SOLUTION ARCHITECTURE

Project : AI BASED LOCALIZATION AND CLASSIFICATION OF SKIN DISEASE WITH ERYTHEMA

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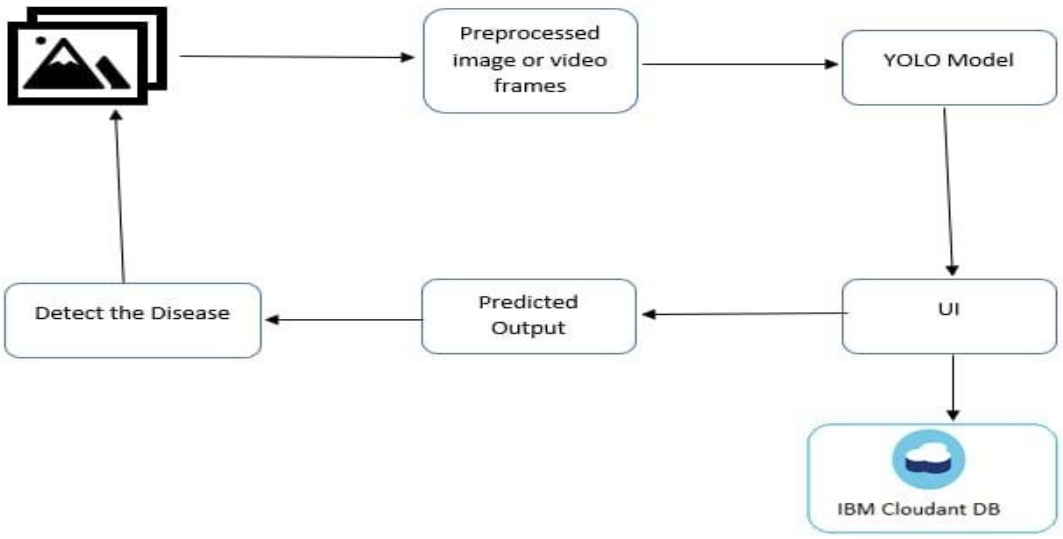
DESCRIPTION:

Although computer-aided diagnosis (CAD) is used to improve the quality of diagnosis in various medical fields such as mammography and colonography, it is not used in dermatology, where non-invasive screening tests are performed only with the naked eye, and avoidable inaccuracies may exist. This study shows that CAD may also be a viable option in dermatology by presenting a novel method to sequentially combine accurate segmentation and classification models. Given an image of the skin, we decompose the image to normalize and extract high-level features. Using a neural network-based segmentation model to create a segmented map of the image, we then cluster sections of abnormal skin and pass this information to a classification model. We classify each cluster into different common skin diseases using another neural network model. Our segmentation model achieves better performance compared to previous studies, and also achieves a near-perfect sensitivity score in unfavourable conditions. Our classification model is more accurate than a baseline model trained without segmentation, while also being able to classify multiple diseases within a single image. This improved performance may be sufficient to use CAD in the field of dermatology.

TECHNICAL ARCHITECTURE:



SOLUTION: Computer-aided diagnosis (CAD) is a computer-based system that is used in the medical imaging field to aid healthcare workers in their diagnoses CAD has become a mainstream tool in several medical fields such as mammography and colonography1,2 However, in dermatology, although skin disease is a common disease, one in which early detection and classification is crucial for the successful treatment and recovery of patients, dermatologists perform most non-invasive screening tests only with the naked eye. This may result in avoidable diagnostic inaccuracies as a result of human error, as the detection of the disease can be easily overlooked. Furthermore, classification of a disease is difficult due to the strong similarities between common skin disease symptoms. Therefore, it would be beneficial to exploit the strengths of CAD using artificial intelligence techniques, in order to improve the accuracy of dermatology diagnosis. This paper shows that CAD may be a viable option in the field of dermatology using state-of-the-art deep learning models. The segmentation and classification of skin diseases has been gaining attention in the field of artificial intelligence because of its promising results. Two of the more prominent approaches for skin disease segmentation and classification are clustering algorithms and support vector machines (SVMs). Clustering algorithms generally have the advantage of being flexible, easy to implement, with the ability to generalize features that have a similar statistical variance. Travels with various clustering algorithms, such as fuzzy c-means, improved fuzzy c-means, and K-means, achieving approximately 83% true positive rates in segmenting a skin disease. An inherent disadvantage of clustering a skin disease is its lack of robustness against noise. Clustering algorithms rely on the identification of a centroid that can generalize a cluster of data. Noisy data, or the presence of outliers, can significantly degrade the performance of these algorithms. Therefore, with noisy datasets, caused by images with different types of lighting, non-clustering algorithms may be preferred; however, Keke et al. implemented an improved version of the fuzzy clustering algorithm using the RGB, HSV, and LAB colour spaces to create a model that is more robust to noisy data. SVMs have gained attention for their effectiveness in high-dimensional data and their capability to decipher "…subtle patterns in noisy and complex dataset". Although more robust than clustering algorithms, SVMs are more reliant on the pre-processing of data for feature extraction. Without pre-processing that allows a clear definition of hyperplanes, SVMs may also underperform. Owing to the disadvantages of these traditional approaches, convolution neural networks (CNNs) have gained popularity because of their ability to extract high-level features with minimal pre-processing CNNs can expand the advantages of SVMs, such as robustness in noisy datasets without the need for optimal pre-processing, by capturing image context and extracting high-level features through down-sampling. CNNs can interpret the pixels of an image within its own image-level context, as opposed to viewing each pixel in a dataset-level context. However, although down-sampling allows CNNs to view an image in its own context, it degrades the resolution of the image. Although context is gained, the location of a target is lost through down-sampling. This is not a problem for classification, but causes some difficulty for segmentation, as both the context and location of the target are essential for optimal performance. To solve this, up-sampling is needed, which works in a manner opposite to that of down-sampling, in the sense that it increases the resolution of the image. While down-sampling takes a matrix and decreases it

to a smaller feature map, up-sampling takes a feature map and increases it to a larger matrix. By learning to accurately create a higher-resolution image, CNNs can determine the location of the targets to segment. Thus, for segmentation, we use a combination of downsampling and up-sampling, whereas for classification, we use only down-sampling. To further leverage the advantages of CNNs, skip-connections were introduced, which provided a solution to the degradation problem that occurs when CNN models become too large and complex. We implement skip-connections in both segmentation and classification models. In the segmentation model, blocks of equal feature numbers are connected between the down and up-sampling sections. In the classification model, these skip-connections exist in the form of inverted residual blocks. This allows our models to grow in complexity without any performance and degradation **Approach**:

In this project, we present a method to sequentially combine two separate models to solve a larger problem. In the past, skin disease models have been applied to either segmentation or classification. In this study, we sequentially combine both models by using the output of a segmentation model as input to a classification model. In addition, although past studies of non-CNN segmentation models used innovative pre-processing methods, recent CNN developments have focused more on the architecture of the model than on the preprocessing of data. As such, we apply an innovative pre-processing method to the data of our CNN segmentation model. The methods described above lack the ability to localize and classify multiple diseases within one image; however, we have developed a method to address this problem. Our objective is two-fold. First, we show that CAD can be used in the field of dermatology. Second, we show that state-of-the-art models can be used with current computing power to solve a wider range of complex problems than previously imagined. We begin by explaining the results of our experimentation, followed by a discussion of our findings, a more detailed description of our methodology, and finally, the conclusions that can be drawn from our study

METHODOLOGY:

Our 2-phase analysis model for localization and classification. We decomposed the original image into its haemoglobin and melanin constituents using pre-processing, to help our model extract valuable information from data that would have been otherwise unavailable. We provide these images as input to our segmentation model, the U-Net, which generated a segmented image. This segmented image was then analysed for clusters, which were subsequently cropped and input to our classification model, the Efficient Net, which then produced a classified label, thus completing our analysis model.

ALGORITHM:

Algorithm 1 Analyse Skin

1: **procedure** SEGMENT(*x*)

2: *h, m* = DECOMPOSE(*x*)

3: *mask* = U-NET([*x, h, m*])
4: CLASSIFY(*mask*)

5: **end procedure**

6: **procedure** CLASSIFY(*mask*)

7: *clusters* = FINDCLUSTERS(*mask*)

8: **for** *cluster* **in** *clusters* **do**

9: *cluster* = FIXRATIO(*cluster*)

10: *cluster* = RESIZE(*cluster*)

11: *class* = EFFICIENTNET(*cluster*)
12. *top prediction* = GETHIGHESTCONFIDENCE(*class*)

12: print(*top prediction*)

13: **end for**

14: **end procedure**

Pre-processing: decomposition

The main constituents of the skin that are visible to humans are melanin and haemoglobin. These constituents provide valuable information for the segmentation of abnormal skin. To ensure that our model can learn to use these features, we used independent component analysis (ICA) to extract the melanin and haemoglobin constituents. Assuming that these components are linearly separable, the separated linear vectors can be represented by the following formula7:

$L_{x,y} = d_m q_{mx,y} + d_h q_{hx,y} + \Delta$ $Lx,y=dmqx,ym+dhqx,yh+\Delta$

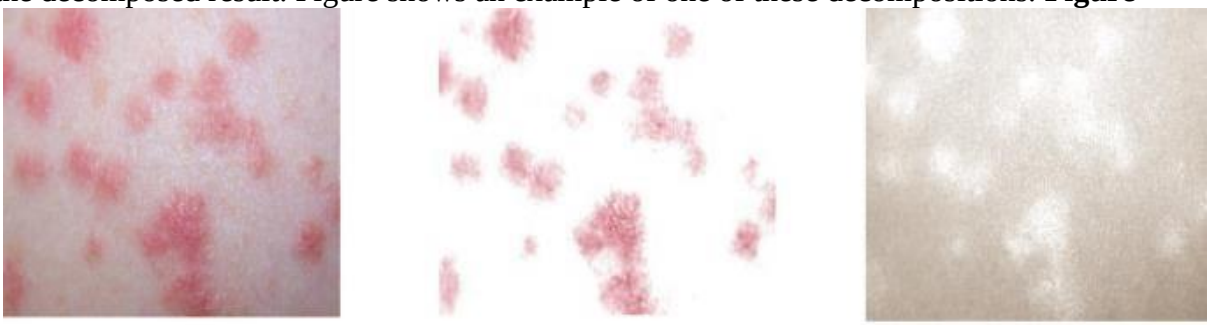
where d_m dm and d_h dh represent the density vectors of melanin and hemoglobin, respectively, $q_{mx,y}$ qx,ym and $q_{hx,y}$ qx,yh represent the quantity of these components, and $\Delta\Delta$ represents values that are caused by other colors. As shown in7, by applying ICA, we can decompose skin as

$[q_{mx,y}, q_{hx,y}] = D^{-1}_{(x,y)} - E[qx,ym, qx,yh] = D^{-1}(x,y) - E$

$E = \min_{x,y}(D^{-1}_{(x,y)}) E = \min x,y(D^{-1}(x,y))$

$I_{x,y} = \exp(-L'_{x,y}) Ix,y = \exp(-L'x,y)$

where D-D^- represents the estimated values of $d_m$dm and $d_h$dh, and $I_{x,y}$Ix,y represents the decomposed result. Figure shows an example of one of these decompositions. **Figure**



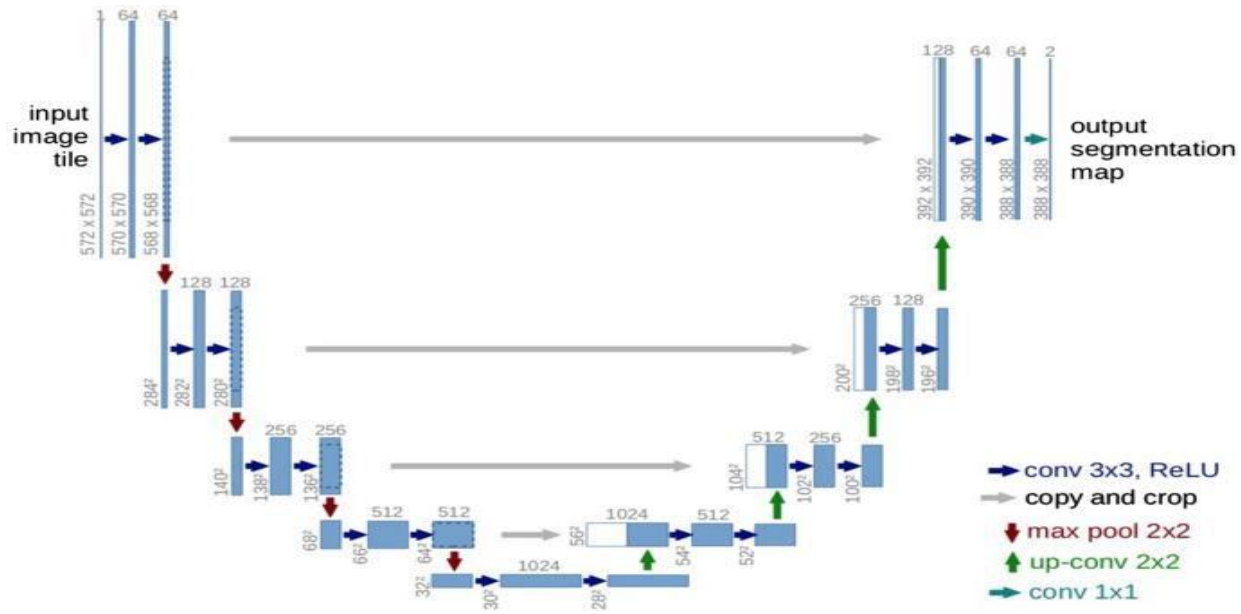
a. Original Image b. Hemoglobin Image c. Melanin Image

Decomposed result of skin. The original image is decomposed into its haemoglobin and melanin constituents through ICA.

Segmentation

The U-Net, , is an architecture created by CNNs, that has attracted attention for accurate biomedical image segmentation through the combination of down-sampling, up-sampling, and skip connections. Its name is attributed to the shape of its architecture, the first half of the 'U' representing down-sampling. Here, the context and key features of the input images are gained at the cost of a decrease in resolution. The second half of the 'U' represents upsampling. Here, the resolution is increased to gain knowledge of the location of the target segment. To combat degradation due to the complexity of the model, skip connections are added to each up-sampling block.

Figure



U-Net architecture. A fully CNN network, comprised of down-sampling, up-sampling, and skip connections.

Although in the original paper, the resolutions of input and output were different, that is, 572 × 572 and 388 × 388 pixels, respectively, we chose to keep our input and output resolution consistent at 304 × 304 pixels. This was done because the images in our dataset were not large enough to warrant the tiling strategy required for extremely large images. Thus, zeropadding allowed us to keep the input and output resolutions consistent, thereby allowing the retention of information present on the border of our images.

Using the decomposed images, in one instance, we input three images, namely, the original, the haemoglobin, and the melanin images, to our U-Net and obtained a single black-andwhite mask image as output as shown

RESULT:

We have shown that even without a large dataset and high-quality images, it is possible to achieve sufficient accuracy rates. In addition, we have shown that current state-of-the-art CNN models can outperform models created by previous research, through proper data pre-processing, selfsupervised learning, transfer learning, and special CNN architecture techniques. Furthermore, with accurate segmentation, we gain knowledge of the location of the disease, which is useful in the preprocessing of data used in classification, as it allows the CNN model to focus on the area of interest. Lastly, unlike previous studies, our method provides a solution to classify multiple diseases within a single image. With higher quality and a larger

quantity of data, it will be viable to use state-of-the-art models to enable the use of CAD in the field of dermatology