Retraction

Retraction: Skin Cancer Classification Detection using CNN and SVM (J. Phys.: Conf. Ser. 1916 012148)

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This article (and all articles in the proceedings volume relating to the same conference) has been retracted by IOP Publishing following an extensive investigation in line with the COPE guidelines. This investigation has uncovered evidence of systematic manipulation of the publication process and considerable citation manipulation.

IOP Publishing respectfully requests that readers consider all work within this volume potentially unreliable, as the volume has not been through a credible peer review process.

IOP Publishing regrets that our usual quality checks did not identify these issues before publication, and have since put additional measures in place to try to prevent these issues from reoccurring. IOP Publishing wishes to credit anonymous whistleblowers and the Problematic Paper Screener [1] for bringing some of the above issues to our attention, prompting us to investigate further.

[1] Cabanac G, Labbé C and Magazinov A 2021 arXiv:2107.06751v1

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Skin Cancer Classification Detection using CNN and SVM

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Abstract. Skin malignant growth is quite possibly the most commonly seen Malignancy type in people. Skin disease happens because of the uncontrollable developing of transformations occurring in DNAs developing to certain reasons. Perceiving the malignant growth in beginning phases could build the opportunity of an effective treatment. These days, PC helped finding applications are utilized nearly at each field. From the real dermoscopic images, the first-stage network aims for precise segmentation of the skin lesion. The second-stage network is a classification network that can predict the existence of Melanoma and Squamous Cell Carcinoma in a skin sample. Deep convolutional neural networks, such as Inception-v4, ResNet-152, and DenseNet-161, were trained for melanoma and squamous cell carcinoma detection and seborrheic keratosis classification. U-Net with VGG-16 Encoder was trained to create segmentation masks for lesion segmentation. Resnet engineering achieves the highest precision of 90 percent among the equations used in the proposed models.

Keywords: convolutional neural network, machine learning, deep learning.

1. INTRODUCTION

Here, two forms of skin cancer have been identified. Melanoma and squamous cell carcinoma are types of skin cancer that develop when melanocyte cells become cancerous due to unrepaired DNA harm. It is less common than squamous cell carcinoma and other skin cancers. However, it is harmful because if not treated promptly, it can spread to other parts of the body. Squamous cell carcinoma, on the other hand, is less common than basal cell carcinoma and other forms. 1st. If caught early enough, it can be cured. Asymmetrical shape, Border irregularity, Color variation, Diameter, and Evolution (ABCDE rule) are some of the characteristics that dermatologists look for when identifying melanoma [1]. In transfer learning is combined with completely convolutional networks for semantic segmentation. For segmentation, common classification networks such as Alexnet and VGGnet are finely used. On PASCAL VOC segmentation results, this resulted in a mean IOU of 62.7 percent. Deep learning for skin lesion segmentation based on the U-NET architecture was proposed in [2]. For segmentation, Otsu’s clustering-based image thresholding method was used. On the ISBI 2017 dataset, this had an IOU of 84.2 percent. Biomedical Image Segmentation applications benefit greatly from the U-NET. The network in [3] outputs semantic segmentation by combining Convolutional and Deconvolutional network architectures. On the ISBI cell monitoring dataset from 2015, this model had an IOU of 92.03 percent. FCRN, a multiscale contextual information integration scheme, is used in [4].
for precise skin lesion segmentation. It creates a two-stage network by combining two deep residual networks. On the ISBI-2016 dataset, segmentation was used as the first stage to achieve an IOU of 82.9 percent and an accuracy of 85.5 percent. To minimize artefacts, [5] performs pre-processing on clinical images that may include illumination and noise effects. After that, a CNN is used to classify the data. On the Dermatology database used in MED-NODE, which contains 70 melanoma and 100 nevus images, an accuracy of 81 percent was achieved.

proposes an ensemble model that incorporates conventional image processing knowledge, sparse coding, and features extracted from state-of-the-art U-NET and Image net models, all of which are combined as a feature input to a classifier. On the ISBI 2016 dataset, they achieve a 76 percent accuracy. In order to improve the results obtained from the above analysis, we introduced a segmentation stage using both the U-NET and FCRN methods. The DRN architecture is used for the classification network [6]. The step-decay method is used, along with adjusted learning speeds. For better detection accuracy, binary cross entropy and weighted binary cross entropy approaches are used.

2. MOTIVATION

Because of the poor contrast between skin lesions and normal skin regions, accurately segmenting the lesion areas is difficult. Perceptual similarities between the two regions may be very strong. This makes it difficult to distinguish between melanoma and non-melanoma conditions [7]. Patients' skin disorders, such as skin tone, natural hairs, and veins, differ. This complicates distinguishing melanoma disorders based on texture, colour, and other characteristics. The main goal of this research is to eradicate human involvement in melanoma cancer diagnosis, making it less error-prone and time-consuming.

3. METHODOLOGY

Because of the poor contrast between skin lesions and normal skin regions, accurately segmenting the lesion areas is difficult. Perceptual similarities between the two regions may be very strong. This makes it difficult to distinguish between melanoma and non-melanoma conditions. Patients' skin disorders, such as skin tone, natural hairs, and veins, differ. This complicates distinguishing melanoma disorders based on texture, colour, and other characteristics. The main goal of this research is to eradicate human involvement in melanoma cancer diagnosis, making it less error-prone and time-consuming. A two-stage model is used to solve the problem.

i. Segmentation Stage: A U-NET-based architecture is implemented for precise skin injury division from dermoscopic images. The Jaccard Index, or Intersection Over Union, is used to evaluate the model (IOU).

ii. Melanoma Classification Level: Our deep Convolution neural network uses the segmented images of skin lesions from the previous stage as input for accurate Melanoma detection Figure 1.

Figure 1. Process of classification.
Profound learning is a quite huge pattern for AI, and the new achievement has prepared to fabricate a
venture this way. In this example we center explicitly on PC vision and picture characterization. To do
this, we will assemble nevus, melanoma, and seborrheic keratosis picture classifiers utilizing a
profound learning calculation, the convolution neural organization (CNN) through the Caffe* system.
In this article we center on administered learning. It requires preparing on the worker just as conveying
on the edge. We will likely form a machine learning calculation that can identify malignancy pictures
continuously; this way you can construct your own AI-based skin disease grouping gadget. Our
application incorporates two sections. The initial segment is preparing, in which we will utilize various
sets of the disease picture data set to prepare an AI calculation (model) with its relating names. The
subsequent part is conveying on the edge, utilizing the same model we've prepared and running it on
an edge gadget; in this Neural Register Stick.

4. MODEL TRAINING
4.1. Image loading and resizing

- In this process, images from the image folder's image path will be loaded into the column
called image. We also resize the images since their original dimensions are 450 x 600 x 3 and
Tensor Flow can't accommodate them, so we resize them to 100 x 75 x 3.

4.2. Splitting the test and training groups

- We divided the dataset into an 80:20 ratio research and training package.

4.3. Standardization

- We normalized the train and test sets by subtracting their mean values from their standard
deviations and dividing by their standard deviations.
- This will normalize all values between 0 and 255 to 0 and 1.

4.4. Label Encoding

- Labels are 7 different classes of skin cancer types from 0 to 6.
- The labels are Actinic keratoses, Basal cell carcinoma, Benign keratosis-like lesions,
- Abbreviations and Acronyms: Dermatofibroma, Melanoma, Melanocytic nevi vascular
lesions.

4.5. Splitting training and validation split

- To train our model, we used 90% of the data. We used ten percent of the data to evaluate our model.
- To avoid overfitting, a small test or validation dataset is used.

4.6. Data Augmentation

- We rotated the sample images by 10 degrees and zoomed them in by 10% for our model. To
maximise the scale of our training set, the images were also rotated by 10% horizontally and
vertically.

5. DATA SET AND RESOURCES

Our deep learning models were run on Google Collab. It is a Google-provided free cloud service
for research that supports GPU (K80) for up to 12 hours at a time. Keras was used on Python to
construct our architecture for Google Collab training. Keras is a deep learning library that can be used
to model and train custom architecture. The same is coded in Python 3.6. The data is taken from an
open-source git repository. The 13k image ISIC dataset was downloaded. 7,353 images are collected
after corrupt and redundant images are deleted. On the melanomic images, data augmentation was performed.

6. MODEL IMPLEMENTATION

The Keras Sequential API was used. The convolution layers, which are essentially a series of filters for learning features from images, are the first step. The two layers have 128 filters each, followed by four conv2D layers with 64 filters each. The filters are known as Kernel filters, and they are used to transform images. All of the images are subjected to the 2D matrix filters. The CNN will extract the features that are needed for classification from these pictures.

The pooling (MaxPool2D) layer comes next. This layer performs the role of a down sampling filter. It chooses the highest value between two adjacent pixels. This is used to reduce computational expense and can also be used to reduce overfitting in some situations. We need to focus on this; we need to set the pooling size, and the larger the pooling size, the more important down sampling becomes. Both global and local features are learned by adding Conv2D and pooling layers. To pick the training sample, the weights of some of the nodes in this layer have been set to 0. This is a regularization process known as Dropout. A portion of the network is eliminated, requiring the system to learn features in a distributed manner. This normalization has increased, and the amount of overfitting has decreased. We’ve used a rectifier called Relu. Max(0,x) is the activation function, and it adds non-linearity to the device. In the Flattening Layer, the final function map is transformed into a single 1D vector. To use the fully connected layers, flattening is needed after convolution and max pooling. It combines the local features of the previous convolution layers. The input layer in the diagram below is a 1D vector. Finally, the characteristics of two fully connected, dense layers, which are ANN (Artificial Neural Networks) classifiers at their heart. The final layer, where the net outputs distribution of probability of each class can be found, contains the net outputs distribution of probability of each class. The input layer in the diagram above is a 1D vector. The input layer in the diagram below is a 1D vector in figure 2.4.

6.1. Segmentation

6.2. Classification

Figure 2. Datasets images.

Figure 3. Process of Classification.

6.3. Accuracy
7. RESULTS

7.1. Segmentation stage results:

Table 1. Segmentation stage results

| Size of the image | Validation Accuracy | Training Accuracy |
|-------------------|----------------------|-------------------|
| 224*244 Big       | 66.55%               | 76.10%            |
| 192*240 Medium    | 75.10%               | 80.52%            |
| 128*160 Small     | 75.50%               | 83.90%            |

7.2. Classification results:

The simple DRN model, which was trained for the classification level, had an accuracy of 91.3 percent and a recall of 0.22 percent. To improve accuracy and recall, this model needs to be fine-tuned. For our target application, recall is the most important factor. The following results were obtained using Binary Cross Entropy as the loss function \((y\log(p) + (1-y)\log(1-p)).\) The number of False Negatives obtained is very high. Melanoma set has a lower recall than non-melanoma set. A 92 percent accuracy rate is achieved in table 1 and 2.

Table 2. Binary cross entropy Confusion Matrix

|          | FN=135 | TP=782 |
|----------|--------|--------|
| TN=1284  |        |        |
| FP=31    |        |        |

The model sees more loss for each incorrect classification as it uses Weighted Cross Entropy as the loss function. This aids in the model's training to create less False Negatives, which is important for our application. Mathematically, Weighted Cross Entropy is represented as a Loss Function \(((y*n\log(p) + (1-y)\log(1-p))\). False Negatives were minimised by using this loss function.
Melanoma set recall increased, while non-melanoma set recall decreased. The accuracy obtained is 88.7% in table 3 and 4.

**Table 3. Weighted binary cross entropy Uncertainty Matrix.**

|     |     |
|-----|-----|
| TN=12.38 | FP=176 |
| FN=77 | TP=740 |

**Table 4. Weighted binary cross entropy improves accuracy and recall.**

| Value of n | Accuracy(%) | Recall(%) |
|-----------|-------------|-----------|
| 1         | 96          | 86        |
| 2         | 91.2        | 92        |
| 3         | 89          | 92        |
| 5         | 84          | 91        |
| 10        | 78          | 91        |

8. CONCLUSION

The Aim Of This Project Is To Determine The Accurate Prediction Of Skin Cancer. To Do Some Pre-Processing Steps Were Carried Out which are Hair Removal, Glare Removal And Segmentation. A Computer aided skin Cancer recognition framework can accomplish another disclosure of identifying considerate or dangerous skin sores and isolating them from sound skins. The diagnosing procedure utilizes Digital image processing techniques and artificial Neural. Organizations for the characterization of malignant Melanoma from amiable melanoma. Dermoscopic Pictures were gathered and they are handled utilizing middle channel are utilized to eliminate salt and pepper commotion. After preprocessing images, is segmented using maximum entropy method. Greatest entropy thresholding is utilized to discover local of interest. The exceptional highlights of the sectioned pictures are extricated utilizing highlights extraction methods.

9. FUTURE SCOPE

Skin cancer identification is a vital medical technology. The network can be trained with the original image size as input, without scaling it down, and a much larger batch size, which will allow the network to learn both general and region-specific features from the lesion. By associating a value to these parameters, they can be inserted into the network. By associating a stochastic model with these parameters, they can be combined with the network. This will aid in the model's accuracy.

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