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Examining Skin Images for Disease Diagnosis Using Statistical Analysis Combined with Machine Learning Techniques

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Abstract

In the early stages of cancer, it is crucial to automatically monitor and analyze the condition. An essential characteristic that is included in the majority of dermoscopy algorithms is the presence of irregular streaks. These streaks are strongly associated with carcinoma and basal cell cancer. One of the most unpleasant and potentially dangerous diagnostic test techniques is used for detection.Unfortunately, this means that machine-driven detection is where our focus will be.In this case, we primarily want to implement the GLCM options for detection. Skin lesion options are derived using GLCMs, which are normalized symmetrical grey level co-occurrence matrices.textural options derived from GLCM A Multi-Class Support vector machine is used for classification purposes, and its input consists of square measures derived from each of the four classes.

Keywords: Skin Cancer , Fuzzy Logic , Mat Lab.

1. Introduction

The skin is the body's outermost layer and a natural defense mechanism against environmental hazards. The human body's biggest organ is its skin. When it comes to controlling metabolic rates, the skin is king. The first line of defense against pathogens and other potentially harmful substances is the skin. Among the many types of skin cells are melanocytes and mesodermal cells. The skin is vulnerable to a wide variety of disorders. Skin cancer stands out among those conditions as the most serious and potentially fatal. The skin may be affected by the fatal skin cancer. A disturbing trend is the exponential growth in the number of cases of skin cancer. There is a lack of appropriate therapy and late diagnosis are the key factors. An aberrant proliferation of cells characterizes cancer. On the other hand, cancer cells may divide and multiply into even more aberrant cells. In a similar vein, melanocytic cell tumors may be defined as skin cancer. The pigment melanin, which serves as a barrier against dangerous radiations, is produced by these melanocytic cells. The aberrant development of melanocytic cells is caused by damage to the DNA of these cells caused by external agents such as ultraviolet radiations and hereditary factors. Cancerous growths are formed when these cells aggregate. Melanoma is another name for skin cancer since it starts in the melanocytic cells. A flattened lesion on the skin's surface is the first sign of skin cancer. A typical mole, it seems. However, it grows larger and develops into a cancerous tumor beyond a certain point. Failure to appropriately treat skin cancer might result in the patient's death. There is little hope for a patient's life when skin cancer spreads to deeper layers of skin. Cancer starts in one area of the body and travels to another via the bloodstream or lymphatic system, where it starts to develop new malignant growth. This is the characteristic that allows skin cancer to progress or spread.

There is less hope of healing the patient if cancer begins to spread. If caught early enough, melanoma may be treated. At first, melanoma is limited to the skin's surface. It is not yet life-threatening, and a full recovery is possible with prompt surgical removal of the lesion if caught early. Curability increases to over 90% with an early diagnosis and drops to below 50% with a late one. As a result, therapy efficacy depends on prompt diagnosis. The DNA of these cells is damaged by ultraviolet radiations and genetic factors, leading to the aberrant creation of melanocytic cells. Cancerous growths are formed when these cells aggregate. Skin cancer is sometimes called as cancer because it develops in melanocytic cells. At first, it seems like a flattened spot on the skin. A typical mole, it seems. However, it grows larger and develops into a cancerous tumor beyond a certain point.

2. Literature Survey

1) BiTr-Unet: A Convolutional Neural Network (CNN) Combined with a Transformer for MRI Brain Tumor Segmentation by Qiran Jia (2020) and Hai Shu (2022). Publication with the DOI 10.1007/978-3-031-09002-8_1.

In order to segment brain tumors in multi-modal MRI images, the suggested model, BiTr-Unet, integrates Convolutional Neural Networks (CNNs) with Transformer networks. On the BraTS2021 dataset, BiTr-Unet accomplishes remarkable results by combining the best features of the two architectures. The median Dice scores for the overall tumor, tumor core, and enhancing tumor on the validation set are 0.9335, 0.9304, and 0.8899, respectively, while the corresponding Hausdorff distances are 2.8284, 2.2361, and 1.4142. Dice scores for the tumor areas on the testing dataset are 0.9257, 0.9350, and 0.8874, whereas the corresponding Hausdorff distances are 3, 2.2361, and 1.4142.

2) Using a U-Net and DCNN Cascaded Learning Algorithm, a Clinical Decision Support Framework is developed for the purpose of segmenting and classifying brain tumor MRIs. With contributions from Tahir Ahmad, Ghada Atteia, Hanaa A. Abdallah, and Atif Rizwan, Nagwan Abdel Samee was a member of the research team in 2002. The citation for this article is 10.3390/healthcare1223440.

The goal of this research is to develop a CAD system that can efficiently and light-weightly categorize brain cancers in magnetic resonance imaging (MRI) images. A simplified U-Net deep network is used in the study to provide a real-time segmentation strategy. A reduced architecture for automated feature extraction and classification is proposed utilizing a deep convolutional neural network (DCNN).Tested on BRATS 2015 datasets, the method achieves competitive results in brain tumor segmentation and improves image classification accuracy from 88% to 88.6% for high-grade gliomas compared to previous studies.

3) To better segment and classify brain tumors, a deep learning framework has been developed that incorporates approaches for preprocessing MRI images. Members of the research team: Khiet Dang, Toi Vo, Lua Ngo, and Huong Ha (2022)

This study employs a deep learning pipeline for accurate glioma grading using MRI-based classification. Utilizing UNet for segmentation, VGG and GoogleNet for classification, and optimizing with data augmentation and window settings, the model achieves impressive Dice coefficients of 0.82, 0.91, and 0.72. The VGG-UNet pipeline attains a notable 97.44% accuracy, underscoring the significance of data augmentation and segmentation in refining glioma detection models.

4) Classification and identification of microscopic brain tumors using 3D convolutional neural network with feature selection architecture Noor Ayesha, Zahid Mehmood, Tanzila Saba, Muhammad Attique Khan, Amjad Rehman, and Usman Tariq (2021). This publication's DOI is 10.1002/jemt.23597.

Using deep learning, this research attempts to solve the critical problem of brain tumor identification and categorization. Given the alarming prevalence of brain tumors and the need for precise grading from MRI scans, the proposed method utilizes a 3D convolutional neural network (CNN) for initial tumor extraction. The extracted tumors then undergo feature extraction using a pre-trained CNN. A correlation-based feature selection method refines these features, which are subsequently employed for classification through a feed-forward neural network. Remarkably, the approach achieves high accuracies of 98.32%, 96.97%, and 92.67% on the BraTS datasets for 2015, 2017, and 2018, respectively. Comparative analysis indicates that the proposed method performs on par with existing techniques.

5) Transfer learning for brain tumor classification using deep convolutional neural network characteristics Deepak S, Ameer P. (2019). CompBioMed. DOI: 10.1016/j.compbiomed.2019.103345.

In order to classify brain tumors, this research employs deep transfer learning with a pre-trained Google Neural Network. With a mean classification accuracy of 98%, the system surpasses state-of-the-art approaches when it comes to differentiating pituitary tumors, gliomas, and meningiomas. Misclassifications are better understood because to the study's focus on transfer learning's effectiveness in situations where medical images are scarce.

6) Using a two-stage feature-level ensemble of deep convolutional neural network (CNN) models, MRI brain tumors may be classified. Mohammad Ali Moni, Nahid Ferdous Aurna, Kazi Abu Taher, Mohammad Abu Yousuf, and A K M Azad. Publication date: 2022, volume 20, issue 5, page 539.

In order to automate the course of cerebrum growth characterization, this study presents an extraordinary two-stage highlight outfit of profound CNNs. The model outperforms previous models with an impressive average accuracy of 99.13% using a combined dataset with three separate MRI datasets. There is a 98.96% overall accuracy, a 99.76% for Dataset 1, a 98.16% for Dataset 2, and a 99.76% for the Merged Dataset. A real-time validation User Interface (UI) is created, and Principal Component Analysis (PCA) is used for feature selection. The model's robustness is assessed through comprehensive performance metrics across three different experiments.

3.Image processing

The electronic realm includes image processing, which involves transforming a picture into a digital memory array of tiny numbers (called pixels) that represent a physical property (such scene radiance) and then processing that array using a computer or other digital appliance.

Imagine for a second that we capture a picture, a photograph, for example. Now, to simplify matters, let's pretend the picture doesn't have any color and is instead black and white (with plenty of shades of grey). According to figure 1, we may think of this picture as a two-dimensional function, where the values of the function represent the image's brightness at any particular location. In this kind of picture, the brightness values may presumably take on any actual value between zero (black) and one (white). While the image's specifics will dictate the x and y ranges, each variable may take on any actual value between the two extremes.

The x, y, and f(x, y) variables of a digital picture are uniquely distinct, setting it apart from a photo. As an example, the picture in figure 1.2 will typically have x and y values somewhere in the range of 1 and 256, and the brilliance values will likewise go from 0 (dark) to 255 (white).They typically only take on integer values. Essentially, a digital picture is just a huge array of individual dots, each of which represents a different level of brightness. These little dots are known as image elements, or pixels, for short. An individual pixel's neighborhood consists of all the pixels immediately around it. Just like a matrix, the geometry of a neighborhood may be used to describe it; for example, a 3*3 neighbourhood or a 5*7 neighbourhood are both valid formats. With the exception of very rare cases, every neighborhood has an odd number of rows and columns. This guarantees that the current pixel is located in the exact middle of the neighborhood. it can be required to identify which local pixel is the "current pixel" in either rows or columns.

4.Image Enhancement

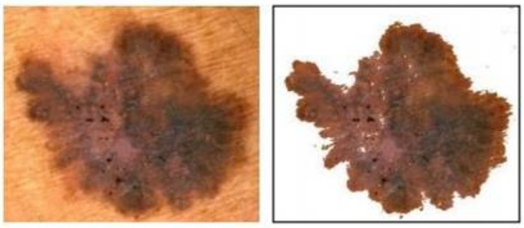

Fig.1 Affected Skin area

The goal of image enhancement is to increase the quality of digital images (for purposes such as visual inspection or machine analysis) without requiring any prior knowledge of how to do so.

The procedure is referred to as picture restoration if the cause of deterioration is identified. In both cases, the input and output are visual representations of some kind.

There are a plethora of approaches to picture improvement, most of them rely on heuristics and simple techniques. Since there is currently no reliable way to quantify picture quality, the issue is naturally vague. Here we go over a few of recipes that have worked for both humans and computers when it comes to recognition. These approaches focus on solving specific problems; what works well for one issue may not be suitable for another.

Automatic image enhancement

Fig.2 Enhanced skin area

Red eye reduction, sharpness adjustments, zoom capabilities, automated cropping, and basic automatic picture enhancing functions are common in camera or computer image editing applications.

These features also fix color hue and brightness imbalances. These are referred to as automated because, in most cases, they do not need any activity from the user and may instead be accessed with a single click of a button, mouse, or menu. On top of that, there are automated editing tools that allow you to do several edits with little to no human intervention.

5. K-MEANS CLUSTERING

Fig.2 Enhanced skin area

The principle of clustering algorithm based on vector quantization of signal processing is k-means and it can be applied to cluster analysis in data mining. The destination of k-means clustering is splitting n observations into k clusters, within which each observation is a prototype representing the mean of the group of the closest mean. The outcome is a data space partitioned into Voronoi cells. This is an NP-hard issue, although there are popular heuristic algorithms that do a good job and converge fast to a local optimum. These two methods adopt a similar strategy of iterative refinement, which is coincidental to the process of Gaussian mixture modeling in which the expectation-maximization procedure is used. Subsequently, these two methods employ the same cluster centers to depict the data, but it should be kept in mind that k-means clustering often places clusters with similar geographical orders whereas expectation-maximization can assign clusters of different shapes and sizes. Because of the similarity in their names, many people mistake this approach for k-means, but in reality, it is more closely related to the widely used k-nearest neighbor classifier. To add new information to the current bunches, one might utilize the 1-closest neighbor classifier on top of the group places delivered utilizing k-implies. The name for this approach is the Rocchio calculation or nearest centroid classifier.

Initialization methods

Methods like Forgy and Random Partition are often used for initialization.In order to establish baseline means, the Forgy technique randomly selects k observations from the dataset. Assigning observations to clusters at random is the first step in the Random Partition technique. Then comes the update step, which calculates the initial mean as the centroid of the clusters. A random partition brings all the initial means around the center of the data set, while the Forgy technique tends to scatter them out. Random Partition is the way to go for algorithms like fuzzy k-means and k-harmonic means, say Hamerly et al. When it comes to ordinary k-means algorithms and expectation maximization, the Forgy initialization approach is highly recommended.

K-means in image segmentation

A common technique for accurately categorizing an image's pixels in a decision-oriented application is image segmentation. It partitions a picture into many individual areas, with the goal of achieving strong contrast between areas and high similarity between pixels within each area. A number of industries may benefit from it, including medicine, image processing, traffic imaging, pattern recognition, and many more. A few methods exist for segmenting images: limit based, edge-based, group based, and brain network-based 1. In view of the numerous strategies, the grouping approach is among the most effective. K-means, fuzzy C-means, the Mountain clustering strategy, and subtractive clustering are just a few of the clustering techniques available.A widely used clustering technique is K-means clustering. After comparing it to Hierarchical clustering, it is both easier to understand and quicker to compute. Furthermore, it is capable of handling a huge number of variables. On the other hand, the output varies depending on the cluster count. There must be an initialization of the correct number of clusters, k 2.Set the k number of centroid as a starting value once again. Altering the original centroid value would produce distinct clusters. Determining the correct starting centroid is, therefore, a crucial step. In recent times, picture segmentation has emerged as a crucial tool in the field of medicine, namely for the extraction of regions of interest from backgrounds. As a result, several techniques are used to segment medical pictures, and the process outputs are subsequent utilized for further analysis within the medical field. In contrast, computer arrays of numbers depict medical pictures in their raw form; these numbers indicate the values of pertinent physical qualities that demonstrate contrast between various bodily sections. Processing and analysis of medical pictures are helpful for several reasons, including turning raw images into a symbolic form that can be quantified, extracting significant qualitative information to help with diagnosis, and combining complementing data from different imaging modalities. Imaging segmentation, which defines the borders of things like organs or aberrant regions in pictures, is one of the cornerstone challenges in medical analysis. An accurate radiation therapy treatment facility, shape analysis, and volume change detection are all made feasible by the segmentation results.One least-squares partitioning approach is K-Means, which divides a set of items into K groups. In two stages, the algorithm iterates:

- Determine the average of every group.
- Using the distance from the cluster mean, determine how far away each point is from each cluster.
- Put each dot in the cluster that is geographically closest to it.
- Repeat steps (a) and (b) until the total of squared errors within the group cannot be reduced any more.

For starters, you may just randomly give points to clusters. During the iterations, the method takes into consideration all groups and aims to minimize the total squared within group error, which is the distance of each point from its group mean. As soon as it becomes impossible to further reduce the goal function (i.e., the residual sum-of-squares), convergence must be achieved. The resulting groups are as geometrically compact as can be around their respective means. For every pixel in the collection of feature photos, a feature vector is built according to.

6.Proposed Methodology

Classifying images of cancer is a crucial step in creating classification maps, as the number of cancers being seen worldwide is steadily rising, and these cancers include various equipment that may capture images periodically and be used for various purposes. Therefore, cancer image categorization is a hotspot for study right now, and the findings from such studies have a wide range of potential real-world applications. Using cancer images, this technique suggested a new way to categorize six distinct types of skin cancer: actinic keratosis, cherry nevus, dermatofibroma, Melanocytic nevus, and melanoma. The system breaks down its work into several stages in order to construct an efficient cancer picture classification framework; each step is critical for providing greater classification accuracy, and each stage is detailed in detail on the next page. One possible interpretation of texture is as a roughness metric for surfaces. The noise produced by cameras, sensors, or films may lead to a certain kind of texture known as random texture. There is no discernible pattern to this kind. photographs with patterned texture are most easily discernible in satellite photographs. The land's texture changes depending on the activities that take place there, such farming or building. Image texture detection often makes use of operators such as rank, range, and gray-level variation. The range of the image's brightness values, from highest to lowest, is measured by the rank operator. The roughness of a surface is proportional to its range value. Using the range operator, we may transform the source picture into a texture-representative one by adjusting the brightness (4). One way to assess gray-level variation is by adding up the squares of the brightness changes between the central pixel and its neighbors.

Proposed System Flow Architecture

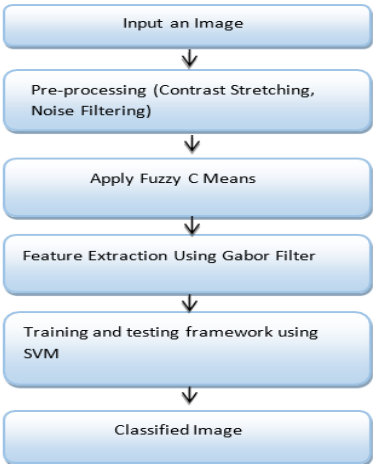

Fig.3 Proposed method

Step 1: - Input Image

We choose a cancer picture for categorization.

Step 2: - Pre-processing (Contrast Stretching, Noise Filtering)

Using the help of the image processing toolkit, noise filtering may eliminate unwanted details and different kinds of noise from photos.

Step 3: - Apply Fuzzy C Means

In order to segment and cluster images, fuzzy C methods are used.

Step 4: - Feature Extraction Using Gabor Filter

Input cancer images, such as texture, are processed to provide feature vectors using GLCM and the Gabor filter. An RGB image's texture element is then extracted. To define these image texture properties, the GLCM algorithms use global color histograms to extract cancer picture color information and compute the frequency with which pairs of pixels with certain values occur in images within a given spatial relationship.

Step 6: - Training and testing framework using SVM

Our suggested structure is trained and prepared using the Support Vector Machine technique, which makes use of these element vectors (texture and color). In order to go on to the next step of classification, the database stores the color and texture properties of every cancer picture.

After considering these component vectors This suggested structure use support vector machines (SVMs) to categorize cancer images according to color and texture.

Image categorization that works makes use of a number of distance metrics that quantify feature similarity. In this case, we conducted a similarity assessment using support vector machine classifiers between the Query Image's features and those of the database pictures.

By comparing the input picture's feature value with the feature value of images in the database, the support vector machine classifier can determine which class the input image belongs to.

Step 7: - Classified Image

Any given input picture may fall into one of six distinct types, or it can fall into one of five.

FEATURE EXTRACTION

To aid in the following learning and generalization processes, and sometimes even to lead to better human interpretations, feature extraction in image processing begins with an initial set of measured data and constructs derived values (features) designed to be useful and non-redundant. Feature extraction and dimensionality reduction go hand in together.

It is possible to minimize the amount of features (also called a features vector) in an input data set that is too big to analyze without some kind of duplication. This might be due to things like identical measurements in feet and meters or the repetitiveness of pictures shown as pixels. This method is known as feature selection. The goal is to carry out the intended activity using this condensed representation rather than the whole original data set, and the chosen features should include the relevant information from the incoming data.

Algorithm implementation issues

Typically, by far the majority of the computational effort and time is spent on calculating the median of each window. Because the filter must process every entry in the signal, for large signals such as images, the efficiency of this median calculation isa critical factor in determining how fast the algorithm can run. The "vanilla" implementation described above sorts every entry in the window to find the median; however, since only the middle value in a list of numbers is required, selection algorithms can be much more efficient. Furthermore, some types of signals (very oftenthe case for images) use whole number representations: in these cases, histogram medians can be far more efficient because it is simple to update the histogram from window to window, and finding the median of a histogram is not particularly onerous.

Edge preservation properties

Median filtering is one kind of smoothing technique, as is linear Gaussian filtering. All smoothing techniques are effective at removing noise in smooth patches or smooth regions of a signal, but adversely affect edges. Often though, at the same timeas reducing the noise in a signal, it is important to preserve the edges. Edges are of critical importance to the visual appearance of images, for example. For small to moderate levels of (Gaussian) noise, the median filter is demonstrably better than Gaussian blur at removing noise whilst preserving edges for a given, fixed window size.However, its performance is not that much better than Gaussian blur for high levels of noise, whereas, for speckle noise and salt and pepper noise (impulsive noise), it is particularly effective. Because of this, median filtering is very widely used in digital image processing.

6. Results

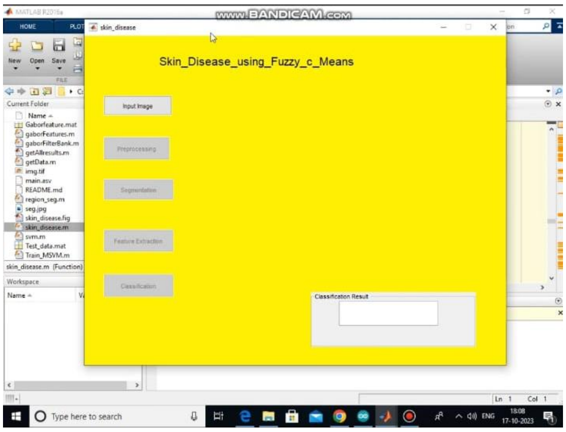

Fig.4 Classifier Output

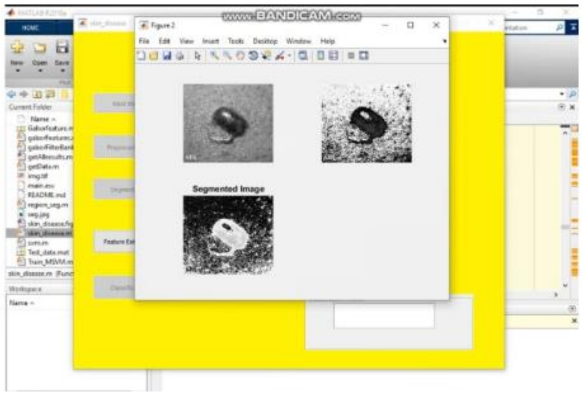

Fig.5 Classified skin image

Fig.6 Output concluded as Basic cell carcinoma

7.Discussion

The goal of this work is to explore digital image processing approaches for the automated detection of early malignant melanoma in a more effective and efficient manner. In this work, we zero in on the preprocessing phase, which comprises analyzing tumor images.

- Finding melanoma cancer early on may improve the likelihood of a successful cure.
- The existence of a significant number of injuries was indicated by the heuristic set threshold limit on the Euler value, which, when exceeded, was considered abnormal. Diseases may be identified by this key trait.
- The worrisome lesion is segregated from normal skin by segmentation. Malignant melanoma differs from benign melanoma in a number of important ways.

In this research, Structural Co-Occurrence matrices are utilized to extract features for the classification of skin diseases. Preprocessing methods involve applying a Median filter to remove salt and pepper noise, thus enhancing image quality. The prevalence of skin diseases underscores their significance as a global health issue.

Many researchers are committed to advancing the early detection and prevention of diseases. Amidst the existing methods, a novel approach has surfaced to improve accuracy in disease classification across networks. In comparison, our method demonstrates marginally lower accuracy rates. Simulation outcomes are outlined, emphasizing metrics such as accuracy. Our proposed approach achieves a classification accuracy of 97%, exceeding that of other established models.

The simplicity of the K-means clustering algorithm makes it widely used for clustering datasets across various domains. However, despite this advantage, its performance is often hindered by inherent implementation issues. Consequently, extensive research has been undertaken to enhance the algorithm's overall performance.

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