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A Simple Point Score Model for Prediction of Covid-19 in Some Egyptian Patients

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Abstract

On a global scale, a substantial number of newly diagnosed cases of the covid-19 virus and a considerable number of associated fatalities are recorded weekly. Its laboratory detection depends on the costly and time-consuming real-time PCR analysis. A simple way to facilitate the diagnosis of Covid-19 is still required. Here, it was aimed to generate a simple point score as a prediction model for fast diagnosis of Covid-19 using simple laboratory analyses. 121 adult individuals with qRT-PCR results served as a training group, whereas 35 individuals were used as a validation group. Different laboratory analyses, including complete blood count (CBC), differential count, D-dimer, C- Reactive Protein (CRP), and Ferritin, have been recruited as predictors using the Receiver Operating Characteristic (ROC) analysis. The results revealed three models, depending on the predictor parameters' ROC area (AUC). The simplest model consisted of the data of the three predictors: lymphocytopenia, CRP, and D-dimer, and resulted in a ROC AUC value of 0.9773. The use of the three models on the validation group provided support for the conclusion that the calculation of lymphocyte count, CRP, and D-dimer is enough for predicting the occurrence of Covid-19.

Keywords: Covid-19; prediction; point-score; model; lab analysis.

Introduction

The outbreaks of MERS (Middle East Respiratory Syndrome) and SARS (Severe Acute Respiratory Syndrome) in 2002 and 2012 led to public health emergencies against coronavirus (CoV). According to etiological reports, at the end of 2019, unknown pneumonia broke out in Wuhan with almost 11 million people (Lu et al, 2020), the most populated city in central China. This SARS-CoV-2, an emerging virus in the coronavirus family, may have originated from a bat-SARS-like coronavirus. After changes in the spike glycoprotein (Protein S) and nucleocapsid N-protein, the virus infected humans (Benvenuto et al., 2020)

The World Health Organization (WHO) has

named this pandemic infection the 2019 Coronavirus Disease (Covid-19); it is considered the greatest global biological threat to humankind. Although the fatality rate is lower than that of SARS and MERS, the virus's low pathogenicity and long incubation time (up to two weeks) increase the danger of SARS-CoV-2 transmission and encourage it (Wu & McGoogan, 2020). Covid-19 is a mysterious respiratory and systemic illness with clinical signs and symptoms, including dry cough, shortness of breath, and fever. In some cases (8-15% depending on geographical area and personal characteristics), it causes critical situations that require special treatment in the intensive care unit (Xu et al., 2020).

Based on the data from the WHO, Covid-19 has spread worldwide. As of June 20, 2020, over 8.9 million sufferers have been diagnosed in over 210 countries, with over 465,000 deaths. As of 19 February 2023, more than 757 million verified Covid-19 cases and 6.8 million deaths have been recorded worldwide [WHO, 2023].

Most published articles related to Covid-19 described clinical aspects and imaging findings; others focused on the diagnostic and prognostic significance of abnormal laboratory data (Lippi & Plebani, 2020). Also, Some recent articles review the diagnostic approach to Covid-19, for example, Laboratory treatment for Several kinds of specimens and sampling problems. La Marca et al. (2020) evaluated the efficiency of laboratory techniques to aid in creating algorithmic treatment methods and healthcare tactics. In a study conducted by Cui and Zhou (2020), they measured and compared biomarkers for the diagnosis of Covid-19. They also identified the appropriate time to collect each sample. The article discussed the challenges associated with diagnosing Covid-19, such as the absence of a universal standard and the challenges of conducting mass screening and testing. This was highlighted by Xu et al. (2020). Li and Ren (2020) conducted a study to investigate the infection potential of domestic and farm animals using human-animal ACE2 receptor sequence analysis. Their findings suggest that SARS-CoV-2 can infect other human species and vice versa.

In this study, it was aimed to apply some blood tests, including complete blood counts such as hemoglobin, RBC, platelet, WBC counts, and differential count (Lymphocyte, Neutrophil lymphocyte Ratio (NLR), CRP, D-dimer, and Ferritin, on some Egyptian patients to make a scoring system for Covid-19 diagnosis and assessment of its diagnostic power.

Materials and Methods

Study population

This study was conducted on patients at the Chest and Clinical Pathology departments at New Damietta Hospital of Al-Azhar University from May 2021 to February 2022**.** Several 156 study participants. Of them, 121 served as a training group to develop the point score model, whereas 35 patients later served as a validation group. The training group consisted of 81 patients diagnosed as Covid-19-positive and confirmed by positive PCR analysis, and 40 individuals had negative PCR and served as a control group. The validation group consisted of 22 positive and 13 negative PCR-diagnosed Covid-19 individuals.

In all cases, children below 16 years old and patients with any chronic illness or viral infection affecting lab results have been excluded.

Data Collection

All participants were subjected to some laboratory tests: 1. CBC including hemoglobin level estimation and the counts of RBCs, Platelet, total WBCs and differential counts (lymphocyte, neutrophil, monocyte, neutrophil-lymphocyte Ratio (NLR), and eosinophils), 2. D-dimer in a citrated plasma sample, 3. CRP, and 4. ferritin levels in the serum.

CBC and its differential count were analyzed using the automated hematology analyzer (Sysmex XS-500i, Japan).

The D-dimer level was used to determine if a subject had a blood clotting disorder. The Roche Cobas C311 Automated Chemistry Analyzer, Germany, tested D-dimer using an immunoturbidimetric assay with a 0 - 0.50 mg/L reference range. The same system was used in the measurement of CRP and Ferritin. CRP is a protein produced by the liver and released into the blood as a reaction to inflammation. Ferritin is a protein found within cells that can store and release iron in a regulated manner. It is a crucial protein for storing iron within the cells of all organisms. Its primary function is to keep iron non-toxic and dissolved.

Real-time PCR was recruited to analyze samples taken from the upper respiratory tract to detect the covid-19 RNA that is the cause of the disease. This test was the reference test for Covid-19 diagnosis. This test used (COBAS 6800) which is completely automated as well.

Statistical analysis

Every evaluation of statistics was performed with Stata software. The mean ± SEM and/or median were used to express continuous data variables. A Kolmogorov-Smirnov test was used to assess the normal distribution of the parameters. The unpaired Student's t-test was used to compare variables between negative and positive Covid-19 values. A significant value was considered to be $p<0.05$. The area under the Receiver Operating Characteristic Curve (AUROC) was utilized to evaluate all scores. Scores can range from 0 to 1, with AUROC's 0.5 indicating no differentiation, scores of 0.7 to 0.8 are considered good, 0.8 to 0.9 very good, and greater than 0.9 exceptional. The stepwise linear regression analysis included only the significant parameters with a high area under AUC to develop a diagnostic model for Covid-19. The AUC was used to measure the diagnostic power of the developed model. The predictive score was formulated by selecting the best cut-off values to achieve the highest possible sum of sensitivity and specificity.

Results

This study aimed to derive a point-score model for predicting the incidence of MERS-CoV-19 from the least measured laboratory analysis parameters. Two patient groups participated in the present study: negative (n-40) and positive Covid-19 patients (n=81). The result of MERS-CoV qPCR positivity differentiated both groups.

Results of laboratory analyses

All participants have been analyzed for complete blood count (CBC), including RBCs, WBCs, and platelets. The differential count has also been included, including lymphocytes, neutrophils, monocytes, and eosinophils. The neutrophil/lymphocyte ratio (NLR) was computed by splitting each sample's total number of neutrophils/lymphocytes. In addition, the three important parameters CRP, D-dimer, and Ferritin have been estimated in the sera of all patients.

As shown in Table 1, Covid-19 positive patients had significantly different values of leukocytes, lymphocytes, NLR, CRP, D-dimer, Ferritin, and platelet count. They were characterized by lymphocytopenia, lower levels of WBCs and platelet counts, and higher levels of CRP, D-dimer, and Ferritin. Covid-19 patients were significantly younger than the control collection.

There is no distinction between both groups in either RBC, monocyte, eosinophil counts or hemoglobin content.

Table 1. Laboratory analysis parameters of patients included in the study

	Negative Covid-19		**Positive Covid-19**		
	Mean±SEM	**Median (q1-q3)**	**Mean±SEM**	**Median (q1-q3)**	**P value**
Age (yr)	45.28±1.57	45.00 (35.75-53.00)	39.70±1.48	39.00 (29.00-49.00)	**0.018**
RBCs (x10^6/µl)	4.97±0.07	5.10 (4.68-5.40)	4.87±0.08	4.80 (4.40-5.20)	0.249
Hb (g/dl)	12.69±3.18	12.65 (11.38-13.83)	13.13±2.19	13.00 (12.00-14.20)	0.090
Platelets (x10^3/µl)	324.30±12.63	287.5 (248.8-382.5)	255.43±14.26	210.0 (183.0-289.0)	**0.002**
WBCs (x10^3/µl)	9.88±0.49	9.00 (6.38-12.00)	8.05±1.63	5.70 (3.60-12.30)	**0.037**
Neutrophils (%)	58.36±1.09	57.95 (52.60-64.45)	62.95±1.88	63.00 (50.60-78.70)	0.123
Lymphocytes (%)	34.41±1.33	32.00 (27.63-40.05)	17.18±1.19	14.00 (10.70-19.00)	**0.000**
NL Ratio	1.94±0.10	1.70 (1.30-2.45)	5.01±0.36	4.37 (2.88-6.57)	**0.000**
Monocytes (%)	5.69±0.14	5.55 (4.60-6.15)	5.61±1.34	4.70 (3.80-6.70)	0.452
Eosinophils (%)	2.02±0.03	2.00 (2.00-2.03)	1.87±0.16	2.00 (1.50-2.00)	0.130
CRP (mg/dl)	6.34±0.29	6.00 (5.00-8.03)	36.14±3.83	24.00 (15.00-48.00)	**0.000**
D-Dimer (mg/L)	0.27±0.02	0.22 (0.12-0.42)	0.99±0.09	0.70 (0.55-0.90)	**0.000**
Ferritin (µg/L)	227.85±13.72	240.0 (153.0-302.0)	322.21±11.12	300.0 (242.0-400.0)	**0.000**

Data are provided as mean, standard error of the mean (SEM), and median (interquartile range: 25th (q1) - 75th (q3)). A Kolmogorov-Smirnov test was used to determine the normality of the quantitative parameter distribution. The unpaired student's t-test was used to compare variables. Statistical significance was defined as a p-value less than 0.05.

Receiver operating characteristic (ROC) analyses

The ROC curve is a graphic illustration of a binary categorization system's performance, which shows how well it performs as the discrimination threshold changes. The ROC curve is created by graphing the true positive rate (TPR) versus the false positive rate (FPR) at different cut-off settings. The term "sensitivity" is used interchangeably with the actual positive rate. The probability of a false positive is commonly called the false alarm probability. It can be calculated by (1-specificity). ROC analysis offers the chance to identify potentially best models while discarding those less than optimal.

To create a ROC curve, you only require the True Positive Rate (TPR) and False Positive Rate (FPR), as shown in the example figure below. The TPR, or True Positive Rate, represents the proportion of positive samples that yield strictly positive results. FPR represents the number of false positives within negative samples. The ROC space is characterized by the FPR (sensitivity) and TPR (1 - specificity), which are the x and y axes, respectively. Thus, the optimal prediction would result in a data point reflecting 100 percent sensitivity (no false negatives) and 100 percent specificity (no false positives). This point serves as the ideal.

Random guesses will lead to a point on the diagonal nondiscrimination line from bottom left to top right (see the following figure as an example). The ROC space is divided by this diagonal line. Points above this represent good prediction outcomes and a point would get a better predictor when it gets closer to the "perfect classifier" point. If points above the diagonal are plotted as a curve, the area between this curve and the diagonal is called "Area Under Curve, AUC"—values of AUC range from 0-to-1. Thus, a 0 value means the curve is lying on the diagonal line, and a 1 value is on the "perfect classifier" point and a perfect prediction.

In the present study, the ROC curve was applied for the parameters as predictors for Covid-19 incidence, considering the PCR result as the dependent parameter. The ROC analysis computed the AUC of all tested parameters from all collected samples (Figure 1). The arrangement of AUC values (Table 2) helped discriminate potential predictive parameters for Covid-19 and calculate the predictive model.

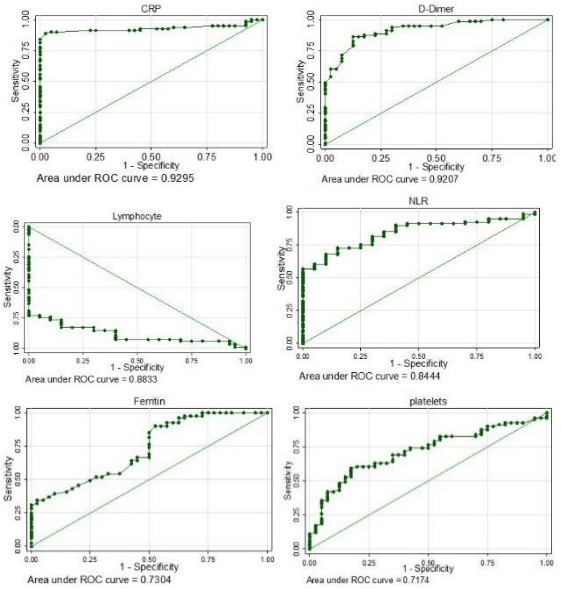

Figure 1a. The good predictors: Receiver operating characteristic curve of different laboratory measured parameters as predictors for Covid-19. The analysis was based on Covid-19 PCR value (positive/negative) as the dependent variable and different parameters as independent variables. Good predictors are those with an AUC value closer to 1.

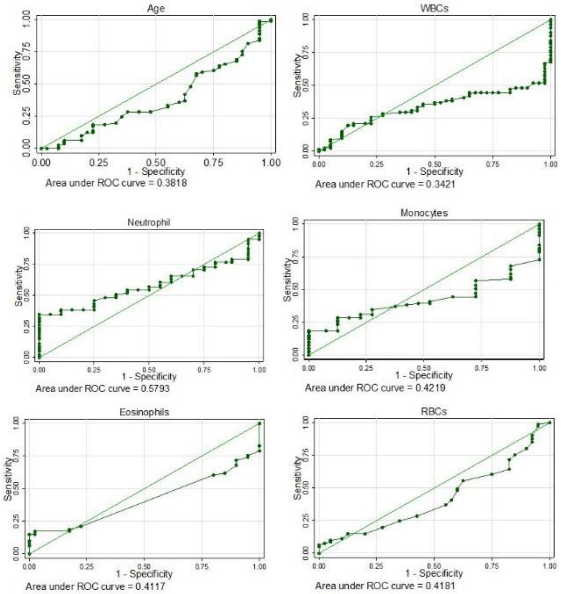

Figure 1b. The bad predictors: Receiver operating characteristic curve of different laboratory measured parameters as predictors for Covid-19. The analysis was based on Covid-19 PCR value (positive/negative) as the dependent variable and different parameters as independent variables. Bad predictors are those with AUC values around or less than 0.5

Table 2. The area under the ROC curve (AUC) for different applied predictors with 95% confidence level intervals

Parameter	AUC area	Std. Err.	[95% Conf. Interval]	
CRP	0.9295	0.0257	0.86350	0.96543
D-dimer	0.9207	0.0243	0.85326	0.95966
Lymphocytes	0.8833	0.0306	0.81349	0.93528
NLR	0.8444	0.0349	0.7657	0.90273
Ferritin	0.7304	0.0485	0.63883	0.80425
Platelets	0.7174	0.0473	0.62482	0.81006
Neutrophils	0.5793	0.0508	0.47983	0.67881
Monocytes	0.4219	0.0507	0.32246	0.52136
RBCs	0.4181	0.0547	0.31077	0.52534
Eosinophils	0.4117	0.0476	0.31842	0.50504
Age	0.3818	0.0546	0.29348	0.47287
WBCs	0.3421	0.0484	0.24723	0.43703

Parameters are descending and arranged according to their AUC areas.

Establishing a predictive model for diagnosis of Covid-19 from blood analysis

To facilitate clinical use and further assessment for diagnosis, three novel scoring models were established according to the nomogram results, which score from 0 to 3 points, as listed in Table 3. The scoring models were developed using logistic regressions. ROC analysis assumes The best model to have the most significant AUC. Based on the previous results, 7 parameters have been selected to build the Covid-19 point score model. The selection depended on two factors: significantly different values for these parameters between negative and positive corona patients and the highest AUC for each of the three models. Lymphocyte count has 4 levels: more than 18% were assigned as score 0, between 15% and 18% were assigned as score 1, between 12% and 15% were assigned as score 2, and less than 12% were assigned as score 3. For CRP, there were 4 levels: CRP between 0.3 mg/dl and 1.0 mg/dl were assigned as score 0, between 1 and 10 were assigned as score 1, between 10 and 50 were assigned as score 2, and more than 50 were assigned as score 3. For D-Dimer, there were 2 levels: up to 0.5 mg/L were assigned as 0, and more than 0.5 mg/L were assigned as 3. For Ferritin, there were 2 levels: up to 200 µg/L (female) or 300 µg/L (male) were assigned a score of 0, and more than 200 µg/L (female) or 300 µg/L (male) were assigned a score of 2. For NLR, there were 4 levels: up to 2 were assigned as score 0, between 2 and 6 were assigned a score 1, between 6 and 9 were assigned as score 2, and more than 9 were assigned as score 3. There were 2 levels for WBCs, between 4.5 $x10^3$/µl and 10 $x10^3$/µl were given a score as 0, less than 4.5 $x10^3$/µl and mg/dl and more than 10 $x10^3$/µl were assigned a score as 1. For platelet count, there were 2 levels between 150 $x10^3$/µl and 440 $x10^3$/µl were assigned a score of 0, and less than 150 $x10^3$/µl and more than 440 $x10^3$/µl were assigned a score of 1.

Table 3. Point score models to predict the incidence of Covid-19

Model 1	**Model 2**	**Model 3**	**Calculated**			**Score**	
16 points	11 points	9 points	components	0	1	2	3
			Lymphocyte-openia	>=18%	<18% - >15%	<15% - >12%	<12%
			CRP	Minor elevation (0.3 - 1.0 mg/dl)	Moderate elevation (>1.0 - 10.0 mg/dl)	Marked elevation (>10 - <50 mg/dl)	Severe elevation (> 50 mg/dl)
			D-Dimer	up to 0.5			>0.5
			Ferritin	up to 200 (female) or 300 (male)		> 200 (female) or 300 (male)	
			NLR*	up to 2	>2 to 6	>6 to 9	>9
			WBCs	4.5-10	<4.5or >10		
			Platelets	150-440	<15- or >440		

The models depended on scores from 0 to 3 for each predictor, which resulted in a maximum of 16, 11, and 9 points for models 1, 2, and 3, respectively.

The 3-point-score models

Based on the data provided in Table 3, it has been determined that three models have been created to score points and predict the likelihood of Covid-19 in patients. The accuracy of predicting severity was assessed using the Model 1 scoring system, which yielded an AUC of 0.9914 (Figure 2). The sensitivity was 91.36%, while the specificity was 97.5%. Each score was calculated, resulting in 0 to 15 cut-off points. Individuals who scored below 6 were considered at minimal risk of Covid-19 infection, while those who scored 6 or higher were classified as having an

increased risk.

In Model 2, 4 parameters (lymphocyte, CRP, D-Dimer, Ferritin) have been recruited, with a maximum score of 11 (Table 6). In this model, AUC was 0.9873 (Figure 2), the sensitivity was 90.12% and the specificity was 97.5% for prediction. Calculate a score for each patient with a cut-off point ranging from 0 to 11. Individuals with a score below 5 were considered to be at minimal risk of Covid-19 infection, and those with a score of 5 or higher were considered to be at high risk.

In model 3, only 3 parameters (lymphocyte, CRP, D-dimer) were used (Table 3), with a maximum score of 9. In this model AUC was 0.9773 (Figure 2), the sensitivity was 92.59% and the specificity was 82.5%. Each score was calculated, resulting in 0 to 9 cut-off points. Individuals with a score below 3 were considered at minimal risk of Covid-19 infection, while 3 or more were defined as having a high risk.

Evaluating and validating different results in Covid-19 models

An independent group of 35 patients was used to validate the models. This group consisted of 22 PCR-diagnosed positive Covid-19 and 13 negative subjects.

The laboratory analysis results of different parameters of the validation group are summarized in Table 4. This table compares the biological blood tests of patients validated with positive and negative RT-PCR. The validation group (n=35) had an average age of 44.38±5.92 and 45.14±3.64 years for the negative and positive Covid-19, respectively. Between positive and negative Covid-19 patients, there was a difference in the number of blood lymphocytes, NLR, D-dimer, and CRP. Positive RT-PCR patients had higher CRP (p = 0.000), neutrophil (0.000), NLR (P = 0.000), and D-dimer (p =0.000) levels in the serum. In addition, lower lymphocyte count (p =0.000), and WBCs (p = 0.000). No significant difference was observed in platelet (p = 0.229) for both.

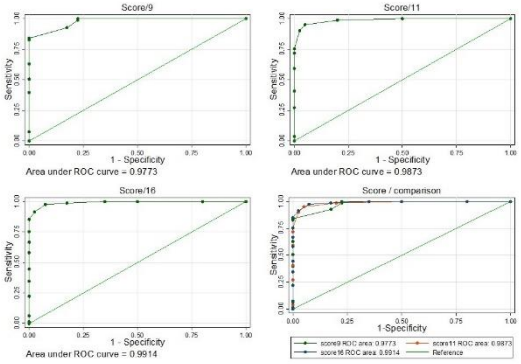

Figure 2. Comparison of ROC analysis between the 3 models applied to the training group. The area under the ROC curve (AUC) is explained for each model.

Table 4 . Laboratory analysis parameters of patients included in the validation group

	Negative Covid-19 (N=13)		Positive Covid-19 (N=22)		
	Mean±SEM	**Median (q1-q3)**	**Mean±SEM**	**Median (q1-q3)**	**P value**
AGE	44.38±5.92	52.00 (31.00-65.00)	45.14±3.64	46.00 (29.75-57.75)	0.454
WBCs	6.74±0.51	6.80 (5.5-7.20)	4.77±0.31	4.30 (4.03-5.18)	0.000
Neutrophil	65.63±1.66	65.00 (62.00-69.50)	73.79±1.15	73.50 (71.58-77.98)	0.000
Lymphocyte	27.67±1.70	28.00 (23.10-30.70)	16.63±1.18	16.05 (13.00-18.90)	0.000
NL Ratio	2.51±0.20	2.43 (1.99-3.04)	4.92±0.37	4.47 (3.86-6.04)	0.000
Platelet	227.46±13.75	212.00 (178.0-266.0)	214.77±10.41	208.5 (190.00-248.75)	0.229
D-Dimer	0.23±0.02	0.22 (0.16-0.26)	0.60±0.05	0.57 (0.52-0.61)	0.000
CRP	7.10±1.34	5.20 (4.80-9.30)	20.36±1.92	18.75 (15.20-24.85)	0.000
Ferritin	144.85±25.10	143.00 (65.0-220.0)	196.86±26.64	220.00 (60.75-295.75)	0.096

Application of the three models on validation group

The 3 models were calculated using predictive parameters from each individual in the validation group. The results are shown in Table 5, which compares the specificity of each model. Model 3 showed neither false negatives (subjects with positive PCR results but negative predictors' data) nor false positives (subjects with negative PCR results, but positive predictors' data). In contrast, model 1 and model 2 similarly gave 7.69% false positives and 4.55% false negatives.

Table 5. False positives and negatives in the validation group after application of the point-score models

Model	Score	False positive	%	False-negative	%
1	16	1/13	7.69	1/22	4.55
2	11	1/13	7.69	1/22	4.55
3	9	0/13	0	0/22	0

ROC analyses of different models applied to validation groups

The AUC curves from different models of the validation group are shown in Figure 3. The AUC was 0.9860, 0.9913, and 1 for models 1, 2, and 3, respectively. Model 3 gave the best ROC AUC value. Taken together, it will be sufficient to estimate only CRP, D-dimer, and lymphocyte count to foretell the incidence of Covid-19.

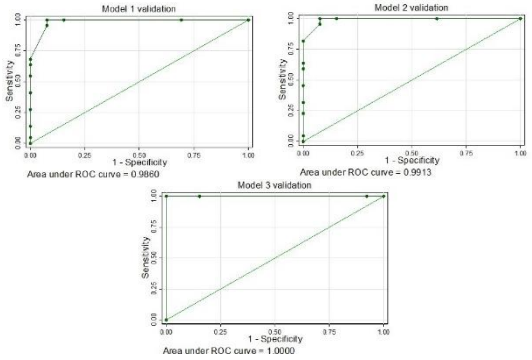

Figure 3. Receiver operating characteristic curve of the three models' validation with the resulting AUC value

Discussion

The Covid-19 pandemic, which began in Wuhan City in China (Covid-19's original center) and spread worldwide in less than 3 months, is regarded as one of the largest pandemics to affect humanity.

In this study, we computed a scoring system based on blood tests, patient features, and clinical indicators to aid in diagnosing Covid-19 infection. Age and NLR have already been linked to severe diseases as an increase in patients with positive RT-PCR (Gong et al., 2020). D-Dimer, CRP, and lymphocytes are chosen as biomarkers to predict disease progression. Similar to other publications published earlier, our results indicated that the lymphocyte percentage decreases with the disease, indicating that viral infection is the direct cause (Wang et al., 2020). Furthermore, we concluded that the higher the severity risk, the higher the D-Dimer, CRP, and neutrophil-lymphocyte (NLR) ratio. There was no association between RBCs and Covid-19, a result that agrees with a previous study (Elkhalifa et al., 2022). In addition, the markers utilized are widely and readily available in the beginning phases of the disease (Havrilesky et al., 2008).

We used three models using the results of 7 laboratory analyses. The selection depended on significantly different values for these parameters between negative and positive Covid-19 patients and the predictors with the highest AUC of the ROC analysis. Thus, the parameters selected were lymphocyte count, CRP, D-dimer, Ferritin, total WBCs count, NLR, and platelets count. All ROC AUC values obtained were near but more significant than those found in the previous reports (e.g. Fink et al., 2021). ROC AUC value was equal to 0.9914, 0.9873, and 0.9773 for model 1, model 2, and model 3, respectively, compared to the AUC value of 0.85 in that study. Comparisons of models scoring system calculated in this present study show no difference. All models appeared to be successful in the diagnosis of Covid-19. Model 3 resulted in the best ROC AUC value on validation. Model 3 also showed neither false negatives nor false positives. Therefore, it will likely be sufficient to estimate only CRP, D-dimer, and lymphocyte count to predict the incidence of Covid-19.

Conclusion

In the present study, some blood tests, including complete blood count such as hemoglobin, RBCs, platelet, WBCs count and differential count (Lymphocyte, Neutrophil lymphocyte Ratio (NLR), CRP, D-dimer, and Ferritin, on some Egyptian patients were used to make a scoring system for Covid-19 diagnosis and assessment of its diagnostic power. This present study yielded 3 predictive models of COVID-19. The three models could demonstrate their effectiveness in predicting COVID-19 positive cases by employing indicators like sensitivity, specificity, and AUROC and using RT-PCR as the gold standard across different contexts. All models appeared to be successful in the diagnosis of Covid-19. The AUC was 0.9860, 0.9913, and 1 for models 1, 2, and 3 on the validation group. We noticed that model 3 resulted in the best ROC AUC.

References

Benvenuto, D., Giovanetti, M., Ciccozzi, A., Spoto, S., Angeletti, S., & Ciccozzi, M. (2020). The 2019-new coronavirus epidemic: evidence for virus evolution. Journal of Medical

Virology, 92(4), 455-459.

Cui, F., & Zhou, H. S. (2020). Diagnostic methods and potential portable biosensors for coronavirus disease 2019. Biosensors and Bioelectronics, 165, 112349-112355.

Elkhalifa, A. M., Elderdery, A. Y., Al Bataj, I. A., Tamomh, A. G., Alyami, M. M., Almakrami, H. A., & Mok, P. L. (2022). Hematological Findings among Covid-19 Patients Attending King Khalid Hospital at Najran, Kingdom of Saudi Arabia. BioMed Research International, 2022, 4620037-4620043.

Fink, D. L., Khan, P. Y., Goldman, N., Cai, J., Hone, L., Mooney, C., & Thomas, S. (2021). Development and internal validation of a diagnostic prediction model for Covid-19 at the time of admission to hospital. QJM: An International Journal of Medicine, 114 (10), 699-705.

Gong, J., Ou, J., Qiu, X., Jie, Y., Chen, Y., Yuan, L., & Hu, B. (2020). A tool for early prediction of severe coronavirus disease 2019 (Covid-19): a multicenter study using the risk nomogram in Wuhan and Guangdong, China. Clinical Infectious Diseases, 71(15), 833-840.

Havrilesky, L. J., Whitehead, C. M., Rubatt, J. M., Cheek, R. L., Groelke, J., He, Q., & Berchuck, A. (2008). Evaluation of biomarker panels for early stage ovarian cancer detection and monitoring for disease recurrence. Gynecologic Oncology, 110 (3), 374-382.

La Marca, A., capuzzo, M., Paglia, T., Roli, L., Trenti, T., &Nelson, SM. (2020). Testing for SARS-coV-2 (cOVId-19): A systematic review and clinical guide to molecular and serological in-vitro diagnostic assays. Reprod Biomed Online, 41, 483-499.

Li, C., & Ren, L. (2020). Recent progress on the diagnosis of 2019 Novel Coronavirus. Transboundary and emerging diseases, 67(4), 1485-1491.

Lippi, G., & Plebani, M. (2020). Laboratory abnormalities in patients with COVID-2019 infection. Clinical chemistry and laboratory medicine (CCLM), 58 (7), 1131-1134.

Lu, H., Stratton, C. W., & Tang, Y. W. (2020). The Wuhan SARS-CoV-2—what's next for China. Journal of Medical Virology, 92(6), 546-548.

Wang, F., Nie, J., Wang, H., Zhao, Q., Xiong, Y., Deng, L., ... & Zhang, Y. (2020). Characteristics of peripheral lymphocyte subset alteration in COVID-19 pneumonia. The Journal of infectious diseases, 221(11), 1762-1769.

WHO, 2023. https://www.who.int/publications/m/item/weekly-epidemiological-update-on-Covid-19---22-february-2023.

Wu, Z., & McGoogan, J. M. (2020). Characteristics of and important lessons from the coronavirus disease 2019 (Covid-19) outbreak in China: summary of a report of 72 314 cases from the Chinese Center for Disease Control and Prevention. jama, 323(13), 1239-1242.

Xu, Z., Shi, L., Wang, Y., Zhang, J., Huang, L., Zhang, C., & Wang, F. S. (2020). Pathological findings of Covid-19 associated with acute respiratory distress syndrome. The Lancet Respiratory Medicine, 8(4), 420-422.

الملخص العربي

عنوان البحث: نموذج نقاط بسيط للتنبؤ بـ الإصابة بكورونا (كوفيد-١٩) في بعض المرضى المصريين

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لا تزال جائحة كوفيد -١٩ نشطًة. على الصعيد العالمي ، لا زال الإبلاغ عن الملايين من حالات Covid-19 الجديدة وآلاف الوفيات أسبوعيًا مستمرا. يعتمد الكشف المختبري على تحليل تفاعل البوليميراز المتسلسل (PCR) المكلف والمستهلك للوقت. لا تزال هناك حاجة إلى طريقة بسيطة لتسهيل تشخيص Covid-19. البحث الحالي كان يهدف إلى إنشاء نموذج نقاط بسيط للتنبؤ والتشخيص السريع لـ Covid-19 باستخدام تحليلات معملية بسيطة. تم استخدام مجموعة مكونة من ١٢١ فردًا بالغًا من حاملي نتيجة تحليل Covid-19 كمجموعة تدريب ، في حين تم استخدام ٣٥ فردًا كمجموعة للتحقق من الصحة. تم استخدام التحليلات المختبرية المختلفة ، بما في ذلك تعداد الدم الكامل ، والعدد النوعي له ، و D-dimer ، و CRP ، و ferritin ، كمتنبئين باستخدام تحليل (Receiver Operating characteristic ROC). كشفت النتائج عن ٣ نماذج ، اعتمادًا على منطقة المساحة تحت المنحنى ROC (AUC) لمعلمات التوقع. يتكون أبسط نموذج من بيانات المتنبئين الثلاثة: قلة الخلايا اللمفية ، CRP ، و D-dimer ، وأسفر عن قيمة ROC AUC تبلغ ٠,٩٧٧٣. دعم تطبيق النماذج الثلاثة على مجموعة التحقق من صحة النتيجة التي مفادها أن تقدير كل من عدد الخلايا الليمفية و CRP و D-dimer سيكون كافياً للتنبؤ بحدوث Covid-19.