**LITERATURE SURVEY**

Several AI based tools have been discussed for the localization and classification of skin disease with erythema. Here, the main proposals available in the specialized literature are highlighted.

Kunio Doi et al [1] 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 colonography.

Trabelsi et al [2] experimented 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.

Rajab et al [3] implemented an ISODATA clustering algorithm to find the optimal threshold for the segmentation of skin lesions. 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.

Keke et al [4] implemented an improved version of the fuzzy clustering algorithm using the RGB, HSV, and LAB color spaces to create a model that is more robust to noisy data.

Lu et al [5] segmented erythema in the skin using the radial basis kernel function that allows SVMs to separate nonlinear hyperplanes.

Sumithra et al [6] combined a linear SVM with a k-NN classifier to segment and classify five different classes of skin lesions.

Maglogiannis et al [7] implemented a threshold on the RGB value for segmentation and used an SVM for classification. Although more robust than clustering algorithms, SVMs are more reliant on the preprocessing of data for feature extraction. Without preprocessing that allows a clear definition of hyperplanes, SVMs may also underperform.

Albawi et al [8] 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 preprocessing10. CNNs can expand the advantages of SVMs, such as robustness in noisy datasets without the need for optimal preprocessing, 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. Tus, for segmentation, we use a combination of down-sampling 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 degradation.

In this paper, 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 preprocessing 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 preprocessing 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.

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