Application of Extension Theory to Analyze Blood Examination Data for Disease Diagnosis

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ABSTRACT

In this study, it reveals that applying the Extension Theory to analyze blood examination data could be an effective way to inspect diseases or even potential ones concealing in the patient's body; besides, this method allows doctors to overcome human negligence or some deficiencies existing in current blood diagnosis methods. With the application of Extension Theory, it discovers that based on the blood examination data transformed in the matter-element model and the calculated correlation function from the comparison between input traits and faulty types, a more precise and accurate diagnosis of pathological threats in patients' bodies could be expected. And according to 600 sets of experimental evidences this study has tested, it could be proved that applying the Extension Theory to analyze blood examination data fulfills high accuracy in diagnosis and which would benefit disease precautions.

Keywords:blood examination, matter-element model, Extension Theory (ET), disease diagnosis

I.INTRODUCTION

Generally, many diseases are potentially risky and sometimes it is truly difficult to realize them until which have caused serious harm to the patients' body. Body examination is one of the important ways to achieve disease precaution because it can effectively monitor and ensure a patient's health condition before diseases do occur. According to some studies, with the blood examination, most of potential disease threats then could be detected and diagnosed. For instance, when the number of red blood cell (RBC) is lower then the normal range requires, Anemia or Anemia with Iron deficiency may occur. Also, an unusual blood platelet count can lead to Leukemia. In most cases, the chronic diseases can be diagnosed through the analysis of blood examination data, in combination with a review on the patient's medical history; hence, the doctor then could provide appropriate treatment to patients based on medical data and expertise.

Normally, analyzing blood examination data is the most effective way to understand a patient's body condition. However, when applying the current methods to analyze blood examination data, some deficiencies in terms of being unable to identify all types of diseases and unable to define disease threats when the data value falling coincidentally on the normal boundary may also affect the accuracy of diagnosis. At present, to resolve this problem, the method of Artificial Intelligence (AI) has been applied to help ascertain the medical uncertainties, overcome faulty diagnosis and increase the rate of accuracy. However, there are several defects that AI method contains: a large amount of data and objective views from examiners are necessary; and for some rare cases, numerical analysis and expertise are extra required for diagnosis. Also, when applying the AI method, the correlation between input and output data is unknown; therefore, diagnosis for multiple faults would be limited and become less effective.

To overcome the drawbacks of current diagnosis methods stated above, in this study, it then suggests the application of the Extension Theory (ET) to improve the present situation. The ET was first introduced in 1983 by a China scholar W. Cai. The ET is adopted as a universal method to resolve contradictory problems which are both subjective and objective in nature. When applying the Extension Theory, the matter-element model of it is functional to reorganize the research data and to integrate both qualitative and quantitative information for data mining and analyzing [1]. As a result, researchers could have a more accurate and thorough view of all the on-hand information; in addition, degrees of how qualitative and quantitative data affect on the research questions then could be defined respectively [2-3]. Based on those advantages, the Extension Theory is then applied to analyze blood examination data in this study. It starts with transforming abnormal blood numerical data in the matter-element model; and next, the extension correlation function is used to calculate the correlation function between blood examination data and the normal blood values; after that, normalized correlation functions is applied to detect whether any abnormal blood data exist. And in order to justify the reliability and validity of the novel method this

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study has referred, 600 sets of experimental data and evidences this study has tested could assure.

II.THE EXTENSION THEORY

The Extension Theory suggests that contradict problems could be solved by applying formalized methods in conjunction with analyzing problems from both quantitative and qualitative aspects. The Extension Theory is composed of the matter-element model and the Extension Set Theory [4]. And in the following, it states and explains partial elements of the Extension Theory that this study has adopted:

Table1. Three different sorts of mathematical sets

Compared item	Cantor set	Fuzzy set	Extension set
objects	Data variables	Linguistic variables	Contradictory problems
Model	Mathematics model	Fuzzy mathematics model	Matter-element model
Descriptive function	Transfer function	Membership function	Correlation function
Descriptive property	Precision	Ambiguity	Extension
Range of set	$C_n(x)\in(0,1)$	$\mu_n(x)\in[0,1]$	$K_n(x)\in[-\infty,\infty]$

Table1 shows three different sorts of mathematical sets [5]. The canter set which can be used to solve a two-value problem and the range of cantor set is {0,1}. The fuzzy set can describe a concept which is related to the inexplicit boundary. The range of fuzzy set is [0, 1] [6]. The extension set is extending fuzzy set, and the range of extension set is [-∞,∞] [7-8]. For this reason, ET can try to solve the incompatibility or contradict problems by the transformation made from the matter-element model.

1 Definition of matter-element

Matter-element model

Defining the name of the matter-element R by N, its characteristic c with value v, and a matter-element R in ET then could be described as follow [9-10]:

$$R=(N,c,v) \tag{2.1}$$

Multi-dimensional matter-element:

Assuming R=(N,c,v) is the matter-element model, C=[c1,c2,…cn] is characteristic vector and V=[v1,v2,…,vn] is value vector; then, a multidimensional matter-element is defined as:

$$R=\begin{bmatrix} N, & c_1, & v_1 \\ & c_2, & v_2 \\ & \cdots & \cdots \\ & c_n, & v_n \end{bmatrix} \tag{2.2}$$

2. Extension Set Theory:

Definition of extension set:

Let U as a space of objects and u as a generic element of U. The u belongs U or $u\in U$, then an extension set A in U is defined as a set of ordered pairs:

$$\tilde{A}=\{(u,y)\,|\,u\in U, y=k(u)\in(-\infty,\infty)\} \tag{2.3}$$

y=K(u) is the relational function for extension set $\tilde{A}$. Every element in U is the K(u) membership, and U is the neighborhood domain. K(u)>0 is the positive domain of $\tilde{A}$, and K(u)<0 is the negative domain of $\tilde{A}$. And K(u)=0 is called zero boundary.(2) Definition of extended distance (∞, -∞) Setting x as a point between (∞, -∞), and Xo=<a,b> is a closed interval, the relation function between x and Xo is defined as follow [11]:

$$\rho(x,X_o)=\left|x-\frac{a+b}{2}\right|-\frac{b-a}{2} \tag{2.4}$$

Value of position:

Setting Xo=<a,b>, X=<c,d> and Xo∈X, the relation function among x, X and Xo is defined as follow:

$$D(x,X_o,X)=\begin{cases}\rho(x,X)-\rho(x,X_o) & x\notin X_o\\ -1 & x\in X_o\end{cases} \tag{2.5}$$

Extended correlation function:

Setting Xo=<a,b>,X=<c,d>, Xo∈X , the extended function can be defined as follow:

$$K(x)=\frac{\rho(x,X_o)}{D(x,X_o,X)} \tag{2.6}$$

The correlation function can be used to calculate the correlation degree between x and X. When K(x)>0, it indicates that x belongs to X; and when K(x)< 0, it describes that x does not belong to X.

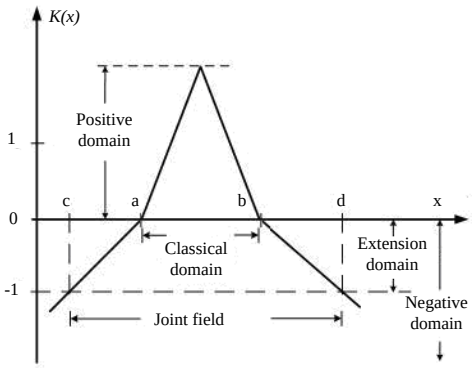

Fig. 1 The graphic relationship of extension

Fig.1 shows the relationship of extension. When K(x) is bigger than zero, the element belongs to the classical domain. When the correlation function is -1<K(x)<0, it is called extension domain. It means the element x may have a chance to become part of the set.

III. APPLY THE EXTENSION THEORY TO ANALYZE BLOOD EXAMINATION DATA

In this section, it explains how the ET is applied to analyze blood examination data for disease

diagnosis. The numerical data from blood examination needs to be compared with the maximum and minimum standard value sets respectively to calculate the ratio for detecting the abnormal blood value. And if the ratio from the maximum one is larger than 1 and the ratio form the minimum one is lower than 1, it then could define that the blood data value is maintained in the normal range. Table2 shows the criteria for diagnosis, and in Table3, it displays different types of diseases that might occur due to different abnormal blood conditions. In Table3, it could be realized that Type1 is normal. Type2 is determined as white blood cell deficiency because the number of white blood cell (WBC) is lower then the normal range. And Type3 is determined as Leukemia because the WBC is over then the normal range.

Table2. The type of avenue

No.	Avenue	examination value upperlimit value	examination value lowerlimit value
1	Normal	>1	<1
2	Less then	<1	<1
3	More then	>1	>1

Table3. The type of diseases

type	Anomalism of type	Name of disease
1	Normal	Normal
2	Less WBC	White blood cell deficiency
3	More WBC	Leukemia
4	Less RBC	Anemia
5	More RBC	Polycyphemia
6	More Hgb	Polycyphemia
7	Less Ht	Anemia
8	Less Plate	Hemophilia
9	More Plate	Hrombocyposis
10	Less MCV	Microcypic
11	Less MCH	Iorn beficiency anemia

1 Organize anomalistic blood data in the matter-element model

As applying the Extension Theory to do disease diagnosis, the first step is building anomalistic blood data in the matter-element model. In this study, the anomalistic data would be divided into three types (the normal type is included as well) as shown in Table4.

In Table4, I={I1,I2,I3,…,I4} is the fault set, the i in Ii represents different anomalistic set and C={c1,c2,…,c8} is the characteristic set. For example: I1 is Type1 in Table3. The Table5 demonstrates the types of characteristics in blood and could be referred to Table4.

Table4. The matter-element model

Fault NO.	1	2	3
matter-element	$R_1=\begin{Bmatrix} I_1 & C_1 & \langle 4,10\rangle \\ & C_2 & \langle 4.15,5.93\rangle \\ & C_3 & \langle 13.2,17.7\rangle \\ & C_4 & \langle 38.8,50.9\rangle \\ & C_5 & \langle 154,432\rangle \\ & C_6 & \langle 81.8,97.7\rangle \\ & C_7 & \langle 28.1,33.8\rangle \\ & C_8 & \langle 33,36\rangle \end{Bmatrix}$	$R_2=\begin{Bmatrix} I_2 & C_1 & \langle 3.2,3.9\rangle \\ & C_2 & \langle 4.2,5.2\rangle \\ & C_3 & \langle 12.4,16.1\rangle \\ & C_4 & \langle 36.2,46.1\rangle \\ & C_5 & \langle 178,320\rangle \\ & C_6 & \langle 82.1,91.4\rangle \\ & C_7 & \langle 27.5,31.6\rangle \\ & C_8 & \langle 33.5,35\rangle \end{Bmatrix}$	$R_3=\begin{Bmatrix} I_3 & C_1 & \langle 10.1,18.2\rangle \\ & C_2 & \langle 4.15,5.65\rangle \\ & C_3 & \langle 13.1,17.5\rangle \\ & C_4 & \langle 38,49.9\rangle \\ & C_5 & \langle 188,433\rangle \\ & C_6 & \langle 82.4,98\rangle \\ & C_7 & \langle 27.1,33.7\rangle \\ & C_8 & \langle 32.9,36\rangle \end{Bmatrix}$
Fault NO.	4	5	6
matter-element	$R_4=\begin{Bmatrix} I_4 & C_1 & \langle 4.3,8.6\rangle \\ & C_2 & \langle 3.89,3.99\rangle \\ & C_3 & \langle 12.4,13.3\rangle \\ & C_4 & \langle 36.1,37.8\rangle \\ & C_5 & \langle 206,368\rangle \\ & C_6 & \langle 91,95.4\rangle \\ & C_7 & \langle 31,33.7\rangle \\ & C_8 & \langle 33.8,35.8\rangle \end{Bmatrix}$	$R_5=\begin{Bmatrix} I_5 & C_1 & \langle 4.3,9.7\rangle \\ & C_2 & \langle 6.02,6.73\rangle \\ & C_3 & \langle 13.1,15.6\rangle \\ & C_4 & \langle 40.3,47.6\rangle \\ & C_5 & \langle 195,3424\rangle \\ & C_6 & \langle 64.6,74.7\rangle \\ & C_7 & \langle 21.3,24.5\rangle \\ & C_8 & \langle 32,33.2\rangle \end{Bmatrix}$	$R_6=\begin{Bmatrix} I_6 & C_1 & \langle 5.8,7.5\rangle \\ & C_2 & \langle 4,5.88\rangle \\ & C_3 & \langle 17,19\rangle \\ & C_4 & \langle 35,54\rangle \\ & C_5 & \langle 256,357\rangle \\ & C_6 & \langle 80,91\rangle \\ & C_7 & \langle 90,233\rangle \\ & C_8 & \langle 32,37\rangle \end{Bmatrix}$
Fault NO.	7	8	9
matter-element	$R_7=\begin{Bmatrix} I_7 & C_1 & \langle 4.2,6.3\rangle \\ & C_2 & \langle 4.13,4.32\rangle \\ & C_3 & \langle 12.1,12.6\rangle \\ & C_4 & \langle 33.9,35.9\rangle \\ & C_5 & \langle 237,377\rangle \\ & C_6 & \langle 81.2,85.2\rangle \\ & C_7 & \langle 29,29.9\rangle \\ & C_8 & \langle 34.4,35.7\rangle \end{Bmatrix}$	$R_8=\begin{Bmatrix} I_8 & C_1 & \langle 4.7,9.4\rangle \\ & C_2 & \langle 4.24,5.69\rangle \\ & C_3 & \langle 13,117\rangle \\ & C_4 & \langle 38,48.5\rangle \\ & C_5 & \langle 90,150\rangle \\ & C_6 & \langle 84.7,93.7\rangle \\ & C_7 & \langle 29.8,32\rangle \\ & C_8 & \langle 33.5,35.2\rangle \end{Bmatrix}$	$R_9=\begin{Bmatrix} I_9 & C_1 & \langle 6.2,9.9\rangle \\ & C_2 & \langle 4.4,5.28\rangle \\ & C_3 & \langle 13.5,15.8\rangle \\ & C_4 & \langle 38,45.8\rangle \\ & C_5 & \langle 452,521\rangle \\ & C_6 & \langle 84.5,90\rangle \\ & C_7 & \langle 29.4,31.7\rangle \\ & C_8 & \langle 33.6,35.6\rangle \end{Bmatrix}$
Fault NO.	10	11	12
matter-element	$R_{10}=\begin{Bmatrix} I_{10} & C_1 & \langle 4,7.7\rangle \\ & C_2 & \langle 5.16,5.93\rangle \\ & C_3 & \langle 12.3,15.4\rangle \\ & C_4 & \langle 37.9,54.1\rangle \\ & C_5 & \langle 221,377\rangle \\ & C_6 & \langle 65.7,79.7\rangle \\ & C_7 & \langle 21.1,27.9\rangle \\ & C_8 & \langle 32.1,35.2\rangle \end{Bmatrix}$	$R_{11}=\begin{Bmatrix} I_{11} & C_1 & \langle 5,9.8\rangle \\ & C_2 & \langle 6.65,7.11\rangle \\ & C_3 & \langle 12.3,12.5\rangle \\ & C_4 & \langle 38.2,42.5\rangle \\ & C_5 & \langle 200,402\rangle \\ & C_6 & \langle 55.7,81.6\rangle \\ & C_7 & \langle 17.3,21\rangle \\ & C_8 & \langle 31.1,32.9\rangle \end{Bmatrix}$	$R_{12}=\begin{Bmatrix} I_{12} & C_1 & \langle 4.5,8.3\rangle \\ & C_2 & \langle 4.01,5.01\rangle \\ & C_3 & \langle 14.1,17.1\rangle \\ & C_4 & \langle 40.5,49.4\rangle \\ & C_5 & \langle 201,371\rangle \\ & C_6 & \langle 95.6,101.1\rangle \\ & C_7 & \langle 34.1,35.1\rangle \\ & C_8 & \langle 34.2,35.9\rangle \end{Bmatrix}$
Fault NO.	13	14	15
matter-element	$R_{13}=\begin{Bmatrix} I_{13} & C_1 & \langle 4.9,9.1\rangle \\ & C_2 & \langle 6,6.64\rangle \\ & C_3 & \langle 13,13.9\rangle \\ & C_4 & \langle 40.9,43.8\rangle \\ & C_5 & \langle 239,330\rangle \\ & C_6 & \langle 62.5,69.5\rangle \\ & C_7 & \langle 19.6,22.1\rangle \\ & C_8 & \langle 31,32\rangle \end{Bmatrix}$	$R_{14}=\begin{Bmatrix} I_{14} & C_1 & \langle 5.1,9.8\rangle \\ & C_2 & \langle 4.26,5.19\rangle \\ & C_3 & \langle 14.1,16.4\rangle \\ & C_4 & \langle 38.6,45.3\rangle \\ & C_5 & \langle 209,366\rangle \\ & C_6 & \langle 84.7,92.2\rangle \\ & C_7 & \langle 30.7,33.6\rangle \\ & C_8 & \langle 36.1,37.4\rangle \end{Bmatrix}$	$R_{15}=\begin{Bmatrix} T & C_1 & \langle 2.13,19.27\rangle \\ & C_2 & \langle 3.34,7.66\rangle \\ & C_3 & \langle 10.39,19.81\rangle \\ & C_4 & \langle 29.575,56.925\rangle \\ & C_5 & \langle 71.8,552.2\rangle \\ & C_6 & \langle 47.86,108.94\rangle \\ & C_7 & \langle 14.68,37.72\rangle \\ & C_8 & \langle 27.675,40.825\rangle \end{Bmatrix}$

Table5. The type of characteristics

type	The name of characteristic
1	White blood cell(WBC)

2	Red blood cell(RBC)
3	Hemoglobin(Hgb)
4	Hematocrit(Ht)
5	Platelet(Plate)
6	Mean corpuscular volume(MCV)
7	Mean corpuscula hemoglobin(MCH)
8	Mean corpuscula-hemoglobin concentration(MCHC)

2. Steps of applying Extension Theory to disease diagnosis

The application of ET to disease diagnosis has been approved in the field of Chinese medical science and the advantages this method provides are:

Integration of both quantitative and qualitative information for analysis

Systematic characteristics could be revealed thoroughly and accurately

Sophisticated analysis of the system structure could be achieved for defining faults precisely

Followings are the steps in terms of applying Extension Theory to analyze blood examination data for disease diagnosis:

Step1: Organize the anomalistic blood data in the matter-element model as:

$$K(x)=\frac{\rho(x,X_O)}{D(x,X_O,X)} \tag{2.6}$$

$$R_i=\begin{bmatrix} I_i & C_1 & V_{i1} \\ & C_2 & V_{i2} \\ & C_3 & V_{i3} \\ & C_4 & V_{i4} \\ & C_5 & V_{i5} \\ & C_6 & V_{i6} \\ & C7 & V_{i7} \\ & C_8 & V_{i8} \end{bmatrix} \quad i=1,2,...,14 \tag{3.1}$$

Vij=<aij,bij>is in classical domain.

Step2: Build the matter-element value T for diagnosis

$$R_t=\begin{bmatrix} T & C_1 & v_{t1} \\ & C_2 & v_{t2} \\ & C_3 & v_{t3} \\ & C_4 & v_{t4} \\ & C_5 & v_{t5} \\ & C_6 & v_{t6} \\ & C_7 & v_{t7} \\ & C_8 & v_{t8} \end{bmatrix} \tag{3.2}$$

Step3:Calculate value of position

$$\rho(v_i,V_i)=\left|x-\frac{a+b}{2}\right|-\frac{b-a}{2},\ v_i\in V_i$$
$$\rho(v_i,V_i')=\left|x-\frac{a+b}{2}\right|-\frac{b-a}{2},\ v_i\notin V_i \tag{3.3}$$

Step4:Calculate correlation functions

$$K_{ij}(v_{tj})=\begin{cases}\dfrac{-\rho(v_i,V_i)}{|V_i|}, & \text{if } v_i\in V_i \\ \dfrac{\rho(v_i,V_i)}{\rho(v_i,V_i')-\rho(v_i,V_i)}, & \text{if } v_i\notin V_i\end{cases} \tag{3.4}$$

$i=1,2,...,14$

Step5: Calculate the correlation degree with the correlation function. The weight set for all would be 1/8.

$$\lambda_i=\sum_{j=1}^{8}w_{ij}K_{ij}(v_{tj}),\quad i=1,2,...,8 \tag{3.5}$$

Step6:Ascertain the state of anomalism. Set λi,max=1 to be anomalism If. When the correlation degree of data is lower 1, it appears to be anomalism. And the anomalistic ratio is set between 1 and -1.

$$\lambda_{new,i}=\frac{2\lambda_i-\lambda_{\max}-\lambda_{\min}}{\lambda_{\max}-\lambda_{\min}} \tag{3.6}$$

Step7:Find the maximum value from the correlation degree.

$$\lambda_{new,max}=\max_{1\le i\le 14}\{\lambda_{new,i}\} \tag{3.7}$$

Step8:Once all of the blood data are examined, the process of complete diagnosis is then accomplished. If not, it has to restart and go through the process from Step 2.

It could be realized that applying correlation degree to examine the blood data allows examiners to detect potential diseases threats effectively and precisely; as a result, patients then could be noticed with disease precautions and prevent diseases from occurring early. When applying the Extension Theory to analyze blood data, it only requires some simple calculation, particular medical experiments are not necessary for data analysis; as a result, it is more feasible and accessible in the medical field.

IV. ANALYSIS AND FINDINGS

To test the reliability and validity in terms of the Extension Theory method applied in this study, 600 sets of blood examination data were experimented and 15 of them are displayed in Table6. Table7 then shows the correlation degree. Based on those two tables, it could be known that No.465 has white blood cell deficiency, because the value of WBC is lower than1. The maximum value of correlation degree of No.465 is defined as Type2 in Table5. No.578 has macroscopic anemia and the maximum value is defined as Type12. Accordingly, it could be found that the outputs and diagnosis are matched.

In terms of fault tolerance of the Extension Theory method applied in this study, it adds ±5% to ±20% error randomly in the calculation of all numerical data, and the results are presented in Table8. It discovers that if there is no error in the test, the accuracy of correlation would be 95.83%. But as ±5% and ±10% error are added, the accuracy would reduce to 90.5% and 75.33% respectively. Also, if the data are set within ±15% and ±20% error, then the accuracy would reduce to 64% and 52%. However, with the examination of both the first and second correlation degree, the accuracy rate would increase and the error made from human negligence would be overcome as

well.

To prove the efficiency of ET on the fault diagnosis, the comparison of accuracy rate between it and the neutral network are displayed in Table9. The accuracy that Extension Theory provides is 95.83%, and that of neural network is only 91%. In the neural

network, the layers are 8-11-14 [12-13].Table6. The blood of pattern (Partial samples)

Table6. The blood of pattern (Partial samples)

NO.	WBC	RBC	Hgb	Ht	Plate	MCV	MCH	MCHC	Fault types
153	5.4	4.49	14.4	40.6	372	90.2	32	35.4	1
465	3.8	4.2	12.8	36.9	211	87.9	30.5	34.7	2
506	11.7	4.67	14.3	41.6	308	89	30.6	34.4	3
515	6.3	3.94	12.7	37.2	252	94.4	32.3	34.2	4
527	7	6.26	14.3	44	272	70.2	22.8	32.4	5
539	5.4	4.17	12.1	33.9	351	81.2	29	35.7	7
547	9.4	4.24	13.1	39	103	92	30.9	33.5	8
563	5.6	5.88	13.1	39.2	253	66.7	22.3	33.5	10
578	5	4.36	15.1	43.1	238	98.7	34.6	35	12
596	5.1	4.44	14.6	39.8	308	89.5	32.9	36.7	14

Table7. The correlation degree of blood (Partial Results)

Type / NO.	1	2	3	4	5	7	8	10	12	14	Output
153	1	0.323	0.741	-0.027	-0.295	-0.248	0.34	0.026	0.251	0.573	1
465	0.894	1	0.633	0.784	-0.741	0.191	0.388	-0.218	-0.138	-0.098	2
478	0.949	0.494	1	0.297	-0.933	-0.607	0.174	-0.018	-0.379	-0.043	3
515	0.176	-0.171	-0.18	1	-0.859	-0.77	-0.385	-0.425	-0.402	-0.328	4
527	-0.07	-0.473	-0.385	-0.736	1	-1	-0.376	0.177	-0.421	-0.458	5
539	0.534	0.05	0.225	0.101	-0.446	1	-0.412	0.1	-0.038	-0.315	7
547	0.862	0.234	0.762	0.005	-0.86	-0.349	1	-0.047	-0.439	-0.214	8
563	-0.1	-0.188	-0.509	-0.419	0.306	-0.738	-0.65	1	-0.674	-0.7	10
578	0.404	-0.1	0.165	-0.328	-0.518	-0.438	-0.051	-0.421	1	-0.06	12
596	0.829	0.256	0.564	-0.089	-0.369	-0.215	0.221	-0.006	0.183	1	14

Table8. The correct rate of system with error

Error added	Correct rate
± 0%	95.83%
± 5%	90.5%
± 10%	75.33%
± 15%	64%
± 20%	52%

Table9. Compared extension theory and neural network

Type	Extension theory	Neural network(8-11-14)
Correct rate	95.83%	91%

V. CONCLUSIONS

This study suggests that the application of Extension Theory to analyze the blood examination data would be an effective way to diagnose potential diseases threats. It not only reduces the probability of faulty diagnosis made from human negligence and personal judgments, but also allows the anomalistic blood data built in the matter-element model for recognizing correlation function between inputted blood examination data and anomalistic

characteristics to define the chronic or potential diseases more precisely. For further research, this study recommends that it could target on some blood data and integrate other blood examination methods for improving the accuracy of diagnosis in particular diseases.

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