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Detectrozen (Disease Detection)

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ABSTRACT

With broad data development in biomedical and healthcare sectors, detailed analyzes of medical data support early detection of illness, patient care and community services. However, the quality of the study is lowered when the content of the medical data is incomplete. Also, various regions exhibit unique features of certain regional diseases. This can hinder disease outbreak forecasting. In this project, we streamline deep learning algorithms to effectively predict chronic disease outbreaks in populations with recurrent diseases. The diagnosis of diseases is a critical and central aspect of medicinal science. Doctors breakdown side effects in the human body more often than not to foresee diseases. In recent times, numerous research strategies have been used with a specific goal to make it more accurate. This system will help to predict the medical results efficiently. In this system, we will provide a user-friendly interface that can be used by the users to detect whether their medical test results are positive or normal, i.e. it will detect the disease.

There is a great growing interest in the domain of deep learning techniques for identifying and classifying images with various dataset. This deep learning project is based on a user interface and its application of the Detrozen real life. It will also describe how the system will perform and under what it must operate. In this document, the user interface will also be shown. Both the stakeholders(users) and the developers of the interface can benefit from this approach.

Keywords : Disease Detection, Feature Selection, Convolutional Neural Network, Deep Learning, Tensorflow.

I. INTRODUCTION

The days are long gone when data on health-care used to be small. The advancement level in devices for the acquisition of images is quite large and that is what makes image processing difficult and fascinating. This significant growth of medical images and techniques requires comprehensive and exhaustive efforts from a medical professional who is susceptible to human error and the result can also vary widely among various

experts. The alternative to this approach is to use machine learning or deep learning strategies for automating the detection process of various diseases.
Machine Learning (ML) and Artificial Intelligence (AI) have made significant progress over the past few years. ML and AI techniques have influenced medical fields such as medical image processing, image recognition, computer-aided diagnosis, image segmentation, and image fusion to name a few. While automated disease detection based on conventional medical imaging methods demonstrated significant accuracies for decades, breakthroughs in machine learning approaches have sparked a growth in deep learning. Deep learningbased algorithms demonstrated remarkable outcomes in various fields such as computer-aided diagnosis, speech recognition etc.
For our project, we have used the above stated idea behind disease detection, to construct a system using Convolutional Neural Network that detects the diseases quickly and also guarantees it to be free of error. By doing so we meant to minimize the human efforts that are required to detect a medical test report. We have tried to make the system user-friendly with the help of GUI, so that it can be used not only by the medical professionals but also by the population at large.

II. Statement of the Problem

This system will help to detect the medical results efficiently. In this detecting system, we will provide a user-friendly interface that can be used by the users to detect whether their medical test results are positive or normal, i.e. it will detect the disease. Decisions are often made based on the doctor's intuition and experience and sometimes that may not be completely correct. In this interface the predictions will be free of unwanted biases and errors- so it will be completely trustworthy. The doctors can also use this system to predict the results better.

III. Objectives of the study

Our team has created a Detectrozen which will detect if a patient is suffering from Malaria, Pneumonia, Breast cancer or Skin cancer by taking an essential input image. The Application of this product is created using Flutter module and for backend, four different custom CNN models are developed for detecting the diseases.

IV. REVIEW OF LITERATURE

BREAST CANCER
There are various ways of detecting breast cancer including mammography, MRI scans, computed tomography (CT) scans, ultrasound, and nuclear imaging. Although, none of these approaches provides a perfectly accurate cancer prediction. Tissue-based diagnosis is done primarily using a method of staining. Some staining elements, usually hematoxylin and eosin (H&E), is being used to colour elements of tissues in this method. Accordingly, cell structures, types and other foreign elements are stained and easily identifiable in high resolution. Pathologists then analyze the stained tissue slides under a microscope or use images taken from the camera in high resolution. A histopathology test is important for the identification of tumours. It is an old method for predicting invasive cancer cells from stained H&E tissues. There are different weaknesses in this procedure because it includes intra-observer variation, cancer cells and tissues can also have multiple appearances, and many other cell figures have the same hyperchromatic characteristics that make identification difficult. The selection of area is also a consideration as the procedure is conducted only on a specific tissue region, so the area chosen should be in the periphery of the tumour. Using deep learning techniques one can solve the aforementioned problems. Deep learning is a popular subcategory of machine learning technology that is inspired by the functioning of the human brain to examine unstructured patterns.

Deep learning models have a high chance of success as they train on representations in the hierarchy. They can also extract and organize unique attributes, and therefore do not require any prior knowledge of the domain. On the other side, trivial methods require rigorous feature engineering to acquire features which involve expertise in the domain. Many methods of deep learning have been proposed for predicting the tumour class. These are mostly binary classification [1,2] but some have used multi-variable classification [3]. Deep learning algorithms just need the data in the correct format and some suitable network parameters for the problem. Pre-designed networks such as AlexNet, MobileNet, Inception and many more can also be used [4]. Different scholars have proposed different methods and manual networks for classifying breast cancer besides the pre-designed networks mentioned above. Artificial neural networks rely, for example, on MLE (Maximum Likelihood Estimation) [5]. RBF Neural Networks on paper [6], the GRU-SVM model which is an ML algorithm coupled with a type of recurrent neural network (RNN) and gated recurrent unit (GRU) with support vector machine (SVM) [7]. Other scholars have developed methodologies including these techniques to achieve better results with less computational complexity. To reduce the size of the input feature, Karabatak et al. have proposed the AR + NN method which reduces the number of features by implementing association rules [8]. A combination of NN and multivariate adaptive regression splines (MARS) is also used for cancer detection [9]. Another method is the Fuzzy-artificial immune system and the KNN algorithm listed in Ref. [10]. Descriptors like CLBP, GLCM, LBP, LPQ, ORB, PFTAS are defined in paper [11] with breast cancer classification up to 85.1% accuracy. As with the BreakHis data set released in 2015, this has only been used by some scholars. For example, Fabio A. Spanhol [12] describes parameters and network configuration that has been accurate between 80 and 85%. The proposed method mentioned herein further reinforces this. Also, we present summaries of other methods along with their accuracies in the Discussion section. A series of tasks are implemented in deep learning algorithms. The first step is the preprocessing of images which is necessary to translate data into the format in which it can be input directly into the network. This step involves multiple image channeling, and then segmentation [13] is done (only if required, e.g. where regions of interest need to be separated from the background or parts which are not needed for training are omitted). At this point, data is ready for use in training, either in a supervised way or in an unsupervised way. The next step is feature extraction. Features represent the image's visual content for histopathology. In the case of supervised extraction of features, the features are known and various methods are used to discover them [14, 15, 16], but in the case of unsupervised feature extraction methods, features are not known and implicitly acquired through the Convolutional Neural Network (CNN) in the proposed solutions. The last phase is classification, which places an image in the respective category (benign or malignant) and can be done utilizing SVM (support vector machine) or using an activation function such as Softmax with a fully connected layer.

PNEUMONIA

Recent advances in deep learning models and the access to large datasets have enabled algorithms to outshine medical workers in various diagnostic imaging tasks,

such as detection of skin cancer [17], haemorrhage identification [18], arrhythmia detection [19], and diabetic retinopathy detection [20]. Automated diagnosis enabled by chest X-rays has taken on huge interest. These algorithms are progressively used to detect pulmonary lung nodule [21] and pulmonary tuberculosis classification [22]. The performance of many convolutional models on various abnormalities relying on the OpenI database available to the public [23] discovered that the same deep convolutional network architecture doesn’t well work across all abnormalities [24], ensemble models dramatically improved classification accuracy compared to a single model, and finally, the deep learning method improved accuracy compared to rule-based approaches.

Statistical dependence amongst labels [25] was studied to arrive at more accurate predictions, thereby outshining other approaches on given 13 images that were selected from 14 classes [26]. Algorithms for mining and predicting labels originating from radiology images were reviewed, as were studies [27–29], however, the image labels were usually limited to disease tags, and therefore lacked contextual information. Disease detection from X-ray images was investigated [30– 32], classifications on chest X-ray image views were performed [33], and segmentation of body parts from chest X-ray images and computed tomography was done [29, 34]. Conversely, the learning of image features using text and the creation of image descriptions are yet to be explored concerning what a person would say.

MALARIA

Malaria is commonly diagnosed by microscopic blood cell analysis using blood films[6]. Nearly 167 million blood films had been tested for malaria using microscopy during 2010 which was less expensive and less complex than the diagnosis based on polymerase chain reaction [36]. Though widely used, a microscopic diagnosis has many drawbacks like- malaria is generally linked to poverty and mostly arises in low-economic countries [37], where most laboratories or diagnostic facilities do not have standard testing facilities. Also, the diagnosis depends on the individual's ability to examine the blood film and the level of the parasites present thereon. Also, the monotonicity of the examination greatly influences the quality of the examination, especially towards the later part of a batch, when the lot has many specimens. Global pathology shortage [38] in general, seriously impacts the health care system in developing nations and malaria is no exception. Several Bangladeshi citizens opt for treatment abroad because of the lack of dependable diagnostic facilities [39] that is sadly not financially viable for the majority of people. Today's modern computer-aided systems utilise deep learning algorithms to analyze medical images [40]. There is a development around the world to simplify the diagnostic method with the assistance of various machine learning techniques to help human specialists make the right diagnosis. Liang et al . have proposed an approach based on deep learning for classifying cells infected with malaria from red blood smears. Their proposed method is based on a 16-layer convolutional neural network that uses the AlexNet architecture[41] pre-trained on the CIFAR-100 [42] dataset to outshine their transfer learning-based model. Dong et al. [43] used a dataset consisting of only about 1000 samples of training and testing and has used transfer learning and reported the outcomes on LeNet[44], AlexNet[45] and GoogleNet[46] architectures.

SKIN CANCER

Deep learning algorithms have recently gained huge success in various computer vision issues. Krizhevsky et al. in 2012 [63]inbuilt a novel technique (AlexNet) using convolutional neural networks for classifying a large data (1,2 million images) containing 1000 categories of objects in the 2010 ImageNet Large Scale Visual Recognition Challenge (ILSVRC2010) and delivers the highest result and, therefore, tremendous interest among academics in the field of computer vision. [68] Esteva et al. made significant progress on the classification of skin cancer through a pretrained model of GoogleNet Inception v3 CNN to categorize 129,450 clinical images of skin cancer including 3,374 dermatoscopic images. Yu et al. [64] developed a convolutional neural network for the classification of malignant melanoma with over 50 layers on ISBI 2016 challenge dataset. Haenssle et al., in 2018 [65] used a deep, convolutional neural network to identify the binary diagnostic group of melanocytic images dermoscopy.

V. Research Methodology

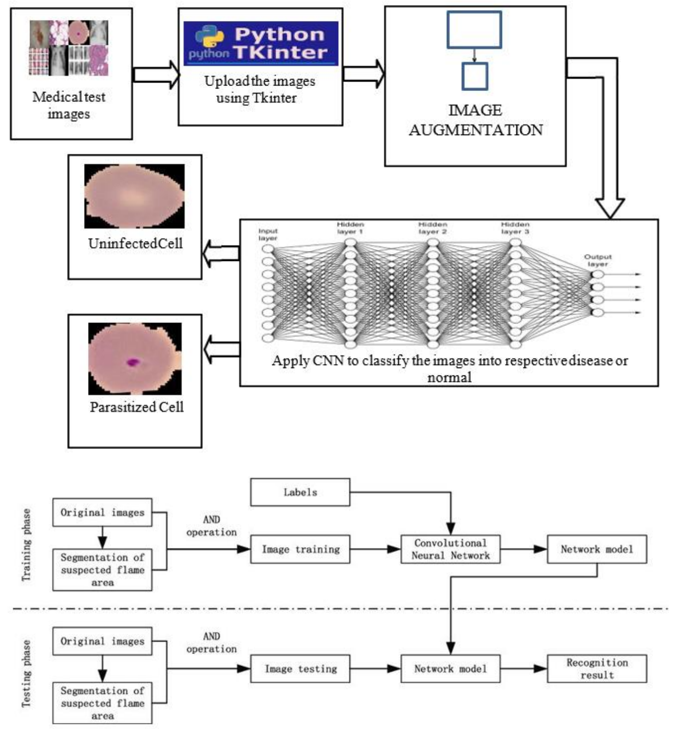


Fig: Researched Approach

CNN Model:

Convolutional Neural Networks (CNNs) are widely used for image recognition and classification tasks due to their ability to effectively learn features from images. In this specific approach, a series of convolution and max-pooling layers were employed in order to learn and extract relevant features from the input images. Convolutional layers are designed to perform feature extraction by applying a set of filters or kernels to the input image. Max-pooling layers are used to downsample the feature maps generated by the convolutional layers, thereby reducing the spatial dimensionality of the data.

Building a CNN (Convolutional Neural Network) model for disease detection involves the following steps:

1. Collect and preprocess the data: The first step is to collect the data for the disease you want to detect. This could include medical images, such as X-rays or MRI scans, or other relevant data. The data should be preprocessed, which may involve resizing, normalization, and augmentation.

2. Split the data into training, validation, and testing sets: Once you have preprocessed the data, you should split it into three sets: a training set, a validation set, and a testing set. The training set is used to train the model, the validation set is used to evaluate the model during training, and the testing set is used to evaluate the model after training.

3. Build the CNN model: The next step is to build the CNN model. This involves defining the architecture of the model, which typically includes several convolutional layers, pooling layers, and fully connected layers. You may also include dropout layers to prevent overfitting.

4. Train the model: Once the model is built, you can train it using the training set. This involves optimizing the model's parameters using an optimization algorithm, such as stochastic gradient descent (SGD). During training, you should monitor the model's performance on the validation set and adjust the model's hyperparameters, such as the learning rate, as necessary.

5. Evaluate the model: After training the model, you should evaluate its performance on the testing set. This will give you an estimate of how well the model will perform on new, unseen data. You can also use various metrics, such as accuracy, precision, and recall, to evaluate the model's performance.

6. Deploy the model: Once you are satisfied with the model's performance, you can deploy it for disease detection. This may involve integrating the model into a web or mobile application, or using it to analyze medical images in a clinical setting.

Overall, building a CNN model for disease detection can be a complex and challenging task, but it has the potential to improve the accuracy and efficiency of medical diagnosis and treatment.

The CNN Architecture is show as follow:

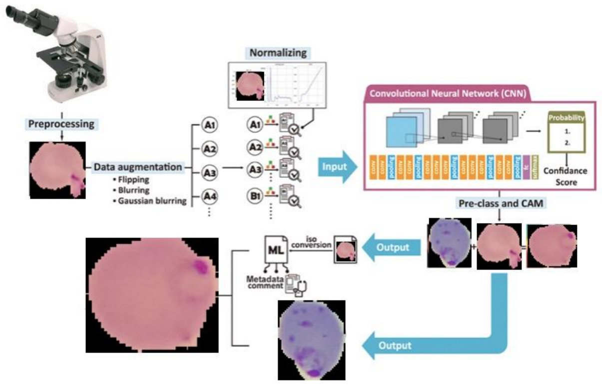


Fig: CNN Architecture

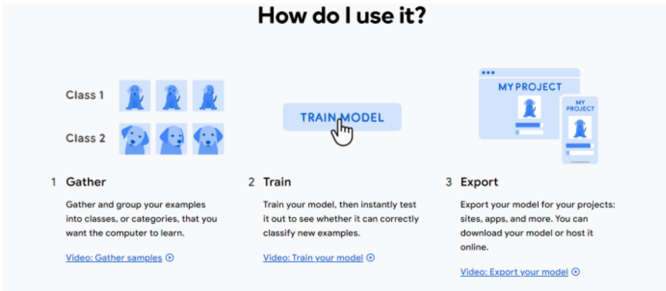
TensorFlow:

TensorFlow is a powerful open-source platform for machine learning that can be used for a wide range of tasks, including disease prediction. TensorFlow can be used to train models using large datasets of medical records and other patient data to predict the likelihood of a patient developing a particular disease. To build a disease prediction model with TensorFlow, you would need to collect a dataset of patient records that includes relevant medical information such as demographics, medical history, test results, and lifestyle factors. This dataset would need to be carefully curated and pre-processed to ensure that it is accurate and complete. Once you have a dataset, you can use TensorFlow to build a predictive model using techniques such as deep learning and neural networks. These models can be trained on the dataset to learn patterns and relationships in the data, and then used to make predictions about new patients based on their data. There are many potential applications for disease prediction using TensorFlow, including early detection of diseases such as cancer and heart disease, as well as personalized medicine and treatment planning. However, it is important to note that building accurate disease prediction models requires careful attention to data quality and model design, and should always be done in collaboration with medical experts to ensure that the models are safe and effective.

In this project Teachable Machine is used based on tensorflow .

Teachable Machine is a simple web-based tool that can be used to create custom machine learning models without any coding. While it can be used for many different applications, including image and sound recognition, it can also be used for disease prediction by training the model on patient data. However, it is important to note that Teachable Machine is a simplified tool and may not have the same level of accuracy or complexity as other machine learning platforms. Additionally, building accurate disease prediction models requires careful attention to data quality and model design, and should always be done in collaboration with medical experts to ensure that the models are safe and effective.

Method:



Dataset Description:

Kaggle is a popular platform for hosting and sharing datasets related to a wide range of topics. The datasets available on Kaggle are typically in a structured format, such as CSV, JSON, or SQL files, and are accompanied by a detailed description of the data, including the source, features, and any known limitations or issues with the data. The datasets on Kaggle cover a wide range of topics, including finance, healthcare, social media, transportation, and more. Some datasets are

public, while others may require registration or payment to access.
Sure! Here are brief descriptions of human disease prediction datasets related to malaria, pneumonia, skin cancer, and breast cancer available on Kaggle:

1. Malaria Cell Images Dataset: This dataset contains images of cells infected with the malaria parasite and uninfected cells, along with corresponding labels indicating whether the cell is infected or not. The dataset includes a total of 27,558 images, with approximately half of them infected with the malaria parasite. This dataset can be used for developing machine learning models to classify malaria-infected cells from uninfected cells based on the images.

2. Chest X-Ray Images (Pneumonia) Dataset: This dataset contains chest X-ray images of patients with and without pneumonia. The dataset includes a total of 5,856 X-ray images from over 3,600 patients. The images were obtained from different sources and have varying resolutions. This dataset can be used for developing machine learning models to accurately diagnose pneumonia from chest X-ray images.

3. Skin Cancer MNIST: HAM10000 Dataset: This dataset contains images of skin lesions, including benign and malignant types of skin cancer. The dataset includes a total of 10,000 images from over 7,000 patients. The images were obtained from different sources and have varying resolutions. This dataset can be used for developing machine learning models to accurately diagnose skin cancer from images of skin lesions.

4. Breast Cancer Wisconsin (Diagnostic) Dataset: This dataset contains features computed from digitized images of breast cancer biopsies, along with corresponding labels indicating whether the biopsy is malignant or benign. The dataset includes a total of 569 biopsy samples, with 212 malignant and 357 benign cases. The features include various measures of the cell nuclei, such as radius, texture, and concavity. This dataset can be used for developing machine learning models to accurately diagnose breast cancer from biopsy images.

These datasets can be used for developing and testing machine learning and statistical models for human disease prediction, which can aid in early detection and diagnosis of the respective diseases, ultimately improving patient outcomes.

Results and Discussion

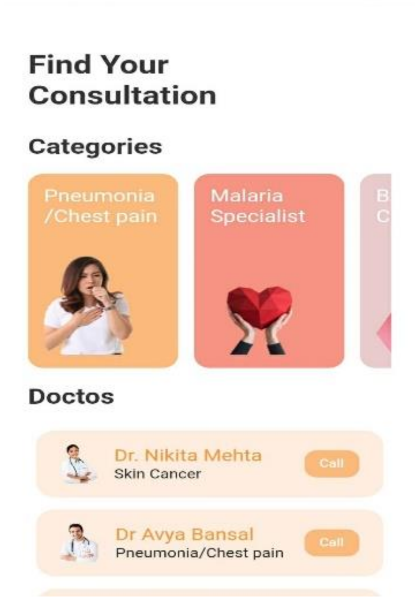


Fig: Home Screen

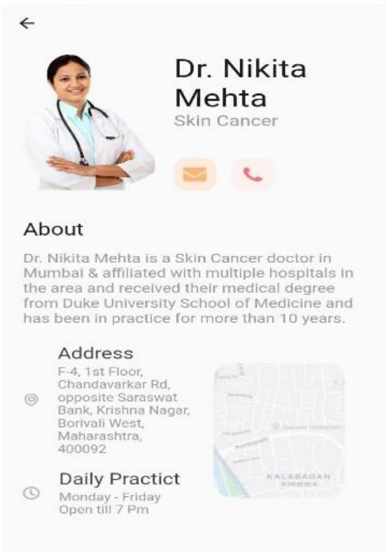


Fig: Consultation page

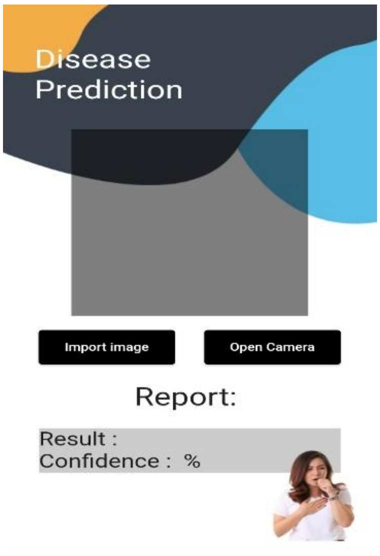


Fig: Disease Prediction page

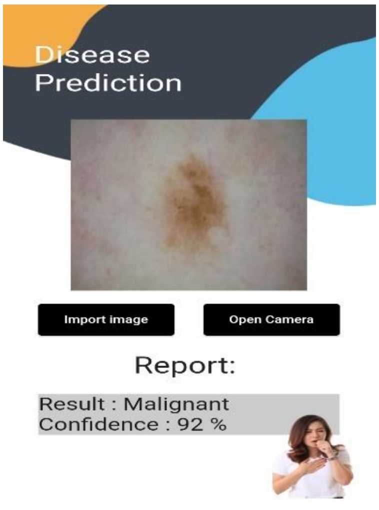


Fig: Detected Image Page

VI. CONCLUSION

In this work, a Detectrozen (Health detection) has been proposed for image classification that will work in real-life scenarios. The proposed method is based on an MVC architecture and the model is responsible for the behavioural aspect of the application. Different sub-models pertaining to the four diseases (malaria, pneumonia, breast cancer, and skin cancer) have been designed using a convolutional neural network (CNN). Each of the sub-models has its own specific set of activation and loss function with a single optimization function across all the models. Each of the models has been trained separately and the performance of the proposed model has been validated using a completely separate test set. Among all the four diseases, the model for skin cancer recorded the lowest accuracy at 84.6%. While classification accuracy to detect the presence of parasitized cells of malaria is seen to be highest at 95.21%. Pneumonia and breast cancer models showed performance accuracy of 90.47% and 86.88% respectively. Although the computational time of training each of the models is high, once the trained model is deployed, testing time is minimal. A GUI based web application has been designed with the help of python Tkinter such that real-life input can be given which will be passed on to the trained model for prediction. Therefore, the proposed work is suitable to be used in real-life situations as it is user friendly and cost-effective in nature.

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