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A hybrid model based on convolutional neural networks and fuzzy kernel k-medoids for lung cancer detection

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ABSTRACT

Lung cancer is the deadliest cancer worldwide. Correct diagnosis of lung cancer is one of the main tasks that is challenging tasks, so the patient can be treated as soon as possible. In this research, we proposed a hybrid model based on convolutional neural networks (CNN) and fuzzy kernel k-medoids (FKKM) for lung cancer detection, where the magnetic resonance imaging (MRI) images are transmitted to CNN, and then the output is used as new input for FKKM. The dataset used in this research consist of MRI images taken from someone who had lung cancer with the treatment of anti programmed cell death-1 (anti-PD1) immunotherapy in 2016 that obtained from the cancer imaging archive. The proposed method obtained accuracy, sensitivity, precision, specificity, and F1-score 100% by using radial basis function (RBF) kernel with sigma of $\{10^{-8}, 10^{-4}, 10^{-3}, 5\text{x}10^{-2}, 10^{-1}, 1, 10^{4}\}$ in 20-fold cross-validation. The computational time is only taking less than 10 seconds to forward dataset to CNN and 3.85 ± 0.6 seconds in FKKM model. So, the proposed method is more efficient in time and has a high performance for detecting lung cancer from MRI images.

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1. INTRODUCTION

One of the cancer types that being the main lead of mortality worldwide is lung cancer. According to the World Health Organization (WHO) publication in 2015 lung cancer has claimed 1,676,000 lives worldwide, and this number is predicted to continue to grow to 2,779,000 deaths is 2030 [1]. According to data held by WHO, in Indonesia, the leading cause of death in men is lung cancer, whereas in women lung cancer ranks number four in the causes of death most [2]. This shows us that lung cancer is a disease that needs to be identified early so that appropriate treatment measures can be taken to prevent the development of these deadly cells and will directly increase the survival rates.

Currently, there are many accepted clinical methods for diagnosing lung cancer, one of which is medical images (magnetic resonance imaging scans). Doctor and medical specialist (radiologist) are used magnetic resonance imaging (MRI) to establish the possibility of the present of cancer in the lungs of a patient [3]. After obtaining the medical images, the correct diagnose of lung cancer is one of the primary challenging tasks, however, even the experienced radiologist cannot correctly tell malignancy from benign in some cases, because lung nodules are so complex [4]. The goal is to classify whether a lung cancer or not, so the patient should be treated as soon as possible. In short, it is a binary classification problem and can be resolved by various machine learning methods that can greatly assist radiologist [5].

In the last years, convolutional neural network (CNN) is a dominant method that improved accuracy in different computer vision task including medical images [6]. Garnier *et al.* [7] used CNN as automatic diagnostics of tuberculosis. Barros *et al.* [8] segmented subarachnoid hemorrhage and Chin *et al.* [9] detected ischemic stroke using CNN. Based on their research, CNN produces good work performance with an accuracy of more than 90%. Kaur *et al*. compared the accuracy of CNN and support vector machine (SVM) in diagnosing ovarian cancer, CNN obtained the highest accuracy, which was 98.8% when SVM was only 85.01% [10]. Then, the compound of CNN and the distinct methods have been expanded [11] and the combination of CNN with the robust classifiers such as SVM [12]. In this study, we proposed a compound of CNN and fuzzy kernel k-medoids (FKKM) for lung cancer detection. The previous studies, FKKM adjusted for anomaly detection propositions [13], classify cancer [14], and classify multiclass multidimensional data [15]. Thereupon, our proposed method is feasible to use, CNN for the feature extraction and FKKM for lung cancer classification model. This study is arranged as follows: first section provides background of details, while the second specifies data and research method used. Along with the proposed method in third section, result and analysis were discussed in fourth, and finally, conclusions in fifth section.

2. RESEARCH METHOD

2.1. The dataset

The dataset in this research consist of MRI images of someone who affected by lung cancer with the treatment of anti-PD1 immunotherapy in 2016 that obtained from the cancer imaging archive [16]. The data obtained were 400 MRI images that were still mixed between normal lung conditions and those that had cancer cells. Please note that the MRI image consists of three dominant colors, namely: 1) black color that indicates the part of the organ that contains air, 2) white color as shows the part of the organ that contains solids such as bone, 3) gray color indicates the part of the organ that has blood.

We manually labeled the data, there are 150 normal lung images and 250 lung cancer images. Starting from Figure 1, there is a circle that is distinguished based on four colors to find out the parts of the human body, namely: 1) For the red circle is the lung organ; because the lungs are like air sacs and are air-filled organs, the MRI image will look black, 2) For the orange colored circle is the heart organ; because the heart is an organ that contains muscle cells and blood, the MRI image will look gray, 3) For green and blue circles are bones where green circles are the backbone and blue circles are ribs or ribs; because bones contain solids, the MRI image will look white.

Next is Figure 2 which shows one sample of MRI image data from lung cancer: 1) For the red circle is lung cancer because lung cancer contains cancer cells and blood, the MRI image will look gray. When seen in Figure 2 cancer cells have grown in the lung organs, so that the color of the lung organs which was initially seen on the MRI image is black, now covered with the color of lung cancer that is gray. 2) For the orange colored circle is the heart organ, because the heart is an organ that contains muscle cells and blood, the MRI image will look gray, if seen in Figure 2 cancer cells have spread to the lungs and began to push the heart organ. 3) For green and blue circles are bones where green circles are the backbone and blue circles are ribs or ribs. Because bones contain solids, the MRI image will look white.

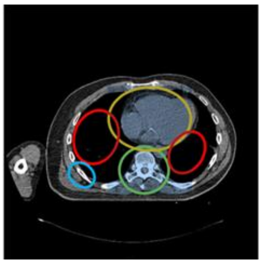

Figure 1. Sample of normal lung MRI image

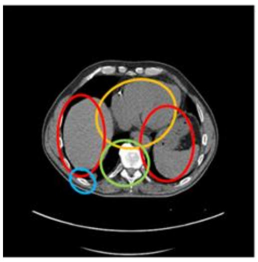

Figure 2. Sample of lung cancer MRI image

2.2. CNN

CNN as one of types of deep neural network is a result of the development of multilayer perceptron (MLP). CNN and MLP have differences; CNN utilizes convolutional, unification, and non-linearity layers [17]. The benefit can be utilized to detect and recognize all aspect of image. CNN consist of 2 stages, namely feature learning (convolutional layer and pooling layer) and trainable classifier (fully connected neural networks) [18].

In this research, we construct the architecture that consist of convolutional layer, pooling layer, activation function, and normalization layer by using keras, as a library. For the activation function, ReLU is utilized as a fast computation contrasted to distinct activation functions like sigmoid and tanh functions [19]. Moreover, for narrowing the input images size by extracting the information, we utilized maximum pooling [20]. As preventing model diverge is important, we did normalization layer after that too. Lastly, dropout with rate of 0.2, implies 80% of the information of each image is guarded. The result of the dropout layer's neuron is flattened as the vector form's length of 6272 on each image.

2.3. Fuzzy k-medoids

Fuzzy k-medoids is way of executes fuzzy clustering to generate the affiliation degree of every cluster then use k-medoids to discover the cluster centre [21]. Let a set of data $\mathbf{X} = \{x_1, x_2, \ldots, x_n\}$, where $x_j \in \mathbb{R}^d, j = 1,2,\ldots,n$, the diversity among object x_i and x_j is signify by $r(x_i, x_j)$. Let $\mathbf{V} = \{v_1, v_2, \ldots, v_c\}$ as medoid set, $v_i \subset \mathbb{R}^d$ and $v_i \in \mathbf{X}$ deputize a subset of $\mathbf{X}$ with cardinality c, along with $\mathbf{X}^c$ deputize the set of all c–subsets $\mathbf{V}$ of $\mathbf{X}$, the diversity among data points x_j and medoid v_i where $v_i \in \mathbf{V}$ is signify by $r(x_j, v_i)$. Let $\mathbf{U} = [u_{ij}]$, where $1 \leq j \leq n, 1 \leq i \leq c$, u_{ij} deputizes the fuzzy or affiliation of x_j in cluster i. The affiliation model is computed as written in (1),

$$u_{ij} = \frac{r^b(x_j,v_i)}{\sum_{k=1}^{c} r^b(x_j,v_i)}, \tag{1}$$

where $1 \leq j \leq n, 1 \leq i \leq c$ and fuzziness degree is signified by m where $b = -\frac{1}{m-1}$. The fuzzy k–medoids algorithm minimizes as seen in (2),

$$J(\mathbf{U}, \mathrm{V}) = \sum_{j=1}^{n} \sum_{i=1}^{c} {u_{ij}}^m r(x_j, v_i), \tag{2}$$

where the minimization is performed over all $\mathbf{V}$ in $\mathbf{X}^c$.

Algorithms of fuzzy k-medoids are as follows [22]:

```
Step 1    Rectify the clusters number of $c$;
Step 2    Opt the initial medoids set of $\mathbf{V} = \{v_1, v_2, \ldots, v_c\}, \forall v_i, 1 \leq i \leq c$ from in $\mathbf{X}^c$;
Step 3    Repeat:
              Tally value of affiliations $u_{ij}$ (2);
              Spot $\mathbf{X}_{(p)i}, i = 1,2,\ldots,c$. $\mathbf{X}_{(p)i}$ as the subset where the set of $p$ objects in $\mathbf{X}$ accord to the top $p$ highest affiliation values in cluster $i$;
              Hold the influx medoids $\mathbf{V}^{\text{old}} = \mathbf{V}$;
              Tally the new value of $v_i \in \mathbf{V}$ by $v_i = x_q$ where $1 \leq i \leq c$;
              $q = arg \min_{x_k \mathbf{X}_{(p)i}} \sum_{j=1}^{n} \sum_{i=1}^{c} {u_{ij}}^m r(x_k, x_j)$;
              $\text{iter} = \text{iter} + 1$;
          Till $\mathbf{V}^{\text{old}} = \mathbf{V}$ or $iter = MAX\_ITER$.
```

2.4. Fuzzy kernel k-medoids

Kernel is used for fuzzy k-medoids to surmount the possibility of linear data inseparability, the major idea of kernel function is altering the dataset into feature space that dimension is higher than data space [23]. However, acquiring is very tough in high dimensional data where clouting the computational tab and made an overfit, but utilizing "connector" among data space and feature space can assist the issues also good performance for the classification sine headlong laboring in the feature space [13]. Let ϕ is a non-linear mapping out of input data space $\mathbb{R}^d$ to feature space F. Discover the range among converted data $\phi(x)$ and $\phi(y)$, where x, y are objects at data space sine wotting explicit form of ϕ with kernel function of K as written in (3) [24].

$$\begin{aligned} d^2\big(\phi(x), \phi(y)\big) &= \|\phi(x) - \phi(y)\|^2. \\ &= \phi(x)^t \phi(x) - 2\phi(x)^t \phi(y) + \phi(y)^t - \phi(y). \\ &= K(x,x) - 2K(x,y) + K(y,y). \end{aligned} \tag{3}$$

Utilized kernel function for this study is Gaussian radial basis function (RBF) with $K(x,y) = \exp\left(-\frac{\|x-y\|^2}{\sigma^2}\right)$ and p_o–th degree polynomial with $K(x,y) = (x^t y + 1)^{p_o}$. Let $K_{ij} = K\big(x_j, v_i\big) = d(x_j, v_i)$ is utilized for compute the range among x_j and v_i, this will supersede the diversity function of fuzzy k–medoids. Fuzzy kernel k-medoids is a merge method of fuzziness degree, fuzzy k-medoids, and kernel. Fuzziness degree (m) at every iteration is computed as (4),

$$m = m_i + \frac{t}{T}(m_j - m_i)\,)\,, \tag{4}$$

where m_j is initial value and m_i end value of m, t is the contrarily of iteration and T is the max amount of iteration.

Algorithm of fuzzy kernel k-medoids are as follows [25]:

```
Step 1  Input $\mathbf{X}, c, m_i, m_j, \varepsilon, T$;
Step 2  Opt the initial set of medoids $\mathbf{V} = \{v_1, v_2, \dots, v_c\}, \forall v_i, 1 \le i \le c$ from in $\mathbf{X}^c$;
Step 3  Towards $t = 1$ to $T$;
            Tally value of fuzziness degree $m$ (4);
            Tally value of affiliations $u_{ij}$ (2);
            Tally value of medoid of $v_i \in \mathbf{V}$ by $v_i = x_q$ where $1 \le i \le c$;
            $q = arg \min_{x_k \mathbf{X}_{(p)i}} \sum_{j=1}^{n} \sum_{i=1}^{c} {u_{ij}}^m r(x_k, x_j)$;
            If $\sum_{k=1}^{c} K^2(v_i t, v_{it-1}) \le \varepsilon$ then halt.
            Otherwise $t = t + 1$.
```

3. THE PROPOSED METHOD

The modeling is applied to Tensorflow, a package framework that supports the machine in the preparing of image data. Furthermore, the MRI image data is classified with the proposed method, we used hybrid CNN-FKKM as a combing model. The performance method was evaluated with accuracy, sensitivity, precision, specificity, F-score and running time. The flow chart of proposed method that was formed and used in this study is shown in Figure 3, along with the summary of the CNN architecture used is shown in Figure 4. This summary includes the number of layers obtained and the output shape, as well as the number formed needed. In Figure 3, we utilized all of 400 labeled images, with 1 towards lung cancer and 0 towards normal lung. The images are resized to the same size of 152x152 pixels and then we examined the input into CNN architecture as Figure 4. Next, the input is forwarded to set of CNN layers as explained in Figure 4. The output was a vector with length 6727, so we had matrix of 400x6272. After that, we divided the matrix data into two datasets as training and testing. Training set is used to train the model which in this research we used FKKM, follow with testing set to validate the model. Lastly, based on the predicted model, we got the predicted class of every data point. The filter size that used in this paper is 3x3 in every convolutional layer, it refers to the previous research that resulted that the small size of filter will help in increasing the accuracy [26].

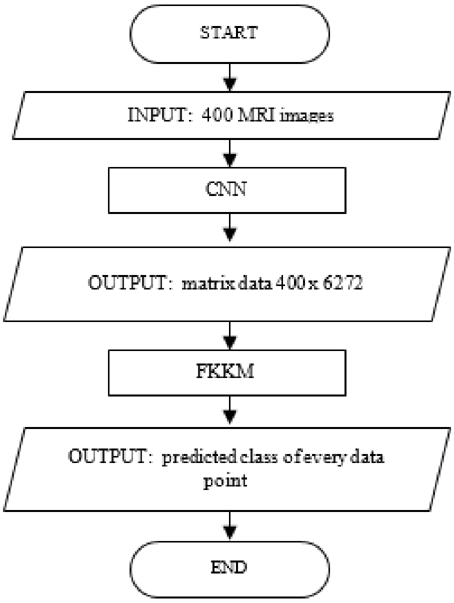

Figure 3. The proposed method

Figure 4 shows the summary of the CNN Architecture Used, starting with input values of 152x152x1. Furthermore, at the convolutional operation stage, five convolutional layers are used. The first layer uses 32–3×3 filters (the value of 32 here means the number of filters used in the 3×3 matrices). Follow with the second layer uses 64–3×3 filters, the third layer uses 96–3×3 filters, the fourth layer uses 64–3×3 filters, and lastly, the fifth layer uses 32–3×3 filters. This proceeds by reducing the size of the Feature Map's or dimension obtained, using the pooling layers. In this model, a max pooling measuring 2×2 was used, which was placed after all the convolutional layers. Due to the pooling layer's use as max pooling with a 2×2 matrix, the largest value was obtained, which create a new feature map. The result or the most recent feature map obtained was reconstructed by flattening and turning it into a one-dimensional array then finally the output.

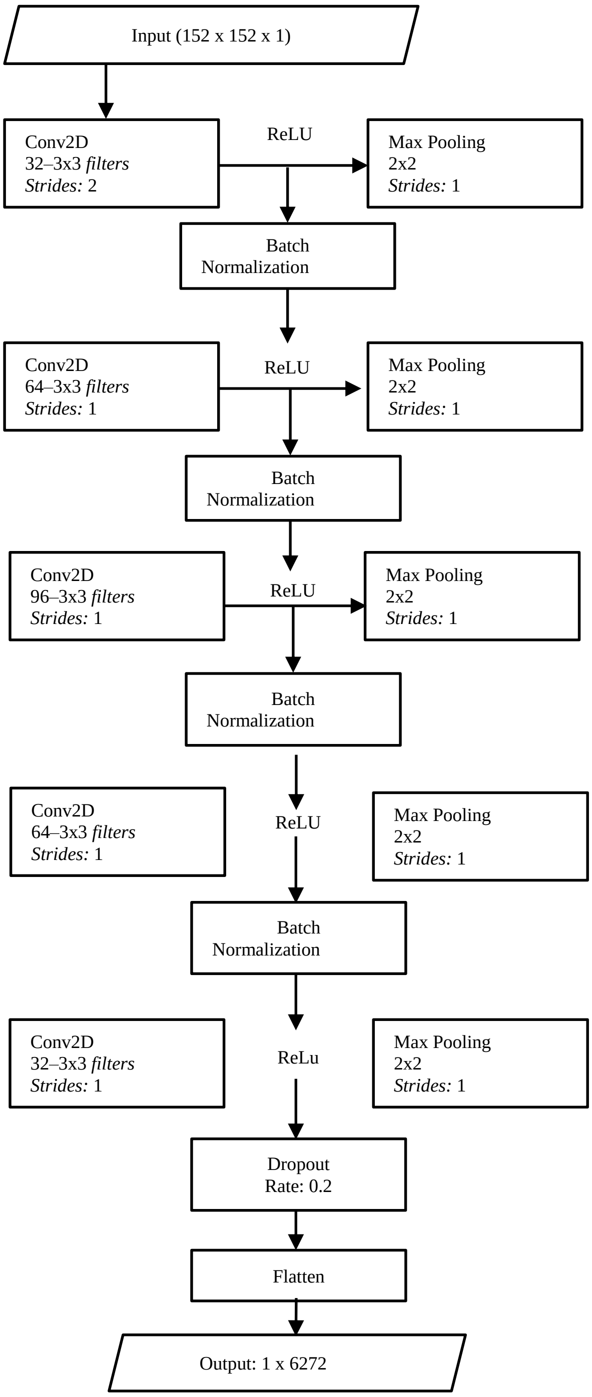

Figure 4. The CNN architecture

4. RESULTS AND ANALYSIS

MRI images processed on CNN for the result of matrix data as we enhanced label in each row as 1 for lung cancer and 0 for normal lung. Table 1 represents us the matrix input that we utilized as the new input for FKKM. As using the matrix data in FKKM based on RBF kernel on 20-fold cross-validation, the performance of this hybrid method is evaluated, as shown in Table 2.

Given some sigma as we can see in Table 2, it was obtained that all sigma delivered the highest performance measure. Almost all the sigma gave 100% of accuracy, specificity, sensitivity, precision, and F1-score. As RBF kernel function with sigma of 1 was one of sigma that produced the highest performance measure, we will evaluate values of k in k-fold cross-validation such as k=12, 14, 16, 18, and 20 to see its behavior, as shown in Table 3.

Table 3 shows us the performance of other k-fold cross-validation that is obtained by CNN–FKKM on RBF kernel function with sigma of 1, we obtained that 20-fold cross validation produced the highest performance measures. The computational time of our proposed method needs less than 10 seconds for forwarding the MRI images to the CNN and 3.85 ± 0.638961 seconds on average running the FKKM. The proposed method that we used is more efficient in time than the deep learning CNN model only for classification with the number of epochs and batch sizes. Then, the performance measures are also competing with several deep learning methods.

Table 1. Matrix input

Data	y_1	y_2	…	y_{6271}	y_{6272}	y
x_1	5.96E-07	4.77E-07	…	7.15E-07	1.53E+00	1
x_2	9.53E-07	1.31E-06	…	2.62E+00	2.00E+00	1
…	…	…	…	…	…	
x_{399}	0.00E+00	7.15E-07	…	2.60E+00	2.04E+00	0
x_{400}	0.00E+00	8.34E-07	…	2.03E+00	230E+00	0

Table 2. The performance of 20-fold cross-validation of CNN-FKKM based on RBF kernel function

σ	Accuracy	Sensitivity	Precision	Specificity	F1-Score
10^{-8}	100	100	100	100	100
10^{-4}	100	100	100	100	100
10^{-3}	100	100	100	100	100
5×10^{-2}	100	100	100	100	100
10^{-1}	100	100	100	100	100
1	100	100	100	100	100
10	96.88	100	92.31	95	96
10^2	96.88	100	92.31	95	96
10^3	96.88	100	92.31	95	96
10^4	100	100	100	100	100

Table 3. The performance of k-fold cross-validation of CNN-FKKM based on RBF kernel function with sigma of 1

k	Accuracy	Sensitivity	Precision	Specificity	F1-Score
12	37.50	100.00	37.50	0.00	54.55
14	81.25	66.67	80.00	90.00	72.73
16	59.38	75.00	47.37	50.00	58.06
18	87.50	66.67	100.00	100.00	80.00
20	**100.00**	**100.00**	**100.00**	**100.00**	**100.00**

5. CONCLUSION

Detecting the lung cancer from the MRI images is a challenging task. Considering the deep learning method, especially CNN, as the reliable method in image classification, we proposed the novelty by building hybrid model based on combining CNN with FKKM for lung cancer detection by using 400 MRI images that taken from someone affected by lung cancer with the treatment of anti-PD1 immunotherapy in 2016 that obtained from the cancer imaging archive. The proposed method obtained accuracy, sensitivity, precision, specificity, and F1-score 100% when using RBF kernel function with sigma of $\{10^{-8}, 10^{-4}, 10^{-3}, 5x10^{-2}, 10^{-1}, 1, 10^{4}\}$ in 20-fold cross-validation. The computational time is only taking less than 10 seconds to forward dataset to CNN and 3.85 ± 0.6 seconds in FKKM model. From our experiments, it was concluded that our proposed method has more efficient in time computation and also delivers competing accuracy with the other deep learning methods.

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