



# CHRONIC DISEASE PREDICTION

An ML Based Application to predict Risk of Chronic Disease

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BATCH - 4





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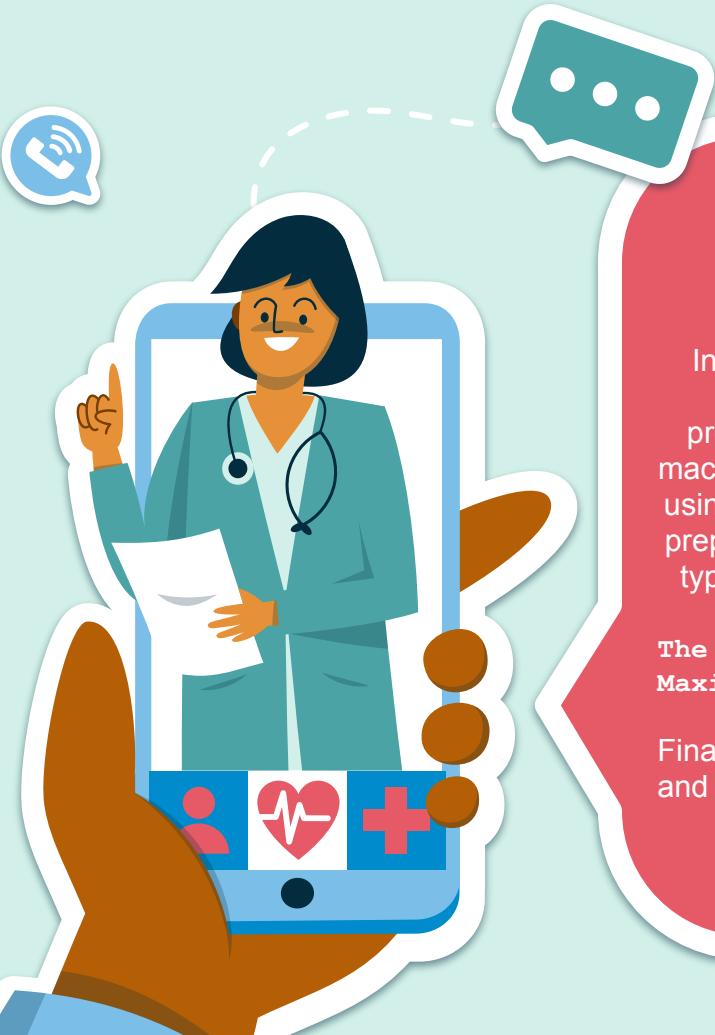
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# INTRODUCTION

In the field of biomedical and healthcare communities the accurate prediction plays the major role to find out the risk of the disease in the patient. The prediction gives the benefits of early disease detection. Here we use a certain machine learning algorithm to state the risk of disease. Prediction process is done using the dataset provided online from certain hospitals, the entire dataset will be preprocessed and the missing values will be reconstructed. Compared to several types of prediction algorithms, the Logistic Regression model gives the highest accuracy of prediction.

The model 'Logistic Regression' has an Average Accuracy: 76.94 %  
Maximum Accuracy that can be obtained: 85.71

Finally, This was integrated to our Web Application, Built on Visual Studio Code and MySQL Work bench

# PROBLEM STATEMENT

To Predict The risk of Chronic Disease in User, By analysing Collected parameters



# OUR OBJECTIVE

CHRONIC ILLNESS PREDICTION

WEB SERVER

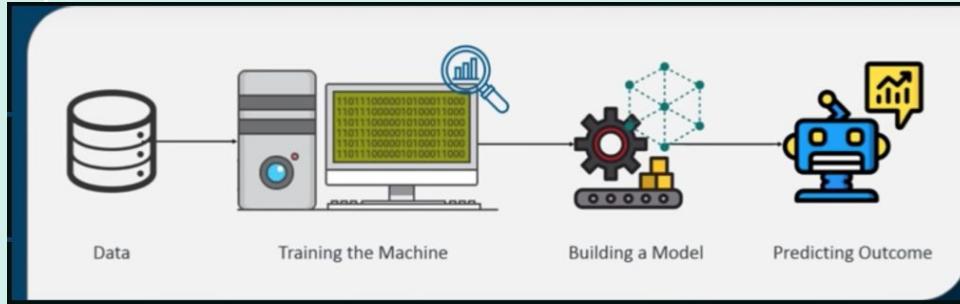
ML PREDICTION ALGORITHM

Flask-Python  
Framework

HTML/CSS

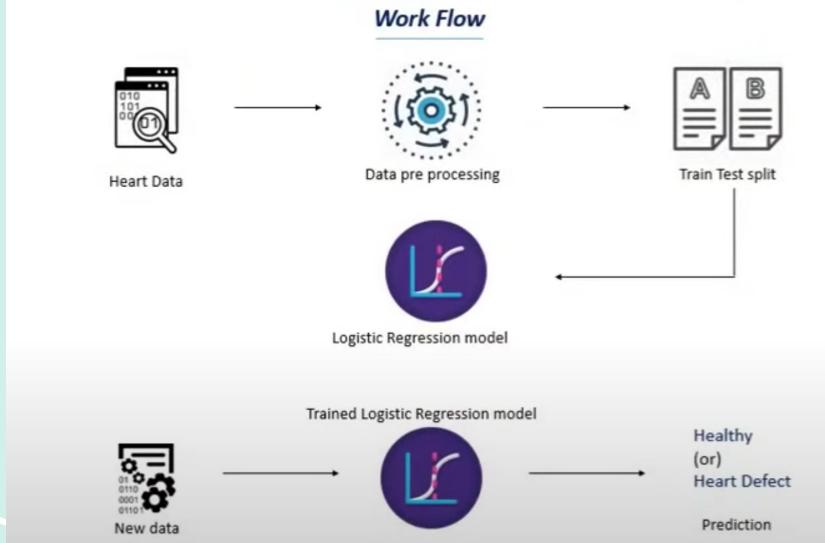
Data Processing  
and training

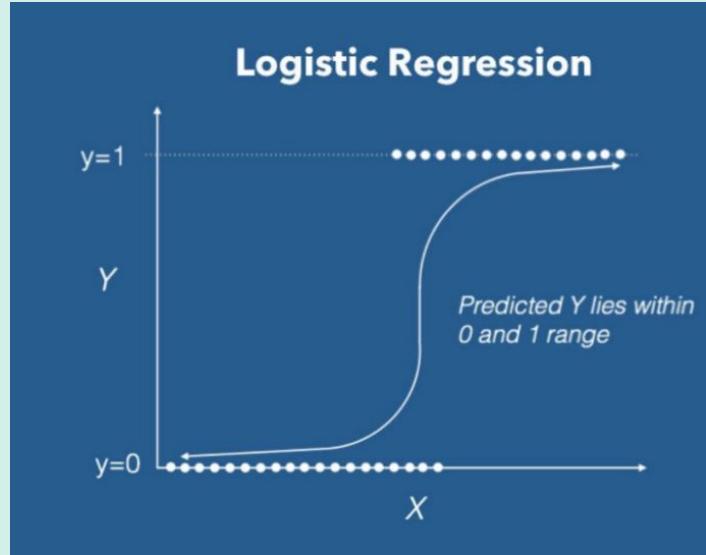
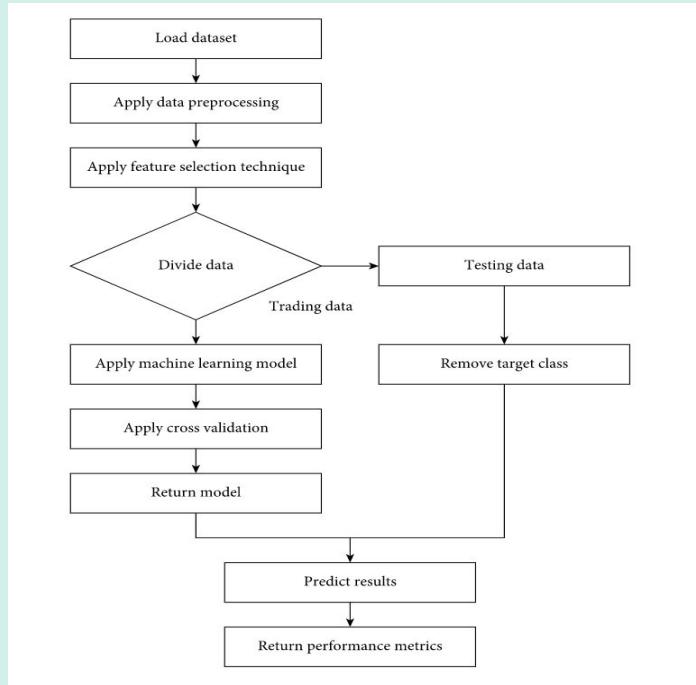
Prediction Model



### Classification

- Supervised Learning
- Output is a categorical quantity
- Main aim is to compute the category of the data
- Eg: Classify emails as spam or non-spam
- Algorithm: Logistic Regression







+ Code + Text

The model 'Logistic Regression' has an Average Accuracy: 76.94 %  
 Maximum Accuracy that can be obtained: 85.71 %  
 Standard Deviation: 0.053713908554226225

The model 'K Nearest Neighbour' has an Average Accuracy: 75.26 %  
 Maximum Accuracy that can be obtained: 82.89 %  
 Standard Deviation: 0.05441598084625328

The model 'Decision Tree' has an Average Accuracy: 69.52 %  
 Maximum Accuracy that can be obtained: 76.62 %  
 Standard Deviation: 0.0477305251276215

The model 'Random Forest' has an Average Accuracy: 76.82 %  
 Maximum Accuracy that can be obtained: 84.42 %  
 Standard Deviation: 0.051902513486997225

The model 'SVM' has an Average Accuracy: 75.9 %  
 Maximum Accuracy that can be obtained: 84.42 %  
 Standard Deviation: 0.05894736252068271

The model 'XGB' has an Average Accuracy: 76.43 %  
 Maximum Accuracy that can be obtained: 81.82 %  
 Standard Deviation: 0.040319660624529706

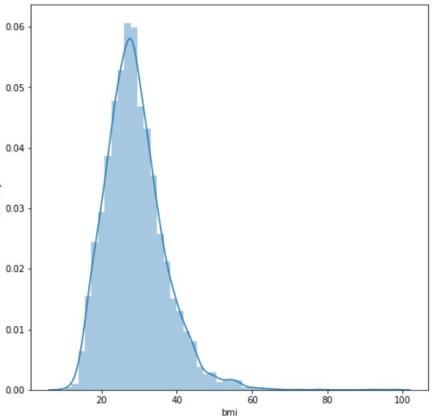
The model 'LightGBM' has an Average Accuracy: 73.96 %  
 Maximum Accuracy that can be obtained: 81.82 %  
 Standard Deviation: 0.062171867376286175

+ Code + Text

We have null values in BMI, so we will replace all null values with the median value

```
[ ] fig, ax = plt.subplots(figsize=(8,8))
sns.distplot(heart_data.bmi)

[ ] /usr/local/lib/python3.7/dist-packages/seaborn/distributions.py:2619: FutureWarning:
  warnings.warn(msg, FutureWarning)
<matplotlib.axes._subplots.AxesSubplot at 0x7f9a756d2e50>
```



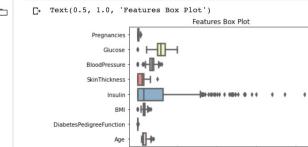
```
[ ] heart_data['bmi'].fillna(heart_data['bmi'].median(),inplace=True)
```

```
[ ] heart_data.isnull().sum()
```

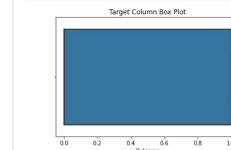
id	0
gender	0
age	0
hypertension	0
heart_disease	0
ever_married	0
work_type	0
Residence_type	0
avg_glucose_level	0
bmi	0
smoking_status	0
stroke	0

+ Code + Text

```
[ ] #First store the features in a separate dataframe.
features = db.drop("Outcome",axis = 1).copy()
#Now plot a boxplot to identify the outliers in our features.
sns.boxplot(data = features, orient = 'h', palette = 'Set3', linewidth = 2.5 )
plt.title('Features Box Plot')
```



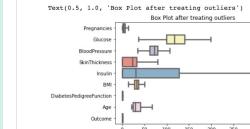
```
[ ] sns.boxplot(x = db["Outcome"], orient = 'h', linewidth = 2.5 )
plt.title('Target Column Box Plot')
plt.show()
```

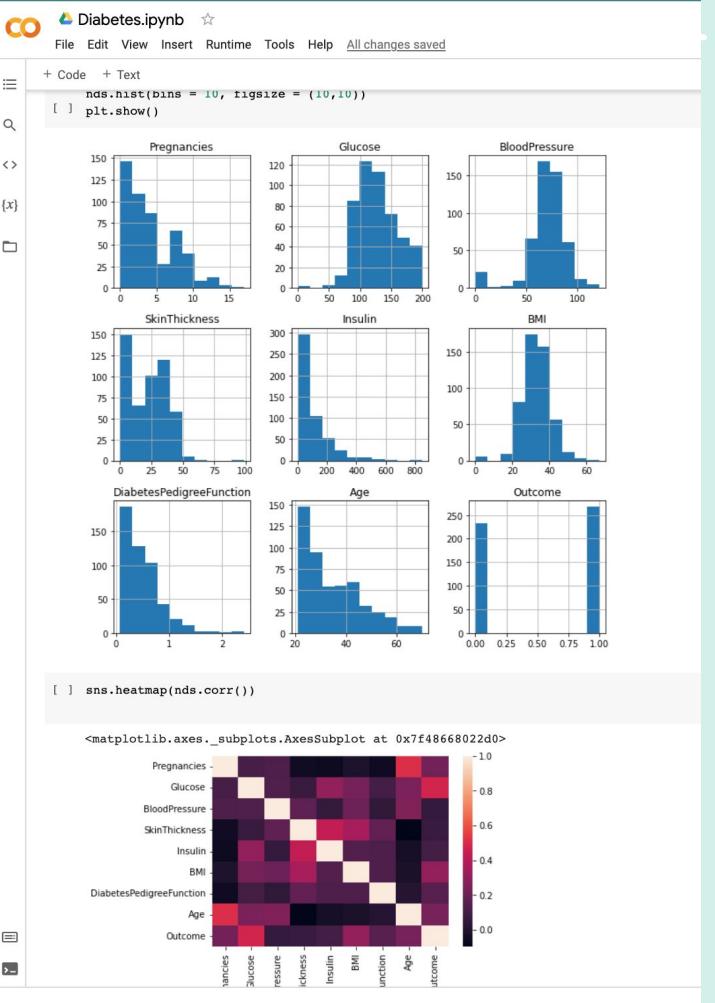


```
[ ] from scipy import stats
[ ] def remove_outliers(dfNone, columns=None):
    for column in columns:
        Q1 = df[column].quantile(0.25)
        Q3 = df[column].quantile(0.75)
        IQR = Q3 - Q1
        lower_bound = Q1 - (1.5 * IQR)
        upper_bound = Q3 + (1.5 * IQR)
        df[column] = df[(df[column]>lower_bound) & (df[column]<upper_bound)]
    print(f"\nThe columns: {column}, has been treated for outliers.\n")
    return df
[ ] df = remove_outliers(db,[col for col in features.columns])
[ ] df
```

The columns: Pregnancies, has been treated for outliers.  
 The columns: Glucose, has been treated for outliers.  
 The columns: BloodPressure, has been treated for outliers.  
 The columns: SkinThickness, has been treated for outliers.  
 The columns: Insulin, has been treated for outliers.  
 The columns: BMI, has been treated for outliers.  
 The columns: DiabetesPedigreeFunction, has been treated for outliers.  
 The columns: Age, has been treated for outliers.

```
[ ] sns.boxplot(data = db, orient = 'h', palette = 'Set3', linewidth = 2.5 )
plt.title('Box Plot after treating outliers')
```







# MAJOR MODULES



## DISEASE PORTAL

Select The Chronic Disease to be tested

## INPUT PARAMETERS

Collect Data from User as required by trained model's dataset

## ANALYSIS AND OUTPUT

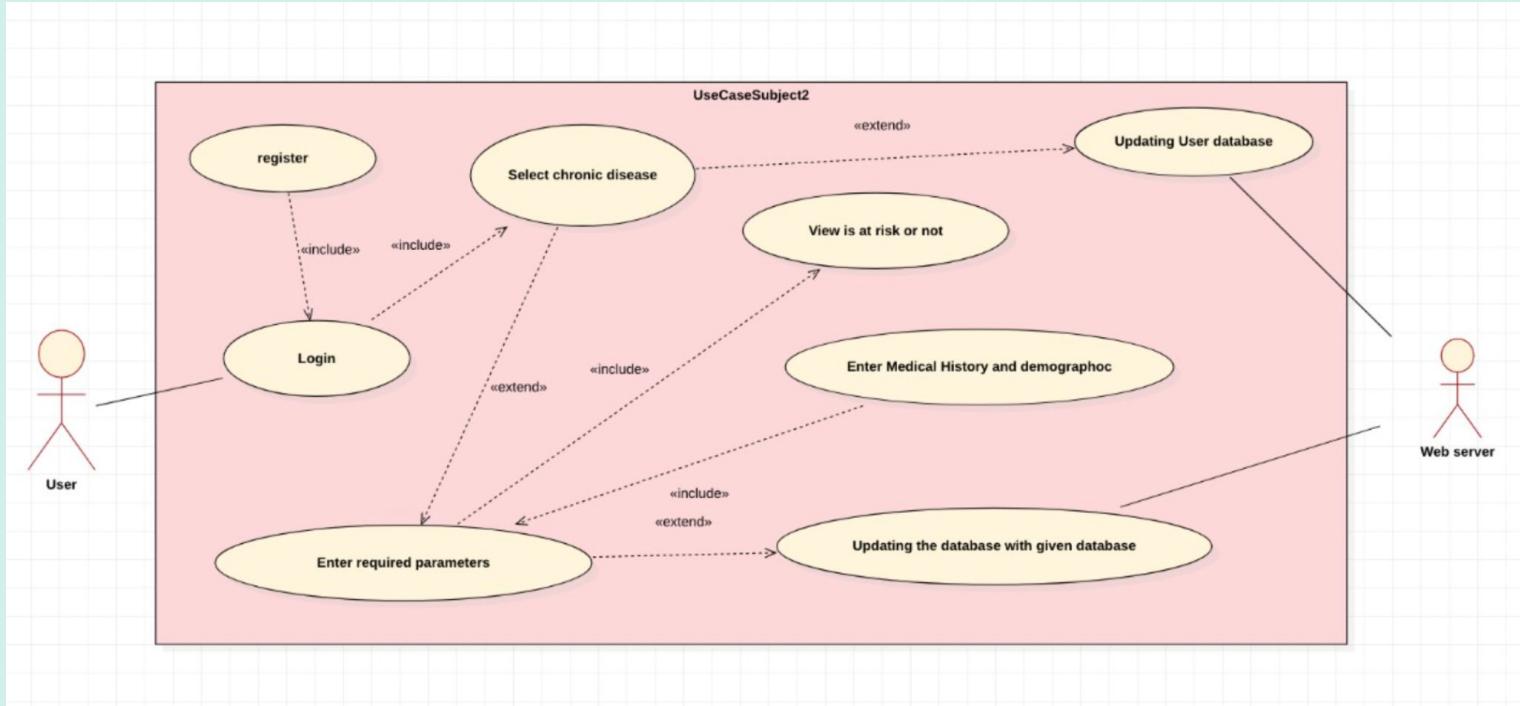
Display the Outcome of the analysis made to the user



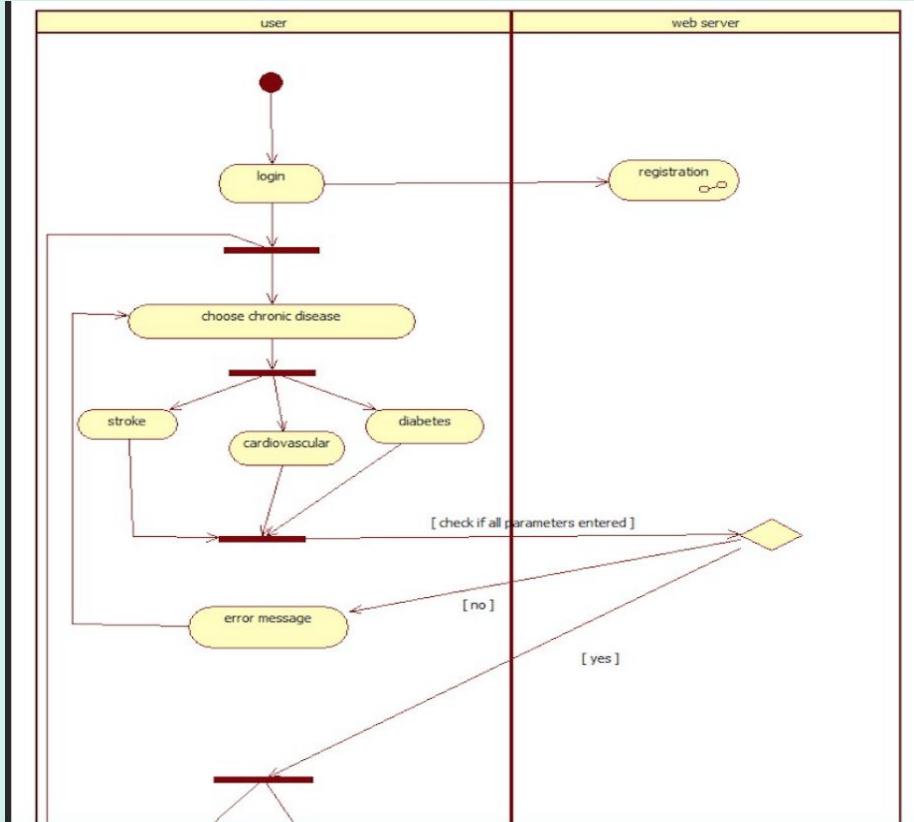
# DESIGN



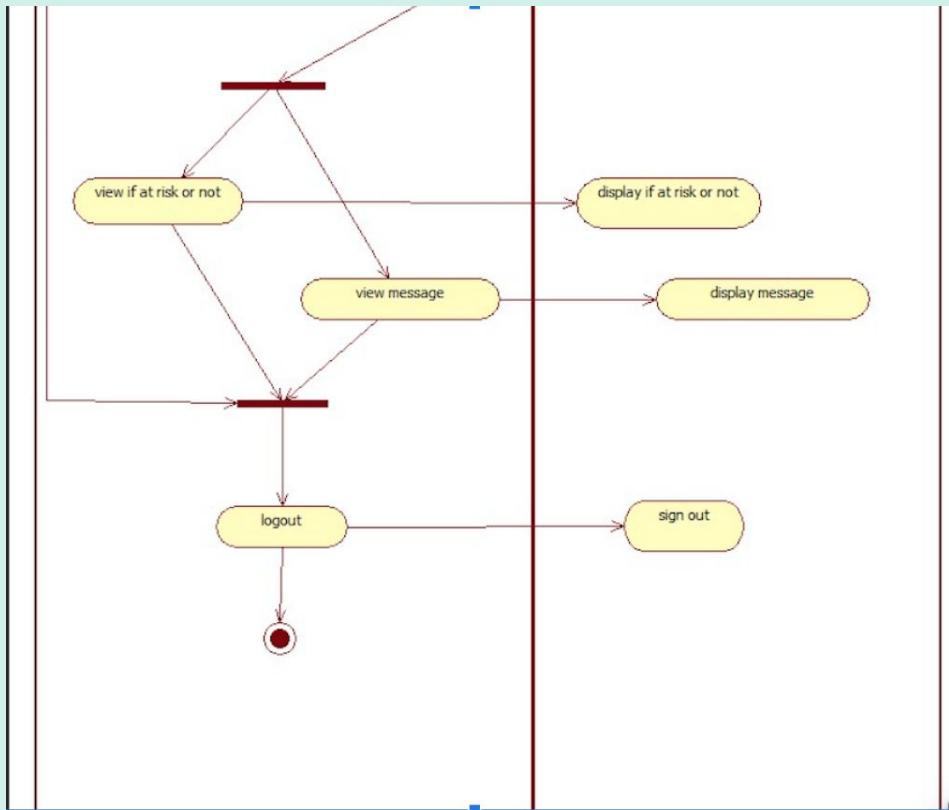
# USECASE DIAGRAM



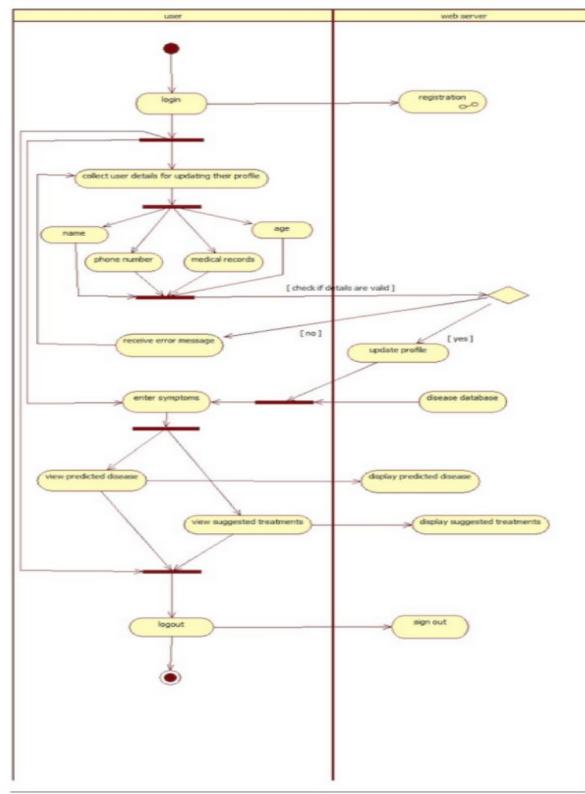
# ACTIVITY DIAGRAM



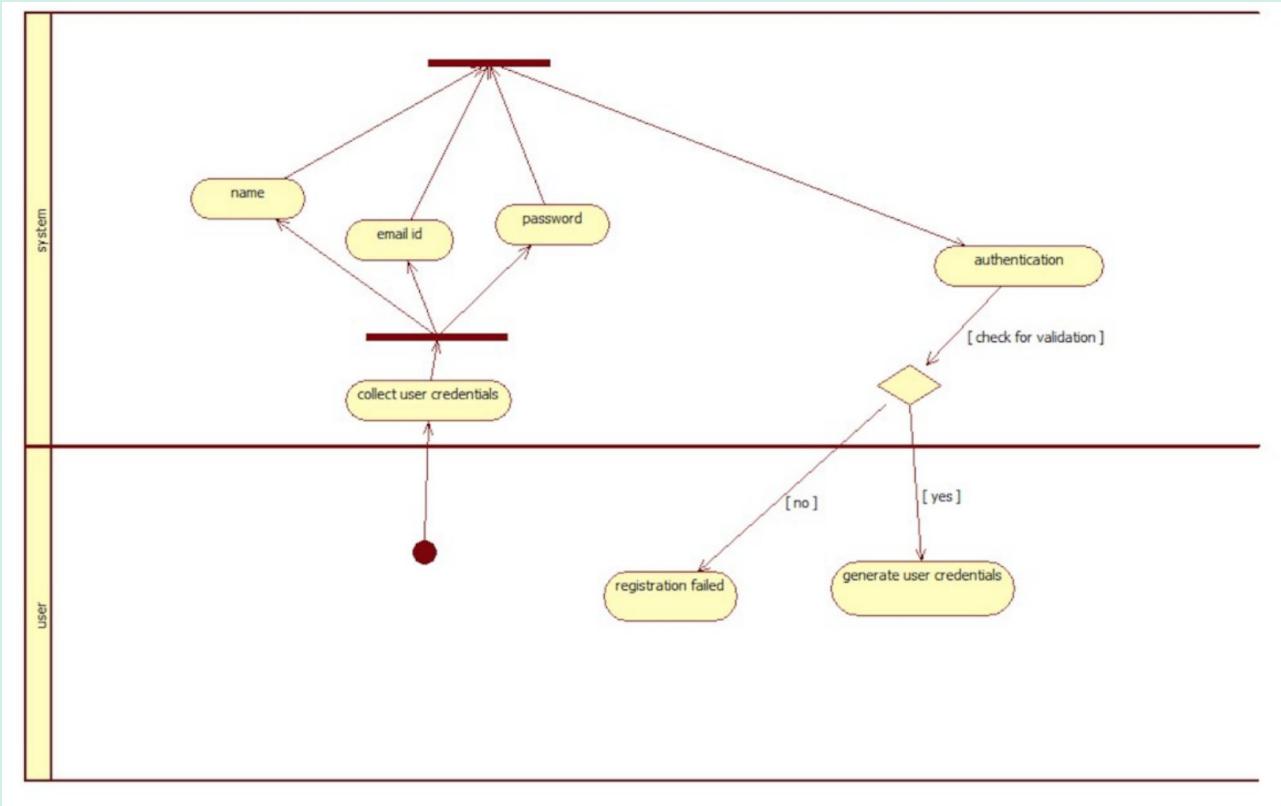
# ACTIVITY DIAGRAM



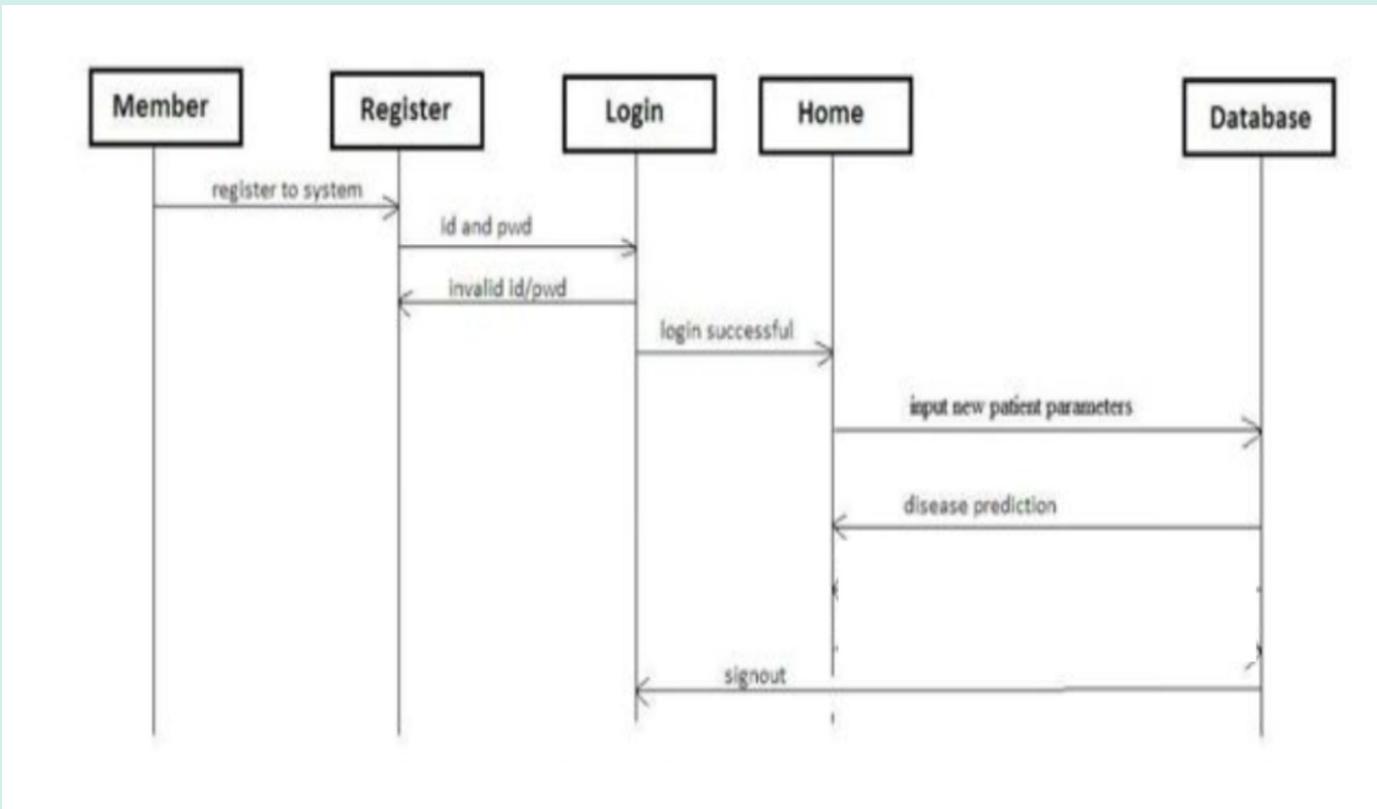
# ACTIVITY DIAGRAM



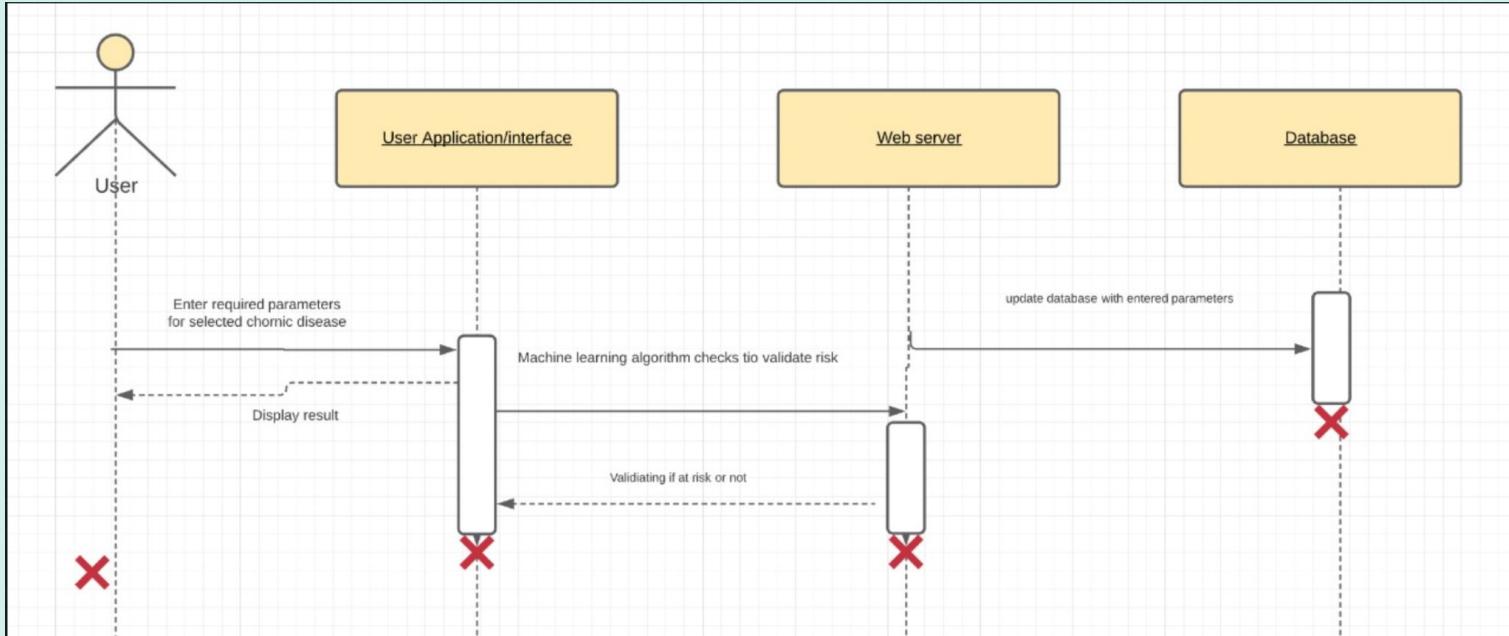
# ACTIVITY DIAGRAM



# SEQUENCE DIAGRAM

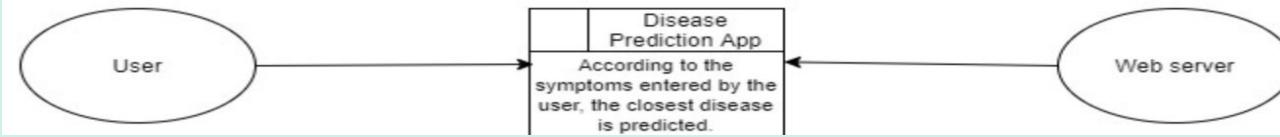


# SEQUENCE DIAGRAM

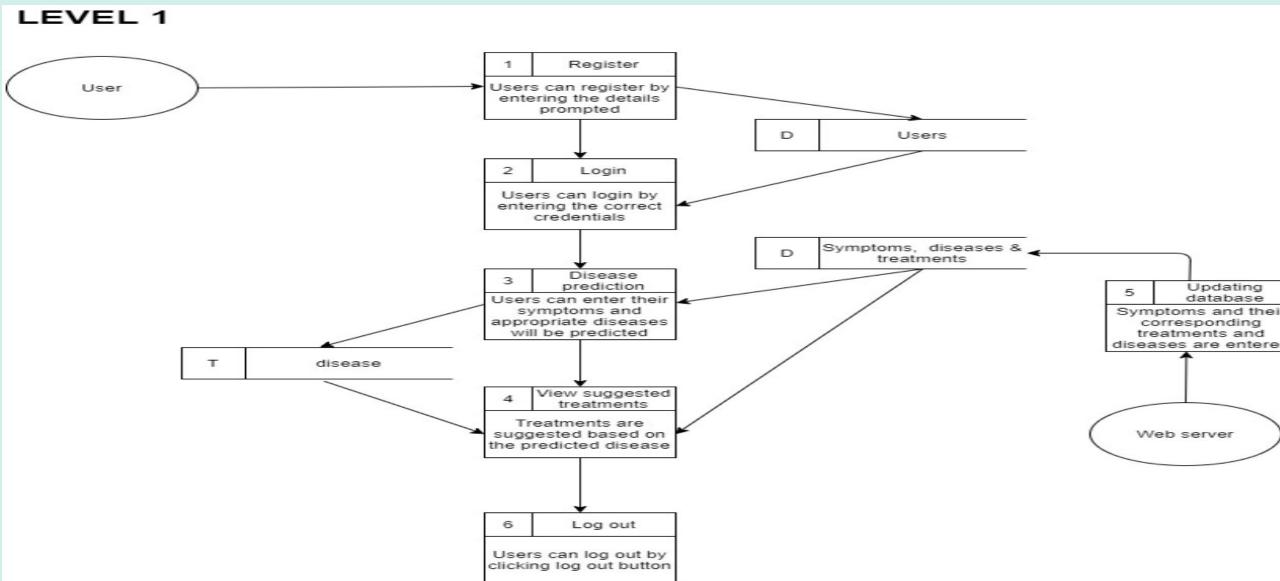


# DFD DIAGRAM

## LEVEL 0

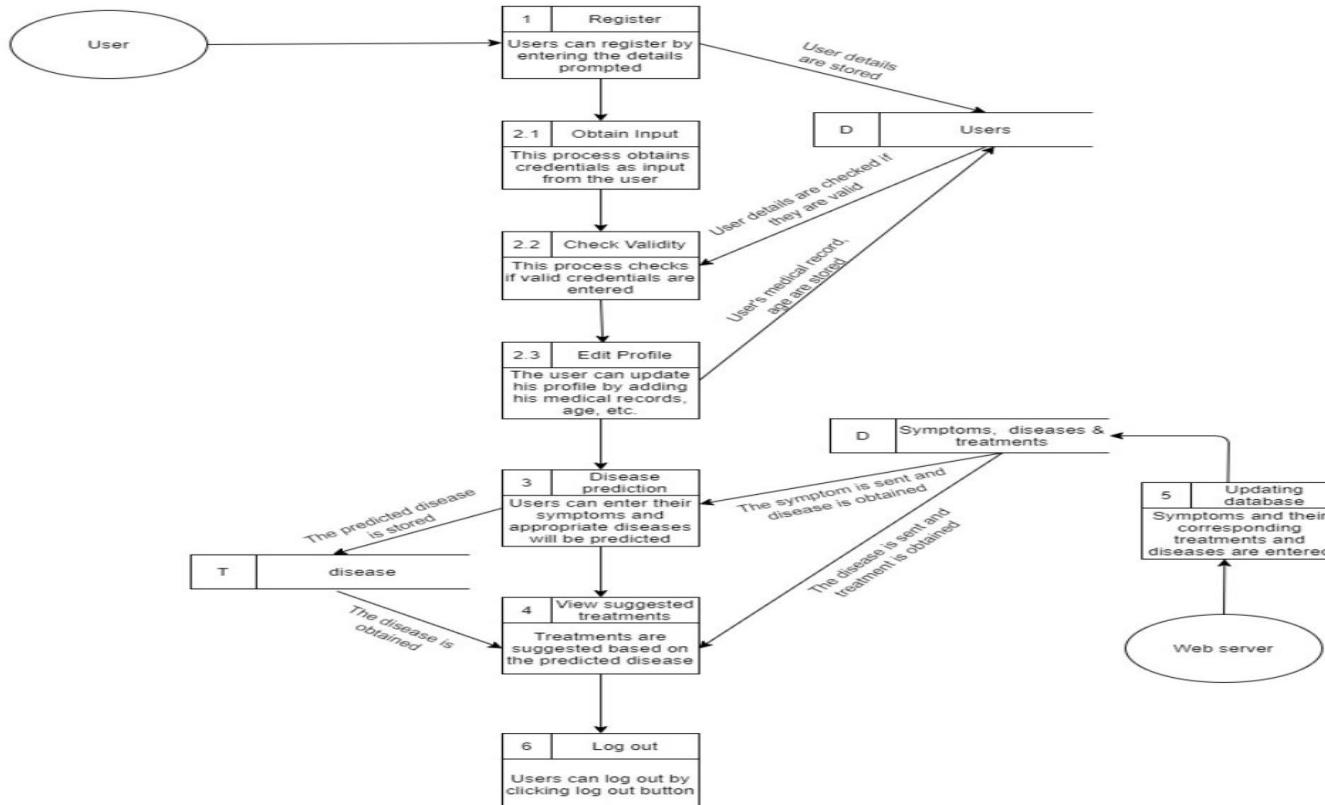


## LEVEL 1



# DFD DIAGRAM

## LEVEL 2





# SYSTEM REQUIREMENT



Software and Hardware Requirements





# SOFTWARE REQUIREMENTS



## FRONTEND

1. HTML
2. CSS



## BACKEND

1. Python



## FRAMEWORK

1. Flask





# SOFTWARE REQUIREMENTS



## IDE

1. Visual Studio Code



## DATABASE

1. MySQL



## ML MODEL

1. Google Collab
2. Jupyter





# HARDWARE REQUIREMENTS



OS-WINDOWS



HARDDISK-40GB



RAM-256 MB



PROCESSOR-PENTIUM ®  
DUAL CORE CPU



# CONTRIBUTIONS



WEB APPLICATION

FRONTEND AND BACKEND

19Z227 - *Monirhithikka S.P*

19Z240 - *Samyuktha Sreekanth*

19Z243 - *Sarayu Miththira V.C*



ML MODEL AND TRAINING

CODE AND DATASETS

19Z202 -*Anita Priyadarshini*



ML MODEL AND DOCUMENTATION

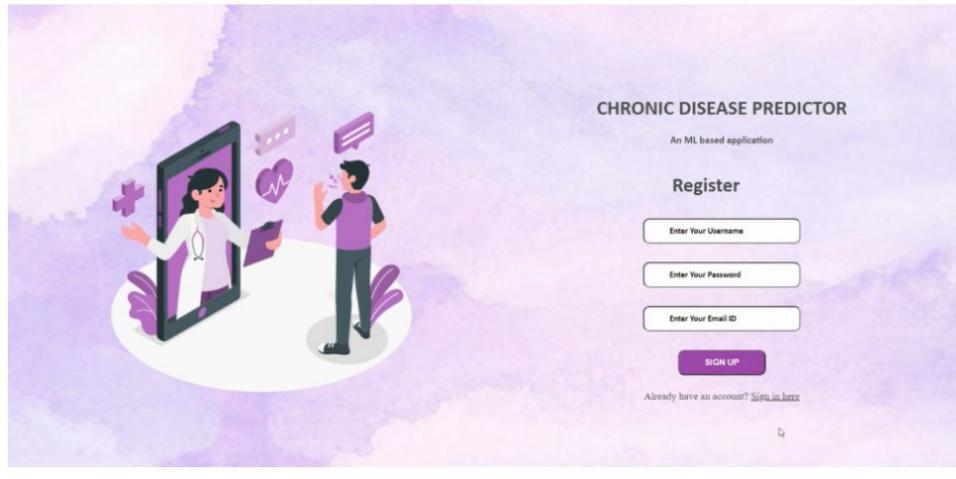
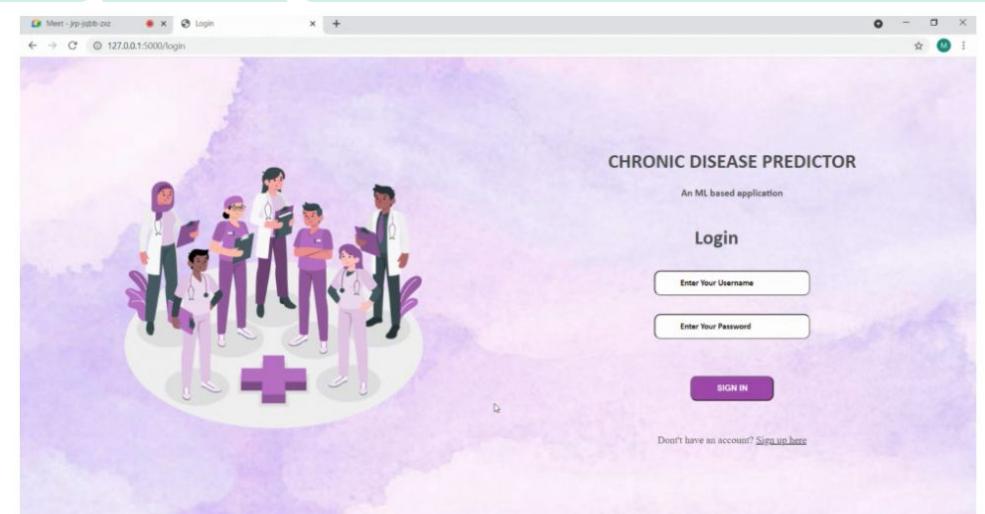
SYSTEM ARCHITECTURE AND  
ML ALGORITHM

19z211-*Divya Darshini R*

19z217- *Hemavarshini B*

# INTERFACE AND DEMO







The image shows two adjacent browser windows on a desktop screen. The top window displays a 'MENU' page with a purple gradient background. It includes a greeting 'Hello mithra', a question 'What would you like to check out?', and three buttons: 'STROKE RISK', 'GENERAL CARDIOVASCULAR DISEASE', and 'DIABETES RISK'. A 'Logout' button is at the bottom. The bottom window displays a 'Details required' form with a purple gradient background. It contains fields for 'Gender' (female), 'Age' (45), 'Experienced hypertension?' (no), 'Any prior heart disease?' (no), 'Ever married?' (yes), and 'Work type'. A dropdown menu for 'Work type' is open, showing options: 'select an option', 'private job', 'children', 'government job', 'never worked', 'partner', and 'self employment'. The status bar at the bottom of the screen shows the time as 01:09.

MENU

Hello mithra  
What would you like to check out?

STROKE RISK

GENERAL CARDIOVASCULAR DISEASE

DIABETES RISK

Logout

Details required

Gender: female

Age: 45

Experienced hypertension?: no

Any prior heart disease?: no

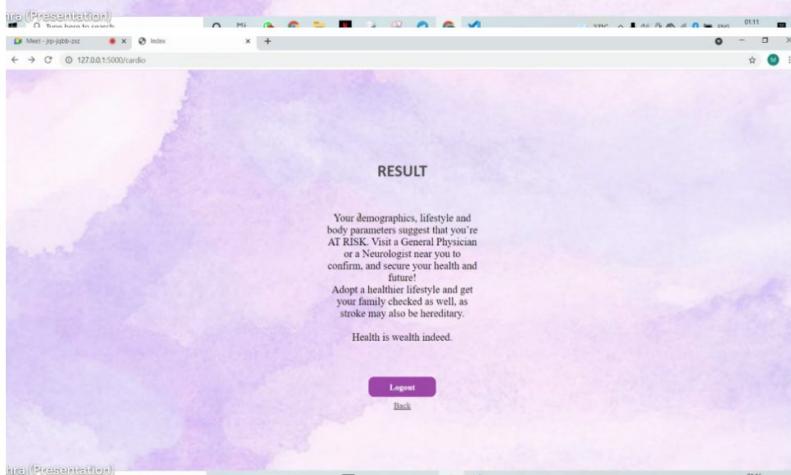
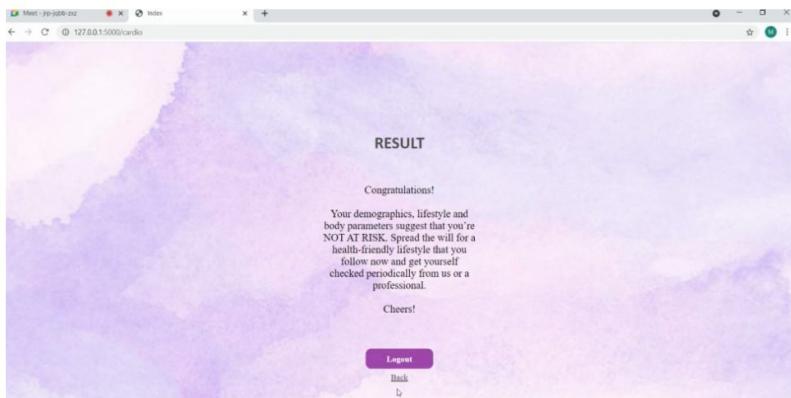
Ever married?: yes

Work type:

- select an option
- private job
- children
- government job
- never worked
- partner
- self employment

Residence type:





**Details required**

Age:  enter value

Gender:  -- Select an option --

Height(cm):  enter value

Weight(kg):  enter value

Systolic blood pressure:  enter value

Diastolic blood pressure:  enter value

Cholesterol level:  -- Select an option --

Glucose level:  -- Select an option --

Smoking:  -- Select an option --

**Details required**

Number of pregnancies:  enter value

Glucose level:  enter value

Blood Pressure:  enter value

Skin Thickness:  enter value

Insulin:  enter value

Enter BMI:  enter value

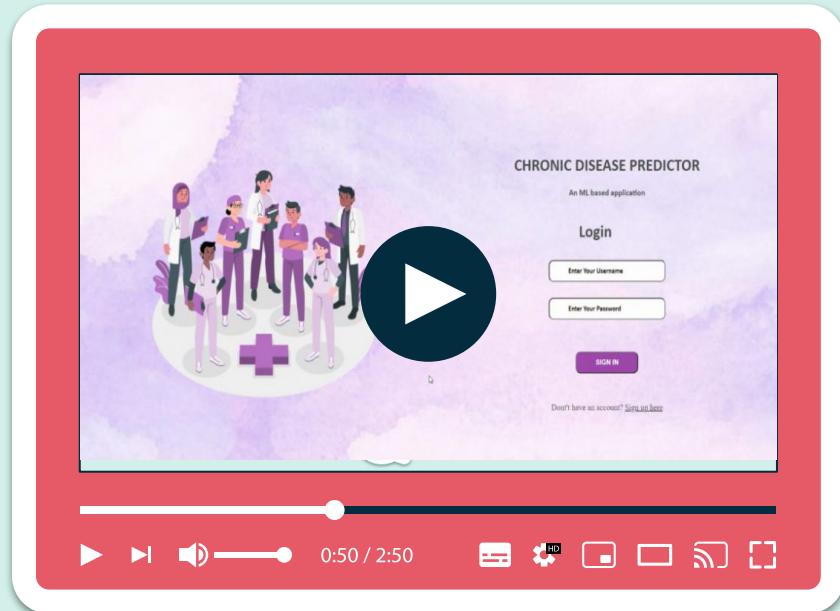
Diabetes pedigree function\*:  enter value

Enter age:  enter value

**SUBMIT**

\*if unsure, enter 1 if there is family history of diabetes else enter 0

# DEMO



# THANK YOU!

We Hope To develop This Project further by adding more Chronic Diseases and training More accurate Analysis Models. We would also like deploy it and have it serve as a stand-alone application so that it can be accessed by all and Detect Chronic diseases in a Timely manner with the power of Data and Efficient Computation

