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APPLICATION OF CLASSIFICATION BASED ASSOCIATION (CBA) FOR MONKEYPOX DISEASE DETECTION

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ABSTRACT

Monkeypox is a zoonotic disease that can be transmitted from animals to humans. The monkeypox virus is the cause of monkeypox disease, which belongs to the orthopoxvirus family. Although the mortality rate from monkeypox is not as high as COVID-19, this virus can be the cause of the next global pandemic if the epidemic worsens. Therefore, it is very important to carry out proper surveillance and prevention to prevent the spread of this disease. In this study, researchers developed another method to detect monkeypox disease based on its symptoms using the classification by association (CBA) method. CBA integrates the advantages of classification and association analysis, allowing the classification process and a deeper understanding of the strength of the relationship between features in the dataset through the analysis of metrics such as support and confidence. Based on the results of the experiments in this study, an accuracy of 68.64%, a precision of 92.21%, and a sensitivity of 71.09% were obtained. In this case, the accuracy obtained is still low, but the results of other metrics show that the CBA model performs fairly well in predicting the positive class with high precision.

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1. INTRODUCTION

The world faces a new issue in 2022 with the introduction of monkeypox following the global impact of COVID-19. A zoonotic disease called monkeypox spreads from animals to people. The orthopoxvirus, which causes this disease, is an uncommon viral disease primarily affecting people in Central and West Africa. The virus is known as the monkeypox virus [1]. According to a report published by CNBC (2023), on November 7, 2023, the total number of monkeypox cases in Indonesia was 35. Monkeypox is an infectious disease, but the mortality rate is not as high as COVID-19; even so, the existence of this disease is enough to make people anxious and afraid. Prevention efforts need to be made to face the pandemic, such as COVID-19. One of the efforts to prevent transmission is the detection of symptoms to control the spread of the disease and provide appropriate care to infected individuals.

Over time, technology has experienced rapid development, one of which is in the field of machine learning (ML). ML has various critical roles in the world of health, one of which is disease diagnosis. ML can help diagnose diseases through medical data such as medical images or patient medical history. Several previous studies have used ML to detect monkeypox disease. Deep learning approach by comparing 13 different methods [2]. The new modified DenseNet-201-based Deep CNN model is called "MonkeyNet" [3]. Detection of the presence or absence of the monkeypox virus by comparing several machine learning classification methods [4]. XGBoost achieved the best performance, and Shapley additive explanations (SHAP) were used to help interpret the XGBoost output [5]. The two primary components of the human monkeypox diagnostic (HMD) strategy are identifying the optimal characteristics using improved binary chimp optimization (IBCO) and diagnosing the illness based on the features identified. [6]. Classification of monkeypox disease using the support vector machine (SVM) method, the accuracy obtained was 65% [7].

Researchers use text datasets in the form of medical history based on symptoms. This detection aims to identify conditions at a stage before the appearance of a rash on the skin and find specific characteristics of monkeypox patients. The monkeypox symptoms dataset was analyzed using data mining methods. Data mining is a crucial stage in knowledge discovery from databases (KDD), encompassing various approaches such as classification, clustering, association rules, and associative classification (AC). This study focuses on the AC technique to detect monkeypox disease based on the symptoms experienced. AC is a classification method that combines association rule mining and classification algorithms. Liu, in 1998, developed an algorithm based on the AC technique called classification-based association (CBA) [8]. Several previous studies using the AC method proposed a new method of weighted classification based on an association rules algorithm (WCBA) for detecting breast cancer [9]. CBA to classify fetal health status [10]. CBA produces the best accuracy in classifying cervical cancer [11]. In AC, there is a subset of association rules where the right side (consequent) is limited by the class attribute or classification target used for the classifier, which is called class association rules (CAR). AC uses two approximate measures to generate association rules: support and confidence.

The main objective of this study is to detect monkeypox using the CBA method. The researchers used the same monkeypox dataset as Anugrah et al. [7]. The researchers used the SVM method but could not provide in-depth insights into the relationships between its features. The dataset we used has many categorical attributes, and the relationships between features are important to understand. CBA generates classifier rules in the form of "if-then," which are easy to understand and interpret, and it can find unexpected or hidden rules or patterns. CBA combines the power of classification and association analysis, which allows for classification and understanding of the strength of the relationship between features in the dataset by analyzing support and confidence metrics.

2. RESEARCH METHODS

The research process involves several steps, as shown in **Figure 1**. The initial steps include problem identification, dataset input, data preprocessing, and data separation into training and test data. The next step is creating CAR rules from training data. CAR rule creation is obtained from frequent rule items built using the apriori algorithm by searching for rule items often appearing in the dataset. The CAR obtained is then selected to be used as a classifier rule by scanning each CAR rule into the training data. Next, the classifier rule is used to test the test data, and then the model evaluation is carried out. Model evaluation is carried out by calculating the classification results: accuracy, precision, and sensitivity values using the CBA method.

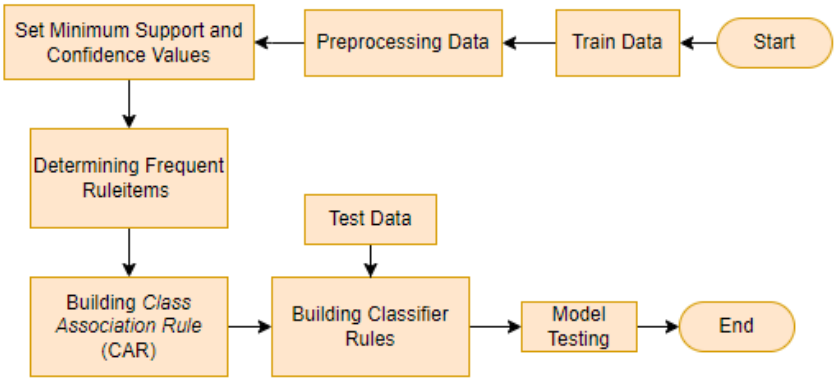

Figure 1. Research Flowchart CBA

2.1 Input dan Preprocessing Data

The data for this study are secondary in the form of patient medical history and patient diagnosis, including whether or not they are positive for monkeypox virus infection. The dataset is taken from kaggle.com. Ten categorical variables, including patient ID, systemic illness, rectal pain, sore throat, penile edema, oral lesions, solitary lesions, swollen tonsils, HIV infection, and sexually transmitted infection, are present in the dataset, which includes 25,000 observations. Where true indicates experiencing one of the symptoms, and false indicates that the patient does not experience one of the symptoms. The target variable also has two classes: positive, identifying patients with monkeypox, and negative, identifying patients who are not infected with monkeypox. **Table 1** below shows a description of the monkeypox dataset.

Table 1. Description of the Monkeypox Dataset

No	Attribute	Category
1.	patient_ID	P0, P1, …, P24999
2.	systemic illness	muscle aches and pain (muscle), fever (fever), swollen lymph nodes (sln)
3.	rectal pain (rp)	True, False
4.	sore throat (st)	True, False
5.	penile edema (pe)	True, False
6.	oral lesions (ol)	True, False
7.	solitary lesion (sl)	True, False
8.	swollen tonsils (swt)	True, False
9.	hiv infection (hiv)	True, False
10.	sexually transmitted infection (sti)	True, False
11.	monkeypox (class)	Positive, Negative

***Data source**: kaggle.com*

In this study, data preprocessing involves a series of steps, such as data cleaning and one-hot encoding. Data cleaning is done to detect and correct or remove incorrect or noisy data from the dataset. Irrelevant data can add noise to the dataset, interfering with the actual pattern and reducing model accuracy **[12]**. The column "patient ID" in the monkeypox dataset was removed because the attribute was irrelevant or did not contribute to model training. Next, checking for missing or empty data values, empty data causes the model to learn from incomplete or incorrect data **[13]**. In the systemic disease column, 6,216 attribute values are none or empty, so the data is removed. Furthermore, column names were changed to help better understand the contents and purposes of each column. The column name 'MonkeyPox' was changed to 'Class' to clarify that the column contains class labels or targets in classification.

The data transformation process uses one-hot encoding. One-hot encoding is a method for transforming discrete (categorical) variables into binary form so that they can work better with classification algorithms **[14]**. One-hot encoding changes each category in a column into a separate column, each filled with a binary value (0 or 1). In the attribute "Type of Systemic Illness," there are three categories: muscle pain and pain, swollen lymph nodes, and fever. Each category will be changed into a column form and named according to its category; the one-hot encoding process is presented in **Table 2** and **Table 3**.

Furthermore, changing the text "Yes" and "Positive" to a binary value of 1, giving a value of 1 identifies the presence of certain symptoms; for example, in the column "Fever" filled with one, means the patient has a fever. While the text "No" and "Negative" into binary 0 identify the absence of certain symptoms, for example, in the column "Fever" filled with 0, it means the patient does not have a fever. **Table 4** shows the data after preprocessing, with the final number of data used being 18,783 rows.

Table 2. Data Before One-Hot Encoding Process

	Type of Systemic Disease
0	Muscle Aches and Pain
1	Swollen Lymph Nodes
2	Fever
3	Fever
4	Muscle Aches and Pain
5	Swollen Lymph Nodes

One-hot encoding

Table 3. Data After One-Hot Encoding Process

Muscle Aches and Pain	Swollen Lymph Nodes	Fever
1	0	0
0	1	0
0	0	1
0	0	1
1	0	0
0	1	0

Table 4. Data After Preprocessing

No.	rp	st	po	ol	sl	swt	hiv	sti	sln	fever	muscle	class
0	1	0	1	1	0	0	1	0	0	1	0	1
1	0	1	1	0	0	0	1	0	0	1	0	1
2	1	1	1	0	0	1	1	0	1	0	0	1
3	0	1	0	0	0	0	0	0	1	0	0	0
4	0	1	0	0	0	0	1	0	0	1	0	1
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
18783	1	1	0	0	1	0	0	0	1	0	0	0

2.2 Classification Based Association (CBA)

By combining association rule mining and classification rule mining, two significant data mining approaches are known as associative classification (AC). This method uses association rules in the classification process to find hidden patterns that can improve the accuracy of the classification process. Class association rules (CAR) are a subset of association rules in AC where the right-hand side (RHS) or consequent is restricted to using a single item of the classification class attribute as a classifier. The AC algorithm generates association rules based on two approximations: confidence and support **[9]**. Suppose a data set D is shown in **Table 5** to explain the concept of AC.

Table 5. Illustration of Sample Dataset D

No.	Attribute 1 (At_1)	Attribute 1 (At_2)	Attribute 1 (At_3)	Class (C)
1.	v_1	v_2	v_1	C_1
2.	v_2	v_2	v_1	C_2
3.	v_1	v_1	v_1	C_1

There is a rule stating that $At_1 \Rightarrow C_1$, C_1 is a class attribute. Data set D has n different attributes $(At_1, At_2, \ldots, At_n)$, and C is a class attribute. Items are described as attribute names At_i and value v_i. As in **Table 4**, (At_1, v_i) is an item and the itemset is a collection of items contained in the training object, for example (At_1, v_1) (At_2, v_2) is an itemset. The itemset rule in the form of $< itemset, C_i >$ is called rule items. In this research $(itemset \Rightarrow C_i)$, itemset as a left-hand side (LHS) in this study states a collection of mpox symptoms, and C_i as a right-hand side (RHS) is a label or class that states whether someone is infected with mpox or not.

Support to measure how often rule items appear in the dataset. Rule items pass the minimum support threshold if $(supp(ruleitem) \geq minsupp)$, and support is calculated using **Equation (1)**.

$$Support = \frac{\text{number of rule item}}{\text{s, the total amount of data}} \quad (1)$$

If there is an association rule $itemset \Rightarrow C_i$ then the rule passes the minimum confidence threshold if $(conf\,(rule\ item) \geq minconf)$. The confidence value can be determined by dividing *supp(ruleitem)* by *supp(itemset)*, as shown in **Equations (2)**.

$$Confidence = \frac{\text{support (rule item)}}{\text{support (itemset)}} \tag{2}$$

One of the well-known methods in classification mining based on association rules is the CBA algorithm proposed by Liu in 1998. The steps in performing associative classification using the CBA algorithm include:

a. Mining the CAR set,

b. Pruning and sorting the rules,

c. Building a classifier from the CAR formed to predict the class.

Algorithm 1. Pseudocode Algorithm CBA

Input: Dataset T, support dan confidence threshold

Output: Prediction

Process:

a. Split (T) ← [train_dataset, test_dataset]

b. txns_train ← Transaction (train_dataset)

c. txns_test ← Transaction (test_dataset)

d. CARS ← generateCARS (txns_train, minimum_support, minimum_confidence)

e. Classifier ← build.classifier(cars, txns_train)

f. Predict(classifier, txns_test)

The first stage of CAR mining will involve applying the apriori algorithm to identify frequency patterns corresponding to association rules that satisfy the predetermined minimum support and minimum confidence limits. All rule items with support values greater than minsup are sought during the CAR mining process. Rule items are in the form of $< itemset, c >$, where the itemset in this study is the set of mpox symptoms, and $c \in C$ is the class label. Rule items that meet minsup are called frequent rule items. The first step is to find a single frequent rule item. Then, use this collection of single frequent rule items to generate new rule items that may appear frequently, called candidate rule items. Identify the often utilized candidate rule items after the process. To generate the CAR from this set of frequently occurring rule items, association rules are constructed by combining elements from the rule items on the frequently occurring rule items that have been located.

In the second step, the candidate association rules are then pruned; this process aims to optimize the results of the CAR rules generated. Pruning can be done based on certain criteria such as confidence, support, lift, or other interest measures. In the third step, a classifier from the CAR is built using the classifier build algorithm developed by Liu **[15]**. Suppose *R* is the set of classification rules built, and *D* is training data. The basic idea of this algorithm is to select a set of rules with high priority in *R* to cover *D*.

2.3 Evaluation of Classification Performance

A popular method for assessing performance in classification issues is the confusion matrix. The comparison between the actual labels on a data set and the model predictions is shown in this matrix. The number of positive events the classifier properly classifies as positive is known as the true positive (TP). The quantity of occurrences that the classifier reports as positive but are actually negative is known as false positives (FP). The number of negative events that the classifier correctly classifies as negative is known as the true negative (TN). The quantity of events categorized as negative but actually positive is known as false negatives (FN) **[16]**. **Equation (5)** states that accuracy is a statistic that assesses how well a model can categorize data**.** Precision is one of the classification performance evaluation metrics that measures the extent

to which positive predictions from the model are correct or relevant (**Equation (6)**). Sensitivity, also known as recall or true positive rate (TPR), is a classification evaluation metric that measures how well the model can identify all true positive data, **Equation (7)**.

$$Accuracy = \frac{TP + TN}{TP + TN + FN + FP} \times 100\% \quad (3)$$

$$Precision = \frac{TP}{TP + FP} \times 100\% \quad (4)$$

$$Sensitivity = \frac{TP}{TP + FN} \times 100\% \quad (5)$$

3. RESULTS AND DISCUSSION

This stage is used to test the proposed method for detection of monkeypox using Python 3.0. The minimum support percentage is set at 1%, and the confidence level is set at 50% based on previous research recommendations **[9]**. The determination of minimum support has an essential influence on the quality of the resulting classifier, if the minimum support is set too high, important rules can be missed. The trial was carried out with several ratios of training data and testing data division, including 90: 10 (90% training data and 10% testing data), 80: 20 (80% training data and 20% testing data), and 70: 30 (70% training data and 30% testing data).

Table 6. CBA Experiment Results

	90 : 10		80 : 20		70 : 30	
	Train	**Test**	**Train**	**Test**	**Train**	**Test**
Accuracy	70.57%	66.83%	70.98%	68.33%	71.22%	68.64%
Precision	87.60%	84.92%	92.44%	91.92%	93.19%	92.21%
Sensitivity	73.55%	71.08%	72.09%	71.01%	72.05%	71.09%
Number of CAR	249,143		249,043		248,472	
Number of classifier rules	524		556		570	

Table 6 describes the performance of monkeypox detection using the CBA method, which is divided into four training and testing data division ratios. The best accuracy is obtained in data division with a ratio of 70: 30, which is 68.64%. The fourth row explains the CAR rules that are built, and the number of CARs with a comparison ratio of 70: 30 is 248,472. CAR, in this case, is a rule built using the apriori algorithm. The rule is selected to produce a classifier rule. The fifth row is the classifier rule after selection with the classifier build algorithm, obtained to predict the testing data. The number of classifier rules is 570. Precision in the context of disease diagnosis ensures that the diagnosis is most likely correct when the system indicates that someone is suffering from a disease. While the sensitivity in disease diagnosis shows a better ability to detect almost all individuals who suffer from the disease. The sensitivity obtained is 71.09%.

Table 7. Comparison Between CBA and other Method

Ratio	Method	Accuracy
70 : 30	SVM	61.80%
	CBA	**68.64%**
80 : 20	SVM	64.80%
	CBA	**68.33%**
90 : 10	SVM	65.00%
	CBA	**66.83%**

Previous research used the same monkeypox dataset using the support vector machine (SVM) method, and the same division of training data and test data was carried out **[7]**. Based on **Table 7**, the CBA method produced better accuracy compared to SVM. In the data sharing ratio of 70% training data and 30% testing data, CBA experienced a significant increase of 6.84%.

Table 8. Classifier Rules of the Monkeypox Dataset

No.	Classifier Rules
1.	HIV infection = 1, sexually transmitted infection = 1, fever = 1, penile edema = 1, solitary lesion = 1,⇒ class = 1 supp: 0.01047 conf: 0.92188
2.	rectal pain = 1, sexually transmitted infection = 1, fever = 1, penile edema = 1, solitary lesion = 1,⇒ class =1 supp: 0.01056 conf: 0.90840
3.	HIV infection = 1, sexually transmitted infection = 1, penile edema = 1, solitary lesions = 1, oral lesions = 1 ⇒ class=1 supp: 0.01863 conf: 0.90129
4.	HIV infection = 1, fever = 1, penile edema = 1, solitary lesions = 1, oral lesions = 1 ⇒ class = 1 sup: 0.01828 conf: 0.89177
5.	HIV infection = 1, sore throat = 1, swollen tonsils = 1, sexually transmitted infections = 1, penile edema = 1 ⇒ class = 1 sup: 0.01011 conf: 0.89062

Table 8 shows five classifier rules with the highest accuracy. The rules have been sorted from the highest confidence value. Confidence shows how true and robust the antecedent is or appears together with the consequent. In the rules, HIV, sexually transmitted infections (STI), fever, penile edema, and solitary lesions have a strong relationship and always appear with the positive class of monkeypox. The symptoms of monkeypox are almost similar to the symptoms of STIs. There are lesions in the genital or anal area, such as in the third rule that rectal pain and penile edema have a strong relationship with the positive class of monkeypox. This can be detected if someone has these symptoms, they can do further examinations such as laboratory tests [17]. Systemic disease or systemic symptoms in monkeypox affect several organs or body systems due to widespread infection and the body's immune response. Fever is one of the systemic symptoms that has a strong relationship with the positive class of monkeypox. High fever often appears before a rash appears on the patient's skin [1].

4. CONCLUSIONS

Monkeypox detection using the CBA algorithm produces better accuracy than the SVM method in previous studies. The dataset has many categorical attributes and relationships between essential features to determine the most significant characteristics of monkeypox disease. Therefore, CBA is more relevant when compared to other methods, such as SVM. The best accuracy of the CBA method was obtained at a data sharing ratio of 70% training data and 30% test data, with an accuracy of 68.64%, a precision of 92.21%, and a sensitivity of 71.09%. The number of CARs obtained was 248,472, and the classifier rules were 570.

The conclusion of this study answers the main objective related to the application of CBA in detecting monkeypox disease. However, this study has limitations in terms of the type of dataset and methodology used, which can affect the generalization of the results. Future research can overcome these limitations by using datasets that have more sophisticated numeric attribute types and analysis techniques. In addition, further development of the CBA method, such as the application of more adaptive learning algorithms, may improve the accuracy and speed of disease detection in the future.

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