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Application of the Mahalanobis-Taguchi System in Renal Profile of the Methadone Flexi Dispensing Program

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Abstract: Patients under the methadone Flexi dispensing (MFlex) program are required to do blood tests like renal profile. To ensure the patient has a kidney failure, a doctor assesses one parameter like creatinine. Unfortunately, the existing system does not have a stable ecosystem towards classification and optimization due to inaccurate measurement methods and lack of justification of significant parameters, which will influence the accuracy of diagnosis. The objective is to apply the Mahalanobis-Taguchi system (MTS) in the MFlex program. The data is collected at Bandar Pekan clinic with 34 parameters. Two types of MTS methods are used, such as RT-Method and T-Method, for classification and optimization. As a result, the RT-Method can classify healthy and unhealthy samples, while the T-Method can evaluate the significant parameters in terms of the degree of contribution. Fifteen unknown samples have been diagnosed with different positive and negative degrees of contribution to achieving lower MD. The best-proposed solution is type 5 of 6 modifications because it shows the highest MD value than others. In conclusion, a pharmacist from Bandar Pekan clinic confirmed that MTS could solve a problem in the classification and optimization of the MFlex program.

Keywords: Mahalanobis-Taguchi system, Mahalanobis distance, renal profile, classification, optimization, and methadone flexi dispensing program.

Introduction

Drug addiction remains one of the big psychological, legal, and public health issues of the globalized era. About 35 million people are estimated to suffer from substance use problems and need recovery facilities [1]. According to a statistic study published by the National Drug Information System (BIONADI), 8613 former drug users relapsed in 2009. Compared to 2009, the rate of relapse among drug addicts in 2010 fell by around 25% [2]. Malaysia has designated the drug problem as the nation's number one adversary since 1983 [3]. The implementation of the MFlex program managed to improve the life of this drug addict. Participation in the MFlex program can also be a platform for patients to detect problems other health such as HIV, hepatitis, and Tibi [4]. MTS is used to create reference scales by generating individual scales of measurement for each parameter [5]. This research work chose MTS over other methods because of the benefits of using MTS compared with other popular techniques such as regression analysis. The MTS process is highly stable and has a better accuracy rating of more than 90% [6]. MTS does better in the sensitivity index, showing good predictive precision in the production of pressure ulcers [7]. Patients under the MFlex program in Bandar Pekan clinic located at Pekan Pahang, Malaysia, must do blood tests such as renal profile involving 34 parameters to determine whether the patient has other diseases or vice versa. A doctor is required to assess one parameter, such as creatinine, to ensure the patient has kidney failure. That procedure proves that the existing system does not have an accurate measurement method and lacks justification of significant parameters. Bandar Pekan clinic has been chosen in this research work because it uses outdated MFlex program management, i.e., written documentation. This research work wants to develop a new data monitoring system for the MFlex program using MTS methods as previous studies have never done in previous studies.

This research aims to analyze the classification and optimization factors in the renal profile and to diagnose the unknown data of the MFlex program. First, the literature review describes related studies on MTS, the most significant research gap. Then, the research methodology explains the methods and strategies used to meet the research objective. Next, the result and discussion elaborate all the evidence possessed during data collection using the MTS method for classification and optimization. Lastly, the conclusion concludes the final findings after the measurements have been handled and recommenddations for the subsequent work.

Methods

Literature Review

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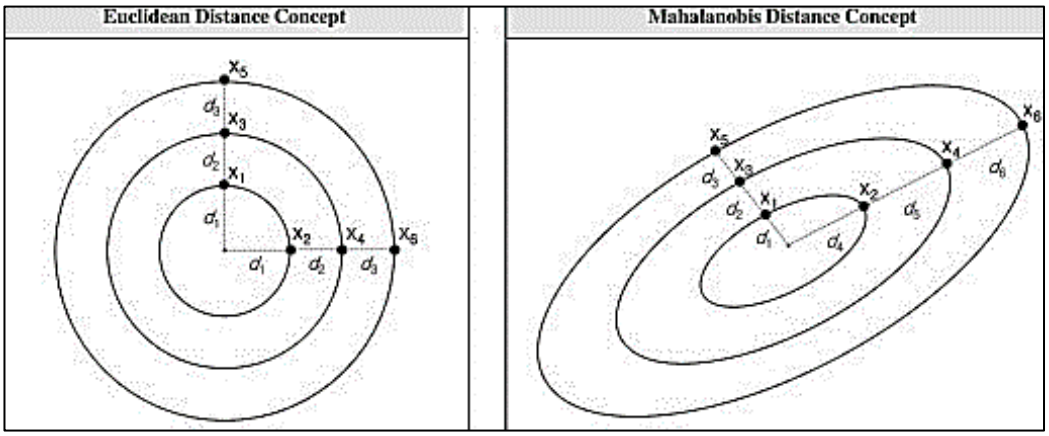


Figure 1. Comparison between MD and ED [14]

HIV and hepatitis C affect about 1.2 million individuals. They share contaminated injection equipment, which puts their health in danger [8]. More than 30 million opioid users globally in 2019, despite the significant danger of lethal overdose [9]. The government has implemented the MFlex program, which is one of the components of harm reduction in October 2005 in the country's efforts to address HIV/AIDS among injecting drug users and at the same time address the issue of opiate addiction, especially heroin in Malaysia [4]. MTS by Genichi Taguchi implements the Taguchi Methods concepts in multivariate applications that help in quantitative decision making by constructing a multivariate scale of measurements using a data-analytical process [10]. MTS is a widely used multisystem pattern recognition tool that has produced successful medical diagnosis, early warning, product identification, fault analysis, market administration, and systematic assessment [11]. The orthogonal arrays (O.A.) and the signal-to-noise ratios (SNR) are then used to determine the contribution of every parameter and to pick a good range of parameters [12]. P.C. Mahalanobis introduced MD in 1930 as an effective technique for determining the similarities between an unknown and known data analysis. The distance between the M.D. and the Euclidian distance (E.D.) has two significant changes, as shown in Figure 1 [13].

The MTS can classify normal and abnormal findings and optimize different criteria for developing a higher-performing product at the workstation [15]. It allowed the identification of abnormalities even though learning data were classified as 'unlabelled' [16]. It is used to create a continuous measurement scale and calculate the abnormality degree [17]. It can define critical and non-critical variables [18], and it measures healthy retrospective observations and unhealthy retrospective observations [19]. In contrast, MTS has a poorer statistical base relative to the classic multivariate processes [17], it can handle issues with binary classification only [20], distinguishing factors may show the covariance matrix. Multicollinearity is singular and irreversible, which is MD cannot be calculated in this way [21], it can decide imperative features, but employments the difficult threshold to choose the features [20]. It lacks a strategy for evaluating an appropriate binary classification threshold [22].

According to Mota-Gutiérrez *et al.* [23], the research of MTS is qualified into seven categories: introduction to the method, case of study/application, comparison with other methods, and construction of MS integration and development with other methods, dimensional reduction, and threshold establishment. This work has used these categories to summarize the research gap of the published work from 2011 to 2020. In the construction of MS, MTS is presented as a reference or normal group that solves the problem of class imbalance [7] includes a multidimensional framework with included knowledge to generate separate measuring scales for each class to create reference scales [24]. MTS also recognized the different fault levels [25]. MD, Taguchi OA, and the major impact plot concept are utilized [26]. The MTS models are employed when faults are found, or anticipated failures are expected. The MS is built by producing 'normal' observations [27].

Abu *et al.* [28] applied MTS to the big-end diameter of connecting rod to distinguish between two distinct ranges within the remanufacturability process spectrum. Abu and Jamaludin [29] provided a systematic analysis of the data set on the main journal diameter of the crankshaft. Abu *et al.* [30] provided a systematic pattern recognition using MTS by constructing a scatter diagram that could support decision making of a particular industry on 14 prominent journals of crankshaft belonging to 7 engine models with different numbers of samples. Abu *et al.* [31] classified crankshafts' end life into recovery operations based on the Mahalanobis-Taguchi system. Nik Mohd Kamil and Abu [32] developed a distinctive pattern of the crankshaft and identified crankshaft's critical and non-critical parameters based on the MTS, then applied the Activity Based Costing (ABC) as a method of estimation for the remanufacturing cost of the crankshaft. Abu *et al.* [33] identified the critical and

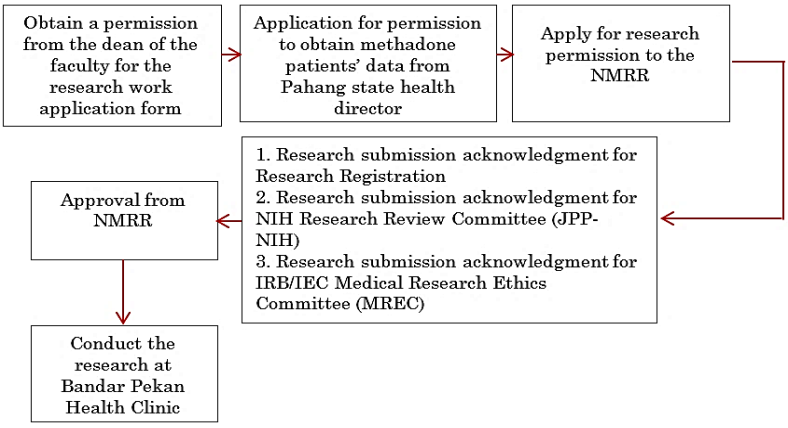


Figure 2. Sequence for research work

non-critical variables during the remanufacturing process using MTS and simultaneously estimated the cost using the ABC method. Abu *et al.* [34] evaluated the criticality of parameters on the end-of-life crankshaft based on Taguchi's orthogonal array. Then, estimate the cost using traditional cost accounting by considering the critical parameters. Azmi *et al.* [35] measured the degree of abnormality using MTS and diagnosed the parameters that influence the system. Nik Mohd Kamil *et al.* [36] proposed MTS and Time-Driven Activity-Based Costing (TDABC) in the electric and electronic industry to evaluate the significant parameters and develop the time equation and capacity cost rate. Nik Mohd Kamil *et al.* [37] identified four insignificant and 11 significant parameters in the visual mechanical inspection workstation using MTS. Safeiee and Abu [15] found that positive gain through SNR indicates the quality of the system still in good condition from February with 0.1244 until December with 0.4432 after the insignificant variable has been removed using MTS. Kamil *et al.* [38] concluded that MTS is a practical method for classification and optimization in the industry. Kamil *et al.* [39] concluded that MTS and TDABC are great tools and feasible to be implemented in the electronic industry. Saad *et al.* [40] developed an MTS-based graphical user interface to analyze and classify normal and abnormal patients under MFlex service for a better monitoring system. Ramlie *et al.* [41] concluded that none of the four thresholding methods outperformed one over the others in (if it is not for all) most of the datasets. Harudin *et al.* [42] proved that incorporating Bitwise Artificial Bee Colony (BitABC) techniques into Taguchi's T-Method methodology effectively improved prediction accuracy.

Research Methodology

To conduct a case study in the MFlex program at Bandar Pekan clinic, the procedures are shown in Figure 2.

This research focused on the MFlex program under the Ministry of Health Malaysia in blood tests. The implementation of the RT-Method and T-Method uses the software MTS provided by Teshima. The 34 parameters of blood tests are defined into four types: FBC, liver function profile, lipid profile, and renal profile used to identify the healthiness of methadone patients. The four types of the diseases are for the classification of the methadone patients whether they had one of the diseases in those four types while joining the MFlex program. Moreover, the significant parameters of the blood tests can be optimized. First, the urine test (types of drugs) of methadone patients is taken to know which drugs are the most addictive in their daily life. After that, blood tests are taken for each methadone patient to classify whether they had any disease in their body. Table 1 shows the parameters of blood tests which contain 34 parameters selection and reference range which classify as a healthy group. The parameters for FBC, liver function profile, lipid profile, and renal profile are 17, 8, 4, and 5, respectively.

RT-Method is used in the MTS for classification problems. The RT-Method describes the "Unit Space," and the distance from its center to the object data is measured as MD [43]. The RT-Method could classify items into two categories within and outside the unit space. Unit data was chosen on the basis of the largest number of samples, among other samples. The RT-Method measured the output value, but the category is clear when more than one unit space exists. The average value for each parameter is calculated as shown in Equation 1, from n number of samples in the healthy group.

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

The sensitivity β, the linear formula L, and the effective divider r, are shown in Equation 2, Equation 3, and Equation 4 respectively.

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)
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)

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

Linear equation: $L_1 = \bar{x}_1 x_{11} + \bar{x}_2 x_{12} + \cdots + \bar{x}_k x_{1k}$ (3)

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

The total variations S_T, variation of proportional term S_β, error variation S_e, and error variance V_e, are shown in Equation 5, Equation 6, Equation 7, and Equation 8 respectively.

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

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

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

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

The standard SN ratio η is then calculated as stated in the Equation 9. The greater the value of η, the stronger the relationship between the input and output.

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

The sensitivity β, and the standard SN ratio η, are then calculated in the healthy group, and the two variables Y_1 and Y_2 are calculated to generate a scatter diagram. The Equation 10 and Equation 11 show the value of Y_1 and Y_2 respectively.

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

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

The prediction of origin is referred to the calculation of average for Y_1 and Y_2 in Equation 12 and Equation 13 respectively.

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

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

Finally, MD is calculated through Equation 14.

$$\text{Mahalanobis distance: } D^2 = \frac{YA^{-1}Y^T}{k} \quad (14)$$

The methadone patients who are under monitoring were classified as an unhealthy group. The linear equation *L*', and the effective divider *r*', are calculated through Equation 15 and Equation 16, respectively. Note that the average values of samples and parameters $\bar{x}$, and the effective divider *r*', are the same values of the healthy group.

$$\text{Linear equation: } L'_1 = \bar{x}_1 x'_{11} + \bar{x}_2 x'_{12} + \cdots + \bar{x}_k x'_{1k} \quad (15)$$

$$\text{Effective divider: } r' = \bar{x}_1^2 + \bar{x}_2^2 + \cdots + \bar{x}_k^2 \quad (16)$$

Next, the value sensitivity β, for each signal data can be calculated as stated in the Equation 17.

$$\beta_1 = \frac{L'_1}{r'} \quad (17)$$

After that, the total variations S_T, variation of proportional term S_β, error variation S_e, and error variance V_e, are calculated through Equation 18, Equation 19, Equation 20, and Equation 21 respectively.

$$\text{Total variation: } S_{T1} = x'^2_{11} + x'^2_{12} + \cdots + x'^2_{1k} \quad (18)$$

$$\text{Variation of proportional term: } S_{\beta 1} = \frac{L'^2_1}{r} \quad (19)$$

$$\text{Error variation: } S_{e1} = S_{T1} - S_{\beta 1} \quad (20)$$

$$\text{Error variance: } V_{e1} = \frac{S_{e1}}{k-1} \quad (21)$$

Eventually, the standard SN ratio η is calculated using Equation 22. The input and output relationship will stronger when the value of SN ratio η is greater.

$$\text{SN ratio: } \eta_1 = \frac{1}{V_{e1}} \quad (22)$$

The value of sensitivity β, and the standard SN ratio η, from the unhealthy group, are used to calculate variables Y_1 and Y_2. The value of sensitivity β is used for Y_1 as stated in Equation 10. Meanwhile, the variable Y_2 is converted first, as stated in the Equation 11, to evaluate any scattering from the normal conditions. The average values for Y_1 and Y_2 are the same as in the Equation 12 and Equation 13, respectively, for predicting healthy group origin. Lastly, the MD value can be found based on the Equation 14.

The T-Method is utilized as an evaluation of the parameters towards the output. The highest sample will be defined as a healthy group, while the remaining samples will be defined as an unhealthy group. The average values for every parameter and the average output value from the number of samples in the healthy group are found as shown in Equation 23 and Equation 24, respectively.

$$\bar{x}_j = \frac{1}{n}\left(x_{1j} + x_{2j} + \cdots + x_{nj}\right) \quad (23)$$

$$\bar{y} = m_0 = \frac{1}{n}(y_1 + y_2 + \cdots + y_n) \quad (24)$$

The balance samples that belong to the healthy group are defined as unhealthy groups. After that, the unhealthy group was normalized using the average value of every parameter and output that belongs to the healthy group. Normalization aims to make the data more flexible by removing their redundancy. The calculation of normalized data for input and output is shown in Equation 25 and Equation 26, respectively.

$$X_{ij} = \acute{x}_{ij} - \bar{x}_j \quad (25)$$

$$M_i = \acute{y}_i - m_0 \quad (26)$$

Proportional coefficient β and SN ratio η for each parameter are calculated as shown in Equation 27, Equation 28, Equation 29, Equation 30, Equation 31, Equation 32, and Equation 33. Then, Table 2 shows the results.

$$\text{Effective divider: } r = M_1^2 + M_2^2 + \cdots + M_l^2 \quad (27)$$

$$\text{Total variation: } S_{T1} = X_{11}^2 + X_{21}^2 + \cdots X_{l1}^2 \quad (28)$$

Variation of proportional term:

$$S_{\beta 1} = \frac{(M_1X_{11} + M_2X_{21} + \cdots + M_lX_{l1})^2}{r} \quad (29)$$

$$\text{Error variation: } S_{e1} = S_{T1} - S_{\beta 1} \quad (30)$$

$$\text{Error variance: } V_{e1} = \frac{S_{e1}}{l-1} \quad (31)$$

Proportional coefficient:

$$\beta_1 = \frac{M_1X_{11} + M_2X_{21} + \cdots + M_lX_{l1}}{r} \quad (32)$$

SN ratio:

$$\eta_1 = \begin{cases} \frac{\frac{1}{r}(S_{\beta 1} - V_{el})}{V_{el}} & (when\ S_{\beta 1} > V_{el}) \\ 0 \end{cases} \quad (33)$$

A positive value of β means that the steepness is ascending to the right, while a negative value of β means that the steepness is descending to the right. The value of η should be in a positive value, but if it turns out to be in a negative value, it will be considered zero, which means there is no longer a significant relationship between input and output.

Table 2. Proportional coefficient β and SN ratio η

β, η	Parameters			
	1	2	…	k
β	β_1	β_1	…	β_1
η	η_1	η_1	…	η_1

Table 3. Actual values and estimated values of unhealthy group

Data No.	Actual value, M	Estimated value, $\widehat{M}$
1	M_1	$\widehat{M}_1$
2	M_2	$\widehat{M}_2$
...	...	...
l	M_l	$\widehat{M}_l$

An unhealthy group's integrated estimate value is computed using the proportional coefficient β and SN ratio η for each parameter. The calculation of the integrated estimate value is shown in Equation 34. Note that, $x_{j1}, x_{j2}, \ldots, x_{j6}$ are the normalized value of each parameter.

Integrated estimate value

$$\widehat{M}_i = \frac{\eta_1 \times \frac{X_{i1}}{\beta_1} + \eta_2 \times \frac{X_{i2}}{\beta_2} + \ldots + \eta_k \times \frac{X_{i6}}{\beta_6}}{\eta_1 + \eta_2 + \cdots + \eta_6} \quad (34)$$

Table 3 shows the actual values and the integrated estimated values of the unhealthy group.

The step by step for calculating estimated SN ratio η are using the following Equation 35, Equation 36, Equation 37, Equation 38, Equation 39, Equation 40, and Equation 41. In fact, the estimated SN ratio η is based on the suitability of OA.

Linear equation: $L = M_1\widehat{M}_1 + M_2\widehat{M}_2 + \cdots + M_l\widehat{M}_l$ (35)

Effective divider: $r = M_1^2 + M_2^2 + \cdots + M_l^2$ (36)

Total variation: $S_T = \widehat{M}_1^2 + \widehat{M}_2^2 + \cdots + \widehat{M}_l^2$ (37)

Variation of propotional term: $S_\beta = \frac{L^2}{r}$ (38)

Error variation: $S_e = S_T - S_\beta$ (39)

Error variance: $V_e = \frac{S_e}{l-1}$ (40)

Estimated SN ratio: $\eta = 10 \log \left[\frac{\frac{1}{r}(S_\beta - V_e)}{V_e} \right]$ (41)

The relative importance of a parameter is determined by how much the estimated SN ratio deteriorates when the parameter is not used. Two-level OA levels 1 and 2 are used for an evaluation. The use of OA enables measurements to be made of the estimated SN ratio under various conditions. The two-level of OA means that level 1 is the parameter that will be used and level 2 is the parameter that will not be used. Concerning the estimated SN ratio, the difference values between level 1 and level 2 for each parameter determine the relative importance of the parameters. When the parameter is used with larger SN ratios, and when the parameter is not used with smaller SN ratios, the degree of contribution turns to be positive. Otherwise, when the parameter is used with lower SN ratios and when the parameter is not used with higher SN ratios, the degree of contribution turns to be negative.

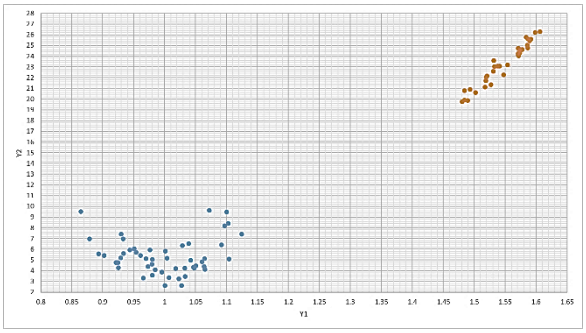


Figure 3. Scatter diagram of renal profile between the healthy and unhealthy group

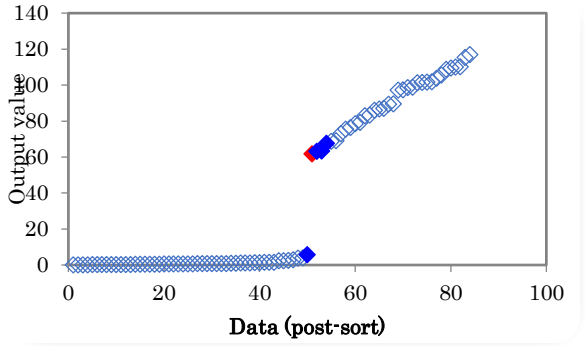
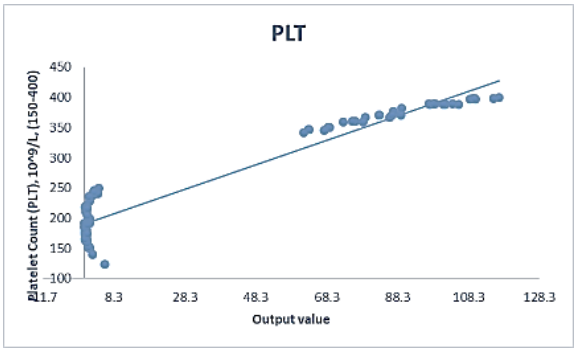


Figure 4. Data (post-sort) for renal profile in blood tests

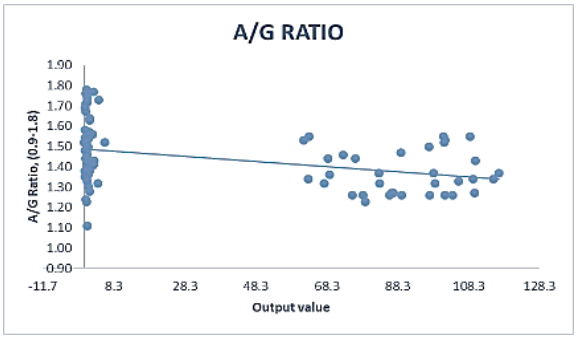
Results and Discussions

The scatter diagrams of the blood tests between healthy and unhealthy groups are created. All the unhealthy groups are computed sample by sample through two variables of Y1 and Y2. The y-axis represents Y2, and the x-axis represents Y1. The blue dot on the graph represents the healthy group with 50 samples, while the orange represents the unhealthy group. These graphs consist of 34 parameters, and the number of samples for the renal profile is 34. Figure 3 shows a scatter diagram of the renal profile between healthy and unhealthy samples. Both samples are scattered but still in their classification group and do not overlap. The minimum and maximum values of MD for unhealthy samples are not overlapped with the minimum and maximum values of MD for healthy samples. The minimum and maximum values of MD for unhealthy samples are 61.7634 and 116.9001, respectively.

Meanwhile, healthy samples' minimum and maximum MD are 0.0111 and 5.6593, respectively. The average MD for unhealthy is 89.9737, and the average MD for healthy is 1.0000. The correlation coefficient r for unhealthy samples (orange dotted) is 0.9729. The correlation is a strong positive correlation, which means that when Y1 variables are high, Y2 variables are also high and vice versa. The healthy samples (blue dotted) correlation coefficient is 0.0585, nearer to zero value. It means the relationship for healthy samples is weak for positive correlation.



(viii)



(xx)

Figure 5. Scatter of normalized output and parameter values of renal profile

In the renal profile of blood tests, healthy and unhealthy samples are 5 and 79, respectively, with 34 parameters. The data is organized in the ascending order of output value, as shown in Figure 4. For example, sample number 11 turns out to be the smallest with 0.011, while sample number 57 turns out to be the largest with 116.900. That means sample numbers 21, 80, 78, 81, and 79 are the center point in blue and red dotted.

The relationship between parameters and their output values is shown in Figure 5. The x-axis represents the normalized output values, and the y-axis represents the values of the normalized parameters. Parameter by parameter computation of the proportional coefficient β and SN ratio η were carried out to determine which of the parameters would be useful for evaluation. The T-Method calculates SN ratios η and proportional coefficients β based on the relationship between the normalized output value and the normalized parameter value.

According to Teshima *et al.* [43], the greater the SN ratios η produces a stronger relationship; in other words, the distribution is closer to a blue line. For example, since Figure 5 (viii), which represents the parameter of platelet count, has a 0.0069 SN ratio η, so the distribution is approaching the blue line, whereas Figure 5 (xx), which represents the parameter of A/G ratio, has 0.00005 SN ratio η, so the distribution is far away from a blue line. This proves

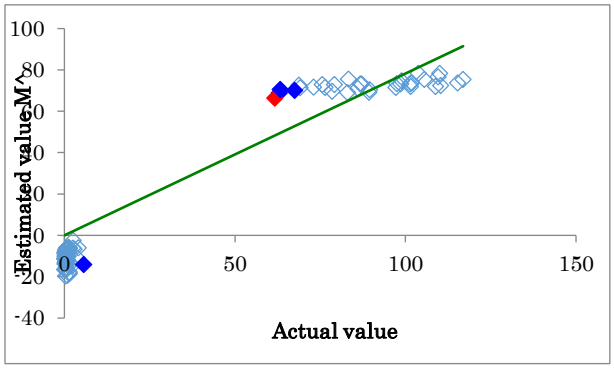


Figure 6. Distribution of actual and estimated signal data values of renal profile

that the greater value of the SN ratio, the closer the distribution to a blue line in a graph.

Furthermore, Teshima *et al.* [43] also stated that ascending the line from left to right indicates the parameter has a positive value of proportional coefficients β. In contrast, the descending line indicates the parameter has a negative value of proportional coefficients β. This has been proven through Figure 5 (xx), which represents the parameter of A/G ratio has -0.0011 of proportional coefficient β, whereas the remaining 33 parameters have a positive value of proportional coefficient β. As a result, those parameters are well suited to calculating integrated estimate value. This study would derive the value of integrated estimate value by using those proportional coefficient β and SN ratios η values. Therefore, the higher the SN ratios η, the greater the degree to which it contributes to the integrated estimates of MD value closer to the actual normalized MD value. Since none of those parameters has a negative SN ratio η value, all those parameters are subsequently considered in an integrated estimate value.

Figure 6 shows a scatter diagram reflecting what happens when actual values are expressed in x-axis terms and the estimated y-axis. If estimated values line up above a straight line, it indicates that a good estimation has been made. Furthermore, the graph will offer additional information regarding an approximately straight line and its attributes. The model contributes to 0.9141 of R2 or -25.11 dB of SN ratios η in general estimation. It means the correlation is high, and the distribution is closer to the green line. The equation of the line is shown in Equation 42.

Nevertheless, some of those parameters are useful for integrated estimation, while others are not. Hence, parameters assessment is performed by utilizing L64 of OA, with level 1 indicating the parameter will be utilized and level 2 indicating the parameter will not be utilized. For example, the value -25.11 dB of integrated estimate SN ratio η refers to the first run

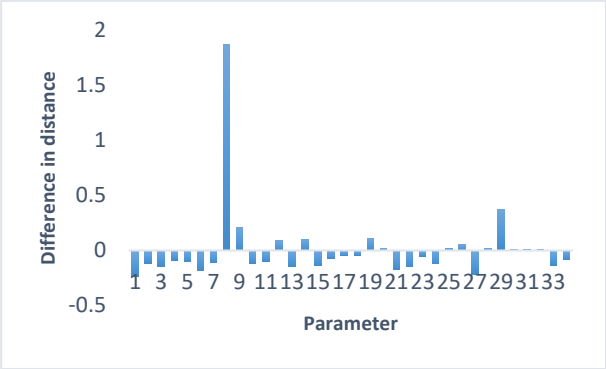


Figure 7. Degree of contribution of renal profile

in L64. Subsequently, the degree of contribution is translated into a bar graph, as shown in Figure 7. From that, it shows how the parameters are significant to the output. For example, when the parameter 8, which represents platelet count (PLT), has been used (level 1) with a greater relationship (SN ratio = -24.37 dB) to the output and when the parameter has not been used (level 2) with a smaller relationship (SN ratio = -26.23 dB) to the output, the parameter would obtain a higher degree of contribution (1.87 dB) which is a positive contribution to the output. On the other hand, the parameter 1, which represents white blood cell (WBC), will have a lower degree of contribution (-0.24 dB), which is a negative contribution to the output. This will happen when the parameter is used (level 1) with a smaller SN ratio, and when the parameter is not used (level 2) with a greater SN ratio.

A positive degree of contribution means that the use of parameter produces the effect of elevating the output of MD, whereas a negative degree of contribution means that the use of parameter produces the effect of lowering the output of MD. Consequently, parameter 8, 9, 12, 14, 19, 20, 25, 26, 28, 29, 30, 31, and 32 are positive degree of contribution whereas parameter 1, 2, 3, 4, 5, 6, 7, 10, 11, 13, 15, 16, 17, 18, 21, 22, 23, 24, 27, 33, and 34 are negative degree of contribution. This research suggests that a positive contribution should be increased while a negative contribution should be maintained for obtaining lower MD.

The purpose of diagnosis unknown data is to measure the MD and evaluate their parameters for each sample. Then, the normalization is performed by subtracting from the average value of the parameters in the healthy group. The estimated value $\widehat{M}$ or MD for unknown data are calculated through Equation 34 and, subsequently, can be seen in Table 4.

Figure 8 shows a scatter diagram of the estimated values after being subjected to the ecosystem, which has been developed during the optimization of the

Table 4. The estimated value $\widehat{M}$ (MD) for unknown data in renal profile

No. of sample	Estimated value $\widehat{M}$(MD)
1	-16.7571
2	-10.7579
3	-5.4491
4	-6.0635
5	-9.6910
6	61.0744
7	70.8809
8	77.9789
9	78.2274
10	71.4827
11	30.7505
12	32.8419
13	38.7317
14	37.4557
15	35.5176

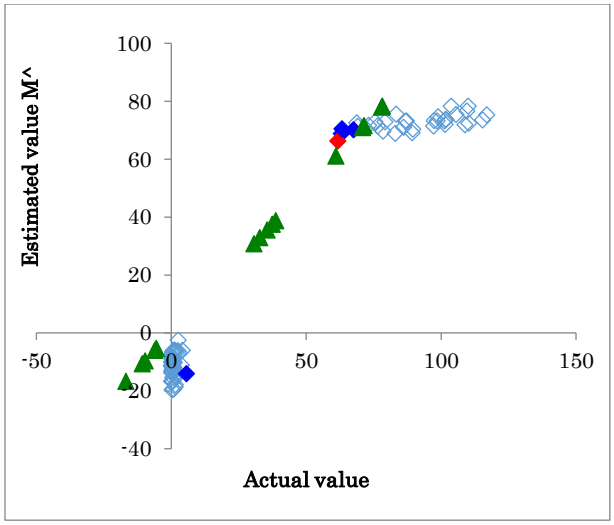


Figure 8. Interpretation of unknown data in renal profile

renal profile of blood tests. The x-axis represents the actual values of the output, M, and the y-axis represents the estimated values of the output, $\widehat{M}$. Since the actual values are unknown, the positions of unknown data on the x-axis use the same estimated values. The position of 15 samples of unknown data is marked as a green triangle in Figure 10. It can be concluded that five unknown samples closely belong to the healthy group, five unknown samples belong to the unhealthy group, and another five unknown samples belong to the outlier.

Figure 9 shows the degree of contribution in the first sample of unknown data in the renal profile. Consequently, parameter 1, 2, 3, 8, 11, 12, 13, 16, 19, 20, 25, 29, 32, and 34 are positive degree of contribution whereas parameter 4, 5, 6, 7, 9, 10, 14, 15, 17, 18, 21, 22, 23, 24, 26, 27, 28, 30, 31, and 33 are negative degree of contribution. This research suggests that to obtain lower MD, a positive degree of contribution should be increased while a negative degree of contribution should be maintained.

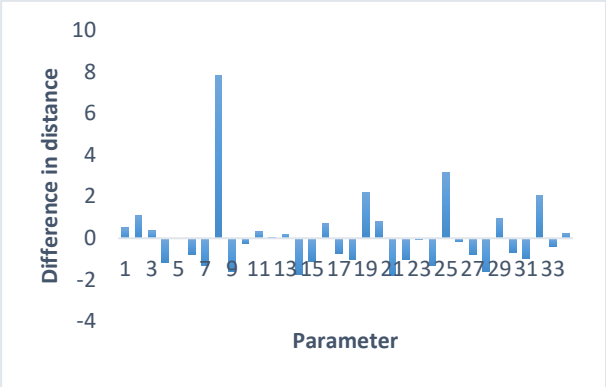


Figure 9. Degree of contribution in first sample of unknown data in renal profile

Table 5. Comparison between original and types of modification

Original	MD	Modification	MD
1	-16.76	Type 1	-17.92
		Type 2	-15.55
		Type 3	-148.88
		Type 4	-120.37
		Type 5	1.51
		Type 6	-36.18

There are two types of degrees of contribution. First is the positive degree of contribution, indicating that using this parameter produces the effect of elevating the output. Therefore, by increasing the value of this parameter, the MD value will be increased as well. Second is, the negative degree of contribution indicates that using this parameter produces the effect of lowering the output. It means that by decreasing the value of this parameter, the MD value will be decreased as well. The purpose of this section is to prove that the purpose solution to the Bandar Pekan clinic, which is lowering the degree of contribution, is the best. Thus, this research has selected blood tests (renal profile) sample 1 as a subject, as shown in Figure 9. The original output for sample 1 renal profile is -16.76, as shown in Table 5. The value is compared with six types of modification.

The MD value for type 1 modification is -17.92, s maller than the original sample. This modification means the higher positive degree of contribution is added with two points (parameter 2, 8, 19, 25, 29, and 32) while the lower positive degree of contribution is added with one point (parameter 1, 3, 11, 12, 13, 16, 20, and 34). On the other hand, the higher negative degree of contribution is subtracted with two points (parameter 4, 6, 7, 9, 14, 15, 18, 21, 22, 24, 28, and 31), while the lower negative degree of contribution is subtracted with one point (parameter 5, 10, 17, 23, 26, 27, 30, and 33). Consequently, this modification as a proposed solution has been rejected.

The MD value for type 2 modification is -15.55, which is higher than the original sample. This modification means the higher positive degree of contribution is subtracted with two points (parameter 2, 8, 19, 25, 29, and 32) while the lower positive degree of contribution is subtracted with one point (parameter 1, 3, 11, 12, 13, 16, 20, and 34). On the other hand, the higher negative degree of contribution is added with two points (parameter 4, 6, 7, 9, 14, 15, 18, 21, 22, 24, 28, and 31), while the lower negative degree of contribution is added with one point (parameter 5, 10, 17, 23, 26, 27, 30, and 33). Consequently, this modification as a proposed solution has been rejected.

The MD value for type 3 modification is -148.88, which is smaller than the original sample. This modification means the higher positive degree of contribution is added with two points (parameter 2, 8, 19, 25, 29, and 32) while the lower positive degree of contribution is added with one point (parameter 1, 3, 11, 12, 13, 16, 20, and 34). On the other hand, the higher and lower negative degree of contribution is set as 0. Consequently, this modification as the proposed solution has been rejected.

The MD value for type 4 modification is -120.37, which is smaller than the original sample. This modification means the higher and lower positive degree of contribution is set as 0. On the other hand, the higher negative degree of contribution is subtracted with two points (parameter 4, 6, 7, 9, 14, 15, 18, 21, 22, 24, 28, and 31), while the lower negative degree of contribution is subtracted with one point (parameter 5, 10, 17, 23, 26, 27, 30, and 33). Consequently, this modification as a proposed solution has been rejected.
The MD value for type 5 modification is 1.51, which is higher than the original sample. This modification means the higher positive degree of contribution is added with two points (parameter 2, 8, 19, 25, 29, and 32) while the lower positive degree of contribution is added with one point (parameter 1, 3, 11, 12, 13, 16, 20, and 34). On the other hand, the higher and lower negative degree of contribution is maintained their value. Consequently, this modification as the proposed solution has been accepted.

The MD value for type 6 modification is -36.18, which is smaller than the original sample. This modification means the higher and lower positive degree of contribution is maintained their value. On the other hand, the higher negative degree of contribution is subtracted with two points (parameter 4, 6, 7, 9, 14, 15, 18, 21, 22, 24, 28, and 31), while the lower negative degree of contribution is subtracted with one point (parameter 5, 10, 17, 23, 26, 27, 30, and 33). Consequently, this modification as a proposed solution has been rejected.

Therefore, the best solution to the Bandar Pekan clinic is modification type 5 because it shows the highest

MD value than others. However, the proposed solution also might be influenced by the total number of positive and negative degrees of contribution and the total number of the higher and lower degree of contribution. Also, the proposed solution might be different from the real practice. The interview session with the pharmacist at Bandar Pekan clinic is done to ask her opinions about the classification and optimization using MTS in MFlex program. The question was asked as follow:

Question: What is your opinion on improving/ renewing the existing system in the MFlex program in Malaysia?

Answer: This MT system is more about categorizing cases. Furthermore, patient data will be available on the computer. So, we can trace directly from the existing system. Using the methods in this MT system is very useful because we need to track data through files only before this. It is a bit cumbersome and harassing when some data is already missing. In addition, in terms of compilation, patient data from other facilities moved to KKBP should have been sent but not available. So, many given medication errors with unnoticed. Therefore, this MT system is beneficial for renewing the existing pharmacy system. It will also help to know the dosage history of the patient and from which facility he/she was previously.

Conclusion

From this research, MTS can classify between the healthy and unhealthy data. Besides, it can identify the significant parameters for the renal profile in the blood tests. In other words, it is proved that MTS is able to analyse the significant factors in the blood tests of the MFlex program. The RT-Method can classify between healthy and unhealthy samples for the blood tests in renal profile because the average MD are not identical and do not overlap with each other as the average MD for healthy is 1.00 and for unhealthy is 89.97. The T-Method is able to evaluate the significant parameters in terms of the degree of contribution for the blood tests where the total positive degree of contribution has 13 while the total negative degree of contribution has 21. Fifteen unknown samples in blood tests of MFlex program have been diagnosed using MTS. They all have different numbers of the positive and negative degree of contribution to achieving lower MD. There are six types of modification to prove the proposed solution, and type 5 modification has been selected as the best solution. A pharmacist from Bandar Pekan clinic has confirmed that MTS is able to solve a problem in classification and optimization in the MFlex program. This research contributes towards the applicability of RT-Method and T-Method of MTS in the health monitoring systems. The methods might be interesting if there are applied for classifying the severe patients of Coronavirus (Covid-19) that hit Malaysia nowadays, the death in a month, and the infection stage.

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