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# Implementation of CRNN Method for Lung Cancer Detection based on Microarray Data

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*Abstract*—Lung Cancer is one of the cancer types with the most significant mortality rate, mainly because of the disease's slow detection. Therefore, the early identification of this disease is crucial. However, the primary issue of microarray is the curse of dimensionality. This problem is related to the characteristic of microarray data, which has a small sample size yet many attributes. Moreover, this problem could lower the accuracy of cancer detection systems. Various machines and deep learning techniques have been researched to solve this problem. This paper implemented a deep learning method named Convolutional Recurrent Neural Network (CRNN) to build the Lung Cancer detection system. Convolutional neural networks (CNN) are used to extract features, and recurrent neural networks (RNN) are used to summarize the derived features. CNN and RNN methods are combined in CRNN to derive the advantages of each of the methods. Several previous research uses CRNN to build a Lung Cancer detection system using medical image biomarkers (MRI or CT scan). Thus, the researchers concluded that CRNN achieved higher accuracy than CNN and RNN independently. Moreover, CRNN was implemented in this research by using a microarray-based Lung Cancer dataset. Furthermore, different dropout values are compared to determine the best drop-out value for the system. Thus, the result shows that CRNN gave a higher accuracy than CNN and RNN methods achieved 83% and 71% accuracy, respectively.

Keywords-Microarray data; lung cancer; classification; deep learning.

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#### I. INTRODUCTION

Cancer is one of the most significant causes of death worldwide. This fatal disease could attack everyone, regardless of their age. The data from IARC in 2020 shows that the number of people with cancer worldwide has increased to 19.3 million patients with 9.9 million deaths [1]. In 2020, the following kinds of cancer will be most prevalent: With 2.26 million instances of breast cancer and 2.21 million cases of lung cancer, respectively. Moreover, the highest cause of cancer was Lung Cancer, with 1.80 million deaths [2].

A new coronavirus known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) began spreading the coronavirus disease at the close of 2019 (COVID-19). As of March 2022, the number of COVID-19 cases has reached over 440 million worldwide. Moreover, 33% of COVID-19 patients were reported to suffer acute respiratory injury, acute respiratory distress syndrome, and severe pneumonia after they were infected by the virus [3]. The outbreak of coronavirus disease is also impacting people with Lung Cancer. Patients with lung cancer are vulnerable to infection

by the SARS-CoV-2 virus, leading to a higher mortality rate. It also discussed that several essential genes for SARS-CoV-2 infection engage in tumorigenesis, which describes the relationship between Lung Cancer and Covid-19 [4]. Thus, the coronavirus disease spread could increase Lung Cancer patients' mortality rate.

The delayed diagnoses of the patients cause a high cancer fatality rate, so the chance of the patient's recovery decreases. Therefore, it is vital to carry out early cancer detection to be given the appropriate treatment. There are some methods to detect cancer; blood tests, ultrasonography (USG), pap smear, endoscope, and DNA microarray. A glass plate with hundreds to thousands of DNA genes is called a microarray. DNA microarray is used as a cancer predictor by examining the gene expression of the genes that cancer attacks[5]. Furthermore, the analysis uses two classes of DNA: the normal genes and the attacked genes. The DNAs are separated and given different fluorescence hues. Additionally, each DNA will emit a different color based on the assigned color [6].

The main challenge of microarray is the curse of dimensionality problem. Microarray is known to have a small

sample number yet extensive feature quantity. Thus, selecting the most valuable features is the key in this field. Many researchers conducted research intending to minimize the data dimension to improve the classification performance [7]. The research of microarray data started in 1997 and continues to develop today. It was challenging to conduct research based on this microarray data because of the limited data and integration. One website that provides microarray data publicly is ONCOMINE [8]. This web-based database was built to systematically perform analyses and provide all available microarray data. The ease of accessing microarray data is the thing that triggers the development of research on cancer detection, one of which is using the classification method.

In classifying cancer cells, many machine learning algorithms can be applied to process data in which the sample is significantly lower than the number of genes. One of the machine learning methods is the deep learning strategy. The Convolutional neural network (CNN) is a part of the deep learning strategy, which imitates our brain function in processing information [9]. Based on previous research [10]–[14], Convolutional Recurrent Neural Network (CRNN) is used to build a Lung Cancer detection system, using medical image biomarkers (CT scan or MRI) as the dataset. Therefore, CRNN is used in image processing in general. The research concluded that CRNN gives higher accuracy than CNN and RNN independently.

Zeebare et al. [9] conduct research to build cancer detection using the deep learning method. The Convolutional Neural Network (CNN) technique was employed in this study. The research used ten different cancer datasets; one is Lung Cancer data. Furthermore, the proposed method's output is contrasted with the output of the SVM-RFE technique. This research concluded that the suggested approach was more precise than the alternate approach. Moreover, the Lung Cancer classification result yielded an accuracy of 72.09%.

Chowdhury et al. [15] proposed a Recurrent Neural Network-based feature selection method. The gene classification on the high dimension, small sample size data is improved by this technique. Furthermore, the researchers used two cancer datasets, Colon Tumor, and Leukemia. This paper concluded that the model performs better in selecting the features subset in some cases. Daoud and Mayo [16] researched to survey the neural network methods for cancer detection. Furthermore, the papers that were reviewed in the research were published from 2013 until 2018. This research concludes that future researchers should choose different network parameters and combine two or more presented approaches.

Khoirunnisa and Adiwijaya [17] conducted research to overcome the overfitting problem of Logistic Regression. The research proposed a new technique combining minimum Redundancy Maximum Relevance (mRMR) and Modified Logistic Regression for data reduction and data classifier. We modify the logistic regression method by including a term in the cost function, and the over-fitting issue is resolved. Moreover, the system gave an average accuracy of 93.33%.

Shah et al. [18] proposed a machine-learning method to improve unstructured data processing. The approach uses a hybrid deep learning model built on a convolutional neural network with a Laplacian score (LS-CNN). This research concluded that LS-CNN could improve the accuracy of cancer detection systems. Additionally, this technique could be applied to multi-class image datasets to achieve greater precision.

In 2021, Iqbal et al. [19] used deep learning long short-term memory (LSTM) and Residual Net (ResNet – 101) to build a cancer detection system. Moreover, the cancer dataset used in this research is the prostate cancer dataset. The suggested approach's results are contrasted with several established machine learning techniques, including Naive Bayes, Decision Tree, SVM Gaussian, KNN-Cosine, and RUSBoost Tree. Furthermore, the research of the proposed methods produced optimal results.

Sori et al. [20] researched deep learning to build a cancer detection system. Moreover, the proposed method in this research is "denoising first" two-path convolutional neural network (DFD-Net). The data used in this research is the CT scan image of the lung. Furthermore, the result of the system is compared with the result of DFD-to, DFD-f, and DFD-s methods. This research concluded that DFD-Net gave better accuracy, sensitivity, and specificity than the others.

In 2021, Jiayi Lu et al. [13] used Convolutional Recurrent Neural Network (CRNN) to build a detection system using publicly available lung tumor 4DCT images. Moreover, this research concluded that CRNN is comparable to the existing deep learning methods for 4DCT images in computation time and system accuracy.

In this paper, instead of using image data from CT scans or MRI, we use the CRNN to build a Lung Cancer detection system based on microarray classification. The dataset that is used in this research is a microarray Lung Cancer dataset, which consists of the gene expression of the observed patients. As a comparison, two other deep learning methods, Convolutional Neural Network (CNN) and Recurrent Neural Network (RNN), are also used. The result of each method will be compared so that the best method for Lung Cancer detection can be determined.

## II. MATERIALS AND METHOD

The overview of the cancer detection system of this research is illustrated in Fig. 1. The system consists of preprocessing the datasets, splitting the dataset, proposing method model building, classification, and system evaluation. The dataset of this research is preprocessed using normalization so that the data would be easier to process by the Machine Learning methods. The preprocessed data will be split into data training and data testing by using a certain proportion. Furthermore, the proposed method model will be built by using the training data, while the testing data will be used to test the model. Finally, the evaluation of the system will be conducted by calculating the system's accuracy.

Generally, CRNN is used in building a Lung Cancer detection system using medical image biomarkers (MRI or CT scans). Meanwhile, CRNN is implemented in this research by using Lung Cancer dataset based on microarray data. Microarray data is a representation of the gene expression of observed patients.



Fig. 1 System Design.

Furthermore, the configuration of CRNN is illustrated in Fig. 2. The proposed method uses two convolution layers and pooling with sequential configuration. Moreover, the input data will be passed to the layers sequentially. The method would be more successful in reducing the unimportant features so that the classification method (RNN) will only accept the essential features.



Convolutional

Lave

Fig. 2 CRNN Configuration on the Proposed Method [21]

CNN

#### A. Dataset

This research uses Lung Cancer Dataset from the Kent-Ridge repository [22]. The dataset consists of 181 records and 7129 features. The term "records" expresses the number of patients observed, while "features" expresses the number of gene expressions of each record.

### B. Convolutional Neural Network (CNN)

Pooling Layer

CNN is a feed-forward network that involves various combinations of convolutional layer, pooling layer, and dense

(fully connected) layer where the convolutional layer is connected to a small part of the previous layer named filter [23], [24]. The filter is used to obtain interrelated and correlated spatial information. In many cases, the filter size is relatively small, for instance,  $3 \times 3$  or  $5 \times 5$  [25].



CNN is a deep learning strategy that processes information by mimicking our brain function. CNN can deal with insufficient data and improve classification performance. This method is also powerful in processing the cancer dataset that is strongly linked. Thus, the performance of data classification could be improved [9]. The standard architecture of CNN can be seen in Fig. 3. It shows that CNN has three main layers: the convolutional layer, the pooling layer, and the dense layer. The layers that play a role in the feature extraction process are the convolutional and pooling layers [25].

### C. Recurrent Neural Network (RNN)

RNN is one of the deep learning-based classification methods that could model sequence data and capture longterm dependencies [26]. Unlike traditional neural network methods, RNN could process the input sequence using the memory (internal state). While other neural networks have independent inputs, the inputs of RNN are related. Moreover, the structure of RNN can be seen in Fig. 4.



Fig. 4 Neural network structure in the RNN [21].

First, RNN takes from the input sequence and then outputs, which are used as the next step. The outputs are then used together with the input in the next step. This way, it keeps the context in mind when training the network.

The formula used in the current state is:

$$h_t = f(h_{t-1}, x_t).$$
 (1)

Moreover, activate the activation function using the formula:

$$h_t = \text{ReLU} \left( W_{hh} h_{t-1} + W_{xh} x_t \right) \tag{2}$$

W is the weight, then h is the vector of the hidden layer,  $W_{hh}$  is the weight of the previously hidden layer,  $W_{xh}$  is the weight at the current input state, **ReLU** is an activation function, which applies non-linearity pressing activation to the range  $[0, \infty]$ . The activation function, threshold function, or transfer function transforms the activation level of a neuron (unit) in the output signal [27]. The ReLU function easily works by setting the value at 0, i.e.,  $f(x) = \max(0, x)$ . To put it simply, when x < 0, it yields 0 and vice versa, which results in a linear function when  $x \ge 0$  [28] looks like equation (3):

$$ReLU(x) = f(x) = \max(0, x)$$
(3)

Furthermore, the output layer is:

$$y_t = sigmoid(W_{hy}h_t) \tag{4}$$

 $y_t$  is the output state.  $W_{hy}$  is the weight on the output state and sigmoid is the activation function for the output layer. Sigmoid is a part of non-linear activation function mostly used in feed-forward neural networks. It is a finite differentiable real function, defined for the original input value, with a ubiquitous positive derivative and some degree of fluency [29]. The Sigmoid function is calculated using the formula:

$$f(x) = \frac{1}{1 + exp^{-x}}$$
(5)

The Sigmoid function is used in a multi-label model where it returns the probability of each class, the value above 0.5 to 1, and the other to 0, where 1 indicates the target class.

## D. Convolutional Recurrent Neural Network (CRNN)

CRNN uses Convolutional Neural Network (CNN) to do the feature extraction and Recurrent Neural Network (RNN) to summarize the extracted features[30]. RNN performs as the last layer, or CNN, to carry out the classification stages. RNN could accept data input that has multiple dimensions. Dissimilar to CNN, which has to do the padding method to uniform the data length across the entire dataset.

This research used CNN to obtain the important features from Lung Cancer data, improving the system performance. CNN is also used to reduce the computational time of the system.

The following is the algorithm from the CRNN that was built in this study:

- Data representation for CNN's input,
- Apply multiple filters and aggregate to capture contextual information and extract important features from each data,
- $x_t$  is the input in time step t. For example,  $x_t$  could be a one-hot vector corresponding to a sentence's second word.
- $h_t$  is the hidden state when step t. This is the "memory" of the network.  $h_t$  is computed from the input of current step, which together with the previous hidden state as we can see in equation 1. Generally, he functions f is nonlinear like tanh or ReLU. In equation 2, we use ReLU as a function  $f(h_{(t-1)})$ , is needed to compute the first hidden state as well as use the identity matrix for initializing weights.
- $y_t$  is the output in step t as we can see in equation 4.
- Repeat steps 1-5 until you reach the minimum error.

## E. System Evaluation

Evaluating a model is one of the essential things in building an effective classification system. There are several techniques to evaluate the model performance, including the confusion matrix. The confusion matrix is also called the error matrix. The confusion matrix compares the model's classification result to the actual classification result. The form of a confusion matrix is a table representing the classification model's performance in several testing data, where the actual value is known. Table 1 below is a confusion matrix with four combinations of different predicted and actual values.

Based on Table 1, 4 different terms represented the classification result in the confusion matrix. Therefore, the terms consist of True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). The explanation of each term is as follows.

*1) True Positive (TP)*: The positive data is predicted as positive. For example, a patient with cancer (class 1), and the model predicts that the patient has cancer (class 1).

2) *True Negative (TN):* The negative data is predicted as negative. For example, a patient without cancer (class 0) and the model predicted that the patient has no cancer (class 0).

3) False Positive (FP): The negative data is predicted as positive. For example, a patient without cancer (class 0) and the model predicted that the patient has cancer (class 1).

4) False Negative (FN): The positive data is predicted as negative. For example, a patient with cancer (class 1) and the model predicted that the patient has no cancer (class 0).

TABLE I Confusion matrix		
	Actual: 1 (Positive)	Actual: 0 (Negative)
Predicted:	TP	FP
1 (Positive)	(True Positive)	(False Positive)
Predicted:	FN	TN
0 (Negative)	(False Negative)	(True Negative

The accuracy of the system then being calculated by using equation (6):

$$accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$
(6)

### III. RESULTS AND DISCUSSION

The results of this study consist of two parts: the result of CRNN with different parameter values and the comparison between CNN, RNN, and CRNN. The proposed method of this research is Convolutional Neural Network (CRNN). The method is implemented by using different values of drop-out. Drop-out is one regularization method used in deep learning to overcome the overfitting problem [31]. Overfitting is a common problem of machine learning models. This problem happens when the model could perform well on training data but perform poorly on the test data. Moreover, the overfitting problem could lead to poor performance of the system.

The drop-out value represents the number of neurons that will not be used during the training process, where one means that there is no drop-out, while 0 means no output from the layer. Srivastava et al. [32] stated that the excellent value of drop-out is between 0.5 - 0.8. Furthermore, the value of drop-out used in this research is between 0.1 - 0.8. This wide range of values is selected so that the best value of drop-out can be concluded.

Table 2 shows that the best accuracy of the cancer detection system in this research is achieved when the dropout value is 0.5, with an accuracy of 91%. The result of CRNN is also compared with the result of RNN and CNN. Moreover, the result can be seen in Table 3. Table 3 shows that the classification process using CRNN gave higher accuracy than RNN and CNN.

TABLE II	

Drop-out Value	Accuracy	
0.1	86%	
0.2	89%	
0.3	86%	
0.4	86%	
0.5	91%	
0.6	81%	
0.7	81%	
0.8	83%	
Without handout	83%	

TABLE III	
RESULT OF RNN, CNN, AND	CRNN METHOD

Method	Accuracy
RNN	73%
CNN	81%
CRNN	91%

The table shows that using two convolution and pooling layers using a sequential configuration could optimize the selected features. Thus, the process in RNN will not be hampered because it does not have to process the features anymore. Moreover, CNN can handle the vanishing gradient problem in RNN, so it can be seen in Table 2 that the accuracy of CNN is higher than RNN.

#### IV. CONCLUSIONS

This research applies a deep learning Convolutional Recurrent Neural Network (CRNN) to classify the Lung Cancer dataset. The dataset consists of 181 records and 7129 features. Moreover, the result of the experiment is compared with the result of the CNN and RNN methods. The first experiment of CRNN is conducted to determine the best value of drop-out to be used in the process. Drop-out is a regularization technique that aims to prevent overfitting the CRNN model. Furthermore, the highest accuracy of 91% is obtained with a 0.5 value of drop-out. This fact shows that half of the neurons are not used during the process. The result also shows that the system's accuracy without drop-out yielded a lower accuracy of 83%, which means that the overfitting problem could be prevented by modifying the drop-out, and a higher system accuracy could be obtained.

The result of the proposed method is also compared with the result of CNN and RNN. It shows that CRNN gave the highest accuracy, which concludes that using two convolutional and pooling layers in CRNN could optimize the selected features. This research could be further developed by implementing the system on various cancer datasets. This research concluded that CRNN could handle the data with a small size yet a large number of attributes so that data with the same characteristic can also be implemented using CRNN.

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