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Modeling of Epidemic Transmission and Predicting the Spread of Infectious Disease

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ABSTRACT
China's Wuhan was the epicenter of coronavirus, reported in December 2019. A month later, there was an intensive outbreak inception. Indeed, epidemiologists and virologists forecasted that the peak of the crisis would be in three months and disappear by the end of the fourth month. However, the virus contagion's healing, prediction, and diagnosis continue to pose critical challenges. In this study, the central objective was to engage in COVID-19 analysis to discern its general diagnosis index via artificial intelligence (AI) application. The motivation was to steer improvements in how accurately the disease could be diagnosed and allow for timely clinical interventions. The sample entailed 85 undiagnosed persons and 32 diagnosed individuals. The research context was in Zhejiang province. To screen the important indexes, four AI technology types were employed. To deal with the problem, some of the feature selection methods that were employed included recursive feature elimination, Gradient boosted feature selection, and the multi-objective decomposition ensemble optimizer (ARMED). In the results, it was noted that out of 18 indexes that were achieved in relation to coronavirus diagnosis, those that matched with the 2019 China virus diagnosis clinical guide included Amyloid-A in the laboratory, 2019 novel coronavirus RNA, Eosinophil rate, Eosinophil count, and white blood cells (WBC). Overall, the method developed was accurate relative to COVID-19 prediction and diagnosis, upon which the rate of confirmed diagnosis could be improved and pave the way for timely clinical interventions.

Keywords: Prediction, diagnosis, 2019 coronavirus, artificial intelligence (AI)

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INTRODUCTION

Following the coronavirus disease outbreak, adverse effects were felt in Wuhan, China, as well as other parts of the world [1]. Currently, much attention has been directed at the trend of ensuring accurate condition diagnosis, upon which the improvements could allow for the timely confirmation of positive patients. From the literature, the timely intervention ensures that there is timely treatment and that any further infections are avoided [2, 3]. Aimed at exploring some of the clinical features and their importance in patients infected with coronavirus, this study applied AI technology. The motivation was to allow for the grasping of the critical index relative to the health condition's diagnosis, allowing further improvements in the rate of confirmed positive cases.

METHODOLOGY

The study was retrospective. Therefore, 85 undiagnosed individuals and 32 diagnosed individuals were selected. Regarding the demographic features of the diagnosed group, female participants were 11, while male participants were 21 within the diagnosed group. Indeed, the participants provided informed consent before participating in the study. For the selected groups, clinical manifestations included chest toughness (2), diarrhea (2), myalgia (1), headache (4), fatigue (4), pharyngalgia (4), sputum (8), cough (20), and fever (29). The table below summarizes the demographic features and clinical manifestations with which the participants presented.

	No.(%)		
	Total (N=117)	Confirmed (N=32)	Unconfirmed (N=85)
Age, years	40 (29-51)	43(34-55)	39 (23-49)
Sex			
Men	69 (59.0)	21(65.6)	48 (56.5)
Women	48 (41.0)	11(34.4)	37 (43.5)
direct Wu Han exposure	67(57.3)	27(84.4)	40(47.1)
Basic disease			
Diabetes	11 (9.4)	2(6.3)	9 (10.6)
Hypertension	13 (11.1)	4(12.5)	9 (10.6)
Cardiovascular disease	15(12.8)	4(12.5)	11 (12.9)
Chronic pulmonary disease	5 (4.3)	2(6.3)	3 (3.5)
Malignancy	7 (6.0)	0 (0.0)	7 (8.2)
Chronic liver disease	5 (4.3)	2(6.3)	3 (3.5)
chronic gastritis	2 (1.7)	2(6.3)	0 (0.0)
Kidney disease	4(3.4)	1(3.1)	3(3.5)

Signs and symptoms			
Fever	54(46.2)	29(90.6)	25(29.4)
Highest temperature, °C			
<37.3	63(53.8)	3(9.4)	60 (70.6)
37.3–38.0	32 (27.4)	19(59.4)	13(15.3)
38.1–39.0	19 (16.2)	8(25.0)	11(12.9)
>39.0	3 (2.6)	2(6.3)	1(1.2)
Cough	71(60.7)	20(62.5)	51(60.0)
Pharyngalgia	22(18.8)	4(12.5)	18(21.2)
Myalgia	1(0.9)	1(3.1)	0(0.0)
Fatigue	13(11.1)	4(12.5)	9(10.6)
Headache	6(5.1)	4(12.5)	2(2.4)
Sputum production	42 (35.9)	8(25.0)	34 (40.0)
Diarrhoea	4 (3.4)	2(6.3)	2 (2.4)
Chest tightness	7(6.0)	2(6.3)	5(5.9)
Systolic pressure, mm Hg	127 (118-138)	129 (120-139)	126 (116-137)
Respiratory rate, per min	19 (18-20)	19 (18-20)	19 (19-20)
CT shows lung changes	101/107(94.4)	32 (100.0)	69/75 (92.0)

Figure 1: Demographic features and clinical manifestations of the participants

To perform the statistical analyses, this study employed SPSS version 25.0 software. For variables that were categorical, they were presented in the forms of percentages and frequency rates. On the other hand, the case of continuous variables saw them presented through values of the interquartile range and the median. Also, P was set at <0.05, perceived to exhibit some statistical significance.

RESULTS AND DISCUSSION

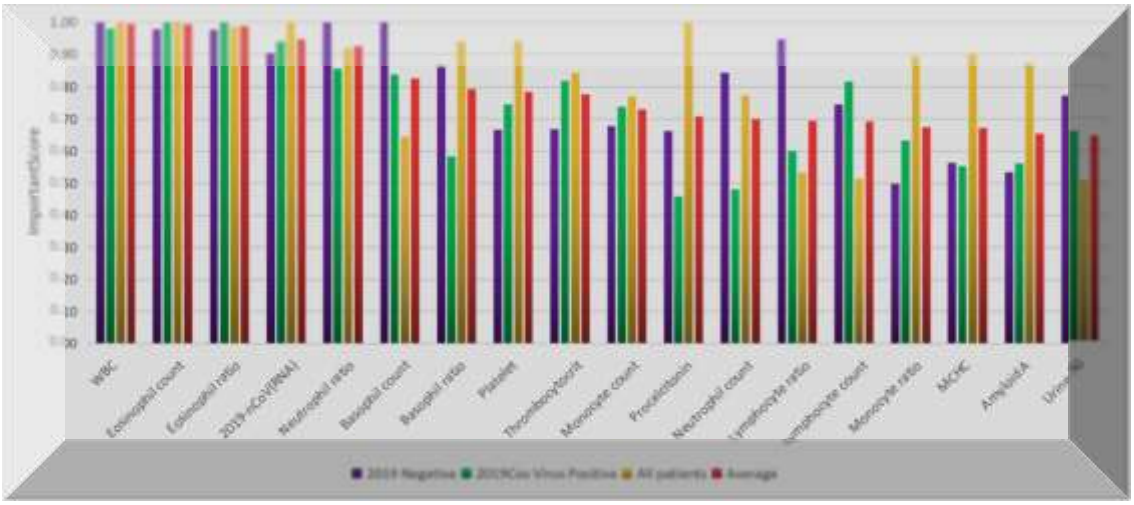

Figure 2: The top 18 critical attributes ranked relative to clinical feature indication

With the characteristics of the individuals analyzed, the most critical indexes that were found to be capable of representing positive Covid-19 diagnosis were 18. The figure above demonstrates the findings, having matched the indexes with the Chinese clinical guide. From the illustration, it can be seen that the negative group exhibited patient characteristics that were unique and differed from the index associated with positive infected confirmed cases. In situations where RT-PCR could not differentiate the patients, other indexes would be used for the evaluation, eventually supplying clinical diagnoses and, in turn, avoiding delayed patient treatment.

From the traditional test relative to patient characteristics, there was a significant difference relative to the clinical guide, including cases of Basophil count, WBC, and Eosinophil rate. For clinical workers, such indexes are likely to be ignored, especially due to the belief that RT-PCR should confirm the positive COVID-19. In the latter scenario, it can be seen that the chances of having increased false negative are higher. However, in this study, with data mining employed, AI technology is seen to demonstrate important disease indications. Also, the use of AI technology posed an advantage, whereby regents' mistakes or other man-made errors did not influence the outcomes.

Based on this study's findings, therefore, it is evident that artificial intelligence strives to respond in a manner similar to that of human intelligence. A key AI characteristic involves reduced workload (because the technology only requires screening the original information and engaging in important attributes' calculation when compared to the case of traditional statistics that demand data unification and neat organization). It is also worth noting that in this investigation, there was the analysis of four types of algorithms, with AI technology aiding in the analysis of three data sets in the total data, the unconfirmed group, and the confirmed group. Particularly, the average would be achieved for the three groups and a cumulative average used for the purpose of sorting the outcomes based on the contribution's size.

Therefore, it can be inferred that the use of AI is changing the world of healthcare, especially in terms of disease diagnosis and prognosis. Furthermore, this study demonstrated that through AI implementation in coronavirus disease diagnosis, a challenge such as man-made deletion could be eliminated, allowing for its usage in big-data environments where samples are large. It was also observed that the use of AI in disease diagnosis steers significant improvements in the prediction and diagnosis accuracy for Covid-19. Based on the test outcomes that were obtained relative to data detection, it was established further that with AI application, there tends to be a a timely mining of correlations among indicators, with the minimum correlations sought and, in turn, reducing indicator redundancy. The latter inferences demonstrate, therefore, that when AI is used towards coronavirus disease prediction and diagnosis, it accounts for screening indicator interoperability. It is further worth noting that the AI implementation approach is promising because the outcomes exhibit some desirable degree of consistency with the outcomes that have been interpreted and interpreted in cases involving traditional statistical techniques.

Indeed, 18 important diagnostic factors associated with the coronavirus disease were mined successfully in this study. The mining was conducted using AI technology. Notably, some that were found to exhibit a desirable degree of clinical significance included Amyloid-A, 2019 new Coronavirus RNA, Eosinophil ratio, Eosinophil count, and WBC. When WBC was evaluated, it was found to be slightly lower or normal. On the other hand, when AI technology was applied to the case of Eosinophil rates, the latter were significantly different when compared to the unproven group, rating at a lower value. It is also notable that the majority of the participants with positive nucleic evaluation samples involved those evaluated via throat swabs.

Regarding the AI method modeling, the objective was to ensure that the important indexes were screened relative to disease prediction and diagnosis, with a particular focus on the COVID-19 disease. Therefore, there was the pre-processing of data sets, including situations that entailed the missing item complement 0 and numerical values. At this stage, some of the state-of-the-art and classical feature selection and attribute reduction techniques that were employed included recursive feature elimination (RFE) [6], Gradient boosted feature selection (GFS) [7], and multi-objective decomposition ensemble optimizer (ARMED) [8] – for attribute reduction. For feature selection, the study gained insights from the outcomes obtained after implementing techniques such as evolutionary non-dominated radial slots based algorithm and sparse re-scaled linear square regression (SRLSR) [9, 10]. For the attribute reduction models, they were used in such a way that each of them engaged in both importance ranking and attribute reduction, whereby for the respective detective indexes, each model's ranking was standardized before taking the average value. As such, the average value became the final ranking. In turn, the following equation was employed for the purpose of calculating the total ranking scores.

$$\text{ImportantS core} = \frac{1}{n}\sum_{j=1}(\text{Ranking}_{j}), \text{j} = 1,\ldots,\text{n}$$

Table 2: Laboratory modeling results summary

	Total (N=117)	Confirmed (N=32)	Unconfirmed (N=85)	Statistics	*P* Value
Blood routine					
White blood cell count, × 10⁹/L	6.2(4.6-8.3)	5.1(4.1-6.0)	6.8(5.0-9.3)	-3.743	0.000
Neutrophil rate , %	69.1(61.2-76.9)	65.8(59.8-71.1)	70.5(61.6-77.4)	-1.605	0.108
Lymphocyte rate , %	22.7(13.8-28.0)	24.0(18.7-28.5)	20.9(12.9-27.4)	-1.593	0.111
Monocytes rate , %	7.7(5.7-10.5)	10.2(6.8-11.5)	7.4(4.9-9.7)	-2.721	0.007
Eosinophil rate , %	0.30(0.00-1.05)	0.00(0.00-0.45)	0.50(0.10-1.50)	-3.499	0.000
Basophil rate , %	0.20(0.20-0.30)	0.20(0.20-0.30)	0.20(0.20-0.40)	-1.206	0.228
Neutrophil count, × 10⁹/L	4.1(2.8-6.4)	3.1(2.5-4.5)	4.6(3.1-6.9)	-3.153	0.002
Lymphocyte count, × 10⁹/L	1.3(0.9-1.8)	1.1(0.9-1.6)	1.3(0.9-1.9)	-1.372	0.170
Monocytes count, × 10⁹/L	0.5(0.3-0.7)	0.4(0.3-0.6)	0.5(0.3-0.7)	-1.363	0.173
Eosinophil count, × 10⁹/L	0.02(0.00-0.75)	0.00(0.00-0.18)	0.04(0.01-0.10)	-3.796	0.000
Basophil count, × 10⁹/L	0.02(0.01-0.02)	0.01(0.01-0.02)	0.02(0.01-0.03)	-3.071	0.002
Red blood cell count, × 10¹²/L	4.68(4.11-5.00)	4.69(4.14-5.09)	4.61(4.10-4.95)	-1.122	0.262
MCH, pg	30.2(29.2-31.1)	30.4(29.2-31.4)	30.1(29.1-31.0)	-0.590	0.555
MCHC, g/L	337(330-344)	337(331-345)	336(329-343)	-1.282	0.200
Haemoglobin, g/L	136(124-151)	142(132-152)	133(123-151)	-1.459	0.145
Platelet count, × 10⁹/L	215(166-251)	197(132-228)	225(187-254)	-2.406	0.016
Thrombocytocrit , %	0.22(0.18-0.26)	0.20(0.15-0.23)	0.23(0.19-0.26)	-2.389	0.017
ESR, mm/H	19(10-36)	15(8-37)	20(10-36)	-0.673	0.501
Interferon-γ, pg/ml	2.8(2.1-4.0)	2.8(1.8-3.7)	2.8(2.8-4.1)	-0.857	0.391

	(0.003-0.010)	(0.002-0.010)	(0.004-0.010)		
Creatine kinase, U/L	79(55-119)	80(67-123)	77(54-119)	-0.229	0.819
Myoglobin, ng/ml	21.0(16-37)	24.1(16.3-39.1)	19.7(15.0-36.3)	-0.565	0.572
Hemagglutination index					
Prothrombin time, s	12.6(11.9-13.5)	12.2(11.6-12.8)	13.0(12.0-13.8)	-2.912	0.004
INR	1.06(1.01-1.11)	1.05(1.01-1.11)	1.07(1.01-1.11)	-0.657	0.511
Activatedpartial	32.2(28.6-37.5)	30.4(28.7-33.0)	32.6(28.6-39.0)	-1.958	0.050
D-dimer, mg/L	0.29(0.20-0.57)	0.24(0.21-0.40)	0.29(0.19-0.65)	-0.787	0.432
Blood gas analysis indicators					
pH	7.42(7.38-7.45)	7.42(7.38-7.44)	7.42(7.39-7.45)	-1.014	0.310
Oxygen saturation, %	97(96-98)	97(95-98)	97(96-98)	-0.843	0.399
PaO2/FiO2	407(339-486)	395(329-476)	419(340-493)	-0.552	0.581
K+, mmol/L	3.5(3.3-3.7)	3.5(3.3-3.6)	3.5(3.3-3.7)	0.497	0.619
Glucose, mmol/L	6.7(5.7-8.7)	6.9(5.8-8.2)	6.7(5.7-10.4)	-0.994	0.320
Total CO2, mmol/L	28.0(26.0-30.0)	28.0(26.0-30.0)	28.0(28.0-30.0)	-0.020	0.984
Cytokine indicators					
CD4, %	30.6(25.2-36.6)	30.1(22.0-35.8)	31.4(26.6-37.0)	-1.416	0.157
Total CD3, %	58.5(51.8-66.3)	58(52-67)	58.5(50.8-68.8)	-0.196	0.845
NK(CD16+CD56), %	16.92(12.10-26.27)	16.92(12.86-27.09)	16.87(11.82-24.37)		0.619
Complement 3, g/L	1.24(1.11-1.40)	1.23(1.07-1.45)	1.27(1.12-1.40)	-1.103	0.270
IL-2, pg/ml	2.4(2.1-2.8)	2.3(1.2-2.6)	2.4(2.2-2.8)	-1.922	0.055
IL-4, pg/ml	2.3(1.6-2.9)	1.9（1.3-2.7）	2.5(2.0-3.1)	-2.697	0.007
IL-6, pg/ml	7.4(4.5-14.3)	9.1(4.5-27.3)	6.9(4.3-12.8)	-0.843	0.399
IL-10, pg/ml	4.2(3.3-6.8)	4.6(3.3-7.9)	3.9(3.3-6.6)	-0.696	0.487
Urine routine					
Urine SG	1.02(1.01-1.03)	1.02(1.01-1.03)	1.02(1.02-1.03)	-0.831	0.406
Urobilinogen	8.1(8/99)	10.7(3/28)	7.0(5/71)	-0.601	0.548
Urobilin	0.0(0/99)	0.0(0/28)	0.0(0/71)	0.000	1.000
Urine protein	25.3(25/99)	28.6(8/28)	24.3(17/70)	-0.475	0.635
Urine VLC	0.0(0/99)	0.0(0/28)	0.0(0/71)	0.000	1.000
Infectious index					
Procalcitonin, ng/ml	0.05(0.02-0.10)	0.04(0.02-0.06)	0.05(0.02-0.155)	-1.614	0.107
C-reactive protein, mg/L	10.0(4.1-27.0)	12.1(3.3-22.1)	9.7(4.3-29.9)	-0.410	0.682
Amyloid A, mg/L	64(20-193)	43(18-183)	81(22-199)	-0.744	0.457
Biochemical Indicators					
ALT, U/L	17(11-30)	21(16-34)	15(10-27)	-2.728	0.006
Alkaline phosphatase, U/L	72(60-86)	69(56.3-81.8)	77(61-89)	-1.945	0.052
Direct Bilirubin, μmol/L	3.8(2.6-5.5)	3.0(2.4-4.8)	4.1(2.7-5.8)	-1.282	0.200
α-L-Fucosidase, U/L	28(22-34)	29(23-35)	28(22-32)	-2.785	0.005
Total protein, g/L	68.4(63.3-73.3)	68.7(63.8-75.8)	68.2(63.2-72.1)	-1.024	0.306
Albumin, g/L	41(38-44)	41(38-44)	41(37-44)	-0.179	0.858
Albumin/Globulin	1.5(1.3-1.6)	1.4(1.3-1.7)	1.5(1.2-1.6)	-0.727	0.467
Phosphorus, mmol/L	1.11(0.92-1.24)	1.12(1.05-1.26)	1.08(0.88-1.23)	-0.816	0.414
Cholesterol, mmol/L	3.97(3.38-4.87)	4.27(3.58-5.03)	3.89(3.36-4.82)	-0.218	0.828
Apolipoprotein A Ⅰ, g/L	1.27(1.09-1.47)	1.26(1.02-1.42)	1.29(1.11-1.50)	-0.502	0.616
Apolipoprotein B, g/L	0.77(0.64-0.99)	0.81(0.66-1.02)	0.76(0.64-0.93)	-0.955	0.339
Creatinine, μmol/L	72(62-86)	75(66-91)	71(58-84)	-1.501	0.133
Troponin-I, ng/ml	0.010	0.009	0.010	-1.564	0.118

In the table above, the mean corpuscular hemoglobin concentration is represented by MCHC, while the mean corpuscular hemoglobin is represented by MCH. Also, values that were deemed statistically significant were set at p<.05. Indeed, P values strived to give insight into differences that could be observed in the modeled scenario for the findings in both the unconfirmed and the confirmed group.

At this stage, it can be seen that in a similar fashion to the case of intelligence that humans exhibit, AI could respond with promising trends relative to disease prediction and diagnosis, COVID-19, in this case. In the modeled cases, findings can be seen to suggest that through AI incorporation into disease prediction and diagnosis, a major beneficial outcome that is felt involves a significant reduction in the workload. It is important to note that the use of traditional statistical techniques has its success in disease prediction depend on the degree to which there is the unification of data, as well as its neat organization. However, in this study, it can be seen that relative to the aspect of epidemic transmission and infection disease spread prediction, the incorporation of AI technology, as modeled in the investigation, only requires the screening of the original data, upon which critical attributes are calculated. The resultant inference is that the proposed method of incorporating AI technology into disease prediction and diagnosis, including the case of COVID-19, poses a beneficial outcome in such a way that it causes a significant reduction in the workload.

The study is, therefore, seen to extend the work of recent scholarly studies that have concentrated on the incorporation of AI into clinical scenarios. Previously, studies have concentrated on cancer disease diagnosis and prognosis [11-13]. Thus, similar to such previous studies, this investigation has demonstrated that through AI usage in infectious disease spread prediction and epidemic transmission in large populations, AI utilization as an approach for predicting the aforementioned variables is a promising approach, whereby the resultant improved state of accuracy ensures that problems such as man-made deletions are eliminated. From the literature, when traditional statistics are applied to situations entailing large sample sizes, they remain prone to the perceived man-made deletions, upon which the accuracy of the approaches in relation to infectious disease spread and epidemic transmission prediction tends to be compromised [14, 15].

Three models were also evaluated, and comparative results obtained. In the modeled approach, the assessment of the three models sought to give insight into a framework that could be deemed ideal to ensure that through AI technology incorporation, it predicts infectious disease spread and epidemic transmission more accurately. These models included the Gompertz model, the Bertalanffy model, and the Logistic model. From the modeling, the results were obtained as shown in the figures below.

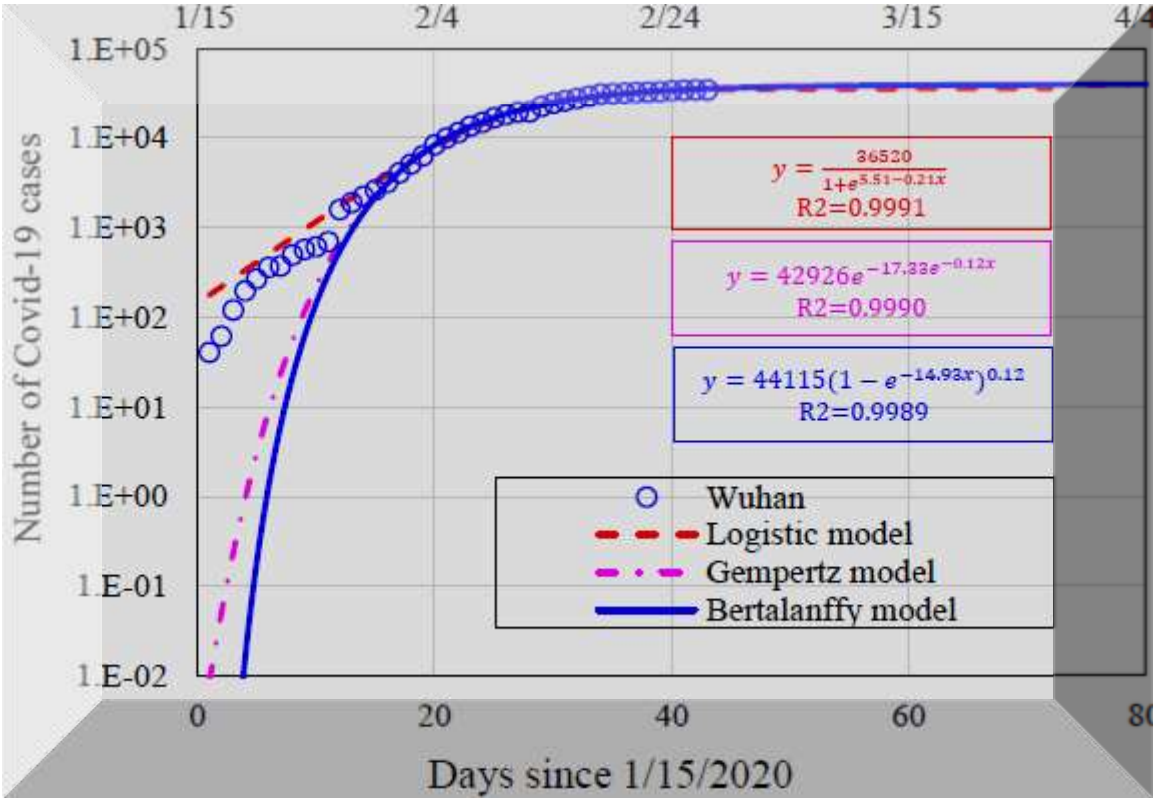

Figure 3: Comparative results for model performance regarding AI technology usage in confirmed case prediction

From Figure 3 above, it is evident that the three frameworks, relative to the incorporation of AI technology into disease prediction, can predict infectious disease spread and epidemic transmission well, both in the late and early stages of the epidemic, COVID-19 in this case. However, it is important to note that the Logistic model outperformed the other two frameworks, especially when the aspect of fitting all the data was considered.

In this case, with the COVID-19 detection data on the focus, it can be observed that the results and many test indicators demonstrate that when the AI approach is utilized, as demonstrated by the modeled approach and results in the study, the correlation between indicators could be mined easily. The latter outcome, thus, suggests that AI utilization in infectious disease spread and epidemic transmission gives real-time results, paving the way for interventions that are so timely that the spread could be contained effectively. Similarly, the modeled results suggest that the use of AI is a targeted approach aimed at seeking minimum correlations. From the literature, this trend demonstrates that for the indicators, redundancy is, in turn, reduced [13]. This modeling has demonstrated further that with the incorporation of AI technology into infectious disease spread and epidemic transmission prediction, the approach accounts for or considers the screening indicators' interoperability, suggesting that it outperforms traditional statistical methods because the path followed ensures consistency in the results obtained.

In this study, 18 critical diagnostic factors were mined successfully using AI technology, with the specific epidemic on the focus being coronavirus. Some of the selected diagnostic factors in the category of the 18 factors included Amyloid-A, 2019n-CoV, Eosinophil ratio, Eosinophil count, and white blood cells (WBC). Given that for nucleic acids, respiratory tract samples were found to be positive, the implication for healthcare systems is that the need to embrace isolation measures could not be overstated, specific examples being the use of impermeable isolation clothing and medical protective masks. Also, it can be seen that whereas feces could be used to detect nucleic acid [2], the fact that fecal-oral transmissions have been documented implies that there is a need for further observation and research to confirm the same [14].

This study also led to the insight that SAA (Amyloid-A) forms one of the most important phase- response proteins and that under normal scenarios, the content is small. However, upon virus- or bacteria-based body simulation, the modeling results demonstrate that SAA secretes much of these proteins. In a span of about five to six hours, the simulation outcomes suggested that there is an increase of about 1000 times in the SAA amount that enters the blood, following body stimulation, either by a virus or bacteria. Given that the latter aspects cause significant declines in recovery from disease, as well as shorter half-life, the resultant observation is that AI utilization in infectious disease spread and epidemic transmission is a promising path because it gives insight into how a diagnostic indicator such as SAA could increase the understanding of infectious disease behavior. In particular, the modeling results depict the superiority of AI technology incorporation in disease prediction, whereby the approach allows for the understanding of the rate at which the SAA amount enters the blood, with Amyloid-A already documented to be an infectious disease indicator. Therefore, AI technology is found to be crucial as revealed in the modeling results because it allows professionals to gain insight into the rate of SAA entry into the blood; hence, allowing for disease prognosis and diagnosis in real-time.

Despite the promising nature of the study, however, which points to the efficacy, effectiveness, and superiority of the performance of a system that integrates AI technology into infectious disease spread and epidemic transmission prediction, this modeling study had the majority of the participants belong to the light and ordinary group. Therefore, for individuals experiencing conditions such as neo-coronary pneumonia, it becomes important to discern the degree to which AI technology usage in the prediction of infectious disease spread and epidemic transmission could be harmful or transformational. For the COVID-19 disease, such further clinical investigations ought to target patients who are approaching or have reached a severe state of hypoxemia, upon which the efficacy of the proposed and modeled approach of AI incorporation into disease behavior prediction could be confirmed – or otherwise. It is also recommended that future studies seeking to extend this work that involves disease prediction modeling to discern the efficacy of AI technology incorporation compare the results with clinical trials, upon which the accuracy of the modeling could be determined, especially when more comprehensive clinical data is available. Overall, however, this study has demonstrated that based on the modeling results, the incorporation of the proposed approach of AI technology into infectious disease spread and epidemic transmission prediction (with coronavirus taken as a selected case to which the modeling is applied) offers assistance and decision support towards accurate disease treatment and diagnosis.

CONCLUSION

In summary, China's Wuhan was the epicenter of coronavirus, reported in December 2019. A month later, there was an intensive outbreak inception. Indeed, epidemiologists and virologists forecasted that the peak of the crisis would be in three months and disappear by the end of the fourth month. However, the virus contagion's healing, prediction, and diagnosis continue to pose critical challenges. In this study, the central objective was to engage in COVID-19 analysis to discern its general diagnosis index via AI application. The motivation was to steer improvements in how accurately the disease could be diagnosed and allow for timely clinical interventions. The sample entailed 85 undiagnosed persons and 32 diagnosed individuals. The research context was in Zhejiang province. To screen important indexes, four AI technology types were employed. To deal with the problem, some of the feature selection methods that were employed included recursive feature elimination, Gradient boosted feature selection, and the ARMED optimizer. In the results, it was noted that out of 18 indexes that were achieved in relation to coronavirus diagnosis, those that matched with the 2019 China virus diagnosis clinical guide included Amyloid-A in a laboratory, 2019 novel coronavirus RNA, Eosinophil rate, Eosinophil count, and WBC. Overall, the method developed was accurate relative to COVID-19 diagnosis, upon which the rate of confirmed diagnosis could be improved and pave the way for clinical interventions.

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