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Multi regression analysis of some parameters using COVID 19 patients as a model

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Abstract

Multi-regression analysis is an important analysis to identify the serial models of dependent variables and independent variables that are associated with Covid 19 patients'. Objective: The goal of the current study is to Identify number of models that may be associated with COVID 19 patients which used to calculate the dependent variables from independent variables. Methods: A group of 158 patients with confirmed SARS CoV-2 RNA testing were collected from Erbil international hospital and analyzed for biochemical and hematological profiles. Multi regression analysis was applied. Results: Biochemical parameters (Procalcitonin, Fe Iron, TIBC, Transferrin, LDH, ALT, AST, Alkaline Phosphatase, Total Bilirubin, Direct Bilirubin, Total protein, and Albumin) appeared alteration in their levels in COVID 19 patients. Regression analysis showed better prediction models for enzymes AST, and ALT, Where as the rest parameters, did not show fit prediction models. The hematological study appeared to fit the production model in most variables like MID, GRA, HGB, MCH, and RBC, whereas LYM, WBC, and MCHC don't show a fit model. Conclusions: Conclusions: Current study findings imply that in COVID 19 patients the level of ALT can be predicted using AST, ALP, and LDH, whereas AST level can be predicted using Levels of ALP, ALT, and LDH. In hematological studies as well, the level of MID, GRA, HGB, MCH, and RBC can be predicted from other independent variables.

Keywords

COVID-19, Enzymes, CBC, Multi regression analysis

The first description of COVID-19 was reported in early December 2019, when some health workers were noted to have symptoms of idiopathic pneumonia. The disease was identified epidemiologically as being associated with a seafood market in Wuhan city, Hubei Province, Mainland China [1]. On the 11th of February 2020, the International-Committee-on-Classification-of-Coronavirus-Study-Group renamed it as SARS-CoV-2, and on the same day, the disease was named COVID-19. On the 11th of March 2020, the WHO declared COVID-19 as a pandemic [2]. Coronaviruses (CoVs) are a group of viruses that are distinguished by positive single-stranded and enveloped RNA and capable of causing various diseases in mammals and birds [3]. The CoVs size has a diameter range of 60-140 nm, and their linear strand and positive-sense RNA genome is relatively large, with a size range of 26-32 Kb [4]. These globular or pleomorphic viruses contain lipid envelope containing a helical nucleocapsid of nucleoproteins (N) bound to the RNA genome. The envelope is embedded with a 2 nm spike glycoprotein (S) trimmer that facilitates virus

binding to host cell receptors. The envelopes of the virus are also composed of integral proteins; membrane (M) and envelope (E) [5]. In severe and critical illness of COVID-19, kidneys, heart and liver, as well as immunological and gastrointestinal systems are involved [6]. Acute-respiratory-distress-syndrome (ARDS), kidney and cardiac failure, and arrhythmias are among the leading causes of death in COVID-19 patients. In the case of hospitalized cases, other necessary laboratory tests have to be performed. These include complete blood count, d-dimer, lactate dehydrogenase, procalcitonin, ferritin and liver function enzymes [7]. Elevated white blood cell count (WBC), lymphopenia and increased neutrophil-to-lymphocyte ratio (NLR) are associated with a poor outcome of disease [8]. Besides, particularly in severe and critical illness, the levels of d-dimer, CRP, ESR, lactate dehydrogenase, IL-6, procalcitonin, ferritin and liver function enzymes are elevated. Some of these tests can be used for evaluating the progression of COVID-19, as well as recovery [9]. In view of the available clinical information, it is noted that abnormal liver function tests are frequently observed in patients infected with the Coronavirus, whose pathological cause is not clearly and completely understood. As liver function tests include damage to liver cells (aspartate transferase and alanine transferase), and bile duct injury. (Alkaline phosphatase and gamma-glutamyl transferase), and signs of bile duct's ability to secrete (bilirubin). As well as prothrombin time and albumin. Liver function tests are not necessarily liver-specific, as it has been suggested that transaminases in the COVID-19 virus can also be caused by polymyositis and not liver damage [10]. In an enormous clear review, the muscle harm marker creatinine kinase was raised in 14% of patients with COVID-19 [11]. Hypoalbuminemia was accounted for in 55% of hospitalized patients with COVID-19 [12,13]. Hypoalbuminemia was an autonomous indicator of mortality [14]. Lower levels of pre-albumen in patients with serious COVID19 were accounted for, recommending diminished hepatic combination [12]. With regards to irritation, hypoalbuminemia may likewise reflect albumin extravasation as a result of expanded fine penetrability [15].The current study aimed to identify number of models that may be associated with COVID 19 patients which used to calculate the dependent variables from independent variables.

Material and Method

Ethical permission for this study was obtained from the Research Ethics committee of scientific of college of science for women department of chemistry with session 14, number 387 at 19/6/2022, and have been conducted according to the ethical standard as set forth in the 1964 Helsinki Declaration and its subsequent corrections or comparable ethical standards. Each individual participant in the study gave their informed consent. 158 patients infected with the SARS CoV -2 RNA testing were collected and analyzed for clinical, biochemical, radiological and hematological profiles. From Patients a 5 ml of blood was obtained from each patient by venipuncture using a 5 ml syringe. A 2 mL was dispensed into a tube containing ethylene diaminetetraacetic acid (EDTA) applied to the hematology autoanalyzer. The obtained serum was used to determine the concentration of (Procalcitonin, Fe_Iron, TIBC, Transferrin, LDH, ALT, AST, Alkaline Phosphatase, Total Bilirubin, Direct Bilirubin, Total protein, and Albumen) All studied parameters were measured using kits provided by Human company. Hematological tests were measured using an automated hematological analyzer

Results and discussion

The results of the current study have been divided into two parts depending on the data: the first part included biochemical parameters and the second part included hematological parameters.

First part: Several biochemical parameters were measured, and the results of the descriptive statistics were presented in table 1

Table 1: Descriptive Statistic table of several biochemical parameters using COVID 19 as a model

Parameters	Mean ± SE
Age	52.53 ± 1.15
Duration	4.72 ± 0.15
Procalcitonin ng/ml	0.7027 ± 0.25
Fe Iron µ/dl	46.16 ± 10.8
TIBC µ/dl	260.33 ± 22.58
Transferrin mg/dl	173.00 ± 23.26
LDH IU/L	451.38 ± 58
ALT U/L	46.29 ± 5.04
AST U/L	41.21 ± 4.71
Alkaline Phosphatase IU/L	134.21 ± 17.27
Total Bilirubin mg/dl	0.73 ± 0.10
Direct Bilirubin mg/dl	0.31 ± 0.04
Bilirubin indirect mg/dl	0.39 ± 0.03
Total protein g/dl	5.91 ± 0.11
Albumin g/dl	8.72 ± 5.31

The mean patients age and duration of disease were demonstrated in table (1). The age and duration of disease were expressed in mean plus minus standard error of patients. According to the

results the mean age was 52.53, duration of disease was 4.72 days.

Two clarifications could be taken to make sense of the age-related results of COVID-19. In the first place, maturing is related with quantitative and subjective changes in the elements of the resistant framework; for example, creation of B and T cells in essential lymphoid organs is diminished and mature lymphocytes in auxiliary lymphoid tissues show declined capability [16]. these progressions impact powerlessness to COVID-19 as well as illness movement and clinical result from there on Bajaj et al. Second, the old will in general have an expanded commonness of ongoing illnesses (for instance, diabetes and cardiovascular sickness) around the world [17], also, it has been obviously clear that individuals with these comorbidities are more powerless to SARS-CoV-2 and are bound to foster an intense course of COVID-19 [18].

Somewhat strange LFTs, particularly AST and ALT, are oftentimes seen in patients with COVID-19 on confirmation and are related with serious illness and expanded provocative markers. As a general rule, strange LFTs in patients with COVID-19 don't prompt critical liver capability disability or disappointment. The pathogenetic systems for strange LFTs in COVID-19 are not completely perceived: They are possible multifactorial and, while direct SARS-CoV-2 contamination in hepatocytes or potentially cholangiocytes seems improbable, microthrombotic endothelialitis, safe dysregulation, drug-prompted liver injury, and hepatic ischemia connected with hypoxia and MOF could all assume a part [19].

Lactate dehydrogenase (LDH) is a compound communicated in virtually all human cells, including cells of the (heart, liver, muscles, kidneys, lungs, and in bone marrow) and catalyzes the creation of pyruvate to lactate. Raised serum LDH might be distinguished following harm to any of the heap cell types that regularly express LDH. Fan et al in their series of COVID-19 patients from Singapore distinguished outright lymphocyte consider and LDH discriminators among ICU and non-ICU patients [20]. As would be expected, height is LDH is normal in COVID-19 patients in the ICU setting and demonstrates an unfortunate result [20].

Bilirubin, which is essential for the heme catabolic pathway in vertebrates, is created in hepatocytes. Expanded serum bilirubin is recognized in various problems including the liver and biliary device, and expanded degrees of all out bilirubin have been displayed to recognize COVID-19 patients confessed to the ICU versus those with less extreme sickness [21].

Procalcitonin is a prohormone, a forerunner of calcitonin, a chemical that assumes a significant part in calcium homeostasis. Raised procalcitonin levels might be found in sepsis and are especially connected with septic shock and organ brokenness requiring mediation. On beginning show, a larger part of COVID-19 patients has procalcitonin levels in the typical reach. Expanded procalcitonin Bacterial superinfection, Increased LDH Pulmonary injury/multiorgan harm, Increased aminotransferases Liver injury/multiorgan harm, Increased bilirubin Liver injury, Decreased egg whites Impaired liver function, Prolonged prothrombin time Consumptive coagulopathy, Prolonged APTT Consumptive coagulopathy, APTT, enacted incomplete thromboplastin time; LDH, lactate dehydrogenase [22].

the results showed a Procalcitonin level was shifted in its range compared to the reference range for the WHO. the same results have been observed in Fe- iron, TIBC, Transferrin, LDH, ALT, AST, and albumin. Authors try to apply multi-regression analysis for the studied parameters to predict the dependent variables from independent variables. Not all study parameters showed a good fit model.

The first model used enzymes variables (LDH, ALP, AST, ALT) variables entered method have been used with, variables entered were ALP, AST, ALT and dependent variable was LDH, Model Summary showed R(multiple correlation coefficient with 0.325 this data considered to be one measure of the quality of the prediction of the dependent variable, so in this case, indicates a week level of prediction. The next value is R square it is known as coefficient of determination, the results appeared 0.10 value for R square that indicate the independent variables (LST, ALT, ALP) explain 10.6 of the variability of dependent variable LDH Model summary 1.

Model 1: Model Summary of Dependent variable LDH

Model Summaryb					
Model	R	R Square	Durbin-Watson	F- ratio	p
1	0.325[a]	0.106	2.150	1.26	0.34
a. Predictors: (Constant), Alkaline_Phosphatase, AST, ALT					
b. Dependent Variable: LDH					

The Anova test (Model 1) showed that F-ratio 1.26 with p> 0.005 indicate that independent variables statistically not significant predict the dependent variable so the regression model is a not good fit of data. Estimated model cofficents were done by applied general form of the equation to predict LDH from ALP, AST, ALT: The general form of the equation to predect LDH = 473.209 +(

3.8x ALT) + (4.6 X AST) − (2.7 X ALP), This means that for each increase in ALT there is an increased in 3.8 unit of LDH.

The Second model variables entered were ALP, AST, LDH, and the dependent variable was ALT Model 2.

Model 2: Model Summary of Dependent variable ALT

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
2	0.771	0.595	1.707	15.6	0.000
Predictors: (Constant), LDH, Alkaline_Phosphatase, AST					
Dependent Variable: ALT					

Model Summary showed R with 0.771 this data considered to be one measure of the quality of the prediction of the dependent variable, so in this case, indicates a strong level of prediction. The next value is R square the results appeared 0.595 value for R square that indicate the independent variables (LST,LDH, ALP) explain 59.5 of the variability of dependent variable ALT. The Anova results table showed that F-ratio 15.6 with p< 0.005 indicate that independent variables statistically significant predict the dependent variable so the regression model is a good fit of data. Estimated model coefficients were done by applied general form of the equation to predict ALT from ALP, AST, LDH : The general form of the equation to predict ALT = 9.559 +(0.52 x AST) + (0.134 X ALP) + (0.003 X LDH). The models appeared that for each increase in AST there is an increase in 0.52 units of ALT

The third model variables entered were ALP, ALT, LDH, and the dependent variable was AST Model 3.

Model 3: Model Summary of Dependent variable AST

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
3	0.730	0.533	1.9	12.1	0.000
Predictors: (Constant), LDH, Alkaline_Phosphatase, ALT					
Dependent Variable: AST					

Model Summary showed R with 0.730, in this case, indicates a strong level of prediction. The next value is R square the results appeared 0.533 value for R square that indicate the independent variables (ALT,LDH, ALP) explain 53.3 of the variability of dependent variable AST

The Anova table showed that F-ratio 12.1 with p< 0.005 indicate that independent variables statistically significant predict the dependent variable so the regression model is a good fit of data.

Estimated model coefficients were done by applied general form of the equation to predict AST from ALP, ALT, LDH: The general form of the equation to predict AST = 1.895 +(0.82 x ALT) - (0.009 X ALP) + (0.006 X LDH), The model coefficients appeared that for each increase in ALT there is an increase in 0.82 units of AST.

The forth model variables entered were ALT, AST, LDH, and the dependent variable was ALP Table 5.

Model 4: Model Summary of Dependent variable ALP

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
4	0.508	0.258	1.8	3.7	0.021
Predictors: (Constant), LDH, AST, ALT					
Dependent Variable: ALP					

Model Summary showed R with 0.508,the next value is R square the results appeared 0.258 value for R square that indicate the independent variables (ALT,LDH, AST) explain 25.8 of the variability of dependent variable ALP. The ANOVA results showed that F-ratio 3.7 with p< 0.05 indicate that independent variables statistically significant predict the dependent variable so the regression model is a good fit of data.

Estimated model coefficients were done by applied general form of the equation to predict ALP from AST, ALT, LDH : The general form of the equation to predict ALP = 69.76 +(1.17 x ALT) - (0.048 X AST) - (0.015 X LDH), the presented results appeared that for each increase in ALT there is an increase in 1.17 units of ALP

Second part: Hematological parameters were measured, and the results of the descriptive statistics were presented in table 2.

Table 2: Descriptive Statistic table of complete blood account using COVID 19 as a model

Parameters	Mean ± SE
INR	1.85 ± 0.35
PT Prothrombin time	20.76 ± 2.86
PTT	39.6 ± 8.39
WBC	15.84 ± 2.59
LYM	6.86 ± 0.65
MID	8.04 ± 1.74
GRA	83.89 ± 2.07
HGB	14.15 ± 2.01
MCH	27.66 ± 0.39
MCHC	32.52 ± 0.212
RBC	4.42 ± 0.08
MCV	84.95 ± 1.02
HCT	37.48 ± 0.75
PLT	214.19 ± 12.40

The results showed that most hematological parameters were altered in COVID 19 patients as

compared to the reference range, So multi-regression analyses were applied for the studied parameters to predict the dependent variables from independent variables. Not all study parameters showed a good fit model.

The platelet counts in combination with different elements related with serious sickness has been accounted for COVID-19 patients, in spite of the fact that it has been uncovered to be useful in SARS. For instance, Zou et al revealed that platelet count, related to hypoxemia, was utilized in prognostic model for SARS that anticipated serious illness with 96.2% accuracy [23,25] likewise, components of the extended CBC helpful in assessment of sepsis, for example, mean platelet volume and reticulated platelet count [23].

The mean of white blood cell (WBC) count increased in COVID-19 cases (15.84), while Prothrombin time (PT) level and platelet count (20.76 and 214.19, respectively) (Table 2). WBC count was an excellent predictor of COVID-19. It is generally agreed that WBC count is increased in most infections and inflammations, with some exceptions. These cells form important cellular components the innate and adaptive immune system, which is responsible for fighting and eliminating infectious agents [24]. However, the WBCs have to be evaluated in terms of their differential counts rather than alone. However, most studies agree that WBC count is significantly increased in COVID-19 and may represent a non-specific indicator of the infection [25].

The First hematological model variables entered were RBC, WBC, MID, MCHC, MCH, GRA, HGB and the dependent variable was LYM Model 1 hematology.

Model 1 hematology: Model Summary of Dependent variable LYM

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
1	0.652	0.425	2.1	4.33	0.001
Predictors: (Constant), RBC, WBC, MID, MCHC, MCH, GRA, HGB					
Dependent Variable: LYM					

Model Summary showed R with 0.652, R square data appeared 0.425 value that indicate the independent variables (RBC, WBC, MID, MCHC, MCH, GRA, HGB) explain 42.5% of the variability of dependent variable LYM. The ANOVA test showed that F-ratio 4.33 with $p< 0.05$ indicate that independent variables statistically significant predict the dependent variable so the regression model is a good fit of data. Estimated model coefficients were done by applied general form of the equation to predict LYM from RBC, WBC, MID, MCHC, MCH, GRA, HGB : The general form of the equation to predict LYM = 64.82 -(0.03 x WBC) - (0.30 X MID) - (0.277 X GRA)+(3.6 x HGB) − (1.52 x MCH) +(0.17 x MCHC) − (8.68 x RBC).

The second hematological model variables entered were RBC, LYM, MID, MCHC, MCH, GRA, HGB and the dependent variable was WBC Model 2 hematology.

Model 2 hematology: Model Summary of Dependent variable WBC

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
2	0.34	0.11	2.1	0.7	0.6
Predictors: (Constant), RBC, LYM, MID, MCHC, MCH, GRA, HGB					
Dependent Variable: WBC					

This model is not a good model as long as R data showed 0.34 and the ANOVA test appeared non-significant results.

The Third hematological model variables entered were RBC, WBC, LYM, MCHC, MCH, GRA, HGB and the dependent variable was MID Model 3 hematology.

Model 3 hematology: Model Summary of Dependent variable MID

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
3	0.855	0.731	2.1	15.8	0.000
Predictors: (Constant), RBC, WBC, LYM, MCHC, MCH, GRA, HGB					
Dependent Variable: MID					

Model Summary showed R with 0.855, and R square results appeared 0.731 value that indicate the independent variables (RBC, WBC, LYM, MCHC, MCH, GRA, HGB) explain 73% of the variability of dependent variable MID. The ANOVA table showed that F-ratio 15.8 with $p< 0.05$ indicate that independent variables statistically significant predict the dependent variable so the regression model is a good fit of data. Estimated model coefficients were done by applied general form of the equation to predict MID from RBC, WBC, LYM, MCHC, MCH, GRA, HGB: The general form of the equation to predict MID = 106.5 -(0.75 x GRA) + (2.52 X HGB) - (1.25X MCH)+(0.2 x MCHC) −(7.2 x RBC) - (1.0 x LYM) + (0.005 x WBC)

The Fourth hematological model variables entered were RBC, WBC, LYM, MCHC, MCH, HGB, MID and the dependent variable was GRA Model 4 hematology.

Model 4 hematology: Model Summary of Dependent variable GRA

odel Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
4	0.867	0.752	2.2	17.7	0.000
Predictors: (Constant), RBC, WBC, LYM, MCHC, MCH, , HGB ,MID					
Dependent Variable: GRA					

Model Summary showed R with 0.867, and R square results appeared 0.752 value that indicate the independent variables (RBC, WBC, LYM, MCHC, MCH, MID, HGB) explain 75% of the variability of dependent variable GRA. The ANOVA table showed that F-ratio 17.7 with p< 0.05 indicate that independent variables statistically significant predict the dependent variable so the regression model is a good fit of data. Estimated model coefficients were done by applied general form of the equation to predict GRA from RBC, WBC, LYM, MCHC, MCH, MID, HGB : The general form of the equation to predict GRA = 56.6 -(3.7 x HGB) + (1.54 X MCH) - (0.083X MCHC)+(8.82 x RBC) −(1.14 x LYM) + (0.028 x WBC) - (0.93 x MID)

The Fifth hematological model variables entered were RBC, WBC, LYM, MCHC, MCH, GRA, MID and the dependent variable was HGB Model 5 hematology.

Model 5 hematology: Model Summary of Dependent variable HGB

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
5	0.998	0.996	1.65	1651.4	0.000
Predictors: (Constant), RBC, WBC, LYM, MCHC, MCH, , GRA,MID					
Dependent Variable: HGB					

Model Summary showed R with 0.998 this data considered to be one measure of the quality of the prediction of the dependent variable, so in this case, indicates a normal level of prediction. R square results appeared 0.996 value that indicate the independent variables (RBC, WBC, LYM, MCHC, MCH, MID, GRA) explain 99% of the variability of dependent variable HGB. The ANOVA table showed that F-ratio 1651.4 with p< 0.05 indicate that independent variables statistically significant predict the dependent variable so the regression model is a good fit of data. Estimated model coefficients were done by applied general form of the equation to predict HGB from RBC, WBC, LYM, MCHC, MCH, MID, GRA: The general form of the equation to predict HGB = - 11.5 + (0.44 x MCH) - (0.011 X MCHC) + (2.68X RBC)+(0.003 x LYM) +(0.00 x WBC) + (0.001 x MID) - (0.001 x GRA)

The Sixth hematological model variables entered were RBC, WBC, LYM, MCHC, GRA, HGB, and MID and the dependent variable was MCH Model 6 hematology.

Model 6 hematology: Model Summary of Dependent variable MCH

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
6	0.996	0.992	1.66	768.3	0.000
Predictors: (Constant), RBC, WBC, LYM, MCHC , GRA,MID,HGB					
Dependent Variable: MCH					

Model Summary showed R with 0.996, and R square results appeared 0.992 value that indicate the independent variables (RBC, WBC, LYM, MCHC, MID, GRA, HGB) explain 99% of the variability of dependent variable MCH. The ANOVA table showed that F-ratio 768.3 with p< 0.05 indicate that independent variables statistically significant predict the dependent variable so the regression model is a good fit of data. Estimated model coefficients were done by applied general form of the equation to predict MCH from RBC, WBC, LYM, MCHC, HGB, MID, GRA : The general form of the equation to predict MCH = 25.6 + (0.04 x MCHC) - (6.0 X RBC) - (0.007X LYM) +(0.00 x WBC) - (0.002 x MID) +(0.002 x GRA)+(2.23 X HGB).

The Seventh hematological model variables entered were RBC, WBC, LYM, MCH, GRA, HGB, and MID and the dependent variable was MCHC Model 7 hematology.

Model 7 hematology: Model Summary of Dependent variable MCHC

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
7	0.629	0.395	1.2	3.82	0.003
Predictors: (Constant), RBC, WBC, LYM, MCH, GRA,MID,HGB					
Dependent Variable: MCHC					

Model Summary showed R with 0.629, and R square result appeared 0.395 value that indicate the independent variables (RBC, WBC, LYM, MCH, MID, GRA, HGB) explain 39% of the variability of dependent variable MCHC

The ANOVA table showed that F-ratio 3.82 with p< 0.05 indicate that independent variables statistically significant predict the dependent variable so the regression model is a good of data. Estimated model coefficients were done by applied general form of the equation to predict MCH from RBC, WBC, LYM, MCH, HGB, MID, GRA: The general form of the equation to predict MCHC =

7.33 + (3.67 x RBC) + (0.018 X LYM) - (0.005X WBC) +(0.008 x MID)- (0.002 x GRA) -(1.24 X HGB) + (0.87 X MCH)

The eighth hematological model variables entered were WBC, LYM, MCH, MCHC, GRA, HGB, and MID and the dependent variable was RBC Model 8 hematology.

Model 8 hematology: Model Summary of Dependent variable RBC

Model Summary					
Model	R	R Square	Durbin-Watson	F- ratio	p
8	0.998	0.995	1.67	1192.36	0.000
Predictors: (Constant): WBC, LYM, MCH , GRA,MID,HGB, MCHC					
Dependent Variable: RBC					

Model Summary showed R with 0.998, and R result appeared 0.995 value that indicate the independent variables (WBC, LYM, MCH, MID, GRA, HGB, MCHC) explain 99% of the variability of dependent variable RBC. The ANOVA table showed that F-ratio 1192.3 with $p< 0.05$ indicate that independent variables statistically significant predict the dependent variable so the regression model is a good of data. Estimated model coefficients were done by applied general form of the equation to predict RBC from MCHC, WBC, LYM, MCH, HGB, MID, GRA : The general form of the equation to predict RBC = 4.28 - (0.001 x LYM) + (0.000 X WBC) + (0.00X MID) +(0.000 x GRA)+ (0.37 x HGB) -(0.16 X MCH) + (0.005 X MCHC).

Conclusion

Multi Regression analysis results using biochemical tests appeared that there are two models considered as a fit good model for predicting the variability, predict ALT from ALP,AST, LDH : The general form of the equation to predict ALT = 9.559 +(0.52 x AST) + (0.134 X ALP) + (0.003 X LDH). , and predict ALP from AST, ALT, LDH : The general form of the equation to predict ALP = 69.76 +(1.17 x ALT) - (0.048 X AST) - (0.015 X LDH). Multi regression analysis using Hematology parameters appeared very good prediction of MID from RBC, WBC, LYM, MCHC, MCH, GRA, HGB uses the general form of the equation to predict MID = 106.5 -(0.75 x GRA) + (2.52 X HGB) - (1.25X MCH)+(0.2 x MCHC) −(7.2 x RBC) - (1.0 x LYM) + (0.005 x WBC); appeared very good prediction of GRA from RBC, WBC, LYM, MCHC, MCH, , HGB ,MID with general form of the equation to predict GRA = 56.6 -(3.7 x HGB) + (1.54 X MCH) - (0.083X MCHC)+(8.82 x RBC) −(1.14 x LYM) + (0.028 x WBC) - (0.93 x MID); appeared very good prediction of HGB from RBC, WBC, LYM, MCHC, MCH, , GRA,MID with general form of the equation to predict HGB = - 11.5 + (0.44 x MCH) - (0.011 X MCHC) + (2.68X RBC)+(0.003 x LYM) +(0.00 x WBC) + (0.001 x MID) - (0.001 x GRA); Good prediction of MCH from RBC, WBC, LYM, MCHC , GRA,MID,HGB with general form of the equation to predict MCH = 25.6 + (0.04 x MCHC) - (6.0 X RBC) - (0.007X LYM) +(0.00 x WBC) - (0.002 x MID) +(0.002 x GRA)+(2.23 X HGB); Good prediction of RBC from WBC, LYM, MCH , GRA,MID,HGB, MCHC with general form of the equation to predict RBC = 4.28 - (0.001 x LYM) + (0.000 X WBC) + (0.00X MID) +(0.000 x GRA)+ (0.37 x HGB) -(0.16 X MCH) + (0.005 X MCHC).

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Ethical approval

The studies have been approved by Committee of the University of Baghdad College of science for women and have been performed in accordance with the ethical standard as laid down in 1964 declaration of Helsinki statement and its later corrections or comparable ethical standards, also accordance to the ministry of Iraqi health protocols. Informed consent was obtained from all individual participants included in the study.

Disclosure of potential conflicts of interest

NO potential conflicts

Contributorship

Ekhlass M. Taha, and fayha M. conceived of the present idea Ekhlass M. Taha, Fayha M., Areej Shawkat, and Gulboy Abdolmajeed have carried out the experiment. Fayha M., Ekhlass M. Taha, Areej Shawkat, and Gulboy Abdolmajeed contributed to the final version of the manuscript.

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