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Forecasting Survival Rates Post-Gastrointestinal Surgery: Integrating The New Japanese Association of Acute Medicine (JAAM Score) and Neural Network Classification

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ABSTRACT

Following gastrointestinal surgery, the incidence of disseminated intravascular coagulation (DIC) has a bad prognosis. Consequently, it is essential to identify the variables that can predict the prognosis of DIC. This study will examine the factors that may affect the outcome of DIC in patients who have had gastrointestinal surgery. From 2003 to 2021, 81 patients were admitted to the intensive care unit at Kyushu University Hospital following gastrointestinal surgery. DIC scores were computed using the new Japanese Association of Acute Medicine (JAAM) score from before and after surgery. Comparisons will be made between DIC values and The Sequential Organ Failure Assessment (SOFA) score, platelet count, lactate level, and a range of biochemical markers. This study utilized machine learning techniques to determine the prognosis of DIC following gastrointestinal surgery. After gastrointestinal

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1. INTRODUCTION

According to The Third International Consensus Definitions for Sepsis and Septic Shock, sepsis is a life-threatening condition caused by impaired regulation of the host's response to infection[1]. Sepsis has still become one of the leading causes of mortality in the world[2]. Sepsis can be caused by a spontaneous perforation or as a complication after abdominal surgery. Sepsis after abdominal surgery mainly occurs in patients with colorectal perforation-associated peritonitis and usually has a poor prognosis[3].

A recent nationwide survey in Japan reported that approximately one-third of patients exhibited shock in patients with sepsis in the intensive care unit, and more than half exhibited DIC. These two significant factors can lead to poor outcomes in sepsis[4].

DIC associated with sepsis is considered a syndrome that should be diagnosed and treated early. Diagnostic criteria play a key role in making an accurate diagnosis and starting therapy early to improve prognosis. There are several diagnostic criteria for DIC. Each criterion has its strengths and weaknesses[5]. The Ministry of Health and Welfare (JMHW) Japan developed scoring systems to diagnose DIC in 1987. In 2001, the International Society on Thrombosis and Haemostasis (ISTH) initiated the first diagnostic criteria for overt DIC. In 2006, the Japanese Association for Acute Medicine (JAAM) proposed new diagnostic criteria to facilitate early identification and intervention[6][7]. Among other diagnostic criteria, the Japanese Association for Acute Medicine criteria (JAAM-DIC) have consistently shown higher sensitivity and predictive accuracy for mortality compared to other DIC criteria[8].

In recent years, there has been growing interest in applying Machine Learning in health services research. Advanced machine-learning models can fit high-order relationships between covariates and outcomes, and therefore, they excel in analyzing complex signals in data-rich environments and can improve clinical decision-making[9]. This study used the JAAM-DIC criteria, SOFA score, and other biochemical parameters and used the machine learning tool to predict the survival rate after gastrointestinal surgery. Machine learning approach is used here to simplify and assist doctors in predicting the prognosis or survival rate of a patient, so that the next appropriate treatment can be known.

The paper is organized as follows: Section 2 will explain some literature, basic knowledge, and tools that we used in this research. In Section 3, we present our research methodology and necessary background for the following parts and the evaluation methods. Section 4 gives a description of the result of experiment and also the analysis, and conclusions are drawn in Section 5.

Scoring system for disseminated intravascular coagulation (DIC) established by the Japanese Association for Acute Medicine.

Table 1. Scoring system for disseminated intravascular coagulation (DIC) established by the Japanese Association for Acute Medicine.

	Score
Systemic inflammatory response syndrome criteria	
· ≥3	1
· 0-2	0
Platelet counts (109/L)	
· <80 or more than 50% decrease within 24 hours	3
· ≥ 80 and < 120 or more than 30% decrease within 24 hours	1
· ≥ 120	0

· Prothrombin time (value of patient/normal value)	
· ≥1.2	1
· <1.2	0
Fibrin / fibrinogen degradation products (mg/L)	
· ≥25	3
· ≥10 and <25	1
· <10	0

The diagnosis of DIC is made if the score is 4 or more

Criteria for systemic inflammatory response syndrome

- Temperature >38°C or <36°C
- Heart rate >90 beats/min
- Respiratory rate >20 breath /min or PaCO2
- White cell blood counts >12,000/mm3, <4000cells?mm3, or 10% immature (band) forms

1.1. The New Japanese Association for Acute Medicine (JAAM) DIC criteria

The Japanese Association for Acute Medicine (JAAM) created the DIC diagnostic criteria in 2006 because the Japanese Ministry of Health and Welfare's (JMHW) DIC diagnostic criteria was often too late for emergency medicine and surgery case [5]. The DIC diagnosis was performed based on the JAAM DIC diagnosis criteria can be seen in Table 1. Patients with a total score ≥ 4 were diagnosed as having[7][10]. The Japanese Association for Acute Medicine (JAAMDIC) criteria consistently showed higher sensitivity and prepredictive accuracy for mortality than other DIC criteria[4]. Fibrinogen was initially included in The JAAM criteria for DIC diagnosis at ≥5 points, but fibrinogen could not be shown to have diagnostic significance in actual application. Fibrinogen was eliminated from the criteria for DIC diagnosis at ≥4 points[5]. The Japanese Clinical Practice Guidelines for the Management of Sepsis and Septic Shock (J-SSCG 2016) build on clinical evidence recommending the use of the JAAM-DIC criteria to decide when to intervene. The JAAM-DIC diagnostic criteria are helpful and still considered to be the standard of practice in Japan[11].

1.2. Machine Learning

Machine Learning (ML) has evolved over the last few decades from a hobby of a few computer enthusiasts who wanted to see if computers could learn to play games to an independent research discipline. ML has not only provided the necessary foundation for statistical-computational principles of learning procedures but has also developed many algorithms that are now widely used. We can say that Machine learning is a paradigm that refers to improving future performance by learning from existing experience (in this case, historical data)[12]. At this time, many fields apply machine learning in it, not only limited to computer-related fields but also many other fields such as business, medical, industry, education, natural science, agronomy, astronomy, and many more.

Machine Learning was a phenomenal result when Computer Science and Statistics merged. Computer Science focuses on building machines that solve a specific problem and identifying whether the problem can be solved. The main approaches that are fundamentally used in Statistics are data inference, hypothesis modeling, and measuring the reliability of conclusions.

1.3. Popular Machine Learning Algorithm

Machine learning is used in many sectors because a lot of studies have been done on it. Various researchers have contributed to ML and introduced many algorithms and techniques. Following are the famous and most commonly used machine learning algorithms along with their use cases and applications[13]:

1) Linear Regression algorithm
2) Logistic Regression algorithm
3) Decision Tree algorithm
4) Support Vector Machine (SVM) algorithm
5) Naïve Bayes algorithm
6) k-Nearest Neighbor algorithm • K-Means Clustering algorithm

1.4. Weka

Weka is one of the machine learning tools that are widely used today, which is an open-source tool with a graphical user interface[14]. WEKA was developed by Waikato University, and now Weka is widely used in science, industry, and education. It includes a variety of built-in tools for common machine learning tasks as well as easy access to many toolboxes. Some of the advantages of this tool are that the algorithm is simple to understand, and Weka is also beneficial for students because it is free. It offers instruction through online courses, multi-platform compatibility, and a straightforward interface. WEKA supports several standard data mining and data processing tasks, including data pre-processing, clustering, classification, regression, visualization, and feature selection[15].

2. METHODS

Machine Learning is used to learn the pattern and generate a classification model. In pattern recognition applications, neural networks are a standard Machine Learning method, and their performance has been proven. Neural Networks were employed in some pattern recognition studies. Some research about pattern recognition application in Medical filed use the Neural Network approach[16][17]. The machine learning process with neural network is depicted in **Figure 2**.

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Hamilton, New Zealand

Figure 1. Weka Application startup screen wek

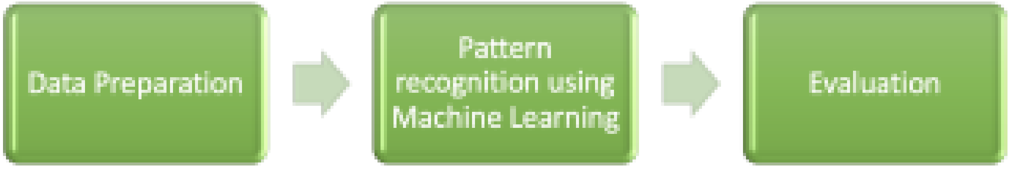

Figure 2. Flow of machine learning process

Testing Data Testing which totaled 25 data and Data Training 75 samples of early childhood data.

2.1. Data

All patients admitted to the Kyushu University Hospital's ICU from 2003 to 2021 were screened retrospectively. Patients were eligible for the study if they had gastrointestinal surgery and met the inclusion criteria during ICU admission: two or more signs of systemic inflammation, at least one sepsis-induced organ dysfunction, and 16 years of age or older. The exclusion criteria were patients with SIRS score ≤1, unknown outcome, not receiving gastrointestinal surgery, and pregnancy. This study included 81 patients who met the inclusion criteria. Extensive medical records data were collected to assess for potential confounding factors. The severity of the patients' illness was evaluated using the Acute Physiology and Chronic Health Evaluation (APACHE) II score and the Sequential Organ Failure Assessment (SOFA) score used to assess organ dysfunction[10]. We calculated DIC scores using the new Japan Acute Medicine Association (JAAM) scores presurgery and day 1, 3, and 7 postsurgery. This study was conducted under the ethical guidelines of the Declaration of Helsinki. This study was performed after approval from the ethical committee at Kyushu University.

In the data preparation step, several things must be done: Data Selection, Data Pre-processing, and Data Transformation. Data Selection is the stage to select the data related to the objective investigation, and we only consider data or attributes that might be useful for our prediction. Data Preprocessing is the stage to remove irrelevant data and validate the data. And Data Transformation means transforming the selected data into appropriate forms used for the following process.

2.2. Training Process

In this training step, data is divided into two groups, which are Training Data, and Testing Data. The algorithm used is 10 FOLD-CROSS VALIDATION. Cross-validation (CV) is a statistical method that can evaluate the performance of a model or algorithm where the data is separated into two subsets, namely learning process data and validation/evaluation process data.

The model or algorithm is trained by the learning subset and validated by the validation subset. Furthermore, the selection of the type of CV can be based on the size of the dataset. Usually, the K-fold CV is used because it can reduce computation time while maintaining the estimate's accuracy. The 10-fold CV is one of the recommended K-fold CVs for selecting the best model because it tends to provide less biased accuracy estimates than the usual, leave-one-out CV. In a ten-fold CV, the data is divided into ten folds of approximately equal size, so we have ten subsets of data to evaluate the performance of the model or algorithm. For each of the 10 data subsets, CV will use nine folds for training and one-fold for testing, as illustrated in **Figure 3**.

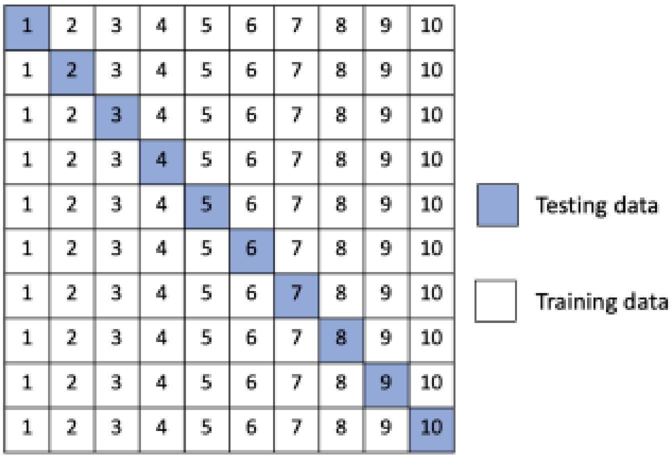

Figure 3. 10-Cross Validation scheme

2.3. Evaluation

After we train our model, we need to evaluate the performance of this model. The performance of model is evaluated by Accuracy in Equation 1.

$$Accuracy = \frac{TP + TN}{T\,P\ +\ T\,N\ +\ F\,P\ +\ F\,N} \tag{1}$$

where :

- $T\,P$ denotes True Positive
- $T\,N$ denotes True Negative
- $F\,P$ denotes False Positive
- $F\,N$ denotes False Negative

The performance of the model will be evaluated by Mean squared error (MSE). MSE value is the average from the absolute value of the difference between an observed value of a quantity and the actual value. Simply, MSE is the average squared difference between outputs of the models and real value. A good MSE value is close to zero

Table 2. Performance comaparison among popular ML algorithm with all variables

Algorithm	Performance	
	Accuracy	MSE
Logistic Regression	85.0746 %	0.1546
Naïve Bayes	92.5373 %	0.1449
Random Forest	88.0597 %	0.0746
SVM	92.5373 %	0.0746

$$MSE\ = \left(\frac{1}{n}\right)\sum_{i=1}^{n} \square\, 1\ (y_i - x_i)^2 \tag{2}$$

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3. RESULTS AND DISCUSSION

Experiments were conducted on two scenarios. The first scenario is to see the performance of some of the most popular machine learning algorithms using all the variables we defined earlier. The second scenario is using the Weka tool, then we rank the existing variables and choose eight variables with the highest correlation level with the prognosis class. Furthermore, the eight variables will be used in the machine learning algorithm, and we can see the performance.

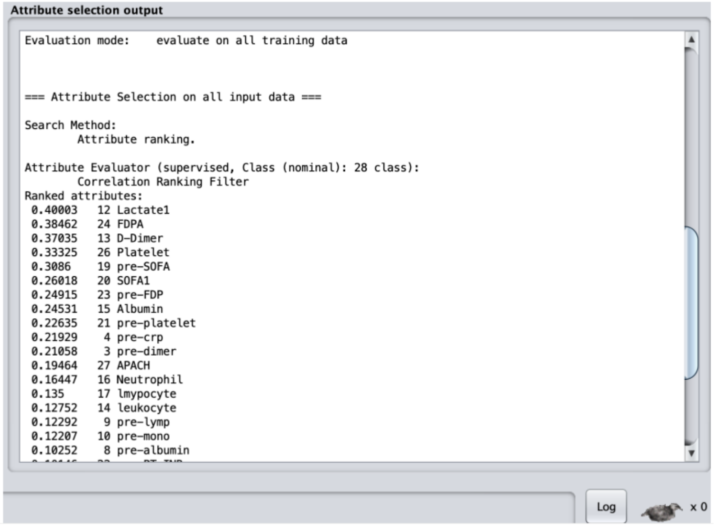
3.1. Scenario I

We used 28 variables which will then be used as input to the machine learning algorithm (including JAAM criteria, laboratory findings, and clinical parameter). The result can be seen in **Table 2.**

3.2. Scenario II

In scenario I we have 28 variables, but in scenario II, we will reduce it to only about 8 variables. The idea is to reduce the number of variables involved because doctors or practitioners can more easily input the data to be processed in machine learning applications.

To process of selecting variables in our data, we need to perform variable selection. There are many variable selection methods in Weka, in this preliminary research we use the Correlation Based Feature Selection. Correlation Based Feature Selection is a popular technique for selecting the most relevant attributes in the dataset. This Correlation is more formally referred to as Pearson's correlation coefficient in statistics. We can calculate the correlation between each attribute and the output variable and pick only those attributes with a high positive or negative correlation (near to 1 or -1), while excluding those with a low correlation (value close to zero). The result from variable / attribute selection can be seen in **Figure 4**.



```
Evaluation mode:    evaluate on all training data



=== Attribute Selection on all input data ===

Search Method:
        Attribute ranking.

Attribute Evaluator (supervised, Class (nominal): 28 class):
        Correlation Ranking Filter
Ranked attributes:
 0.40003   12 Lactate1
 0.38462   24 FDPA
 0.37035   13 D-Dimer
 0.33325   26 Platelet
 0.3086    19 pre-SOFA
 0.26018   20 SOFA1
 0.24915   23 pre-FDP
 0.24531   15 Albumin
 0.22635   21 pre-platelet
 0.21929    4 pre-crp
 0.21058    3 pre-dimer
 0.19464   27 APACH
 0.16447   16 Neutrophil
 0.135     17 lmypocyte
 0.12752   14 leukocyte
 0.12292    9 pre-lymp
 0.12207   10 pre-mono
 0.10252    8 pre-albumin
```

Figure 4. Variable / Attribute Selection Result

Table 3. Performance comaparison among popular ML algorithm with 8 selected variables

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Algorithm	Performance	
	Accuracy	MSE
Logistic Regression	85.0746 %	0.1454
Naïve Bayes	89.5522 %	0.1071
Random Forest	92.5373 %	0.1093
SVM	92.5373 %	0.0746

After we get the ranking of variables, then we need to use the top 8 variables only to be processed to the Machine Learning application. The 8 selected attributes are as follows: • Lactate day-1

1) FDP
2) D-Dimer
3) Platelet
4) pre-SOFA
5) SOFA day-1
6) pre-FDP
7) Albumin

These eight variables have the highest correlation with the patient's prognosis. FDP and D-dimer have great significance in diagnosing DIC, and they are included as essential test items in almost all DIC diagnostic criteria. A decreased platelet count has a high sensitivity for DIC diagnosis, but the specificity is low [5].The input results showed that the lactate level on the first day and albumin also affected the patient's prognosis. Lactate level is used as an indicator of the occurrence of shock in patients. Albumin levels as one of the factors that affect the prognosis can be further analyzed.

From Table 2 and Table 3, we can see there is no significant different. In average the accuracy from all those algorithm is around 90%. This machine learning application is reliable enough to help doctors quickly get early predictions about patients' emergency status. From the use of 28 or 8 variables shows that the accuracy is not much different. This may be because from the data we have, these 8 variables have a very close correlation with the patient's prognostic condition. However, this is still a very early analysis and requires further evidence and a larger amount of data in order to better understand which variables have the most influence in determining the patient's prognosis.

4. CONCLUSION

Early Prediction of Survival Rate after Gastrointestinal Surgery Based on The New Japanese Association for Acute Medicine (JAAM Score) can be carried out by implementing machine learning method. Average accuracy is more than 90% either with all variables and subset variables. There are still many possibilities that can be elaborated more in this research, for example exploring other sophisticated machine learning algorithm, add more data, and investigating the effect from every variable. Also From this preliminary research, we can make a simple application in small device to predict the Survival Rate after Gastrointestinal Surgery so we can help the surgeon or practitioner to get the additional insight to take the next treatment process quickly and get early predictions about patients' emergency status.

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6. AUTHORS' NOTE

The authors declare that there is no conflict of interest regarding the publication of this article. Authors confirmed that the paper was free of plagiarism.

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