SKIN CANCER PREDICTION

A PROJECT REPORT

Submitted by

S.R. VIDHYAMBIKA

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ABSTRACT

In recent days, skin cancer is seen as one of the most Hazardous form of the cancers found in Humans. Online Dataset from all around the world is gathered to cancer diagnosis. The lack of robust prognosis models results in difficulty for doctors to prepare a treatment plan that may prolong patient survival time. Hence, this necessitates the requirement to develop prediction algorithms to predict the disease with minimum error to increase accuracy. Many machine learning algorithms are available for cancer diagnosis and prediction.

This project uses Artificial Neural Network along with two machine learning algorithms: Logistic Regression and Support Vector Machines for cancer prediction using python as a simulation environment and compares the accuracy. The algorithm with higher accuracy is then deployed as a webapp.

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LIST OF ABBREVIATIONS

ACRONYMS	ABBREVIATIONS
ANN	Artificial Neural Network
BC	Breast Cancer
BSD	Berkeley Software Distribution
CNN	Convolutional Neural Networks
IDE	Integrated Development Environment
NUMPY	Numerical Python
PCA	Principal Component Analysis
SVM	Support Vector Machines
URL	Uniform Resource Locator
WSGI	Web Server Gateway Interface

CHAPTER 1

INTRODUCTION

Cancer is a dangerous disease that characterized by the nature of the cell inside the body which has no control. Cancer is not a single disease but rather more than 100 types of disease. Cancer damages the human body gradually when cells starts growing uncontrollably to form many lumps of tissue inside the human body called tumors. Tumors may grow and interact with the other parts of the body. That parts may be nervous system, digestive system or circulatory system. The effect of infected parts of the body releases the hormones that causes change in the body. Mainly There are two types of cancer: Malignant and Benign.

Malignant is spread into the surrounding tissue. Cell can grow to other cell and destroy the surrounding tissue that causes other tumor to develop. So malignant tumor can be a life-threatening and more dangerous in nature. Benign tumor usually do not cause much damage but can become more dangerous if they grow a lot or they might become malignant after certain amount of time.

CHAPTER 2

LITERATURE SURVEY

2.1 COMPUTER VISION FOR SKIN CANCER DIAGNOSIS AND RECOGNITION USING RBF AND SOM

Digital image processing technique is used for enhancing the image to recognize and predict different types of skin cancers. Sample skin cancer image were taken from American cancer society research center and DERMOFIT. The combination of Self Organizing Map (SOM) and Radial Basis Function (RBF) was made to classify the image into predefined classes of the type of skin cancer. The best classification accuracy of 88% for basal cell carcinoma, 96.15 for melanoma and 94.45 for squamous cell carcinoma was obtained.[1]

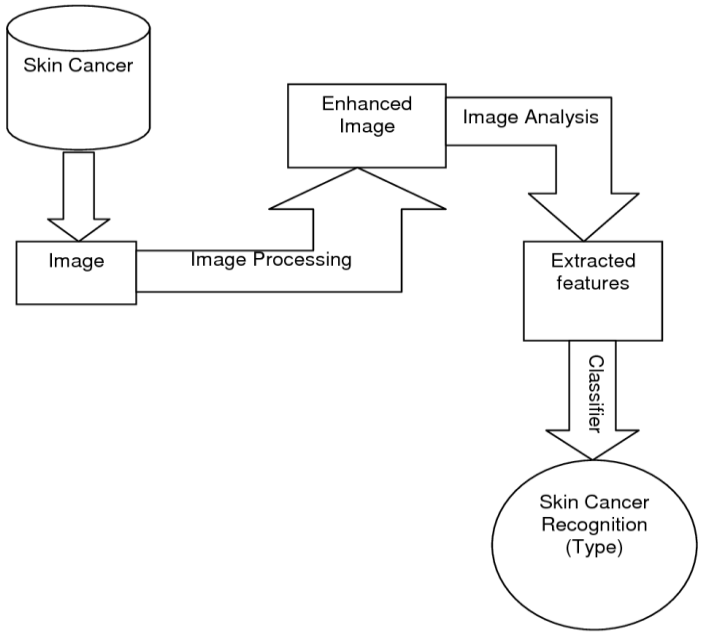


Fig 2.1

2.2 DIFFERENT TECHNIQUES FOR SKIN CANCER DETECTION USING DERMOSCOPY IMAGES

For predicting the melanoma type skin cancer, first pre-processing of input skin image is made using image segmentation. Feature extraction is performed on segmented lesion. Then, the extracted features are used to classify the image as normal skin and melanoma cancer lesion.[2]

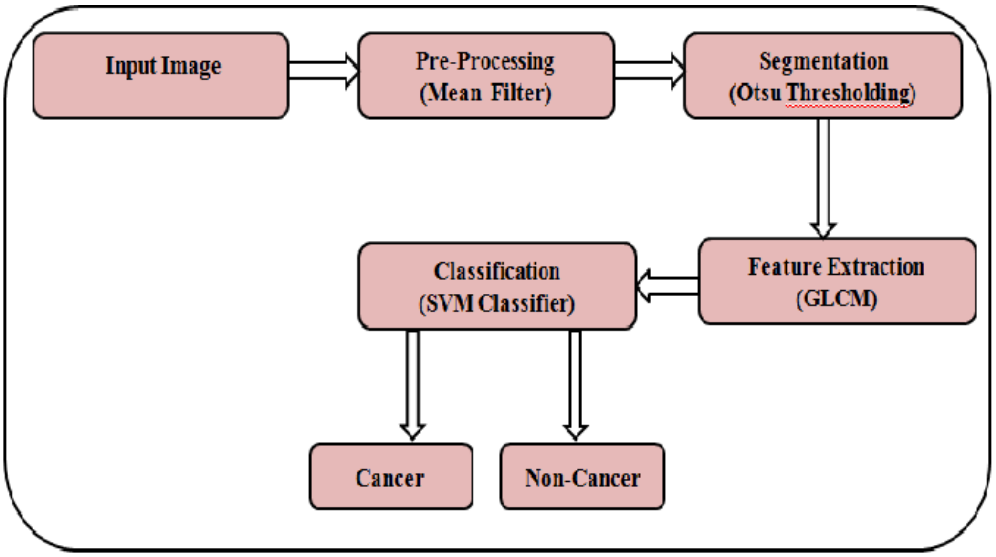


Fig 2.2

2.3 DETECTION OF SKIN CANCER USING SVM

The type of skin cancer is predicted using Image processing. The input to the system is the skin lesion image and then by applying image processing techniques, it analyses to conclude about the presence of skin cancer.

The Lesion Image analysis is done using LBP algorithm which checks for the various Melanoma parameters like Color, Area perimeter, diameter, texture, size and shape analysis for image segmentation and feature stages. The

extracted feature parameters are used to classify the image as Non Melanoma and Melanoma cancer or benign and malignant.[3]

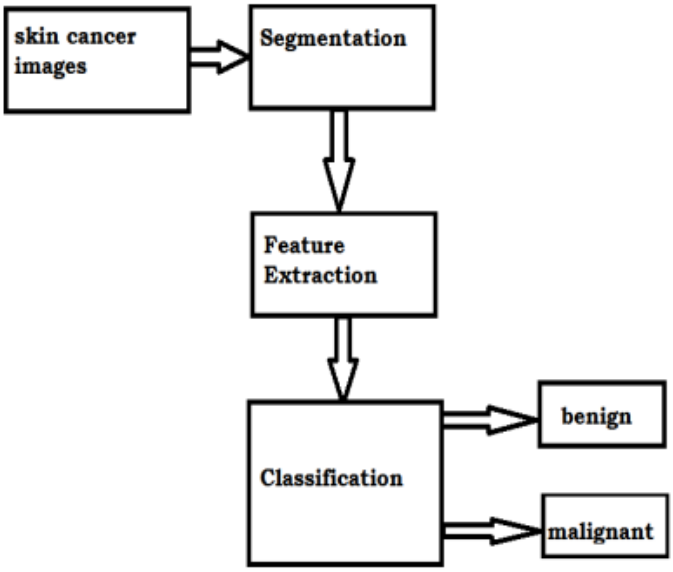


Fig 2.3

2.4 SKIN LESION ANALYSIS TOWARDS MELANOMA DETECTION USING DEEP LEARNING NETWORK

Two deep learning methods: Lesion Segmentation and Classification, Lesion Indexing Network are used. Three main tasks emerging in the area of skin lesion image processing: lesion segmentation, lesion dermoscopic feature extraction and lesion classification.

The Support Vector Machines consisting of two fully convolutional residual networks (FCRN) is proposed to simultaneously produce the segmentation result and the coarse classification result. A lesion index calculation unit (LICU) is developed to refine the coarse classification results by calculating the distance heat-map. A straight-forward CNN is proposed for the dermoscopic feature extraction task.[4]

2.5 DEEP LEARNING FOR MEDICAL IMAGE PROCESSING: OVERVIEW, CHALLENGES AND FUTURE

Healthcare sector is totally different from other industry as most of the interpretations of medical data is being done by medical expert and is quite limited due to its subjectivity, complexity of the image, extensive variations exist across different interpreters, and fatigue.

Different deep learning algorithms like Support Vector Machines(SVM), Convolutional Neural Networks (CNN), Recurrent Neural Network(RNN), Long Short Term Memory(LSTM), Extreme Learning Model(ELM), Generative Adversarial Networks(GAN), Deep Neural Network(DNN), Deep Belief Network, Deep Auto Encoder(DA), Deep Boltzmann Machine(DBM) for feature extraction, classification of medical data for processing.[5]

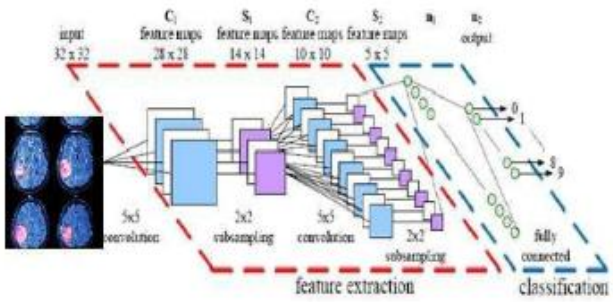


Fig 2.4

2.6 A PROPOSAL FOR AN EXPLAINABLE FUZZY – BASED DEEP LEARNING SYSTEM FOR SKIN CANCER PREDICTION

The theoretical fundamentals of an explainable fuzzy-based deep learning (EFBDL) system that is both precise and explainable was proposed. The system comprises two main parts. First, the deep network part composed of a

convolutional neural network (CNN) based on Inception V4 for image classification, a transfer learning mechanism, and a feature extraction algorithm based on neuron perturbation. Second, a soft computing part comprised of a fuzzy rule-based system (FRBS), a hierarchical network for natural language generation named granular linguistic model of a phenomenon (GLMP), and a human-machine integration methodology for linguistic rules named highly interpretable linguistic knowledge (HILK).

The output of the overall system is an explanation of the neural network decision using natural language. This system focuses on preventing skin cancer rather than healing it. Thus, governments could use this kind of system for implementing policies focused on prevention and save in overall treatment costs of the disease.[6]

2.7 TRANSFER LEARNING BASED METHOD FOR TWO-STEP SKIN CANCER IMAGES CLASSIFICATION

Classification of skin cancer images is done using classification models which are developed in Python using the PyTorch machine learning library and the dataset used as experimental support for testing and validating the transfer learning based method is Human Against Machine with 10000 training images (HAM10000) dataset. In the first step the accuracy of the prediction model for testing data is 85% and in the second step the accuracy of the prediction model for testing data is 75%.[7]

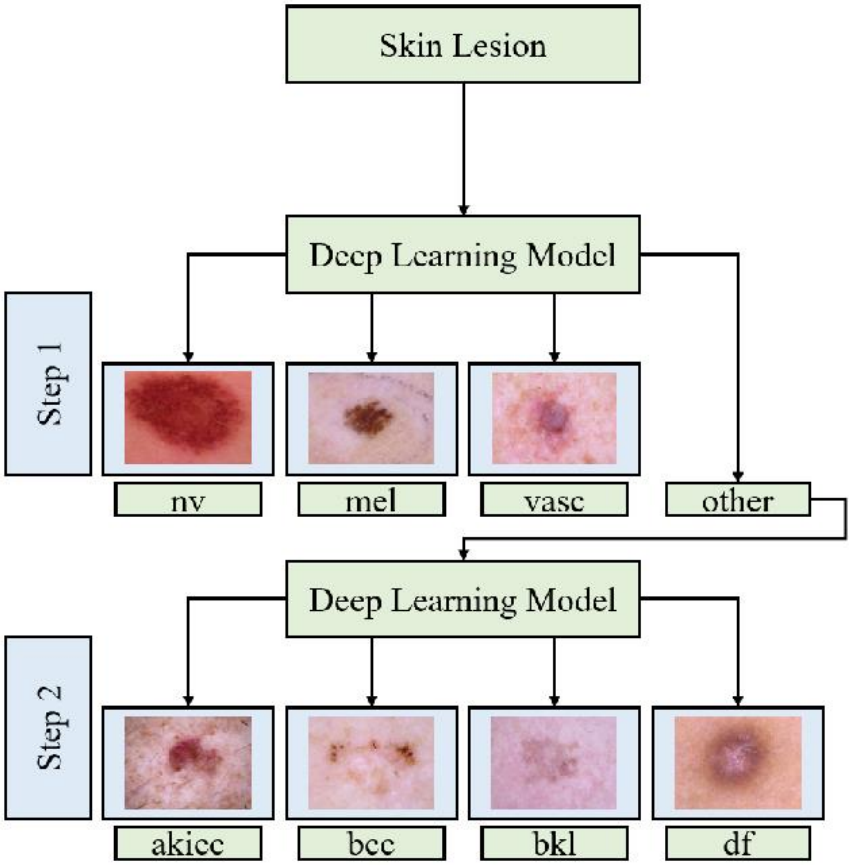


Fig 2.5

2.8 MELANOMA SKIN CANCER DETECTION USING DEEP LEARNING AND CLASSICAL MACHINE LEARNING TECHNIQUES: A HYBRID APPROACH

A convolutional neural network and two classical machine learning classifiers trained with a set of features describing the borders, texture and the color of a skin lesion are used. These methods are then combined to improve their performances using majority voting. The experiments have shown that using the three methods together, gives the highest accuracy level.[8]

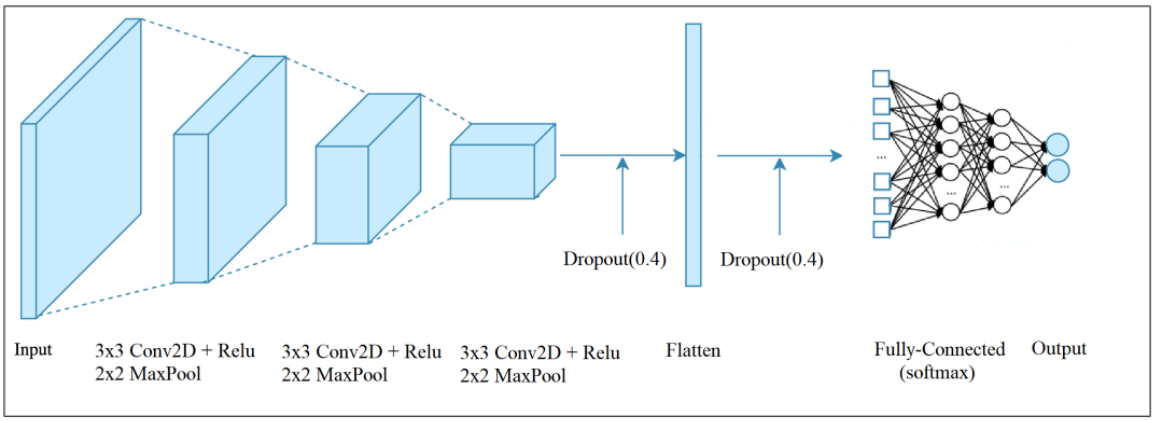


Fig 2.6

2.9 ENHANCE SKIN CONDITION PREDICTION THROUGH MACHINE LEARNING USING DYNAMIC TRAINING AND TESTING AUGMENTATION

Only limited researches are focused on dynamic data augmentation, even in the fields of machine learning and computer vision. The dynamic training and testing augmentation are capable of increasing performance significantly and are used here. The searching augmentation framework used requires fewer GPU hours than a conventional search algorithm. Speeding up of the search algorithm is achieved by using Bayesian optimization on a trained model, for every time new model creation need not be peformed. Instead, new augmentation policy is proposed.

The performance of this method is compared with single model and ensemble model which happens to be the winner of the ISIC 2019 challenge. Furthermore, accurate network architecture EfficientNet is used as the backbone system. This delivers a superior result, and also shares the searched augmentation policy utilized, which requires extraordinary resources. Thus, other researchers can use the searched augmentation policies for dermoscopic images to improve performance.[9]

2.10 INTERPRETING MECHANISMS OF PREDICTION FOR SKIN CANCER DIAGNOSIS USING MULTI- TASK LEARNING

Interpretation of predictions is presented in better way on a skin lesion dataset by the use of a multi-task learning framework and a set of learnable gates. The model detects a set of clinically significant attributes in addition to the final diagnosis and learns the association between tasks by selecting which features to share among them.

Conventional multi-task learning algorithms generally share all the features among tasks and lack a way of determining the amount of sharing between tasks. On the other hand, this method provides a simple way to inspect which features are being shared between tasks in the form of gates that can be learned in an end-to-end fashion. Experiments have been carried out on the publicly available Derm7pt dataset, which provides diagnosis information as well as the attributes needed for the well-known 7-point checklist method.[10]

2.11 SKIN CANCER CLASSIFICATION USING CONVOLUTIONAL NEURAL NETWORKS

Convolution neural networks are used to detect and classify the classes of cancer based on historical data of clinical images. Some of our objectives through this research are ,to build a CNN model to detect skin cancer with an accuracy of >80% ,to keep the false negativity rate in the prediction to below 10%, to reach the precision of above 80% and do visualization on our Data. Simulation results show that this method has superiority towards other compared methods.[11]

2.12 CANCER PREDICTION SYSTEM USING DATA MINING TECHNIQUES

The gathered data is preprocessed, fed into the database and classified to yield significant patterns using decision tree algorithm. Then, the data is clustered using K- means clustering algorithm to separate cancer and noncancer patient data. Further the cancer cluster is subdivided into six clusters namely lung, breast, oral, stomach, brain and blood cancer. Finally, a prediction system predicts the type of cancer by analyzing risk levels which help in prognosis. Thus, this helps in detection of a person's predisposition for cancer before going for clinical and lab tests which is cost and time consuming.[12]

2.13 APPLICATIONS OF MACHINE LEARNING IN CANCER DETECTION AND CLASSIFICATION

Diagnosis of Breast Cancer(BC) and classification of patients into malignant or benign groups is done using critical features detection from complex BC datasets, data mining and classification with machine learning (ML) which is widely recognized as the methodology of choice in BC pattern classification and forecast modelling. [13]

2.14 MACHINE LEARNING APPLICATIONS IN CANCER PROGNOSIS AND PREDICTION

Cancer is detected using prediction and is evaluated by splitting labelled dataset into subsets using Holdout Method, Random Sampling, Cross-Validation and Bootstrap and extracting different features. The predictive models used are based on various Supervised ML techniques like Decision Trees, Artificial Neural Networks, Batch Normalization, Support Vector Machines.[14]

2.15 APPLICATIONS OF MACHINE LEARNING IN CANCER DETECTION AND PROGNOSIS

The types of data being integrated and the performance of these methods in cancer prediction and prognosis are enhanced by 10-15% using protein biomarkers and microarray data towards applications in prostate and breast cancer, and a heavy reliance on technologies such artificial neural networks (ANNs) and Support Vector Machines(SVM).[15]

2.16 EXISTING SYSTEM

ML is useful in order to infer the learning outcome on the basis of behavior of data samples. There are mainly two phases of learning process: (i) On the basis of dataset provided, the unknown dependencies are to be estimated for the system and (ii) New output of the system is to predict if estimated dependencies are known. In existing system, the labelled training data is used to estimate to the desired output. Some of the examples are Gaussian Process regression, Naïve Bayes Classifier, Max Entropy classifier, K-means, PCA, Latent variable model, Hebbian learning. When these algorithms are used on unlabelled dataset of skin cancer, false prediction of type of skin cancer occurred and it also didn’t focused on severity of disease.

2.12.1 Drawbacks of Existing System

1) Result Classification and prediction is difficult.

2) Less Accuracy due to support vector machine, because does not efficient for multiclass classification.

3) Does not concentrate on the severity of the disease.

CHAPTER 3

PROPOSED WORK

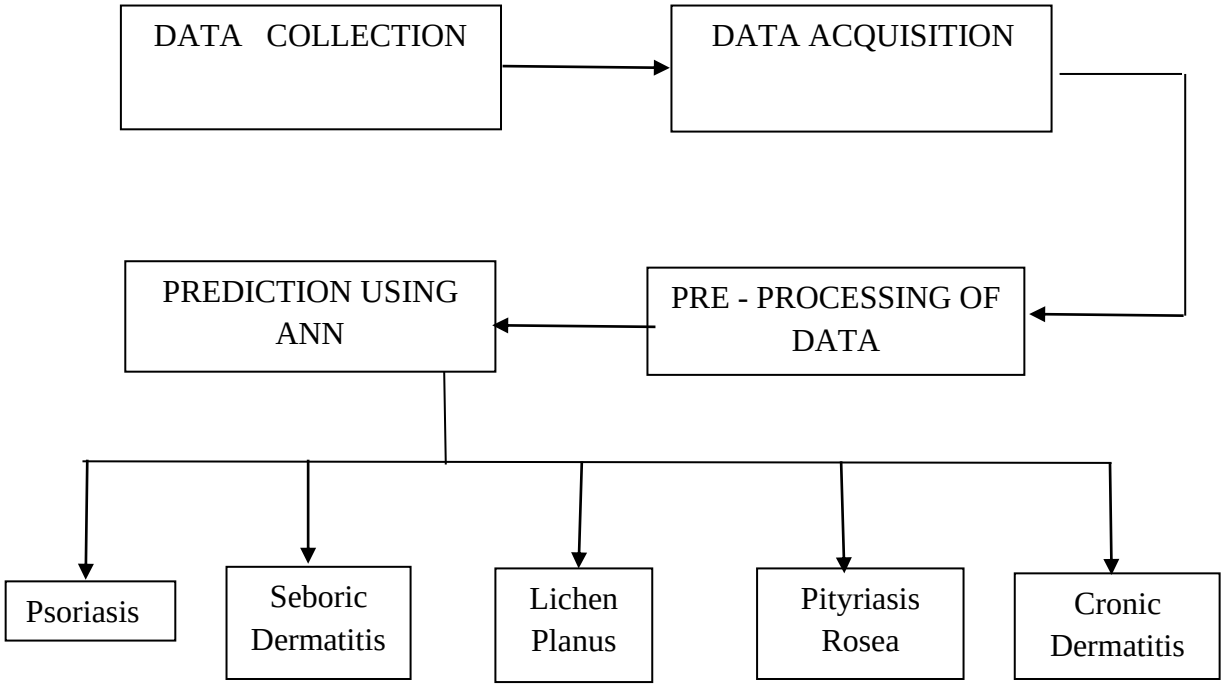
3.1 METHODOLOGY

In my proposed system, The existing system is enhanced by using Aritificial Neural Networks (ANN) for classification, using labelled dataset using Support Vector Machines (SVM) Algorithm and the user is also provided with an option to use varying values from 0-3 for every attribute to denote the severity of the disease. This variation in attribute values denotes the severity of each symptom and predicts the disease into the most accurate category.

Advantages

- Prediction accuracy of original and enhanced datasets, the value is around 0.85 with mean 0.8479 for the original dataset
- Result Classification and prediction is accurate.
- Does efficient multi type skin cancer classification.

3.2 BLOCK DIAGRAM



3.3 ADMIN MODULE

3.3.1 Data collection

The first phase is to collect the data that we are interested in collecting for pre-processing and to apply prediction and machine learing methods. This step is very important because the quality and quantity of data that is gathered and used will directly determine how good your predictive model can be. In this project, Dermatology Dataset from UCI Machine Learning Repository which is available in Kaggle is used as training dataset.

3.3.2 Data acquisition

Data Preparation, loadimg our data into a suitable place and prepare it for use in our machine learning training. All the data are collected and stored in a dataframe using pandas, and then randomized the ordering

3.3.3 Preprocessing the data

Real world data is often incomplete, inconsistent, and lacking certain and contains many errors. Data pre-processing is a proven method of resolving such issues by preparing raw data into understandable format for further processing. For pre-processing, feature selection, also known as variable selection, attribute selection which is the process of selection a subset of relevant features by comparison with input values and data set values for use in model construction is done using pandas.

3.3.4 Classification using ANN

Data Set from https://archive.ics.uci.edu/ml/datasets/dermatology (UCI Machine Learning Repository in Kaggle).There are 33 parameters in this dataset: Erythema, scaling, definite, itching, koebner, polygonal, follicular, oral, knee, scalp, family, melanin, eosinophils, PNL, fibrosis, exocytosis, acanthosis, hyperkeratosis, parakeratosis, clubbing, elongation, thinning, spongiform, munro, focal, disappearance, vacuolisation, spongiosis, saw_tooth, follicular, perifollicular, inflammatory, band, Age which acts here as the independent variable.

My target parameter/output is classification of type of cancer using multiclass classifier through diagnosis – whether it is psoriasis, seboreic

dermatitis, lichen planus, pityriasis rosea, cronic dermatitis, pityriasis rubra pilaris.

Supervised learning is the method in which the machine is trained on the data which the input and output are well labelled. The model can learn on the training data and can process the future data to predict outcome. In our dataset we have the outcome variable or Dependent variable i.e. Y having only six set of values like psoriasis, seboreic dermatitis, lichen planus, pityriasis rosea, cronic dermatitis, pityriasis rubra pilaris.

Artificial Neural Network and two different types of Supervised Machine Learning algorithm: Logistic Regression and Support Vector Machines are used to improve accuracy.

Since this model will be deployed, it is saved into a pickle file (model.pkl) created by pickle.

Pickle is a python module that enables python objects to be written to files on the disk and read back into the python program runtime.

3.3.5 Deploy the model on the webpage using Flask

This project is conducted using libraries from Anaconda Tool machine learning environment. In Experimental studies we have partition 70-30% for training & testing. SYPDER IDE contains a collection of machine learning algorithms for data pre-processing and prediction. Machine learning techniques implemented in SPYDER are applied to a variety of real-world problems. The results of the data analysis are reported.

In deploying this skin cancer prediction model into production, a web application framework called Flask is used. In Flask, writing and developing

web applications is easy. In this project, the Flask environment with an API endpoint is constructed which takes in the model and enables it to receive input from users and return output. After this, a python file app.py is created, and the required libraries are imported.

3.4 USER MODULE

3.4.1 Add health attribute details

In this module, user can add the attribute details like

- Erythema
- Scaling
- Definite
- Itching
- Koebner
- Polygonal
- Follicular
- Oral
- Knee
- Scalpfamily
- Melanin
- Eosinophils
- PNL
- Fibrosis
- Exocytosis
- Acanthosis
- Hyperkeratosis
- Parakeratosis
- Clubbing
- Elongation
- Thinning
- Spongiform
- Munro
- Focal
- Disappearance
- Vacuolisation

- Spongiosis
- Saw_tooth
- Follicular
- Perifollicular
- Inflammatory
- Band
- Age

3.4.2 View Prediction

Then user health attribute details will be compared with the trained dataset values. Then the type of skin cancer disease like

- Psoriasis
- Seboreic dermatitis
- Lichen planus
- Pityriasis rosea
- Cronic dermatitis
- Pityriasis rubra pilaris will be predicted.

CHAPTER 4

IMPLEMENTATION DETAILS

4.1 HARDWARE SPECIFICATION

PROCESSOR	:	DUAL CORE
HARD DISK CAPACITY	:	400 GB
MONITOR	:	14 “SAMTRON MONITOR
INTERNAL MEMORY CA	:	2 GB
KEYBOARD	:	LOGITECH OF 104 KEYS
CPU CLOCK	:	1.08 GHz
MOUSE	:	LOGITECH MOUSE
HARD DISK	:	1TB HDD / 512GB SSD

4.2 SOFTWARE SPECIFICATION

OPERATING SYSTEM	:	WINDOWS 7
LANGUAGE	:	PYTHON
TOOLS USED	:	FLASK

4.3 SOFTWARE DESCRIPTION

4.3.1 FLASK

Flask is a micro web app framework written in Python. Armin Ronacher, who leads an international group of Python enthusiasts named Pocco, develops it. Flask is based on Werkzeug WSGI toolkit and Jinja2 template engine.

It has no database abstraction layer, form validation, or any other components where pre-existing third-party libraries provide common functions.

However, Flask supports extensions that can add application features as if they were implemented in Flask itself. Web Server Gateway Interface (WSGI) is a specification for a universal interface between the web server and the web applications.

Modern web frameworks use the routing technique to help a user access the desired page directly. The route() decorator in Flask is used to bind URL to a function. So, if a user visits http://localhost:5000/hello URL, the output of the hello_world() function will be rendered in the browser.

The add_url_rule() function of an application object is also available to bind a URL with a function. It is possible to build a URL dynamically, by adding variable parts i.e., <variable-name> to the rule parameter as keyword argument to the function with which the rule is associated.

Why Flask?

- Easy to use
- Unicode based
- Built in development server and debugger
- Integrated unit testing support
- RESTful request dispatching
- Uses Jinja2 templating,
- Support for secure cookies (client side sessions)
- 100% WSGI 1.0 compliant

4.3.2 WERKZEUG

Werkzeug is a toolkit for Web Server Gateway Interface (WSGI) applications, licensed under a BSD License. Werkzeug can realize software objects for request, response, and utility functions. It can be used to build a custom software framework on top of it and supports Python 2.6, 2.7 and 3.3 Jinja.

4.3.3 JINJA (TEMPLATE ENGINE)

Jinja, also by Armin Ronacher, is a template engine for the Python programming language and is licensed under a BSD License. Similar to the Django web framework, it provides that templates are evaluated in a sandbox.

4.3.4 SPYDER

Spyder is a free and open-source scientific environment written in Python, for Python, and designed by and for scientists, engineers and data analysts. It features a unique combination of the advanced editing, analysis, debugging, and profiling functionality of a comprehensive development tool with the data exploration, interactive execution, deep inspection, and beautiful visualization capabilities of a scientific package.

Beyond its many built-in features, its abilities can be extended even further via its plugin system and API. Furthermore, Spyder can also be used as a PyQt5 extension library, allowing you to build upon its functionality and embed its components, such as the interactive console, in your own software.

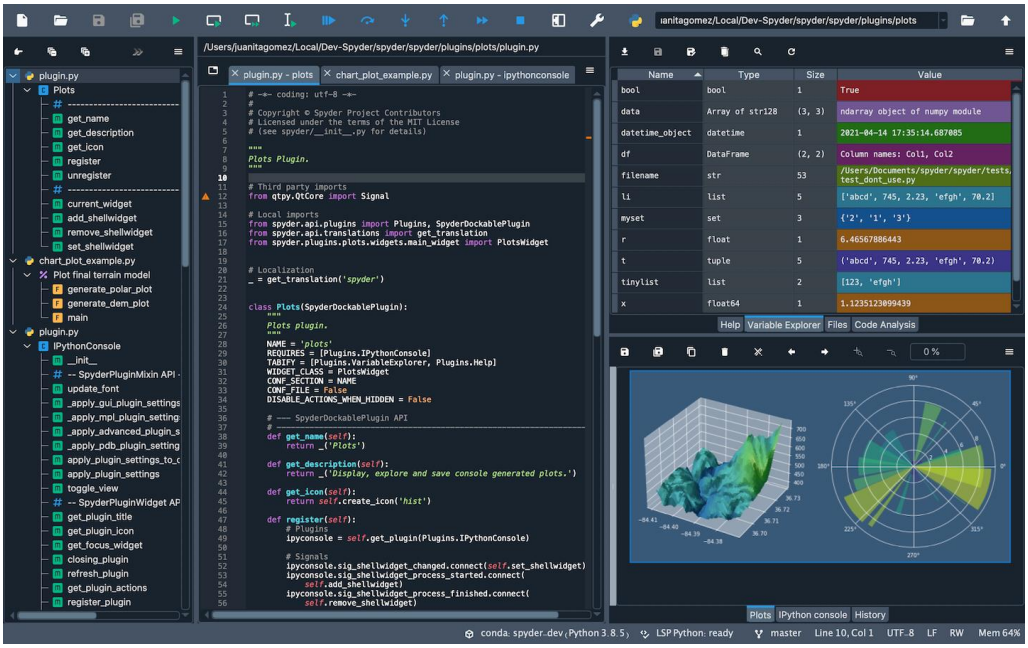


Fig 4.1: Spyder IDE

CHAPTER 5

RESULTS

The public, labelled dataset used to train the AI to predict the different types of skin cancer. Both the machine learning algorithms: Logistic Regression and SVC or SVM are applied along with the Artificial Neural Networks and comparison of accuracy with these algorithms is made using graph to find which algorithm is more accurate.

Then the algorithm which gives high accuracy upon combined with Artificial Neural Network and tested on dataset is deployed in the web application for skin cancer prediction by diagnosis.

Users say, doctors upon entering the values for each type of symptoms from 0-3 based on the severity,. The type of cancer is predicted based on the user's inputs.

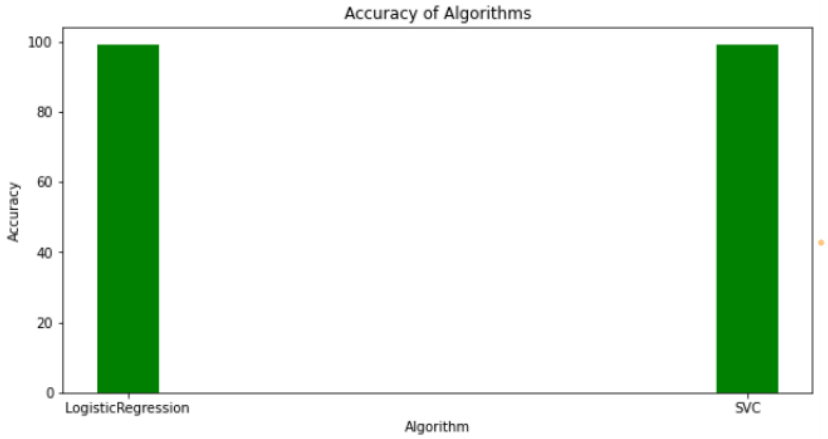


Fig 5.1

The above bar graph shows the accuracy of both machine learning algorithms used along with Artifical Neural Networks for classification. Logistic Regression algorithm has an accuracy of 99.16% and Support Vector Machines has an accuracy of 99.72%.

CHAPTER 6

CONCLUSION AND FUTURE WORK

6.1 CONCLUSION

This paper focuses on determining the stage of the skin cancer, based on various feature etc. The analysis can be made with the help of machine learning algorithm. A comparison can be made with the existing systems, machine learning reduces the computational time. Hence, the treatment can begin faster. classification of skin cancer is performed. With the aim to help the patient to identify the skin cancer without going to hospitals. This diagnosis research work includes prediction using algorithm like LogisticRegression, SVM with the highest accuracy. The proposed system classify six different types of skin cancer like psoriasis, seboreic dermatitis, lichen planus, pityriasis rosea, cronic dermatitis, pityriasis rubra pilaris.

6.2 FUTURE WORK

In future, this project can be improved by using convolutional neural network model to diagnose and detect skin cancer from lesion images. It also explored the data augmentation technique as a pre-processing step to strengthen the classification robustness of the CNN model. The best model, namely Inception Residual Networks (Resnet) can achieve an average accuracy of 91%

APPENDICES

A.1 SOURCE CODE

Classifier.py

```
import pandas as pd

import numpy as np

import pickle

from sklearn.linear_model import LogisticRegression

from sklearn import svm

import matplotlib.pyplot as plt

df=pd.read_csv('skincancer_data.csv')

cdf=df[['erythema','scaling','definite','itching','koebner','polygonal','follicular','oral','knee','scalp','family','melanin','eosinophils','PNL','fibrosis','exocytosis','acanthosis','hyperkeratosis','parakeratosis','clubbing','elongation','thinning','spongiform','munro','focal','disappearance','vacuolisation','spongiosis','sawtooth','follicular','perifollicular','inflammatory','band','Age','types']]

x = cdf.iloc[:, :34]

y = cdf.iloc[:, -1]

clf=LogisticRegression()

clf.fit(x,y)

SVM = svm.LinearSVC()

SVM.fit(x, y)
```

```
print(clf.predict([[2,2,1,0,1,0,0,0,0,0,0,0,0,0,0,3,2,0,2,0,0,0,0,0,0,0,0,2,0,0,0,2,0,30]]))

print(SVM.predict([[2,2,1,0,1,0,0,0,0,0,0,0,0,0,0,3,2,0,2,0,0,0,0,0,0,0,0,2,0,0,0,2,0,30]]))

round(clf.score(x,y), 4)

round(SVM.score(x,y), 4)

file=open('model.pkl','wb')

pickle.dump(clf,file,protocol=2)
```

App.py

```
import numpy as np

from flask import Flask,jsonify,render_template,request

import pickle

# from keras import models

file=open('model.pkl','rb')

clf=pickle.load(file)

#file.close()

app=Flask(__name__)

@app.route('/',methods=['GET','POST'])

def hello_world():

    if request.method == 'POST':
```

```
erythema = int(request.form['erythema'])

scaling = int(request.form['scaling'])

definite = int(request.form['definite'])

itching = int(request.form['itching'])

koebner = int(request.form['koebner'])

polygonal = int(request.form['polygonal'])

follicular = int(request.form['follicular'])

oral = int(request.form['oral'])

knee = int(request.form['knee'])

scalp = int(request.form['scalp'])

family = int(request.form['family'])

melanin = int(request.form['melanin'])

eosinophils = int(request.form['eosinophils'])

PNL = int(request.form['PNL'])

fibrosis = int(request.form['fibrosis'])

exocytosis = int(request.form['exocytosis'])

acanthosis = int(request.form['acanthosis'])

hyperkeratosis = int(request.form['hyperkeratosis'])

parakeratosis = int(request.form['parakeratosis'])

clubbing = int(request.form['clubbing'])
```

```
elongation = int(request.form['elongation'])

thinning = int(request.form['thinning'])

spongiform = int(request.form['spongiform'])

munro = int(request.form['munro'])

focal = int(request.form['focal'])

disappearance = int(request.form['disappearance'])

vacuolisation = int(request.form['vacuolisation'])

spongiosis = int(request.form['spongiosis'])

saw_tooth = int(request.form['saw-tooth'])

follicular = int(request.form['follicular'])

perifollicular = int(request.form['perifollicular'])

inflammatory = int(request.form['inflammatory'])

band = int(request.form['band'])

Age = int(request.form['Age'])


  input_feature=[erythema,scaling,definite,itching,koebner,polygonal,follic
  ular,oral,knee,scalp,family,melanin,eosinophils,PNL,fibrosis,exocytosis,a
  canthosis,hyperkeratosis,parakeratosis,clubbing,elongation,thinning,spon
  giform,munro,focal,disappearance,vacuolisation,spongiosis,saw_tooth,fol
  licular,perifollicular,inflammatory,band,Age]

#input_feature=[5,1,1,1,2,1,3,1,1]
```

```
        infprob=clf.predict([input_feature])


        #infprob = round(infprob*100,4)
        return render_template('result.html',inf=infprob)
    return render_template('home.html')
if __name__ == '__main__'  :
    app.run(debug=True)
```

A.2 SCREEN SHOTS

DATASET

acanthosis	hyperkera	parakerat	clubbing	elongatio	thinning	spongifor	munro	focal	disappear	vacuolisat	spongiosis	saw-tooth	follicular	perifollicu	inflamma	band	Age	types
2	0	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	55	2
2	0	2	2	2	2	2	1	0	0	0	0	0	0	0	1	0	8	1
2	0	2	0	0	0	0	0	2	0	2	3	2	0	0	2	3	26	3
2	0	3	2	2	2	2	0	0	3	0	0	0	0	0	3	0	40	1
2	0	0	0	0	0	0	0	2	2	3	2	3	0	0	2	3	45	3
2	0	2	0	0	0	1	0	0	0	0	2	0	0	0	1	0	41	2
3	0	0	0	2	0	0	0	0	0	0	0	0	0	0	2	0	18	5
3	0	0	0	0	0	0	0	0	2	2	3	2	0	0	3	3	57	3
1	0	1	0	0	0	0	0	0	0	0	2	0	0	0	2	0	22	4
2	0	2	0	0	0	0	0	0	0	0	2	0	0	0	2	0	30	4
3	2	3	2	2	2	1	1	0	0	0	0	0	0	0	1	0	20	1
2	0	0	0	0	0	1	0	0	0	0	3	0	0	0	1	0	21	2
1	0	1	0	0	0	0	0	0	0	0	2	0	0	0	1	0	22	2
2	1	2	1	2	3	0	2	0	0	0	0	0	0	0	2	0	10	1
1	1	1	0	0	0	0	0	2	0	3	0	3	0	0	1	3	65	3
1	0	1	0	0	0	0	0	0	0	0	2	0	0	0	2	0	40	4
1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	30	2
2	0	2	3	3	3	2	3	0	3	0	0	0	0	0	2	0	38	1
2	0	1	0	0	0	0	0	3	0	2	0	3	0	0	2	3	23	3
3	2	2	0	3	0	0	0	0	0	0	1	0	0	0	2	0	17	5
1	2	2	0	1	0	1	0	0	0	0	0	0	1	2	1	0	8	6
2	1	2	0	2	1	2	0	0	0	0	3	0	0	0	2	0	51	2
3	1	2	0	2	1	0	0	0	0	0	1	0	1	0	2	0	42	5
2	1	1	0	0	0	0	0	3	0	3	0	2	0	0	2	3	44	3
2	0	0	0	3	0	0	0	0	0	0	0	0	0	0	2	0	22	5
2	2	2	2	2	2	1	2	0	2	0	0	0	0	0	2	0	33	1

INPUT VALUES

SKIN CANCER PREDICTOR

Skin Cancer Screening and Diagnosis

erythema	1	scaling	2	definite borders	4	itching	3
koebner phenomenon	6	polygonal papules	45	follicular papules	37	oral mucosal involvement	36
knee and elbow involvement	9	scalp involvement	7	family history	5	melanin incontinence	437
eosinophils in the infiltrate	9	PNL infiltrate	86	fibrosis of the papillary dermis	4	exocytosis	780
acanthosis	645	hyperkeratosis	7698	parakeratosis	054	clubbing of the rete ridges	35
elongation of the rete ridges	8	thinning of the suprapapillary epidermis	6	spongiform pustule	3	munro microabcess	70
focal hypergranulosis	8	disappearance of the granular layer	6	vacuolisation and damage of basal layer	5	spongiosis	9

PREDICTED VALUES

SKIN CANCER PREDICTOR

Prediction

You have cronic dermatitis .

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