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APPLICATION OF MT METHOD OF MAHALANOBIS-TAGUCHI SYSTEM IN METHADONE FLEXI DISPENSING PROGRAM

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Abstract— Patient under methadone flexi dispensing (MFlex) program are required to perform blood tests like lipid profile. To verify the patient does have a lipid disorder, a doctor analyses 3 parameters such as cholesterol, HDL cholesterol, and LDL cholesterol. However, the present system lacks a robust ecology for categorization and optimization due to imprecise measuring methods and a lack of rationale for major elements that impact diagnostic accuracy. The goal is to implement the Mahalanobis-Taguchi system (MTS) into the MFlex programme. The data was acquired at the Bandar Pekan clinic and included 34 lipid profile measures. For classification and optimization, two categories of MTS

techniques are being used, which are RT-Method and T-Method. As a result of the lipid profile analysis, the healthy Mahalanobis distance (MD) is 1.0000, whereas the unhealthy MD is 79.5876. Positive contributions are made by parameters 1, 3, 4, 6, 7, 8, 9, 11, 12, 17, 18, 23, 26, 27, 28, 30, 31, 33, and 34. 15 unknown samples were diagnosed with varying degrees of positive and negative contribution to obtain a smaller MD. The best recommended way has been typed 5 from overall 6 modifications. Finally, the pharmacist acknowledged that MTS could tackle the issue of MFlex programme categorization.

I. Introduction

The illegal drugs of incidence are 6.9 deaths per 100,000 people [1]. These deaths are the result in the use of illicit drugs raises the risk of illness and disability, involving suicide, liver damage, hepatitis, cancer, and HIV [2]. Drug misuse is a complex and severe public health issue in Malaysia [3]. The statistics released by the National Anti-Drugs Agency (NADA) for 2013 where the age involved in drug abuse is comprised of those aged 13 years and above [4]. Opioids are among the most widely misused narcotics in the world, with more users than cocaine and ecstasy [5]. Approximately 550,000 people died in 2019 from drug overdoses, and 18 million years of healthy life were lost because of drug use disorders [6].

Drug addiction is a complex issue in Malaysia that has become a serious public health concern, which has remained over 50% high for decades [3]. For more than 30 years, Malaysians have claimed drugs to be the country's number one threat [7]. The MFlex program

has been shown to be successful in terms of HIV/AIDS problems and improving the life of this drug user [8]. Patients involved in the MFlex programme must undergo blood tests such as a lipid profile comprising 34 parameters to evaluate if they have other illnesses or vice versa. To verify if the patient has a lipid disorder, a doctor is required to assess 3 parameters such as cholesterol, HDL cholesterol, and LDL cholesterol.

This proves that the existing system has lack of justification on significant parameters. The goal of this study is to examine the categorization and optimization variables in the lipid profile, as well as to diagnose the MFlex program's unknown data. The literature review discusses relevant works on MTS, highlighting the most essential research gaps. The research methodology describes the procedures and approaches utilized to accomplish the research's aim. The results and discussions concentrate on all the evidence gathered by utilizing MTS classification and optimization methods. Finally, the conclusion summarizes the final outcomes once the assessment has been analyzed and makes several suggestions for further study.

II. Literature Review

Deaths from opioids have recently altered mortality rates in some high-income nations that almost 11 million people globally inject drugs, with 1.4 million infected with HIV and 5.6 million infected with hepatitis C [9]. Drug addiction is a major public health concern in Malaysia for every 20 new instances of drug abusers reported daily on average in 2009 [3]. The application of MFlex program has proven successful in reducing HIV infection in Malaysia. The program also proved to be cost-effective in terms of providing cost savings and returns [8]. Addicts who consume drugs through injection have an extra 29 times possibilities to get HIV compared to the general public [6]. Malaysia has been using the MFlex Iharm reductionI program to reduce HIV transmission among those who inject drugs since 2005 [7]. The implementation of this program

has proven successful in reducing HIV infection in Malaysia as observed in other countries such as Australia, United Kingdom, and Hong Kong which earlier implemented this program [8].

MTS is a multivariate application developed by Genichi Taguchi that applies Taguchi Methods concepts to generate a multivariate scale of measurements using a data-analytical method to assist in quantitative decision making [10]. Prasanta Chandra Mahalanobis originally developed the MD in 1936. The Mahalanobis space (MS) is calculated using uniform variables from healthy or normal data in MTS. The MS might be used to distinguish between healthy and unhealthy items. When this MS is specified, the number of features is reduced by measuring the input of each attribute using the Iorthogonal array (OA) and the signal-to-noise ratio (SNR) [11]. To construct a continuous scale of measurement and determine the degree of abnormality, MTS has been used [12], to identify critical and non-critical elements [13], and to assess healthy and unhealthy retrospective observations [14].

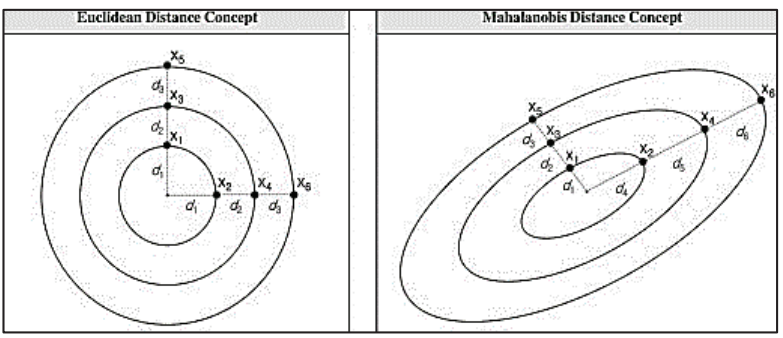

Figure 1: Comparison between MD and ED [17]

MTS, on the other hand, can only deal with binary classification issues [15]. Characteristic factors may show the covariance matrix, and multicollinearity is singular and irreversible, so MD cannot be determined [16]. Figure 1 shows the distance between the MD and the Euclidian distance (ED).

MD is used to determine the "nearness" of an unknown point to the group's middle point (s). ED also shows the distance between the "unknown" point and the group mean point, but it has a weakness as it calculates only a proportional distance from the group mean point without considering the distribution of the points in the group [10].

The MTS can categorize normal and abnormal outcomes and utilize various element for the advancement of a greater product at the workstation [18], it enables the recognition of abnormalities even when learning data is categorized as 'unlabelled' [19], and it measures healthy and unhealthy retrospective observations [14]. MTS, on the other hand, has a weaker statistical framework than standard multivariate processes [12], it can only manage binary classification difficulties [15], and lacks a mechanism for determining an acceptable binary classification threshold [20].

Mota-Gutiérrez et al., [21] classified MTS research into seven categories which are the method's introduction, case study or application, comparison with other methods, development of MS, integration and advancement with other methods, dimensional minimization, and threshold establishment. These categories were included in this analysis to highlight the research gap of published work from 2011 to 2020. In threshold establishment, MTS classified normal and abnormal findings and optimized different parameters at the production line to create a higher performance product [18]. Road surface conditions, such as manhole cover, pothole, and speed hump, can be well distinguished from the MTS system [15]. MTS has been the most promising binary classification technique to manage imbalanced data [20]. MTS used MD-based threshold values for grouping objects into binary groups [22]. MD expanded the form of the super pixels to best suit the dynamic structure of the real world [23], calculated in the right direction to determine the value of a random sample [24], classified participants listed as outsiders,

based on a basic regression study [25], has received an index of the health of the tool [26], and provided more precise results for the right decision-making process [27].

On the other side of dimensional reduction, MTS has improved the critical parameter and reduced the rejected electric and electronic (E&E) product [28]. MTS has detected progress in anterior cruciate ligament reconstruction (ACLR) recovery with a reduced number of important features [29]. On the basis of waveform knowledge on noise and vibration, MTS resolved the quality inspection of the motor fan in the region [30]. Moreover, MTS Original, MTS-binary particle swarm optimization (MTS-BPSO), and MTS-genetic binary particle swarm optimization (MTS-GBPSO) conducted optimum dimensional reductions for an accurate diagnosis [31]. MTS decreased the cost of system control [32], increased the accuracy of classification [33], also eliminated shaft errors and decreased variation across the optimal hardness profile by the design of experiments [34]. The combination of the rough set (RS) and the MD minimized the costs and time required for a proper diagnosis [35].

Abu and Jamaludin [36] performed MTS to differentiate two unique ranges on the connecting rod's large end diameter in the remanufacturability process spectrum. Then, they have conducted a comprehensive study of the data set on crankshaft main journal diameter [37]. Abu et al., [38] developed a systematic pattern recognition with MTS by generating a scatter diagram that might assist in decision making for 14 primary journals of crankshaft belonging to 7 type of engines with varying sample sizes. Furthermore, by utilising MTS, Abu et al., [39] have categorized crankshafts' end life into recovery activities. In other report, Kamil and Abu [40] used the MTS to generate a particular pattern of crankshaft and later on used Activity Based Costing (ABC) as a method to estimate the remanufacturing budget of crankshaft. Abu et al., [41] used both MTS and ABC methods to identify critical and non-critical

variables throughout the remanufacturing process and to estimate the cost, respectively. Abu et al., [42] applied Taguchi's orthogonal array to assess the criticality of parameters on an end-of-life crankshaft. Then, by applying the conventional cost accounting approach, the cost can be estimated while keeping the important characteristics in mind. Meanwhile, Azmi et al., [43] used MTS to assess the degree of malfunction and identify the parameters that affected the system.

Kamil et al., [44] recommended MTS and Time-Driven Activity-Based Costing (TDABC) to be used in the electric and electronic sectors in order to analyse critical factors and generate time equations and capacity cost rates. In other report by Kamil et al., [45] they have adopted MTS to recognize 4 irrelevant and 11 significant parameters in the visual mechanical inspection workstation. Kamil et al., [46] also found that MTS and TDABC are excellent tools that may be applied in the electronic field. For a comprehensive monitoring system, Saad et al., [47] created an MTS-based graphical user interface for assessing and categorizing normal and abnormal patients under the MFlex service. Ramli et al., [48] determined that none of the four thresholding strategies outperformed the others in most datasets. In other report by Ramlie et al., [49] that they have revealed combining Bitwise Artificial Bee Colony (BitABC) approaches with Taguchi's T-Method methodology enhanced prediction performance significantly.

III. Research Design and Methodology

The 34 blood test parameters are used to determine the health level of methadone consumers. The parameters are initially classified into four types, to be specific, Full Blood Count (FBC), liver function profile, lipid profile, and renal profile. The four types of illnesses are used to categorize methadone patients based on either they had one of those four types or not when they enrolled the MFlex programme. Furthermore, the

important parameters of the blood tests may indeed be improved. Methadone users' urine tests are performed to determine which substances are the most addictive in their ordinary activities. Following that, blood tests are performed on each methadone patient to check if they have any ailment in their body. Table 1 displays the parameters of blood tests, that include 34 parameters selection and a reference range for the healthy group. The parameter for FBC, liver function profile, lipid profile, and renal profile are 17, 8, 4, and 5, accordingly.

Table 1: Units for Magnetic Properties

Parameters	Unit	Reference range
Full Blood Count (FBC)		
1. White Blood Cell (WBC)	10^9/L	(4.0-11.0)
2. Red Blood Cell (RBC)	10^12/L	(3.5-5.6)
3. Haemoglobin (HGB)	g/dL	(11.5-16.4)
4. Hematocrit (HCT)	%	(36-47)
5. Mean Corpuscular Volume (MCV)	fL	(76-96)
6. Mean Corpuscular Haemoglobin (MCH)	pg	(27-32)
7. Mean Cell Haemoglobin Concentration (MCHC)	g/dL	(30-35)
8. Platelet Count (PLT)	10^9/L	(150-400)
9. Lymphocyte % (LYM%)	%	(20.0-45.0)
10. Lymphocyte # (LYM#)	10^9/L	(1.5-3.5)
11. MXD %	%	(3.0-10.0)
12. MXD #	10^9/L	(2.0-7.7)
13. NEUT %	%	(40.0-75.0)
14. NEUT #	10^9/L	(2.5-7.5)
15. MPV	fL	(5.0-10.0)
16. PDW	fL	(12.0-18.0)
17. Fasting Blood Sugar	mmol/L	(4.1-5.9)
Liver Function Profile		
18. Total Protein	g/L	(65-85)
19. Albumin	g/L	(35-52)
20. Globulin	g/L	(20-39)
21. A/G Ratio	-	(0.9-1.8)
22. Total Bilirubin	umol/L	(2-24)
23. Alk Phosphatase	U/L	(30-115)
24. ALT (SGPT)	U/L	(0-41)
25. AST (SGOT)	U/L	(0-41)

Lipid Profile		
26. Cholesterol	mmol/L	(3.60-5.20)
27. Triglycerides	mmol/L	(0.50-2.00)
28. HDL Cholesterol	mmol/L	(0.90-1.55)
29. LDL Cholesterol	mmol/L	(2.3-4.4)
Renal Profile		
30. BUN	mmol/L	(1.7-8.5)
31. Creatinine	umol/L	(62-150)
32. Sodium	mmol/L	(135-152)
33. Potassium	mmol/L	(3.5-5.5)
34. Chloride	mmol/L	(95-114)

The RT-Method may divide samples into two categories, that are within and outside the unit space. Among other things, the unit data was selected based on the greatest number of samples. The RT-Method assessed the output value, but the category is distinct when there are several unit spaces. The average value for each parameter is computed from n samples in the healthy group, as indicated in Equation (1).

Equations (2), (3), and (4) illustrate the sensitivity β, the linear formula L, and the effective divider r, respectively.

$$\bar{x}_j = \frac{1}{n}\left(x_{1j} + \cdots + x_{nj}\right) \quad (1)$$

$$Sensitivity, \beta_1 = \frac{L_1}{r} \quad (2)$$

$$Linear\ equation, L_1 = \bar{x}_1 x_{11} + \cdots + \bar{x}_k x_{1k} \quad (3)$$

$$Effective\ divider, r = \bar{x}_1^2 + \bar{x}_2^2 + \cdots + \bar{x}_k^2 \quad (4)$$

The total variations S_T, variation of proportional term S_β, error variation S_e, and error variance V_e, are depicted in Equations (5), (6), (7), and (8) accordingly.

$$Total\ variation, S_{T1} = x_{11}^2 + x_{12}^2 + \cdots + x_{1k}^2 \quad (5)$$

$$Variation\ of\ proportional\ term, S_{\beta 1} = \frac{L_1^2}{r} \quad (6)$$

$$Error\ variation, S_{e1} = S_{T1} - S_{\beta 1} \quad (7)$$

$$Error\ variance = \frac{S_{e1}}{k-1} \quad (8)$$

The standard SN ratio η is then computed using the Equation (9). The higher the value of η, the greater the relationship between the input and output.

$$SN\ ratio, \eta_1 = \frac{1}{V_{e1}} \quad (9)$$

In the healthy group, the sensitivity β and standard SN ratio η are generated, and the two variables Y_1 and Y_2 are determined to form a scatter diagram. Equations (10) and (11) reveal the values of Y_1 and Y_2, separately.

$$\boldsymbol{Y_{i1} = \beta_i} \quad (10)$$

$$\boldsymbol{Y_{i2} = \frac{1}{\sqrt{\eta_i}} = \sqrt{V_{ei}}} \quad (11)$$

The prediction of origin is addressed in Equations (12) and (13) by the computation of average for Y_1 and Y_2.

$$\bar{Y}_1 = \frac{1}{n}(Y_{11} + \cdots + Y_{n1}) \quad (12)$$

$$\bar{Y}_2 = \frac{1}{n}(Y_{12} + \cdots + Y_{n2}) \quad (13)$$

Finally, Equation (14) shows the calculation to obtain MD value.

$$Mahalanobis\ distance, D^2 = \frac{YAY^T}{k} \quad (14)$$

Methadone patients who are being monitored were identified as an unhealthy group. When compute the unhealthy group, the same equation as for the healthy group is used, however the distinction between the two groups is in the normalisation of the unhealthy group. In the healthy group, the linear equation L' and the effective divider r' are determined to be identical equation, that are Equation (3) and Equation (4), accordingly. It is worth noting that the healthy group's average values for samples and parameters $\bar{x}$, as well as the effective divider r', are the same. Following that, the value sensitivity β for every unhealthy category may be computed using the Equation (2). Despite determining the total variations S_T, variation of the proportional term S_β, error variation S_e, and error variance V_e, by using Equations (5), (6), (7), and (8) consecutively, the sensitivity value and standard SN ratio from the unhealthy group are also utilized in order to calculate variables Y_1 and Y_2. The sensitivity value is taken for Y_1 as indicated in Equation (10), whereas the variable Y_2 is transformed first as stated in Equation (11) to enable assessment of any scattering

from ordinary situations. For the prediction of healthy group origin, the average value for Y_1 and Y_2 are as similar as indicated in Equations (12) and (13). Finally, as shown in Equation (14), the MD value can be identified.

The T-Method is used to analyze the parameters leading to the outcome. The greatest sample will be considered a healthy group, while the remaining samples will be considered as an unhealthy group. Equations (15) and (16) indicate the average values for each parameter as well as the output average value based on the number of samples in the healthy group.

$$\bar{x}_j = \left(x_{1j} + \cdots + x_{nj}\right) \quad (15)$$

$$\bar{y} = m_0 = \frac{1}{n}\left(y_1 + \cdots + y_n\right) \quad (16)$$

The unhealthy group is being classified when there are remaining samples from the healthy group. The unhealthy group was then adjusted by taking the average value of each parameter and output from the healthy group. The goal of normalization is to make data more adaptable by eliminating duplication. Equations (17) and (18) demonstrate the computation of normalized data for input and output, accordingly.

$$X_{ij} = \acute{x}_{ij} - \bar{x}_j \quad (17)$$

$$M_i = \acute{y}_i - m_0 \quad (18)$$

Proportional coefficient β and SN ratio η for each parameter are calculated as shown in Equations (19), (20), (21), (22), (23), (24) and (25).

$$Effective\ divider, r = M_1^2 + M_2^2 + \cdots + M_l^2 \quad (19)$$

$$Total\ variation, S_{T1} = X_{11}^2 + X_{21}^2 + \cdots X_{l1}^2 \quad (20)$$

$$Variation\ of\ proportional\ term, S_{\beta 1} = \frac{(M_1X_{11} + \cdots + M_lX_{l1})^2}{r} \quad (21)$$

$$Error\ variation, S_{e1} = S_{T1} - S_{\beta 1} \quad (22)$$

$$Error\ variance, V_{e1} = \frac{S_{e1}}{l-1} \quad (23)$$

$$Proportional\ Coefficint, \beta_1 = \frac{M_1X_{11} + \cdots + M_lX_{l1}}{r} \quad (24)$$

$$SN\ ratio\ \eta_1 = \begin{cases} \frac{\frac{1}{r}(S_{\beta 1} - V_{el})}{V_{el}} \\ 0 \end{cases} \quad (25)$$

A positive number of proportional coefficients indicates that the slope is advancing to the right, whereas a negative value proportional coefficient indicates that the slope is declining to the right. The value of SN ratio ought to be positive, however if it is negative, it is declared zero, indicating the absence of substantial interaction between input and output.

The proportional coefficient and SN ratio from each parameter are used to obtain the integrated estimate value of the unhealthy group. Equation (26) depicts the computation of the integrated estimate value. It should be noted that X_{i1}, X_{i2}, ..., X_{i6} are the normalized values of each parameter.

$$Integrated\ estimate\ value, \widehat{M}_i = \frac{\eta_1 \times \frac{X_{i1}}{\beta_1} + \ldots + \eta_k \times \frac{X_{ik}}{\beta_k}}{\eta_1 + \cdots + \eta_k} \quad (26)$$

The following Equations (27), (28), (29), (30), (31), (32), and (33) are used to calculate the estimated SN ratio. Indeed, the anticipated SN ratio is determined by the suitability of OA.

$$Linear\ equation, L = M_1\widehat{M}_1 + \cdots + M_l\widehat{M}_l \quad (27)$$

$$Effective\ divider, r = M_1^2 + \cdots + M_l^2 \quad (28)$$

$$Total\ variation, S_T = \widehat{M}_1^2 + \cdots + \widehat{M}_l^2 \quad (29)$$

$$Variation\ of\ proportional\ term, S_\beta = \frac{L^2}{r} \quad (30)$$

$$Error\ variation, S_e = S_T - S_\beta \quad (31)$$

$$Error\ variance, V_e = \frac{S_e}{l-1} \quad (32)$$

$$Integrated\ estimate\ value, \widehat{M}_i = 10 \quad (33)$$

The significance of a parameter is measured by how much the estimated SN ratio deteriorates when the parameter is not utilized. A two-level OA, level 1 and level 2 is applied for analysis. The implementation of OA allows for evaluations of the estimated SN ratio under diverse circumstances. The two-level of OA indicates that level 1 is a used parameter and level 2 is an unused parameter. In terms of the estimated SN ratio, the gap between the SN ratio averages for levels 1 and 2 for every parameter is important in order to figure out the relative significance of the parameters.

When the parameter is utilized with greater SN ratios and not used with smaller SN ratios, the degree of contribution becomes positive. Conversely, when the parameter is employed with smaller SN ratios and not with greater SN ratios, the degree of contribution becomes negative.

IV. Results and Discussion

Blood tests' scatter diagrams are made to differentiate between healthy and unhealthy groups. The unhealthy group is calculated sample by sample using two variables, Y_1 and Y_2. Y_2 is portrayed by the y-axis, and Y_1 is portrayed by the x-axis. The blue dotted on the graph denotes the healthy group with 50 samples, whereas the orange dotted denotes the unhealthy group with same number of samples. These graphs include 34 blood test parameters and 17 samples for the lipid profile. A scatter diagram of the lipid profile between healthy and unhealthy samples is depicted in Figure 2. Due to the varied range of MD values, the samples do not overlap and generate an aggregate of their own. The highest MD value for health is 5.6593, while the lowest MD value for healthy is 0.0111. Likewise, the highest and lowest MD values for unhealthy are 108.1481 and 53.3469 respectively. The average MD values for healthy and unhealthy are 1.0000 and 79.5876, indicating that the two samples are non-identical.

With 34 parameters, the number of healthy and unhealthy samples in the lipid profile of blood tests are 5 and 62, accordingly. As illustrated in Figure 3, the data is grouped in increasing order of output value. Sample number 11 has the smallest value of 0.011, while sample number 55 has the biggest value of 108.148. Nevertheless, sample numbers 8, 36, 13, 3, and 21 are assigned to be the blue and red dotted centre points.

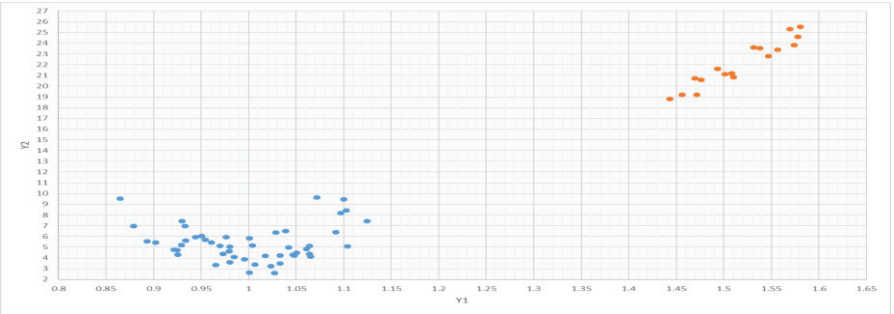

Figure 2: Scatter diagram of lipid profile between healthy and unhealthy

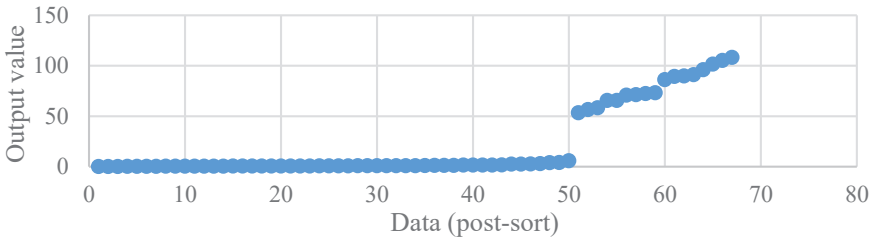

Figure 3: Data (post-sort) for lipid profile in blood tests

Figure 4 depicts the interaction between parameters and their desired outputs. The x-axis shows the normalized output values, while the y-axis shows the normalized parameter values. To decide the characteristics for assessment, the proportional coefficient and SN ratio were computed parameter after parameter. Using the connection between the normalized output value and the normalized parameter value, the T-Method computes SN ratios and proportional coefficients. According to [50], the higher the SN ratios, the stronger the relationship or the closer the distribution is to a blue line. Because Figure 4 (a) represents the parameter of A/G ratio and has 0.0002 SN ratio, the distribution is far from a blue line, but Figure 4 (b) represents the parameter of PDW and has 0.0040 SN ratio, the distribution is becoming closer to the blue line. This demonstrates that the higher the SN ratio, the closer the distribution is to a blue line in a graph.

Additionally, [50] claimed a positive value of proportional coefficients existed when there is a line ascending from left to

right. In the other hand, the descending line shows a negative value of proportional coefficients. This is seen in Figure 4 (a), which shows that the A/G ratio parameter has a proportional coefficient of -0.0021, while the other 33 parameters have a positive proportional coefficient. Consequently, such characteristics are ideal for computing integrated estimate value. Using the proportional value. Using the proportional coefficient and SN ratio data, this study would generate the integrated estimate value. As a result, the greater the SN ratios, the more it benefits to integrated estimations of MD value that are closer to the real normalized MD value. Because none of those parameters has a negative SN ratio value, all of them are accounted in the integrated estimate value.

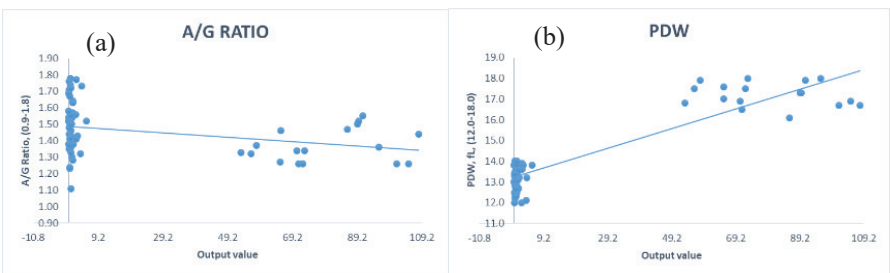

Figure 4: Scatter of normalized output and parameter values of lipid profile

Figure 5 illustrates a scatter diagram of real values when stated in x-axis terms and estimated values when expressed in y-axis terms. Estimated values that line up above a straight line suggest that a decent estimate was performed. Additionally, the graph provides extra information about an approximate straight line and its characteristics. In general, the model provides 0.9399 of R_2 or -19.19 db of SN ratios. It indicates that the correlation is high, and the distribution is approaching ithe green line. The line's equation is stated in Equation (34).

$$y = 1.0027x \quad (34)$$

Nonetheless, a few of these parameters are helpful for

integrated prediction while the remaining are not. As an outcome, parameters are assessed using L_{64} of OA, with level 1 stating for the used parameter and level 2 stating for the unused parameter. The integrated estimate SN ratio of -19.19 db corresponds to the initial run in L_{64}. The degree of contribution is then transformed into a bar graph, as illustrated in Figure 6. This demonstrates how well the parameters influence the output. When parameter 8 (PLT) is used (level 1) with a greater relationship (SN ratio = -19.41 db) to the output and when the parameter 8 is not used (level 2) with a smaller relationship (SN ratio = -19.88 db) to the output, the parameter acquires a higher degree of contribution (0.47 db), that has a positive contribution to the output. Then, when the parameter 29 (BUN) is used (level 1) with a smaller relationship (SN ratio = -19.72 db) to the output and when the parameter is not used (level 2) with a greater relationship (SN ratio = -19.57 db) to the output, the parameter receives a lower degree of contribution (-0.15 db) which indicates a negative contribution to the output.

Positive degree of contribution implies that the usage of parameter results in an increase in MD output, whilst negative degree of contribution implies that the use of parameter results in a decrease in MD output. As a result, parameters 1, 3, 4, 6, 7, 8, 9, 11, 12, 17, 18, 23, 26, 27, 28, 30, 31, 33, and 34 have a positive contribution degree, while parameters 2, 5, 10, 13, 14, 15, 16, 19, 20, 21, 22, 24, 25, 29, and 32 have a negative contribution degree. According to the findings of this study, in order to achieve a lower MD, the positive degree of contribution should be raised while the negative degree of contribution must be retained.

The objective of analyzing unknown data is to calculate the MD and assess its parameters for each sample. Normalization is accomplished by deducting from the healthy group's average value of the parameters. The outputs of the estimated MD value for unknown data are determined using Equation (26) and are shown in Table 2.

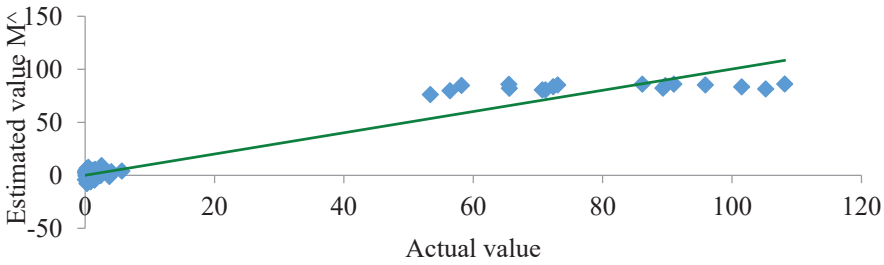

Figure 5: Distribution of actual and estimated signal data values of lipid profile

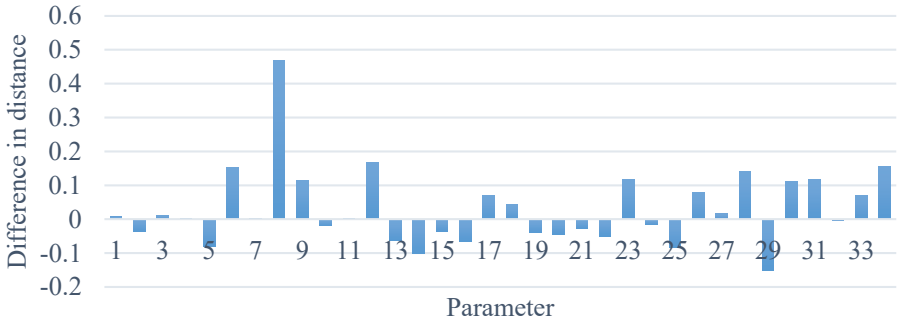

Figure 6: Degree of contribution of lipid profile

Figure 7 displays a scatter diagram of the estimated values after being subjected to the ecosystem generated during the optimization of the lipid profile of blood tests. The x-axis indicates the actual values of the output, *M*, while the y-axis displays the estimated values of the output, *M^*. Because the real values are uncertain, the unknown data spots on the x-axis have similar numbers as the estimated values. Figure 7 depicts the location of 15 samples with unknown data as a green triangle. It is possible to deduce that 5 unknown samples are closely related to the healthy group, 5 unknown samples are related to the unhealthy group, and 5 unknown samples are associated to the outlier.

Table 2: The estimated value Mˆ (MD) for unknown data in lipid profile

No. of sample	Estimated value Mˆ (MD)
1.	-11.0858
2.	-0.5437
3.	6.2553
4.	13.2806
5.	11.3406
6.	65.1200
7.	80.3015
8.	81.2553
9.	86.4674
10.	85.1327
11.	54.8708
12.	57.2702
13.	60.4310
14.	63.5181
15.	62.3254

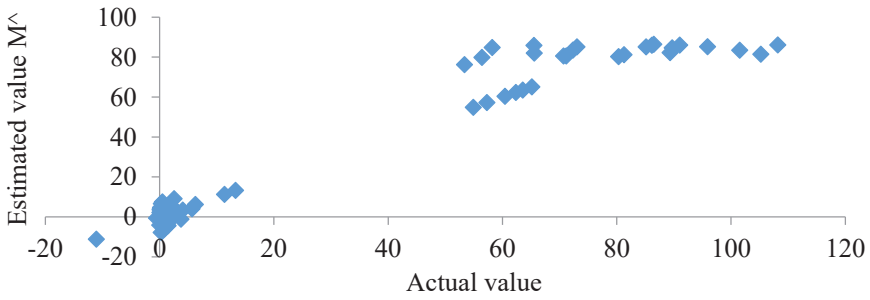

Figure 7: Interpretation of unknown data in lipid profile

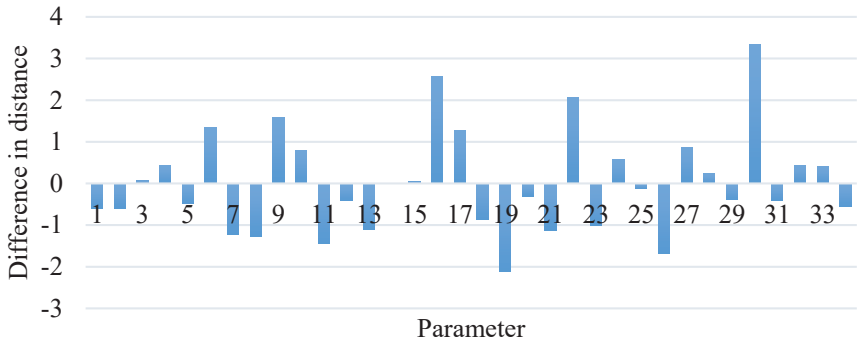

Figure 8: Degree of contribution in first sample of unknown data in lipid profile

Table 3: Comparison between original and types of modification

Original	MD	Modification	MD
1	-11.09	Type 1	-5.58
		Type 2	-13.12
		Type 3	-99.76
		Type 4	-148.77
		Type 5	6.42
		Type 6	-23.09

Figure 8 demonstrates the degree of contribution in the first unknown data sample in the lipid profile. As a result, parameters 3, 4, 6, 9, 10, 14, 15, 16, 17, 22, 24, 27, 28, 30, 32, and 33 have a positive contribution degree, while parameters 1, 2, 5, 7, 8, 11, 12, 13, 18, 19, 20, 21, 23, 25, 26, 29, 31, and 34 have a negative contribution degree. According to the findings of this study, to achieve a lower MD, the positive degree of contribution should be raised while the negative degree of contribution should be retained.

There are two sorts of contribution degrees. The first is the positive degree of contribution, that suggests the parameter has the impact of increasing the output. This means that raising the value of this parameter will also raise the MD value. Secondly, the negative degree of contribution implies that using the parameter has the impact of decreasing output. This means that lowering the value of this parameter will lowers the MD value too. The goal of this section is to demonstrate that the proposed solution is optimal to the Bandar Pekan clinic by decreasing the degree of contribution. As indicated in Figure 8, this study used blood tests (lipid profile) sample 1 as a specific subject. Table 3 shows the actual result for lipid profile (-11.09) which is from sample 1. The value is then compared to six other forms of modification.

The MD value for type 1 modification is -5.58, which is less than the MD value for the original sample. This adjustment indicates that the greater positive degree of contribution is increased by two points (parameters 6, 9, 16, 17, 22, and 30), whereas the lower positive

degree of contribution is increased by one point (parameter 3, 4, 10, 14, 15, 24, 27, 28, 32, and 33). The larger negative degree of contribution, on the other hand, is deducted with two points (parameters 7, 8, 11, 13, 19, 21, 23, and 26), while the lower negative degree of contribution is deducted with one point (parameter 1, 2, 5, 12, 18, 20, 25, 29, 31, and 34). As a result, this change has been rejected.

The MD value for type 2 modification is -13.12, which is greater than the value from the original sample. This change indicates that the greater positive degree of contribution is deducted by two points (parameters 6, 9, 16, 17, 22, and 30), whereas the lower positive degree of contribution is deducted by one point (parameter 3, 4, 10, 14, 15, 24, 27, 28, 32, and 33). The greater negative degree of contribution, on the other hand, is added with two points (parameters 7, 8, 11, 13, 19, 21, 23, and 26), whereas the lower negative degree of contribution is added with one point (parameter 1, 2, 5, 12, 18, 20, 25, 29, 31, and 34). As a result, this change has indeed been rejected.

The MD value for type 3 modification is -99.76, which is less than the value for the original sample. This adjustment indicates that the greater positive degree of contribution is added by two points (parameters 6, 9, 16, 17, 22, and 30), whereas the lower positive degree of contribution is added by one point (parameter 3, 4, 10, 14, 15, 24, 27, 28, 32, and 33). The greater and lower negative degrees of contribution, on the other hand, are both set to 0. As a result, this change has been rejected.

The MD value for type 4 modification is -148.77, which is less than the value for the original sample. This change means that the higher and lower positive degrees of contribution are both set to 0. The greater negative degree of contribution, on the other hand, is deducted with two points (parameters 7, 8, 11, 13, 19, 21, 23, and 26), while the lower negative degree of contribution is deducted with one point (parameter 1, 2, 5, 12, 18, 20, 25, 29, 31, and 34). As a result, this change has also been

rejected.

The MD value for type 5 modification is 6.42, which is more than the MD value for the original sample. This adjustment indicates that the greater positive degree of contribution is added by two points (parameters 6, 9, 16, 17, 22, and 30), whereas the lower positive degree of contribution is added by one point (parameter 3, 4, 10, 14, 15, 24, 27, 28, 32, and 33). The greater and lower negative degrees of contribution, on the other hand, retain their value. As a result, this modification has been accepted.

The MD value for type 6 modification is -23.09, which is less than the value for the original sample. This change means that the higher and lower positive degrees of contribution retain their value. The larger negative degree of contribution, on the other hand, is deducted with two points (parameters 7, 8, 11, 13, 19, 21, 23, and 26), while the lower negative degree of contribution is deducted with one point (parameter 1, 2, 5, 12, 18, 20, 25, 29, 31, and 34). As a result, this change has been rejected.

As a result, modification type 5 is the ultimate choice for the Bandar Pekan clinic since it has the highest MD value compared to others, which is a positive value. Nevertheless, the proposed alternative may be impacted by the total number of positive and negative contribution degrees, as well as the total number of higher and lower contribution degrees. This research demonstrates that the most crucial sort of modifications is merely a recommendation and is not implemented in clinics. The interview with the pharmacist at the Bandar Pekan clinic is conducted to get her feedback on the classification and optimization of the MFlex programme using MTS.

The following question was asked:

Question: In your viewpoint, does the T-Method make blood tests easier for the health department when just specific parameters are utilized to diagnose a disease, with a positive contribution to the output?

Answer: According to the explanation, the T-Method is

effective in assisting with disease diagnosis since it takes less time and makes it simpler to analyse the findings of diseases or blood tests.

V. Conclusion

In a nutshell, MTS can distinguish between healthy and unhealthy data based on this study's findings. Furthermore, it helps detect the important parameters for the lipid profile in blood tests. In other terms, it demonstrated that MTS could evaluate the key components in the MFlex program's blood test. The healthy group have an average MD of 1.0000, whereas unhealthy group have an average MD of 79.58. Parameters 1, 3, 4, 6, 7, 8, 9, 11, 12, 17, 18, 23, 26, 27, 28, 30, 31, 33, and 34 are positive degree of contribution, whereas parameters 2, 5, 10, 13, 14, 15, 16, 19, 20, 21, 22, 24, 25, 29, and 32 are negative degree of contribution. MTS was used to diagnosis 15 unknown samples in MFlex programme blood testing. They all have varying degrees of positive and negative contribution to obtain smaller MD. There are six types of modifications that may be used to prove the suggested solution, with type 5 being the best. A pharmacist from the Bandar Pekan clinic verified that MTS could handle classification and optimization difficulty in the MFlex system. This study offers benefits for the application of MTS's RT-Method and T-Method in health monitoring systems. It will be intriguing to identify if the approaches can be used for system upgrades, medicine selection, and patient identification from prior facilities.

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