Alzheimer's Disease Prediction

A MINI-PROJECT REPORT

Submitted by

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BONAFIDE CERTIFICATE

Certified that this mini project "**Alzheimer's Disease Prediction**" is the bonafide work of "**NAVEEN KUMAR K - 2116220701183)"** who carried out the project work under my supervision.

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Submitted for the End semester practical examination to be held on

INTERNAL EXAMINER **EXTERNAL EXAMINER**

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Abstract

Alzheimer's Disease (AD) is a progressive neurodegenerative disorder that impairs cognitive functioning, affecting millions globally. Early detection is critical, as it can slow disease progression and improve the quality of life for patients. Traditional diagnostic methods, including neuroimaging and genetic testing, are often costly, invasive, and inaccessible in remote areas. In response to these limitations, *CognitiveX* introduces a non-invasive, accessible solution for early AD prediction through speech analysis.

CognitiveX leverages machine learning and natural language processing (NLP) to identify subtle linguistic and acoustic markers in speech that are indicative of cognitive decline. Extensive research has shown that individuals with early-stage Alzheimer's often exhibit distinct changes in language patterns, including pauses, reduced vocabulary, and slower speech rates. Our system analyses these speech characteristics to predict the likelihood of Alzheimer's in individuals, potentially years before symptoms become clinically significant.

The project methodology involves collecting speech samples from diverse datasets and employing advanced signal processing to isolate relevant features. Using supervised learning algorithms, these features are then correlated with clinical data to develop a predictive model with high accuracy. The final model is integrated into a user-friendly application that allows clinicians and caretakers to screen individuals quickly and efficiently.

Preliminary results demonstrate promising accuracy rates, indicating that *CognitiveX* could significantly augment traditional diagnostic methods. By providing an accessible, cost-effective, and non-invasive tool, this project has the potential to reshape Alzheimer's detection, making early intervention more widely achievable.

Beyond early detection, *CognitiveX* advances research into speech as a diagnostic tool for neurological health. By leveraging AI, it contributes to the development of accessible, non-invasive solutions that could reshape diagnostic practices. This approach not only aids Alzheimer's detection but also highlights the potential for scalable, speech-based assessments to support proactive cognitive health globally.

TABLE OF CONTENTS

CHAPTER 1

1.1 INTRODUCTION

Alzheimer's Disease (AD) is a progressive neurodegenerative disorder that severely impacts cognitive functions, affecting memory, language, and thought processes. With an aging global population, AD prevalence is projected to rise, presenting a significant public health challenge worldwide. Early detection is crucial, as timely interventions can potentially slow cognitive decline, improving patients' quality of life. However, current diagnostic methods often rely on costly and invasive procedures, such as neuroimaging and biomarker testing, which may not be readily accessible. *CognitiveX* addresses this gap by introducing a non-invasive, cost-effective approach that leverages speech analysis for early AD prediction. By examining subtle linguistic and acoustic cues in speech patterns, *CognitiveX* utilises advanced machine learning algorithms to provide an accessible screening tool that empowers clinicians, caregivers, and individuals alike. This project not only underscores the potential of speech as a biomarker for cognitive health but also aligns with the broader mission to democratise access to early diagnostic tools.

1.2 SCOPE OF THE WORK

The scope of *CognitiveX: Alzheimer's Disease Prediction through Speech Analysis* involves developing a robust application that includes the following features:

- **Alzheimer's Risk Prediction**
  Utilizing machine learning models to analyze speech patterns and assess the likelihood of cognitive decline, focusing on early detection of Alzheimer's.
- **Feature Extraction and Analysis**
  Identifying linguistic and acoustic markers (e.g., speech rate, pauses, vocabulary) associated with Alzheimer's to provide meaningful insights into cognitive health.
- **User-Friendly Interface**
  An intuitive interface for clinicians and caregivers, allowing easy data input and clear presentation of risk scores and assessments.

- **Data Visualization**
  Graphical representations of analyzed speech features over time, enabling users to understand trends and potential risk indicators.
- **Secure Data Handling**
  Ensuring user data privacy and security through encryption and compliance with healthcare regulations for safe data management.

1.3 AIM AND OBJECTIVES OF THE PROJECT

Aim:

The primary aim of *CognitiveX* is to develop a machine learning-based application that utilizes speech analysis to predict the risk of Alzheimer's Disease, thereby facilitating early detection and intervention. By leveraging linguistic and acoustic features in speech, the project seeks to provide a non-invasive, accessible tool for clinicians and caregivers to monitor cognitive health.

Objectives:

- **To Develop Predictive Models**
  Create and validate machine learning models capable of accurately predicting Alzheimer's risk based on speech patterns, utilizing techniques such as neural networks and support vector machines.
- **To Analyze Speech Features**
  Conduct comprehensive analysis to identify key linguistic and acoustic markers associated with cognitive decline, ensuring the features used in the model are relevant and significant.
- **To Design a User-Friendly Application**
  Develop an intuitive interface that allows users to easily input speech samples and receive actionable insights, ensuring accessibility for both healthcare professionals and individuals.
- **To Implement Data Visualization**
  Incorporate visual tools that present the analysis results, trends, and risk assessments in a clear and understandable manner, enhancing user comprehension of cognitive health indicators.

CHAPTER 2

SYSTEMSPECIFICATIONS

1. HARDWARE SPECIFICATIONS

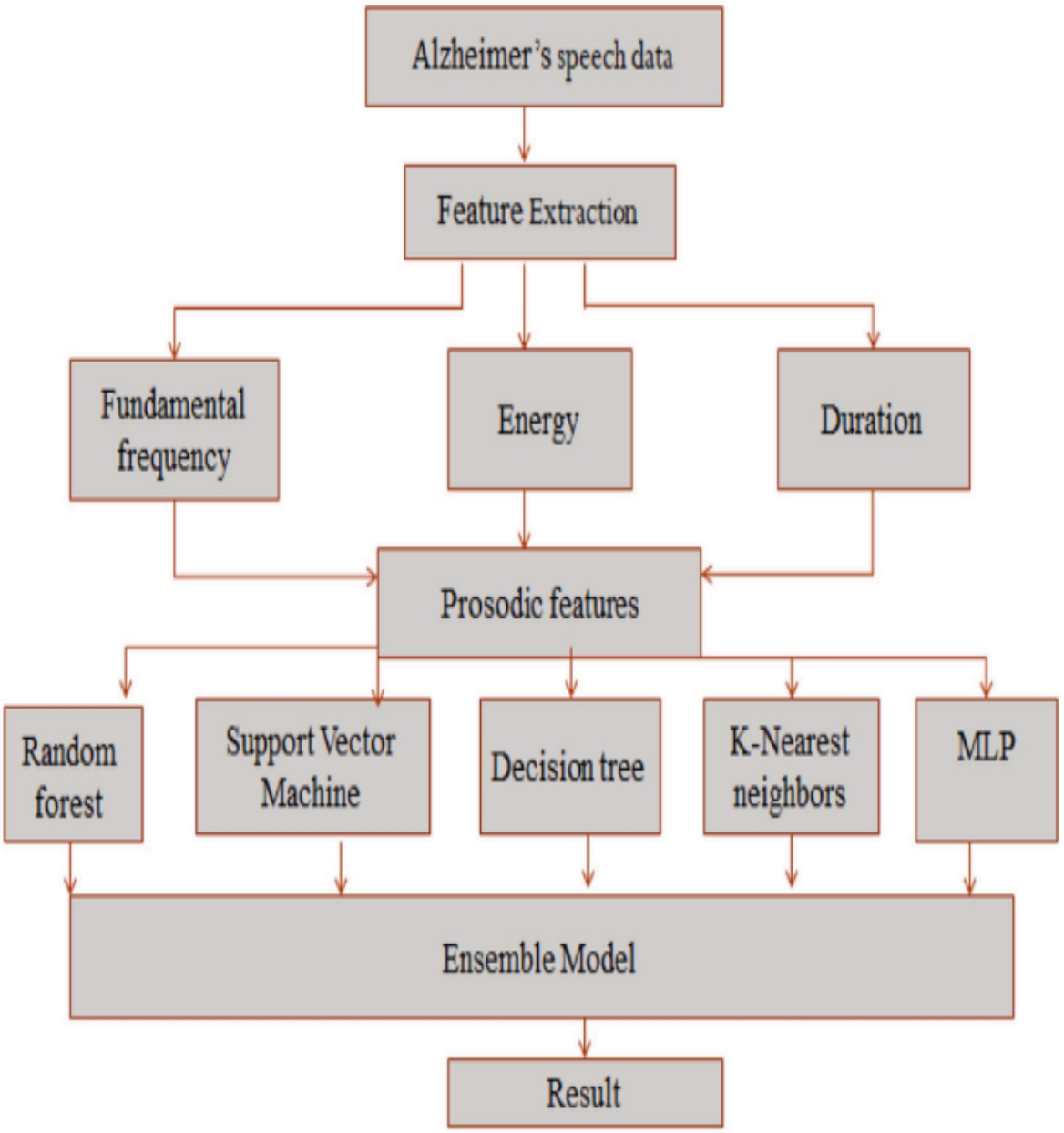
Processor	:	Pentium IV Or Higher
Memory Size	:	128 GB (Minimum)
HDD	:	40 GB (Minimum)

2. SOFTWARE SPECIFICATIONS

Operating System	:	WINDOWS 7 AND PLUS
Front – End	:	HTML,CSS, JAVASCRIPT
Back – End	:	PYTHON, CSV, SQL

CHAPTER 3

ARCHITECTURE DIAGRAM



CHAPTER 4

MODULE DESCRIPTION

4.1 Web Application Interface (Flask App)

- **Description**: A user-friendly interface allowing clinicians and caregivers to upload speech samples and view cognitive health predictions.
- **Functionality**:
    - Users can upload recorded speech files through a form, which then processes the data for analysis.
- **Routes**:
    - index(): Displays the homepage where users can input and upload speech samples.
    - analyze(): Processes the uploaded file, runs it through prediction models, and displays results.
- **Templates**: Templates like index.html and results.html render the user interface, making it accessible and visually informative.

4.2 Speech Data Processing Module

- **Description**: Processes and prepares speech files for analysis, extracting essential acoustic and linguistic features.
- **Functionality**:
    - Applies noise reduction and segmentation techniques to prepare the speech data.
    - Extracts features such as speech rate, pauses, vocabulary, and prosody for further analysis.
    - Stores processed data in a structured format for efficient model training and predictions.

4.3 Machine Learning Model (Prediction Module)

- **Description**: Uses machine learning algorithms to analyze extracted features and predict Alzheimer's risk.
- **Functionality**:
    - Trains and optimizes machine learning models like support vector machines (SVM) or neural networks on labeled speech data.
    - Outputs predictions that gauge the likelihood of cognitive decline based on the analyzed speech patterns.
    - Displays an accuracy metric (e.g., AUC or sensitivity) for model reliability.

4.4 Linguistic and Acoustic Feature Analysis Module

- **Description**: Identifies key features in speech indicative of cognitive decline, providing detailed insights into cognitive health.
- **Functionality**:
    - Analyzes metrics like speech fluency, word choice, and timing, pinpointing patterns associated with Alzheimer's symptoms.
    - Generates feature-specific results, which allow users to see specific markers contributing to the risk assessment.

4.5 Data Visualization Module

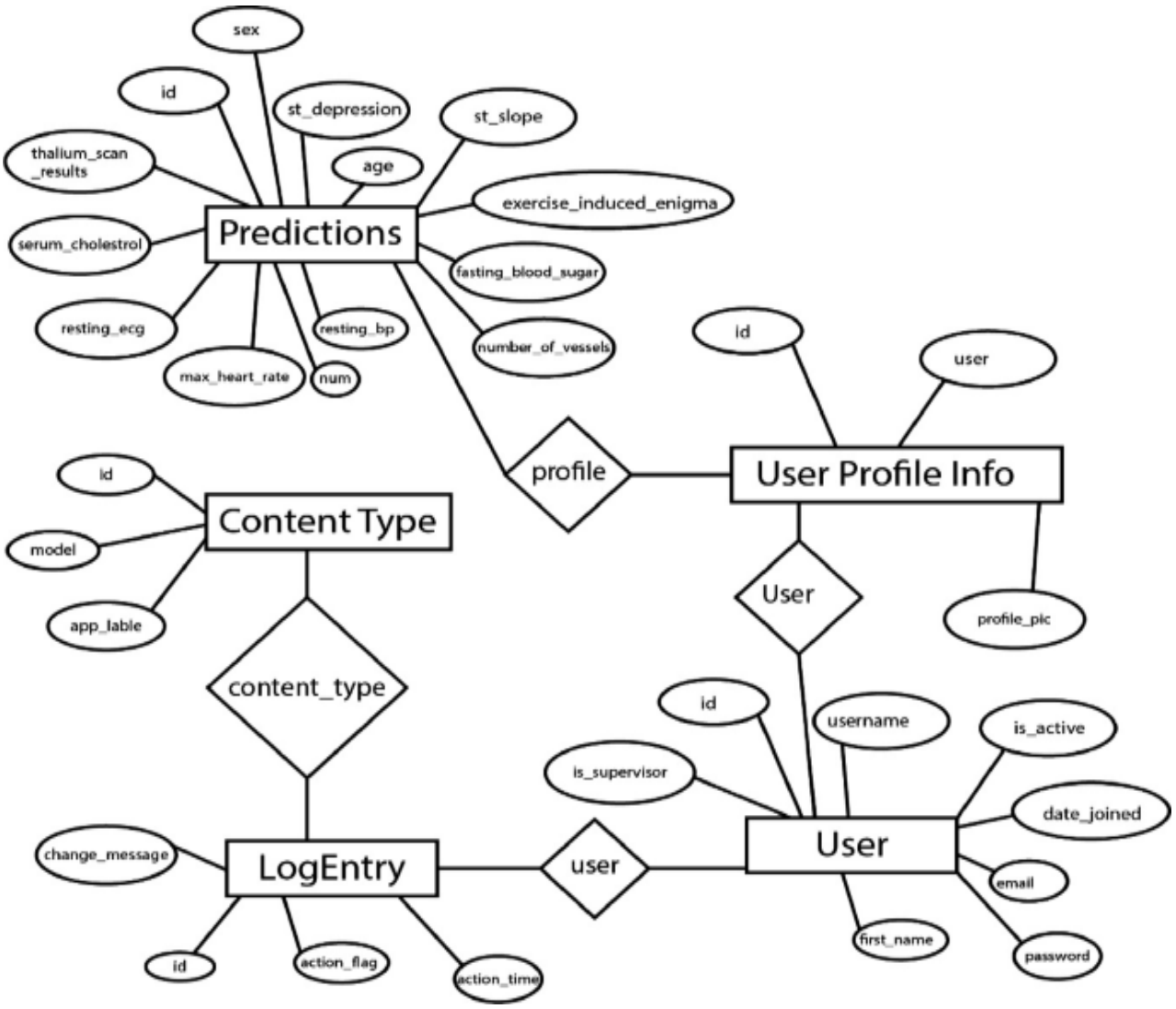
- **Description**: Visualizes the results of the speech analysis and Alzheimer's risk prediction in a clear and accessible format.
- **Functionality**:
    - Produces charts and graphs showing trends in speech patterns over time.
    - Provides visual comparisons of actual speech markers versus normal ranges, helping users interpret potential risk factors.
    - Displays cognitive risk scores and allows tracking changes over multiple assessments for ongoing monitoring.

CHAPTER 5

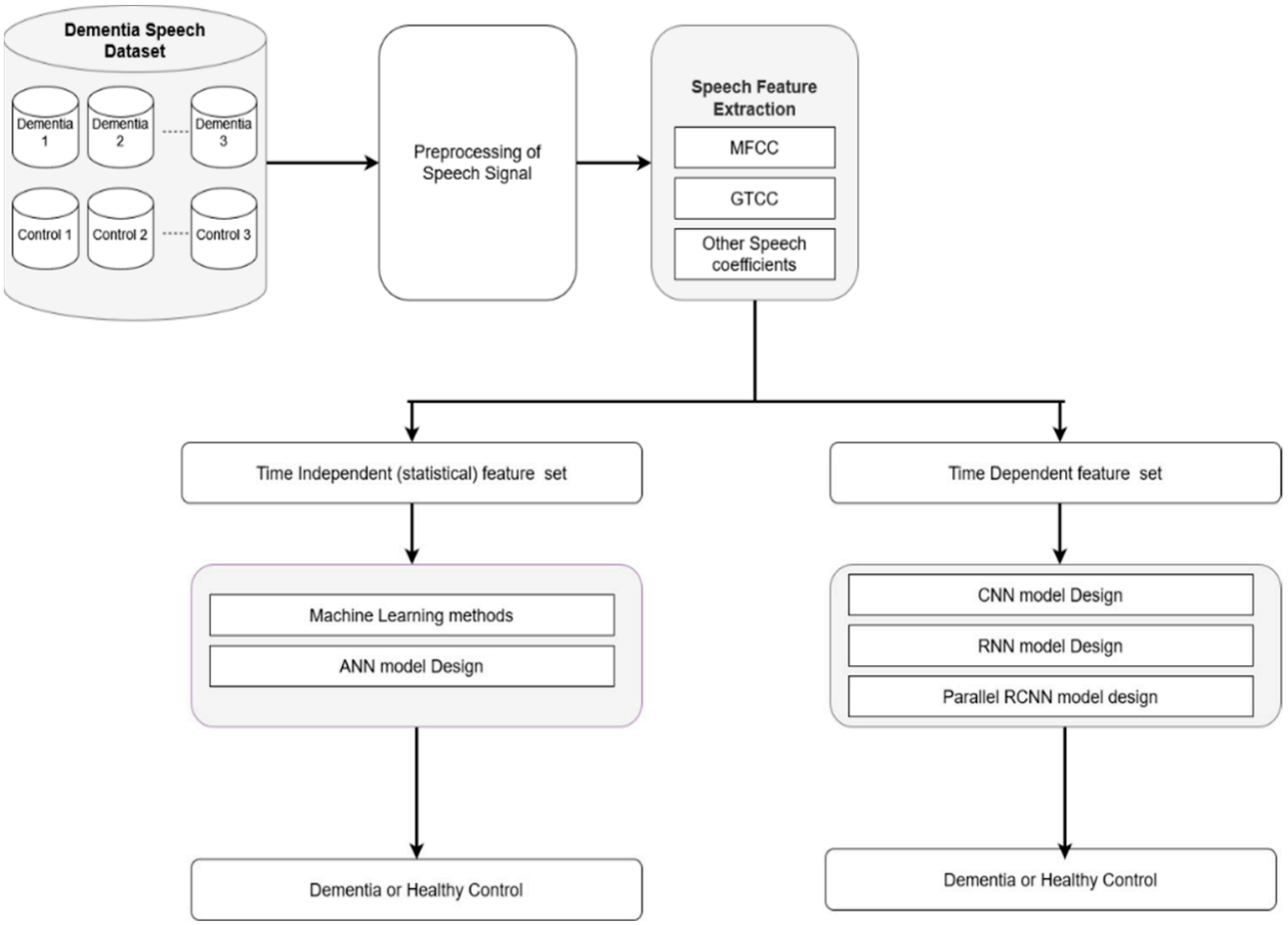
SYSTEM DESIGN

5.1 USE CASE DIAGRAM

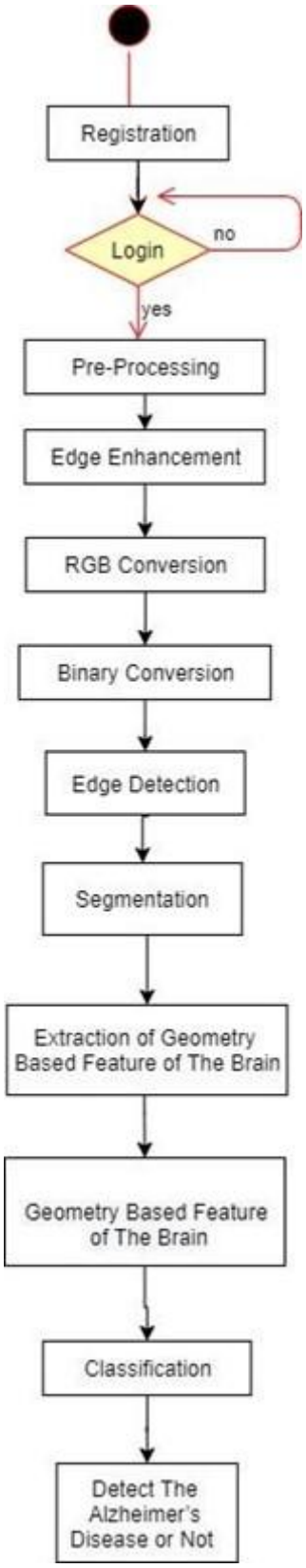
5.2 ER DIAGRAM



5.3. DFD DIAGRAM



5.4. ACTIVITY DIAGRAM



CHAPTER 6

SAMPLE CODING

```
import librosa
import librosa.display
import matplotlib.pyplot as plt
import numpy as np
import os
import warnings
warnings.filterwarnings("ignore", category=FutureWarning)
import csv

from glob import glob
from pydub import AudioSegment, silence

import parselmouth
from torch import segment_reduce
from parselmouth.praat import call # type: ignore

import noisereduce as nr

import pandas as pd

### PROSODIC FEATURES - PITCH RELATED / PHONETICS FEATURES
def prosodic_features(sound, f0min, f0max, unit, interpol):
```

```
    # Unit -> "Hertz", sound -> parselmouth.Sound(voiceID), interpol -> "None", "Parabolic", etc


    ### Pitch Related

    pitch = call(sound, "To Pitch", 0.0, f0min, f0max) # Getting the Pitch object

    meanF0 = call(pitch, "Get mean", 0, 0, unit) # Get mean pitch / Average fundamental frequency

    minF0 = call(pitch, "Get minimum", 0.0, 0.0, unit, interpol) # Get minimum pitch

    maxF0 = call(pitch, "Get maximum", 0.0, 0.0, unit, interpol) # Get maximum pitch

    stdF0 = call(pitch, "Get standard deviation", 0 ,0, unit) # Get standard deviation of fundamental frequency


    ### Intensity Related

    intensity = sound.to_intensity()

    mean_intensity = call(intensity, "Get mean", 0.0, 0.0)

    min_intensity = call(intensity, "Get minimum", 0.0, 0.0, interpol)

    max_intensity = call(intensity, "Get maximum", 0.0, 0.0, interpol)

    std_intensity = call(intensity, "Get standard deviation", 0.0, 0.0)


    ### Harmonicity Related

    harmonicity = call(sound, "To Harmonicity (cc)", 0.01, 75, 0.1, 1.0) # Harmonicity vector

    hnr = call(harmonicity, "Get mean", 0, 0) # Harmonic to Noise Ratio


    ### Prosodic Features

    pointProcess = call(sound, "To PointProcess (periodic, cc)", f0min, f0max)
```

```
    # Parameters Explained for Jitters and Shimmers -> ((Time range:) 0->, 0 (=the whole signal), shortest period=0.0001, longest period=0.02, maximum period factor=1.3, maximum amplitude factor=1.6)

    localJitter = call(pointProcess, "Get jitter (local)", 0, 0, 0.0001, 0.02, 1.3)

    localabsoluteJitter = call(pointProcess, "Get jitter (local, absolute)", 0, 0, 0.0001, 0.02, 1.3)

    rapJitter = call(pointProcess, "Get jitter (rap)", 0, 0, 0.0001, 0.02, 1.3)

    ppq5Jitter = call(pointProcess, "Get jitter (ppq5)", 0, 0, 0.0001, 0.02, 1.3)

    ddpJitter = call(pointProcess, "Get jitter (ddp)", 0, 0, 0.0001, 0.02, 1.3)

    localShimmer =  call([sound, pointProcess], "Get shimmer (local)", 0, 0, 0.0001, 0.02, 1.3, 1.6)

    localdbShimmer = call([sound, pointProcess], "Get shimmer (local_dB)", 0, 0, 0.0001, 0.02, 1.3, 1.6)

    apq3Shimmer = call([sound, pointProcess], "Get shimmer (apq3)", 0, 0, 0.0001, 0.02, 1.3, 1.6)

    apq5Shimmer = call([sound, pointProcess], "Get shimmer (apq5)", 0, 0, 0.0001, 0.02, 1.3, 1.6)

    apq11Shimmer =  call([sound, pointProcess], "Get shimmer (apq11)", 0, 0, 0.0001, 0.02, 1.3, 1.6)

    ddaShimmer = call([sound, pointProcess], "Get shimmer (dda)", 0, 0, 0.0001, 0.02, 1.3, 1.6)


    pros_feat = [meanF0, minF0, maxF0, stdF0, mean_intensity, min_intensity, max_intensity, std_intensity, hnr, localJitter, localabsoluteJitter, rapJitter, ppq5Jitter, ddpJitter, localShimmer, localdbShimmer, apq3Shimmer, apq5Shimmer, apq11Shimmer, ddaShimmer]


    return pros_feat


def get_prosodic_features(file_loc):
```

```
    unit="Hertz"

    filename = file_loc
    sound = parselmouth.Sound(file_loc)
    y, sr = librosa.load(file_loc)
    duration = librosa.get_duration(y=y, sr=sr)
    energy = librosa.feature.rms(y=y)
    #1
    SD_energy = np.std(energy)
    #2
    pitch = call(sound, "To Pitch", 0.0, 75, 300)

    #3
    voiced_frames = pitch.count_voiced_frames()
    total_frames = pitch.get_number_of_frames()
    #4
    voiced_to_total_ratio = voiced_frames/total_frames
    #5
    voiced_to_unvoiced_ratio =  voiced_frames / (total_frames - voiced_frames)



    return [SD_energy, voiced_frames, voiced_to_total_ratio,
voiced_to_unvoiced_ratio]
```

```
## SILENCE FEATURES EXTRACTED USING pydub.silence
# Plot the signal and silences detected on it
def plot_silences(y, silences,color,title):
    plt.figure(figsize=(12,3))
    librosa.display.waveshow(y, alpha=0.5)
    for i in range(len(silences)):
        plt.plot(list(silences[i]),list([0])*len(silences[i]),color=color)
    plt.title(title)
    plt.ylim((-0.3,0.3))
    plt.show()

# Silence detection
def sil_det_normal(myaudio,long=False):
    thresh = myaudio.dBFS + myaudio.dBFS*0.5
    print("Thresh:",thresh)
    sil = silence.detect_silence(myaudio, min_silence_len=500,
silence_thresh=thresh)
    sil = [((start/1000),(stop/1000)) for start,stop in sil] #convert to sec
    # print(sil)
    non_sil = silence.detect_nonsilent(myaudio,min_silence_len=500,
silence_thresh=thresh)
    non_sil = [((start/1000),(stop/1000)) for start,stop in non_sil] #convert to sec

    # non_sil = []
    # for i in range(1,len(sil)):
    #     non_sil.append(tuple([list(sil[i-1])[1],list(sil[i])[0]]))
    # # print(non_sil)
```

```
    return sil,non_sil



# Features for silences
def sil_features(silences, non_sil):
    silence_features = []
    # Finding durations for each silence
    durations_of_silence = [list(silences[i])[1]-list(silences[i])[0] for i in
range(len(silences))]
    # # # print(durations_of_silence)
    # Finding the total duration of silences
    sum_durations_sil = sum(durations_of_silence)
    silence_features.append(sum_durations_sil)
    # # # print(sum_durations_sil)
    # Number of silences
    no_of_silences = len(durations_of_silence)
    silence_features.append(no_of_silences)
    # # # print(no_of_silences)
    # Average silence duration
    if(no_of_silences>0):
        average_silence_duration = sum_durations_sil/no_of_silences
        silence_features.append(average_silence_duration)
        # Median of the silence durations
        med_sil = np.median(durations_of_silence)
        silence_features.append(med_sil)
        # Standard deviation of silence duration
```

```
    std_sil = np.std(durations_of_silence)
    silence_features.append(std_sil)
    # Min Max
    silence_features.append(np.min(durations_of_silence))
    silence_features.append(np.max(durations_of_silence))
    # Q1-Q3 Quartiles
    Q1_sil = np.percentile(durations_of_silence, 25)
    Q3_sil = np.percentile(durations_of_silence, 75)
    silence_features.append(Q1_sil)
    silence_features.append(Q3_sil)
else:
    average_silence_duration = 0
    silence_features.append(average_silence_duration)
    # Median of the silence durations
    med_sil = 0
    silence_features.append(med_sil)
    # Standard deviation of silence duration
    std_sil = 0
    silence_features.append(std_sil)
    # Min Max
    silence_features.append(0)
    silence_features.append(0)
    # Q1-Q3 Quartiles
    Q1_sil = 0
    Q3_sil = 0
    silence_features.append(Q1_sil)
```

```
        silence_features.append(Q3_sil)


    # Finding durations for non silent
    durations_of_non_sil = [list(non_sil[i])[1]-list(non_sil[i])[0] for i in
range(len(non_sil))]
    # Sum of durations of non silent regions
    sum_durations_non_sil = sum(durations_of_non_sil)
    silence_features.append(sum_durations_non_sil)
    # Number of non silent regions
    no_of_non_sil = len(durations_of_non_sil)
    silence_features.append(no_of_non_sil)
    # Average non-silent duration - Mean
    average_non_sil_duration = sum_durations_non_sil/no_of_non_sil
    silence_features.append(average_non_sil_duration)
    # Median of the non-silent durations
    med_non_sil = np.median(durations_of_non_sil)
    silence_features.append(med_non_sil)
    # Standard deviation of non silenct duration
    std_non_sil = np.std(durations_of_non_sil)
    silence_features.append(std_non_sil)
    # Min Max
    silence_features.append(np.min(durations_of_non_sil))
    silence_features.append(np.max(durations_of_non_sil))
    # Q1-Q3 Quartiles
    Q1_non_sil = np.percentile(durations_of_non_sil, 25)
    Q3_non_sil = np.percentile(durations_of_non_sil, 75)
```

```
    silence_features.append(Q1_non_sil)
    silence_features.append(Q3_non_sil)

    # Ratio of silent vs non silent durations
    ratio_sil_non_sil = sum_durations_sil/sum_durations_non_sil
    silence_features.append(ratio_sil_non_sil)
    # Ratio of number of silent vs non silent regions
    ratio_sil_non_sil_no = no_of_silences/no_of_non_sil
    silence_features.append(ratio_sil_non_sil_no)
    # Ratio of average_silence_duration vs average_non_sil_duration - Mean
    ratio_average_sil_non_sil =
average_silence_duration/average_non_sil_duration
    silence_features.append(ratio_average_sil_non_sil)
    # Ratio of medians
    ratio_med = med_sil/med_non_sil
    silence_features.append(ratio_med)
    # Ratio of std
    ratio_std = std_sil/std_non_sil
    silence_features.append(ratio_std)
    # Ratio of Q1
    ratio_Q1 = Q1_sil/Q1_non_sil
    silence_features.append(ratio_Q1)
    ratio_Q3 = Q3_sil/Q3_non_sil
    silence_features.append(ratio_Q3)

    return silence_features
```

```
### ZERO CROSSING FEATURES
def zero_crossing_features(sound):
    # Zero crossings
    zc = librosa.zero_crossings(sound, pad=False)
    zc = sum(zc)
    # ZCR
    dur = librosa.get_duration(sound)
    zcr = zc/dur
    zcr = librosa.feature.zero_crossing_rate(sound)

    ## ZCR lowerst and highest instantaneous value
    min_zcr = zcr.min()
    max_zcr = zcr.max()

    ## ZCR mean
    zcr = zcr.mean()

    return [zc,min_zcr,max_zcr,zcr]



def feature_extraction_per_stage(files_No, output_name, going_for_all=False):
    ## going_for_all -> bool to say if we want feature extraction for a new file
(TRUE)
    ##              or if we want to use the function for a new person and thus
    ##              only write the new features on an existing csv file.
```

```
    # Feature names and feature array intialization
    names = []
    silence_feature_names = ['Total_Duration_Silence','# of Silences','Average Silence Duration','Median of Silence Duration','Std of Silence','Min Duration of Silence','Max Duration of Silence','Q1 Sil Duration','Q3 Sil Duration','Total non-Silent Duration','# of non-Silent','Average non-Silent Duration','Median of non-Silent Duration','Std of non-Silent Duration','Min Duration of non-Silent','Max Duration of non-Silent','Q1 non-Sil Duration','Q3 non-Sil Duration','Ratio Sil non-Sil','Ratio # Sil non-sil','Ratio Average Sil non-sil','Ratio medians','Ratio STDs','Ratio Q1','Ratio Q3']
    prosodic_feature_names = ['meanF0', 'minF0', 'maxF0', 'stdF0', 'mean_intensity', 'min_intensity', 'max_intensity', 'std_intensity', 'hnr', 'localJitter', 'localabsoluteJitter', 'rapJitter', 'ppq5Jitter', 'ddpJitter', 'localShimmer', 'localdbShimmer', 'apq3Shimmer', 'apq5Shimmer', 'apq11Shimmer', 'ddaShimmer']
    zcr_feature_names = ['ZeroCrossings','Min zcr','Max zcr','zcr']
    feature_names = silence_feature_names + prosodic_feature_names + zcr_feature_names
    features = np.empty((0,len((feature_names))),float)
    print(len(files_No)," files are expected to go through feature extraction.")
    i = 1
    # Basic loop
    for file in files_No:
        temp_features = np.array([])
        names.append(os.path.basename(file))
        snd = parselmouth.Sound(file)
        myaudio = AudioSegment.from_wav(file)
        y, sr = librosa.load(file)
```

```
        # Extracting silence features
        silences,non_silent = sil_det_normal(myaudio)
        # plot_silences(y, silences,'r',os.path.basename(file))
        silence_features = sil_features(silences,non_silent)
        # print("Number of silence features extracted: ", len(silence_features))
        temp_features = np.append(temp_features,silence_features)

        # Prosodic features
        pros_features = prosodic_features(snd, 75, 500.0, "Hertz", "parabolic")
        temp_features = np.append(temp_features,pros_features)
        # print("Number of prosodic features extracted: ", len(pros_features))

        # Zero-crossing features
        zcr_features = zero_crossing_features(y)
        temp_features = np.append(temp_features,zcr_features)
        # print("Number of zcr features extracted: ", len(zcr_features))

        # print("Total Number of features extracted: ", len(features))
        print(i/len(files_No)*100," % ","of Feature extraction Completed. File : ",
i, " out of ", len(files_No))
        i = i+1

        features = np.append(features, [temp_features], axis=0)

    ## Writing a new file
    if going_for_all:
```

```
        df = pd.DataFrame(features, columns=feature_names,index=names)
        df.to_csv(output_name)
    ## Writing on existing file (when adding new people to the database)
    else:
        df = pd.DataFrame(features,columns=feature_names, index=names)
        df.to_csv(output_name, mode='a', index=True, header=False)



### Function to extract and save features for new people to the database
def feature_extraction_new_person(persons_folder,csv_output_names):
    # Getting different bunches of files according to stage of the recording
    files1 = glob(persons_folder+'/*[1].wav')
    files2 = glob(persons_folder+'/*[2].wav')
    files3 = glob(persons_folder+'/*[3].wav')
    files4 = glob(persons_folder+'/*[4].wav')
    files5 = glob(persons_folder+'/*[5].wav')
    files = [files1, files2, files3, files4, files5]
    for i in range(5):
        print("Stage ", i+1, " :")
        feature_extraction_per_stage(files[i],csv_output_names[i],
going_for_all=False)

# Files stored per stage of recording
files1 = glob(seg_recs_path+'/*[1].wav')
files2 = glob(seg_recs_path+'/*[2].wav')
```

```
files3 = glob(seg_recs_path+'/*[3].wav')

files4 = glob(seg_recs_path+'/*[4].wav')

files5 = glob(seg_recs_path+'/*[5].wav')



# feature_extraction_per_stage(files2,
'Features_Stage_2.csv',going_for_all=True)

folder = 'C:/Users/MSI User/OneDrive - Speech/Speech Data/Segmented
Recs/name'

csv_names = ['test.csv','test2.csv','test3.csv','test4.csv','test5.csv']

feature_extraction_new_person(folder,csv_names)


import numpy as np

import matplotlib.pyplot as plt

from pydantic import Extra

import seaborn as sns

import pandas as pd

from sklearn import svm

from sklearn.preprocessing import StandardScaler, LabelEncoder,
OneHotEncoder

from sklearn.model_selection import train_test_split, RepeatedStratifiedKFold,
StratifiedKFold

from sklearn.ensemble import RandomForestClassifier

from sklearn.metrics import f1_score,confusion_matrix, roc_auc_score

from sklearn.metrics import accuracy_score, recall_score

import pickle

import warnings
```

```
from sklearn.metrics import classification_report

from sklearn.model_selection import cross_val_predict, cross_val_score
from sklearn.ensemble import ExtraTreesClassifier
import joblib

warnings.filterwarnings('ignore')



### Train Models
def train_model(model, df, df_test, save_model_name, save_scaler_name,
age_flag, education_flag, gender_flag, scaling, binary):

    ### Drop NaN and Inf
    df.replace([np.inf, -np.inf], np.nan, inplace=True)
    df = df.dropna().reset_index(drop = True)

    df_test.replace([np.inf, -np.inf], np.nan, inplace=True)
    df_test = df_test.fillna(0).reset_index(drop = True)
    dft = df_test

    # Drop according to binary
    if binary == 'hs':
        df['Diagnosis'] = df['Diagnosis'].replace(['E-MCI'],'MCI')
        df['Diagnosis'] = df['Diagnosis'].replace(['L-MCI'],'MCI')
```

```
    df = df[df.Diagnosis != 'MCI']
    Y = df.Diagnosis
    dft['Diagnosis'] = dft['Diagnosis'].replace(['E-MCI'],'MCI')
    dft['Diagnosis'] = dft['Diagnosis'].replace(['L-MCI'],'MCI')
    dft = dft[dft.Diagnosis != 'MCI']
    Y_test = dft.Diagnosis

elif binary == 'hm':
    df['Diagnosis'] = df['Diagnosis'].replace(['E-MCI'],'MCI')
    df['Diagnosis'] = df['Diagnosis'].replace(['L-MCI'],'MCI')
    df = df[df.Diagnosis != 'SCD']
    dft['Diagnosis'] = dft['Diagnosis'].replace(['E-MCI'],'MCI')
    dft['Diagnosis'] = dft['Diagnosis'].replace(['L-MCI'],'MCI')
    dft = dft[dft.Diagnosis != 'SCD']
    Y = df.Diagnosis
    Y_test = dft.Diagnosis
elif binary == 'sm':
    df['Diagnosis'] = df['Diagnosis'].replace(['E-MCI'],'MCI')
    df['Diagnosis'] = df['Diagnosis'].replace(['L-MCI'],'MCI')
    df = df[df.Diagnosis != 'Healthy']
    dft['Diagnosis'] = dft['Diagnosis'].replace(['E-MCI'],'MCI')
    dft['Diagnosis'] = dft['Diagnosis'].replace(['L-MCI'],'MCI')
    dft = dft[dft.Diagnosis != 'Healthy']
    Y = df.Diagnosis
    Y_test = dft.Diagnosis
```

```
    ### Prepare the data-set
    print(Y_test.value_counts())
    label_1 = LabelEncoder()

    if age_flag and education_flag and gender_flag:
        X = df[df.columns[~df.columns.isin(['Unnamed: 0','Ratio Q1',
'Name','Diagnosis','Min zcr'])]]
        X['Gender']= label_1.fit_transform(X['Gender'])
        X['Gender'] = pd.get_dummies(X['Gender'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)
        X['Education'] = pd.get_dummies(X['Education'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)
        X_test = dft[dft.columns[~dft.columns.isin(['Unnamed: 0','Ratio Q1',
'Name','Diagnosis','Min zcr'])]]
        X_test['Gender']= label_1.transform(X_test['Gender'])
        X_test['Gender'] = pd.get_dummies(X_test['Gender'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)
        X_test['Education'] = pd.get_dummies(X_test['Education'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)

        s = '_AEG.sav'

    elif education_flag and gender_flag:
        X = df[df.columns[~df.columns.isin(['Unnamed: 0','Ratio Q1',
'Name','Diagnosis','Min zcr','Age'])]]
        X['Gender']= label_1.fit_transform(X['Gender'])
```

```
        X['Gender'] = pd.get_dummies(X['Gender'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)

        X['Education'] = pd.get_dummies(X['Education'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)

        X_test = dft[dft.columns[~dft.columns.isin(['Unnamed: 0','Ratio Q1',
'Name','Diagnosis','Min zcr','Age'])]]

        X_test['Gender']= label_1.transform(X_test['Gender'])

        X_test['Gender'] = pd.get_dummies(X_test['Gender'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)

        X_test['Education'] = pd.get_dummies(X_test['Education'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)

        s = '_EG.sav'

    elif gender_flag:

        X = df[df.columns[~df.columns.isin(['Unnamed: 0','Ratio Q1',
'Name','Diagnosis','Min zcr','Age','Education'])]]

        X['Gender']= label_1.fit_transform(X['Gender'])

        X['Gender'] = pd.get_dummies(X['Gender'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)

        X_test = dft[dft.columns[~dft.columns.isin(['Unnamed: 0','Ratio Q1',
'Name','Diagnosis','Min zcr','Age','Education'])]]

        X_test['Gender']= label_1.transform(X_test['Gender'])

        X_test['Gender'] = pd.get_dummies(X_test['Gender'],prefix_sep='_',
dummy_na=False, columns=None,sparse=False, drop_first=False)

        s = '_G.sav'

    else:

        X = df[df.columns[~df.columns.isin(['Unnamed: 0','Ratio Q1',
'Name','Diagnosis','Min zcr','Age','Education','Gender'])]]

        X_test = dft[dft.columns[~dft.columns.isin(['Unnamed: 0','Ratio Q1',
'Name','Diagnosis','Min zcr','Age','Education','Gender'])]]
```

```
        s = '.sav'


    ### Encoding
    X['Stress_Depression']= label_1.fit_transform(X['Stress_Depression'])
    X['Stress_Depression'] =
pd.get_dummies(X['Stress_Depression'],prefix_sep='_', dummy_na=False,
columns=None,sparse=False, drop_first=False)
    X_test['Stress_Depression']= label_1.transform(X_test['Stress_Depression'])
    X_test['Stress_Depression'] =
pd.get_dummies(X_test['Stress_Depression'],prefix_sep='_', dummy_na=False,
columns=None,sparse=False, drop_first=False)
    X_test_1 = X_test
    ### Train-test split
    x_train, x_test, y_train, y_test = train_test_split(X, Y, test_size=0.2)


    ### Scaling if need to
    if scaling:
        scaler = StandardScaler()
        x_train = scaler.fit_transform(x_train)
        x_test = scaler.transform(x_test)
        X = scaler.transform(X)
        X_test = scaler.transform(X_test)
        joblib.dump(scaler, save_scaler_name)



    ### Model
    clf = model
```

```
    clf.fit(x_train, y_train)



    # feat_importances = pd.Series(clf.feature_importances_,
index=X_test_1.columns)
    # feat_importances.nlargest(30).plot(kind='barh')
    # most_important_feat = feat_importances.nlargest(30).index.tolist()
    # plt.show()


    ### Print model metrics
    if binary == 'hs':
        print('Classification Report for Train Set: ')
        print(classification_report(y_test, clf.predict(x_test),
target_names=['Healthy','SCD']))
        cv = RepeatedStratifiedKFold(n_splits=10, n_repeats=3)
        n_scores = cross_val_score(clf, X, Y, scoring='accuracy', cv=cv,
n_jobs=-1, error_score='raise')
        print('Cross-Validated Accuracy : %.3f ± (%.3f)' % (np.mean(n_scores),
np.std(n_scores)))


        print('Classification Report for Test Set: ')
        print(Y_test.shape)
        print(X_test.shape)
        print(classification_report(Y_test, clf.predict(X_test),
target_names=['Healthy','SCD']))


    elif binary == 'hm':
        print('Classification Report for Train Set: ')
```

```
        print(classification_report(y_test, clf.predict(x_test),
target_names=['Healthy','MCI']))

        cv = RepeatedStratifiedKFold(n_splits=10, n_repeats=3)

        n_scores = cross_val_score(clf, X, Y, scoring='accuracy', cv=cv,
n_jobs=-1, error_score='raise')

        print('Cross-Validated Accuracy : %.3f ± (%.3f)' % (np.mean(n_scores),
np.std(n_scores)))


        print('Classification Report for Test Set: ')

        print(classification_report(Y_test, clf.predict(X_test),
target_names=['Healthy','MCI']))


    elif binary == 'sm':

        print('Classification Report for Train Set: ')

        print(classification_report(y_test, clf.predict(x_test),
target_names=['MCI','SCD']))

        cv = RepeatedStratifiedKFold(n_splits=10, n_repeats=3)

        n_scores = cross_val_score(clf, X, Y, scoring='accuracy', cv=cv,
n_jobs=-1, error_score='raise')

        print('Cross-Validated Accuracy : %.3f ± (%.3f)' % (np.mean(n_scores),
np.std(n_scores)))


        print('Classification Report for Test Set: ')

        print(classification_report(Y_test, clf.predict(X_test),
target_names=['MCI','SCD']))
```

```
    # Save the model to disk
    filename = save_model_name+s
    pickle.dump(model, open(filename, 'wb'))
```

Load data sets

```
df1_train = pd.read_csv('df_some_train_1.csv').dropna().reset_index(drop = True)
df2_train = pd.read_csv('df_some_train_2.csv').dropna().reset_index(drop = True)
df3_train = pd.read_csv('df_some_train_3.csv').dropna().reset_index(drop = True)
df4_train = pd.read_csv('df_some_train_4.csv').dropna().reset_index(drop = True)
df5_train = pd.read_csv('df_some_train_5.csv').dropna().reset_index(drop = True)

dfs_train = [df1_train, df2_train, df3_train, df4_train, df5_train]

df1_test = pd.read_csv('df_some_test_1.csv').dropna().reset_index(drop = True)
df2_test = pd.read_csv('df_some_test_2.csv').dropna().reset_index(drop = True)
df3_test = pd.read_csv('df_some_test_3.csv').dropna().reset_index(drop = True)
df4_test = pd.read_csv('df_some_test_4.csv').dropna().reset_index(drop = True)
df5_test = pd.read_csv('df_some_test_5.csv').dropna().reset_index(drop = True)
```

dfs_test = [df1_test, df2_test, df3_test, df4_test, df5_test]

models =
[svm.SVC(kernel='rbf',C=10,probability=True),svm.SVC(kernel='rbf',C=20,probability=True), svm.SVC(kernel='rbf',C=12,probability=True),
svm.SVC(kernel='rbf',C=14,probability=True),
svm.SVC(kernel='rbf',C=14,probability=True),
svm.SVC(kernel='rbf',C=14,probability=True),
svm.SVC(kernel='rbf',C=14,probability=True),
svm.SVC(kernel='rbf',C=10,probability=True),
svm.SVC(kernel='rbf',C=25,probability=True),
svm.SVC(kernel='rbf',C=10,probability=True),]

models = [ExtraTreesClassifier(),ExtraTreesClassifier(),ExtraTreesClassifier(),
ExtraTreesClassifier(),ExtraTreesClassifier()]

################## Some people out Testing 5 models:

model_names =
['SVM_1_hs','SVM_2_hs','SVM_3_hs','SVM_4_hs','SVM_5_hs']

scaler_names =
['Scaler_1_hs.gz','Scaler_2_hs.gz','Scaler_3_hs.gz','Scaler_4_hs.gz','Scaler_5_hs.gz']

model_names =
['SVM_1_hm','SVM_2_hm','SVM_3_hm','SVM_4_hm','SVM_5_hm']

scaler_names =
['Scaler_1_hm.gz','Scaler_2_hs.gz','Scaler_3_hm.gz','Scaler_4_hm.gz','Scaler_5_hm.gz']

```
# model_names =
['SVM_1_sm','SVM_2_sm','SVM_3_sm','SVM_4_sm','SVM_5_sm']

# scaler_names =
['Scaler_1_sm.gz','Scaler_2_sm.gz','Scaler_3_sm.gz','Scaler_4_sm.gz','Scaler_5
_sm.gz']



for i in range(5):

    train_model(models[i], dfs_train[i], dfs_test[i], model_names[i],
scaler_names[i], age_flag=False, education_flag=False, gender_flag=False,
scaling=True, binary='hm')

    # train_model(models[i], dfs_train[i], dfs_test[i], model_names[i],
scaler_names[i], age_flag=True, education_flag=True, gender_flag=True,
scaling=True)

    # train_model(models[i], dfs_train[i], dfs_test[i], model_names[i],
scaler_names[i], age_flag=True, education_flag=True, gender_flag=True,
scaling=False)

    # train_model(models[i], dfs_train[i], dfs_test[i], model_names[i],
scaler_names[i], age_flag=False, education_flag=False, gender_flag=False,
scaling=False)
```

CHAPTER 7

SCREENSHOTS

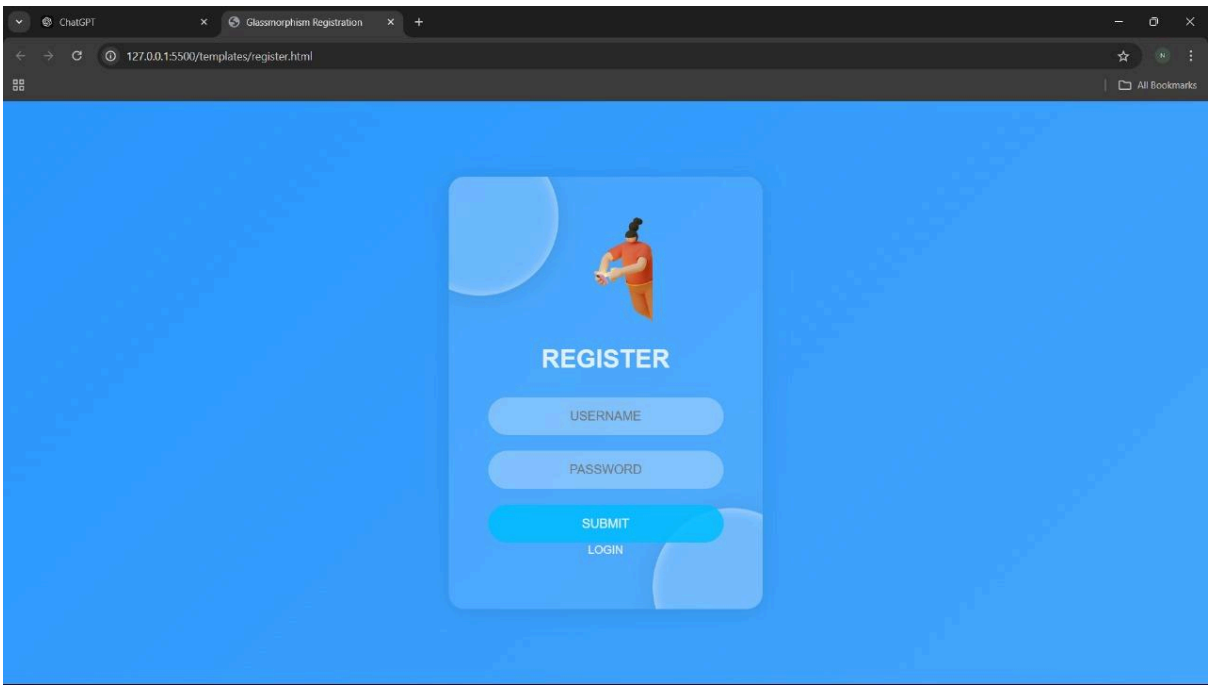


Fig 7.1 Register Page

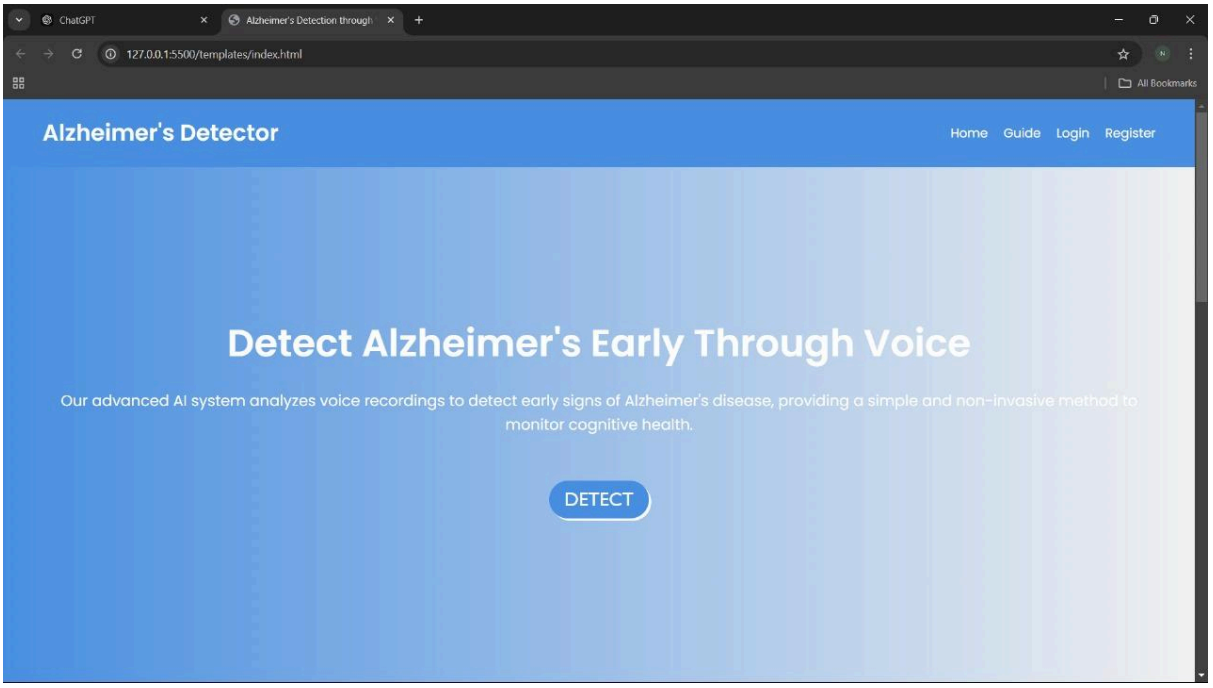


Fig 7.2 Home Page

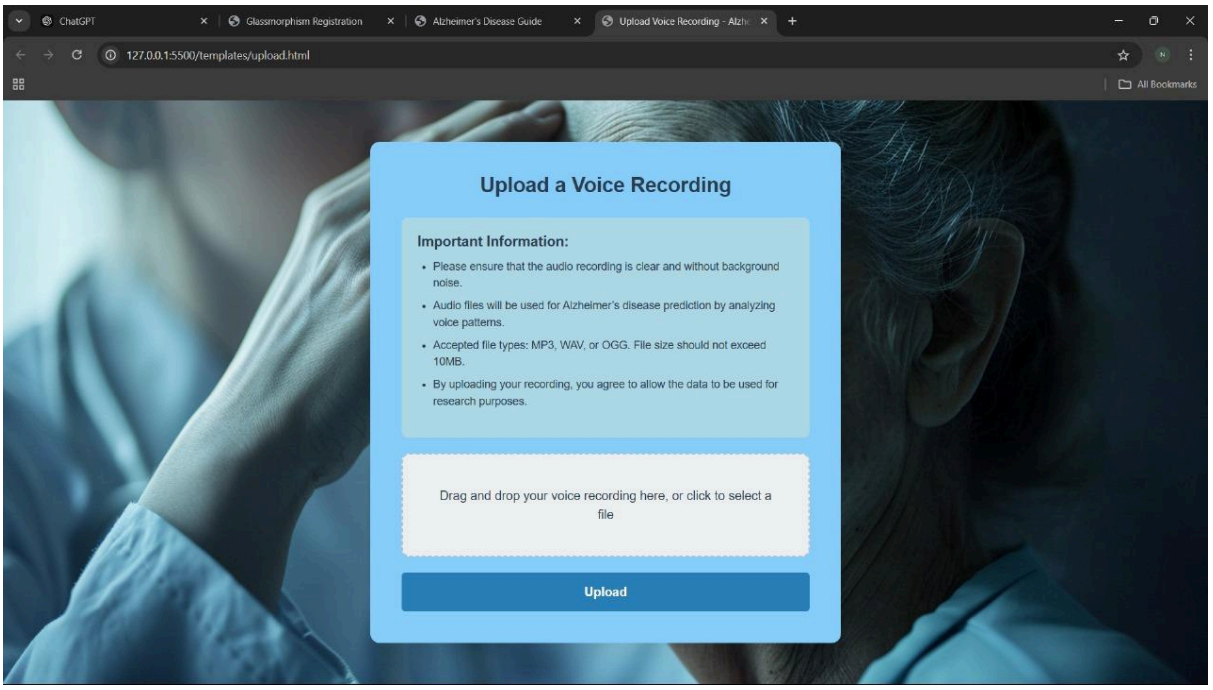


Fig 7.3 Upload Page

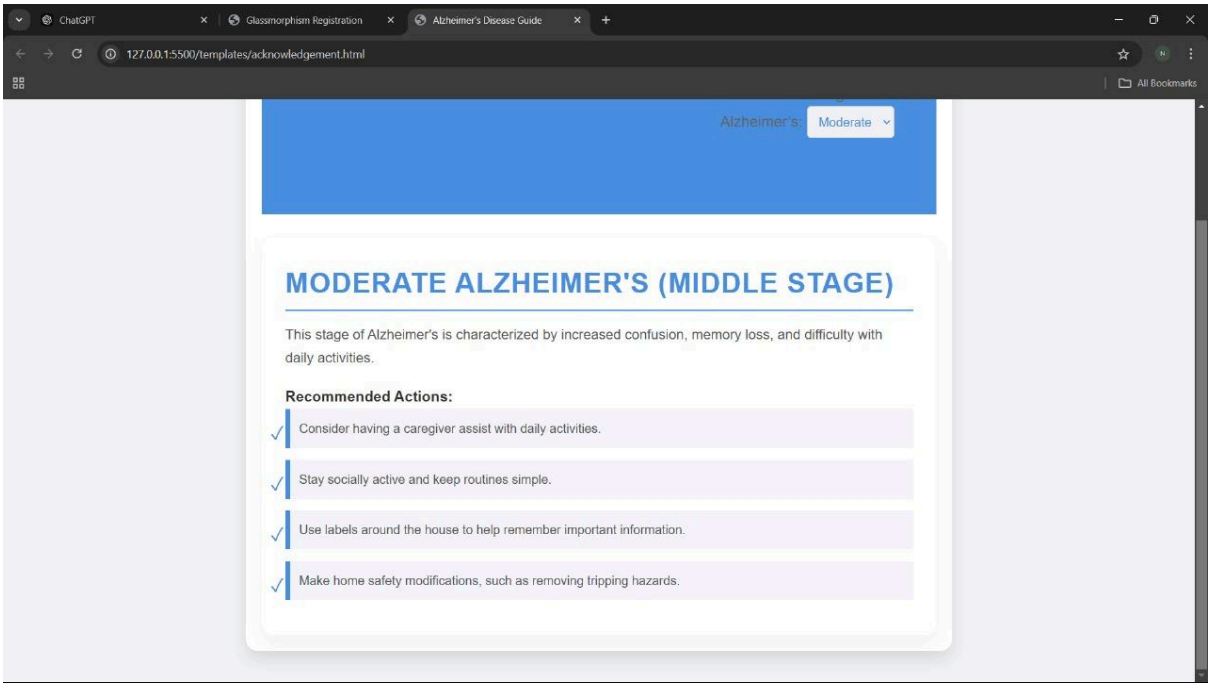


Fig 7.4 Prediction Page

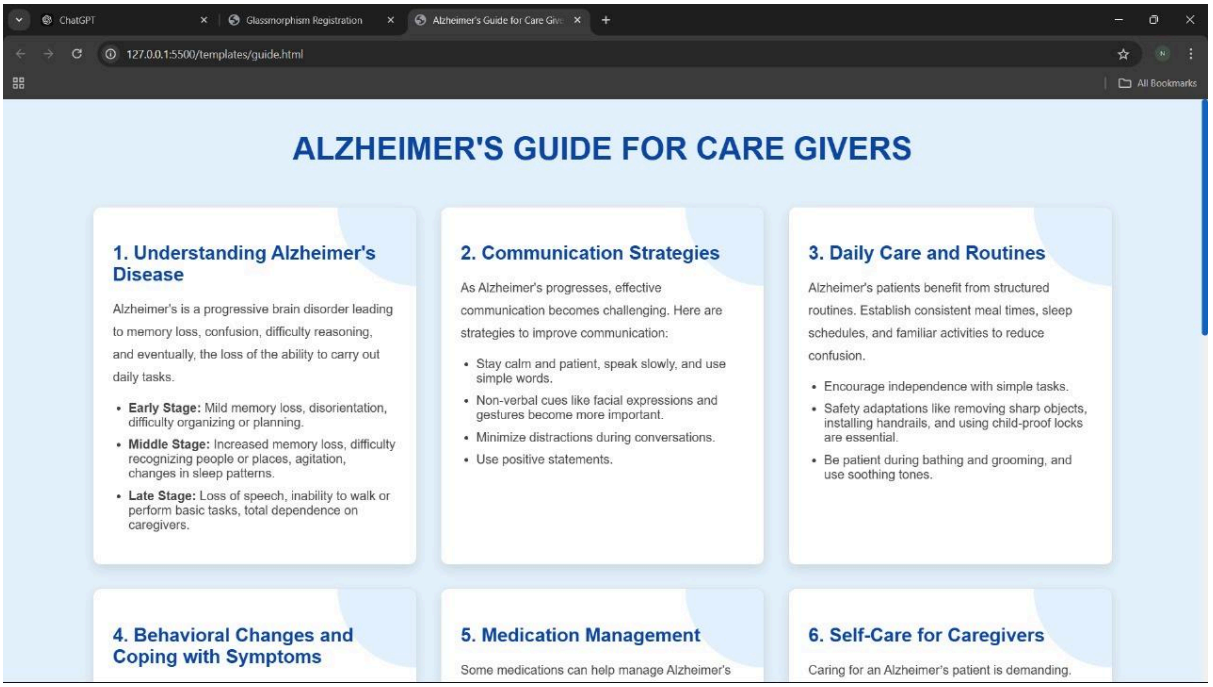


Fig 7.5 Guide page

CHAPTER 8

CONCLUSION

In conclusion, *CognitiveX: Alzheimer's Disease Prediction through Speech Analysis* is a promising tool for non-invasive and accessible early detection of Alzheimer's Disease. By leveraging machine learning to analyze linguistic and acoustic features in speech, the system provides a novel approach to identifying cognitive decline at an early stage. The user-friendly interface, coupled with data visualizations, allows for easy interpretation of results, making it valuable for clinicians and caregivers alike. With secure data handling protocols, *CognitiveX* also ensures user privacy while supporting proactive cognitive health management. Future enhancements, such as incorporating multi-language capabilities and refining model accuracy, could further expand its effectiveness. Overall, *CognitiveX* contributes to the growing field of preventive healthcare by empowering users with an innovative tool for Alzheimer's monitoring and early intervention.

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