenza, where patients suffer nausea, vomiting and diarrhoea, fever, headache, cough, sore throat, exhaustion, weak appetite, ambiguous muscle and joint aches, and sore throat. Any of the symptoms can grow into pneumonia, acute respiratory distress syndrome (ARDS) and multi-organ failure in people with many diseases. The reviewer of the report [10] addresses that COVID-19 is an often occurring virus that could be responsible for pandemics. We can see that, since the majority of cases identified for this disease require more serious treatments, the mortality rate for this disease is poor. In [11], the author addresses AI and big data, then describes AI as a method for detecting COVID-19, then highlights numerous problems and problems, such as the lack of a consistent reference point and the lack of an in-depth understanding of COVID-19, then concludes with a set of communications guidelines aimed at effectively reducing the COVID-19 problem. In [12], the author introduces a new interactive visual interface that displays and compares the pace of spread of the COVID-19 pandemic over time across various countries. We surveyed current visualisation methods used in different websites and media outlets and adopted the use of a knee detection algorithm that divides exponential distribution across several linear components. It was found that during the pandemic, people in European countries travelled five times to reach their favourite destinations, that they wanted to fly to their destination five times, that they selected their destination five times (5), and that they played a random-combination of their U-VNO-VNO journey within their origin-transportation-destination (OTD) network.

In [13], the author used details on the outbreak curve of cases of 2019-nCoV from January 10 to January 24 and used the exponential growth model to predict the number of cases of 2019-nCoV in mainland China from January 10 to January 24, 2020. Using the evolution rate μ and the number of serial intervals (such as 400SI), we calculated the measurement unknown as μ , the evolution rate, using a number such as 400SI of two other well-known coronaviruses. In his article in the "Scandinavian Journal of Infectious Diseases" the author adapted the recorded serial interval (mean and standard deviation) to the gamma distribution and applied the "earlyR" package in R to approximate R_0 at the early stage of the outbreak of COVID-19. The "projections" kit in R was used to predict the predicted projected disease trajectories and potential daily occurrence by fitting the current daily incidence data, the distribution of serial intervals, and the projected R_0 into a model based on the assumption that daily investigators roughly follow Poisson's daily infectious distribution.

In [14], suggest a computational model for the epidemic of Wuhan COVID-19 that takes into account human (e.g. behavioural responses such as accommodation) and government activities such as restricted holidays and quarantine for infected people. In this

publication (under the title “Tick bite poisoning: a fascinating new world of toxicity”), the scientists collected the dates of onset of the disease in cases of tick bites that could lead to tick-borne diseases. All the proof they examined was classified on a scale of 1 to 7 by the review committee in order to convert it into a grade. These ratings were then extended to a subset of pairs with the highest reporting certainty. We correct for the left truncation of the data by using an approximation that is different from the values we have previously measured. [15] records a newly discharged asymptomatic patient with COVID-19 who has been screened positive for SARS-CoV-2. The question is that COVID-19 was the cause of the latest hospitalisation of the patient and other asymptomatic hard-to-diagnose patients. The explanation that 987 new coronavirus cases were identified by Iran as of 1 March 2020 is that, as of 1 March, the country had reported 54 related deaths. We studied the epidemiology of COVID-19 in several Middle East countries and found that at least six neighbouring countries registered imported cases. In this report, data on air transport and the number of cases smuggled from Iran to other Middle Eastern countries were used to approximate the number of COVID-19 cases in Iran. The overall number of cases in Iran was projected to be 16,533 (95% confidence interval: 5925–35,538) by 25 February 2020 before the UAE and other Gulf Cooperation Council countries suspended inbound and outbound flights from Iran.

In [16], the author addresses that the number of new cases of coronavirus (COVID-19) tends to rise worldwide, and the discrepancy between data from China and statistical estimates of occurrence based on cases diagnosed outside of China suggests that a large number of cases remain under-diagnosed (Nishiura et al., 2020a). In [17], the author makes it clear that the viral load dynamics between imported and non-imported patients with clinical characteristics of COVID-19 are distinct. While it will start mostly as pneumonia, there is a small risk of SARS-CoV2 in some patients and the severity of their symptoms may steadily decrease. A family cluster of 2023 novel coronavirus disease (COVID-19) was documented here in [18] to determine its possible transmission during the incubation phase. During the early presymptomatic process, the first patient in this family cluster was identified as the near contact of the reported patient. During the incubation time of this patient, five family members had a close relationship with the first patient. Four of the family members were found to be positive for extreme acute respiratory syndrome coronavirus (SARS-CoV) in the study. In [19], the author indicates that subtle and asymptomatic transmission exists but has not been well described among possible people who may be carriers. Here, we record another set of cases and further illustrate the repeatability of COVID-19 transmission by pre-symptomatic carriers.

Many of the approaches discussed above are affected by higher success in forecasting and defining vulnerable sources.

3. Convolution neural network based Covid infection transmission analysis (CNN-CITA) MODEL

The proposed search engine for the transmission of infection to Covid-19 was developed to assist remote sensing data and GIS for government posts. The process reads all data from the data collection. From remote sensing data, the method extracts various climatic conditions such as temperature, humidity and rainfall. Similar to the Global Information System data collection, the coordinates of the citizens are retrieved and combined. The combined data has been separated into the number of time frames, and at each condition the data sets are merged. Such combined data has been trained in deep learning networks that support the search for location and mobility of humans. Based on the findings and the data collection retained by the governments, support for infection transmission has been assessed on a regional basis. Based on the importance of the ITR in various areas, the system chooses a collection of individuals as susceptible sources. This segment provides a detailed strategy.

The architecture of proposed CNN-CITA model has been presented in the above Fig. 1 where the functional components are detailed in this section.

4. Data preparation

Both satellite and GIS data are merged to produce the image data which is being used in training the network. From satellite images, the features required about humidity, temperature and rainfall are extracted. Similarly, the set of mobile phones located in different region are identified and added to a set. Consider a set of person P located in the region R, then the GIS data has been merged to produce a set GCS which is used to perform infection transition analysis.

Pseudo Code of Data Preparation:

Given: GIS Data Gd, satellite Image Set Sis, Government Data GoD.

Obtain: Region set Rs.

Start

Read Gd, SIS.

Initialize Gabor Filer GF = $GF(Coefficients, i)$
 $i = 1$

Identify set of regions Rs = $\sum_{i=1}^{size(Gd)} Regions \in GD$

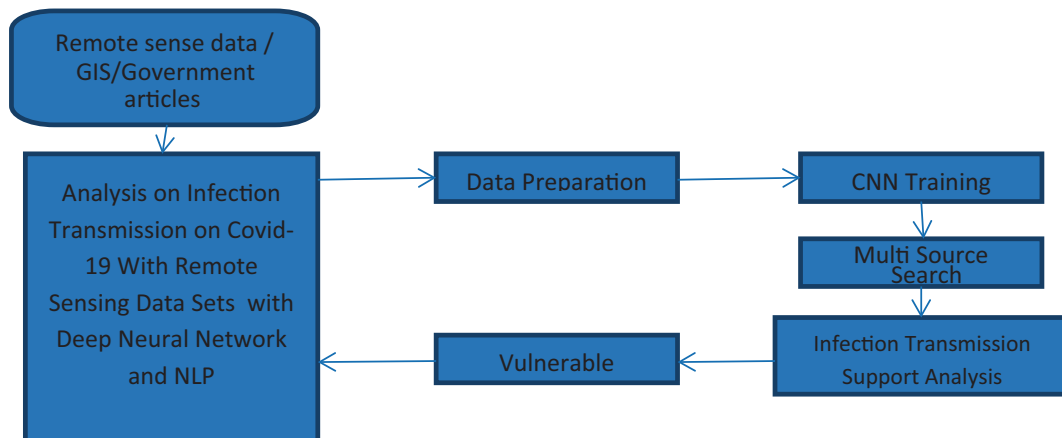


Fig. 1. Architecture of the proposed model.

```

For each region r
  For each time stamp Ti
    SI = Gabor(Gf,SI (r))
    Simp = HistogramEqualization(SI)
    Find list of persons Pl =  $\sum_{i=1}^{size(Gd(r))} Persons \in Gd(r)$ 
    Extract temperature RTemp =  $Temp \in RemoteSenseData(r)$ 
    Extract Humidity RHum =  $Humidity \in RemoteSenseData(r)$ 
    Extract Rainfall Rf =  $Rainfall \in RemoteSenseData(r)$ 
    Extract Infection in region as RI =  $Infection \in GoD(r)$ 
    Feature vector Fv = {Rtemp,Rhum,Rf,RI,Pl}
    Add to region set Rs =  $\sum(Fv \in Rs) \cup Fv$ 
  End
End
Stop

```

The working of data preparation on GIS, Satellite Image and government data towards Covid analysis is presented in the above pseudo code. The method uses all these data to extract different features like the number of persons present in the region, temperature, humidity, rainfall and the infection found at each time window. Each case has been converted into feature vector to support infection transmission analysis.

5. CNN training

The network is trained for number of region where the number of layers are decided by the number of region. The network has been trained with number of layers which is decided by the number of regions identified. Also, for each layer, there will be number of neurons will be generated and initialized according to the number of time stamp found. If the time stamp is about one week or one day, then if the data available is one month, then there will be 30 number of neurons will be generated for each layer. Each neuron has been initialized with the feature extracted in the previous stage. The neurons are designed to measure the infection transmission rate (ITR) which is measured according to the number of previous infection and number of post infection which is measured based on the specific person. According to that, for each person, the method would measure the value of Infection Transmission Support (ITS).

Pseudo Code of CNN Training Algorithm:

```

Given: region set Rs
Obtain: CNN
Start
  Read Rs.
  Initialize convolution neural network CNN.
  For each time window T
    Generate layer l.
    For each region R
      Generate Neuron N
      Initialize neuron with N = Rs(R(T))
      Add to layer.
    End
  End
End
Stop

```

The above algorithm shows how the neural network has been trained to support infection transmission analysis with different data sets.

6. Multi source search

The mobility of persons has great impact in the infection rate of Covid-19. By having GIS data of specific person, the method searches the mobility of a person in each time stamp in different geographic region. According to the GIS data, the method searches

mobility of specific person in multiple regions. Similarly, for each person mobility, the list of regions they moved are identified. According to that, the method person infection transmission analysis to support the control of pandemic. For a specific person, the list of mobility is identified and for each region they moved, the method estimates the infection rate to support the pandemic restriction.

Pseudo Code of Multi Source Search:

Given: GIS Data GD, Government Data GoD

Obtain: Source set Ss

Start

Read GD, GoD.

For each instance I from GoD

Extract text features Tf = $\sum_{i=1}^{size(GoD)} GoD(i).TextFeatures$

Split terms to produce terms set Ts = $Split(Tf, ",")$

For each term Ti

If $Ti \in Stopwordset$ then

 Ts = $Ts \cap Ti$

End

If Ti is name && Result == Positive then

 Add to source set SS = $\sum(Sources \in Ss) \cup Name$

End

End

Stop

The above algorithm represents how the multiple source of Covid transmission is identified. The method uses the government data set and GIS data set to identify such sources towards pandemic restriction.

7. Infection transmission support analysis

The infection transmission analysis is performed according to the value of infection transmission support. To perform this, the method first identifies the list of sources using the document available. According to the details obtained, the CNN Testing is performed where the neurons at the different layer verifies the presence of the person in the region and estimates the infection transmission support ITS according to various features available in the trained sets. Each neuron measure the ITS value and finally yield a cumulative ITS value. Based on the value of ITS, the source has been selected as vulnerable source to help pandemic restriction.

Pseudo Code of Infection Transmission Support Analysis:

Given: CNN, Government Data set GDS.

Obtain: Vulnerable Set Vs.

Start

Read CNN, GDS.

Perform Data Preparation.

Perform CNN Training.

Source set Ss = Perform Multiple Source Search (Government Data set GDS)

For each source s

For each layer l

For each neuron n

 size(N)

 If $Fv(Pl) \in s$ then

 i = 1

 Count = count + 1.

 Compute Current Infection CI = $\frac{Fv(Temp+Humidity)}{Fv(Rainfall)} \times Fv(NI)$

 Compute Infection rate in previous layer IrPl.

 IrPl = $\frac{Fv(l-1)(Temp+Humidity)}{Fv(l-1)(Rainfall)} \times Fv(l-1)(NI)$

 Compute infection rate IR = $\frac{CI}{IrPl}$

 End

End

Compute Infection Transmission Support ITS.

$$ITS = \left(\frac{Fv(Temp+Humidity)}{Fv(Rainfall)} \times Fv(NI) \right) \times Std(IR)$$

If ITS > Th then

Add to vulnerable set VS = $\sum (Sources \in Vs) \cup s$

End
Stop

Table 1
Details of Data set.

Parameters	Value
Tool Used	Advanced java
Data set	GIS, Covid Data set
Number of regions	35
Number of Users	1 million
Time Line	3 months

Table 2
Performance on Infection Transmission Analysis.

Methods	3 Lakhs users	5 Lakhs Users	1 Million Users
Infection Disease System	72	76	79
Hygienic Measures	76	79	83
Screen NC	79	84	86
CNNCITA	86	91	97

Table 3
Analysis on false ratio.

False Ratio on Infection Transmission Analysis			
Methods	3 Lakhs users	5 Lakhs Users	1 Million Users
Infection Disease System	28	24	21
Hygienic Measures	24	21	17
Screen NC	21	16	14
CNNCITA	14	9	3

Table 4
Analysis on time complexity.

Time Complexity in Millie Seconds			
Methods	3 Lakhs users	5 Lakhs Users	1 Million Users
Infection Disease System	73	79	89
Hygienic Measures	69	74	83
Screen NC	56	69	78
CNNCITA	14	21	29

Infection Transmission Analysis Performance

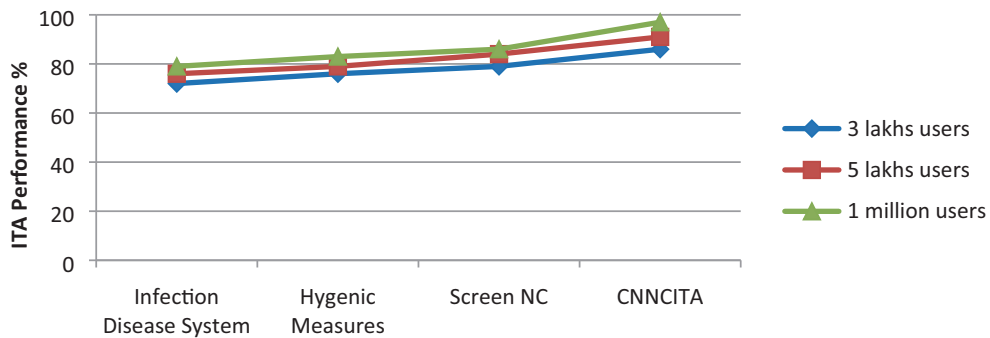


Fig. 2. Analysis on Infection Transmission Analysis.

False Ratio in ITA

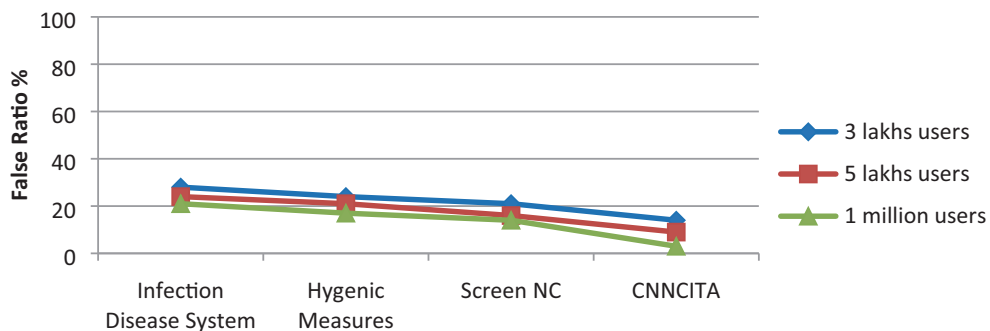


Fig. 3. Analysis on false classification ratio.

Time Complexity in ITA

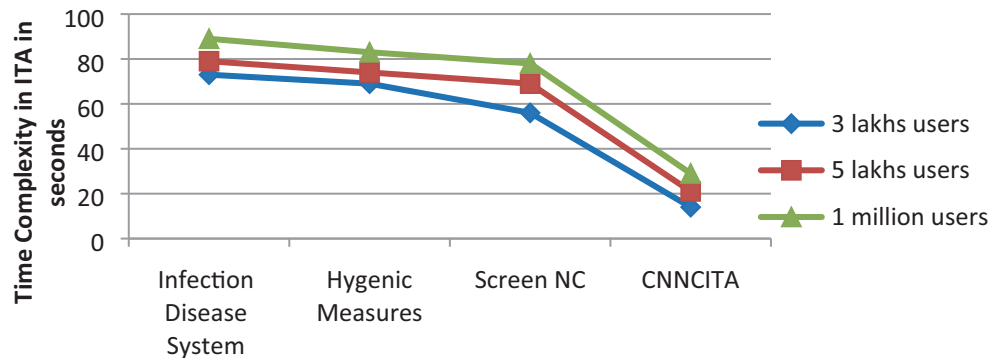


Fig. 4. Analysis in Time Complexity.

The working of infection transmission support analysis is presented in the above pseudo code which measure infection rate on different time stamp at different region and based on that the value of ITS is measured to select vulnerable sources.

8. Results and discussion

The proposed convolution neural network based infection transmission support analysis model is implemented using advanced java and its performance in restricting the pandemic is measured. The performance of the method has been validated under various parameters. The method has been validated for its performance using different data sets. The results obtained have been presented in this section.

The data set being used to evaluate the performance of proposed algorithm has been presented in the Table 1. According to the details in Table 1, the performance of the method has been measured and presented in this section.

The performance on infection transmission analysis produced by different methods are measured and presented in Table 2. The results indicate that the proposed CNNCITA approach has produced higher performance in infection transmission analysis.

The performance in analyzing and identifying the infection transmission produced by different method are measured and presented in Fig. 2. The proposed CNNCITS approach has produced higher performance than other methods (Fig. 3).

The false ratio produced by different infection transmission analysis approaches has been measured and presented in Table 3. The proposed CNNCITA approach has produced less false ratio compare to other techniques.

The performance in classifying the infection transmission in false manner is measured and false ratio is computed for different conditions according to number of persons in each region. According to that, the proposed CNNCITA approach has produced less false ratio than other methods.

The time complexity introduced by different methods are measured and presented in Table 4, which shows the proposed CNNCITA approach has produced less time complexity than other techniques.

The time complexity incurs by different methods in analyzing the infection transmission is measured and presented in Fig. 4. The proposed CNNCITA approach has produced less time complexity in ITA than other methods.

9. Summary

This paper presented a detailed implementation on the CNN based Covid Infection Transmission analysis model. The model starts with data processing or preprocessing which extracts several features from both GIS and remote sense and government data. using the data extracted, the method trains the network with number of layers and neurons. Further the list of persons present in each region are identified and for each of them the method perform ITA which measures the infection transmission support (ITS) based on which the list of vulnerable sources are identified. The proposed model improves the performance of predicting the infection transmission and reduces the false ratio and time complexity.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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International Journal of Environment and Climate Change. He has been awarded with the **BEST RESEARCHER AWARD** on September 5, 2020 on Teacher day by the **GLOBAL EDUCATIONAL AWARD 2020** and has Strong synthesizing, writing, and information technology skills: wrote scientific articles in international peer-reviewed journals, as well as the highly technical replies to the questions raised by the reviewers.