

An Approach to Recognise Lung Diseases Using Segmentation and Classification

Prabakaran J¹, Selvaraj P^{2*}

¹*Department of Networking and Communications, Faculty of Engineering and Technology, College of Engineering and Technology, SRM Institute of Science and Technology, Chennai, Tamil Nadu 603203, India, prabakaj@srmist.edu.in*

²*Department of Computing Technologies, Faculty of Engineering and Technology, College of Engineering and Technology, SRM Institute of Science and Technology, Chennai, Tamil Nadu 603203, India, selvarap@srmist.edu.in*

Abstract: Lung cancer is one of the most common causes of death in people worldwide. One of the key procedures for early detection of cancer is segmentation or analysis and classification or assessment of lung images. Radiotherapists have to invest a lot of effort into the manual segmentation of medical images. To solve this issue, early-stage lung cancer is detected using Computed Tomography (CT) scan images. The proposed system for diagnosing lung cancer is divided into two main components: the first part is an analyser component built on the upper layer of the U-shaped Network Transformer (UNT), and the second component is an assessment component built on the upper layer of the self-supervised network, which is used to categorise the output segmentation component as benign or cancerous. The proposed method provides a powerful tool for the early detection and treatment of lung cancer by combining CT scan data with 2D input. Numerous experiments are conducted to improve the analysis and evaluation of the findings. Using the public dataset, both test and training experiments were conducted. New state-of-the-art performances were achieved with experimental results: an analyser accuracy of 96.9% and an assessment accuracy of 96.98%. The proposed approach provides a new powerful tool for leveraging 2D-input CT scan data for early detection and treatment of lung cancer using a variety of methods.

Keywords: Classification, segmentation, COVID, tuberculosis, prediction, pneumonia, lung cancer.

1. INTRODUCTION

Cancer is known as collection of related diseases. In many cancers, some parts of the body's cells begin to break down and spread to neighbouring tissues. The human body is made up of billions of cells. Tumours can develop anywhere in these cells. Human cells are constantly developing and shedding cells to make new cells according to their needs [1]. When old cells die, they are regularly replaced by new cells. But when cancer strikes, the process does not work as well as it should. Mature cells do not die and new cells are formed unnecessarily. The cells continue to divide without restriction and produce a growth in the body called a tumour. These tumours are regularly rigid and contain more mass. Malignancies of the blood, for example leukaemia, do not usually form aggressive tumours. Tumours can spread or attack the tissue near them, which is why they are called malignant [2]. In addition, when these tumours develop, some of the growth cells can rupture and move to distant parts of the body or into the blood or lymph nodes, forming new tumours that are far away from the tumour site. Except benign tumours are not similar to malignant tumours. They do not spread and do not affect the tissue surrounding them or the tissue in their vicinity [3]. After elimination, either by surgery

or additional treatment measures, the tumour does not return. This is in contrast to malignant tumours, which sometimes continue to grow after removal. Mild tumours are generally not serious, apart from mild tumours that occur in the brain. Mild brain tumours can be dangerous and still lead to death [4], [5].

Normal cell physiology consists of growth, division, and apoptosis of cells in a planned manner. When this physiological process becomes uncontrollable, the cells develop too rapidly and become a lump called a tumour. Tumours can be divided into two groups: benign and cancerous. While a benign tumour is confined to the site of growth and does not grow that fast, a malignant tumour basically has fast-growing cancer cells can spread away from the original site, attack surrounding tissue and also spread to different regions of the body, which is called metastasis. Early lung cancer detection is extremely useful as it prolongs survival as well as the appropriate stages of threat [6]-[8].

2. LITERATURE REVIEW

There are several types of computerised diagnostic systems for lung cancer. Some of these methods are discussed in this section. The authors [9] propose the use of Computer-Aided

Diagnosis (CAD), the recently urbanised mobile-category Computed Tomography (CT) scanner, which is mainly used to screen for lung cancer. In this novel Lung Cancer Screening CT (LSCT) method, one of the main consequences is to increase the amount of data to 30 images per person from X-ray films. To get around this, the authors are trying to significantly reduce the image data to present to clinicians using imaging techniques. The distribution of hybrid lungs in CT imaging for chest for CA analysis [10]. The projected system consists of three phases:

- In the first phase, the lungs and airways are unconnected by a growing reverse seed region and connected with component labelling.
- In the second phase, the airways and large airways are removed from the lungs by growing 3-dimensional regions.
- In the final phase, the correct lung boundary is determined by eliminating the results of the second phase from the first.

The urbanised computer-based analytic circuitry is based on the architecture of a two-dimensional Artificial Neural Network (ANN). The original ANN identifies suspicious areas in low-resolution images [11]. The inputs provided by the second ANN are curved peaks measured for each pixel in each suspect area. This is evidenced by the fact that even tiny tumours have a recognisable signature in the space of the vertebral peak, with the curve being the centre of the image information at which time was looked out, this is an auxiliary record. The output of the network is set to a certain level to provide an optimistic identity. A computerised method for diagnosing lung cancer is based on helical CT imagery. This method will both reduce time and increase diagnostic certainty. The system includes the phase of examination and the phase of identification. In the phase of lung and 27 vascular analyses, the lungs were extracted and the features of these areas were examined with imaging techniques [12]-[14]. In the diagnosis phase, diagnostic rules are characterised by features and tumour regions are identified based on these diagnostic rules.

The computerised diagnostic system to assist in the relative reading of lung cancer depends on CSV imaging. This work provides a novel and automated system for the detection of early-stage lung cancer based on a computerised scanning system that reads all CT images. In addition, the CAD scheme is equipped with features that identify doubtful parts of the chest CT images and provide comparable reports. The segmentation algorithm has been used in this way to compare individual images from current and previous CT scans and interfaces to characterise suspect areas [15], [16].

The proposed work offers a number of extra benefits over other innovative works by providing a complete system for lung cancer analysis and also for diagnosis through assessment head. Most innovative work focuses on only one task, usually a classification or segmentation assignment. In the proposed study, the two objectives are combined to provide a comprehensive system for prior identification of lung cancer. The proposed model will make a significant contribution to the early detection of lung cancer as well as mitigating the circumstances. The proposed model will also help medical professionals and specialists to plan radiation therapy.

A. Motivation of the work

To distinguish between benign and cancerous nodules, detection methods for lung cancer based on computerised technique need to analyse the imaging properties of lung nodules in CT images.

Building an autonomous segmentation system is becoming increasingly important for early lung cancer diagnosis. It is very challenging to build such a system using traditional approaches.

Deep learning-based architectures have seen substantial growth in recent years and have been used extensively in the healthcare industry.

Therefore, the main objective of this work was to develop a reliable and accurate 2D-segmentation method for lung cancer.

B. Objective of the work

The primary objective of this work is to build an advance detection of lung disease.

To achieve this objective, the proposed model divides the system into two parts, namely analyser head and assessment head for lung cancer segmentation.

The rest of this article is divided as follows: The different components of the proposed model used for early detection of lung cancer are described in detail in section 2. The experiments carried out to add to the created model are all described in section 3. The discussion on the proposed model is explained in section 4 and section 5 provides a summary of the model.

3. PROPOSED SYSTEM MODEL

A. Analyser head

The analysing section is an earlier proposal by the author [25], which is a combination of a U-shaped network and transformers. To successfully record information at multiple scales globally and explore successive representations of the input data set, this network uses a transformer for the encoding technique. Both the encoding and decoding procedures are developed using this network. To determine the final result of the semantic analyser head outcome, the transformer in the encoder is directly connected to a decoder in different resolutions via hops. The encoder in the U-shaped Network Transformer (UNT) is built from a heap of transformers. Both the decoder units and the encoder unit are connected by hop networks in a design of shrinking and expanding. Transformers have been used extensively in natural language processing. Transformers work with a 1D input array. The input information is:

$$X \in Res^{ch \times h \times w}$$

where ch represents the number of channels,

$$X_p \in Res^{n \times (PT^3 \cdot ch)}$$

where every resolution of the patch is denoted by

$$(PT, PT, PT), N = (h \times w \times d) / PT^3$$

A linear layer is then used to project the patches onto a K -dimensional anchoring space that is continuous across all transformer levels. The approach incorporates a 1D learnable, positional, embedding E_{pos} that allows the retention of the geographic data of the retrieved patches:

$$Z_0 = [x_v^1 E, x_v^2 E, \dots, x_v^N E] E_{pos} \quad (1)$$

The transformer blocks consisting of Multi-head Self-Attention (MSA) and Multilayer Perceptron (MLP) sub-layers are then applied after the embedding layer. Equations (2) and (3) define MSA and MLP , respectively:

$$Z'_i = MSA(Norm(Z_i - 1)) + Z_i - 1, i = 1 \dots L \quad (2)$$

$$Z_i = MLP(Norm(Z'_i)) + Z'_i, i = 1 \dots L \quad (3)$$

The $Norm$ indicates normalisation of the layer. The MLP is composed of $Z \in R^{n \times k}$ and is learned with a parameterised function known as the SA block. Comparing two entries in z and their key-value pairs yields the attention weights (A), as shown in (4):

$$A = softmax \frac{QK^T}{\sqrt{K_h}} \quad (4)$$

where $K_h = K/n$ acts as a scaling factor to keep the key's values, which use the estimated attention weights, at a constant value. For v values in sequence z , the output of the SA layers is determined as in (5):

$$SA(z) = Av \quad (5)$$

Here v represents the values in the input sequence and a scaling factor, $K_h = K/n$ is used. In addition, the output of MSA is evaluated as in (6):

$$MSA(z) = [SAL_1(z); SAL_2(z); \dots; SAL_n(z)] w_{msa} \quad (6)$$

where the values of the weights of the different parameters that can be trained are reflected in w_{msa} . The developed architecture of the UNT model for lung cancer segmentation is shown in Fig. 1 below.

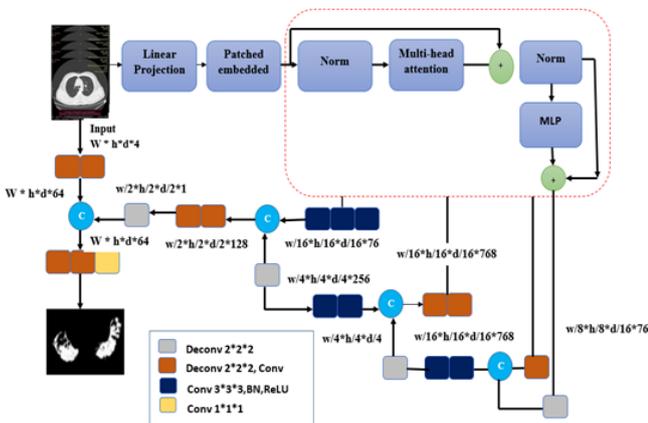


Fig. 1. The analyst head of UNT architecture during segmentation.

B. Assessment head

The output of segmentation is given to the classification head, which categorises the input data as benign or cancerous module, ensuring early identification of cancer cells in the lung. The proposed identification system's classification procedure was carried out using the "self-supervised neural network". This architecture provides a state-of-the-art, point-to-point, self-supervised categorisation training approach. To optimise same-class prophecy of two augmented views of the same sample, the Self-Classifier synchronously learns both labels and representations in a single stage point-to-point process. A theoretically motivated cross-entropy loss differentiation with a uniform prior for the projected labels is used to ensure non-degenerate solutions.

Attention to the self-supervised pictorial representation acquisition has increased recently. To learn representations with semantic meaning without the aid of human-annotated labels, a pretext job must be defined and finished. Even without annotations labels, it is possible to study useful patterns. A smaller dataset is then refined to apply the newly learnt patterns to subsequent tasks. Contrastive learning mind is the basis of modern self-supervised models. These techniques maximise the resemblance between two separate augmentations of the same image, while simultaneously minimising the similarity between different images in different contexts. In this case, the "self-supervised neural network" provides a classification-based pretext task with a target that is closely related to the main objective. To categorise two different augmentations of the same image, knowing only the C number of classes, an unsupervised classifier has been developed. In practise, such a task is prone to degenerate solutions where each sample is assigned to the same class.

The best solution to this problem is to set a uniform prior for the common cross-entropy loss function to prevent it from providing an answer that divides the data evenly. In fact, this design shows that the collection of optimal solutions no longer includes degenerating alternatives. In this design, deep unsupervised clustering architectures and contrastive learning are combined. In a single-phase point-to-point process, the self-supervised architecture learns representations and cluster labels using mini batch Stochastic Gradient Descent (SGD). This model proposes a point-to-point classification and representation learning approach, self-supervised, and single-stage, both simple and effective. This approach requires no pre-training, no expectation-maximisation technique, no pseudo-labelling and no external clustering.

Let us use the symbols x_1 and x_2 to represent two separate, enhanced perspectives of the same image sample x . The main goal of this architecture is to study a classifier with the formula $y = f(x_i) e [C]$, where C is the predetermined number of classes that can classify two different perspectives of the same sample. An obvious solution to this problem is to minimise the resulting cross-entropy loss:

$$l(x_1, x_2) = \sum_{y \in [C]} P(x_1) \log P(y|x_2) \quad (7)$$

where, $P(x_1)$ is the softmax row of the logits S matrix generated by our model (classifier + backbone) for all classes and batch samples. The network makes a constant y -value

prediction, which is x -independent. Without further regularisation, attempts to reduce (7) will therefore quickly converge to this degenerate solution. Applying the Bayes and total probability laws would solve this problem and lead to the following results:

$$P(x_1) = \frac{P(y)P(x_1)}{P(y)} = \frac{P(y)P(x_1)}{\sum_{x_1 \in B_1} P(x_1) P(x_1)} \quad (8)$$

where S is the previously mentioned matrix of logits, $P(y)$ is a softmax column, and B_1 is a collection of N samples. The cross-entropy function is represented by [10] because the authors assume that $P(y)$ has a uniform prior and that $P(x_1)$ and $P(x_2)$ are uniform in the self-supervised network.

$$l(x_1, x_2) = -\sum_{y \in [c]} \frac{P(y)}{\sum_y P(y)} \log \left(\frac{N}{ch} \frac{P(x_1)}{\sum_y P(x_2)} \right) \quad (9)$$

The self-supervised network was used in the proposed UNT model to fully diagnose the type of disease and to categorise the segmented input image as benign or cancerous. To perform a prior identification of lung cancer, UNT and a self-supervised network work together. The central architecture of the proposed UNT model is shown in Fig. 2.

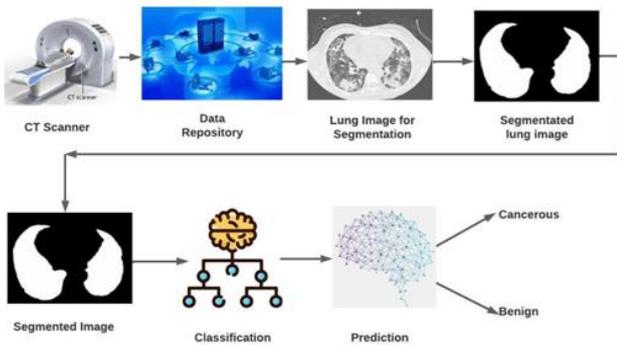


Fig. 2. The entire process of lung cancer identification using analyser and assessment head.

4. RESULTS AND DISCUSSION

The main goal of this endeavour is to develop a segmentation and classification tool that allows early detection of lung cancer. Datasets with the lung images are widely used to assess the effectiveness of deep learning-based techniques for classification and identification of lung cancer. The proposed model was trained and tested on a public dataset available in the Kaggle and GitHub repositories, containing a total dataset of 25000 CT images, including 5000 COVID images, 5000 pneumonia images, 6000 tuberculosis images, and 9000 lung cancer images, including normal images. The repository images are open for image segmentation with updated images. The entire dataset is verified and validated by the experts for CT scan images.

In the proposed work, an analyser head and an assessment head are combined to form the diagnostic system. A 2D CT scan serves as the input data for the segmentation part, and the segmentation in semantic format is the resulting output of the proposed UNT model. The self-supervised network is built on the segmentation part, and the classification part uses the output of this part to perform classification and check whether it is benign or cancerous.

A. Image analyser

Using the Decathlon dataset, both training and testing were conducted. The CT images are provided as input in the ratio of 8:2. The accuracy of the segmentation directly affects whether it is successful or unsuccessful. Therefore, specificity, accuracy and sensitivity are used as the four measurement variables. True positives Tr_P , true negatives Tr_N , false negatives Fa_N and false positives Fa_P are additional factors that affect the assessment.

$$Specificity = \frac{Tr_N}{Tr_N + Fa_P} \quad (10)$$

$$Accuracy = \frac{Tr_N + Tr_P}{Tr_N + Fa_N + Fa_P + Tr_P} \quad (11)$$

$$Sensitivity = \frac{Tr_P}{Tr_P + Fa_N} \quad (12)$$

Different experiment settings were used for both testing and training. The parametric values used for the proposed UNT model are given in Table 1.

Table 1. Parametric values of the proposed model.

Count	Parameter	Value
1	Encoder	VIT-B/16
2	Weight	0.00001
3	Learning rate	0.0001
4	Input size	12*12*12
5	Optimizer	Nadam/AdamW

The lung cancer segmentation method created provides encouraging results that surpass the most recent results on the dataset, as shown in Table 2. We trained and tested the network with different optimisers – AdamW and Nadam in this study – to achieve the best segmentation performance. Table 2 lists the results obtained.

Table 2. Performance during segmentation with and without optimiser

Without / With Optimiser	Optimiser	Accuracy (%)	Sensitivity (%)	Recall (%)
Without	Encoder	97.25	96.75	97.21
With	AdamW	96.98	95.89	96.08
With	Nadam	95.35	94.01	96.33

As can be seen in Table 2, we were able to improve the segmentation results by changing the network optimiser. Better segmentation performance was obtained with the Nadam optimiser. When comparing the segmentation accuracy with the AdamW network optimiser, a 1% improvement was observed.

B. Image assessment

The aim is to create a comprehensive method for diagnosing lung cancer early in the planned work. The proposed system consists of two key components: an analyser head and the assessment part based on the technique of self-supervision. To help develop a system for diagnosing lung

cancer, we need to incorporate a classification component for the segmentation results. The segmented CT scan data from this task is given as input to the classification part to be categorised as either cancerous or benign. The experiment settings used in the training phase are listed in Table 3.

Table 3. Parameters considered by the proposed UNT model for classification.

Count	Parameter	Value
1	Activation function	ReLU
2	Weight	0.00001
3	Learning rate	0.01
	Iterations	100
4	Batch size	20
5	Optimizer	Adam/SGD/Gan/RMSProp

To achieve better results, the network optimiser is crucial. For this purpose, the optimisers Adam, RMSProp, SGD and Gan are tested. The network classification performance is improved by using the Adam optimiser compared to the other optimiser techniques, as shown in the comparative section. The Adam optimiser provided the highest categorisation rates.

C. Comparative classification results

To analyse the performance of the proposed system, the results of the UNT mode are presented in comparison with the existing methods. The CT scan images of the lungs were converted into binary images (Fig. 3) before being fed into the UNT model. The comparative analysis of the proposed UNT model including the analyser head and the assessment head is presented.

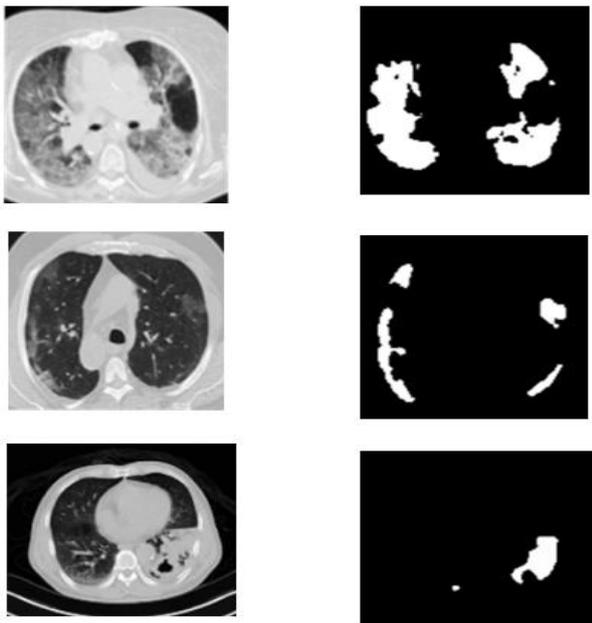


Fig. 3. CT scan image of the lung.

Table 4 shows the comparative performance metric analysis for lung cancer classification.

The proposed UNT method outperformed the existing optimisers in terms of classification accuracy. The existing

models were compared with the proposed approach under different optimiser models as shown in Fig. 4.

Table 4. Performance analysis for the proposed method.

Diseases	Learning model	Optimizer	Accuracy (%)	Sensitivity (%)	Recall (%)
Lung Cancer	ResNet-50	Adam	89.67	87.45	85.2
		SGD	89.26	86.25	86.0
		RMSProp	90.58	85.26	83.4
	Inception-ResNet	Adam	92.45	90.56	90.5
		SGD	94.30	91.79	89.7
		RMSProp	93.70	92.35	86.5
	VGG-19	Adam	93.90	91.05	92.3
		SGD	92.50	90.68	91.8
		RMSProp	91.70	89.74	90.7
	Proposed UNT	Adam	96.90	94.80	95.7
		SGD	95.30	93.74	92.6
		RMSProp	95.80	94.12	91.8

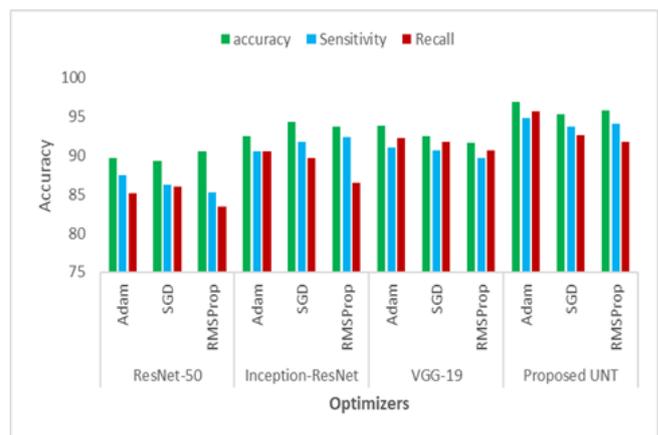


Fig. 4. Performance of classification optimisers in the proposed UNT method compared to the existing methods for lung cancer diagnosis.

5. CONCLUSION

People worldwide are at high risk of lung cancer and numerous solutions are attempted to deal with the addressed problem, but exiting techniques are still successful because they segment or categorise the problem of lung cancer. Numerous tests have been run to improve the segmentation and classification results. To achieve this goal, in this paper we have created a 3-dimensional lung cancer diagnostic technique for CT scan imaging. The proposed system consists of two primary components: the analyser component, which is built on the UNT network, and the assessment component, which is based on the self-supervised network and used to classify the segmentation result. The proposed approach provides a novel tool for the 2-dimensional lung cancer identification as well as for the CT scan. The proposed approach is effective enough to help radiologists and medical professionals in the fight against lung cancer due to the very encouraging segmentation and classification results. A classification performance of 98.77% and a segmentation accuracy of 97.83% are achieved. The major drawbacks of the proposed model include its high processing demands and

the need for a powerful GPU to function properly. The proposed paradigm can be used on high-capability local machines or cloud-based systems to overcome this limitation.

FUNDING

The authors declare no funding applied.

CONFLICTS OF INTEREST

The authors declare they have no conflicts of interest to report regarding the present study.

DATA AVAILABILITY STATEMENT

Available on Request. The datasets generated and/or analysed during the current study are not publicly available due to the extent of the submitted research. They are available upon reasonable request from the corresponding author.

REFERENCES

- [1] Aoki, T., Nakaata, H., Watanabe, H., Nakamura, K., Kasai, T., Hashimoto, H., Yasumoto, K., Kido, M. (2000). Evolution of peripheral lung adenocarcinomas: CT findings correlated with histology and tumor doubling times. *American Journal of Roentgenology*, 174 (3), 763-768. <https://doi.org/10.2214/ajr.174.3.1740763>
- [2] Arun, R., Singaravelan, S. (2020). Automated communication system for detection of lung cancer using catastrophe features. *Informatologia*, 53 (3-4), 184-190. <https://doi.org/10.32914/i.53.3-4.5>
- [3] Alam, J., Alam, S., Hossan, A. (2018). Multi-stage lung cancer detection and prediction using multi-class SVM classifier. In *2018 International Conference on Computer, Communication, Chemical, Material and Electronic Engineering (IC4ME2)*. IEEE. <http://dx.doi.org/10.1109/IC4ME2.2018.8465593>
- [4] Alizadeh, G., Frounchi, J., Baradaran Nia, M., Asgarifar, S., Zarifi, M. H. (2008). An FPGA implementation of an Artificial Neural Network for prediction of cetane number. In *2008 International Conference on Computer and Communication Engineering*. IEEE, 605-608. <https://doi.org/10.1109/ICCCE.2008.4580675>
- [5] Sathees Kumar, B., Sathiyaprasad, B. (2021). Bone cancer detection using feature extraction with classification using k-nearest neighbor and decision tree algorithm. In *Smart Intelligent Computing and Communication Technology*. IOS Press, APC Vol. 38, 347-353. <http://dx.doi.org/10.3233/APC210064>
- [6] Satheeshkumar, B., Sathiyaprasad, B. (2022). Medical data analysis using feature extraction and classification based on machine learning and metaheuristic optimization algorithm. In *Applications of Computational Science in Artificial Intelligence*. IGI Global, 132-156. <https://doi.org/10.4018/978-1-7998-9012-6.ch006>
- [7] Parameswari, A., Vinoth Kumar, K., Gopinath, S. (2022). Thermal analysis of Alzheimer's disease prediction using random forest classification model. *Materials Today: Proceedings*, 66 (3), 815-821. <https://doi.org/10.1016/j.matpr.2022.04.357>
- [8] Sathiyaprasad, B., Satheesh Kumar, B. (2022). Multi spectral image retrieval in remote sensing big data using fast recurrent convolutional neural network. In *2022 International Conference for Advancement in Technology (ICONAT)*. IEEE. <https://doi.org/10.1109/ICONAT53423.2022.9725921>
- [9] El-Baz, A., Gimel'farb, G., Falk, R., El-Ghar, M. A. (2007). A new CAD system for early diagnosis of detected lung nodules. In *2007 IEEE International Conference on Image Processing*. IEEE, 461-464. <https://doi.org/10.1109/ICIP.2007.4379192>
- [10] Lin, D.-T., Yan, C.-R. (2002). Lung nodules identification rules extraction with neural fuzzy network. In *Proceedings of the 9th International Conference on Neural Information Processing*. IEEE, 2049-2053. <https://doi.org/10.1109/ICONIP.2002.1199035>
- [11] Vinod, D. N., Prabakaran, S. R. S. (2023). COVID-19- The role of artificial intelligence, machine learning, and deep learning: A newfangled. *Archives of Computational Methods in Engineering*, 30 (4), 2667-2682. <https://doi.org/10.1007%2Fs11831-023-09882-4>
- [12] Vinod, D. N., Prabakaran, S. R. S. (2023). Elucidation of infection asperity of CT scan images of COVID-19 positive cases: A Machine Learning perspective. *Scientific African*, 20, e01681. <https://doi.org/10.1016%2Fj.sciaf.2023.e01681>
- [13] Storcz, T., Várady, G., Ercsey, Z. (2021). Identification of shadowed areas to improve ragweed leaf segmentation. *Tehnicki Gazette*, 28 (4), 1236-1243. <https://doi.org/10.17559/TV-20190604092100>
- [14] Winkler, A. M., Renaud, O., Smith, S. M., Nichols, T. E. (2020). Permutation inference for canonical correlation analysis. *NeuroImage*, 220, 117065. <https://doi.org/10.1016/j.neuroimage.2020.117065>
- [15] Hatamizadeh, A., Tang, Y., Nath, V., Yang, D., Myronenko, A., Landman, B., Roth, H. R., Xu, D. (2022). UNETR: Transformers for 3D medical image segmentation. In *2022 IEEE/CVF Winter Conference on Applications of Computer Vision (WACV)*. IEEE, 574-584. <https://doi.org/10.1109/WACV51458.2022.00181>
- [16] Ivković, R., Petrović, M., Daković, B., Jakšić, B., Milošević, I. (2020). Segmentation and classification of Bi-Rads medical images with the imaging biomarkers according to level of detail. *Tehnicki Gazette*, 27 (2), 527-534. <https://doi.org/10.17559/TV-20181221151205>

Received May 25, 2023
Accepted October 16, 2023