AIML MINI PROJECT

GROUP MEMBERS:
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BATCH: A
CLASS; TE IT
COURSE: AIML LAB

AIM: To detect various diseases in a person using various machine learning models.

GITHUB LINK: https://github.com/smrithi1912/AIML

PROBLEM STATEMENT:

In today's time we see a lot of the shortage of doctors in the world especially in India. A lot of people are suffering without a proper medical checkup. Also, most of the cases that arise lead to death due to lack of timely medical attention. So, to cope up with all of those problems, we have designed this web application that predicts if a person suffers from a particular disease or not using Machine Learning

APPLICATIONS:

- To remove the dependencies on the doctors
- To help out the poor and helpless people with the normal medical checkup
- To help people avoid paying huge amount to the doctors unnecessarily
- To extend the role of the technology in the medical field

ALGORITHMS USED:

1. Logistic Regression

   Logistic regression is a statistical model that in its basic form uses a logistic function to model a binary dependent variable, although many more complex extensions exist. In regression analysis, logistic regression[1] (or logit regression) is estimating the parameters of a logistic model (a form of binary regression). Mathematically, a binary logistic model has a dependent variable with two possible values, such as pass/fail which is represented by an indicator variable, where the two values are labeled "0" and "1".
   Model :
   Output = 0 or 1
   Hypothesis => Z = WX + B

hΘ(x) = sigmoid (

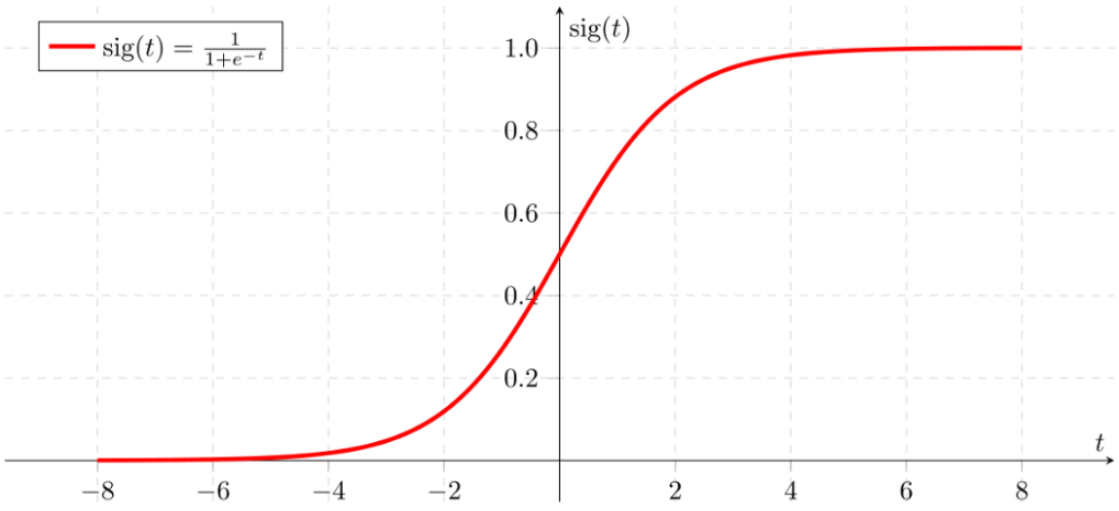
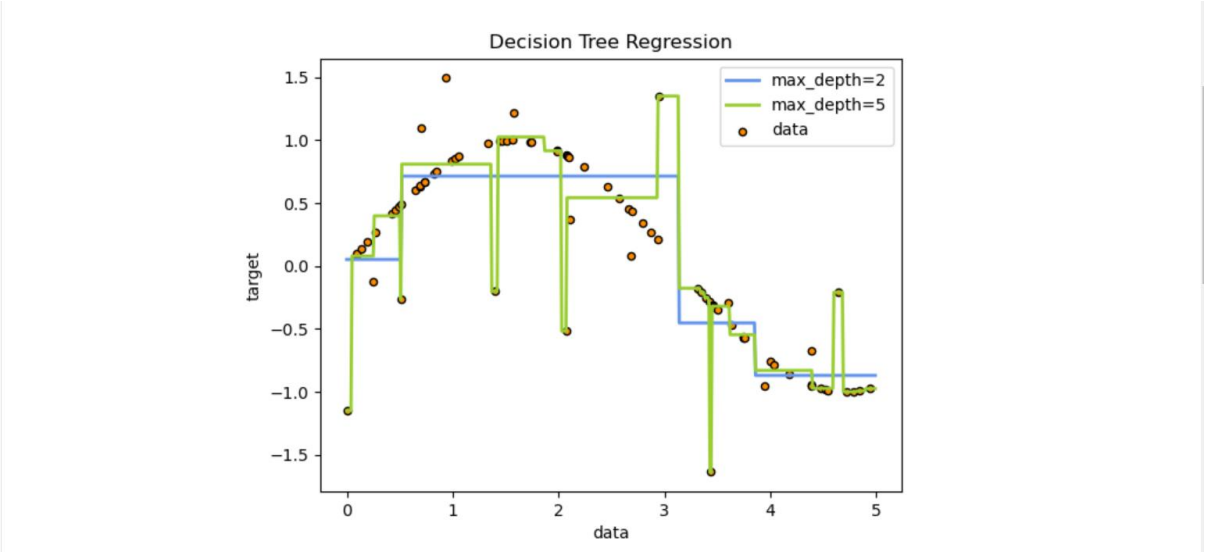


Figure 2: Sigmoid Activation Function

Analysis of the hypothesis: The output from the hypothesis is the estimated probability. This is used to infer how confident can predicted value be actual value when given an input X. Consider the below example,

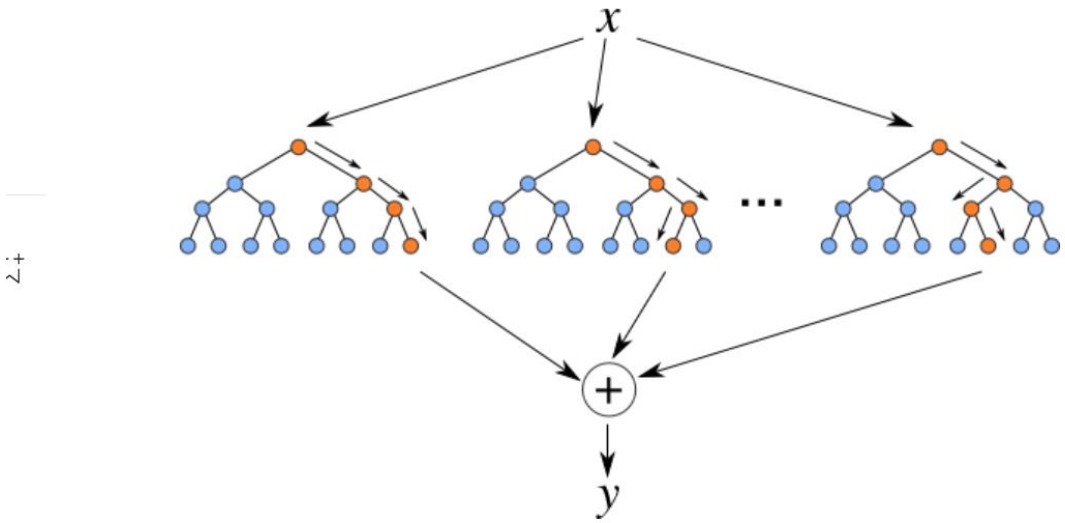
2. Decision Tree Regressor

Decision trees build regression or classification models in the form of a tree structure. It breaks down a dataset into smaller and smaller subsets while at the same time an associated decision tree is incrementally developed. The final result is a tree with decision nodes and leaf nodes. A decision tree is built top-down from a root node and involves partitioning the data into subsets that contain instances with similar values (homogenous). We use standard deviation to calculate the homogeneity of a numerical sample. If the numerical sample is completely homogeneous its standard deviation is zero.



3. **Random Forest Regression**

Random Forest Regression is a supervised learning algorithm that uses ensemble learning method for regression. Ensemble learning method is a technique that combines predictions from multiple machine learning algorithms to make a more accurate prediction than a single model.



A Random Forest operates by constructing several decision trees during training time and outputting the mean of the classes as the prediction of all the trees. To get a better understanding of the Random Forest algorithm, let's walk through the steps:

a. Pick at random k data points from the training set.
b. Build a decision tree associated with these k data points.
c. Choose the number N of trees you want to build and repeat steps 1 and 2.
d. For a new data point, make each one of your N-tree trees predict the value of y for the data point in question and assign the new data point to the average across all of the predicted y values.

MODEL FILES USED:

Cancer Model = model
Diabetes Model = model1
Heart Model = model2

DATASETS USED:

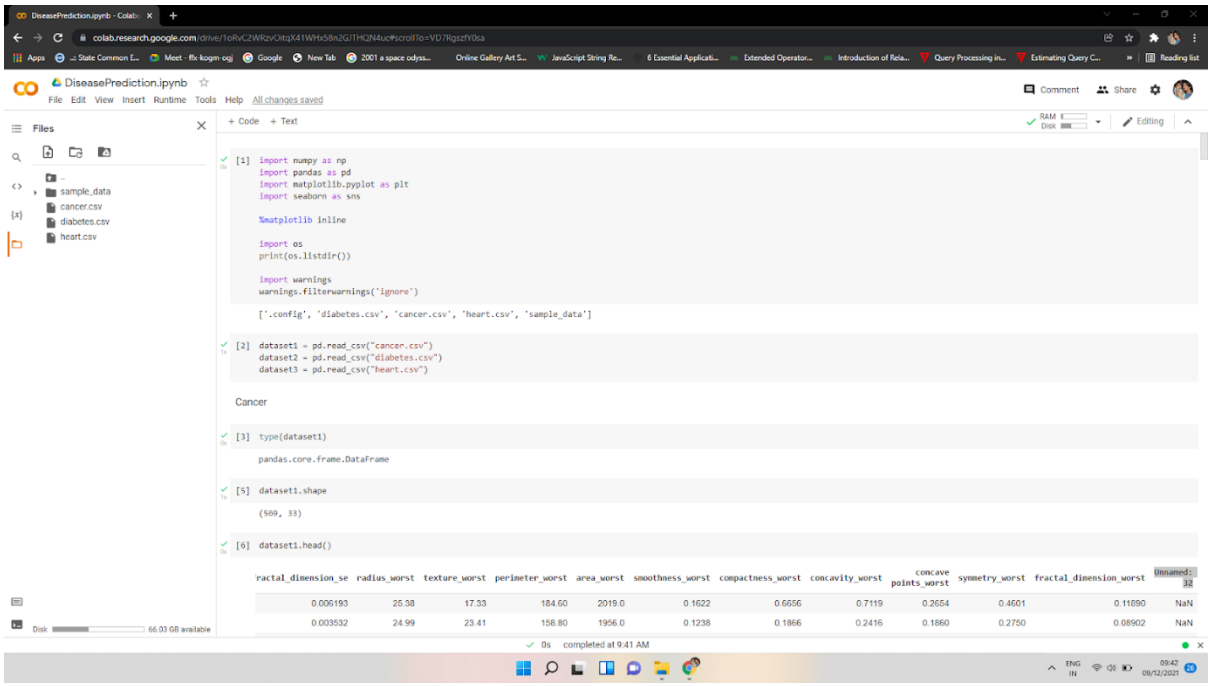
Drive Link
Cancer = cancer.csv
Diabetes = diabetes.csv
Heart = heart.csv

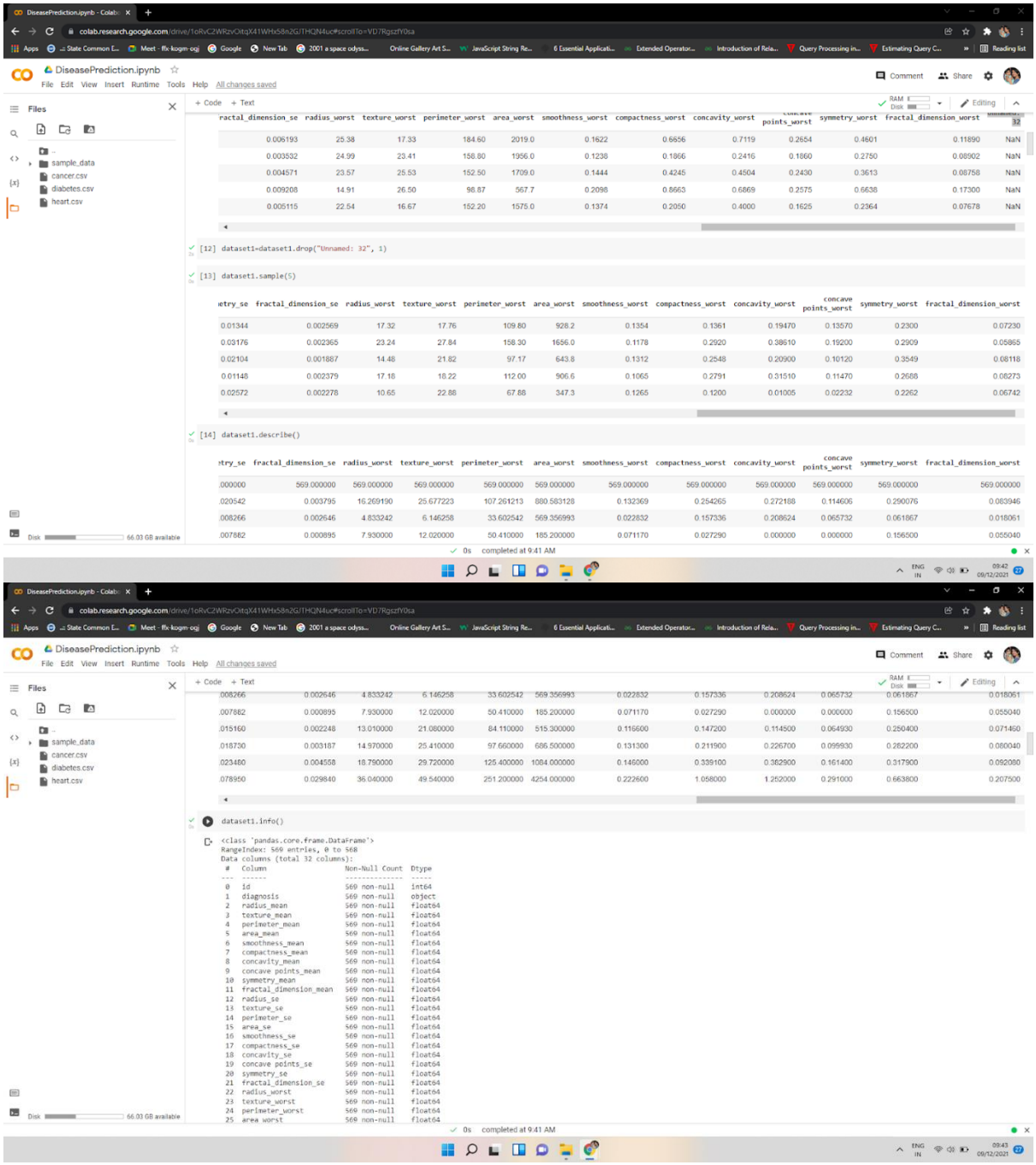
TOOLS NEEDED:

Python
Flask
TensorFlow
pillow

scikit
pandas
numpy
HTML
CSS

Colab File:

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fractal_dimension_se radius_worst texture_worst perimeter_worst area_worst smoothness_worst compactness_worst concavity_worst concave points_worst symmetry_worst fractal_dimension_worst
0.005193 25.38 17.33 184.60 2019.0 0.1622 0.6656 0.7119 0.2654 0.4601 0.11890 NaN
0.003532 24.99 23.41 158.80 1956.0 0.1238 0.1866 0.2416 0.1860 0.2750 0.08902 NaN
0.004571 23.57 25.53 152.50 1709.0 0.1444 0.4245 0.4504 0.2430 0.3613 0.08758 NaN
0.009208 14.91 26.50 98.87 567.7 0.2098 0.8663 0.6869 0.2575 0.6638 0.17300 NaN
0.005115 22.54 16.67 152.20 1575.0 0.1374 0.2050 0.4000 0.1625 0.2364 0.07678 NaN
[12] dataset1=dataset1.drop("Unnamed: 32", 1)
[13] dataset1.sample(5)
[14] dataset1.describe()
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dataset1.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 32 columns):
Column Non-Null Count Dtype
0 id 569 non-null int64
1 diagnosis 569 non-null object
2 radius_mean 569 non-null float64
3 texture_mean 569 non-null float64
4 perimeter_mean 569 non-null float64
5 area_mean 569 non-null float64
6 smoothness_mean 569 non-null float64
7 compactness_mean 569 non-null float64
8 concavity_mean 569 non-null float64
9 concave points_mean 569 non-null float64
10 symmetry_mean 569 non-null float64
11 fractal_dimension_mean 569 non-null float64
12 radius_se 569 non-null float64
13 texture_se 569 non-null float64
14 perimeter_se 569 non-null float64
15 area_se 569 non-null float64
16 smoothness_se 569 non-null float64
17 compactness_se 569 non-null float64
18 concavity_se 569 non-null float64
19 concave points_se 569 non-null float64
20 symmetry_se 569 non-null float64
21 fractal_dimension_se 569 non-null float64
22 radius_worst 569 non-null float64
23 texture_worst 569 non-null float64
24 perimeter_worst 569 non-null float64
25 area_worst 569 non-null float64
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DiseasePrediction.ipynb

```
dataset1.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 32 columns):
 #   Column                   Non-Null Count  Dtype
---  ------                   --------------  -----
 0   id                       569 non-null    int64
 1   diagnosis                569 non-null    object
 2   radius_mean              569 non-null    float64
 3   texture_mean             569 non-null    float64
 4   perimeter_mean           569 non-null    float64
 5   area_mean                569 non-null    float64
 6   smoothness_mean          569 non-null    float64
 7   compactness_mean         569 non-null    float64
 8   concavity_mean           569 non-null    float64
 9   concave points_mean      569 non-null    float64
 10  symmetry_mean            569 non-null    float64
 11  fractal_dimension_mean   569 non-null    float64
 12  radius_se                569 non-null    float64
 13  texture_se               569 non-null    float64
 14  perimeter_se             569 non-null    float64
 15  area_se                  569 non-null    float64
 16  smoothness_se            569 non-null    float64
 17  compactness_se           569 non-null    float64
 18  concavity_se             569 non-null    float64
 19  concave points_se        569 non-null    float64
 20  symmetry_se              569 non-null    float64
 21  fractal_dimension_se     569 non-null    float64
 22  radius_worst             569 non-null    float64
 23  texture_worst            569 non-null    float64
 24  perimeter_worst          569 non-null    float64
 25  area_worst               569 non-null    float64
 26  smoothness_worst         569 non-null    float64
 27  compactness_worst        569 non-null    float64
 28  concavity_worst          569 non-null    float64
 29  concave points_worst     569 non-null    float64
 30  symmetry_worst           569 non-null    float64
 31  fractal_dimension_worst  569 non-null    float64
dtypes: float64(30), int64(1), object(1)
memory usage: 142.4+ KB
```

```
[16] dataset1["diagnosis"].describe()
```

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DiseasePrediction.ipynb

```
[16] dataset1["diagnosis"].describe()
```

```
count     569
unique      2
top         B
freq      357
Name: diagnosis, dtype: object
```

```
[17] # M - Malignant, B - Benign
     dataset1["diagnosis"].unique()
```

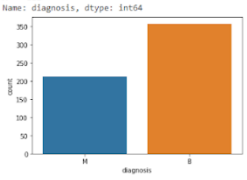
```
array(['M', 'B'], dtype=object)
```

Exploratory Data Analysis

```
[19] y = dataset1["diagnosis"]
     sns.countplot(y)

     diag_temp = dataset1.diagnosis.value_counts()
     print(diag_temp)
```

```
B    357
M    212
Name: diagnosis, dtype: int64
```




```
[21] print("Percentage of people having M form of cancer: " + str(round(diag_temp[1]*100/569, 2)))
```

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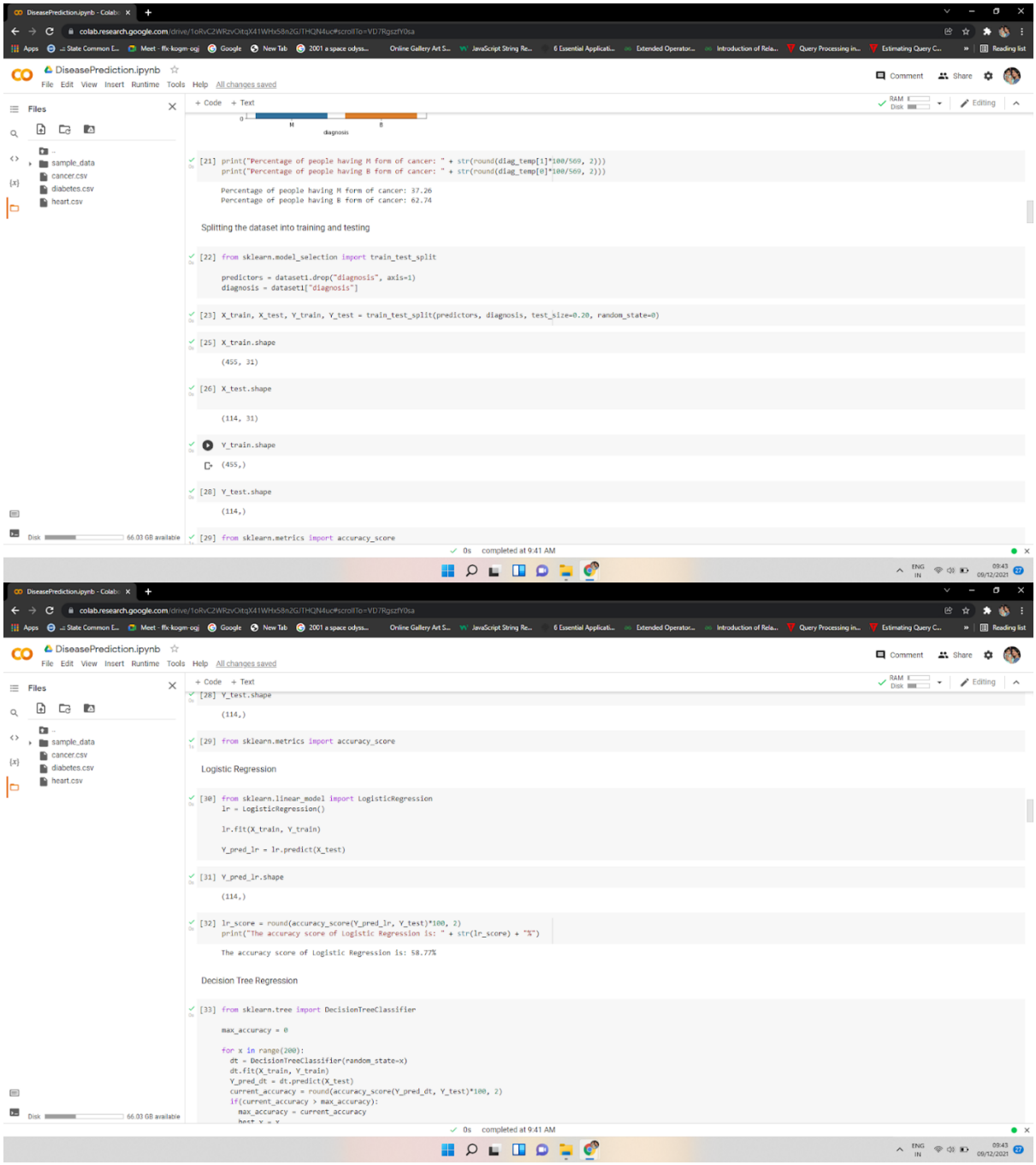
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cancer.csv
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diagnosis
[21] print("Percentage of people having M form of cancer: " + str(round(diag_temp[1]*100/569, 2)))
print("Percentage of people having B form of cancer: " + str(round(diag_temp[0]*100/569, 2)))
Percentage of people having M form of cancer: 37.26
Percentage of people having B form of cancer: 62.74
Splitting the dataset into training and testing
[22] from sklearn.model_selection import train_test_split
predictors = dataset1.drop("diagnosis", axis=1)
diagnosis = dataset1["diagnosis"]
[23] X_train, X_test, Y_train, Y_test = train_test_split(predictors, diagnosis, test_size=0.20, random_state=0)
[25] X_train.shape
(455, 31)
[26] X_test.shape
(114, 31)
Y_train.shape
(455,)
[28] Y_test.shape
(114,)
[29] from sklearn.metrics import accuracy_score
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sample_data
cancer.csv
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[28] Y_test.shape
(114,)
[29] from sklearn.metrics import accuracy_score
Logistic Regression
[30] from sklearn.linear_model import LogisticRegression
lr = LogisticRegression()
lr.fit(X_train, Y_train)
Y_pred_lr = lr.predict(X_test)
[31] Y_pred_lr.shape
(114,)
[32] lr_score = round(accuracy_score(Y_pred_lr, Y_test)*100, 2)
print("The accuracy score of Logistic Regression is: " + str(lr_score) + "%")
The accuracy score of Logistic Regression is: 58.77%
Decision Tree Regression
[33] from sklearn.tree import DecisionTreeClassifier
max_accuracy = 0
for x in range(200):
dt = DecisionTreeClassifier(random_state=x)
dt.fit(X_train, Y_train)
Y_pred_dt = dt.predict(X_test)
current_accuracy = round(accuracy_score(Y_pred_dt, Y_test)*100, 2)
if(current_accuracy > max_accuracy):
max_accuracy = current_accuracy
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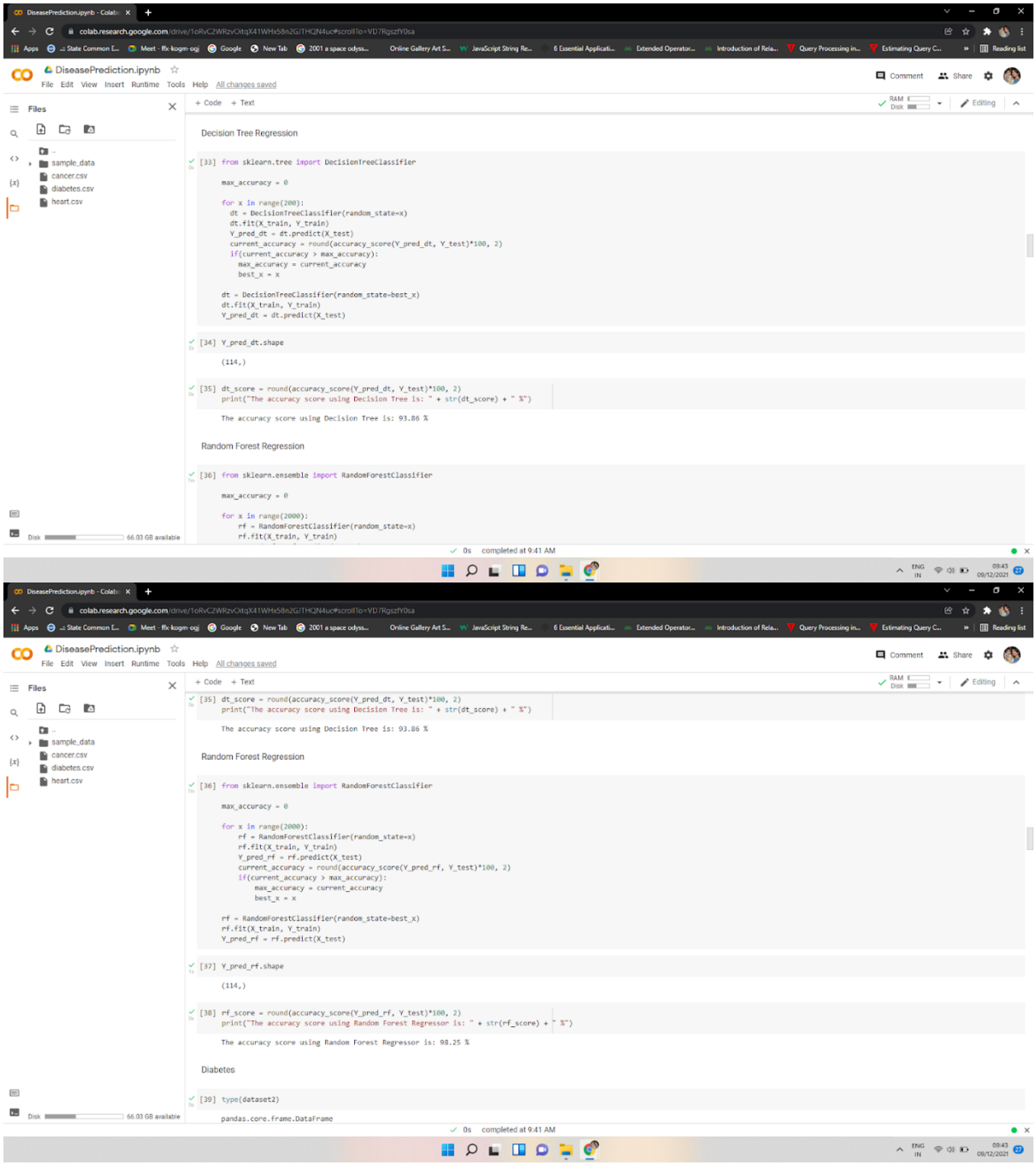
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sample_data
cancer.csv
diabetes.csv
heart.csv
Decision Tree Regression
[33] from sklearn.tree import DecisionTreeClassifier
max_accuracy = 0
for x in range(200):
dt = DecisionTreeClassifier(random_state=x)
dt.fit(X_train, Y_train)
Y_pred_dt = dt.predict(X_test)
current_accuracy = round(accuracy_score(Y_pred_dt, Y_test)*100, 2)
if(current_accuracy > max_accuracy):
max_accuracy = current_accuracy
best_x = x
dt = DecisionTreeClassifier(random_state=best_x)
dt.fit(X_train, Y_train)
Y_pred_dt = dt.predict(X_test)
[34] Y_pred_dt.shape
(114,)
[35] dt_score = round(accuracy_score(Y_pred_dt, Y_test)*100, 2)
print("The accuracy score using Decision Tree is: " + str(dt_score) + " %")
The accuracy score using Decision Tree is: 93.86 %
Random Forest Regression
[36] from sklearn.ensemble import RandomForestClassifier
max_accuracy = 0
for x in range(2000):
rf = RandomForestClassifier(random_state=x)
rf.fit(X_train, Y_train)
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sample_data
cancer.csv
diabetes.csv
heart.csv
[35] dt_score = round(accuracy_score(Y_pred_dt, Y_test)*100, 2)
print("The accuracy score using Decision Tree is: " + str(dt_score) + " %")
The accuracy score using Decision Tree is: 93.86 %
Random Forest Regression
[36] from sklearn.ensemble import RandomForestClassifier
max_accuracy = 0
for x in range(2000):
rf = RandomForestClassifier(random_state=x)
rf.fit(X_train, Y_train)
Y_pred_rf = rf.predict(X_test)
current_accuracy = round(accuracy_score(Y_pred_rf, Y_test)*100, 2)
if(current_accuracy > max_accuracy):
max_accuracy = current_accuracy
best_x = x
rf = RandomForestClassifier(random_state=best_x)
rf.fit(X_train, Y_train)
Y_pred_rf = rf.predict(X_test)
[37] Y_pred_rf.shape
(114,)
[38] rf_score = round(accuracy_score(Y_pred_rf, Y_test)*100, 2)
print("The accuracy score using Random Forest Regressor is: " + str(rf_score) + " %")
The accuracy score using Random Forest Regressor is: 98.25 %
Diabetes
[39] type(dataset2)
pandas.core.frame.DataFrame
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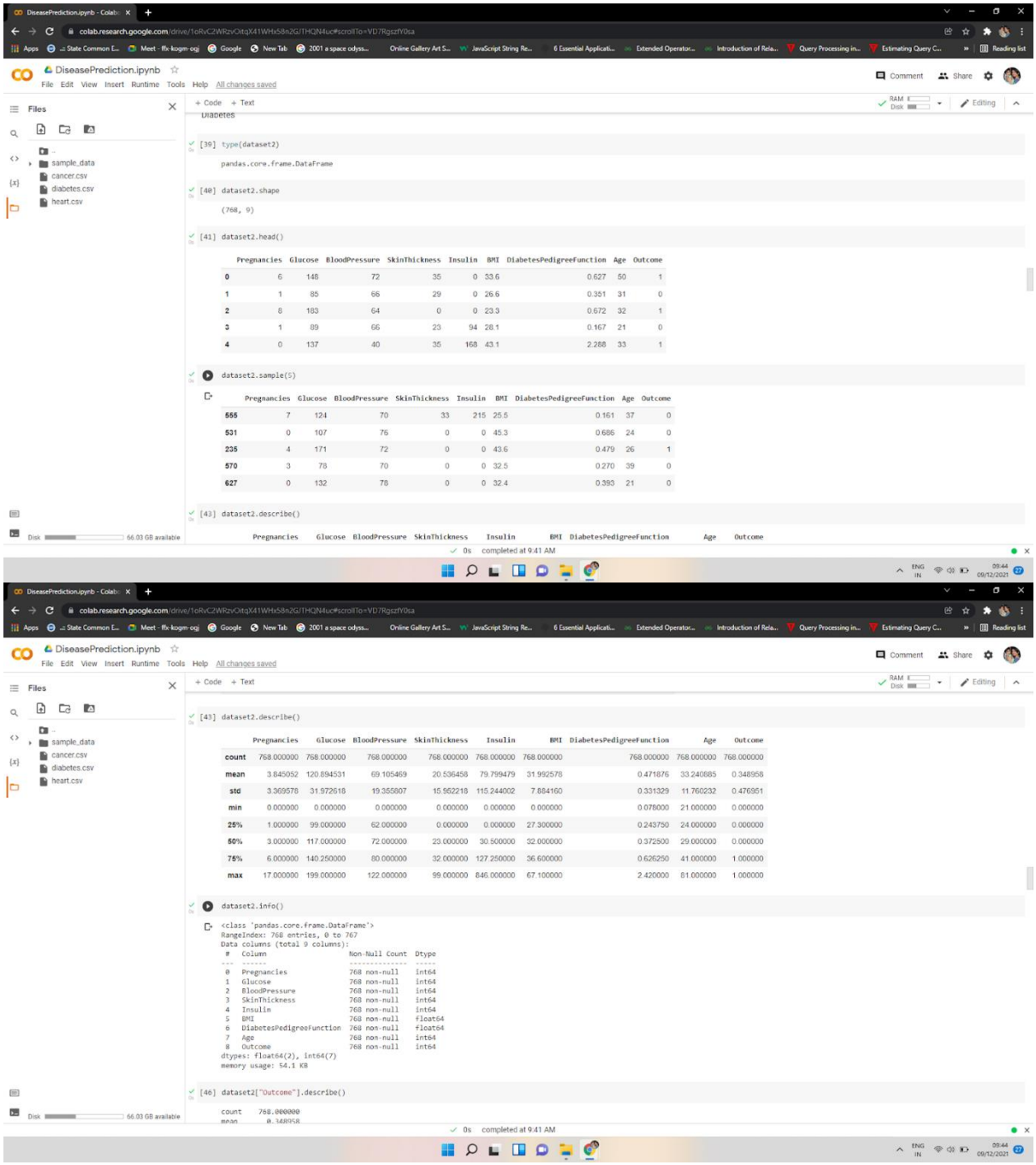
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Diabetes
[39] type(dataset2)
pandas.core.frame.DataFrame
[40] dataset2.shape
(768, 9)
[41] dataset2.head()
Pregnancies Glucose BloodPressure SkinThickness Insulin BMI DiabetesPedigreeFunction Age Outcome
0 6 148 72 35 0 33.6 0.627 50 1
1 1 85 66 29 0 26.6 0.351 31 0
2 8 183 64 0 0 23.3 0.672 32 1
3 1 89 66 23 94 28.1 0.167 21 0
4 0 137 40 35 168 43.1 2.288 33 1
dataset2.sample(5)
Pregnancies Glucose BloodPressure SkinThickness Insulin BMI DiabetesPedigreeFunction Age Outcome
555 7 124 70 33 215 25.5 0.161 37 0
531 0 107 76 0 0 45.3 0.686 24 0
235 4 171 72 0 0 43.6 0.479 26 1
570 3 78 70 0 0 32.5 0.270 39 0
627 0 132 78 0 0 32.4 0.393 21 0
[43] dataset2.describe()
Pregnancies Glucose BloodPressure SkinThickness Insulin BMI DiabetesPedigreeFunction Age Outcome
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[43] dataset2.describe()
Pregnancies Glucose BloodPressure SkinThickness Insulin BMI DiabetesPedigreeFunction Age Outcome
count 768.000000 768.000000 768.000000 768.000000 768.000000 768.000000 768.000000 768.000000 768.000000
mean 3.845052 120.894531 69.105469 20.536458 79.799479 31.992578 0.471876 33.240885 0.348958
std 3.369578 31.972618 19.355807 15.952218 115.244002 7.884160 0.331329 11.760232 0.476951
min 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.078000 21.000000 0.000000
25% 1.000000 99.000000 62.000000 0.000000 0.000000 27.300000 0.243750 24.000000 0.000000
50% 3.000000 117.000000 72.000000 23.000000 30.500000 32.000000 0.372500 29.000000 0.000000
75% 6.000000 140.250000 80.000000 32.000000 127.250000 36.600000 0.626250 41.000000 1.000000
max 17.000000 199.000000 122.000000 99.000000 846.000000 67.100000 2.420000 81.000000 1.000000
dataset2.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
Column Non-Null Count Dtype
0 Pregnancies 768 non-null int64
1 Glucose 768 non-null int64
2 BloodPressure 768 non-null int64
3 SkinThickness 768 non-null int64
4 Insulin 768 non-null int64
5 BMI 768 non-null float64
6 DiabetesPedigreeFunction 768 non-null float64
7 Age 768 non-null int64
8 Outcome 768 non-null int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
[46] dataset2["Outcome"].describe()
count 768.000000
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heart.csv

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```
[46] dataset2["Outcome"].describe()
```

```
count    768.000000
mean       0.348958
std        0.476951
min        0.000000
25%        0.000000
50%        0.000000
75%        1.000000
max        1.000000
Name: Outcome, dtype: float64
```

```
[47] dataset2["Outcome"].unique()
```

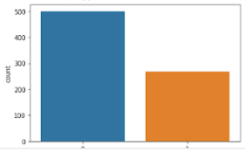
```
array([1, 0])
```

Exploratory Data Anaylsis

```
y = dataset2["Outcome"]
sns.countplot(y)

out_temp = dataset2.Outcome.value_counts()
print(out_temp)
```

```
0    500
1    268
Name: Outcome, dtype: int64
```



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heart.csv

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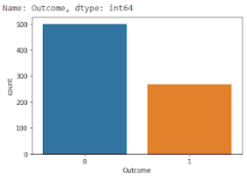
Exploratory Data Anaylsis

```
y = dataset2["Outcome"]
sns.countplot(y)

out_temp = dataset2.Outcome.value_counts()
print(out_temp)
```

```
0    500
1    268
Name: Outcome, dtype: int64
```




```
[49] # 0 -> No Diabetes
     # 1 -> Has Diabetes
```

```
[50] print("Percentage of people having diabetes: " + str(round(out_temp[1]*100/768, 2)))
     print("Percentage of people not having diabetes: " + str(round(out_temp[0]*100/768, 2)))
```

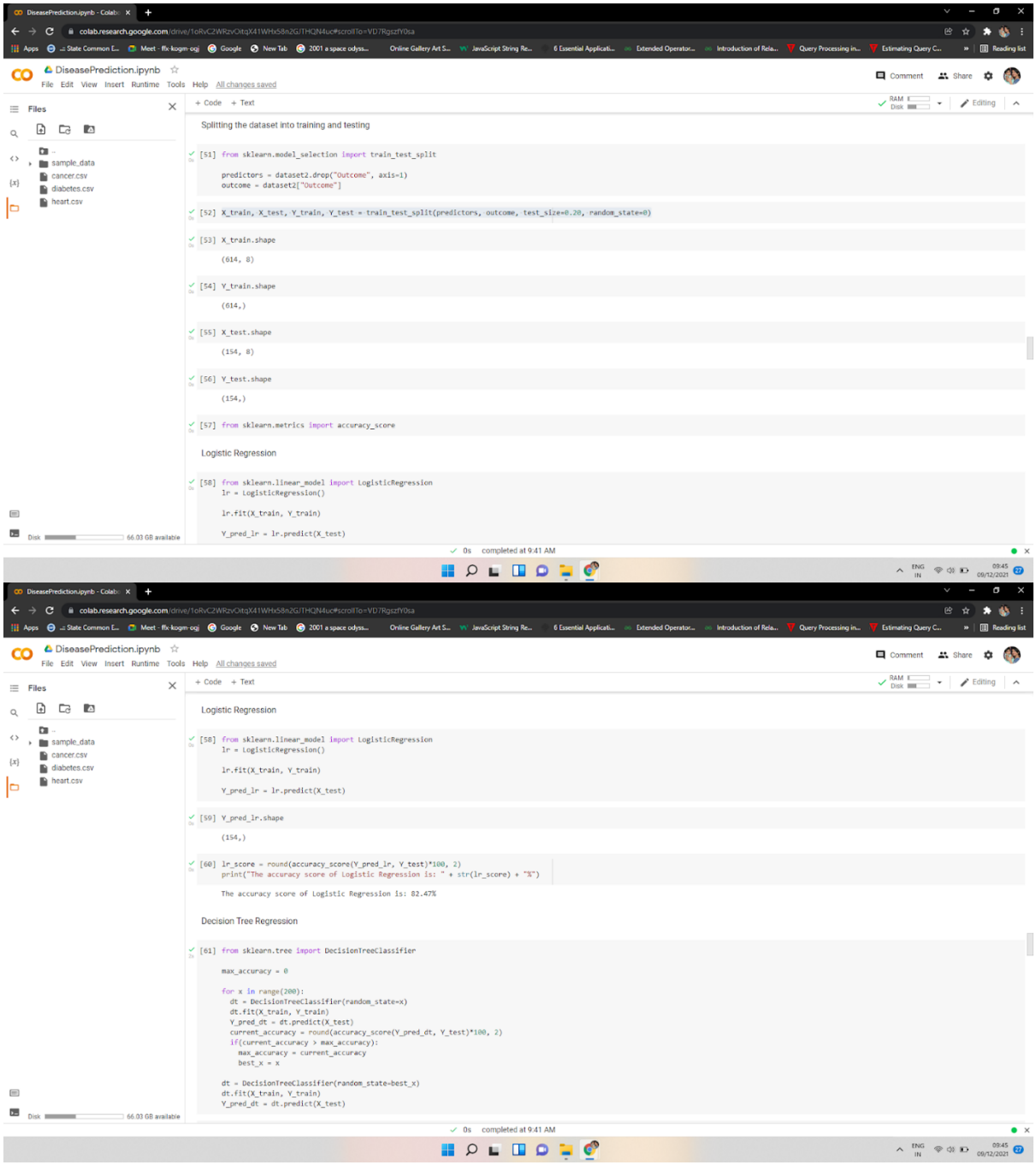
```
Percentage of people having diabetes: 34.9
Percentage of people not having diabetes: 65.1
```

Splitting the dataset into training and testing

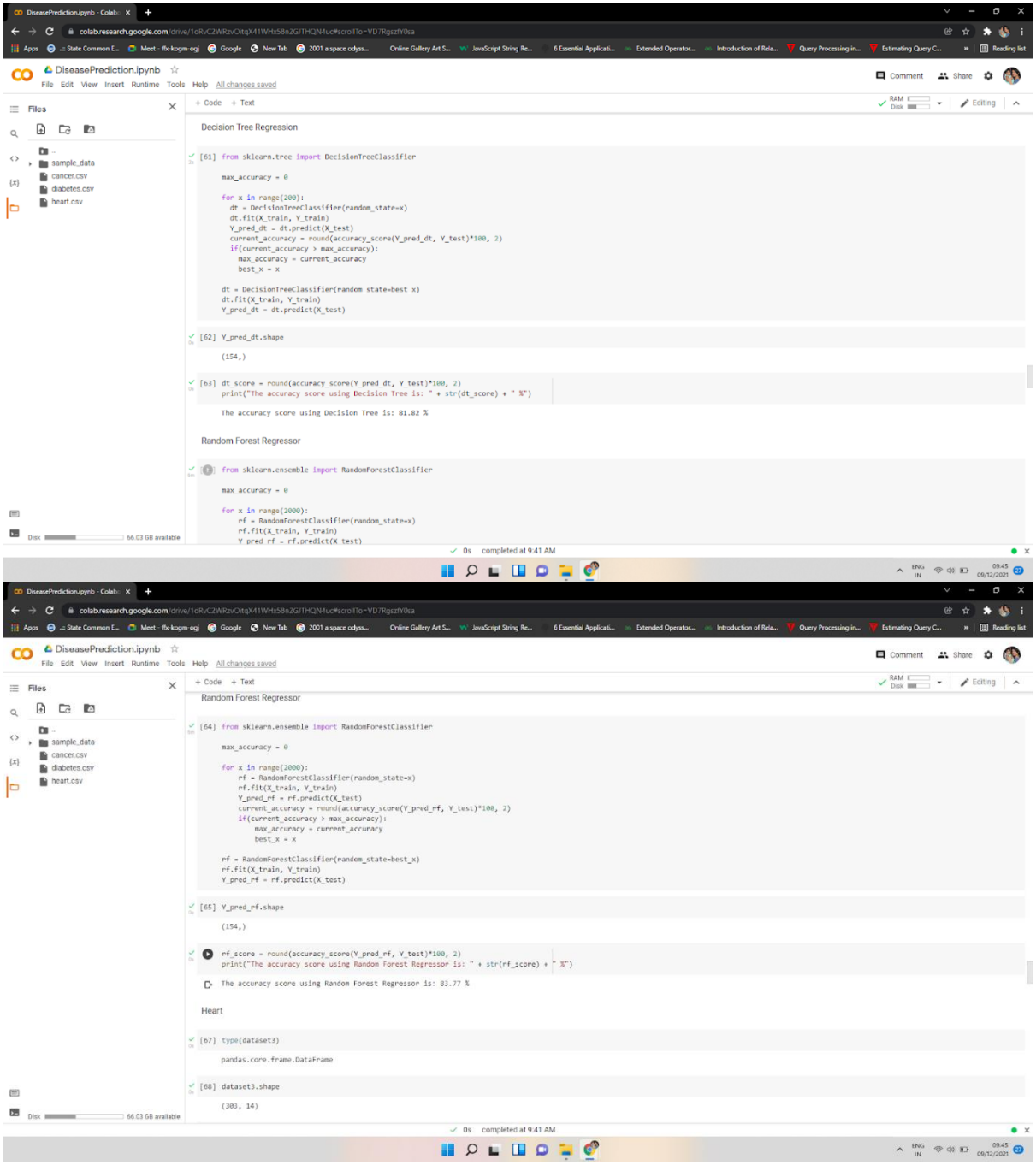
```
[51] from sklearn.model_selection import train_test_split
```

0s completed at 9:41 AM

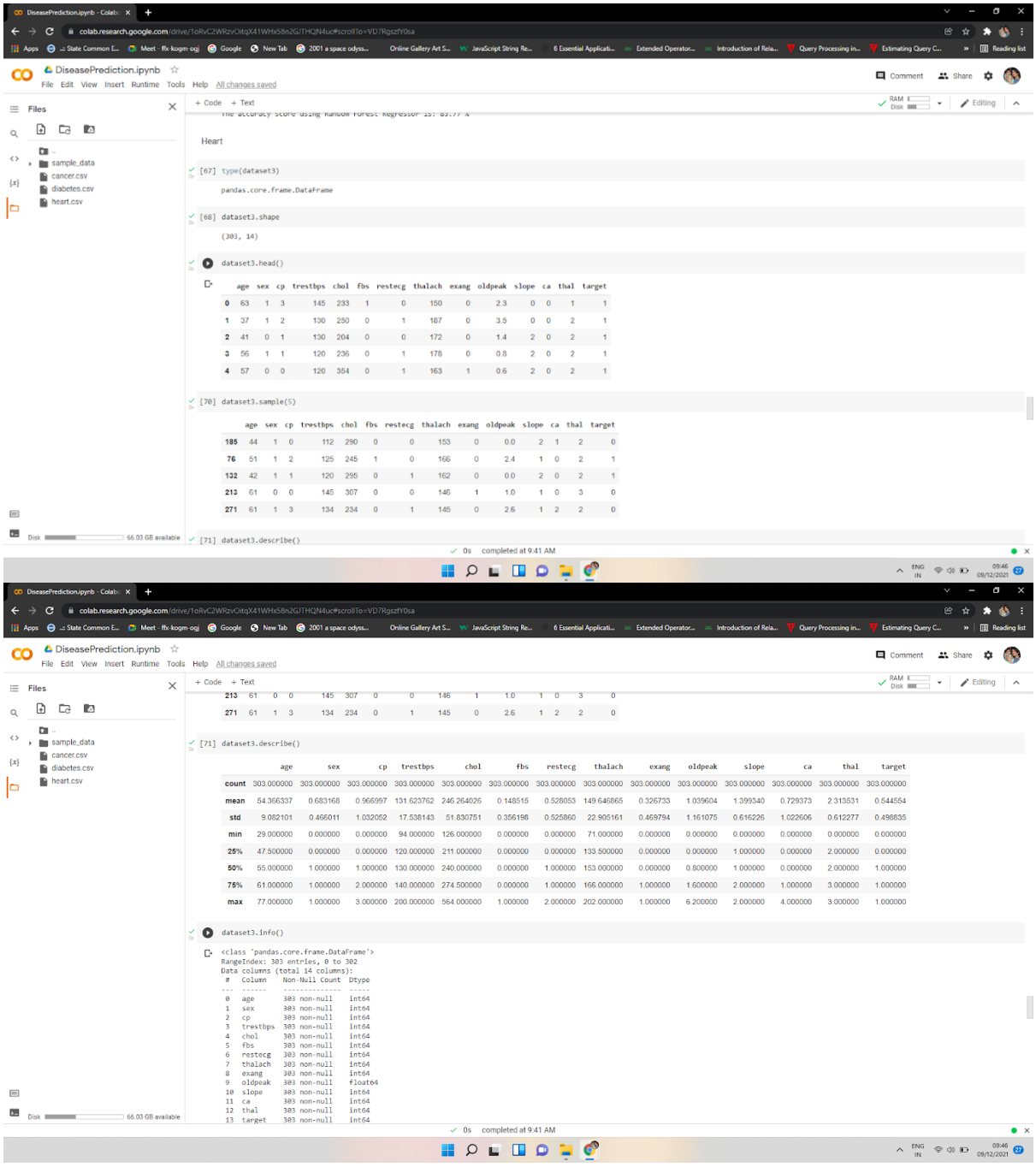
ENG IN 09:45 09/12/2021


DiseasePrediction.ipynb - Colabo
colab.research.google.com/drive/1oRvC2WRzvOitqX41WHx58n2GJ1HQN4uc#scrollTo=VD7RgszfY0sa
DiseasePrediction.ipynb
File Edit View Insert Runtime Tools Help All changes saved
Comment Share
Files
sample_data
cancer.csv
diabetes.csv
heart.csv
Disk 66.03 GB available
+ Code + Text
RAM Disk
Editing
Splitting the dataset into training and testing
[51] from sklearn.model_selection import train_test_split
predictors = dataset2.drop("Outcome", axis=1)
outcome = dataset2["Outcome"]
[52] X_train, X_test, Y_train, Y_test = train_test_split(predictors, outcome, test_size=0.20, random_state=0)
[53] X_train.shape
(614, 8)
[54] Y_train.shape
(614,)
[55] X_test.shape
(154, 8)
[56] Y_test.shape
(154,)
[57] from sklearn.metrics import accuracy_score
Logistic Regression
[58] from sklearn.linear_model import LogisticRegression
lr = LogisticRegression()
lr.fit(X_train, Y_train)
Y_pred_lr = lr.predict(X_test)
0s completed at 9:41 AM
ENG IN
09:45
09/12/2021

DiseasePrediction.ipynb - Colabo
colab.research.google.com/drive/1oRvC2WRzvOitqX41WHx58n2GJ1HQN4uc#scrollTo=VD7RgszfY0sa
DiseasePrediction.ipynb
File Edit View Insert Runtime Tools Help All changes saved
Comment Share
Files
sample_data
cancer.csv
diabetes.csv
heart.csv
Disk 66.03 GB available
+ Code + Text
RAM Disk
Editing
Logistic Regression
[58] from sklearn.linear_model import LogisticRegression
lr = LogisticRegression()
lr.fit(X_train, Y_train)
Y_pred_lr = lr.predict(X_test)
[59] Y_pred_lr.shape
(154,)
[60] lr_score = round(accuracy_score(Y_pred_lr, Y_test)*100, 2)
print("The accuracy score of Logistic Regression is: " + str(lr_score) + "%")
The accuracy score of Logistic Regression is: 82.47%
Decision Tree Regression
[61] from sklearn.tree import DecisionTreeClassifier
max_accuracy = 0
for x in range(200):
dt = DecisionTreeClassifier(random_state=x)
dt.fit(X_train, Y_train)
Y_pred_dt = dt.predict(X_test)
current_accuracy = round(accuracy_score(Y_pred_dt, Y_test)*100, 2)
if(current_accuracy > max_accuracy):
max_accuracy = current_accuracy
best_x = x
dt = DecisionTreeClassifier(random_state=best_x)
dt.fit(X_train, Y_train)
Y_pred_dt = dt.predict(X_test)
0s completed at 9:41 AM
ENG IN
09:45
09/12/2021


DiseasePrediction.ipynb
File Edit View Insert Runtime Tools Help All changes saved
Comment Share
Files
sample_data
cancer.csv
diabetes.csv
heart.csv
+ Code + Text
Editing
Decision Tree Regression
[61] from sklearn.tree import DecisionTreeClassifier
max_accuracy = 0
for x in range(200):
dt = DecisionTreeClassifier(random_state=x)
dt.fit(X_train, Y_train)
Y_pred_dt = dt.predict(X_test)
current_accuracy = round(accuracy_score(Y_pred_dt, Y_test)*100, 2)
if(current_accuracy > max_accuracy):
max_accuracy = current_accuracy
best_x = x
dt = DecisionTreeClassifier(random_state=best_x)
dt.fit(X_train, Y_train)
Y_pred_dt = dt.predict(X_test)
[62] Y_pred_dt.shape
(154,)
[63] dt_score = round(accuracy_score(Y_pred_dt, Y_test)*100, 2)
print("The accuracy score using Decision Tree is: " + str(dt_score) + " %")
The accuracy score using Decision Tree is: 81.82 %
Random Forest Regressor
from sklearn.ensemble import RandomForestClassifier
max_accuracy = 0
for x in range(2000):
rf = RandomForestClassifier(random_state=x)
rf.fit(X_train, Y_train)
Y_pred_rf = rf.predict(X_test)
Disk 66.03 GB available
0s completed at 9:41 AM

DiseasePrediction.ipynb
File Edit View Insert Runtime Tools Help All changes saved
Comment Share
Files
sample_data
cancer.csv
diabetes.csv
heart.csv
+ Code + Text
Editing
Random Forest Regressor
[64] from sklearn.ensemble import RandomForestClassifier
max_accuracy = 0
for x in range(2000):
rf = RandomForestClassifier(random_state=x)
rf.fit(X_train, Y_train)
Y_pred_rf = rf.predict(X_test)
current_accuracy = round(accuracy_score(Y_pred_rf, Y_test)*100, 2)
if(current_accuracy > max_accuracy):
max_accuracy = current_accuracy
best_x = x
rf = RandomForestClassifier(random_state=best_x)
rf.fit(X_train, Y_train)
Y_pred_rf = rf.predict(X_test)
[65] Y_pred_rf.shape
(154,)
rf_score = round(accuracy_score(Y_pred_rf, Y_test)*100, 2)
print("The accuracy score using Random Forest Regressor is: " + str(rf_score) + " %")
The accuracy score using Random Forest Regressor is: 83.77 %
Heart
[67] type(dataset3)
pandas.core.frame.DataFrame
[68] dataset3.shape
(303, 14)
Disk 66.03 GB available
0s completed at 9:41 AM

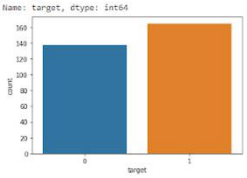

DiseasePrediction.ipynb
File Edit View Insert Runtime Tools Help All changes saved
Comment
Share
Files
sample_data
cancer.csv
diabetes.csv
heart.csv
+ Code + Text
Editing
Heart
[67] type(dataset3)
pandas.core.frame.DataFrame
[68] dataset3.shape
(303, 14)
dataset3.head()
age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal target
0 63 1 3 145 233 1 0 150 0 2.3 0 0 1 1
1 37 1 2 130 250 0 1 187 0 3.5 0 0 2 1
2 41 0 1 130 204 0 0 172 0 1.4 2 0 2 1
3 56 1 1 120 236 0 1 178 0 0.8 2 0 2 1
4 57 0 0 120 354 0 1 163 1 0.6 2 0 2 1
[70] dataset3.sample(5)
age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal target
185 44 1 0 112 290 0 0 153 0 0.0 2 1 2 0
76 51 1 2 125 245 1 0 166 0 2.4 1 0 2 1
132 42 1 1 120 295 0 1 162 0 0.0 2 0 2 1
213 61 0 0 145 307 0 0 146 1 1.0 1 0 3 0
271 61 1 3 134 234 0 1 145 0 2.6 1 2 2 0
[71] dataset3.describe()
Disk 66.03 GB available
0s completed at 9:41 AM

DiseasePrediction.ipynb
File Edit View Insert Runtime Tools Help All changes saved
Comment
Share
Files
sample_data
cancer.csv
diabetes.csv
heart.csv
+ Code + Text
Editing
213 61 0 0 145 307 0 0 146 1 1.0 1 0 3 0
271 61 1 3 134 234 0 1 145 0 2.6 1 2 2 0
[71] dataset3.describe()
age sex cp trestbps chol fbs restecg thalach exang oldpeak slope ca thal target
count 303.000000 303.000000 303.000000 303.000000 303.000000 303.000000 303.000000 303.000000 303.000000 303.000000 303.000000 303.000000 303.000000 303.000000
mean 54.366337 0.683168 0.966997 131.623762 246.264026 0.148515 0.528053 149.646865 0.326733 1.039604 1.399340 0.729373 2.313531 0.544554
std 9.082101 0.466011 1.032052 17.538143 51.830751 0.356198 0.525860 22.905161 0.469794 1.161075 0.616226 1.022606 0.612277 0.498835
min 29.000000 0.000000 0.000000 94.000000 126.000000 0.000000 0.000000 71.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000
25% 47.500000 0.000000 0.000000 120.000000 211.000000 0.000000 0.000000 133.500000 0.000000 0.000000 1.000000 0.000000 2.000000 0.000000
50% 55.000000 1.000000 1.000000 130.000000 240.000000 0.000000 1.000000 153.000000 0.000000 0.800000 1.000000 0.000000 2.000000 1.000000
75% 61.000000 1.000000 2.000000 140.000000 274.500000 0.000000 1.000000 166.000000 1.000000 1.600000 2.000000 1.000000 3.000000 1.000000
max 77.000000 1.000000 3.000000 200.000000 564.000000 1.000000 2.000000 202.000000 1.000000 6.200000 2.000000 4.000000 3.000000 1.000000
dataset3.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
Column Non-Null Count Dtype
0 age 303 non-null int64
1 sex 303 non-null int64
2 cp 303 non-null int64
3 trestbps 303 non-null int64
4 chol 303 non-null int64
5 fbs 303 non-null int64
6 restecg 303 non-null int64
7 thalach 303 non-null int64
8 exang 303 non-null int64
9 oldpeak 303 non-null float64
10 slope 303 non-null int64
11 ca 303 non-null int64
12 thal 303 non-null int64
13 target 303 non-null int64
Disk 66.03 GB available
0s completed at 9:41 AM

```
[72] dataset3.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype
---  ------    --------------  -----
 0   age       303 non-null    int64
 1   sex       303 non-null    int64
 2   cp        303 non-null    int64
 3   trestbps  303 non-null    int64
 4   chol      303 non-null    int64
 5   fbs       303 non-null    int64
 6   restecg   303 non-null    int64
 7   thalach   303 non-null    int64
 8   exang     303 non-null    int64
 9   oldpeak   303 non-null    float64
 10  slope     303 non-null    int64
 11  ca        303 non-null    int64
 12  thal      303 non-null    int64
 13  target    303 non-null    int64
dtypes: float64(1), int64(13)
memory usage: 33.3 KB

dataset3["target"].describe()

count    303.000000
mean       0.544554
std        0.498835
min        0.000000
25%        0.000000
50%        1.000000
75%        1.000000
max        1.000000
Name: target, dtype: float64

[74] dataset3["target"].unique()

array([1, 0])
```

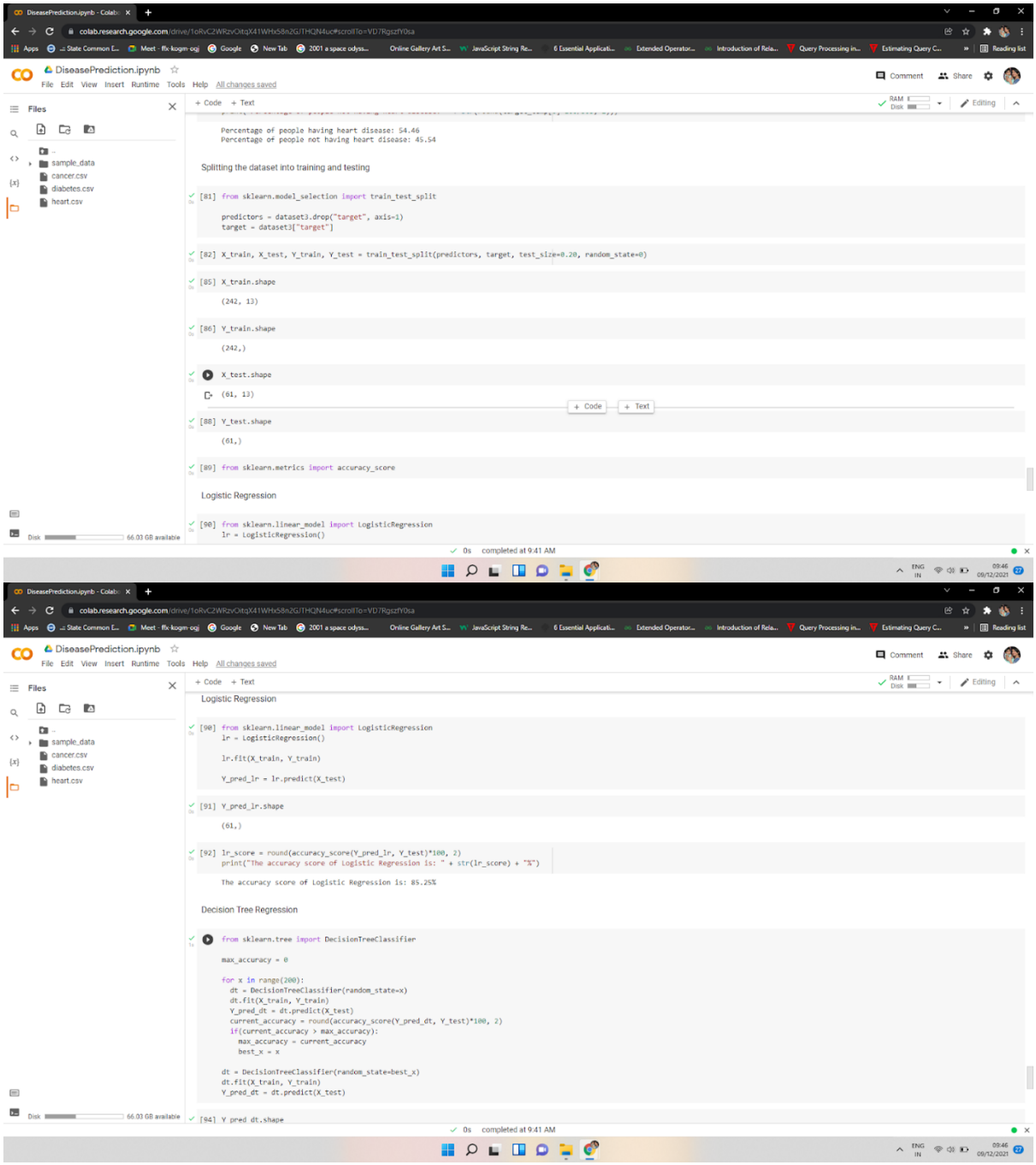
Exploratory Data Analysis

```
y = dataset3["target"]
sns.countplot(y)

target_temp = dataset3.target.value_counts()
print(target_temp)

1    165
0    138
Name: target, dtype: int64
```

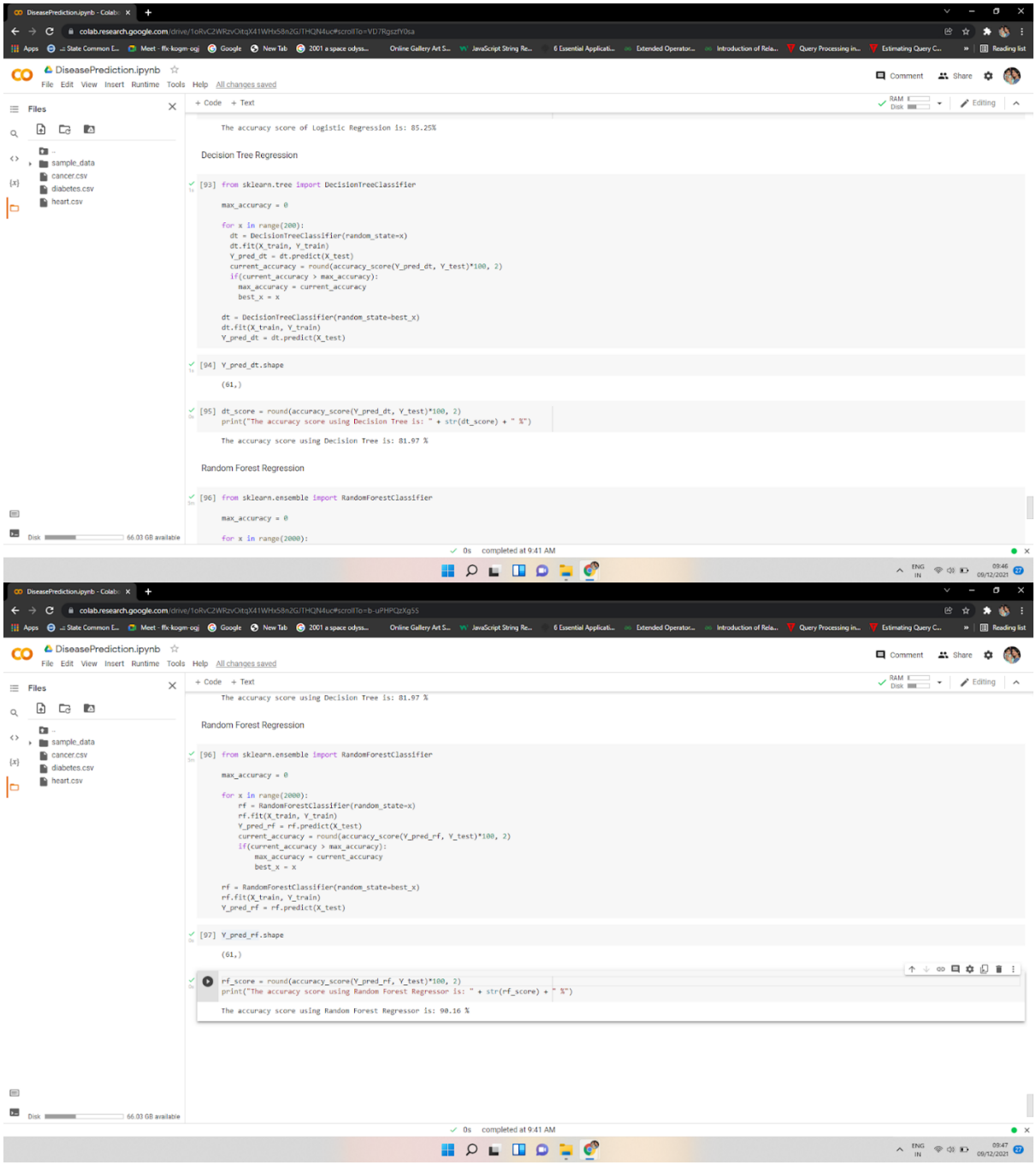



```
[76] # 0 -> No heart disease
     # 1 -> Has heart disease

[78] print("Percentage of people having heart disease: " + str(round(target_temp[1]*100/303, 2)))
     print("Percentage of people not having heart disease: " + str(round(target_temp[0]*100/303, 2)))

     Percentage of people having heart disease: 54.46
     Percentage of people not having heart disease: 45.54
```

Splitting the dataset into training and testing


DiseasePrediction.ipynb
Percentage of people having heart disease: 54.46
Percentage of people not having heart disease: 45.54
Splitting the dataset into training and testing
[81] from sklearn.model_selection import train_test_split
predictors = dataset3.drop("target", axis=1)
target = dataset3["target"]
[82] X_train, X_test, Y_train, Y_test = train_test_split(predictors, target, test_size=0.20, random_state=0)
[85] X_train.shape
(242, 13)
[86] Y_train.shape
(242,)
X_test.shape
(61, 13)
[88] Y_test.shape
(61,)
[89] from sklearn.metrics import accuracy_score
Logistic Regression
[90] from sklearn.linear_model import LogisticRegression
lr = LogisticRegression()
Files
sample_data
cancer.csv
diabetes.csv
heart.csv
66.03 GB available
completed at 9:41 AM

DiseasePrediction.ipynb
Logistic Regression
[90] from sklearn.linear_model import LogisticRegression
lr = LogisticRegression()
lr.fit(X_train, Y_train)
Y_pred_lr = lr.predict(X_test)
[91] Y_pred_lr.shape
(61,)
[92] lr_score = round(accuracy_score(Y_pred_lr, Y_test)*100, 2)
print("The accuracy score of Logistic Regression is: " + str(lr_score) + "%")
The accuracy score of Logistic Regression is: 85.25%
Decision Tree Regression
from sklearn.tree import DecisionTreeClassifier
max_accuracy = 0
for x in range(200):
dt = DecisionTreeClassifier(random_state=x)
dt.fit(X_train, Y_train)
Y_pred_dt = dt.predict(X_test)
current_accuracy = round(accuracy_score(Y_pred_dt, Y_test)*100, 2)
if(current_accuracy > max_accuracy):
max_accuracy = current_accuracy
best_x = x
dt = DecisionTreeClassifier(random_state=best_x)
dt.fit(X_train, Y_train)
Y_pred_dt = dt.predict(X_test)
[94] Y_pred_dt.shape
Files
sample_data
cancer.csv
diabetes.csv
heart.csv
66.03 GB available
completed at 9:41 AM



Website Output:

127.0.0.1:5000

Disease Prediction Home About Cancer Diabetes Heart

Details

Welcome to the home page of the app.

This is mainly based on as the application of the machine learning,meant to be employed in the remote and the downtrodden area.

Overview

In todays time we see a lot of the shortage of the doctors in the world especially in India.A lot of people are suffering a lot without the help of the proper medical checkup.Also most of the cases many cases arise leading to dealth due to lack of timely medical checkup

So to cope up with all of those problems this app is designed which would prove its benefits upto much extent.

Application

- To remove the dependencies on the doctors
- To help out the poor and helpless people with the normal medical checkup
- To help people avoid paying huge amount to the doctors unnecessarily
- To extend the role of the technology in the medical field

Creator :

Smrithi Agrawal & Karen Castelino

Disease Prediction Home About Cancer Diabetes Heart

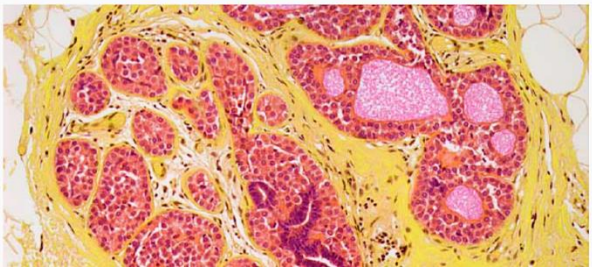
Details :

This is a basic machine learning and deep learning based medical app.

The prediction about the disease is made with the help of the machine learning model which itself is trained on the thousands of the datasets

So with the following paragraph I gonna be describing about the types of the diseases which gonna be getting employed in this app.

1. Breast Cancer



127.0.0.1:5000/about

Disease Prediction Home About Cancer Diabetes Heart

Breast cancer is cancer that develops from breast tissue. Signs of breast cancer may include a lump in the breast, a change in breast shape, dimpling of the skin, fluid coming from the nipple, a newly inverted nipple, or a red or scaly patch of skin.

Symptoms

Signs and symptoms of breast cancer may include:

- A breast lump or thickening that feels different from the surrounding tissue
- Change in the size, shape or appearance of a breast
- Changes to the skin over the breast, such as dimpling
- A newly inverted nipple
- Peeling, scaling, crusting or flaking of the pigmented area of skin surrounding the nipple (areola) or breast skin
- Redness or pitting of the skin over your breast, like the skin of an orange

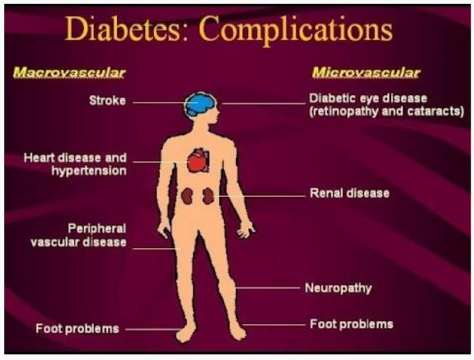
Causes

Doctors know that breast cancer occurs when some breast cells begin to grow abnormally. These cells divide more rapidly than healthy cells do and continue to accumulate, forming a lump or mass. Cells may spread (metastasize) through your breast to your lymph nodes or to other parts of your body.
Breast cancer most often begins with cells in the milk-producing ducts (invasive ductal carcinoma). Breast cancer may also begin in the glandular tissue called lobules (invasive lobular carcinoma) or in other cells or tissue within the breast.
Researchers have identified hormonal, lifestyle and environmental factors that may increase your risk of breast cancer. But it's not clear why some people who have no risk factors develop cancer, yet other people with risk factors never do. It's likely that breast cancer is caused by a complex interaction of your genetic makeup and your environment.

127.0.0.1:5000/about

Disease Prediction Home About Cancer Diabetes Heart

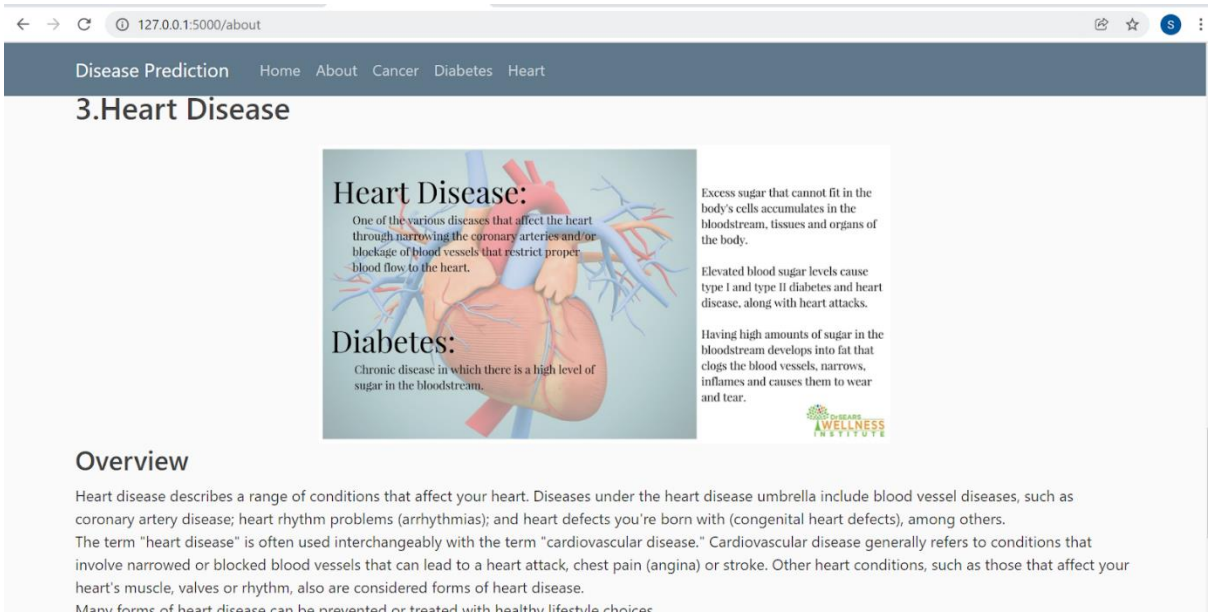
2. Diabetes



Diabetes is a disease that occurs when your blood glucose, also called blood sugar, is too high. Blood glucose is your main source of energy and comes from the food you eat. Insulin, a hormone made by the pancreas, helps glucose from food get into your cells to be used for energy.

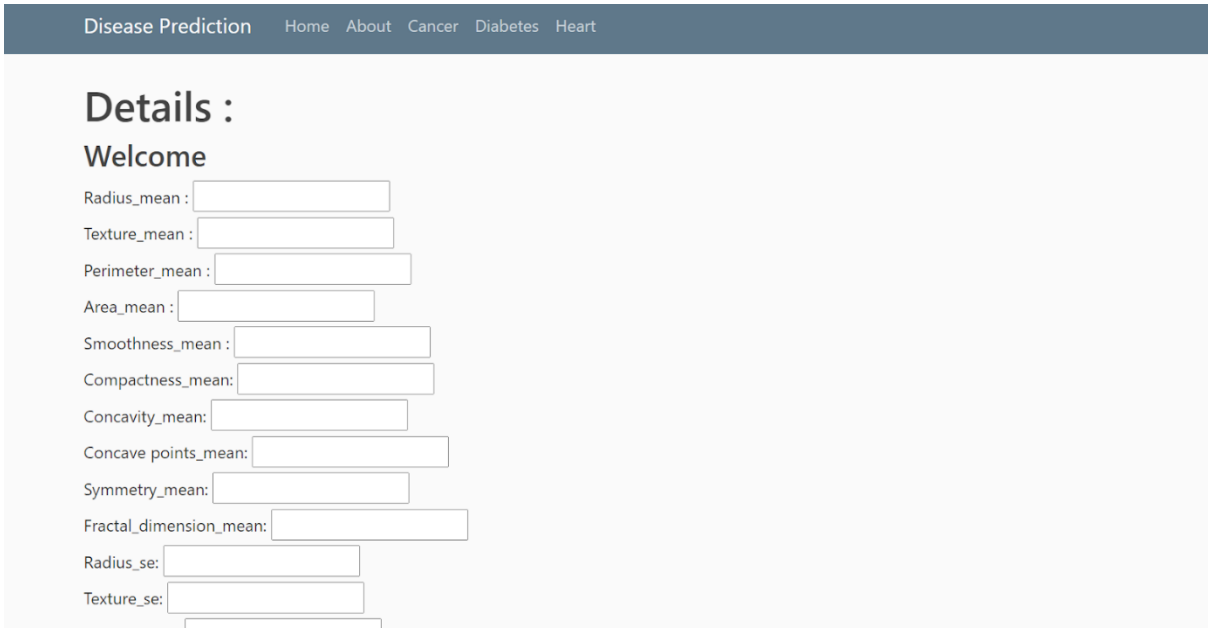
What health problems can people with diabetes develop?

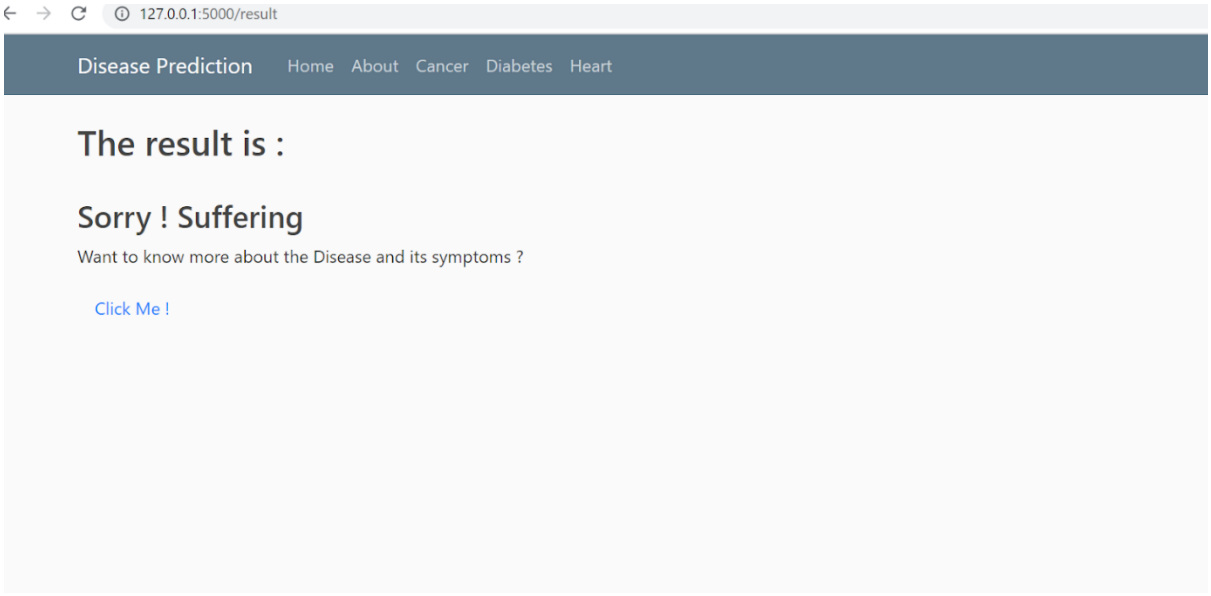
Over time, high blood glucose leads to problems such as



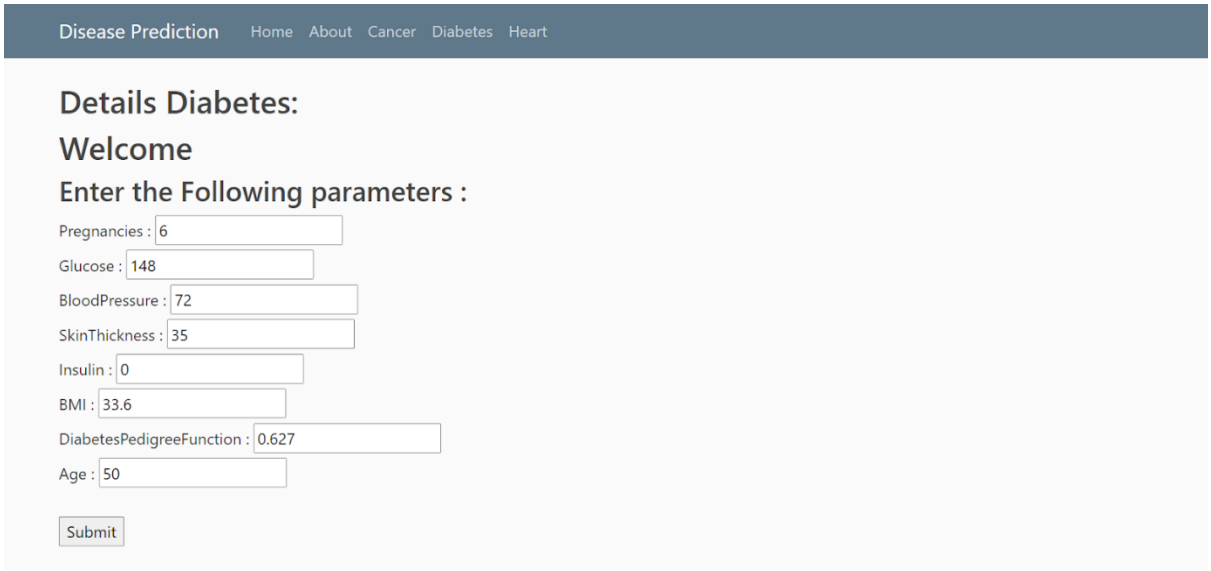
Final Output:

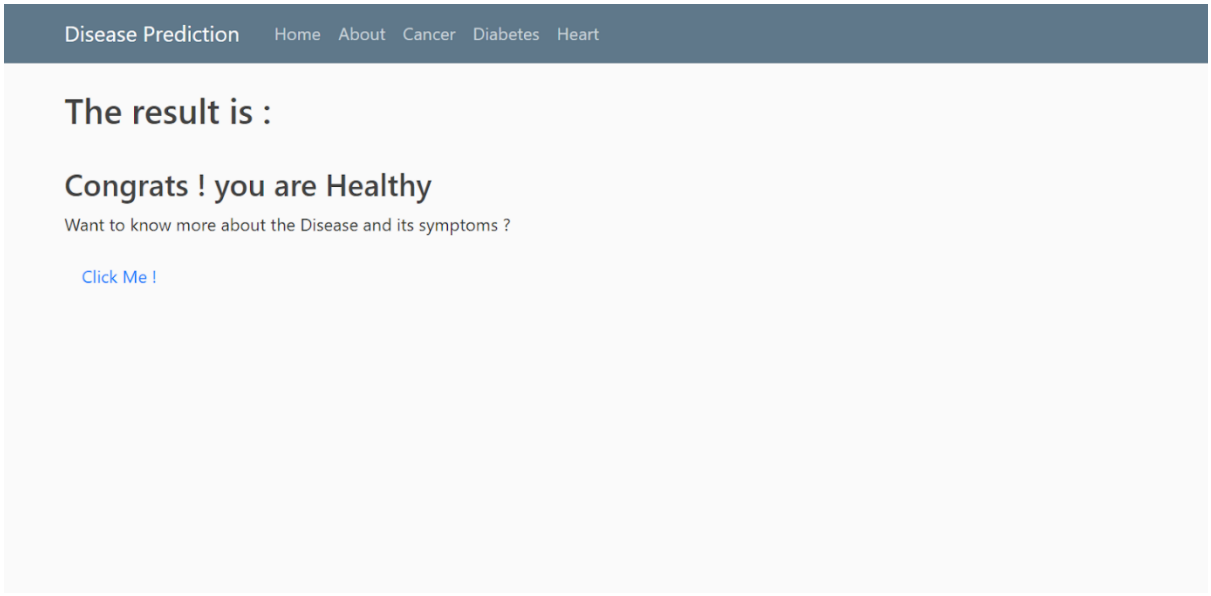
Cancer.html



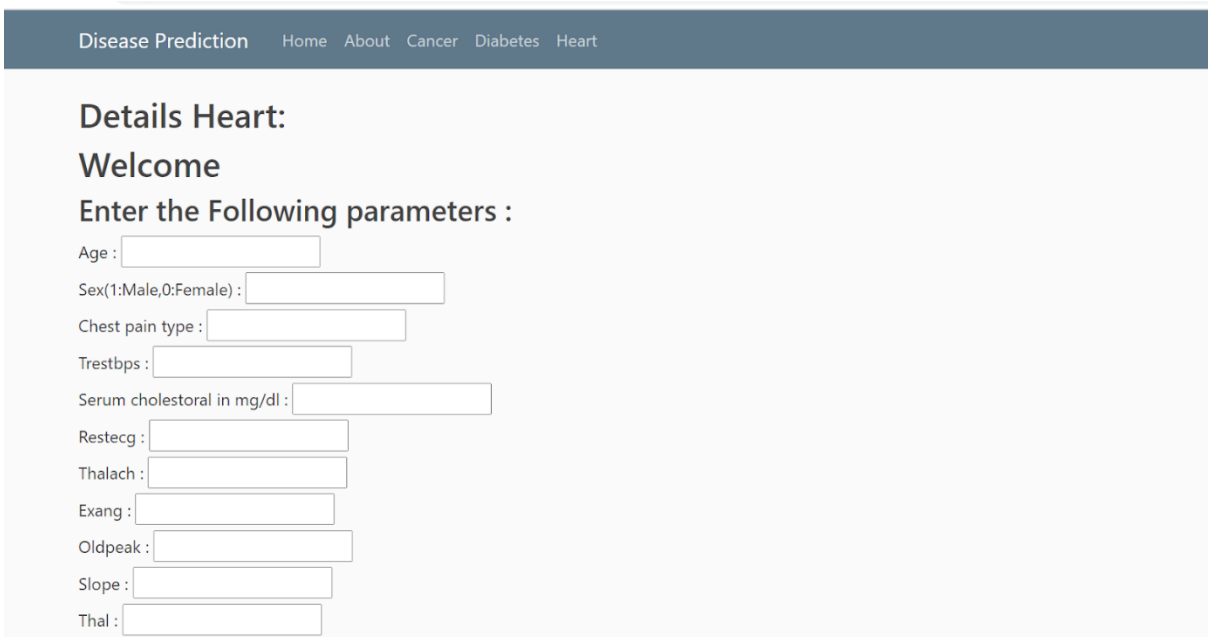


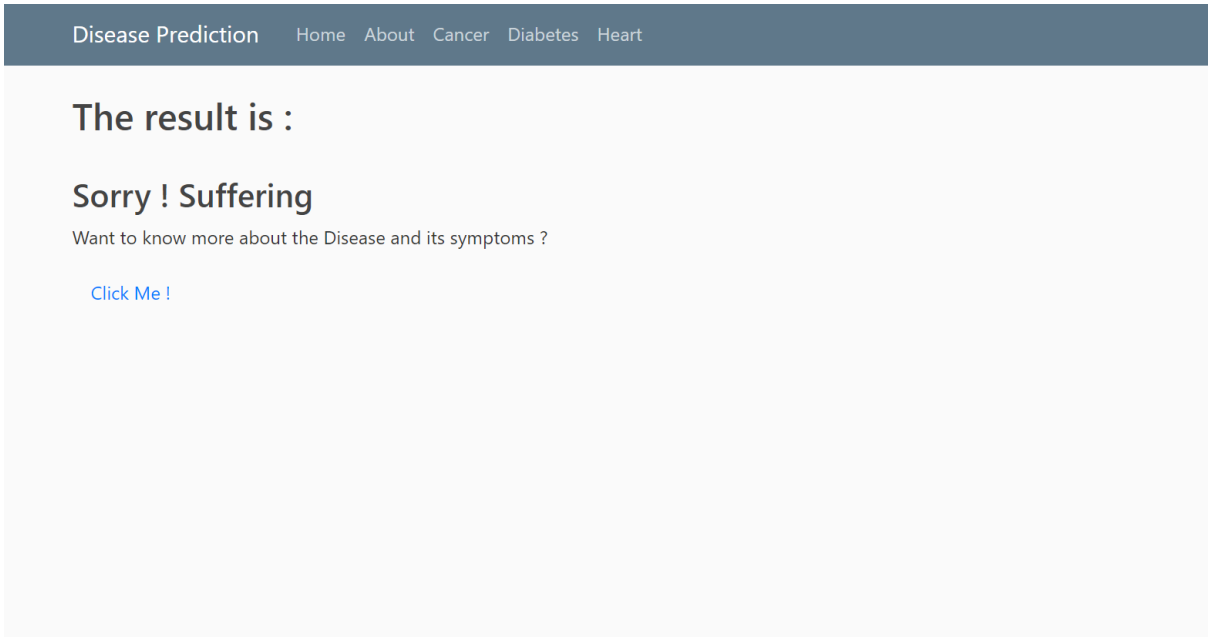
Diabetes.html




Disease Prediction
Home
About
Cancer
Diabetes
Heart
The result is :
Congrats ! you are Healthy
Want to know more about the Disease and its symptoms ?
Click Me !

Heart.html


Disease Prediction
Home
About
Cancer
Diabetes
Heart
Details Heart:
Welcome
Enter the Following parameters :
Age :
Sex(1:Male,0:Female) :
Chest pain type :
Trestbps :
Serum cholestoral in mg/dl :
Restecg :
Thalach :
Exang :
Oldpeak :
Slope :
Thal :



Conclusion:

The methods logistic regression, decision tree and random forest are analyzed for predicting the type of treatment that can be offered for the patient with cancer, diabetes or heart disease.

The success rate of classification for cancer is 58.77% obtained by Logistic Regression. The accuracy using Decision Tree Regression is 93.86%. The prediction percentage using Random Forest Regression is 98.25%.

The success rate of classification for Diabetes is 82.47% obtained by Logistic Regression. The accuracy using Decision Tree Regression is 81.82%. The prediction percentage using Random Forest Regression is 83.77%.

The success rate of classification for Heart Disease is 85.25% obtained by Logistic Regression. The accuracy using Decision Tree regression is 81.97%. The prediction percentage using Random Forest Regression is 90.16%.

Future Scope

As a future enhancement, how the preprocessing of dataset can be improvised for increasing the success rate in classification and prediction process. Implementation of various other diseases can be done by the use of different algorithms to achieve better accuracy (most probably neural networks). An improved and user-friendly front-end can be useful for better accessibility to the website.

Limitations

- All the necessary input values must be present and accurate.
- The accuracy is not as good as we expect it to be, and sometimes this might result in a wrong prediction.
- The prediction might change after some time depending on the input attributes

References:

https://www.geeksforgeeks.org/random-forest-regression-in-python/
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