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BIOMEDICAL MODELLING THROUGH PATH ANALYSIS APPROACH

Arshed A. AHMAD[1], Murat SARI[2] and Ibrahim DEMİR[3]

[1]College of Education for Pure Science, University of Diyala, IRAQ
[2]Department of Mathematical Engineering, Faculty of Science and Letters, Istanbul Technical University, Istanbul 34469, TÜRKİYE
[3]Turkish Statistical Institute, Çankaya, 06420, Ankara, TÜRKİYE

Abstract. Since blood disease markers are one of the most prevalent health problems in this era, the aim of this study is to forecast pathological subjects from a population through biomedical variables of individuals using the currently produced path analysis (PA) model. In terms of the dataset, 539 subjects were used to implement this study. A mathematical approach based on the PA has been used to create a reliable biomedical model in this research that investigates if there exists a relation between the various anemia types and the biomedical variables through observational variables (the blood variables, age, and sex) and anemia types. Other linear approaches were taken into consideration for comparison, in terms of R^2 value of the model, which has a value of 0.699. The findings reveal that the model has great predictive potential. It is believed that the developed model, which includes observational variables, will help healthcare providers predictively plan appropriate treatment programs for their patients.

1. Introduction

Medical models are frequently used in many healthcare processes and also as a tool for analyzing pathological features. Modelling has become a substantial tool in studies of prediction because of its ease of interpretation for pathological data; therefore, these studies commonly use mathematical modeling to portray the interrelationship among the multiple variables in a mathematical equation. According

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[1] arshed980@gmail.com-Corresponding author; 0000-0003-1393-1253;
[2] muratsari@itu.edu.tr; 0000-0003-0508-2917;
[3] idemir@gmail.com; 0000-0002-2734-4116.

to the research [1–5], how effectively any aim can be achieved depends on knowledge about the problem and how well the modeling is done. Any disease state has different effects for a single disease, which may be used to evaluate the circumstances shown in hospitals. As a result, several endogenous variables determine the majority of outcomes in real-life problems.

The purpose of this study is to use biomedical variables and anemia types to predict pathological people in a population and know the relationship between blood variables. The literature [6, 7] indicates that there has been an increase in anemia among various segments of the population of the community; thus, it is crucial to predict the anemia types. Therefore, our aim is to develop a new biomedical model to study the effect of the blood variables, sex, and age together and their effect on the anemia types.

Our model differs from the other models contained in the literature [8–10] and has been successfully used to predict several anemia types using a wide range of blood variables, sex, and age.

The previous studies [8, 9, 11–13] produced relatively less accurate results by using a relatively small or limited number of blood variables to predict anemia types or a small number of anemia types.

The PA is a generalization of multiple regression that allows one to estimate the strength and sign of directional relationships for complicated causal schemes with multiple dependent variables. A major advantage of the PA is that, in addition to studying the direct effects, indirect effects through intervening variables can be studied, as can estimating the values of coefficients in the model, adding non-recurring paths, reporting additional appropriate indicators, and estimating residuals and their potential relationships with each other. Also, it is seen when there are two or more dependent variables. Therefore, a great deal of research has been done in a variety of fields using the PA found in the literature. Examples of these include the COVID-19 emergency [14], stability analysis and an epidemic model [15], odds of elevated systolic blood pressure [16], blood-associated parasites [17], predicting blood donation behavior among donors [18], the relationship between iron deficiency anemia and blood cadmium and vitamin D [19], the relationship between blood pressure and the structures of the health promotion model [20], and assessing the healthcare empowerment model among HIV-positive individuals [21]. In this study, a realistic model has been developed that allows the best relationship between blood variables to be found through the PA by using many input variables. Because there are more input variables in the created model, it is therefore more realistic in the field of biomedicine. Therefore, the primary goal of the current study is to identify the different forms of anemia utilizing a large number of practical observational characteristics. As a result, it is believed that this study significantly advances the understanding of anemia types

2. Materials and Methods

2.1. **Collection of the study samples.** Here the samples for people and for each subject readings of blood variables are [22, 23] Hemoglobin (HB), Red Blood Cells (RBC), White Blood Cell (WBC), Mean Corpuscular Volume (MCV), Mean Corpuscular Hemoglobin (MCH), Hematocrit (HCT), Mean Corpuscular Hemoglobin Concentration (MCHC), Platelets (PLT) and sex and age. The following explanation applies to the blood variables. Within the RBC, the HB is a transportable protein that is made of iron atoms. The worthless nucleus of the RBCs, which are concave cells, contains the HB. The computed result obtained from the HB measurement and a few red cells is the MCH. The immune system cells known as WBCs are responsible for defending the body against infectious diseases. The volume of RBCs in total blood volume divided by the percentage is the HCT. The estimated amount of HB in a particular volume of RBC is known as the MCHC. The PLT is a haphazard, disc-shaped component of blood that promotes blood coagulation. The MCV calculates the average size of the red blood cells in a sample.

Table 1 displays the many forms of anemia and the biological variables used to collect the data. Table 3 additionally lists the many forms of anemia.

Table 1. Some study samples of the data

HB	RBC	MCH	WBC	MCV	HCT	MCHC	PLT	Sex	Age	Anemia type
11	4.16	26.5	7.7	88	36.6	30.1	180	2	10	0
16.3	6.07	26.9	8.16	80.9	49.1	33.2	349	1	23	0
14.1	4.5	31.2	5.5	90	40.3	34.9	198	1	56	0
11	4.86	22.6	13.6	78	37.7	29.2	482	2	6	1
5.79	9.3	16	14.6	60	34.8	26.6	411	1	16	1
4.65	10.2	21.9	6.7	77	35.8	28.5	409	2	48	1
4.1	1.13	36.2	1.6	114	12.8	31.8	6	2	9	2
10.4	3.7	28	9.2	91	33.7	30.7	607	1	16	2
1.46	4.4	30.4	59.8	108	15.8	28.2	330	2	29	2
7.4	3.1	23.9	5.37	70.6	21.9	33.8	233	1	6	3
10.6	4.78	22.1	16.4	76	36.2	29.2	351	2	27	3
5.4	1.92	28	21.2	94	18	29.9	107	1	54	3
8.3	2.58	31.9	12.4	103	26.7	30.9	458	1	11	4
2.73	8.9	32.6	21.78	94.9	25.9	34.4	546	2	20	4
2.66	8.2	30.8	15.7	90.6	24.1	34	437	1	29	4
11.5	4.63	24.9	7	78	35.9	32	180	1	7	5
7.3	2.06	35.4	15.6	117	24.2	30.2	478	2	16	5
4.41	11	24.9	8.67	73.5	32.4	34	280	1	37	5

The purpose of the paper is to predict diseased people from a community using various biomedical data. In order to determine whether a subject was healthy or infected, data were collected through observations of blood variables, and 539 patients provided from the work of Sari and Ahmad [2, 24], we ran investigative analysis using SPSS, AMOS. Some related calculated variables are shown and the anemia types and the number of individuals (see Tables 2, 3)

Table 2. Descriptive statistics about the values of the sample

Parameters	HB	RBC	MCH	WBC	MCV	HCT	MCHC	PLT	Sex	Age
Average	9.59	5.10	26.67	13.18	82.60	33.18	32.08	363.26	1.54	21.48
Min.	1.46	0.96	11.7	1.6	38.6	7.7	22.6	2	1	6
Max.	18.2	11.9	77	146.1	117	51.7	60.5	1892	2	56
Standard deviation	4.34	2.26	4.56	16.23	8.71	9.01	3.15	210.13	0.499	10.65
Sig.	0.000	0.001	0.054	0.549	0.988	0.565	0.643	0.009	0.000	0.022

Table 3. The anemia types and their population

Parameters	Type0	Type1	Type2	Type3	Type4	Type5
Definition	Healthy	Iron Deficiency Anemia	Deficiency Vitamin B12	Thalassemia	Sickle Cell	Spherocytosis
No. of subjects	211	83	9	217	10	9

2.2. **Path Analysis.** The directed dependencies between a group of variables are described by the PA, which was created as a technique for examining the direct and indirect impacts of variables. Furthermore, the PA is viewed as a type of multiple regression that focuses on causation; its goal is to clarify the plausibility of the causal models that researchers develop using their theoretical understanding and knowledge, rather than to identify causes.

In path models, the independent and dependent variables are shown as boxes or rectangles. Single-headed arrows are emanating from the exogenous; a double-headed arrow signifies that the variables are only correlated. 'Endogenous' variables are those that are dependent variables. There is one or more single-headed arrows pointing at endogenous variables [25].

While determining the amount and direction of the relation between two or more variables by correlation analysis, the mathematical structure of the relation is determined by regression analysis. For this reason, correlation and regression analysis are often used to examine causal relationships. However, in some cases, these methods are often insufficient to reveal the relationship between variables. In multivariate regression analysis, this situation becomes somewhat complicated. Entering independent variables with a high correlation between them can distort the importance of the model, or make transactions in the model meaningless, or either make the effect on the model more or less necessary or make it act against the outcome of the correlation. Because of this, it is critical to assess the structural relationship between quantitative variables and illustrate the connections between independent variables by analyzing the pathway.

3. Results and Discussion

According to the literature, various strategies of many approaches are used to analyze blood variables [8, 9, 12, 26, 27]. Many researchers [28–34] have taken into account the multiple regression analysis while addressing various anemia problems at various levels. Also, the PA has been studied of blood disease in the literature [16, 17, 19, 20]. Although they investigated a relationship for the prediction of various types of anemia, they only used a few blood factors and were aware of the relationship between them. As a result, the current study focuses on the relationship between a number of observational variables and different forms of anemia. However, some of the observed factors have a greater effect than others.

The correlation analysis was carried out to determine the link between blood variables. Pearson correlation analysis was used to determine the relationship between blood variables. The connections between the blood variables were as follows: HB and RBC (-0.307), HB and MCH (0.420), HB and WBC (-0.276), HB and MCV (0.195), HB and HCT (0.807), HB and MCHC (0.504), HB and PLT (-0.335), HB and sex (-0.2), HB and age (0.258), and other blood variables. Pearson correlation analysis was performed to examine whether our data is suitable for path analysis or to understand the relationship between variables (see Table 4 and Figure 1).

Table 4. Correlations relationship between the blood variables

Independent variables	HB	RBC	MCH	WBC	MCV	HCT	MCHC	PLT	Sex	Age
HB	1.000	-0.307***	0.420***	-0.276***	0.195***	0.807***	0.504***	-0.335***	-0.200***	0.258***
RBC	-0.307***	1.000	-0.131**	0.016	-0.050	0.268***	-0.178***	0.015	0.202***	0.323***
MCH	0.420***	-0.131**	1.000	-0.096*	0.570***	0.266***	0.564***	-0.211***	-0.126**	0.197***
WBC	-0.276***	0.016	-0.096*	1.000	0.050	-0.249***	-0.183***	0.574***	0.006	-0.077
MCV	0.195***	-0.050	0.570***	0.050	1.000	0.254***	0.231***	-0.113**	-0.034	0.149***
HCT	0.807***	0.268***	0.266***	-0.249***	0.254***	1.000	0.310***	-0.322***	-0.051	0.434***
MCHC	0.504***	-0.178***	0.564***	-0.183***	0.231***	0.310***	1.000	-0.221***	-0.234***	0.265***
PLT	-0.335***	0.015	-0.211***	0.574***	-0.113**	-0.322***	-0.221***	1.000	-0.013	-0.113**
sex	-0.200***	0.202***	-0.126**	0.006	-0.034	-0.051	-0.234***	-0.013	1.000	-0.049
age	0.258***	0.323***	0.197***	-0.077	0.149***	0.434***	0.265***	-0.113**	-0.049	1.000

$*P < 0.05, **p < 0.01$

Some blood variables had a beneficial effect on anemia types, whilst others had a negative effect. That is, the value of the anemia will rise as the value of the variable rises, and fall as the value of the variable declines. As a result, the standardized coefficient assesses the relative impact of each blood characteristic, sex, and age on different anemia types. It is thus given by $Standard\ Estimate_j = B_j * SD(X_j)/SD(Y)$.

In comparison to the other variables, the HB absolute value of the coefficient, which is (-0.663), has the largest correlation with the disease categories, i.e., when HB goes up by 1 standard deviation, anemia types go down by 0.663 standard deviations, also, the other blood variables. The Standard Estimate value for the HB, means that the dependent variable will vary by the Standard Estimate coefficient value for every change in the HB (see Table 5).

The regression weight for HB in the prediction of anemia types is significantly different from zero at the 0.001 level. Also, RBC and sex are significantly different from zero at the 0.001 level, PLT at the 0.01 level and age at the 0.05 level. As for MCH, WBC, MCV, HCT, and MCHC, the regression weight in the prediction of anemia types is not significantly different from zero at the 0.05 level (see Table 5). As for the regression weight estimate, when HB goes up by 1, anemia types go down by 0.224. In addition, when RBC, MCH, HCT, sex, and age go up by 1, anemia types go down by (0.224), (0.029), (0.016), (0.311), and (0.009), respectively. Also,

Table 5. Regression weights of the blood variables and Anemia by using the PA

	Estimate	Standard Estimate	S.E.	C.R.	P
Diseases < − − − HB	-0.224	-0.663	0.062	-3.615	***
Diseases < − − − RBC	-0.224	-0.345	0.065	-3.424	***
Diseases < − − − MCH	-0.029	-0.090	0.015	-1.949	0.051
Diseases < − − − WBC	0.001	0.016	0.003	0.554	0.580
Diseases < − − − MCV	0.000	-0.001	0.007	-0.015	0.988
Diseases < − − − HCT	-0.016	-0.100	0.028	-0.581	0.561
Diseases < − − − MCHC	0.007	0.016	0.016	0.469	0.639
Diseases < − − − PLT	0.001	0.080	0.000	2.662	0.008
Diseases < − − − sex	-0.311	-0.106	0.073	-4.231	***
Diseases < − − − age	-0.009	-0.065	0.004	-2.325	0.020

when WBC, MCV, MCHC, and PLT go up by 1, anemia types go up by (0.001), (0.000), (0.007), and (0.001), respectively.

The P values were applied to measure the partial effect of the observations of blood variables, sex, and age on the various anemia types compare with $p < 0.05$. The biomedical variables have been seen to affect the various anemia types but in varying rates (see Table 5).

The critical ratio (C.R.) is equal to the parameter estimate divided by the parameter's standard error estimate. This statistic has a conventional normal distribution under the null hypothesis that the parameter has a population value of zero if the necessary distributional assumptions are made. The critical ratio was used to calculate the partial effect of age, sex, and variables on the various anemia types. These biomedical variables have been demonstrated to have differing degrees of effect on the various anemia types (see Table 5).

As for the standard error, the regression weight estimate, -0.224, -0.224, -0.029, 0.001, 0.000, -0.016, 0.007, 0.001, -0.311, and -0.009 have a standard error of about 0.062, 0.065, 0.015, 0.003, 0.007, 0.028, 0.016, 0.000, 0.073, and 0.004, respectively (see Table 5). This means that each blood variable has a different effect than the other on anemia types.

Variance is a statistical measure of how much a set of observations differ from each other, it measures how far a data set is spread out. The variance of HB is estimated to be 18.831, has a standard error of about 1.148. In addition, the variance of RBC, MCH, WBC, MCV, HCT, MCHC, PLT, sex, and age are estimated and have a standard error (see Table 6). The results have been shown that the variance estimate for blood variables is significantly different from zero at the 0.001 level.

In the outcome of the current PA, the biomedical model has been found to be highly effective, on the prediction of the various anemia types, it is 0.699 of the model. Which clarify 69.90% of the change in the relationship of the biomedical model between all the observational variables and the various anemia types. In other words, the error variance of anemia types is approximately 30.1% (see Table 7). As a result, it is concluded that the model including the blood variables, sex,

Table 6. Variances

	Estimate	S.E.	C.R.	P
HB	18.831	1.148	16.401	***
RBC	5.113	0.312	16.401	***
MCH	20.777	1.267	16.401	***
WBC	263.233	16.050	16.401	***
MCV	75.850	4.625	16.401	***
HCT	81.030	4.941	16.401	***
MCHC	9.966	0.608	16.401	***
PLT	44075.983	2687.360	16.401	***
sex	0.248	0.015	16.401	***
age	113.296	6.908	16.401	***
e	0.645	0.039	16.401	***

and age is significant ($p < 0.000$). By correlating the independent variables among themselves, the model achieved similar results in this study.

In this study, the concept was used principle of whether the approach provides an acceptable prediction or not. In comparison to the other approaches [2,24,34], the findings show that the PA has a good fit for the initial dataset (see Table 7). Therefore, the current study offers a reliable model for predicting the various anemia types.

Table 7. Comparison of the PA results with the other approaches

Approaches	R^2
PA	0.699
Particle Swarm Optimization [24]	0.699
Linear Regression Analysis [2,34]	0.699
Linear Deep Learning Methods (LSTM) [2]	0.695

LSTM: Long Short-Term Memory

To know how significant the model, results were investigated of the root mean square residual (RMR) is the square root of the average squared amount by which the sample variances and covariances differ from their estimates obtained for the model. Therefore, the smaller the RMR is indicating the better fit. Thus, the result shows that, according to RMR=0.001 (see Table 8). However, value for the normed fit index (NFI) should range between 0 and 1, NFI values close to 1 indicate a perfect fit.

Incremental Fit Index (IFI): adjusts the NFI for sample size and degrees of freedom. IFI values close to 1 indicate a good fit. The comparative fit index (CFI) analyzes the model fit by examining the discrepancy between the data and the hypothesized model. CFI values range from 0 to 1, CFI values close to 1 indicate a very good fit. Thus, the results show that each from NFI, IFI, and CFI is equal to 1.000. Therefore, the model is considered a suitable fit (see Table 8).

Table 8. Model fit

CMIN	RMR	NFI	IFI	CFI
0.000	0.001	1.000	1.000	1.000

Since blood variables and anemia types are related to each other, blood variables are displayed double-headed arrows between boxes. As the blood variables affect anemia types, therefore, the model has consisted of single-headed arrows when creating the model. The coefficients obtained from the PA are displayed in the model (see Figure 1).

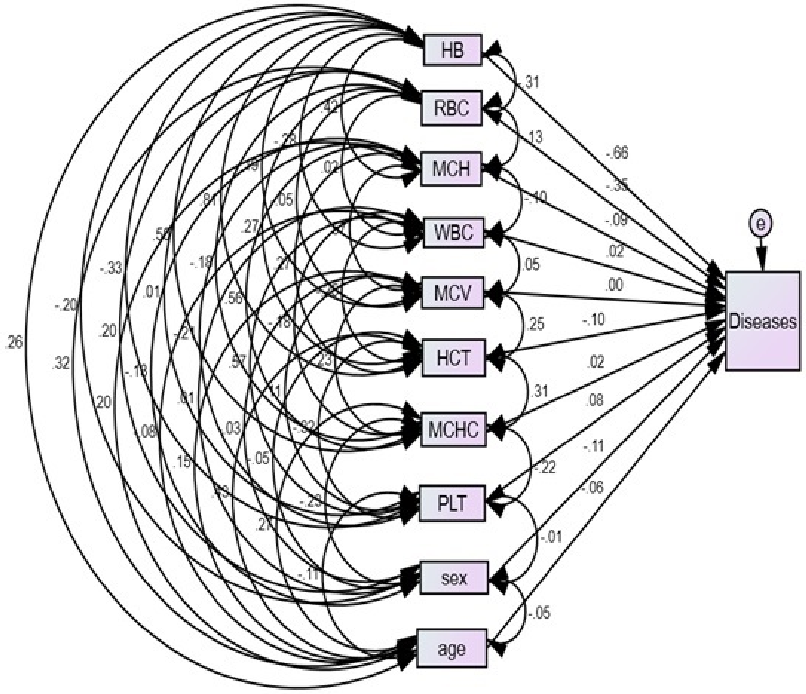

Figure 1. Diagram of the PA for prediction of anemia

4. Conclusions and Future Research

This study has predicted the anemia types through biomedical information (the blood variables, age, and sex of individuals). A mathematical method based on the PA has been implemented for the first time because it is a form of multiple regression centering on causality and sheds light on the tenability of the causal models a researcher formulates based on knowledge and theoretical considerations. So, it was achieved to develop a biomedical model that investigates whether there is a relationship between the various anemia types and the blood variables and finds the best relationship between biomedical variables through the PA in predicting the anemia types. The outcomes showed that the present biomedical model is highly promising and capable of making predictions. In analyzing the present anemia problem, the PA approach has been discovered to be significant compared to other linear methods. It has been concluded that the biomedical model is predicted to be beneficial for the diagnosis of the various anemia types and the provision of effective treatment plans for their patients. This model could be improved in further studies by taking into account various statistical techniques and apply the model to other data and compare it.

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References

[1] Narwal, Y., Rathee, S., Fractional order mathematical modeling of lumpy skin disease, *Communications Faculty of Sciences University of Ankara Series A1 Mathematics and Statistics,* 73(1) (2024), 192-210. https://DOI:10.31801/cfsuasmas.1207144

[2] Sari, M., Ahmad, A. A., Anemia modelling using the multiple regression analysis, *International Journal of Analysis and Applications,* 17(5) (2019), 838-49. https://doi.org/10.28924/2291-8639-17-2019-838

[3] Sari, M., Ahmad, A. A., Uslu, H., Medical model estimation with particle swarm optimization, *Communications Faculty of Sciences University of Ankara Series A1 Mathematics and Statistics*, 70(1) (2021), 468-82. https://DOI: 10.31801/cfsuasmas.644071

[4] Malehi, A. S., Pourmotahari, F., Angali, K. A., Statistical models for the analysis of skewed healthcare cost data: a simulation study, *Health Economics Review*, 5(1) (2015), 11. https://doi.org/10.1186/s13561-015-0045-7

[5] Liddell, C., Owusu-Brackett, N., Wallace, D., A mathematical model of sickle cell genome frequency in response to selective pressure from malaria, *Bull. Math. Biol.*, 76 (2014), 2292-2305. https://DOI: 10.1007/s11538-014-9993-z

[6] Li, X., Dao, M., Lykotrafitis, G., Karniadakis, G. E., Biomechanics and biorheology of red blood cells in sickle cell anemia, *J Biomech.*, 50 (2017), 34-41. https://doi.org/10.1016/j.jbiomech.2016.11.022

[7] Kim, A., Rivera, S., Shprung, D., Limbrick, D., Gabayan, V., Nemeth, E., Ganz, T., Mouse models of anemia of cancer, *PLoS One*, 9 (2014), e93283. https://doi.org/10.1371/ journal.pone.0093283

[8] Sirachainan, N., Iamsirirak, P., Charoenkwan, P., Kadegasem, P., Wongwerawattanakoon, P., Sasanakul, W., Chansatitporn, N., Chuansumrit, A., New mathematical formula for differentiating thalassemia trait and iron deficiency anemia in thalassemia prevalent area: a study in healthy school-age children, *Southeast Asian J Trop. Med. Public. Health.*, 45 (2014), 174.

[9] Roth, I. L., Lachover, B., Koren, G., Levin, C., Zalman, L., Koren, A., Detection of β -thalassemia carriers by red cell parameters obtained from automatic counters using mathematical formulas, *Mediterr. J Hematol. Infect. Dis.*, (2018), 10. https://doi: 10.4084/MJHID.2018.008

[10] Ngwira, A., Kazembe, L. N., Analysis of severity of childhood anemia in Malawi: a Bayesian ordered categories model, *Open Access Medical Statistics*, 6 (2016), 9-20. https://doi.org/10.2147/OAMS.S95159

[11] Jiménez, C. V., Iron-deficiency anemia and thalassemia trait differentiated by simple hematological tests and serum iron concentrations, *Clin. Chem.*, 39 (1993), 2271-2275.

[12] Soleimani, N., Relationship between anaemia, caused from the iron deficiency, and academic achievement among third grade high school female students, *Procedia-Soc. Behav. Sci.*, 29 (2011), 1877-1884. https://doi.org/10.1016/j.sbspro.2011.11.437

[13] Piplani, S., Madaan, M., Mannan, R., Manjari, M., Singh, T., Lalit, M., Evaluation of various discrimination indices in differentiating Iron deficiency anemia and Beta Thalassemia trait: A practical low cost solution, *Annals of Pathology and Laboratory Medicine*, 3 (2016), A551-559.

[14] De La Fuente, J., A path analysis model of protection and risk factors for university academic stress: analysis and psychoeducational implications for the COVID-19 emergency, *Frontiers in Psychology*, 13(12) (2021), 562372. https://doi.org/10.3389/fpsyg.2021.562372

[15] Zhou, Y., Ding, Y., Guo, M., Path analysis method in an epidemic model and stability analysis, *Frontiers in Physics*, 11 (2023), 1158814. https://doi.org/10.3389/fphy.2023.1158814

[16] Ortiz, R. M., Rodriguez, R., Depaoli, S., Weffer, S. E., Increased physical activity reduces the odds of elevated systolic blood pressure independent of body mass or ethnicity in rural adolescents, *J Hypertens*, 3(3) (2014), 1-8. https://DOI:10.4172/2167-1095.1000150

[17] Cohen, C., Einav, M., Hawlena, H., Path analyses of cross-sectional and longitudinal data suggest that variability in natural communities of blood-associated parasites is derived from host characteristics and not interspecific interactions, *Parasites & Vectors*, 8(1) (2015), 429. https://doi: 10.1186/s13071-015-1029-5

[18] Masser, B. M., White, K. M., Hyde, M. K., Terry, D. J., Robinson, N. G., Predicting blood donation intentions and behavior among Australian blood donors: testing an extended theory of planned behavior model, *Transfusion*, 49(2) (2009), 320-9. https://doi.org/10.1111/j.1537-2995.2008.01981.x

[19] Suh, Y. J., Lee, J. E., Lee, D. H., Yi, H. G., Lee, M. H., Kim, C. S., Nah, J. W., Kim, S. K., Prevalence and relationships of iron deficiency anemia with blood cadmium and vitamin D levels in Korean women, *Journal of Korean medical science*, 31(1) (2016), 25-32. https://doi: 10.3346/jkms.2016.31.1.25

[20] Kamran, A., Azadbakht, L., Sharifirad, G., Mahaki, B., Mohebi, S., The relationship between blood pressure and the structures of Pender's health promotion model in rural hypertensive patients, *Journal of education and health promotion*, 4 (2015). https://doi: 10.4103/2277-9531.154124

[21] van den Berg, J. J., Neilands, T. B., Johnson, M. O., Chen, B., Saberi, P., Using path analysis to evaluate the healthcare empowerment model among persons living with HIV for antiretroviral therapy adherence, *AIDS patient care and STDs*, 30(11) (2016), 497-505. https://doi: 10.1089/apc.2016.0159

[22] World Health Organization. Worldwide Prevalence of Anaemia 1993-2005: WHO Global Database on Anaemia, (2008). https://www.who.int/publications/i/item/9789241596657

[23] Hébert, P. C., Wells, G., Blajchman, M. A., Marshall, J., Martin, C., Pagliarello, G., Tweeddale, M., Schweitzer, I., Yetisir, E., A multicenter, randomized, controlled clinical trial of transfusion requirements in critical care, *N. Engl. J Med.*, 340 (1999), 409-417. https://doi: 10.1056/NEJM199902113400601

[24] Ahmad, A. A., Sari, M., Parameter estimation to an anemia model using the particle swarm optimization, *Sigma: Journal of Engineering & Natural Sciences*, 37(4) (2019), 1331-1343.

[25] Streiner, D. L., Finding our way: an introduction to path analysis, *The Canadian Journal of Psychiatry*, 50(2) (2015), 115-22. https://doi.org/10.1177/070674370505000207

[26] Rondanelli, M., Perna, S., Alalwan, T., A., Cazzola, R., Gasparri, C., Infantino, V., Perdoni, F., Iannello, G., Pepe, D., Guido, D., A structural equation model to assess the pathways of body adiposity and inflammation status on dysmetabolic biomarkers via red cell distribution width and mean corpuscular volume: a cross-sectional study in overweight and obese subjects, *Lipids in Health and Disease*, 19 (2020), 1-1. https://doi.org/10.1186/s12944-020-01308-5

[27] Mohammed, S. J., Ahmed, A. A., Ahmad, A. A., Mohammed, M. S., Anemia prediction based on rule classification, *In2020 13th International Conference on Developments in eSystems Engineering (DeSE) IEEE*, (2020), 427-431. https://DOI: 10.1109/DeSE51703.2020.9450234

[28] Nguyen, P. H., Scott, S., Avula, R., Tran, L. M., Menon, P., Trends and drivers of change in the prevalence of anaemia among 1 million women and children in India, 2006 to 2016, *BMJ global health*, 3 (2018), e001010. https://doi.org/10.1136/bmjgh-2018-001010

[29] Kawo, K. N., Asfaw, Z. G., Yohannes, N., Multilevel analysis of determinants of anemia prevalence among children aged 6–59 months in ethiopia: classical and bayesian approaches, *Anemia*, (2018). https://doi.org/10.1155/2018/3087354

[30] Reso, M. C., Dewi, Y. L., Budihastuti, U. R., Path analysis on the biological and social-economic determinants of anemia in pregnant mothers in bantul, yogyakarta, *Journal of Maternal and Child Health*, 4(6) (2019), 415-26. https://DOI:10.26911/thejmch.2019.04.06.03

[31] Little, M., Zivot, C., Humphries, S., Dodd, W., Patel, K., Dewey, C., Burden and determinants of anemia in a rural population in South India: a cross-sectional study, *Anemia*, 2018. https://doi.org/10.1155/2018/7123976

[32] Huang, X. Z., Yang, Y. C., Chen, Y., Wu, C. C., Lin, R. F., Wang, Z. N., Zhang, X., Preoperative anemia or low hemoglobin predicts poor prognosis in gastric cancer patients: a meta-analysis, *Dis. Markers*, (2019). https://doi: 10.1155/2019/7606128

[33] Ahmad, A. A., Sari, M., Anemia prediction with multiple regression support in system medicinal internet of things, *Journal of Medical Imaging and Health Informatics*, 10(1) (2020), 261-7. https://doi.org/10.1166/jmihi.2020.2839

[34] Ahmad, A. A., Alzaidi, K., Sari, M., Uslu, H., Prediction of anemia with a particle swarm optimization-based approach, *An International Journal of Optimization and Control: Theories & Applications (IJOCTA)*, 13(2) (2023). https://DOI: 10.11121/ijocta.2023.1269