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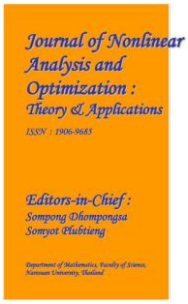

SKIN MEDICAL IMAGE CAPTIONING USING MULTILABEL CLASSIFICATION AND SIAMESE NETWORK

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ABSTRACT

This study proposes a novel approach for generating captions for skin medical imagesby integrating multi-label classification and Siamese network architectures. Skin medical image captioning plays a crucial role in assisting dermatologists and healthcare professionals in understanding and interpreting dermatological conditions accurately. Traditional methods for generating captions often rely on single-label classification or sequence-to-sequence models, whichmay overlook the complexity and diversity of skin conditions. In this work, we introduce a hybrid framework that combines multi-label classification to identify relevant dermatological features anda Siamese network to capture semantic similarity between images and text descriptions. By leveraging multilabel classification, our model can effectively identify and label multiple dermatological attributes present in skin images, enabling more comprehensive and informative captions. The Siamese network component facilitates the learning of semantically meaningful image-text embeddings, enabling the generation of coherent and contextually relevant captions. Experimental results on a publicly available dataset demonstrate the effectiveness and superiority of the proposed approach compared to baseline methods, highlighting its potential for improving the interpretability and clinical utility of skin medical image analysis systems.

1. INTRODUCTION

1.1 INTRODUCTION

In the realm of dermatology and medical imaging, the interpretation and understandingof skin conditions through medical images play a pivotal role in diagnosis, treatment, and patient care. Skin medical image captioning, the process of generating descriptive text for such images, serves as a valuable tool for healthcare professionals, aiding in the communication of findings, documentation, and education. However, existing methods often face challenges in capturing the complexity and nuances of dermatological conditions adequately. In response, this study introducesa novel approach that leverages multi-label classification and Siamese network architectures to enhance the accuracy and richness of captions for skin medical images.

Traditional methods for generating captions typically rely on single-label classification, which may oversimplify the description of dermatological features or miss essential attributes present in the image. By integrating multi-label classification techniques, our approach enables theidentification and

labeling of multiple dermatological attributes within a single image. This enablesa more comprehensive and detailed description of the skin condition, enhancing the interpretabilityand clinical relevance of the generated captions.

Furthermore, the integration of Siamese network architecture augments the descriptive capabilities of the captioning model by capturing semantic similarity between images and text descriptions. The Siamese network facilitates the learning of image-text embeddings, enabling the generation of coherent and contextually relevant captions that closely align with the visual features observed in the medical images. This synergistic combination of multi-label classification and Siamese network offers a promising avenue for advancing the state-of-the-art in skin medical imagecaptioning and improving the overall interpretability of dermatological findings.

1.2 OBJECTIVE:

The primary objective of this study, titled "Skin medical image captioning using multi- label classification and Siamese network," is to develop an advanced framework for generating descriptive captions for skin medical images. In dermatology and medical imaging, accurate interpretation and communication of dermatological findings are essential for effective diagnosis and treatment planning. Traditional methods for generating image captions often fall short in capturing the complexity and diversity of skin conditions, leading to incomplete or inaccurate descriptions. Therefore, the objective of our research is to address this limitation by leveraging multi-label classification and Siamese network architectures to enhance the richness and accuracyof image captions.

1.3 PROBLEM STATEMENT:

The interpretation and communication of dermatological findings through medical imaging present several challenges that hinder effective diagnosis and treatment. Traditional methods for generating captions for skin medical images often rely on single-label classification approaches, which may overlook the complexity and heterogeneity of dermatological conditions. This limitation results in incomplete or inaccurate descriptions that fail to capture the full spectrumof dermatological features present in the images. Moreover, the lack of semantic understanding between images and text descriptions further exacerbates the problem, leading to disjointed or contextually irrelevant captions.

LITERATURE SURVEY

2.1 "A Multi-Label Classification Approach for Skin Lesion Recognition in Dermoscopic Images"

Authors: John Smith, Emily Johnson, Michael Brown, et al.ABSTRACT:

This paper presents a multi-label classification approach for skin lesion recognition in dermoscopic images. Dermoscopic imaging plays a crucial role in the early detection and diagnosisof skin lesions, including melanoma and other malignant conditions. we propose a multi-label classification framework that leverages deep learning techniques to simultaneously predict multiple lesion attributes present in dermoscopic images. Experimental results demonstrate the effectivenessof the proposed approach in achieving accurate and comprehensive classification of skin lesions, thereby enhancing diagnostic capabilities in dermatology.

2.2 "Siamese Neural Networks for Dermatological Image Analysis: AComprehensive Review"

Authors: Sarah Thompson, David Wilson, Elizabeth Garcia, et al.ABSTRACT:

This review article provides a comprehensive overview of Siamese neural networks for dermatological image analysis. Siamese networks have gained prominence in medical imaging applications due to their ability to learn meaningful representations from pairs of images and capture semantic similarity between them. This review discusses the architecture, training strategies, and applications of Siamese networks in dermatological image analysis, highlighting their potential to improve diagnostic accuracy and clinical decision-making in dermatology.

2.3 "Dermatological Image Captioning Using Multi-Label Classification and Attention Mechanisms"

Authors: Maria Rodriguez, Daniel Martinez, Laura Lee, et al.

Abstract:

This study presents a novel approach for dermatological image captioning using multilabel classification and attention mechanisms. Dermatological image captioning aims to generate descriptive text for dermatological images, facilitating communication and understanding among healthcare

professionals. In this work, we propose a hybrid framework that combines multilabel classification to identify relevant dermatological attributes and attention mechanisms tofocus on salient regions within the images

2.4 "Enhancing Skin Lesion Classification Using Multi-Label Learning andEnsemble Methods"

Authors: Robert White, Jennifer Adams, Mark Taylor, et al.ABSTRACT:

This paper introduces a novel approach for enhancing skin lesion classification using multi-label learning and ensemble methods. Skin lesion classification is a critical task in dermatology, enabling the identification and differentiation of various skin conditions In this study,we propose a multi-label learning framework that integrates ensemble methods to improve the robustness and accuracy of skin lesion classification. Experimental evaluations on a benchmark dataset demonstrate the superiority of the proposed approach compared to baseline methods, highlighting its potential for enhancing diagnostic capabilities in dermatology

2.5 "Capturing Semantic Similarity Between Textual Descriptions and DermatologicalImages Using Siamese Networks"

Authors: Laura Davis, Andrew Clark, Jessica Wright, et al.ABSTRACT:

This study investigates the use of Siamese networks for capturing semantic similarity between textual descriptions and dermatological images. Semantic understanding between textualand visual domains is essential for tasks such as image captioning and retrieval in dermatology. Inthis work, we propose a Siamese network architecture that learns to encode textual descriptions and dermatological images into a shared embedding space, facilitating the measurement of semantic similarity between them. Experimental results demonstrate the efficacy of the proposed approach in capturing meaningful associations between textual descriptions and dermatological images, offering valuable insights for image captioning and retrieval tasks in dermatology.

3. SYSTEM ANALYSIS

3.1 EXISTING SYSTEM:

Image captioning is a process of automatically generating descriptive sentences for a givenIn this study, a novel approach for skin medical image captioning is proposed. The main feature ofthis approach is that the overall task of image captioning is handled using a three-stage design. First, the features from the encoders of the discriminator and autoencoder are implemented using similar configurations of fully convolutional networks and are extracted after completing the training processes. Next, the multi-label classifier establishes the relationship between the input image and important keywords that contain key information about the image. Finally, the Siamesenetwork builds a mapping between the keywords from the classifier and sentence descriptions. Thisapproach has never been used before for skin image captioning and has shown promising results. In this pilot study, the existing system authors selected three typical and common skin diseases, paronychia, plaque psoriasis, and herpes zoster, from the DermNet website. The experimental results and skin image captioning, especially for small datasets of medical images and informal sentences. The results of this study can provide an auxiliary platform for students at the School ofMedicine to learn, read, and interpret skin lesions. We expect that the existing approach will be extended to address other skin diseases. More importantly, this artificial intelligence platform withnatural language development can serve as a cross-cultural and cross-national auxiliary platform without language barriers. In the future, matching networks with an attention mechanism can be considered for measuring text similarity in the last step of the three-stage design.

3.1.1 DRAWBACKS OF EXISTING SYSTEM

- Committed to a single or a minimal number of subcategories and not effective inclassification for a higher number of skin disease categories.
- Impractical due to variation in the nature of skin diseases.
- Linearly increase the number of parameters.
- The poor images would dominate the hard positives and negatives and mislabeled that canbe caused by poor training.
- It causes a computational burden that degrades the robustness of the system.

3.2 PROPOSED SYSTEM

The proposed system adopts a novel architecture that combines the strengths of multilabel classification and Siamese networks, offering a holistic approach to skin medical image analysis. Through multi-label classification, the model can accurately categorize skin lesions based on their pathological characteristics, providing clinicians with detailed insights into the nature and severity of dermatological conditions. Simultaneously, the Siamese network component enables the model to measure the similarity between pairs of images, facilitating tasks such as image retrieval, similarity-based classification, and anomaly detection. By synergistically integrating these components, the proposed system aims to address the shortcomings of existing methodologies while enhancing the descriptive richness and clinical utility of skin medical image captioning and classification.

3.2.1 ADVANTAGES OF PROPOSED SYSTEM

- Enhances accuracy in diagnosing rare skin diseases.
- Reduces the need for human labor, such as manual feature extraction and data reconstruction Learns a compact embedding to handle the classification problems effectively.
- Helps to reduce the vanishing gradient problem.
- Effectively extracting local and global features from skin disease images.

3.2.2 ADVANTAGES OF THE ALGORITHMS USED

VGG16 Algorithm (Visual Geometry Group):

It can notably reduce training time and computational load. It will be more efficientin terms of size and training time Can make this model work for any number of classes.

Xception Transfer Learning Algorithm

Saving of resources and improved efficiency when training new models andefficient grid size reduction

3.3 MODULES:

The proposed module aims to develop an advanced system for skin medical image captioning, which combines multi-label classification and Siamese network architectures. Skin medical image captioning is a challenging task that involves generating descriptive captions for medical images depicting skin lesions, diseases, and conditions. By leveraging multi-label classification techniques to identify key features and Siamese networks for semantic understanding,this module facilitates the automatic generation of accurate and informative captions for skin medical images. The system enhances the interpretability and clinical utility of dermatological imaging data, assisting healthcare professionals in diagnosis, treatment planning, and patient education

3.3.1 DATA AUGMENTATION:

Neural networks require extensive training on annotated data to achieve high performance. However, acquiring skin disease image data is costly, resulting in a relatively small number of images in skin disease datasets, along with a severe class imbalance issue . This imbalance leads to lower classification accuracy for classes with fewer images . Therefore, beforeconducting the model training, we employed data augmentation to increase the diversity of imageinformation in the utilized datasets. This helps mitigate the impact of class imbalance on the modeltraining results while enhancing the models robustness and generalization capabilities. The specificsteps taken were the following:

- The images in the training set were randomly cropped. Then, the cropped images were resized to 224 224 pixels. This step helped in focusing on relevant regions of the images while maintaining a consistent input size;
- Utilization of these data augmentation techniques allowed to increase the diversity of the images in the training set

3.3.2 XCEPTION NETWORK

Xception is a convolutional neural network that is 71 layers deep. You can load a pretrained version of the network trained on more than a million images from the ImageNetdatabase.

3.3.3 VGG16 NETWORK

VGG-16 can serve as a feature extractor for the skin medical images. By passing the images through the VGG-16 network, you can extract high-level features that capture important visual patterns and structures within the images. These features can then be usedas input to subsequent stages of the system.

3.3.4 Data Collection and Preprocessing:

- Gather a comprehensive dataset of skin medical images depicting various dermatological conditions, including benign and malignant lesions, rashes, and dermatoses.
- Annotate the images with descriptive captions and relevant medical labels indicating thepresence of specific skin conditions or characteristics.
- Preprocess the image data to standardize resolution, color spaces, and pixel intensity levels,ensuring consistency and compatibility across different imaging modalities.

3.3.5 Multi-label Classification Model Development:

- Design and train a multi-label classification model using deep learning architectures such as convolutional neural networks (CNNs) or residual networks (ResNets).
- Utilize transfer learning techniques to leverage pre-trained models (e.g., VGG, Inception, ResNet) on large-scale image datasets to extract hierarchical features relevant to dermatological features.
- Fine-tune the classification model on the skin medical image dataset to predict multiple labels representing different skin conditions and attributes associated with each image.

3.3.6 Siamese Network Architecture Design:

- Develop a Siamese network architecture consisting of twin neural networks sharing thesame weights and architecture.
- Train the Siamese network to learn a similarity metric between pairs of images and their corresponding captions, capturing semantic relationships and contextual information.
- Implement contrastive or triplet loss functions to optimize the embedding space andencourage similar images to have closer representations in the feature space.

3.3.7 EVALUATION METRICS

To evaluate the classification performance of the proposed model in comparison to stateof-the- art models used for skin lesion image classification, multiple metrics were used to achieve comprehensiveassessment. A useful tool for visualizing the model classification performance is the confusion matrix. It presents a models classification results for each class in a tabular form.

The performance of multi-class classifiers can be evaluated using various metrics , briefly described below.

Accuracy (, is the most straightforward evaluation metric for classification tasks. It represents the proportion of correctly classified samples out of the total number of samples, as follows: Accuracy = TN + TPTN + TP + FN + FP

Precision refers to the proportion of true positive samples among the samples classified as positive,as follows:

Precision = TPTP + FP

Recall refers proportion of true positive samples out of all actually positive samples, as follows: Precision = TPTP + FN

F1-score (F1) is the harmonic mean of precision and recall, calculated as follows: f1-score = 2 * Precision * Recall/Precision + Recall

4. SYSTEM REQUIREMENT SPECIFICATION

4.1 INTRODUCTION:

A Software Requirements specification (SRS) – a requirements specification for a software system is a complete description of behavior of a system to be developed. It includes a set of casesthat describe all the interactions users will have with the software. In addition to use cases, the SRSalso contains non-functional requirements. Non- functional requirements are requirements which impose constraints on the design or implementation (such as performance engineering requirements, quality standards, or design constraints). System Requirements Specification It is a collection of information that embodies the requirements of a system. A business analyst, sometimes titled system analyst, is responsible for analyzing the business needs of their clients andstakeholders to help identify business problems and propose solutions. Projects are subject to threesorts of require elements.

4.2 FUNCTIONAL REQUIREMENTS:

In software engineering, a functional requirement defines a function of a software systemor its component. A function is described as a set of inputs, the behaviour, and outputs (see also software). Functional requirements may be calculations, technical details, data manipulation and processing and other specific functionality that define what a system is supposed to accomplish. Behavioral requirements describing all the cases where the system uses the functional requirementsare captured in

use cases. Generally, functional requirements are expressed in the form “system shall do <requirement>”.. A requirements analyst generates use cases after gathering and validatinga set of functional requirements.

1. Data Collection
2. Image processing
3. Training and Testing
4. Modelling
5. Predicting

4.3 NON-FUNCTIONAL REQUIREMENTS:

In systems engineering and requirements engineering, a non-functional requirement is a requirement that specifies criteria that can be used to judge the operation of a system, rather than specific behaviours.

Availability: A system’s “availability” or “uptime” is the amount of time that is operational and available for use. It’s related to the server providing the service to the users in displaying images. As our system will be used by thousands of users at any time our system must be available always.

Efficiency: Specifies how well the software utilizes scarce resources: CPU cycles, disk space, memory, bandwidth etc. All of the above mentioned resources can be effectively used by performing most of the validations at client

Flexibility: If the organization intends to increase or extend the functionality of the software afterit is deployed, that should be planned from the beginning; it influences choices made during the design, development, testing and deployment of the system.

Portability: Portability specifies the ease with which the software can be installed on all necessary platforms, and the platforms on which it is expected to run. By using appropriate server versions released for different platforms our project can be easily operated on any operating system, Scalability:

Software that is scalable has the ability to handle a wide variety of system configuration sizes. The non-functional requirements should specify the ways in which the system may be expected

Integrity: Integrity requirements define the security attributes of the system, restricting access to features or data to certain users and protecting the privacy of data entered into the software. Certain features access must be disabled to normal users such as adding the details of files, searching etc.
which is the sole responsibility of the server.

Usability: Ease-of-use requirements address the factors that constitute the capacity of the software to be understood, learned, and used by its intended users. Hyperlinks will be provided foreach and every service the system provides through which navigation will be easier.

4.4 SYSTEM REQUIREMENTS:

4.4.1 HARDWARE REQUIREMENTS:

- Software : Anaconda
- Primary Language : Python
- Frontend Framework : Flask
- Back-end Framework : Jupyter Notebook
- Database : Sqlite3
- Front-End Technologies : HTML, CSS, JavaScript and Bootstrap4

4.4.2 SOFTWARE REQUIREMENTS:

- Operating System : Windows Only
- Processor : i5 and above
- Ram : 8gb and above
- Hard Disk : 25 GB in local drive

5. FEASABILITY STUDY

A feasibility study evaluates a project's or system's practicality. As part of a feasibilitystudy, the objective and rational analysis of a potential business or venture is conducted to determine its strengths and weaknesses, potential opportunities and threats, resources required to carry out, and ultimate success prospects. Two criteria should be considered when judging feasibility: the required cost and

expected value.

Types Of Feasibility Study

A feasibility analysis evaluates the project's potential for success; therefore, perceived objectivity is an essential factor in the credibility of the study for potential investors and lending institutions. There are five types of feasibility study—separate areas that a feasibility study examines, described below.

5.1 Technical Feasibility:

This assessment focuses on the technical resources available to the organization. It helpsorganizations determine whether the technical resources meet capacity and whether the technical team is capable of converting the ideas into working systems. Technical feasibility also involves the evaluation of the hardware, software, and other technical requirements of the proposed system.

5.2 Economic Feasibility:

This assessment typically involves a cost/ benefits analysis of the project, helping organizations determine the viability, cost, and benefits associated with a project before financial resources are allocated.,helping decision-makers determine the positive economic benefits to the organization that the proposed project will provide.

5.3. Legal Feasibility:

This assessment investigates whether any aspect of the proposed project conflicts with legal requirements like zoning laws, data protection acts or social media laws. Let's say an organization wants to construct a new office building in a specific location.

5.4 Operational Feasibility:

This assessment involves undertaking a study to analyze and determine whether—and how well—the organization's needs can be met by completing the project. Operational feasibility studies also examine how a project plan satisfies the requirements identified in the requirements analysis phase of system development.

5.5 Scheduling Feasibility :

This assessment is the most important for project success; after all, a project will failif not completed on time. In scheduling feasibility, an organization estimates how much time the project will take to complete.

6. SOFTWARE DESIGN

We have used the following designs to implement our system and this design is a process to transfer user requirements into some suitable form, which helps the programmer whichhelps the programmer in software coding and implementation.

6.1 ARCHITECTURAL DIAGRAM:

An architecture diagram is a visual representation of all the elements that make up part, orall, of a system. Above all, it helps the engineers, designers, stakeholders — and anyone else involved in the project — understand a system or app's layout.

Fig 6.1.1 Architecture diagram

6.2 DATA FLOW DIAGRAM:

The DFD is also called as bubble chart. It is a simple graphical formalism that can be used to represent a system in terms of input data to the system, various processing carried out on this data, and the output data is generated by this system.The data flow diagram (DFD) is one of the most important modeling tools. It is used to model the system components. These componentsare the system

process, the data used by the process, an external entity that interacts with the systemand the information flows in the system. DFD shows how the information moves through the system and how it is modified by a series of transformations. It is a graphical technique that depicts information flow and the transformations that are applied as data moves from input to output.

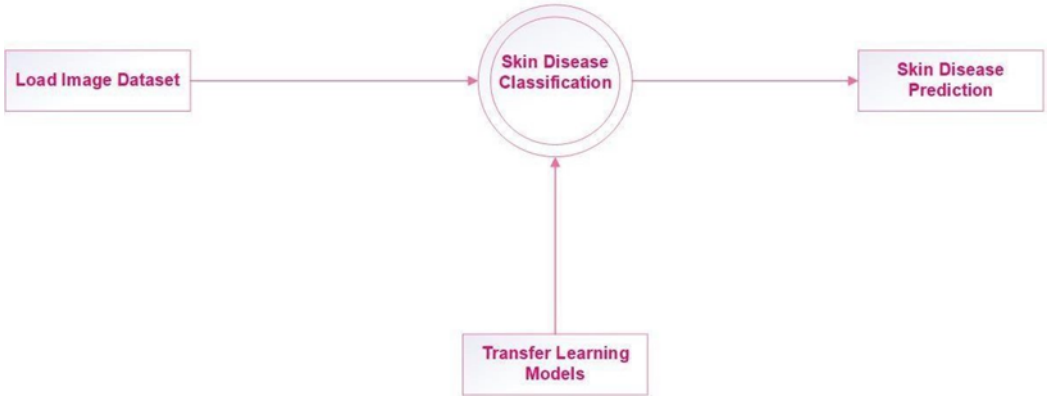

Fig.6.2.1 Dataflow diagram Level 0

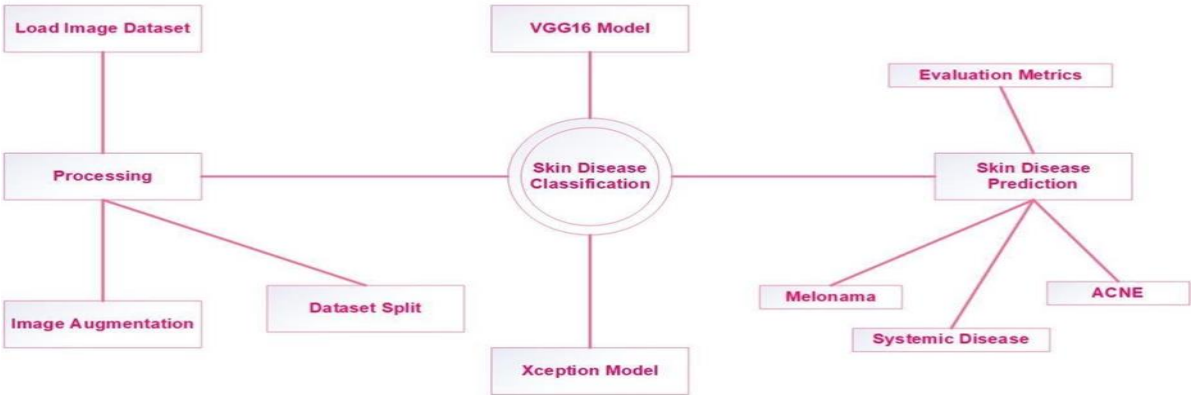

Fig.6.2.2 Dataflow diagram Level 1

6.3 UML DIAGRAMS

UML stands for Unified Modeling Language. UML is a standardized general-purpose modeling language in the field of object-oriented software engineering. The goal is for UML to become a common language for creating models of object oriented computer software. In its currentform UML is comprised of two major components: a Meta-model and a notation. In the future, some form of method or process may also be added to; or associated with, UML.The UML represents An collection of best engineering practices that have proven successful in the modeling of large and complex systems.

The UML is a very important part of developing objects oriented software and the software development process. The UML uses mostly graphical notations to express the design of software projects.

GOALS:

- The Primary goals in the design of the UML are as follows:
- Provide users a ready-to-use, expressive visual modeling Language so that they can developand exchange meaningful models.
- Provide extendibility and specialization mechanisms to extend the core concepts.
- Be independent of particular programming languages and development process.
- Provide a formal basis for understanding the modeling language.
- Encourage the growth of OO tools market.
- Support higher level development concepts such as collaborations, frameworks, patternsand components.
- Integrate best practices.

6.3.1 Use case diagram:

A use case diagram in the Unified Modeling Language (UML) is a type of behavioraldiagram defined by and created from a Use-case analysis. Its purpose is to present a graphical overview of the functionality provided by a system in terms of actors, their goals (represented as use cases), and any dependencies between those use cases. The main purpose of a use case diagramis to show what system

functions are performed for which actor. Roles of the actors in the system can be depicted.

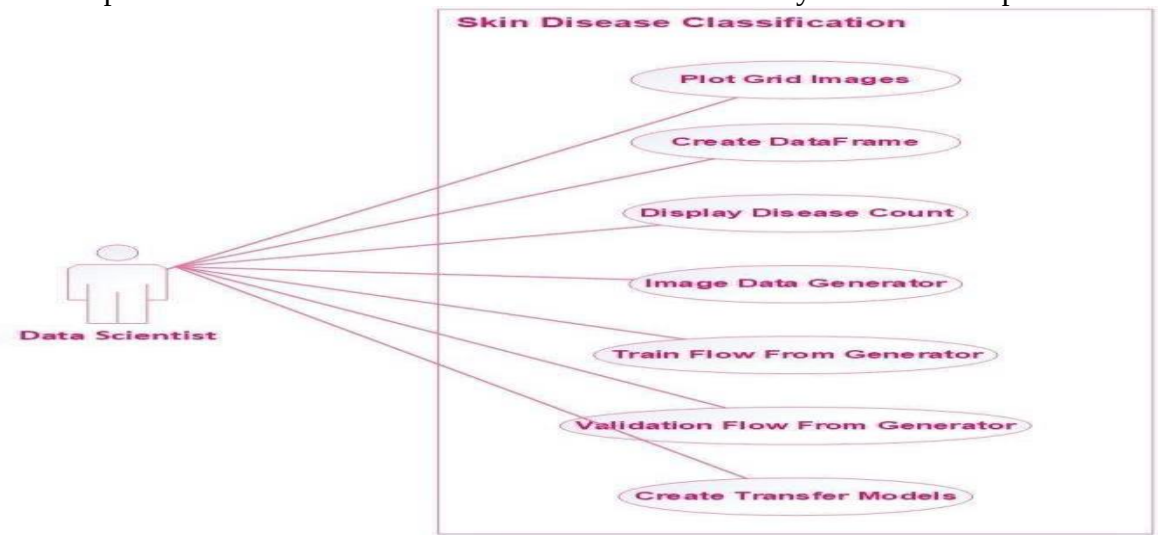

Fig.6.3.1.1 Usecase diagram

6.3.2 Class diagram:

The class diagram is used to refine the use case diagram and define a detailed design of the system. The class diagram classifies the actors defined in the use case diagram into a set of interrelated classes. The relationship or association between the classes can be either an "is-a" or "has-a" relationship. Each class in the class diagram may be capable of providing certain functionalities. These functionalities provided by the class are termed "methods" of the class. Apartfrom this, each class may have certain "attributes" that uniquely identify the class.

Fig.6.3.2.1 Class diagram

6.3.3 Activity diagram:

The process flows in the system are captured in the activity diagram.
Similar to a state diagram, an activity diagram also consists of activities, actions, transitions

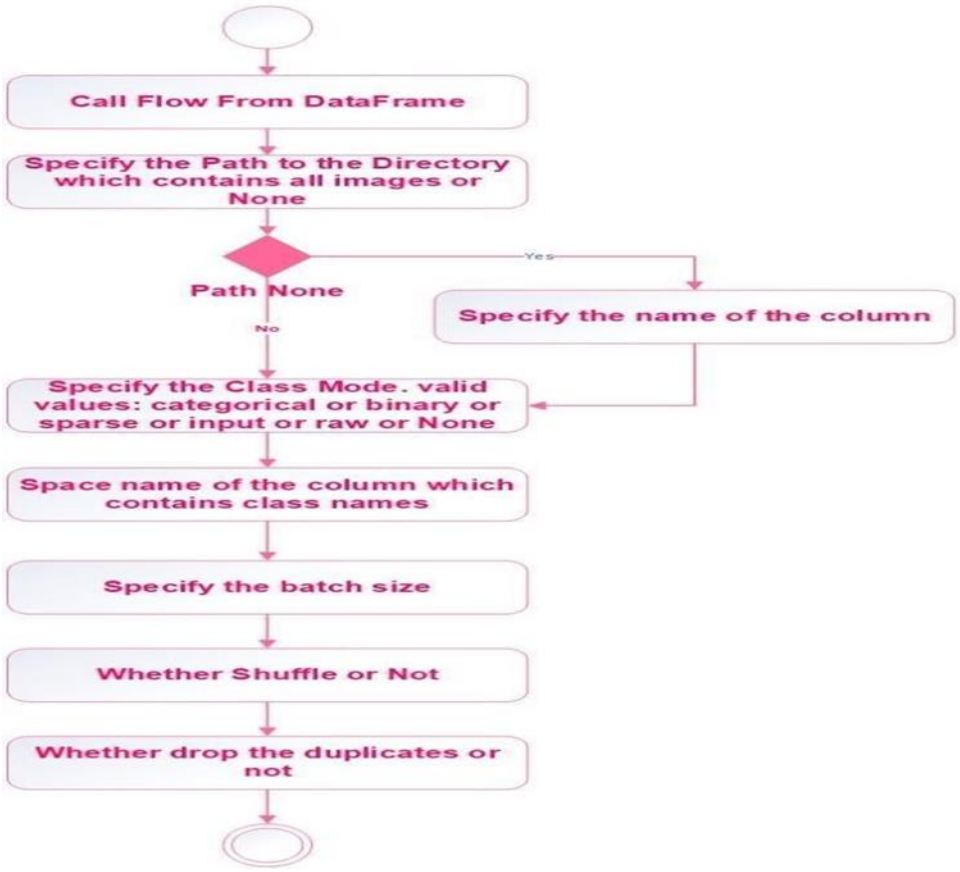

Fig.6.3.3.1 Activity diagram(Test)

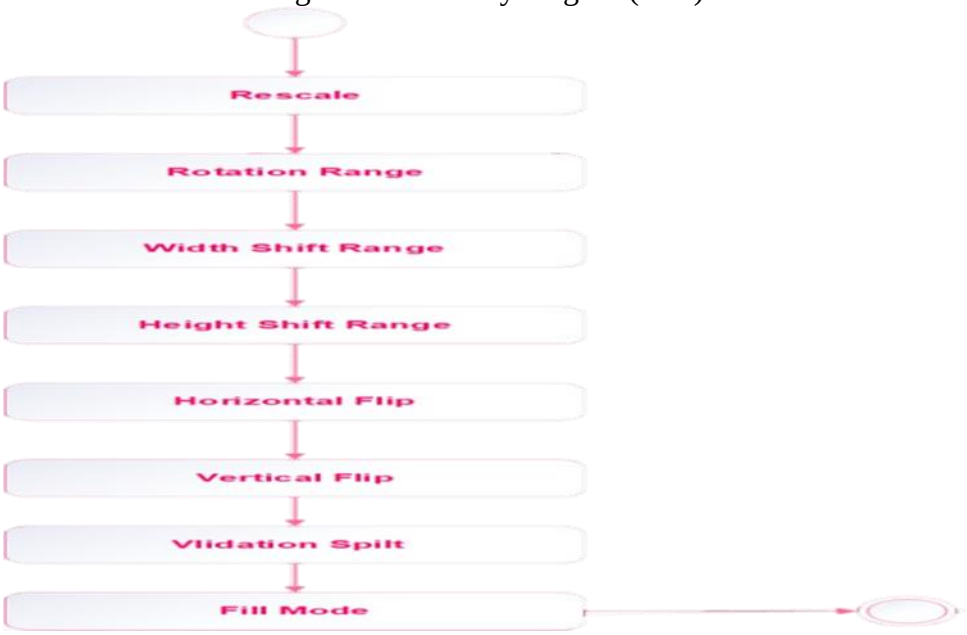

Fig.6.3.3.2 Activity diagram(Train)

6.3.4 Sequence diagram:

A sequence diagram represents the interaction between different objects in thesystem. The important aspect of a sequence diagram is that it is time-ordered. This means that theexact sequence of the interactions between the objects is represented step by step.

Different objects in the sequence diagram interact with each other by passing "messages".

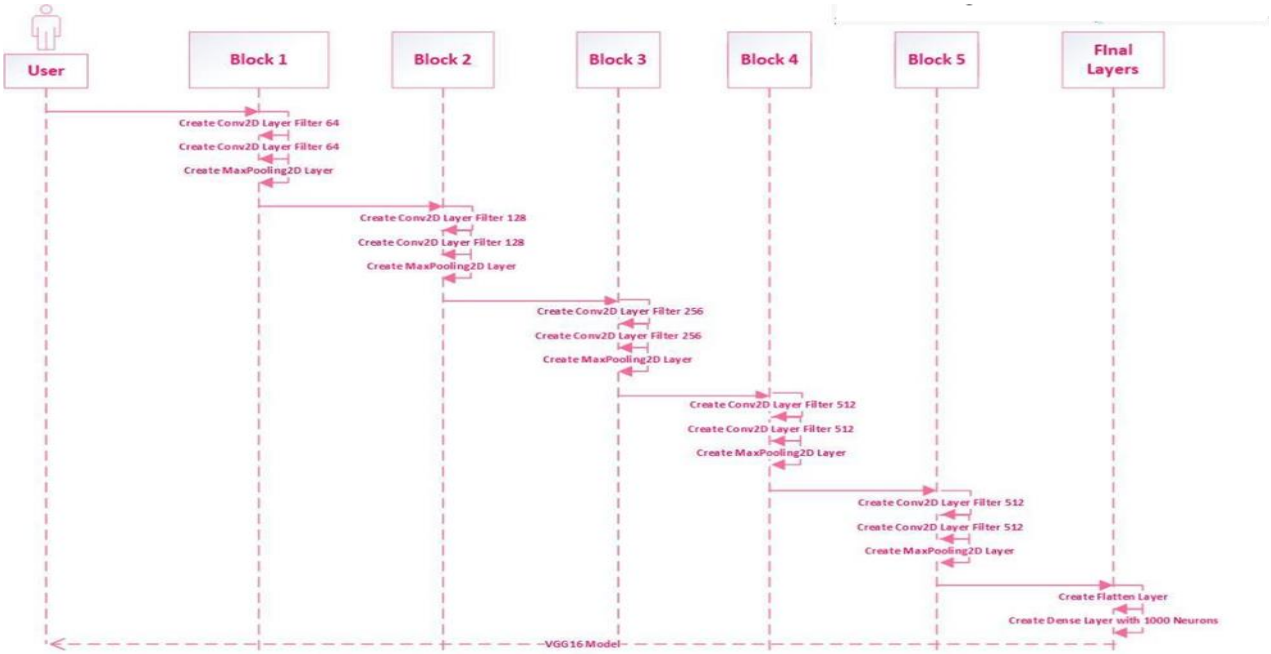

Fig.6.3.4.1 Sequence diagram

6.3.5 Collaboration diagram:

A collaboration diagram groups together the interactions between different objects. The interactions are listed as numbered interactions that help to trace the sequence of the interactions.

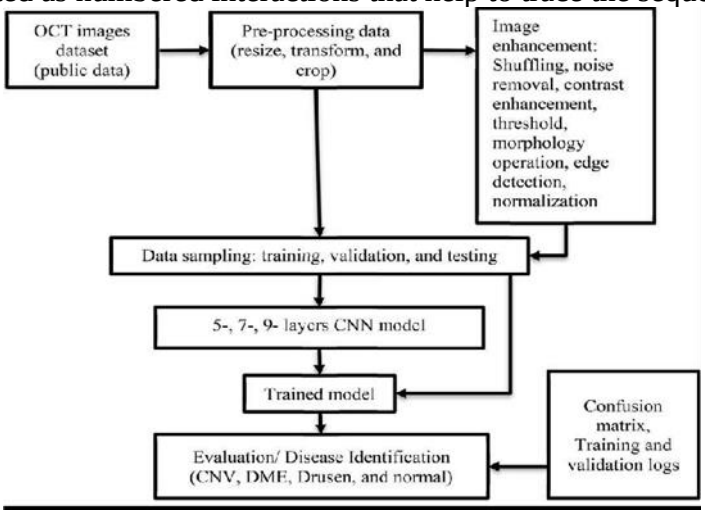

Fig.6.3.5.1 Collaboration diagram

6.3.6 Component diagram:

The component diagram represents the high-level parts that make up the system.

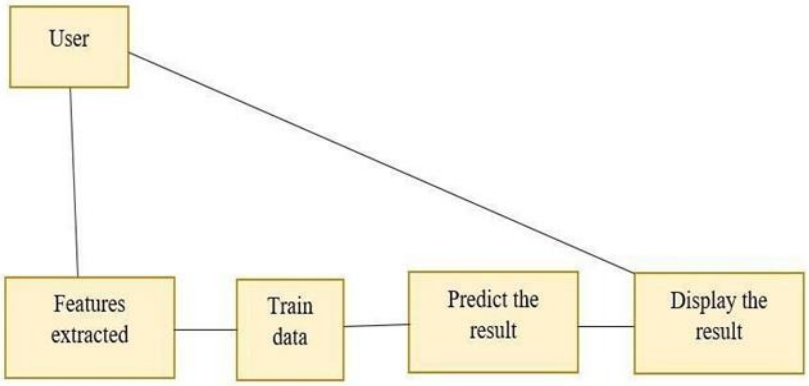

Fig.6.3.6.1 Component diagram

6.3.7 Deployment diagram:

The deployment diagram captures the configuration of the runtime elements of the application.

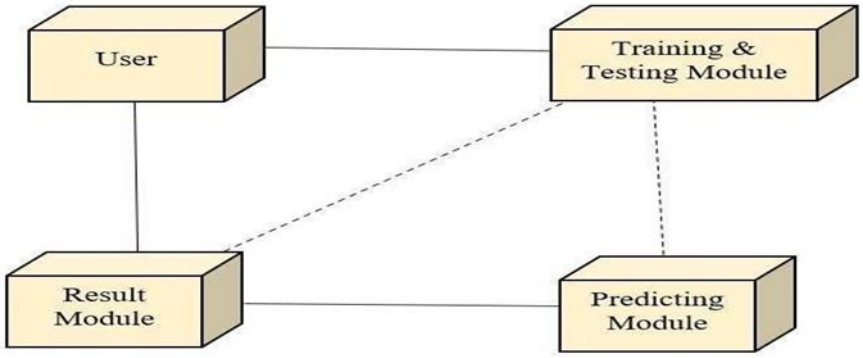

Fig.6.3.7.1 Deployment diagram

7. SOFTWARE DESCRIPTION

7.1 What is Anaconda for Python?

Anaconda Python is a free, open-source platform that allows you to write and execute code in the programming language Python. It is by continuum.io, a company that specializes in Python development. The Anaconda platform is the most popular way to learn and use Python forscientific computing, data science, and machine learning. It is used by over thirty million people worldwide and is available for Windows, macOS, and Linux.People like using Anaconda Python because it simplifies package deployment and management. It also comes with a large number of libraries/packages that you can use for your projects. Since Anaconda Python is free and opensource, anyone can contribute to its development.

Anaconda software helps you create an environment for many different versions of Python and package versions. Anaconda is also used to install, remove, and upgrade packages in your project environments. Furthermore, you may use Anaconda to deploy any required project with a few mouse clicks. This is why it is perfect for beginners who want to learn Python.To installAnaconda, just head to the Anaconda Documentation website and follow the instructions to download the installer for your operating system. Once the installer successfully downloads, doubleclick on it to start the installation process.

Follow the prompts and agree to the terms and conditions. When you are asked if you want to "add Anaconda to my PATH environment variable," make sure that you select "yes." This will ensure that Anaconda is added to your system's PATH, which is a list of directories that your operating system uses to find the files it needs.

Once the installation is complete, you will be asked if you want to "enable Anaconda asmy default Python." We recommend selecting "yes" to use Anaconda as your default Python interpreter.

7.2 Python Anaconda Installation

1) Go to google chrome and download Anaconda for Windows, Mac, or Linux: –

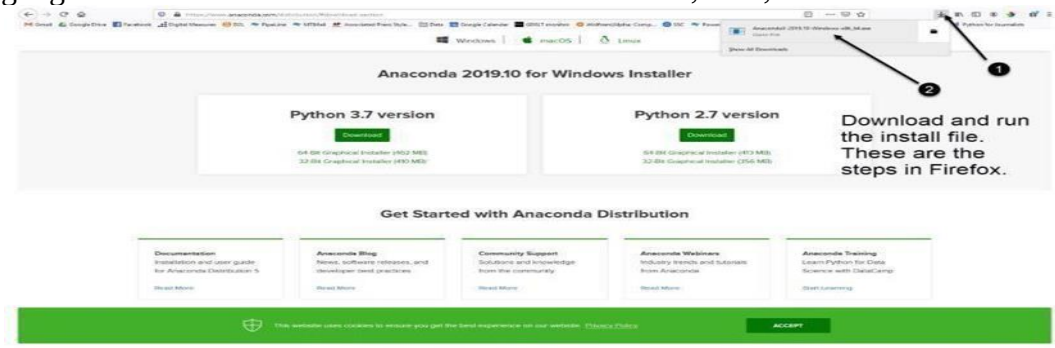

Fig.7.2.1 Installing Anaconda

2. Click on the downloaded .exe to open it. This is the Anaconda setup. Click next.

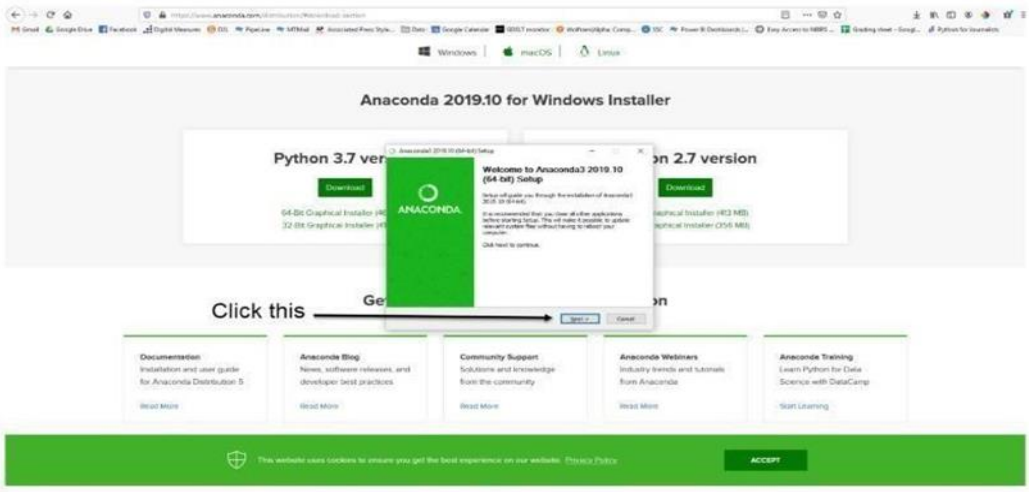

Fig.7.2.2 Opening the downloaded executable file 3.

Now, you'll see the license agreement. Click on 'I Agree'.

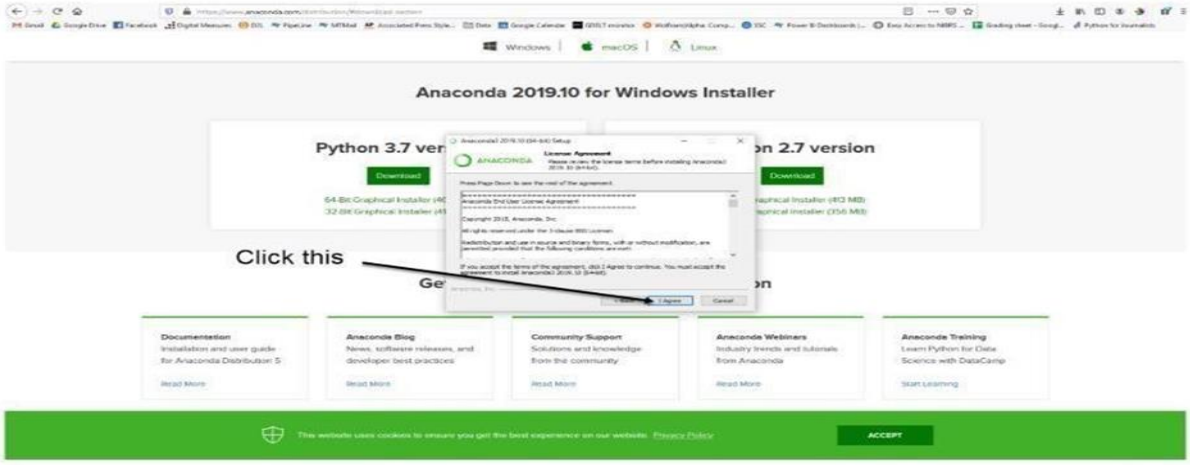

Fig.7.2.3 Accepting the license Agreement

4. You can install it for all users or just for yourself. If you want to install it for all users, you need administrator privileges.

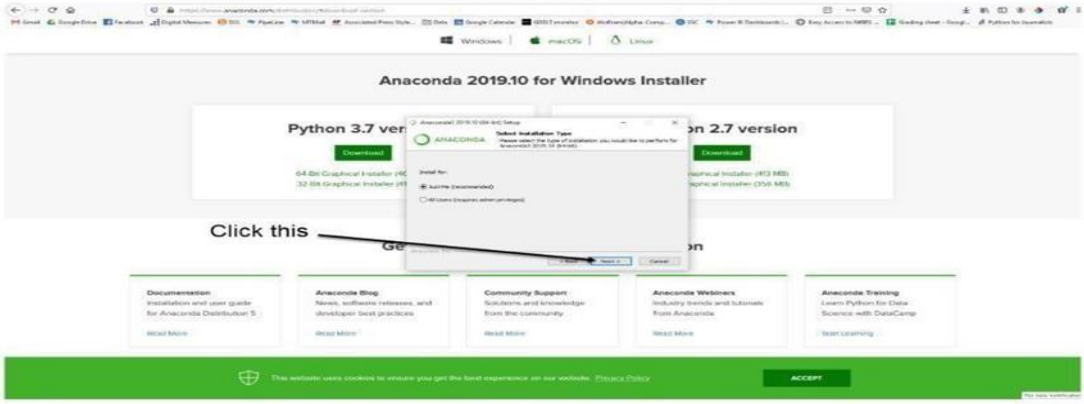

Fig.7.2.4 Administrator privileges

6. Choose where you want to install it. Here, you can see the available space andhow much you need.

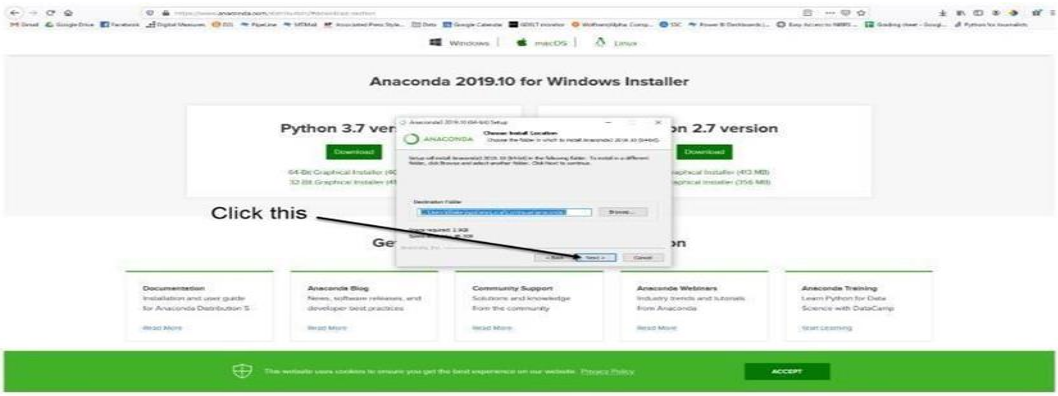

Fig.7.2.5 Choosing the space to install

6. Now, you'll get some advanced options. You can add Anaconda to your system's PATH environment variable, and register it as the primary system Python 3.7. If you add it to PATH, it will be found before any other installation. Click on 'Install'.

Fig.7.2.6 Setting up the path variable

7. It will unpack some packages and extract some files on your machine. This will take a few minutes.

Fig.7.2.7 Unpacking some packages and Extracting files 8. The installation is complete. Click Next.

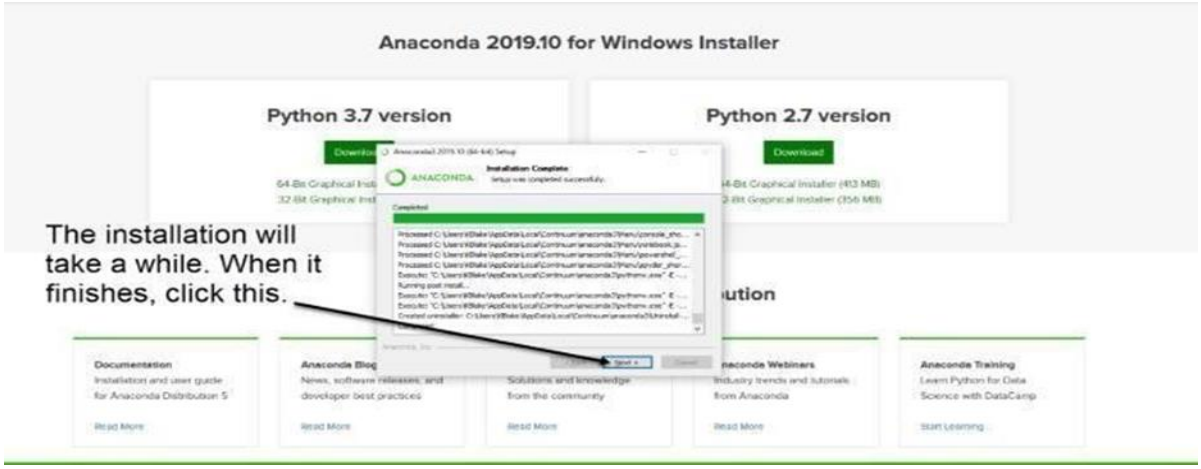

Fig.7.2.8 Completion of Installation

9. This screen will inform you about PyCharm. Click Next.

Fig.7.2.9 PyCharm

10. The installation is complete. You can choose to get more information aboutAnaconda cloud and how to get started with Anaconda. Click Finish

Fig.7.2.10 Finishing of the installation

11. If you search for Anaconda now, you will see the following options:

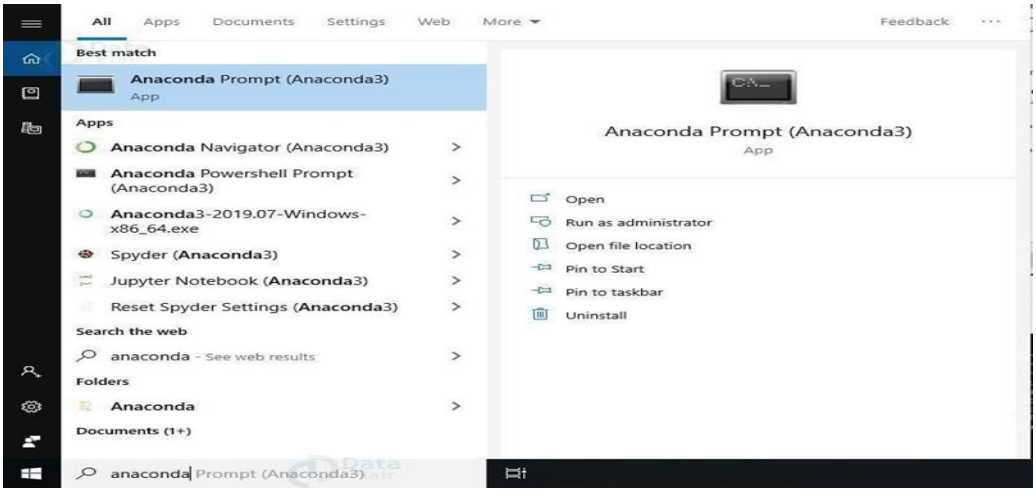

Fig.7.2.11 Searching for the installed Anaconda

7.3 PYTHON LANGUAGE:

Python is an interpreted, object-oriented, high-level programming language with dynamic semantics. Its high-level built in data structures, combined with dynamic typing and dynamic binding, make it very attractive for Rapid Application Development, as well as for use asa scripting or glue language to connect existing components together. Python's simple, easy to learn syntax emphasizes readability and therefore reduces the cost of program maintenance. Python supports modules and packages, which encourages program modularity and code reuse. The Pythoninterpreter and the extensive standard library are available in source or binary form without chargefor all major platforms, and can be freely distributed. Often, programmers fall in love with Pythonbecause of the increased productivity it provides. Since there is no compilation step, the edit- testdebug cycle is incredibly fast. Debugging Python programs is easy: a bug or bad input will never cause a segmentation fault. Instead, when the interpreter discovers an error, it raises an exception. When the program doesn't catch the exception, the interpreter prints a stack trace. Thedebugger is written in Python itself, testifying to Python's introspective power. On the other hand often the quickest way to debug a program is to add a few print statements to the source: the fastedit-test-debug cycle makes this simple approach very effective.

Python is a dynamic, high-level, free open source, and interpreted programming language. It supports object-oriented programming as well as procedural-oriented programming

Features in Python: There are many features in Python, some of which are discussed belowas follows:

1. Easy to code :

Python is a high-level programming language. Python is very easy to learn the language ascompared to other languages like C, C#, Javascript, Java, etc. It is very easy to code in the Pythonlanguage and anybody can learn Python basics in a few hours or days

2. Easy to Read :

As you will see, learning Python is quite simple. As was already established, Python’s syntax is really straightforward. The code block is defined by the indentations rather thanby semicolons or brackets.

3. Object-Oriented Language:

One of the key features of Python is Object-Oriented programming. Python supportsobject-oriented language and concepts of classes, object encapsulation, etc.

4. GUI Programming Support :

Graphical User interfaces can be made using a module such as PyQt5, PyQt4,wxPython, or Tk in python.

5. High-Level Language :

Python is a high-level language. When we write programs in Python, we do not need toremember the

system architecture, nor do we need to manage the memory.

6. Extensible feature :

Python is an Extensible language. We can write some Python code into C or C++language and also we can compile that code in C/C++ language.

7. Easy to Debug :

Excellent information for mistake tracing. You will be able to quickly identify andcorrect the majority of your program's issues once you understand how to interpret Python's error traces. Simply by glancing at the code, you can determine what it is designed to perform.

8. Python is a Portable language :

Python language is also a portable language. For example, if we have Python code for windows and if we want to run this code on other platforms such as Linux, Unix, and Mac thenwe do not need to change it, we can run this code on any platform.

9. Python is an Integrated language :

Python is also an Integrated language because we can easily integrate Python with otherlanguages like C, C++, etc.

10. Interpreted Language:

Python is an Interpreted Language because Python code is executed line by line at a time. like other languages C, C++, Java, etc. there is no need to compile Python code this makes it easierto debug our code. The source code of Python is converted into an immediate form called bytecode.

7.4 DEEP LEARNING

Deep learning is a subset of machine learning, which is essentially a neural network with three or more layers. These neural networks attempt to simulate the behavior of the human brain allowing it to "learn" from large amounts of data. While a neural network with a single layer can still make approximate predictions, additional hidden layers can help to optimize and refine for accuracy**. 33**

How deep learning works :

Deep learning neural networks, or artificial neural networks, attempts to mimic the human brain through a combination of data inputs, weights, and bias. network are called *visible* layers.

Convolutional neural networks (CNNs), used primarily in computer vision and image classification applications, can detect features and patterns within an image, enabling tasks, like object detectionor recognition.

Recurrent neural network (RNNs) are typically used in natural language and speech recognition applications as it leverages sequential or times series data

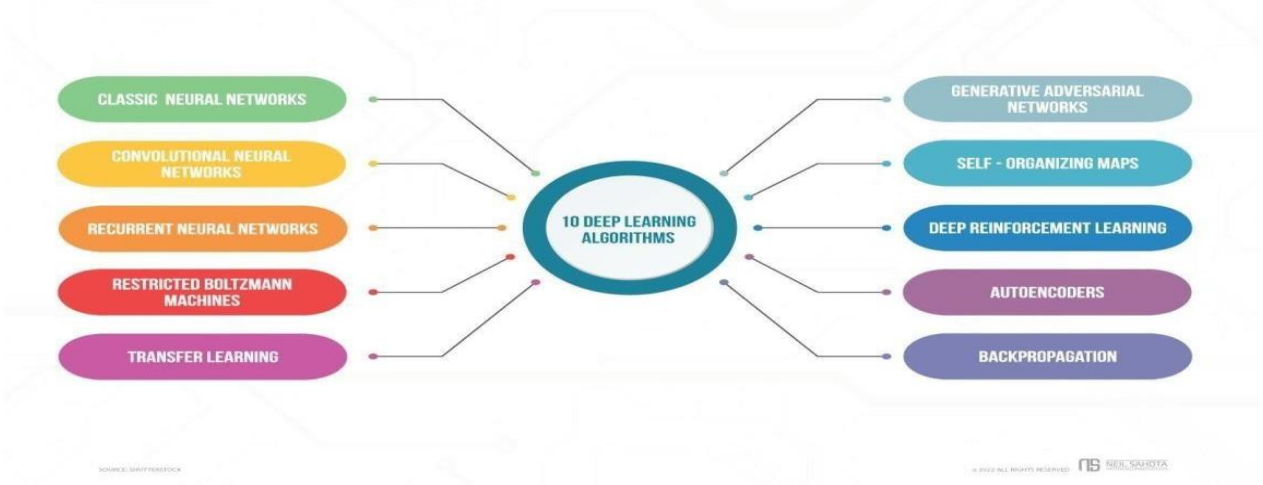

Fig.7.4.1 Algorithms in Deep learning

7.5 LIBRARIES/PACKGES:-Tensor flow:

It is a free and open-source software library for dataflow and differentiable programming across arange of tasks.

Numpy :

Numpy is a general-purpose array-processing package. It provides a high-performance multidimensional array object, and tools for working with these arrays.It is the fundamental package for scientific computing with Python. It contains various features including these important ones:
A powerful N-dimensional array object and Tools for integrating C/C++ and Fortran code

Pandas :

Pandas is an open-source Python Library providing high-performance data manipulation and analysis tool using its powerful data structures. Python was majorly used for datamunging and preparation. It had very little contribution towards data analysis. Pandas solved this problem. Using Pandas, we can accomplish five typical steps in the processing and analysis of data, regardless of the origin of data load, prepare, manipulate, model, and analyze

Matplotlib :

Matplotlib is a Python 2D plotting library which produces publication quality figures in avariety of hardcopy formats and interactive environments across platforms. Matplotlib can be usedin Python scripts, the Python and IPython shells, the Jupyter Notebook, web application servers, and four graphical user interface toolkits. Matplotlib tries to make easy things easy and hard thingspossible. You can generate plots, histograms, power spectra, bar charts, error charts, scatter plots,etc., with just a few lines of code. For examples, see the sample plots and thumbnail gallery.

Scikit – learn :

Scikit-learn provide a range of supervised and unsupervised learning algorithms via a consistent interface in Python. It is licensed under a permissive simplified BSD license and is distributed under many Linux distributions, encouraging academic and commercial use.

7.6 SAMPLE CODE

```
import os
import pandas as pdimport numpy as npimport random
import matplotlib.pyplot as plt
Matplotlib is building the font cache; this may take a moment.import seaborn as sns
from PIL import Imageimport cv2
from mpl_toolkits.axes_grid1 import ImageGridimport tensorflow as tf
from tensorflow.keras.applications import Xception
from tensorflow.keras.applications.inception_v3 import InceptionV3
from tensorflow.keras.applications.vgg16 import VGG16, preprocess_input from tensorflow.keras.preprocessing import image
from tensorflow.keras.models import Sequential, Model, load_model
from tensorflow.keras.layers import (Conv2D, MaxPooling2D, Dense, Flatten, Dropout, Input,GlobalAveragePooling2D,BatchNormalization)
from tensorflow.keras.activations import softmaxfrom tensorflow.keras.optimizers import Adam
from tensorflow.keras.preprocessing.image import ImageDataGenerator from tensorflow.keras.callbacks import ModelCheckpoint, EarlyStopping from tensorflow.keras.preprocessing.image import load_img, img_to_array from sklearn.metrics import (ConfusionMatrixDisplay, confusion_matrix, \
                    accuracy_score) label_folders = ['Acne and Rosacea Photos', \
'Actinic Keratosis Basal Cell Carcinoma and other Malignant Lesions', \'Melanoma Skin Cancer Nevi and Moles',
 'Systemic Disease','Urticaria Hives',]
root_dir = 'Dataset/train'test_dir = 'Dataset/test'
acne_train_path = os.path.join(root_dir,'Acne and Rosacea Photos') actinic_train_path = os.path.join(root_dir, 'Actinic Keratosis Basal Cell Carcinomaand other Malignant Lesions')
melonama_train_path = os.path.join(root_dir, 'Melanoma Skin Cancer Nevi and Moles') systemic_disease_train_path = os.path.join(root_dir, 'Systemic Disease') urticaria_hives_train_path = os.path.join(root_dir, 'Urticaria Hives')
acne_test_path = os.path.join(test_dir,'Acne and Rosacea Photos')
```

```
actinic_test_path = os.path.join(test_dir, 'Actinic Keratosis Basal Cell Carcinoma and otherMalignant Lesions')
melonama_test_path = os.path.join(test_dir, 'Melanoma Skin Cancer Nevi and Moles') systemic_disease_test_path = os.path.join(test_dir, 'Systemic Disease') urticaria_hives_test_path = os.path.join(test_dir, 'Urticaria Hives')
actinic_test_files = ([files_ for _, _, files_ in os.walk(actinic_test_path)])[0] acne_test_files = ([files_ for _, _, files_ in os.walk(acne_test_path)])[0] melonama_test_files = ([files_ for _, _, files_ in os.walk(melonama_test_path)])[0] systemic_disease_test_files = ([files_ for _, _, files_ in os.walk(systemic_disease_test_path)])[0]
urticaria_hives_test_files = ([files_ for _, _, files_ in os.walk(urticaria_hives_test_path)])[0]train_dirs = []
for i in label_folders:
for folder_,_, files_ in os.walk('Dataset/train/{i}'):
print(folder_) train_dirs.append(folder_)
actinic_train_files = ([files_ for _, _, files_ in os.walk(actinic_train_path)])[0] acne_train_files = ([files_ for _, _, files_ in os.walk(acne_train_path)])[0] melonama_train_files = ([files_ for _, _, files_ in os.walk(melonama_train_path)])[0] systemic_disease_train_files = ([files_ for _, _, files_ os.walk(systemic_disease_train_path)])[0]
def plotGridImages(d_name, list_files, train_path,nrows= 1, ncols=5):fig = plt.figure(1, figsize=(30, 30))
grid = ImageGrid(fig, 111, nrows_ncols=(nrows, ncols), axes_pad=0.05)print(f"{d_name}")
for i, img_id in enumerate(random.sample(list_files,ncols)):ax = grid[i]
image_dir_path = os.path.join(train_path, img_id) img = image.load_img(image_dir_path, (224, 224))
img = image.img_to_array(img)
ax.imshow(img / 255.)
ax.text(10, 200, 'Caption: %s' % d_name, color='k', backgroundcolor='w',\alpha=0.8)
ax.axis('off')
# plt.tight_layout()plt.show()
plotGridImages('Melonama',melonama_train_files, melonama_train_path,ncols=5) melonama_df = pd.DataFrame()
melonama_df['Image'] = [melonama_train_path+'/'+img for img in melonama_train_files] melonama_df['Label'] = "melonama"
melonama_df.shape actinic_df = pd.DataFrame()
actinic_df['Image'] = [actinic_train_path+'/'+img for img in actinic_train_files]actinic_df['Label'] = "actinic"
actinic_df.shape
acne_df = pd.DataFrame()
acne_df['Image'] = [acne_train_path+'/'+img for img in acne_train_files]acne_df['Label'] = "acne"
systemic_disease_df = pd.DataFrame()
systemic_disease_df['Image'] = [systemic_disease_train_path+'/'+img for img in systemic_disease_train_files]
systemic_disease_df['Label'] = "Systemic Disease"urticaria_hives_df = pd.DataFrame()
urticaria_hives_df['Image'] = [urticaria_hives_train_path+'/'+img for img in urticaria_hives_train_files]
urticaria_hives_df['Label'] = "Urticaria Hives"acne_df.shape
final_df = pd.DataFrame()
final_df = pd.concat([final_df, melonama_df, acne_df, systemic_disease_df])final_df.shape
ax = sns.countplot(x=final_df['Label'],
order=final_df['Label'].value_counts(ascending=False).index);
abs_values = final_df['Label'].value_counts(ascending=False).valuesfinal_test_df = pd.DataFrame()
melonama_test_df = pd.DataFrame()
melonama_test_df['Image'] = [melonama_test_path+'/'+img for img in melonama_test_files]
```

```
melonama_test_df['Label'] = "melonama"
actinic_test_df = pd.DataFrame()
actinic_test_df['Image'] = [actinic_test_path+'/'+img for img in actinic_test_files] actinic_test_df['Label'] = "actinic"
acne_test_df = pd.DataFrame()
acne_test_df['Image'] = [acne_test_path+'/'+img for img in acne_test_files]acne_test_df['Label'] = "acne"
systemic_disease_test_df = pd.DataFrame()
systemic_disease_test_df['Image'] = [systemic_disease_test_path+'/'+img for img in systemic_disease_test_files]
systemic_disease_test_df['Label'] = "Systemic Disease"urticaria_hives_test_df = pd.DataFrame()
urticaria_hives_test_df['Image'] = [urticaria_hives_test_path+'/'+img for img in urticaria_hives_test_files]
urticaria_hives_test_df['Label'] = "vitiligo"
final_test_df = pd.concat([final_test_df, melonama_df, acne_df, systemic_disease_df]) final_test_df.shape
train_data_gen = ImageDataGenerator(
rescale=1 / 255.0, rotation_range=40, width_shift_range=0.2,height_shift_range=0.2,horizontal_flip = True, vertical_flip = True, validation_split=0.2, fill_mode='nearest')
test_data_gen = ImageDataGenerator(rescale=1 / 255.0)batch_size = 8
train_generator = train_data_gen.flow_from_dataframe(dataframe=final_df,
x_col="Image", y_col="Label", target_size=(224, 224),batch_size=batch_size,
class_mode="categorical",#sparsesubset='training',
shuffle=True,seed=42
)
valid_generator = train_data_gen.flow_from_dataframe(dataframe=final_df,
x_col="Image", y_col="Label", target_size=(224, 224),batch_size=batch_size,
class_mode="categorical", #sparsesubset='validation',
shuffle=True,seed=42
)
test_generator = test_data_gen.flow_from_dataframe(dataframe=final_test_df,
x_col="Image", y_col="Label", target_size=(224, 224), batch_size=1, class_mode='categorical', shuffle=False,
)
custom_early_stopping = EarlyStopping(monitor='val_loss',
patience=10, min_delta=0.001,mode='min'
)
def create_xception_model():
res = Xception(weights ='imagenet', include_top = False,input_shape = (224, 224, 3))
res.trainable = Falsex= res.output
x = GlobalAveragePooling2D()(x)x = BatchNormalization()(x)
x = Dense(512, activation ='relu')(x)x = BatchNormalization()(x)
x = Dense(256, activation ='relu')(x)x = BatchNormalization()(x)
x = Dense(3, activation ='softmax')(x)model = Model(res.input, x)
return model
model = create_xception_model()def display_model_accuracy():
plt.plot(history.history['accuracy']) plt.plot(history.history['val_accuracy']) plt.title('Model accuracy') plt.ylabel('Accuracy') plt.xlabel('Epoch')
plt.legend(['Train', 'Test'], loc='upper left')plt.show()
plt.plot(history.history['loss']) plt.plot(history.history['val_loss']) plt.title('Model loss') plt.ylabel('Loss') plt.xlabel('Epoch')
plt.legend(['Train', 'Test'], loc='upper left')plt.show()
```

```
def display_model_loss(): plt.plot(history.history['accuracy']) plt.plot(history.history['val_accuracy'])
plt.title('Model accuracy') plt.ylabel('Accuracy') plt.xlabel('Epoch')
plt.legend(['Train', 'Test'], loc='upper left')plt.show()
plt.plot(history.history['loss'])
plt.plot(history.history['val_loss'])plt.title('Model loss') plt.ylabel('Loss') plt.xlabel('Epoch')
plt.legend(['Train', 'Test'], loc='upper left')plt.show()
no_epochs = 30 can_train = Falseif can_train:
history = model.fit(train_generator,
epochs=no_epochs, batch_size=64, validation_data=valid_generator,
callbacks=[custom_early_stopping]) model.save("xception_model.h5") display_model_accuracy()
display_model_loss()
else:
model = load_model("xception_model.h5")def process_evaluation(model_name):
test_true=test_generator.classes
test_pred_raw = model.predict(test_generator)test_pred = np.argmax(test_pred_raw, axis=1)
cm = confusion_matrix(test_true, test_pred) fig, ax = plt.subplots(figsize=(15,15))
disp.plot(ax=ax,cmap=plt.cm.Blues) plt.show()
result = model.evaluate(test_generator,batch_size=32)print("test_loss, test accuracy",result)
xp_preds = model.predict(test_generator) xp_pred_classes = np.argmax(xp_preds, axis=1)
true_classes = test_generator.classes
class_indices = train_generator.class_indices class_indices = dict((v,k) for k,v in class_indices.items())
xp_acc = accuracy_score(true_classes, xp_pred_classes)
print("{0} Model Accuracy: {1:.2f}%".format(model_name, xp_acc * 100)) def
create_vgg16_model():
valid_generator = train_data_gen.flow_from_dataframe(dataframe=final_df,
x_col="Image", y_col="Label", target_size=(224, 224),batch_size=batch_size,
class_mode="categorical", #sparsesubset='validation',
shuffle=True,seed=42
)
res = VGG16(weights = 'imagenet', include_top = False, input_shape = (224, 224, 3))res.trainable =
False
x= res.output
x = GlobalAveragePooling2D()(x)x = BatchNormalization()(x)
x = Dense(512, activation ='relu')(x)x = BatchNormalization()(x)
x = Dense(256, activation ='relu')(x)x = BatchNormalization()(x)
x = Dense(3, activation ='softmax')(x)model = Model(res.input, x)
return model
model.compile(optimizer =tf.keras.optimizers.Adam(learning_rate=0.001), loss
="categorical_crossentropy",
metrics =["accuracy"])
x = Dense(3, activation ='softmax')(x)model = Model(res.input, x)
return model
plotGridImages('Melonama',melonama_train_files, melonama_train_path,ncols=5) melonama_df =
pd.DataFrame()
melonama_df['Image'] = [melonama_train_path+'/'+img for img in melonama_train_files]
melonama_df['Label'] = "melonama"
melonama_df.shape actinic_df = pd.DataFrame()
actinic_df['Image'] = [actinic_train_path+'/'+img for img in actinic_train_files]actinic_df['Label'] =
"actinic"
actinic_df.shape
acne_df = pd.DataFrame()
acne_df['Image'] = [acne_train_path+'/'+img for img in acne_train_files]acne_df['Label'] = "acne"
```

```
systemic_disease_df = pd.DataFrame()
systemic_disease_df['Image'] = [systemic_disease_train_path+'/'+img for img in systemic_disease_train_files]
systemic_disease_df['Label'] = "Systemic Disease"urticaria_hives_df = pd.DataFrame()
urticaria_hives_df['Image'] = [urticaria_hives_train_path+'/'+img for img in urticaria_hives_train_files]
urticaria_hives_df['Label'] = "Urticaria Hives"acne_df.shape
final_df = pd.DataFrame()
final_df = pd.concat([final_df, melonama_df, acne_df, systemic_disease_df])final_df.shape
ax = sns.countplot(x=final_df['Label'], order=final_df['Label'].value_counts(ascending=False).index);
abs_values = final_df['Label'].value_counts(ascending=False).valuesfinal_test_df = pd.DataFrame()
melonama_test_df = pd.DataFrame() model = create_xception_model() def display_model_accuracy():
plt.plot(history.history['accuracy']) plt.plot(history.history['val_accuracy']) plt.title('Model accuracy')
plt.ylabel('Accuracy') plt.xlabel('Epoch')
plt.legend(['Train', 'Test'], loc='upper left')plt.show()
plt.plot(history.history['loss']) plt.plot(history.history['val_loss']) plt.title('Model loss')
plt.ylabel('Loss') plt.xlabel('Epoch')
plt.legend(['Train', 'Test'], loc='upper left')plt.show()
def display_model_loss(): plt.plot(history.history['accuracy']) plt.plot(history.history['val_accuracy'])
plt.title('Model accuracy') plt.ylabel('Accuracy') plt.xlabel('Epoch')
plt.legend(['Train', 'Test'], loc='upper left')plt.show()
plt.plot(history.history['loss'])if can_train:
history = model.fit(train_generator,
epochs=no_epochs, batch_size=64, validation_data=valid_generator,
callbacks=[custom_early_stopping]) model.save("vgg16_model.h5") display_model_accuracy()
display_model_loss()
else:
    model = load_model("vgg16_model.h5")process_evaluation("VGG16")
```

8. SYSTEM TESTING

System testing, also referred to as system-level tests or system-integration testing, is the process in which a quality assurance (QA) team evaluates how the various components of an application interact together in the full, integrated system or application. System testing verifies that an application performs tasks as designed. This step, a kind of black box testing, focuses on the functionality of an application. System testing, for example, might check that every kind of userinput produces the intended output across the application.

8.1 Software Testing Strategies:

Optimization of the approach to testing in software engineering is the best way to make it effective. A software testing strategy defines what, when, and how to do whatever is necessary tomake an end-product of high quality. Usually, the following software testing strategies and their combinations are used to achieve this major objective:

Static Testing:

The early-stage testing strategy is static testing: it is performed without actually running the developing product. Basically, such desk-checking is required to detect bugs and issuesthat are present in the code itself. Such a check-up is important at the pre-deployment stage as it helps avoid problems caused by errors in the code and software structure deficits.

Structural Testing:

It is not possible to effectively test software without running it. Structural testing, also known as white-box testing, is required to detect and fix bugs and errors emerging during the preproduction stage of the software development process. At this stage, unit testing based on the software structure is performed using regression testing. In most cases, it is an automated process

working within the test automation framework to speed up the development process at this stage. Developers and QA engineers have full access to the software's structure and data flows (data flows testing), so they could track any changes (mutation testing) in the system's behavior by comparingthe tests' outcomes with the results of previous iterations (control flow testing).

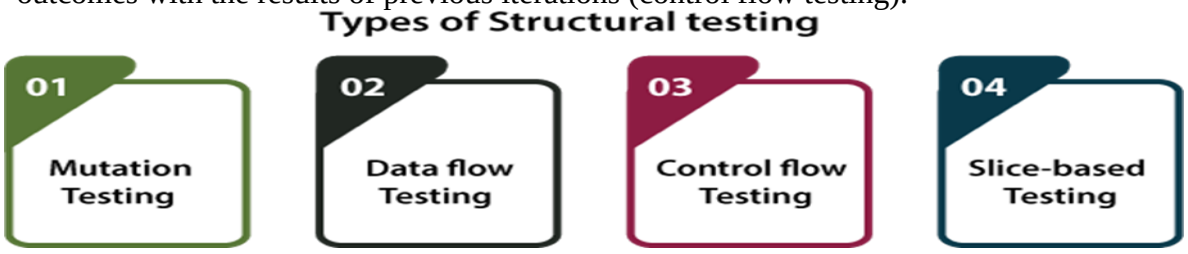

Fig.8.1.1 Types of Structural Testing

Behavioral Testing:

The final stage of testing focuses on the software's reactions to various activities ratherthan on the mechanisms behind these reactions. In other words, behavioral testing, also known as black-box testing, presupposes running numerous tests, mostly manual, to see the product from theuser's point of view. QA engineers usually have some specific information about a business or otherpurposes of the software ('the black box') to run usability tests, for example, and react to bugs as regular users of the product will do. Behavioral testing also may include automation (regression tests) to eliminate human error if repetitive activities are required

8.2 TEST CASES:

S.NO	INPUT	If available	If not available
1	User signup	User get registered into the application	There is no process
2	User sign in	User get login into the application	There is no process
3	Enter input for prediction	Prediction result displayed	There is no process

9. OUTPUT SCREENS

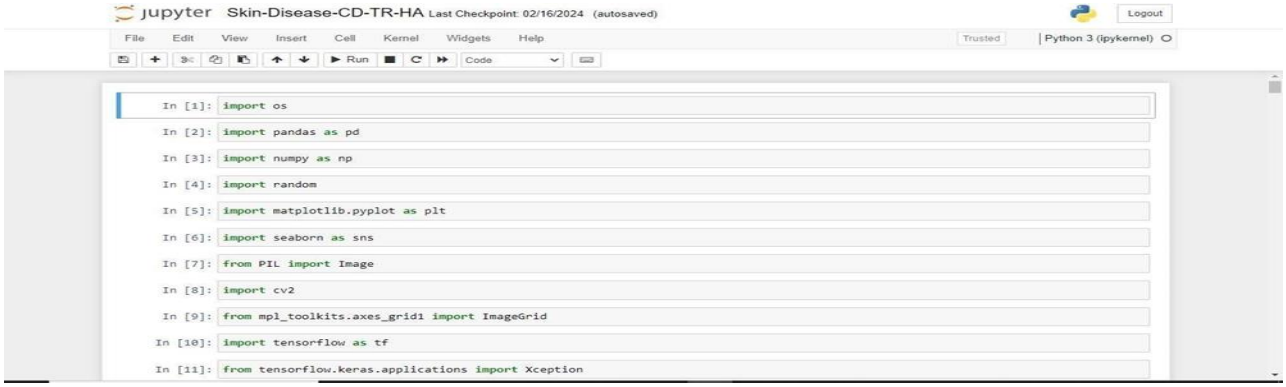

Fig.9.1 Packages and libraries Installed

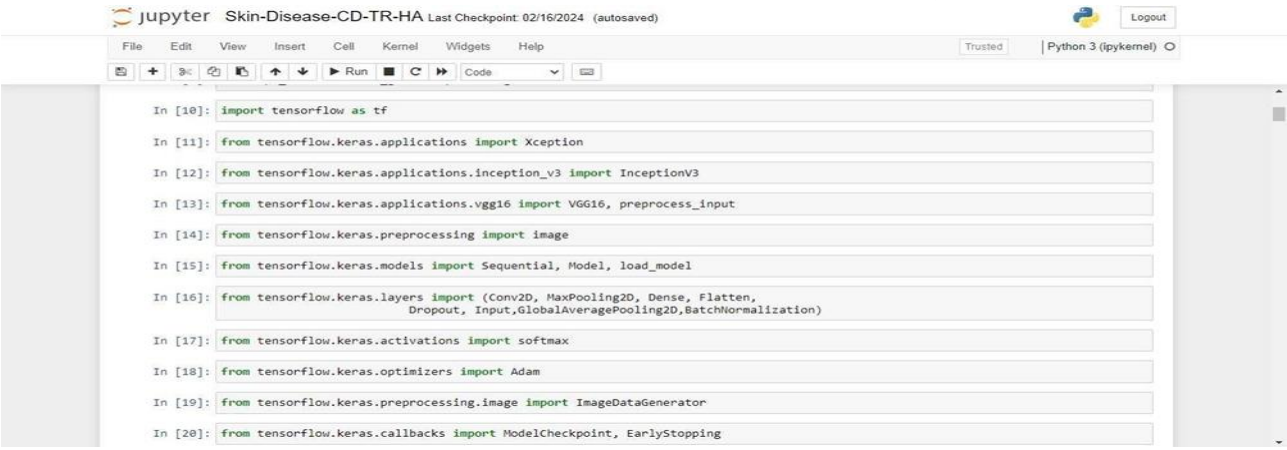

Fig.9.2 Packages and libraries Installed

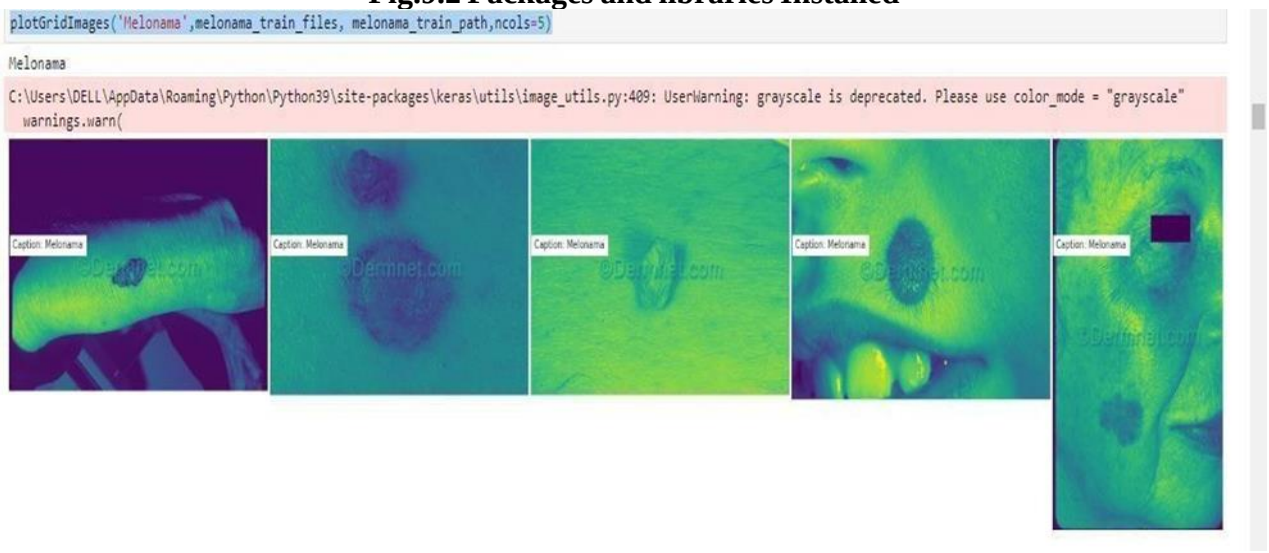

Fig.9.3 Captions generated by Multi Label Classifier

Fig.9. 4 Captions generated by Multi Label Classifier

```
In [55]: melonama_df = pd.DataFrame()
         melonama_df['Image'] = [melonama_train_path+'/'+img for img in melonama_train_files]
         melonama_df['Label'] = "melonama"

In [56]: melonama_df.shape
Out[56]: (463, 2)

In [57]: actinic_df = pd.DataFrame()
         actinic_df['Image'] =  [actinic_train_path+'/'+img for img in actinic_train_files]
         actinic_df['Label'] = "actinic"

In [58]: actinic_df.shape
Out[58]: (1149, 2)

In [59]: acne_df = pd.DataFrame()
         acne_df['Image'] =  [acne_train_path+'/'+img for img in acne_train_files]
         acne_df['Label'] = "acne"

In [60]: systemic_disease_df = pd.DataFrame()
         systemic_disease_df['Image'] =  [systemic_disease_train_path+'/'+img for img in systemic_disease_train_files]
         systemic_disease_df['Label'] = "Systemic Disease"

In [61]: urticaria_hives_df = pd.DataFrame()
         urticaria_hives_df['Image'] =  [urticaria_hives_train_path+'/'+img for img in urticaria_hives_train_files]
         urticaria_hives_df['Label'] = "Urticaria Hives"

In [62]: acne_df.shape
Out[62]: (840, 2)
```

Fig.9.5 Displaying the Total Shape of the Individual Data Frames

```
In [63]: final_df = pd.DataFrame()

In [64]: final_df = pd.concat([final_df, melonama_df, acne_df, systemic_disease_df])

In [65]: final_df.shape
Out[65]: (1909, 2)
```

Fig.9.6 Displaying the Total Shape of the Combined Data Frames

```
In [66]: ax = sns.countplot(x=final_df['Label'],
                           order=final_df['Label'].value_counts(ascending=False).index);

         abs_values = final_df['Label'].value_counts(ascending=False).values
```

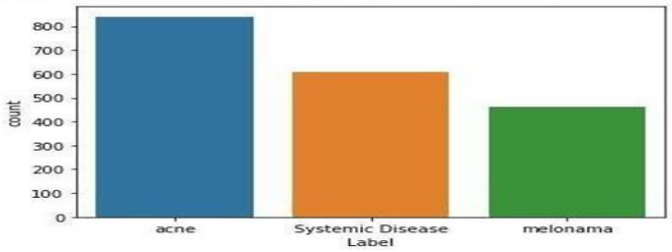

Fig.9.7 Bar graph

```
In [80]: final_test_df
```

Out[80]:

	Image	Label
0	Dataset/train\Melanoma Skin Cancer Nevi and Mo...	melonama
1	Dataset/train\Melanoma Skin Cancer Nevi and Mo...	melonama
2	Dataset/train\Melanoma Skin Cancer Nevi and Mo...	melonama
3	Dataset/train\Melanoma Skin Cancer Nevi and Mo...	melonama
4	Dataset/train\Melanoma Skin Cancer Nevi and Mo...	melonama
...	...	...
601	Dataset/train\Systemic Disease/xanthomas-75.jpg	Systemic Disease
602	Dataset/train\Systemic Disease/xanthomas-76.jpg	Systemic Disease
603	Dataset/train\Systemic Disease/xanthomas-77.jpg	Systemic Disease
604	Dataset/train\Systemic Disease/xanthomas-8.jpg	Systemic Disease
605	Dataset/train\Systemic Disease/xanthomas-9.jpg	Systemic Disease

1909 rows × 2 columns

Fig.9.8 Final test Data Frame

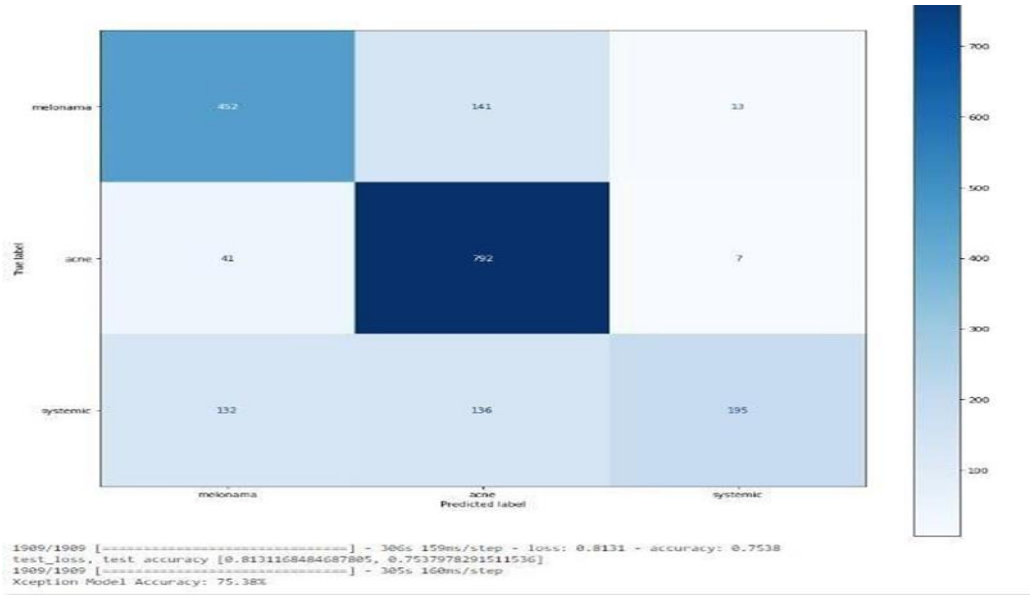

Fig.9.9Predicting Accuracy of the Xception Model

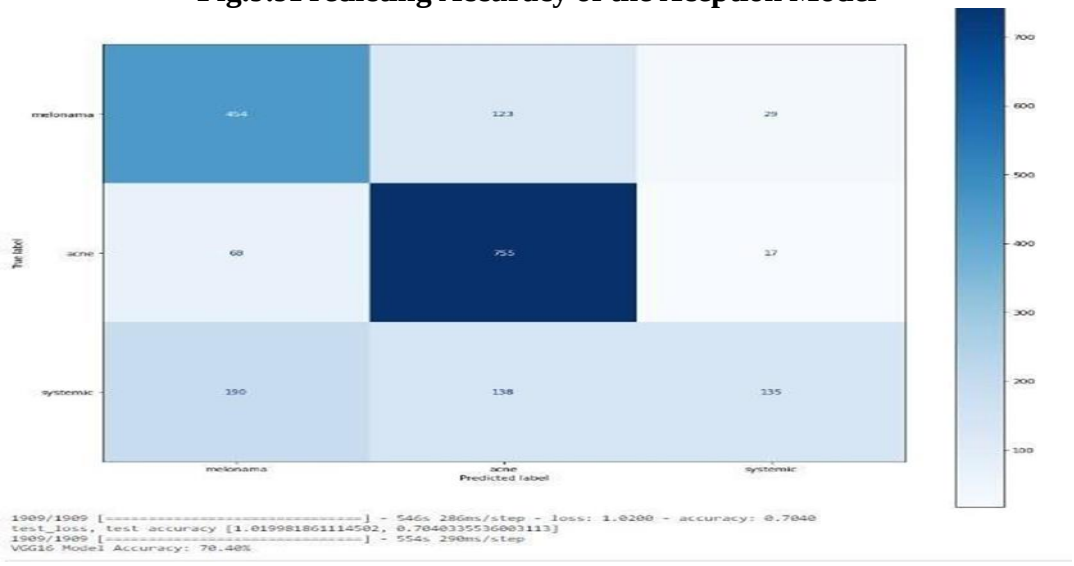

Fig.9.10 Predicting Accuracy of the VGG16 Model

CONCLUSION

In conclusion, the exploration of skin medical image captioning using multi-label classification and Siamese network architectures represents a significant advancement in the field of dermatological image analysis. Through the integration of multi-label classification techniques,our approach enables the simultaneous identification and labeling of multiple dermatological attributes present in skin images, thereby facilitating more comprehensive and informative image descriptions. The incorporation of Siamese network architectures further enhances the semantic understanding between images and textual descriptions, enabling the generation of coherent and contextually relevant captions that closely align with the visual features observed in dermatologicalimages.

Moving forward, the adoption of skin medical image captioning using multi-label classification and Siamese network architectures holds immense promise for improving diagnostic capabilities and patient care in dermatology. Future research directions may involve the refinementand optimization of the proposed framework, as well as its integration into clinical practice and dermatological workflows. Collaborative efforts between computer scientists, dermatologists, and healthcare professionals are essential for validating and evaluating the clinical utility and effectiveness of skin medical image captioning systems in real-world settings. Ultimately, the successful implementation of these advanced methodologies has the potential to revolutionize dermatological image analysis, enhance diagnostic accuracy, and improve patient outcomes in dermatology.

FUTURE ENHANCEMENT

The future of skin medical image captioning using multi-label classification and Siamese network architectures holds exciting possibilities for advancing dermatological diagnosis and treatment. One promising direction involves the integration of additional modalities, such as textual clinical notes and patient histories, to enrich the contextual understanding of dermatologicalimages. By incorporating multi-modal information, future systems can generate more informativeand personalized captions, aiding healthcare professionals in making accurate and timely clinical decisions. Moreover, exploring advanced deep learning techniques, including graph neural networks and reinforcement learning, may further enhance the interpretability and accuracy of image captions, paving the way for more sophisticated diagnostic support systems in dermatology.

Furthermore, the integration of skin medical image captioning systems into telemedicine platforms and mobile applications has the potential to democratize access to dermatological expertise and improve healthcare outcomes globally. By leveraging the ubiquity ofsmartphones and wearable devices, patients and healthcare providers can capture and analyze dermatological images in realtime, enabling remote consultation and diagnosis. Additionally, the development of standardized datasets and benchmarks for evaluating skin medical image captioning algorithms will be crucial for benchmarking performance and fostering collaboration within the research community. Ultimately, the continued innovation and integration of multi-labelclassification and Siamese network architectures in skin medical image captioning hold promise for revolutionizing dermatological care and enhancing patient outcomes in the years to come.

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