

# AI BASED DIABETES PREDICTION SYSTEM

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*PHASE 5 SUBMISSION*

## PROJECT DOCUMENTATION & SUBMISSION

*SUBMITTED BY*

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### Introduction:

The problem we aim to address is the early prediction of diabetes using artificial intelligence. Diabetes is a prevalent and chronic health condition that can lead to severe complications if not detected and managed in its early stages. Early prediction allows for timely intervention and lifestyle changes, potentially preventing or delaying the onset of diabetes-related complications.

### Design Thinking Process:

#### Empathize:

- Understand the needs and concerns of individuals at risk of diabetes.
- Gather insights from healthcare professionals, patients, and relevant stakeholders.

## Define:

Clearly define the problem based on insights gathered. Identify key criteria for predicting diabetes risk, such as lifestyle factors, genetic predisposition, and existing health conditions.

## Ideate:

Brainstorm and generate ideas for AI-based solutions. Consider features like machine learning algorithms, data sources (biometric, lifestyle, etc.), and user interface for seamless interaction.

## Prototype:

- Create a prototype of the AI-based diabetes prediction model.
- Develop a user-friendly interface for inputting relevant data.
- Test the prototype with a diverse group of potential users to gather feedback.

## Test:

- Evaluate the prototype's performance using real-world data.
- Gather feedback from users and healthcare professionals to refine the model.
- Ensure the model's accuracy and reliability in predicting diabetes risk.

## Implement:

- Develop the final version of the AI-based diabetes prediction tool.
- Integrate it into existing healthcare systems or make it accessible through user-friendly platforms.

## Iterate:

- Continuously improve the model based on user feedback and emerging research.
- Stay updated with advancements in AI and diabetes research to enhance prediction accuracy.

## Phases of Development:

### 1.Data Collection:

Tool Used : jupyter Notebook

#### DATA SOURCE:

<https://www.kaggle.com/datasets/mathchi/diabetes-data-set/>

This dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases. The objective of the dataset is to diagnostically predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. Several constraints were placed on the selection of these instances from a larger database. In particular, all patients here are females at least 21 years old of Pima Indian heritage.

### 2.Data Preprocessing:

Clean and preprocess the data to remove noise and ensure consistency.

Handle missing or incomplete data using appropriate techniques.

Missing Data Handling:

Address missing values through techniques like mean imputation or advanced methods like multiple imputation.

Outlier Detection and Removal:

Identify and remove outliers that could skew the model's performance.

Normalization/Scaling:

Normalize or scale numerical features to ensure that they contribute equally to the model.

### 3.Feature Selection:

Identify key features that contribute to diabetes prediction.

Use statistical methods or machine learning techniques to select the most relevant features.

#### 4. Model Development:

Choice of Machine Learning Algorithm:

The choice of machine learning algorithm for the diabetes prediction system is often based on experimentation and performance evaluation. Commonly used algorithms include:

- Logistic Regression
- Decision Trees
- Random Forest
- Support Vector Machines
- Neural Networks

Splitting the Dataset:

Divide the dataset into training and testing sets to assess the model's performance on unseen data.

Training the Model:

Train the selected machine learning algorithm on the training set, optimizing its parameters for the best performance.

From analysing the accuracy, precision of the data with multiple machine learning algorithm, we can come up it one algorithm(here we achieve random forest tree algorithm)

#### 5. Validation:

Validate the model using a separate dataset to ensure its generalization to new, unseen data.

Fine-tune the model parameters based on validation results.

## 6. Save the model:

Integrate the developed model into the overall AI-based diabetes prediction system.

Ensure compatibility with existing healthcare infrastructure. Then save the developed model using **pickle library**.

## 7. Deployment:

Deploy the system in real-world application like web app. In this project we use streamlit framework for loading the ai model as web application.

**Tool used: STREAMLIT**

By following this structured approach, we create a robust and user-friendly AI-based diabetes prediction system that addresses the identified problem effectively.

Note:

All the phases of code are implemented on **google collab**

## Innovative Technique used:

### Ensemble Learning:

Implemented ensemble learning techniques such as Random Forest or Gradient Boosting to combine predictions from multiple models. This helps in improving overall predictive performance and robustness.

## Implementation

1. First create a jupyter notebook to develop the ai based model. For that we have to import required libraries like pandas, numpy, pickle etc.
2. Continue developing the model using the above discussed method
3. Then save the model as .pkl format

- 4.This saved model i.e .pkl format file is used for loading the input for web application
- 5.Streamlit is python web app framework which is simple framework to develop the web application
- 6.This web app provide accuracy info about diabetes prediction with well supported user interface

## Code

### 1.Jupyter Notebook

#### 1. import libraries

```
#import libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
```

#### 2. Load the dataset

```
#Reading the dataset
df = pd.read_csv("/kaggle/input/diabetes-predictionsys/diabetes.csv")
df.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
0	6	148	72	35	0	33.6	
1	1	85	66	29	0	26.6	
2	8	183	64	0	0	23.3	
3	1	89	66	23	94	28.1	
4	0	137	40	35	168	43.1	

	DiabetesPedigreeFunction	Age	Outcome
0	0.627	50	1
1	0.351	31	0
2	0.672	32	1
3	0.167	21	0
4	2.288	33	1

#### 3. Analysis the dataset

```
#columns available in our dataset
df.columns
```

```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
      'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

*#Information about the data*

```
df.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
```

*#more about the dataset*

```
df.describe().T
```

	count	mean	std	min	25%	\
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	
Glucose	768.0	120.894531	31.972618	0.000	99.00000	
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	
Insulin	768.0	79.799479	115.244002	0.000	0.00000	
BMI	768.0	31.992578	7.884160	0.000	27.30000	
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	
Age	768.0	33.240885	11.760232	21.000	24.00000	
Outcome	768.0	0.348958	0.476951	0.000	0.00000	

	50%	75%	max
Pregnancies	3.0000	6.00000	17.00
Glucose	117.0000	140.25000	199.00
BloodPressure	72.0000	80.00000	122.00
SkinThickness	23.0000	32.00000	99.00
Insulin	30.5000	127.25000	846.00
BMI	32.0000	36.60000	67.10
DiabetesPedigreeFunction	0.3725	0.62625	2.42
Age	29.0000	41.00000	81.00
Outcome	0.0000	1.00000	1.00

## 4. Clean the data

*Clean the data after analyse the null , impossible value and duplicated value*

*#analyse the null and duplicated values*

```
print(f'Duplicated rows are: \n { df.duplicated().sum()} \n \n \n Null values per
column are: \n {df.isnull().sum()}\n \n \n Zero values per column are: \n {(df ==
0).sum()} , \n \n \n data types of each column is: \n {df.dtypes}  ')
```

Duplicated rows are:

0

Null values per column are:

Pregnancies	0
Glucose	0
BloodPressure	0
SkinThickness	0
Insulin	0
BMI	0
DiabetesPedigreeFunction	0
Age	0
Outcome	0

dtype: int64

Zero values per column are:

Pregnancies	111
Glucose	5
BloodPressure	35
SkinThickness	227
Insulin	374
BMI	11
DiabetesPedigreeFunction	0
Age	0
Outcome	500

dtype: int64 ,

data types of each column is:

Pregnancies	int64
Glucose	int64
BloodPressure	int64
SkinThickness	int64
Insulin	int64
BMI	float64
DiabetesPedigreeFunction	float64
Age	int64
Outcome	int64

dtype: object

*#analyse the impossible values*

```
impossible_values = (df["Glucose"] == 0) | (df["BloodPressure"] == 0) |  
(df["SkinThickness"] == 0) | (df["Insulin"] == 0) | (df["BMI"] == 0)  
impossible_values.sum()
```

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*Replace the null value with median value*

*#replace the null value with median value*

```
lst=['Glucose','BloodPressure','SkinThickness','Insulin','BMI']  
for i in lst:  
    df[i].replace(0, np.nan, inplace=True)  
    df[i].fillna(df[i].median(), inplace=True)  
df.head()
```



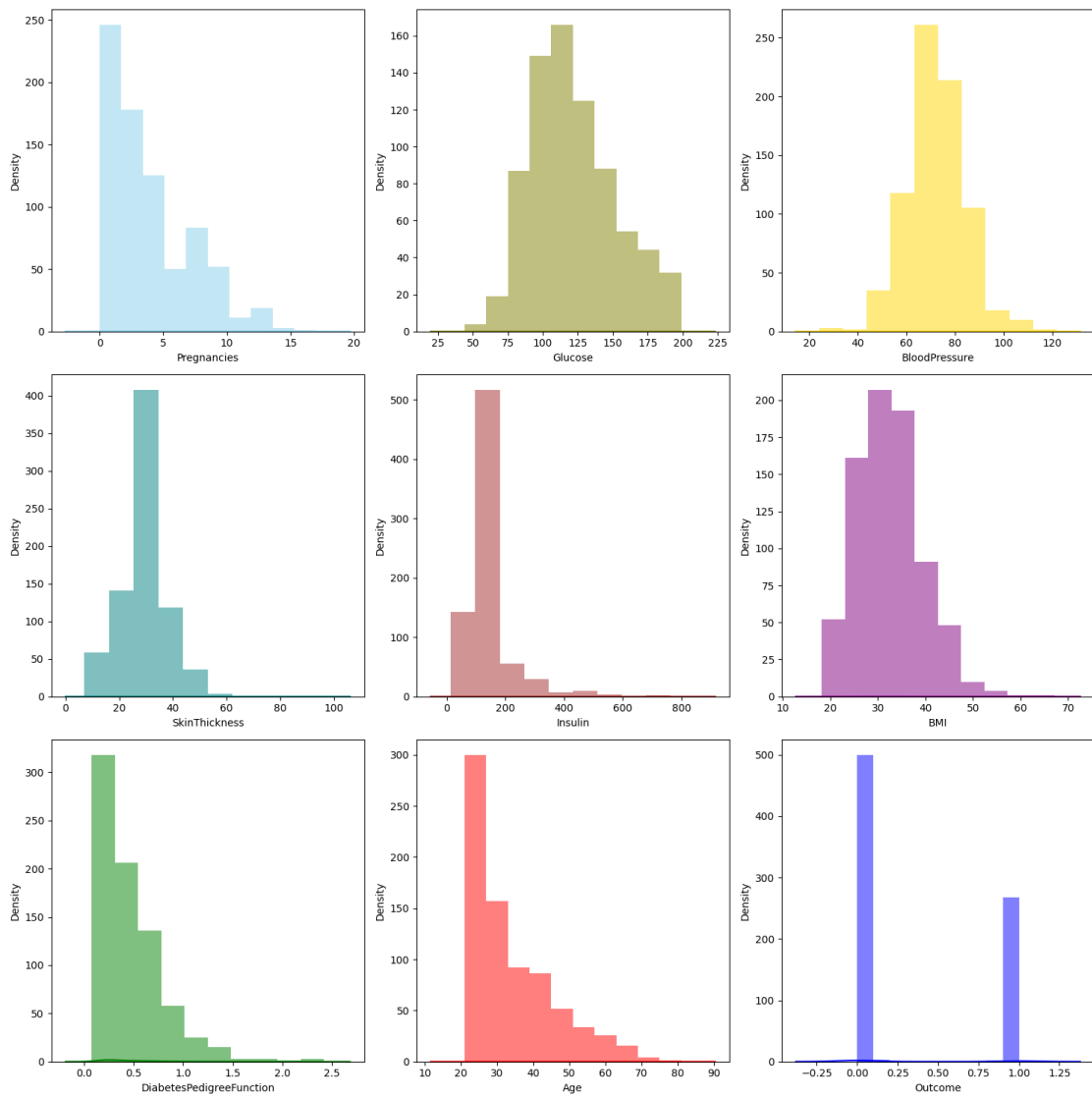
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
0	6	148.0	72.0	35.0	125.0	33.6	
1	1	85.0	66.0	29.0	125.0	26.6	
2	8	183.0	64.0	29.0	125.0	23.3	
3	1	89.0	66.0	23.0	94.0	28.1	
4	0	137.0	40.0	35.0	168.0	43.1	

	DiabetesPedigreeFunction	Age	Outcome
0	0.627	50	1
1	0.351	31	0
2	0.672	32	1
3	0.167	21	0
4	2.288	33	1

## 5. Visualize the dataset

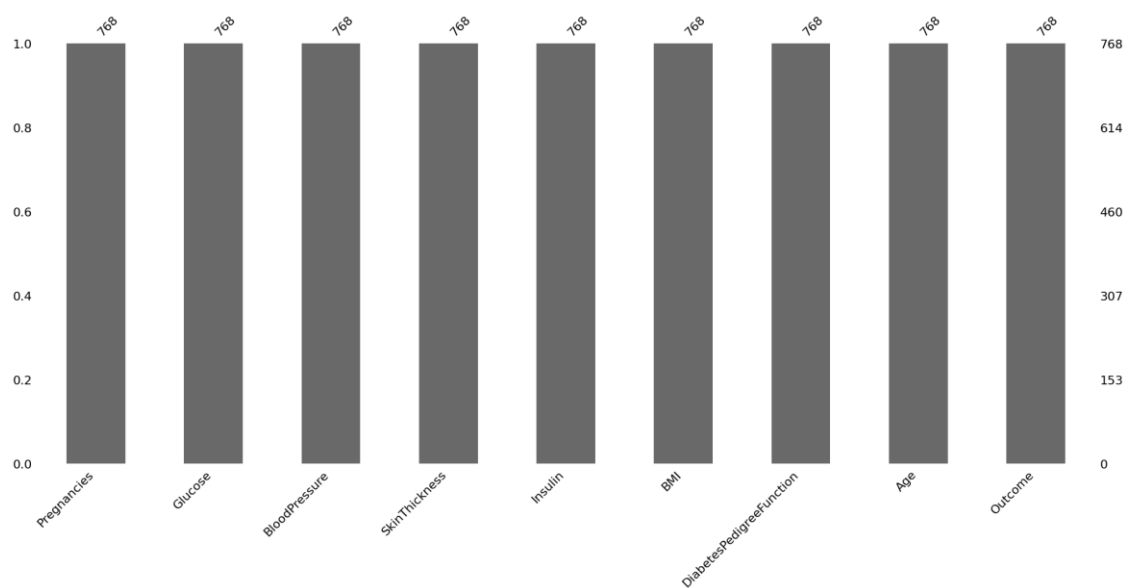
*After clean the data visualize the data distribution by plotting it as histogram*

```
lst1=['Pregnancies','Glucose','BloodPressure','SkinThickness','Insulin','BMI','DiabetesPedigreeFunction','Age','Outcome']
lst_col=['skyblue','olive','gold','teal','brown','purple','green','red','blue']
f, axes = plt.subplots(3, 3, figsize=(15, 15), sharex=False) # Set up the matplotlib figure
axes = axes.flatten() # Plot a simple histogram with binsize determined automatically
for ax,k,m in zip(axes,lst1,lst_col):
    ax.hist(df[k], color=m, bins=10, alpha=0.5)
    sns.distplot(df[k], color=m, ax=ax)
plt.tight_layout()
```



## Plotting Null Count Analysis Plot

```
import missingno as msno
p = msno.bar(df)
```



*Inference: Now in the above graph also we can clearly see that there are no null values in the dataset.*

## *check that how well our outcome column is balanced*

dataset **is** completely imbalanced **in** fact the number of patients who are diabetic **is** half of the patients who are non-diabetic

Cell In[85], line 1

dataset is completely imbalanced in fact the number of patients who are diabetic is half of the patients who are non-diabetic

^

SyntaxError: invalid syntax

```
color_wheel = {1: "#0392cf", 2: "#7bc043"}
colors = df["Outcome"].map(lambda x: color_wheel.get(x + 1))
print(df.Outcome.value_counts())
p=df.Outcome.value_counts().plot(kind="bar")
```

Interference: dataset is completely imbalanced in fact the number of patients who are diabetic is half of the patients who are non-diabetic

### • Visualization of Outliers

```
# Generate a box plot for each feature
lst1=['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome']
lst_col=['skyblue', 'olive', 'gold', 'teal', 'brown', 'purple', 'green', 'red', 'blue']
f, axes = plt.subplots(3, 3, figsize=(15, 15), sharex=False) # Set up the matplotlib figure
axes = axes.flatten() # Plot a simple histogram with binsize determined automatically
for ax,k,m in zip(axes,lst1,lst_col):
    sns.boxplot(data=df, x=k, color=m, ax=ax)
plt.tight_layout()
plt.show()
```

### • Check the Relationship Between Variables

Then we wanna check the relationships between the different variables(columns). This can provide insights into which variables are strongly or weakly associated with each other.

```
corr = df.corr() # Compute the correlation matrix
mask = np.triu(np.ones_like(corr, dtype=bool)) # Generate a mask for the upper triangle
f, ax = plt.subplots(figsize=(11, 9)) # Set up the matplotlib figure
cmap = sns.diverging_palette(230, 20, as_cmap=True) # Generate a custom diverging colormap
sns.heatmap(corr, mask=mask, cmap=cmap, vmax=0.3, center=0, square=True, linewidths=.5, cbar_kws={"shrink": .5}, annot=True) # Draw the heatmap with the mask and correct aspect ratio
plt.tight_layout()
```

Interference: The correlation coefficient values range from -1 to 1. If the correlation coefficient is close to 1, it means that there is a strong positive correlation between the two variables. When it is close to -1, the variables have a strong negative correlation. Glucose, Age and BMI are moderately correlated with Outcome. Pregnancies and Age show a strong correlation.

- Pairwise Variable Relationship

This can be very helpful to understand how the variables interact with each other and identify any potential patterns or trends in the data.

```
# We'll use a sample of the data to make the pairplot faster to generate
df_sample = df.sample(100, random_state=1)
```

```
# Create a pairplot
sns.pairplot(df_sample, hue="Outcome")
plt.show()
```

## 6.Split the data

we need to split the data into a training set and a test set. This allows us to evaluate how well our model generalizes to unseen data. We'll use 80% of the data for training and 20% for testing.

```
from sklearn.model_selection import train_test_split
X = df.drop("Outcome", axis=1)
y = df["Outcome"]
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
random_state=42)# Split the data into a training set and a test set
X_train.shape, X_test.shape

((614, 8), (154, 8))
```

## 7.Data Transformation

Transform data as needed, for example, scaling

### a)Before Scaling

```
df.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
0	6	148.0	72.0	35.0	125.0	33.6	
1	1	85.0	66.0	29.0	125.0	26.6	
2	8	183.0	64.0	29.0	125.0	23.3	
3	1	89.0	66.0	23.0	94.0	28.1	
4	0	137.0	40.0	35.0	168.0	43.1	

	DiabetesPedigreeFunction	Age	Outcome
0	0.627	50	1
1	0.351	31	0
2	0.672	32	1
3	0.167	21	0
4	2.288	33	1

### b)After Scaling

## Scaled it by trained model

```
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler() # Initialize the scaler
scaler.fit(X_train) # Fit the scaler to the training data
X_train_scaled = scaler.transform(X_train)
X_test_scaled = scaler.transform(X_test)
pd.DataFrame(X_train_scaled, columns=['Pregnancies',
'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI',
'DiabetesPedigreeFunction', 'Age']).head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
0	-0.526397	-1.256881	-0.018995	0.034298	-0.175620	-0.007450	
1	1.588046	-0.326051	0.808174	-0.560583	-0.175620	-0.599092	
2	-0.828460	0.571536	-2.169636	-1.155463	-0.652193	-0.526941	
3	-1.130523	1.302903	-1.838768	0.034298	-0.175620	-1.508200	
4	0.681856	0.405316	0.642740	0.986106	2.604392	1.998360	

	DiabetesPedigreeFunction	Age
0	-0.490735	-1.035940
1	2.415030	1.487101
2	0.549161	-0.948939
3	-0.639291	2.792122
4	-0.686829	1.139095

## Scaled it by test model

```
X_test_scaled = scaler.transform(X_test)
pd.DataFrame(X_test_scaled, columns=['Pregnancies',
'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI',
'DiabetesPedigreeFunction', 'Age']).head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
0	0.681856	-0.791466	-1.177033	0.510202	0.561935	0.237865	
1	-0.526397	-0.326051	0.229156	0.391226	-0.175620	0.483180	
2	-0.526397	-0.459026	-0.680731	0.034298	-0.175620	-0.223904	
3	1.285983	-0.492270	0.642740	0.034298	-0.175620	-1.118582	
4	0.983919	0.471804	1.469910	0.034298	-0.175620	-0.353777	

	DiabetesPedigreeFunction	Age
0	-0.116372	0.878091
1	-0.954231	-1.035940
2	-0.924520	-1.035940
3	1.149329	0.095078
4	-0.770021	1.487101

## 8.BUILDING THE ML MODEL

scaling help our ML model to give a better result.

```
from sklearn.metrics import accuracy_score
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
```

```

from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
def fit_and_evaluate(model):# Define a function to fit a model
    model.fit(X_train_scaled, y_train) # Fit the model
    train_preds = model.predict(X_train_scaled) # Make predictions on the
training set and compute the accuracy
    train_acc = accuracy_score(y_train, train_preds)
    test_preds = model.predict(X_test_scaled) # Make predictions on the test
set and compute the accuracy
    test_acc = accuracy_score(y_test, test_preds)
    return train_acc, test_acc
res=[]
models=[LogisticRegression(random_state=42),DecisionTreeClassifier(random_s
tate=42),RandomForestClassifier(random_state=42),SVC(random_state=42)]
for i in models:
    res.append(fit_and_evaluate(i))
for mod,result in zip(models,res):
    print(f'train and test accuracy of {mod} respectively is: \n {result}
\n \n')

```

train and test accuracy of LogisticRegression(random\_state=42) respectively is:  
(0.7703583061889251, 0.7532467532467533)

train and test accuracy of DecisionTreeClassifier(random\_state=42) respectively  
is:  
(1.0, 0.7142857142857143)

train and test accuracy of RandomForestClassifier(random\_state=42) respectively  
is:  
(1.0, 0.7337662337662337)

train and test accuracy of SVC(random\_state=42) respectively is:  
(0.8289902280130294, 0.7467532467532467)

## Result & Discussion

- Logistic Regression: The training accuracy is approximately 77.04% and the test accuracy is approximately 75.32%.
- Decision Tree: The training accuracy is 100%, indicating that the model has perfectly fit the training data. However, the test accuracy drops to approximately 71.43%, suggesting that the model might be overfitting the training data.
- Random Forest: Similar to the Decision Tree, the training accuracy is 100%, but the test accuracy is approximately 73.38%, indicating potential overfitting.

- Support Vector Machine (SVM): The training accuracy is approximately 82.90% and the test accuracy is approximately 74.68%.

From the results, it appears that the Logistic Regression and SVM models are performing the best on this dataset based on accuracy. They are not overfitting the training data as much as the Decision Tree and Random Forest models, and are achieving a good balance between bias and variance.

## The Conclusion from Model Building

**Random forest** is the best model for this prediction since it has an accuracy\_score of 0.76.

## 9.Feature Importance

Knowing about the feature importance is quite necessary as it shows that how much weightage each feature provides in the model building phase.

```
#Getting feature importances

from sklearn.ensemble import RandomForestClassifier

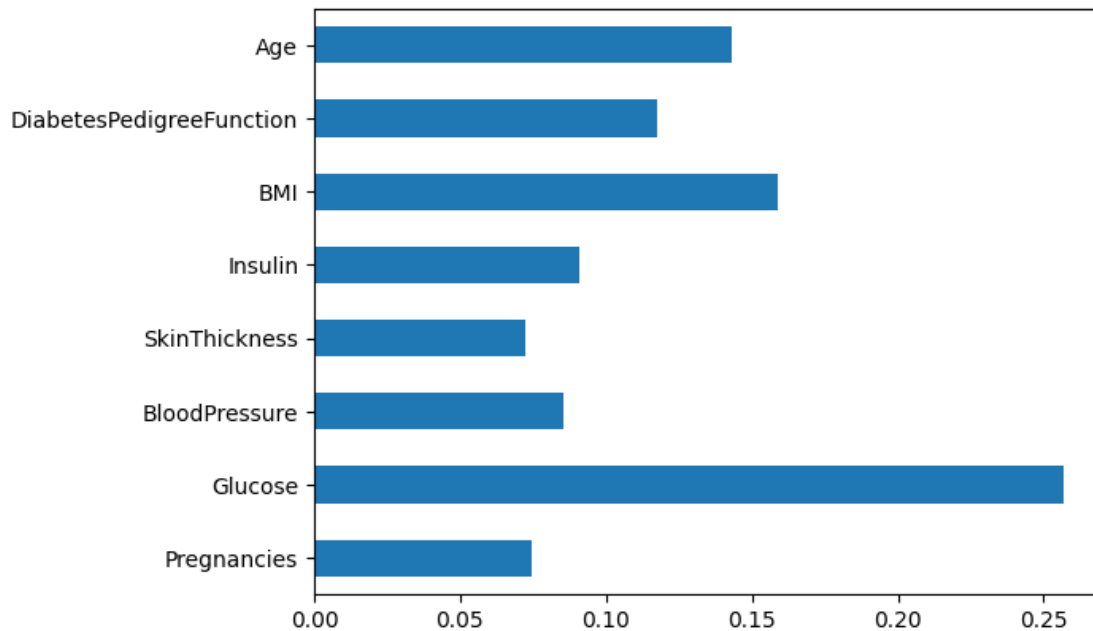
rfc = RandomForestClassifier(n_estimators=200)
rfc.fit(X_train, y_train)
rfc.feature_importances_

array([0.07477938, 0.24613127, 0.08375199, 0.0720271 , 0.09390982,
       0.16086506, 0.12181228, 0.1467231 ])
```

From the above output, it is not clear about feature is important so we will now make a visualization of the same.

```
#Plotting feature importances
(pd.Series(rfc.feature_importances_, index=X.columns).plot(kind='barh'))
```

<Axes: >



*From the above graph, it is clearly visible that Glucose as a feature is the most important in this dataset.*

## 9.Saving Model – Random Forest

```
input_data = (5,166,72,19,175,25.8,0.587,51)
# Change the input_data to numpy array

input_data_as_numpy_array = np.asarray(input_data)
# Reshape the array for one instance

input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

prediction = rfc.predict(input_data_reshaped)
print(prediction)

if (prediction[0] == 0):
    print('The person is not diabetic')
else:
    print('The person is diabetic')

    The person is diabetic
```



## 10. Save the model

```
# Save the trained model

import pickle

filename = 'trained_model.pkl'

pickle.dump(rfc, open(filename, 'wb'))


# Load the saved model

loaded_model = pickle.load(open('trained_model.pkl', 'rb'))
```

---

*our ai prediction system successfully developed*

---

## 2. for deploying python code:

```
import numpy as np
import pickle
import streamlit as st

# Load the saved model
loaded_model = pickle.load(open('trained_model.pkl', 'rb'))

# Create a function for Prediction
def diabetes_prediction(input_data):

    # Change the input_data to numpy array
    input_data_as_numpy_array = np.asarray(input_data)

    # Reshape the array as we are predicting for one instance
    input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

    prediction = loaded_model.predict(input_data_reshaped)
    print(prediction)

    if (prediction[0] == 0):
        return 'The person is not diabetic'
    else:
        return 'The person is diabetic'
```

```

def main():

    # Give a title
    st.title('Diabetes Prediction Web App')

    # To get the input data from the user
    Pregnancies = st.text_input('Number of Pregnancies')
    Glucose = st.text_input('Glucose Level')
    BloodPressure = st.text_input('Blood Pressure value')
    SkinThickness = st.text_input('Skin Thickness value')
    Insulin = st.text_input('Insulin Level')
    BMI = st.text_input('BMI value')
    DiabetesPedigreeFunction = st.text_input('Diabetes Pedigree Function value')
    Age = st.text_input('Age of the Person')

    # Code for Prediction
    diagnosis = ""

    # Create a button for Prediction

    if st.button('Diabetes Test Result'):
        diagnosis = diabetes_prediction([Pregnancies, Glucose, BloodPressure, SkinThickness, Insulin, BMI,
        DiabetesPedigreeFunction, Age])

    st.success(diagnosis)

if __name__ == '__main__':
    main()

```

save this file as app.py

## How to deploy the code on the web app using google colab:

- I. Go to google colab
- II. Import the 'app.py' file
- III. Import the saved model file 'trained\_model.pkl'
- IV. Type the following command

```
!pip install streamlit -q
```

```
!wget -q -O - ipv4.icanhazip.com

! streamlit run app.py & npx localtunnel --port 8501
```

And the result will be



Conclusion:

our AI-based diabetes prediction system, built through innovative techniques and user-centric design, is now fully deployed. This robust tool combines accuracy, transparency, and personalized risk assessment, empowering healthcare professionals and individuals for proactive diabetes management. With continuous updates and adaptability, it stands as a dynamic solution at the forefront of early intervention and improved health outcomes.

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