International Journal of Medical Toxicology & Legal Medicine Volume 27, No. 2, 2024
e-ISSN: 0974-4614
p-ISSN: 0972-0448

Related Weighted Feature Subset Model for Skin Cancer Classification using Resnet50 Model

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Received: 10.08.2024 Revised: 12.09.2024 Accepted: 20.10.2024

ABSTRACT
Among all diseases, skin cancer is among the deadliest disease if not detected early as per the records from World Health Organization (WHO). Early and accurate skin lesion classification could improve clinical decision-making by facilitating more precise disease identification, which in turn could improve treatment outcomes by halting the progression of cancer. The bulk of skin disease images utilized for training purposes are imbalanced and in low supply, which makes automatic skin cancer classification challenging. Additionally, the model's cross-domain adaptability and robustness pose key obstacles. In order to address these concerns and obtain satisfying results, numerous deep learning-based approaches have recently been extensively utilized in skin cancer categorization. However, there is a dearth of reviews that address the aforementioned cutting-edge issues with skin cancer classification. Using features taken from pre processed images in the publicly accessible datasets, this research intends to build a deep learning based model that can accurately classify skin cancer. It is well-known that pre processed features capture visual qualities pertinent to the classification task, making them more informative than raw image data. Improving the accuracy and interpretability of deep learning classification, this research proposed a model that detects the diseases more accurately from dermoscopy images. The 50-layer ResNet is constructed using a bottleneck architecture. With ResNet50, users can train a state-of-the-art image classification model on massive datasets. The utilization of residual connections is a major innovation that enables the network to learn a set of functions that translate the input into the intended output. By utilizing these residual connections, the network is able to overcome the issue of vanishing gradients and learn more complex topologies than before. This research proposes a Related Feature Subset Model using ResNet50 for Skin Cancer Classification (RFSM-ResNet50-SCC). The proposed model when compared with the traditional models performs better in feature subset generation and skin cancer classification.

Keywords: Skin Cancer, Feature Extraction, Feature Selection Model, Related Feature Set, Deep Learning, ResNet50, Classification Accuracy.

1. INTRODUCTION

Cancer ranks high among the leading global killers as per the records from World Health Organization (WHO). About 10.4 million people died in 2020 as a result of cancer and related disorders, based on the WHO records. Cancer is a disease characterized by the uncontrolled proliferation of aberrant cells in the body, which can metastasize to other organs [1]. One of the most frequent types of cancer, skin cancer can spread quickly and even kill. Our skin protects several internal organs, including muscles and bones, from the elements. As a whole, the body reacts strongly to anything that messes with the skin [2]. Many lesions are subdivided based on their point of origin, which is the sick spot on the skin. Squamous Cell Carcinoma (SCC) and Basal Cell Carcinoma (BCC) are two types of skin cancer [3]. One of the main causes of these malignancies, which are called keratinocyte cancers, is being exposed to the sun.

The face and hands are common areas where they manifest because of direct sunlight. SCC is able to rapidly spread to neighbouring organs or lymph nodes [4], while BCC is relatively inactive in other parts of the body. Melanoma, another rare and deadly skin cancer, starts in the melanocytes [5]. Early detection is necessary because it allows for surgical treatment; later stages make survival very challenging, if not impossible. Melanoma is a type of skin cancer that primarily strikes white people. It often develops on the chest of men and the lower limbs of women, but it can spread to other parts of the body. While just 5% of skin cancers are melanoma, it is believed to be responsible for 75% of deaths from skin cancer. The types of skin cancer are shown in Figure 1.

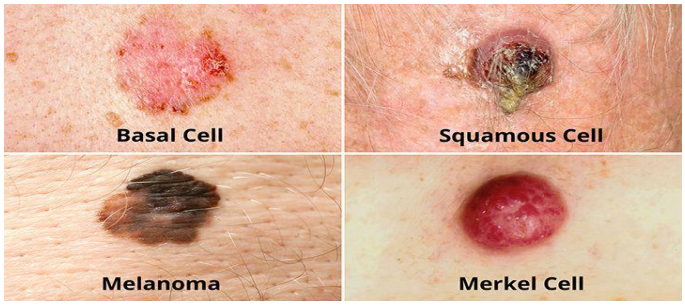

Fig 1: Types of Skin Cancer

There is a significant risk to human life from cancer. There are instances when it directly causes death in humans [6]. Although the human body is capable of generating a wide variety of cancers, skin cancer ranks high among its most aggressive and fatal forms. Some things that can set it off include smoking, consuming alcoholic beverages, having allergies, being ill, exercising, experiencing changes in surroundings, being exposed to Ultraviolet (UV) rays [7], and so on. Sunlight, which contains UV light, can damage skin cells' DNA. An additional risk factor for skin cancer is the development of abnormal swellings in humans. The four most prevalent types of skin cancer are melanoma, carcinoma of the basal cell [8], carcinoma of the squamous and actinic keratoses[9]. An important weapon in the process against skin cancer mortality is, early detection and treatment leads to a better cure rate [10]. The conventional approach to screening for skin cancer, which relies on visual examination, is time-consuming, subjective, and error-prone.

The skin lesion can be better seen with dermoscopy, a non-invasive imaging technique that takes images of the affected area and magnifies them. It achieves this by removing the skin's surface reflection [11]. However, in real-world clinical settings, dermatologists missed melanoma by more than 80% when using dermoscopyimages. To improve the accuracy and timeliness of skin cancer screening, doctors need a computerized diagnostic tool to help them make better judgments [12]. Typical Deep Learning (DL) approaches are used to classify melanoma and non-melanoma in order to generate automated diagnostic tools. Nevertheless, achieving exceptional diagnosis accuracy with DL algorithms is incredibly challenging when dealing with dermoscopyimages due to their low inter-class variances and high intra-class variations [13].

Worldwide, the incidence of melanoma has been steadily rising over the past few decades. Because it aids medical professionals in deriving useful information from images, dermoscopy Computer-aided design (CAD) fusion has emerged as a significant area of study in recent years. When developing a diagnostic system, feature extraction is an essential first step, and choosing the right feature is a key process [14]. Feature extraction allows for the extraction of hundreds of features from a single image. However, not all of the traits that were retrieved are applicable to lesion categorization [15]. The classifier becomes more complicated and computationally intensive with the addition of many unnecessary features, which in turn lowers the classification accuracy [16]. The ideal attributes for skin cancer images should reflect the region's characteristics. In order to get the best feature out of an image, there are a few different approaches taken. The proposed model makes use of ResNet50 model that effectively detects and classifies the skin cancer. The general flowchart of feature selection is shown in Figure 2.

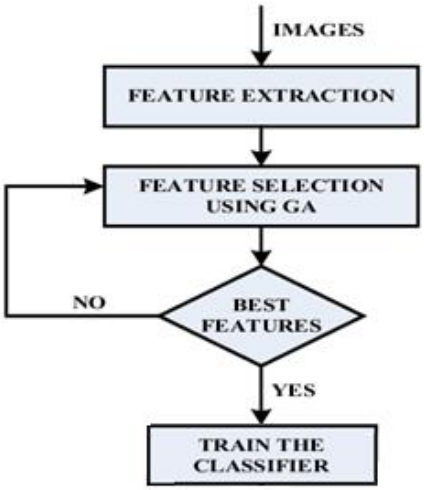

Fig 2: Feature Selection Flowchart

As a 50-layer residual network, ResNet50 is able to provide residual learnin. To circumvent the issue of vanishing gradients and train extremely deep networks, the ResNet architecture includes skip connections, also known as residual connections [17]. This can improve the model's performance. In ResNet design, residual networks play a significant role. In these networks, the input to a block is used to train the intermediate layers to learn a residual function. There are four steps to the ResNet50 architecture. The network accepts inputs in 32-bit increments with a channel width of 3. With 7x7 and 3x3 kernel sizes, the first convolution and max-pooling are executed by eachResNet architecture. The input is shrunk in half in height and width at each level, while the channel width is doubled [18]. There are three residual blocks with three layers in each stage. Every block of residuals has three layers of 1x1, 3x3, and 1x1 convolutions. The dimensionality reduction and restoration processes are carried out using the 1x1 convolution layers. The network concludes with a fully linked layer and an average pooling layer. The ResNet50 architecture is shown in Figure 3.

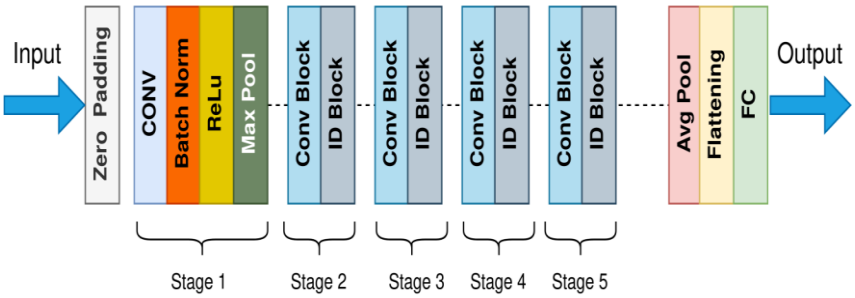

Fig 3: ResNet50 Architecture

Utilizing pre-trained weights, various Neural Network (NN) models were trained to extract features from each dermoscopy image [19]. Feature representation matrices were subsequently acquired. It is common practice for later layers of a deep learning architecture to capture task-specific data, while earlier layers attempt to extract general features [20]. As a result, feature extraction is performed from subsequent layers in this research. Since the CNN-obtained feature maps exist in a three-dimensional space, a layer of global average pooling is applied to reduce their dimensionality. To guarantee the data's efficacy and avoid over-fitting, a 20% drop out layer has been implemented after a pooling layer to eliminate neurons during training. This research proposes a Related Feature Subset Model using ResNet50 for Skin Cancer Classification.

2. LITERATURE REVIEW

The survival percentage of patients with skin cancer, a common type of cancer worldwide, is greatly improved by prompt and precise detection. Despite its importance, clinical evaluation for skin lesions is fraught with difficulties, such as lengthy wait periods and subjective interpretations. To help dermatologists overcome these obstacles and make more precise diagnoses, deep learning approaches have been created. The only way to stop skin cancer in its tracks and save lives is to treat it quickly. With the help of deep learning algorithms, doctors can make more precise diagnoses more quickly, which means patients can get the help they need sooner. Also, it can make doctors and nurses' jobs easier, so they have more time to focus on patients with more complicated needs. Mridha et al. [1] created atrustworthy DL predictive models over skin cancer classification, addressed the common issue of a very small class of patients with skin-related diseases compared to healthy controls, and decipher the model's output in order to comprehend the reasoning behind its decisions. A skin lesion categorization system based on XAI was created, with the model's decisions explained by Grad-CAM and Grad-CAM++.

Saeed et al. [2] analyzed and identified that skin cancer a malignant melanoma subtype in particular, are extremely dangerous cancers caused by the aberrant development of melanocyte cells. But there are a lot of obstacles to overcome, such as skin lesion classification and diagnosis and the automatic detection of malignant tumors using dermoscopy images. To determine the most effective of these generative processes, the author compared and contrasted them. Typically, predictions are made solely using images of skin lesions by computer-assisted skin cancer categorization systems that are constructed with deep neural networks. Although the results are encouraging, they may be even better if the patient demographics were considered; these are key indicators that human professionals look for when screening for skin lesions. The difficulty of using deep learning models for skin cancer classification through the integration of image and metadata components is addressed by Pacheco et al. [3] in this study. To aid in data categorization, the author introducedMetaBlock, a novel approach that improves upon the most important image features extracted from the classification pipeline. It was compared to other combination approaches, like the one that used features concatenation and the

MetaNet.

Even while there may be benefits to having them perform both tasks simultaneously, most deep learning models are only designed to handle one. Xie et al. [4] proposed amutually bootstrapping deep neural networks (MB-DCNN) mode designed to simultaneously segment and classify skin lesions. Three networks coarse-SN for coarse segmentation, mask-CN for mask-guided classification, and enhanced-SN for enhanced segmentation form the model. One benefit of using coarse-SN-generated rough lesion masks as a bootstrapping step is that mask-CN improves the detection and classification of skin lesions.

As a result of breast cancer, there may be noticeable and quantifiable changes in the skin linked to changes in the interstitial network and lymph system. The purpose of this research done by Andreasen et al. [5] was to identify any differences in skin electrical resistance between benign and malignant breast cancer lesions, with the hope that this information could be used as a biomarker for diagnosis and treatment. In all, forty-eight women participated, including twenty-four with cancer and twenty-three with benign lesions. During the same session along with a week after the initial measurement, the skin resistance of the breast lymphatic region and non-breast lymphatic areas was measured many times. To find out how repeatable the method was both within and across sessions, the author computed intraclass correlation coefficients. Next, the data was standardized so that the cross-sectional differences between benign and malignant breast lesions can be compared. In order to determine the efficacy of treatment, six patients who underwent therapy had their six-month longitudinal data examined. To compare the ratiometric differences between the groups, standard statistical methods were utilized. Breast cancer lesions were diagnosed using an automated learning random forest categorization algorithm that was trained on skin resistance data.

Numerous clinical investigations have shown that various skin pathological conditions share a great deal of biological DNA. Research into and development of novel intelligent systems for clinical decision-support are motivated by the fact that these commonalities make efficient skin cancer diagnosis challenging. Therefore, finding genes with different expressions (DEGs) that can concurrently identify numerous skin disease conditions in a single test is possible with gene expression analysis. Automated classification evaluation, fast biomarker identification, and appropriate batch merging are all steps in a well-designed pipeline that facilitates the integration of diverse transcriptome datasets. Gálvez et al. [6] offered a fresh perspective on skin cancer diagnosis by tackling all these technical concerns in a unique way. While further research into improved biomarkers for identifying particular skin pathologies is required, this study did identify a set of eight highly relevant multiclass differentially expressed genes (DEGs) capable of distinguishing between ten skin pathologies, including two a priori healthy skin conditions, two precancerous skin diseases that have been identified, and six skin cancers. Classification models that had been trained before extensively tested their diagnostic capabilities on new samples.

In order to streamline the procedure of skin lesion classification and segmentation with the aim of skin cancer detection, Adegun et al. [7] introduced an innovative framework. The first step of the proposed framework learns the difficult and inhomogeneous elements of the skin lesion using encoder-decoder Fully Convolutional neural networks (FCN). This stage also acquires the coarse appearance and details of the lesion borders. This is followed by the second step. The FCN differs from the conventional one in that it uses both long skip and short-cut connections in its sub-networks, allowing for a more efficient residual learning method and training. Additionally, the network incorporates the Conditional Randomized Field (CRF) component, which employs paired edge potentials for both the refinement of contours and the localization of lesion boundaries. It makes use of a linear combination with kernels that are Gaussian. In the second section, the author introduced an updated DenseNet design that makes use of FCNs. A transition layer and the concatenation technique combined dense pieces to form this design.

One form of skin cancer that can be deadly is melanoma. It can be difficult to tell it apart from nevus because the two conditions have similar symptoms and look same. This disease has the highest fatality rate of all consolidated cancers associated to the skin. The number of cancer cases is on the rise among young individuals, although the survival chances can be significantly improved with early diagnosis. It takes a lot of time and money for doctors to diagnose every patient for melanoma. Using cutting-edge image processing methods, Khan et al. [8] provided an intelligent system that can detect melanoma and differentiate it from nevus. The lesion's texture and color traits are extracted to create a unique hybrid super feature vector. The use of support vector machines (SVMs) allows for the differentiation of melanoma and nevus, two forms of skin cancer. The author evaluated the suggested segmentation method, pull out the best characteristics, and then contrasted the classification outcomes to those of other methods in the literature.

Among the most prominent uses of e-health and telemedicine is teledermatology, experts in this discipline receive patient records through the use of communications technology. Because skin is mostly transparent, teledermatology can be a useful technique for diagnosing skin lesions, particularly in rural locations. Triaging dermatology cases and reducing unnecessary clinician referrals are two other potential benefits. Classifying skin lesion image samples obtained from several servers is the purpose of this research. Classification and skin lesion localization/segmentation are the two main components of the suggested system. Khan et al. [9] proposed a

hybrid strategy for the localization module that merges 16-layered CNN model's binary images with a saliency segmentation technique that utilizes a better high-dimensional contrast transform. The segmentation RGB lesion image can be returned using a maximum information sharing strategy, which makes the most of the data acquired through the binary images. via the segmented lesion images, the classification module retrains a previously trained DenseNet201 model via transfer learning.

Using electromagnetic waves in conjunction with radio frequency technologies and circuits, Shafi et al. [10] presented an alternate approach to skin cancer screening that allows for the non-invasive detection and tracking of skin lesions. A powerful electromagnetic sensor, specialized circuitry for analyzing radio frequency waves, with machine learning algorithms make up the SkanMD, the proposed portable device. There are a total of 46 participants in the clinical trials using the device; There are a total of 36 patients: 18 with pre-cancerous skin lesions, 10 with normal nevi, 7 with other diseases, and 11 healthy people. These studies captured the complicated data produced by measuring the value of the coefficient for reflection, S11, on multiple skin patches in order to build a Support Vector Machine, or SVM, based classification model.

3. PROPOSED METHOD

Observation of suspicious lesions manually from dermoscopy images is the typical procedure followed by an experienced dermatologist. Time would be required, and the patient might progress to later phases as a result. Also, the competence of the doctor makes a big difference when it comes to making a correct diagnosis. Research shows that even the most skilled dermatologists can only diagnose skin cancer with an accuracy of around 76%. The scarcity of qualified dermatologists working in public healthcare systems around the world compounds these problems [21].Extensive research has been conducted to address the aforementioned issues and speed up the early detection of skin cancer through the development of computer image analysis algorithms [22]. The data have to follow a normal distribution for most of these computational techniques to work. These methods fall short in precisely diagnosing the condition since data cannot be controlled in their nature. Nonetheless, the assumption that the data follows a normal distribution is not necessary for non-parametric solutions [23].

The typical method for diagnosing skin cancer is a biopsy, which can be time-consuming and inaccurate. When it comes to skin examination, dermatologists now rely heavily on noninvasive procedures like macroscopic and dermoscopy imaging [24]. By illuminating deeper layers of skin and providing high-resolution images that are imperceptible to the human eye, dermoscopy improves skin cancer detection. Recent years have seen the rise of computer vision and digital image processing as powerful resources for improving visualization speed and decreasing room for human mistake [25]. The use of digital image processing and computer vision algorithms has significantly sped up vision processing and decreased human error in recent years. Dermatologists may now more accurately diagnose melanoma with the use of technological advancements like image processing and artificial intelligence, which improves melanoma diagnosis and decreases biopsy-related suspicion [26].

In order to detect cancer cells, conventional computer vision methods examine multiple properties, including size, color, and texture. The problem is that these characteristics aren't always enough to differentiate across images. In the present day, these issues are being resolved by means of AI. Detection of skin cancer is an active area of study, and melanoma markers in dermoscopy images have been identified using deep learning algorithms [27]. Automatic extraction of both low-level behaviorssuch as edges and forms and high-level characteristics such as semantics and patterns is made possible by the abstraction capacity of neural network layers in Convolutional Neural Networks (CNNs). With this capability, this approach is able to diagnose cutaneous melanoma more accurately. Bringing more attention to the issue can benefit both skin cancer groups and dermatologists, as CNNs did better than all professionals on both diagnoses.

Algorithms based on deep learning and artificial intelligence are among the many classification methods used to enhance classification outcomes. The extraction of hand-crafted features important for skin disease classification is carried out based on methods utilized by dermatologists for skin cancer diagnosis, particularly the ABCD dermoscopy method. For the purpose of feature extraction, image segmentation isolates the skin lesion from the surrounding skin backdrop. Using real-time analysis, 200 dermoscopy images are analyzed for relevant aspects. The dataset under consideration is used to determine the threshold range of each feature in order for the image to be classified as melanoma cancer [28]. A melanoma image is defined as one whose value falls inside the range. Because not all visual characteristics provide values within that range, an artificial neural network makes the call. From the 80 benign and 120 malignant photos that were considered, the average value of each feature for the two types of images was also calculated. The proposed model framework is shown in Figure 4.

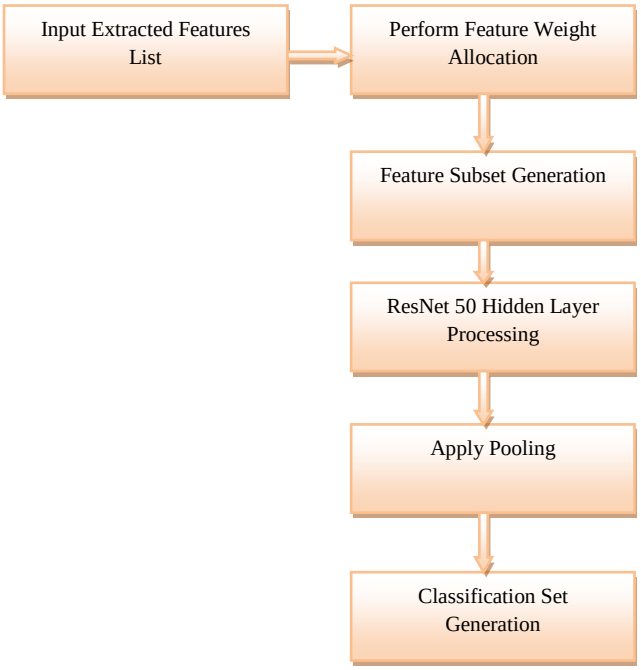

Fig 4: Proposed Model Framework

The proposed model makes use of the features of ResNet50 model to design an efficient methodology for designing a model for accurate classification of melanoma. Each of ResNet-50's five blocks contains a set of residual blocks, and the network's fifty levels make up its architecture. By preserving data from previous layers in the residual blocks, the network is able to learn more accurate representations of the input data. The vanishing gradient problem states that gradients become very small when they propagate across many layers of a neural network, which happens in typical or basic deep neural networks. Basically, the training or test error gets worse as the number of layers increases. In extremely deep architectures, this might cause learning to be sluggish or nonexistent altogether. ResNets circumvent this issue by implementing skip connections, which are also called residual connections. These connections enable the gradient to evade specific network layers. The Residual Network Model is shown in Figure 5.

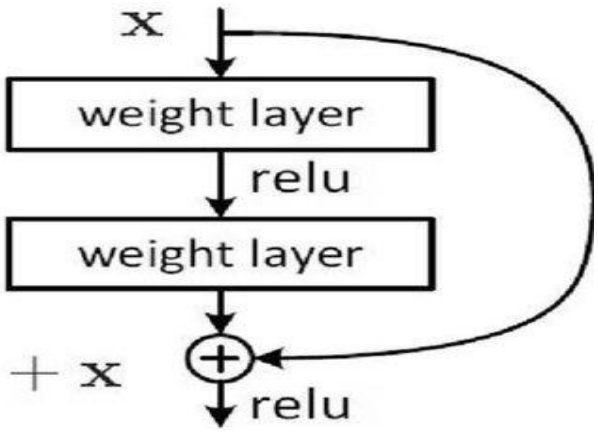

Fig 5: Residual Network Model

Adding additional layers to a sufficiently deep model results in increased training error, as previously reported and experimentally confirmed, and this degradation is unexpectedly not caused by overfitting. This drop in accuracy shows that optimizing some systems is easier than others. Fortunately, this is something that residual/identity mapping (block) can tackle. Bypassing the convolution blocks between two Relu Activation units allows us to input the output of the first Relu directly into the second Relu, so avoiding these blocks. The network may now learn the residual function rather than the underlying mapping directly with the addition of this residual connection. This has the potential to enhance performance and contribute to more efficient learning, particularly in extremely deep systems. There is no need to worry about performance dropping as the number of layers are increased from 20 to 50 or 50 to 100 because regularization and weights will not impact performance at that point. By utilizing these residual connections, the network is able to overcome the issue of vanishing

gradients and learn more complex topologies than before. This research proposes a Related Feature Subset Model using ResNet50 for Skin Cancer Classification.

Algorithm RFSM-ResNet50-SCC
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Input: Extracted Features Set [EFset}
Output: Classification Set {Cset}
Step-1: The extracted features are analyzed and the range of features is considered that are used to assign weights. The maximum range and minimum range of feature ranges are calculated as

$$MinFeSet\quad[M] = \sum_{f=1}^{M} getattr\quad(f) + \frac{getmaxrange\quad(f) - getminrange\quad(f)}{M-f} + std\quad(\frac{attr\quad(f+1)}{attr\quad(f)})$$

$$MaxFeSet\quad[M] = \sum_{f=1}^{M} getattr\quad(f) + \frac{getminrange\quad(f) - MinFeSet\quad(f)}{M-f} + std\quad(\frac{attr\quad(f+1)}{attr\quad(f)}) + \frac{\sum max\quad(f, f+1)}{M}$$

Here f is considered as current feature and M is the total features in the dataset, getattr() is used to consider each and every feature attribute, $getmaxrange\quad(f)$ is used to identify the maximum range of values of features and $getminrange\quad(f)$is used to identify minimum range of features, std() model calculates the standard deviation among the feature values.
Step-2: The extracted features are analyzed and the correlation factor and dependency relation is calculated. The weight allocation is performed by calculating the correlation among the features. The weight allocation is performed as

$$Fweig\quad h[M] = \sum_{f=1}^{M} getattr\quad(MaxFeSet\quad(f)) + maxrange\quad(MaxFeSet\quad(f, f+1)) \begin{cases} Fweig\quad h \leftarrow W++\ if\quad maxrange\quad(f) > Th \\ Continue\quad\quad\quad\quad\quad\quad\quad\quad\quad\quad\quad\quad Otherwise \end{cases}$$

Here getattr() considers each and every value in the feature set, W is the flag variable that allocates the weights, Th is the threshold value considered for weight allocation.
Step-3: In feature selection, subset of the features is selected to feed into a model in order to filter out the irrelevant ones. The overall accuracy of the model will be decreased, complexity will be increased, generalization capability will be limited if unnecessary features are selected. In order to decrease the likelihood of over fitting occurring in a model, feature selection is a method for decreasing the number of variables used to train the model. The feature subset generation process is performed as

$$FSset\quad[M] = \sum_{f=1}^{M} \frac{\max(Fweig\quad h(f))}{M-f} + \omega\left(\max\left(Fweig\quad h(f, f+1)\right)\right) - \min(\text{Fweigh(f, f + 1)})$$

Here ω is the model that considers the features set that are having maximum weight.
Step-4: The 50-layer ResNet is constructed using bottleneck architecture. In order to decrease the amount of parameters and matrix multiplications, a bottleneck residual block utilizes 1×1 convolutions. As a result, training each layer becomes substantially quicker. Instead of two layers, proposed model employs a stack of three. The network is able to learn a set of residual functions that translate the input into the intended output with residual connections, which is one of its main features. To keep the gradients from disappearing and the information flowing through the network, ResNet50 incorporates residual connections. Bypassing one or more network levels and going straight to the output is possible with residual connection. The ResNet50 hidden layer processing is performed as

$$HLProc\quad[M] = \sum_{f=1}^{M}\sum_{i=1}^{f} \frac{\lim_{f\to M}\left(\max\left(FSset\quad(f)\right) + \frac{\max\left(Fweig\quad h(f, f+1)\right)}{len\quad(FSset\quad)}\right)}{\sum_{f=1}^{M} maxrange\quad(FSset\quad) - \min(Fweig\quad h(f, f+1))} + \frac{\beta(FSset\quad(f, f+1))}{R}$$

$$FHkernel\quad[M] = \sum_{f=1}^{M} \frac{\gamma\,(HLProc\quad(f, f+1))}{M} + \lim_{f \to M}\left(\min(\omega(FSset\quad(f))) + \frac{\max(FeSet\quad(f, f+1))}{M-f}\right)^2$$

Here γ is the model used for fixing the kernel window size, R is the total number of batches.

Step-5: To enlarge the input geographically, max pooling works independently on each depth slice. Reducing the amount of data in an image without sacrificing the key features needed for precise image recognition is max pooling's major goal. One pooling procedure is max pooling, which takes the filter-covered area of the feature map and chooses the largest element from there. After max pooling, final classification will be performed by generating class labels that predicts the disease accurately. The max pooling operation and classification set generation is performed as

$$Maxpool\quad[M] = \left[\left(\frac{1}{|\gamma|}\sum FHkernel\quad\frac{\omega}{f}\right)\right]$$

$$Class\quad[M] = \sum_{f=1}^{M} \frac{\max(FSset\quad(f, f+1))}{M} + maxpool\quad(FHkernel\quad(f, f+1)) + diff\quad(FHkernel\quad(FSset\quad(f, f+1))) + \max(\min(\omega(FSset\quad(f)))) + \tau\,(HLProc\quad(f, f+1))\backslash$$

Here τ is the model for class labelling based on the feature differences and hidden layer processing.

}

4. RESULTS

Melanoma develops when the pigment-producing cells called melanocytes develop malignant cells. While most people detect pigment cells in their skin, they can also appear in other areas of the body and even the eyes. The face, chest, and back are all possible locations. In females, it manifests in the lower extremities.When it comes to skin cancers, melanoma is the most hazardous kind since it metastasizes and damages tissues more severely than the others. There is hope for a cure for seborrhoea keratosis because it is not malignant. However, melanoma is a common misconception.Medical professionals can save time and effort with the use of CADs models. Skin cancer detection using CADs systems and a variety of supervised, unsupervised, and semi-supervised learning algorithms has been the subject of considerable research. Natural picture classification is a good area for Deep Learning Medical professionals can save time and effort with the use of CAD. In order to train the learning model more effectively and decrease overfitting, more data is required. Overfitting occurs when a model fits the training data too closely or completely, making it unable to generalize well. Due to difficulty in creating datasets, particularly when dealing with image data, there is often insufficient data in learning problems. For big datasets, the tagging process can be somewhat time-consuming. Increasing the amount of images in the dataset is thus one of the primary objectives of every learning challenge.

Characteristic extraction and categorization are carried out simultaneously in deep learning architectures. In image processing, feature extraction from regions with a higher likelihood of containing the desired information is of utmost importance. The majority of the problematic skin areas in skin cancer statistics tend to cluster in the image's central region. The feature extraction component of this study has been enhanced by utilizing this fact. The hallmark of cancer is the uncontrolled proliferation of abnormal cells that eventually metastasize to other organs. Skin cancer stands out among cancers as one of the most hazardous and damaging types. Early detection is a key factor for skin cancer patients seeking a cure. Skin covers every aspect of the body, including bones and muscles, and it is an essential component of the human body. A minor alteration to the skin's function can have far-reaching effects on the body's systems, highlighting the importance of this organ. A lesion area is the medical term for the affected skin area.

Determining whether the lesion is benign or a malignant tumor is the next stage. If the lesion is found in the second category, it is categorized into one of the several skin lesion kinds. These judgments are also made according on a collection of dermoscopy features. This research proposes a Related Feature Subset Model using ResNet50 for Skin Cancer Classification (RFSM-ResNet50-SCC). The proposed model is compared with thetraditional Interpretable Skin Cancer Classification using Optimized Convolutional Neural Network (ISCC-OCNN) and Mutual Bootstrapping Model for Automated Skin Lesion Segmentation and Classification (MBM-ASLSC) models.

Feature extraction is a way to decrease processing resources without sacrificing valuable or relevant information. In order to handle data efficiently, it is necessary to reduce its dimensionality, and feature extraction helps with that. It is the process of developing improved features from the source data while retaining all of the relevant information. The proposed model extracts all the features from the segmented image to perform accurate predictions. The Feature Extraction Time Levels are indicated in Table 1 and Figure 6.

Table 1: Feature Extraction Time Levels

No.of Images Considered	Models Considered		
	RFSM-ResNet50-SCC Model	ISCC-OCNN Model	MBM-ASLSC Model
10000	16.9	26.0	27.9
20000	17.0	26.1	28.1
30000	17.3	26.3	28.3
40000	17.5	26.5	28.6
50000	17.8	26.8	28.8
60000	18	27	29

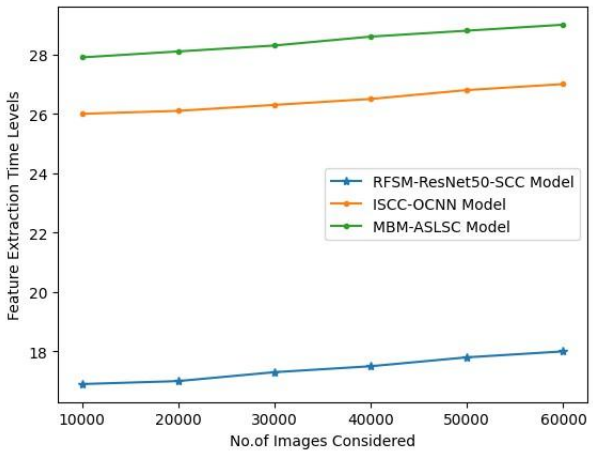

Fig 6: Feature Extraction Time Levels

To the extracted features, the proposed model allocates weights based on the correlation factor and dependency levels. These weights are helpful in selecting the most relevant features instead of using all the features to train the deep learning model. The Feature Weight Allocation Accuracy Levels are depicted in Table 2 and Figure 7.

Table 2: Feature Weight Allocation Accuracy Levels

No.of Images Considered	Models Considered		
	RFSM-ResNet50-SCC Model	ISCC-OCNN Model	MBM-ASLSC Model
10000	97.6	92.6	93.3
20000	97.8	92.8	93.6
30000	98.1	93.1	93.8
40000	98.3	93.4	94.0
50000	98.5	93.6	94.2
60000	98.7	93.8	94.4

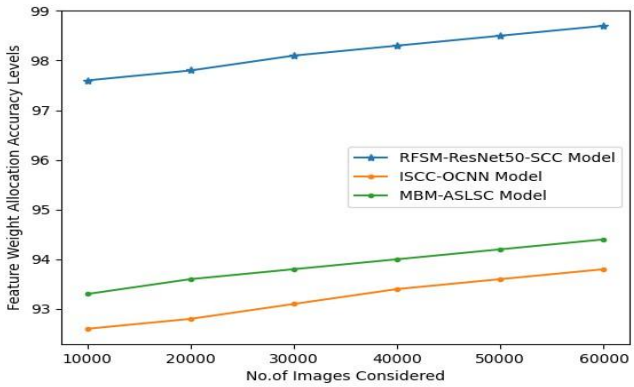

Fig 7: Feature Weight Allocation Accuracy Levels

In feature selection, a subset of the original features is chosen in order to minimize the feature space to an ideal level according to some criterion. When building a predictive model, feature selection is the method used to

decrease the amount of input variables. In order to decrease the computational cost of modeling and, in certain instances, to enhance the model's performance, it is desired to decrease the number of input variables. The Feature Subset Generation Time Levels of the proposed and existing models are shown in Table 3 and Figure 8.

Table 3: Feature Subset Generation Time Levels

No.of Images Considered	Models Considered		
	RFSM-ResNet50-SCC Model	ISCC-OCNN Model	MBM-ASLSC Model
10000	14.9	20.1	23.9
20000	15.1	20.3	24.1
30000	15.2	20.5	24.3
40000	15.5	20.7	24.6
50000	15.8	20.8	24.8
60000	16	21	25

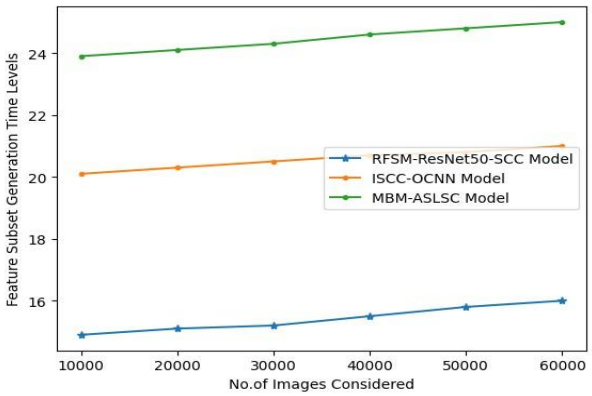

Fig 8: Feature Subset Generation Time Levels

The values of the nodes in the hidden layer are determined by adding together all of the input node values and then multiplying them by their respective weights. Transformation describes this action. The sum also includes the bias node, which has a weight of 1.0. To learn important qualities from this raw data and make it more meaningful and compact, hidden layers are crucial in processing the features. This method lowers the data's dimensionality, which allows higher-level layers to more easily extract useful information and generate reliable predictions. Table 4 and Figure 9 represents the Hidden Layer Processing Accuracy Levels.

Table 4: Hidden Layer Processing Accuracy Levels

No.of Images Considered	Models Considered		
	RFSM-ResNet50-SCC Model	ISCC-OCNN Model	MBM-ASLSC Model
10000	97.5	92.9	94.3
20000	97.7	93.1	94.5
30000	97.9	93.3	94.7
40000	98.1	93.5	94.9
50000	98.3	93.8	95.1
60000	98.5	94	95.3

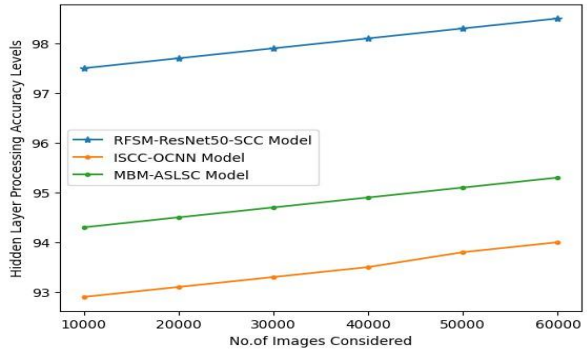

Fig 9: Hidden Layer Processing Accuracy Levels

Pooling layers are added to a Convolutional neural network subsequent to the convolutional layer. Reducing the amount of training parameters allows for faster computation, which is the primary goal of feature map reduction by pooling. In order to pool features, a two-dimensional filter is slid over each feature map channel and the features included within the filter's coverage area are summarised. A typical CNN model consists of multiple consecutively stacked convolution and pooling layers. The Pooling Accuracy Levels are indicated in Table 5 and Figure 10.

Table 5: Pooling Accuracy Levels

No.of Images Considered	Models Considered		
	RFSM-ResNet50-SCC Model	ISCC-OCNN Model	MBM-ASLSC Model
10000	97.4	92.7	93.3
20000	97.6	92.9	93.5
30000	97.9	93.1	93.7
40000	98.0	93.2	93.9
50000	98.2	93.4	94.0
60000	98.4	93.6	94.2

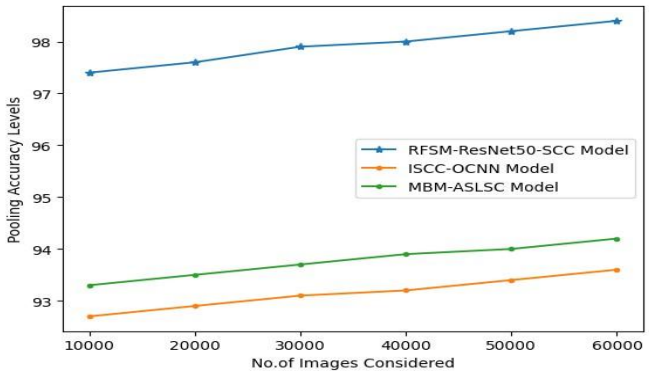

Fig 10: Pooling Accuracy Levels

Putting something into a category is called classification. One of the worst diseases is skin cancer, especially melanoma. The similarities between various skin lesions, such as melanoma and nevus, in color skin imaging make detection and diagnosis more challenging. This research presents a method for automatically classifying skin lesions. The Classification Accuracy Levels are represented in Table 6 and Figure 11.

Table 6: Classification Accuracy Levels

No.of Images Considered	Models Considered		
	RFSM-ResNet50-SCC Model	ISCC-OCNN Model	MBM-ASLSC Model
10000	98.0	94.6	93.7
20000	98.1	94.8	93.9
30000	98.3	95.0	94.0
40000	98.5	95.2	94.2
50000	98.6	95.4	94.5
60000	98.8	95.6	94.7

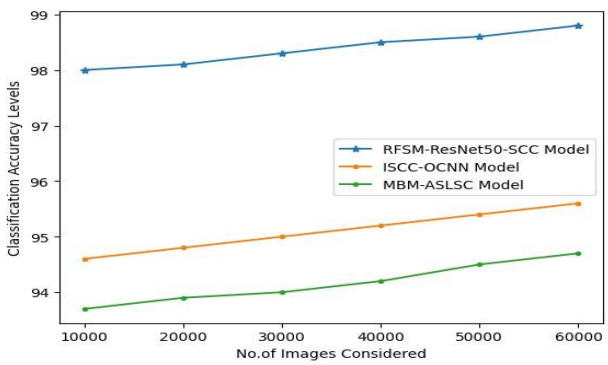

Fig 11: Classification Accuracy Levels

The degree to which a model's predictions deviate from the genuine model is quantified by its error rate. Classification models frequently make use of the phrase error rate. The excluded sample is used for testing, whereas N −1 samples are used for training. An error will be recorded if something is incorrectly classified. This process is iterated N times, with a new sample being excluded with each iteration. Estimation of the probability of classification error is based on the total number of errors. The Table 7 and Figure 12 indicates the Error Rate levels.

No.of Images Considered	Models Considered		
	RFSM-ResNet50-SCC Model	ISCC-OCNN Model	MBM-ASLSC Model
10000	4.9	12.9	15.9
20000	5.1	13.1	16.1
30000	5.3	13.4	16.3
40000	5.7	13.6	16.6
50000	5.8	13.8	16.8
60000	6	14	17

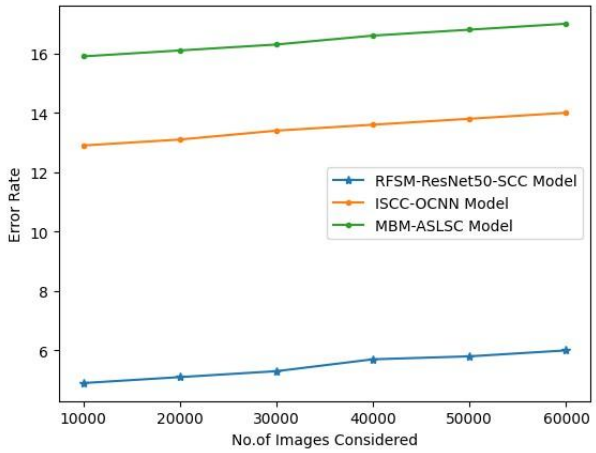

Fig 12: Error Rate

5. CONCLUSION

When left untreated, melanoma is far more likely to spread to other parts of the body, making it one of the most dangerous forms of skin cancer. Melanoma also accounts for most skin cancer deaths. Melanomas cannot be treated unless they are detected early. As a result, early identification is crucial for melanoma treatment. Because of its often-misdiagnosed benign appearance, melanoma is notoriously hard to detect. Cancer, like any other malignancy, is devastating if not treated early; it develops when aberrant epidermal cells proliferate uncontrollably. On the other hand, cancer detection via a machine-assisted approach is more efficient. When it comes to data organization and pattern design for decision making, deep learning is an AI operation that mimics the human brain's functioning. Artificial neural networks, and more specifically Convolutional neural networks, are the basis of the majority of current deep learning models. If this type of cancer is detected and treated quickly, it can become significantly less dangerous. The use of tried-and-true diagnostic tools that help doctors spot cancerous tumors earlier rather than later is a key component in reaching this goal. These imaging techniques are based on assessments developed by specialists in the detection of melanoma while the cancer is still locally contained in lymph nodes. This research introduced a Resnet50-based learning method for distinguishing between malignant and benign skin lesions. To differentiate between benign and malignant diseases, a Melanoma dataset is used that includes images of skin cancer disorders. This research proposes a Related Feature Subset Model using ResNet50 for Skin Cancer Classification. The proposed model achieved 98.7% accuracy in Feature Weight Allocation and 98.8% accuracy in classification. In future, optimization models and hybrid deep learning models can be used for achieving better classification rates and also for reducing false predictions.

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