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ORIGINAL ARTICLE

# Methadone Flexi Dispensing (MFlex) Intelligence System utilizing the Mahalanobis-Taguchi System

N.S. Pinueh[1], M.Y. Abu[1*], S.K.M. Saad[1], N.H. Aris[1] and E. Sari[2]

[1]Faculty of Manufacturing and Mechatronic Engineering Technology, Universiti Malaysia Pahang Al-Sultan Abdullah, 26600 Pahang, Malaysia.

[2]Universitas Trisakti, Faculty of Industrial Technology, Department of Industrial Engineering, 11440 Kyai Tapa No 1, West Jakarta, Indonesia

**ABSTRACT** – Patients who are participating in the methadone flexi dispensing (MFlex) program are obliged to provide their blood samples for various testing, such as lipid profiles. A doctor evaluates three parameters, including cholesterol, HDL cholesterol, and LDL cholesterol to determine whether or not the patient has a lipid issue. Since, the current structure lacks an ideal atmosphere for classification and optimization caused by inaccuracies in measurement methodologies and a lack of explanation for significant aspects that have an effect on the accuracy of diagnostics. The objective is to implement the Mahalanobis-Taguchi system (MTS) in the MFlex program. Utilizing a total of 34 parameters, there are two different types of MTS techniques used for classification and optimization: the RT method and T method. The average Mahalanobis distance (MD) for healthy conditions is 1.0000 whereas for unhealthy is 79.5876. As a result, there is 19 parameters indicate a positive degree of contribution. 15 unknown samples were diagnosed with a variety of positive and negative degree of contribution to achieving a lower MD. Type 5 of 6 alterations was chosen as the best suggested possibility. In conclusion, MTS is able to be applied in medical environment.

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## INTRODUCTION

According to [1], the average rate of mortality caused by illegal substances is 6.9 deaths per 100,000 individuals. These deaths happened because using illegal substances increases the chance of getting sick or disabled, including getting HIV, liver damage, suicide, and hepatitis [2]. Misuse of drugs is a complicated and serious problem that affects the public's health in Malaysia [3]. According to the numbers that were made public by the National Anti-Drug Agency (NADA) for the year 2013, the category of individuals who engage in drug abuse is constituted of those who are at least 13 years old [4]. The MFlex program was established with the intention of reducing HIV infections and other blood-borne illnesses, particularly among injecting drug users [5]. Blood tests, such as a lipid profile that includes 34 parameters, are required to be performed on patients who are participating in the MFlex program. These tests are used to determine whether or not the patient has other medical conditions. To determine if a patient has a lipid issue, the doctor needs to examine three parameters: cholesterol, HDL cholesterol, and LDL cholesterol. This demonstrates that the current system lacks a reliable measuring technique and lack an explanation for major parameters. The purpose of this study is to analyze the classification and optimization elements in the lipid profile, as well as to diagnose the unknown data in the MFlex program. The literature review highlights relevant MTS studies and identifies the most important study gaps. Research methodology describes the processes and techniques utilized to achieve the research's objective. The results and discussions expand on all of the documentation obtained during collecting data utilizing MTS techniques for classification and optimization. In a nutshell the conclusion concludes by providing a summary of the final findings after the measurements have been accomplished while providing some recommendations for additional research.

## LITERATURE REVIEW

Deaths from opioids, especially prescription opioids, have drastically impacted mortality statistics in numerous high-income countries. Nearly 11 million individuals worldwide inject narcotics, with 1.4 million infected with HIV and 5.6 million with hepatitis C [6]. For every twenty new cases of drug abusers that were reported on a daily basis on average in 2009, drug addiction is a serious public health problem in Malaysia [3]. The MFlex program has been effective in

*CORRESPONDING AUTHOR | M. Y. Abu | myazid@umpsa.edu.my

lowering HIV infection in Malaysia. The program also demonstrated cost-effectiveness in terms of cost reductions and returns [5].

MTS created by Genichi Taguchi is a multivariate group that employs Taguchi Methods concepts to generate a multivariate scale of measurements using a data-analytical method to assist in quantitative decision making [7]. The MD was first developed in 1936 by Prasanta Chandra Mahalanobis. A calculation of the Mahalanobis space (MS) is performed by using uniform variables derived from healthy or normal data in MTS. The MS may be used to identify between healthy and unhealthy data. In the scenario this MS is chosen, the number of features is reduced to the highest level possible by using an orthogonal array (OA) and the signal-to-noise ratio (SNR) to measure the input of each characteristic [8]. An illustration of the distance between the MD and the Euclidian distance (ED) may be seen in Figure 1. The "nearness" of an unknown point to the group's midpoint (s) may be estimated with the help of MD algorithm. It is also possible to determine the distance between the "unknown" point and the group mean point using ED. However, this method has a limitation in that it only calculates a proportional distance from the group mean point, without taking into account the distribution of the points that are included in the group [9].

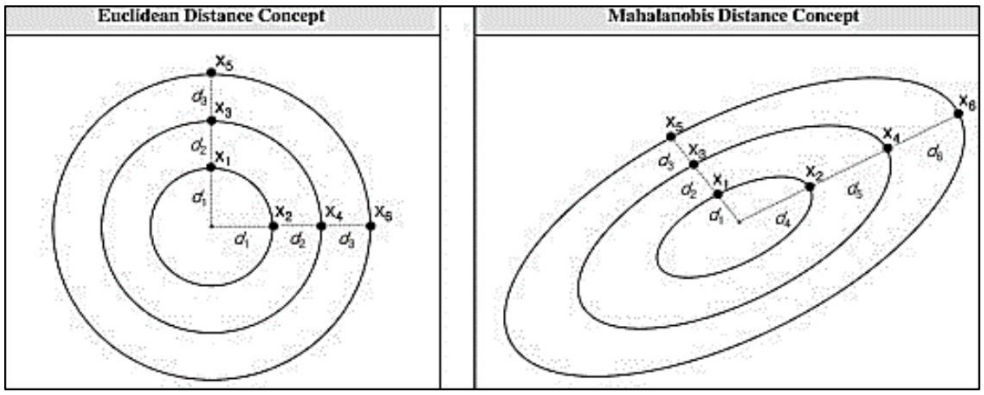


Figure 1. Comparison between MD and ED [10]

It is possible for the MTS to identify abnormalities even when learning data were classified as "unlabelled" [12], as well as to measure healthy and unhealthy retrospective observations [13]. Additionally, the MTS is able to classify normal and abnormal findings and optimise various criteria for the development of a product that performs better at the workstation [11]. MTS, on the other hand, has a statistical framework that is less robust than that of typical multivariate processes [14], it can only handle problems with binary classification [15], and it does not have a method for obtaining an acceptable binary classification threshold [16].

According to [17], MTS research is classified into seven categories: introduction to the method, case of study/application, comparison with other methods, construction of MS, integration, and development with other methods, dimensional reduction, and threshold establishment. These groups are used to summarize the gaps in research that have been released from 2011 to 2020 in this study. MTS assessed normal and abnormal data during threshold establishment and optimized numerous parameters on the manufacturing line to provide an improved product [11]. From the MTS system, it is easy to tell the difference between road surface conditions like manhole cover, pothole, and speed hump [18]. MTS has been the most promising method for using binary classification to deal with uneven data [16]. MTS put objects into two groups by using MD-based cutoff values [19]. MD changed the shape of the super pixels to better fit the changing structure of the real world [20], figured out the right way to find the value of a random sample [21], put people on the outside of the study based on a basic regression study [22], got an indicator of the tool's health [23], and gave more accurate results for the right decision-making process [24].

[25] used MTS to the connecting rod's large end diameter to differentiate between two separate ranges in the re-manufacturability process spectrum. [26] conducted a comprehensive examination of the data collected on the primary journal diameter of the crankshaft. [27] used MTS to create a scatter diagram that could help people make decisions in an industry. The diagram showed 14 main journals of crankshafts from 7 different engine types, with different numbers of samples. [28] used the Mahalanobis-Taguchi technique to classify the end of crankshafts life into recovery operations. [29] made a new crankshaft design and used the MTS to figure out which crankshaft factors were important and which were not. They then used Activity Based Costing (ABC) to guess how much it would cost to remanufacture the crankshaft. [30] used MTS to identify critical and non-critical factors throughout the remanufacturing process while also estimating cost using the ABC technique. Using Taguchi's orthogonal array, [31] analyzed the criticality of parameters on an end-of-life crankshaft. Then, using typical cost accounting, estimate the cost taking into consideration the important characteristics. [32] used MTS to assess the degree of contribution and identify the parameters influencing the system.

[33] suggested that the electric and electronic industries use MTS and Time-Driven Activity-Based Costing (TDABC) to look at important variables and come up with time equations and capacity cost rates, respectively. [34] used MTS to identify four unimportant and eleven important parameters in a visual mechanical inspection workstation. [11] discovered that a positive rise in SNR implies that the system's quality remained acceptable from February (0.1244) to December (0.4432), after unimportant parameters using MTS. [35] found that MTS is advantageous for classification and optimization in industry. [36] found that MTS and TDABC are a great resource that can be easily used in the electronic industry. [37] used the MFlex service to make the tracking system better by creating an MTS-based graphical user interface for analyzing and sorting patients into groups of normal and abnormal variants. According to [38], none of the four thresholding approaches outperformed the others in almost all of the datasets. [39] showed that combining Bitwise Artificial Bee Colony (BitABC) methods along with Taguchi's T-Method greatly improved the accuracy of predictions.

## RESEARCH METHODOLOGY

This study focuses on the MFlex program administered by the Ministry of Health Malaysia in the blood testing. There are four groups of 34 factors in blood tests that are used to check on the health of people who are on methadone: FBC, liver function profile, lipid profile, and renal profile. Patients on methadone are put into one of four groups based on whether they had one of those problems when they started the MFlex program. Also, the essential elements of blood tests may be made improved. Methadone individual urine tests (types of drugs) are used to determine which substances are more addictive in daily life. Following that, blood tests are performed on each methadone patient to see if they have any ailment in their body. The parameters of blood tests are shown in Table 1, which includes a selection of 34 parameters and a reference range that indicates a healthy condition. The parameters for the FBC, liver function profile, lipid profile, and renal profile are 17, 8, 4, and 5 accordingly.

Table 1. Parameters in Blood Tests

| 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) |
| 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 things into two categories: inside and outside the unit region. Unit data was chosen because, among other things, it had the greatest number of samples. The RT-Method validated the output value, but the group can be perceived when there is more than one unit place. From n samples in the healthy group, equation (1) is used to find the average number for each parameter.

$$\bar{x}_j = \frac{1}{n}(x_{1j} + x_{2j} + \cdots + x_{nj}) \ (j = 1, 2, \ldots k) \tag{1}$$

$$\text{Sensitivity}, \beta_1 = \frac{L_1}{r} \tag{2}$$

$$\text{Linear equation}, L_1 = \bar{x}_1 x_{11} + \bar{x}_2 x_{12} + \cdots + \bar{x}_k x_{1k} \tag{3}$$

$$\text{Effective divider}, r = \bar{x}_1^2 + \bar{x}_2^2 + \cdots + \bar{x}_k^2 \tag{4}$$

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

$$\text{Variation of proportional term}, S_{\beta 1} = \frac{1}{r} \tag{6}$$

$$\text{Error variation}, S_{e1} = S_{T1} - S_{\beta 1} \tag{7}$$

$$\text{Error variance}, V_{e1} = \frac{S_{e1}}{k-1} \tag{8}$$

Equation (9) is used to get the standard SN ratio, $\eta$. The higher the value of $\eta$, the stronger the correlation between input and output.

$$\text{SN ratio}, \eta_1 = \frac{1}{V_{e1}} \tag{9}$$

The healthy group's sensitivity $\beta$, and the standard SN ratio $\eta$ are computed, followed by the two variables (Y1 and Y2) to construct a scatter diagram. Equations (10) and (11) reveal the values of Y1 and Y2, respectively.

$$Y_{i1} = \beta_i \tag{10}$$

$$Y_{i2} = \frac{1}{\sqrt{y_i}} = \sqrt{V_{ei}} \tag{11}$$

The prediction of origin is based on the computation of averages for Y1 and Y2 in equations (12) and (13) respectively. Finally, MD is determined using Equation 14.

$$\bar{Y}_1 = \frac{1}{n}(Y_{11} + Y_{21} + \cdots + Y_{n1}) \tag{12}$$

$$\bar{Y}_2 = \frac{1}{n}(Y_{12} + Y_{22} + \cdots + Y_{n2}) \tag{13}$$

$$\text{Mahalanobis distance}, D^2 = \frac{YA^{-1}Y^T}{k} \tag{14}$$

Those patients who are currently being tracked for methadone have been determined to be unhealthy. The unhealthy group is calculated using the same equation as the healthy group, with the only difference being the normalization of the unhealthy group. Evaluation of the parameters in relation to the final outcome is accomplished via the use of the T-Method. All of the samples will be categorized as unhealthy, with the exception of the biggest sample, which will be declared to be a healthy group. Using equations (15) and (16), respectively, one can determine the average values for each parameter as well as the output average value depending on the number of samples received from the healthy group.

$$\bar{x}_j = \frac{1}{n}(x_{1j} + x_{2j} + \cdots + x_{nj}) \tag{15}$$

$$\bar{y} = m_0 = \frac{1}{n}(y_1 + y_2 + \cdots + y_n) \tag{16}$$

It is determined that the balance samples that are part of the healthy group are considered to be unhealthy. After that, the unhealthy group was normalized by calculating the average value of each parameter and output from the healthy group. This was accomplished through the process of normalization. Normalization aims to increase data flexibility by reducing duplication. The equations (17) and (18) are used to determine the normalised data for the input and output, respectively.

$$X_{ij} = x'_{ij} - x_j \tag{17}$$

$$M_i = y'_i - m_0 \tag{18}$$

$$\text{Effective divider, } r = M_1^2 + M_2^2 + \cdots + M_l^2 \tag{19}$$

$$\text{Total variation, } S_{T1} = X_{11}^2 + X_{21}^2 + \cdots X_{l1}^2 \tag{20}$$

$$\text{Variation of proportional term, } S_{\beta 1} = \frac{(M_1X_{11} + M_2X_{21} + \cdots + M_lX_{l1})^2}{r} \tag{21}$$

$$\text{Error variation, } S_{e1} = S_{T1} - S_{\beta 1} \tag{22}$$

$$\text{Error variance, } V_{e1} = \frac{S_{e1}}{l-1} \tag{23}$$

$$\text{Proportional Coefficient, } \beta_1 = \frac{M_1X_{11} + M_2X_{21} + \cdots + M_lX_{l1}}{r} \tag{24}$$

$$\text{SN ratio, } \eta_1 = \begin{cases} \frac{\frac{1}{r}(S_{\beta 1} - V_{el})}{V_{el}} & (when\ S_{\beta 1} > V_{el}) \\ 0 & (when\ S_{\beta 1} \le V_{el}) \end{cases} \tag{25}$$

A positive value of $\beta$ indicates steepness increasing to the right, whereas a negative value indicates steepness descending to the right. If $\eta$ is negative, it is regarded zero, indicating no substantial relationship between input and output. The number should be positive.

A calculation is made to determine the integrated estimate value of the unhealthy group by using the β and ŋ values for each parameter. A demonstration of how to compute the integrated estimate value is provided by Equation (26). It should be noted that the normalized value of each parameter is represented by the values *xj1*, *xj2*, …, *xj6*. As a matter of fact, the SN ratio ŋ that is expected is dependent upon the suitableness of OA.

$$\text{Integrated estimate value, } \hat{M}_i = \frac{y_1 \times \frac{X_{i1}}{\beta_1} + y_2 \times \frac{X_{i2}}{\beta_2} + \ldots + y_k \times \frac{X_{i6}}{\beta_6}}{y_1 + y_2 + \cdots + y_6} \tag{26}$$

$$\text{Linear equation, } L = M_1\hat{M}_1 + M_2\hat{M}_2 + \cdots + M_l\hat{M}_l \tag{27}$$

$$\text{Effective divider, } r = M_1^2 + M_2^2 + \cdots + M_l^2 \tag{28}$$

$$\text{Total variation, } S_T = \hat{M}_1^2 + \hat{M}_2^2 + \cdots + \hat{M}_l^2 \tag{29}$$

$$\text{Variation of proportional term, } S_\beta - \frac{L^2}{r} \tag{30}$$

$$\text{Error variation, } S_e = S_T - S_\beta \tag{31}$$

$$\text{Error variance, } V_e = \frac{S_e}{l-1} \tag{32}$$

$$\text{Estimated SN ratio, } \eta = 10 \log \left[ \frac{\frac{1}{r}(S_\beta - V_e)}{V_e} \right] \tag{33}$$

The relative significance of a parameter is measured by how much the estimated SN ratio deteriorates when it is not employed. The assessment is conducted using a two-level OA (level 1 and level 2). The use of OA provides measurements

of the estimated SN ratio under a variety of circumstances. The two-level of OA signifies that level 1 parameters will be utilized and level 2 parameters will be ignored. In terms of the estimated SN ratio, the significance of the parameters is determined by calculating the difference between the SN ratio averages for levels 1 and 2 for each parameter. This difference has been calculated for each parameter. When the parameter is used with larger SN ratios, rather than with smaller SN ratios, the degree of contribution transforms into a positive value. On the other hand, the degree of contribution is shown to be negative when the parameter is used with lower SN ratios and is not utilized with bigger SN ratios.

## RESULTS AND DISCUSSIONS

The scatter diagrams of blood tests between healthy and unhealthy groups are generated. All unhealthy groups are estimated sample per sample using two variables: Y1 and Y2. The y-axis indicates Y2, whereas the x-axis represents Y1. The blue dots on the graph reflect the healthy group of 50 samples, while the orange dots represent the unhealthy group. This figure shows 34 blood test parameters and the lipid profile was created using 17 samples. Figure 2 depicts a scatter diagram of the lipid profile in healthy and unhealthy samples. It is because of the wide range of MD values that these samples do not overlap and instead create their own aggregate with one another. The highest value of MD for healthy is 5.6593, while the smallest value is 0.0111. On the other hand, the greatest MD value for unhealthy is 108.1481, while the lowest MD value is 53.3469. It is evident that the two samples are not similar since the average MD values for healthy and unhealthy are 1.0000 and 79.5876, respectively.

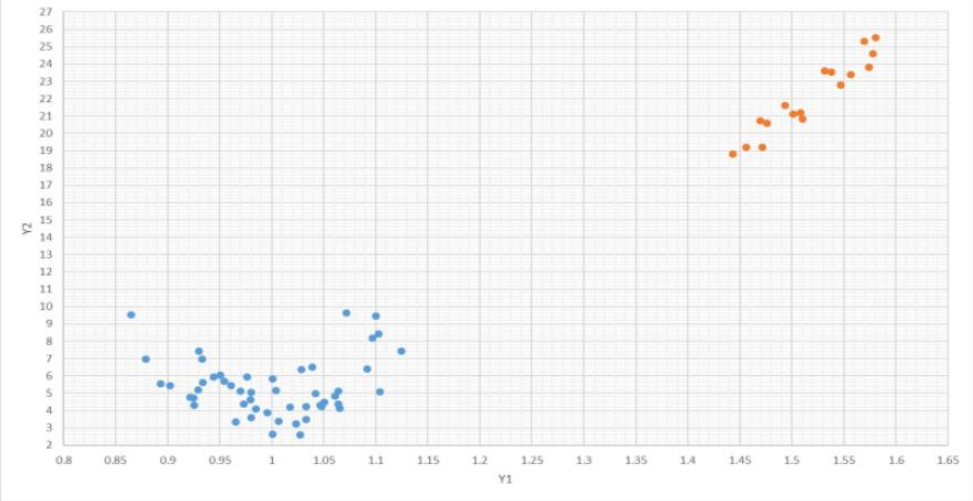


Figure 2. Scatter diagram of lipid profile between healthy and unhealthy

In the lipid profile of blood tests, there are 5 healthy samples and 62 unhealthy samples, each with 34 parameters. Figure 3 illustrates how the data is organized in ascending order of output value. Sample number 11 is the smallest with 0.011, while sample number is the biggest with 108.148. That is the fact sample numbers 8, 36, 13, 3, and 21 are designated as the center points in blue and red dots.

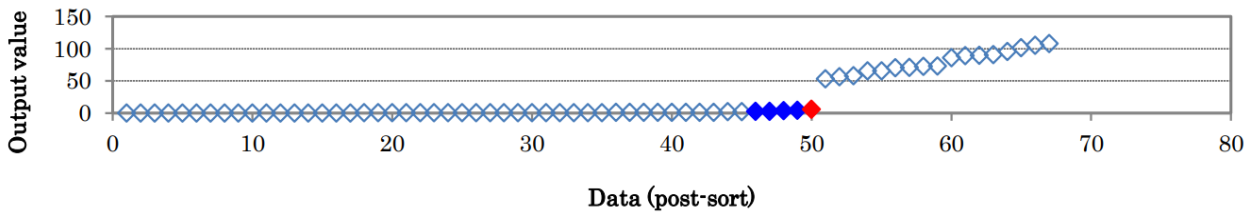


Figure 3. Data (post-sort) for lipid profile in blood tests

Figure 4 depicts the relation between parameters and their respective output values. The values of the normalized output are shown along the x-axis, while the values of the normalized parameters are represented along the y-axis. A parameter-by-parameter calculation of the β and the ŋ was carried out in order to determine which parameters would be advantageous for consideration throughout the process of evaluation. In the T-Method, the computation of ŋ and β is based on the relation between the normalized output and the parameter values. According to [40], higher SN ratios $\eta$ result in a stronger connection or closer distribution to a blue line. Figure 4 (xx) displays the A/G ratio parameter with

0.0002 SN ratio $\eta$, whereas Figure 4 (xvi) represents the PDW parameter with 0.0040 SN ratio $\eta$, indicating a distribution closer to the blue line. It is clear that the distribution is more closely aligned with a blue line on a graph when the SN ratio is lower.

As stated in reference [40], when the line is ascending from left to right, it represents a positive value β, whereas when the line is descending, it implies a negative value β. Figure 4 (xx) shows that the A/G Ratio parameter has a $\beta$ of -0.0021, whereas the other 33 parameters have a positive $\beta$. As a consequence, these characteristics are ideal for determining the integrated estimate value. This study uses $\beta$ and $\eta$ data to calculate integrated estimate values. Higher $\eta$ lead to more accurate MD value predictions that are closer to the real normalized value. Due to the fact that none of these parameters contain a negative ŋ value, they are all included into the calculation of the integrated estimate value.

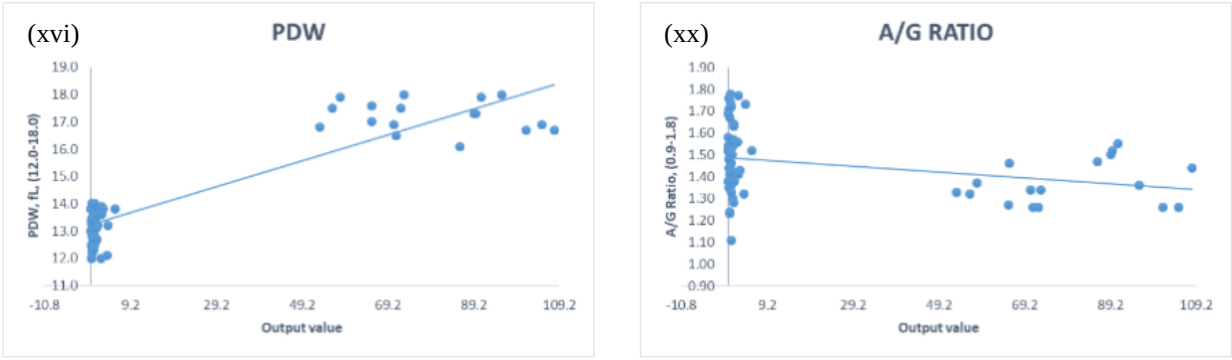


Figure 4. Scatter of normalized output and parameter values of lipid profile

The scatter diagram that is shown in Figure 5 illustrates the results that are obtained when the x-axis represents actual values and the y-axis represents estimated values. A reasonable estimate was generated if the estimated values are higher than a straight line, which indicates that the estimate was accurate. In addition, the graph will provide further details about an approximate straight line and the characteristics it's has. The model provides 0.9399 of $R^2$ or -19.19 db of $\eta$ in general estimate. Furthermore, it demonstrates that the connection is strong and that the distribution is becoming closer to the green line. The equation that describes the line may be found in equation (34).

$$y = 1.0027x \tag{34}$$

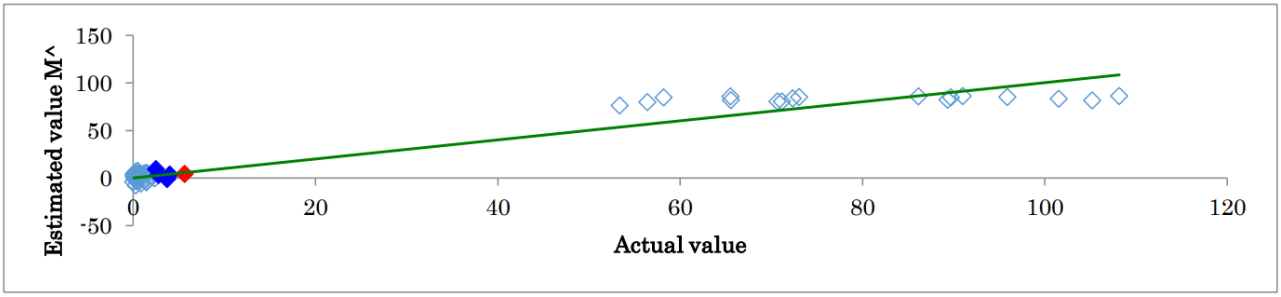


Figure 5. Distribution of actual and estimated signal data values of lipid profile

Nonetheless, some of these parameters are beneficial for integrated estimation, while others are not. As a result, parameters are assessed using L64 of OA, where level 1 indicates that the parameter will be used and level 2 indicates that it will not be used. The first run in L64 yielded an integrated estimate $\eta$ of -19.19 db. The degree of contribution will be converted into a bar graph as seen in Figure 6. This shows how the result is affected by the parameters that are selected. There is a stronger relationship (c = -19.41 db) between parameter 8 (platelet count, PLT) and the output when it is used (level 1) and a weaker relationship (β = -19.88 db) when it is not used (level 2). When parameter 8 is not used, it has a higher degree of contribution (0.47 db), which is a positive contribution to the output. On the other hand, parameter 29, which stands for BUN, has a smaller relationship (β = -19.72 db) to the output when it is used (level 1) and a larger relationship (β = -19.57 db) when it is not used (level 2). The parameter has a lower degree of contribution (-0.15 db), which means it has a negative relationship with the output.

The utilization of a parameter results in an increase in the production of MD when the degree of contribution is positive, while the utilization of a parameter results in a decrease in the output of MD when the degree of contribution is negative. As a result, parameters 1, 3, 4, 6, 7, 8, 9, 11, 12, 17, 18, 23, 26, 27, 28, 30, 31, 33, and 34 contribute positively, whereas parameters 2, 5, 10, 13, 14, 15, 16, 19, 20, 21, 22, 24, 25, 29, and 32 contribute negatively. According to the findings of this study, in order to achieve a lower MD, it is recommended that the positive degree of contribution be increased while the negative degree of contribution remain unchanged.

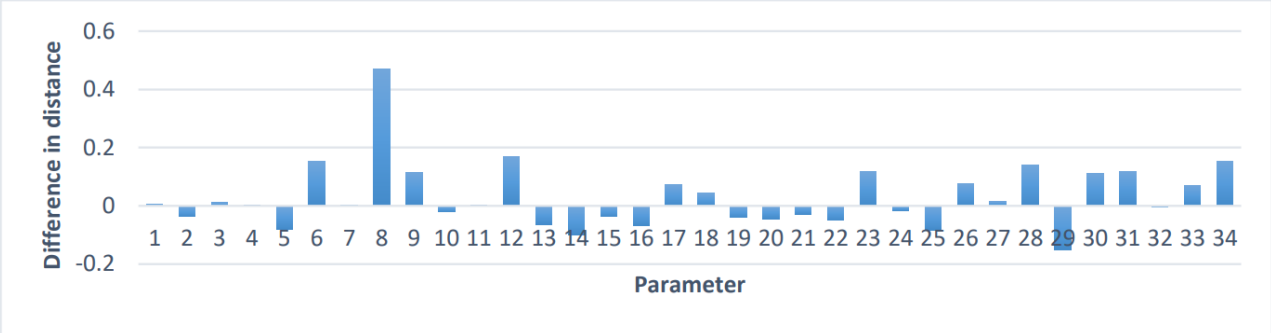


Figure 6. Degree of contribution of lipid profile

For each sample, the objective of the diagnostic of unknown data is to ascertain the MD and the parameters associated with it. The removal of the parameters' average values in the healthy group is the method that is used to accomplish normalization. The equation (26) calculates the estimated value $M\hat{}$ or MD for unknown data, which is then shown in Table 2.

Table 2. The estimated value $M\hat{}$ (MD) for unknown data in lipid profile

| No. of sample | Estimated value $M\hat{}$ (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 depicts a scatter diagram of the estimated values after receiving exposure to the ecosystem created during the optimization of the lipid profile of blood tests. The x-axis depicts the actual output values $M$ and the y-axis represents the estimated output values of $M\hat{}$. Because of the real values are unknown, the unknown data places on the x-axis use are based on the estimated values. Figure 7 shows the whereabouts of 15 unknown data samples represented by a green triangle. It is feasible to draw the conclusion that 5 unknown samples are closely connected to the healthy group, 5 unknown samples belong to the unhealthy group, and another 5 unknown samples belong to the outlier.

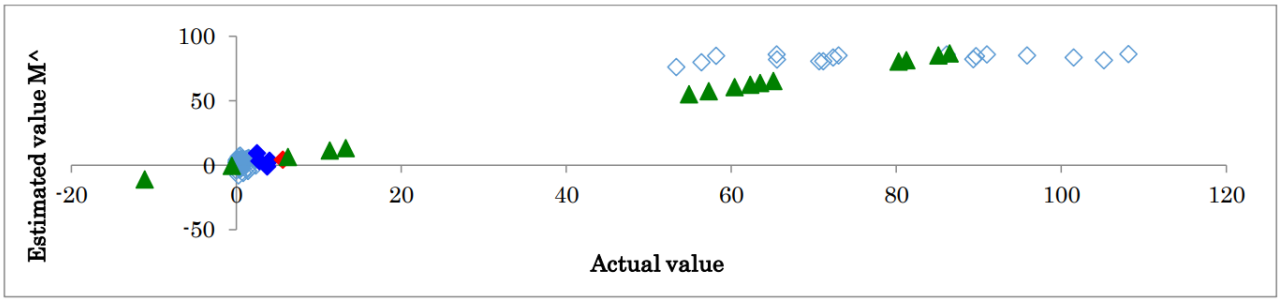


Figure 7. Interpretation of unknown data in lipid profile

Figure 8 depicts the degree of contribution to the lipid profile of unknown data in the first sample. As a result, parameters 3, 4, 6, 9, 10, 14, 15, 16, 17, 22, 24, 27, 28, 30, 32, and 33 contribute positively, whereas parameters 1, 2, 5, 7, 8, 11, 12, 13, 18, 19, 20, 21, 23, 25, 26, 29, 31, and 34 contribute negatively. According to the findings of this research, in order to achieve a lower MD, it is recommended that enhancements be made to the positive degree of contribution while the negative degree of contribution should be maintained.

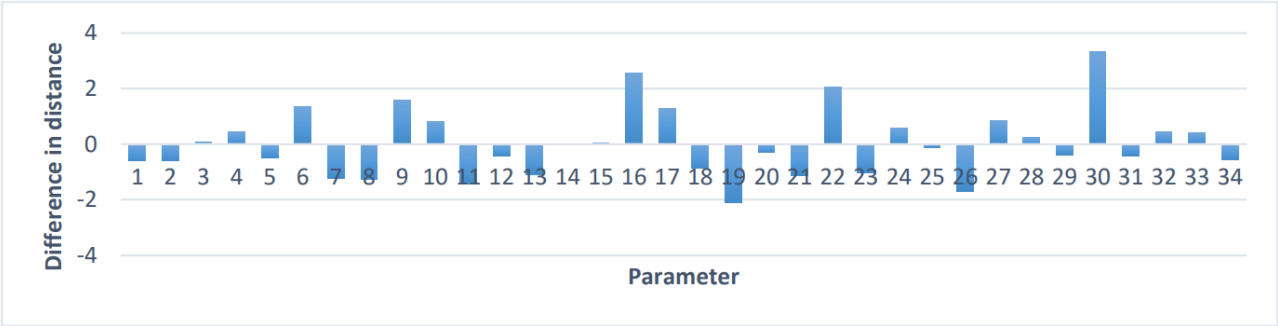


Figure 8. Degree of contribution in first sample of unknown data in lipid profile

The first is a positive degree of contribution, which means that this measure has the effect of making the result higher. This means that the MD will increase when the number of this parameter increases. Second, the fact that the degree of contribution is negative means that using this parameter lowers the result. When this parameter's value is lowered, the MD number will also be lowered. The objective of this phase is to show that the suggested solution to the Bandar Pekan clinic, which includes lowering the degree of contribution, is an optimal alternative. As illustrated in Figure 8, the focus of this blood tests (lipid profile) sample 1. The original outcome for sample 1 lipid profile is -11.09 as stated in Table 3. There are six different types of modifications that are compared to the value.

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 |

This suggests, the ideal alternative for the Bandar Pekan clinic is modification type 5, which has a higher MD value than the others, indicating a positive value. However, the solution that has been suggested could be affected by the total number of degree contributions that are of a positive and negative, as well as the total number of degree contributions that are of a higher and lower. This study demonstrates that the most essential kind of modification are just suggestions and are not often implemented in clinics. The interview with the pharmacist at the Bandar Pekan clinic proceeded to find out what she thought about using MTS for classification and optimization in the MFlex program. The question was posed as follow.

Question: From your point of view, does the T-Method make it simpler for the health department to conduct blood tests when just certain parameters are required to detect an illness, and does this result in a positive contribution to the output?

Answer: According to the explanation, the T-Method is effective in assisting with illness diagnose since it saves time and simplifies the interpretation of diseases or blood tests results.

## CONCLUSION

Based on this study, MTS can distinguish between healthy and unhealthy data. Furthermore, it may detect significant parameters for the lipid profile in the blood testing. In other words, MTS demonstrated its ability to assess significant elements in the MFlex program's blood tests. The average MD for a healthy is 1.0000, whereas an unhealthy one is 79.5876. Parameters 1, 3, 4, 6, 7, 8, 9, 11, 12, 17, 18, 23, 26, 27, 28, 30, 31, 33, and 34 are all degree of contribution positively, whereas parameters 2, 5, 10, 13, 14, 15, 16, 19, 20, 21, 22, 24, 25, 29, and 32 are degree of contribution negatively. MTS was used to diagnosis 15 unknown samples in blood testing from the MFlex program. All of them assist to decrease MD in varying degree of contributions, both positively and negatively. There are six distinct types of modifications that may be used to demonstrate that the suggested solution is the best one, and type 5 has been selected as the ideal alternative. A pharmacist from the Bandar Pekan clinic verified that MTS can handle a classification and optimization difficulties in the MFlex program. Regarding the use of the RT Method and the T Method of MTS in health monitoring systems, this study combines both of those approaches. It would be fascinating to see whether the approaches might be used to update systems, determine prescription dosages, and identify patients from previous hospitals.

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