Fatty liver Prediction

Predict whether a person has fatty liver or not.

Challenges

1. General data analysis.
2. Data preprocessing and cleaning.
3. Split dataset to test & train data.
4. ANN model design.
5. Model Training & evaluation.
6. Prediction
7. Wrong prediction and suggestions for improvement (false negetive/positive).
8. Callbacks APIs (EarlyStopping & ModelCheckpoint)

1. General data analysis

Before training a machine learning model, it's crucial to perform data analysis and preparation. Here are some essential steps.

In [ ]:
```
# Importing essential libraries
import numpy as np
import pandas as pd
```

In [ ]:
```
# Loading the dataset
df = pd.read_csv('data.csv')
df
```

Out[6]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction
0	2	138	62	35	0	33.6	0.127
1	0	84	82	31	125	38.2	0.233
2	0	145	0	0	0	44.2	0.630
3	0	135	68	42	250	42.3	0.365
4	1	139	62	41	480	40.7	0.536
...	...	...	...	...	...	...	...
1995	2	75	64	24	55	29.7	0.370
1996	8	179	72	42	130	32.7	0.719
1997	6	85	78	0	0	31.2	0.382
1998	0	129	110	46	130	67.1	0.319
1999	2	81	72	15	76	30.1	0.547

Exploring the dataset

In [ ]:
```
# Returns number of rows and columns of the dataset
df.shape
```

Out[7]:
```
(2000, 9)
```

In [ ]:
```
# Returns an object with all of the column headers
df.columns
```

Out[8]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insul
in',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

In [ ]:
```
# Returns different datatypes for each columns (float, int, string, bool, e
df.dtypes
```

Out[9]:
```
Pregnancies                   int64
Glucose                       int64
BloodPressure                 int64
SkinThickness                 int64
Insulin                       int64
BMI                         float64
DiabetesPedigreeFunction    float64
Age                           int64
Outcome                       int64
dtype: object
```

In [ ]:
```
# Returns the first x number of rows when head(num). Without a number it re
df.head()
```

Out[10]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Ag
0	2	138	62	35	0	33.6	0.127	4
1	0	84	82	31	125	38.2	0.233	2
2	0	145	0	0	0	44.2	0.630	3
3	0	135	68	42	250	42.3	0.365	2
4	1	139	62	41	480	40.7	0.536	2

In [ ]:
```
# Returns basic information on all columns
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2000 entries, 0 to 1999
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype  
---  ------                    --------------  -----  
 0   Pregnancies               2000 non-null   int64  
 1   Glucose                   2000 non-null   int64  
 2   BloodPressure             2000 non-null   int64  
 3   SkinThickness             2000 non-null   int64  
 4   Insulin                   2000 non-null   int64  
 5   BMI                       2000 non-null   float64
 6   DiabetesPedigreeFunction  2000 non-null   float64
 7   Age                       2000 non-null   int64  
 8   Outcome                   2000 non-null   int64  
dtypes: float64(2), int64(7)
memory usage: 140.8 KB
```

In [ ]:
```
# Returns basic statistics on numeric columns
df.describe().T
```

Out[12]:

	count	mean	std	min	25%	50%	75%	max
Pregnancies	2000.0	3.70350	3.306063	0.000	1.000	3.000	6.000	17.00
Glucose	2000.0	121.18250	32.068636	0.000	99.000	117.000	141.000	199.00
BloodPressure	2000.0	69.14550	19.188315	0.000	63.500	72.000	80.000	122.00
SkinThickness	2000.0	20.93500	16.103243	0.000	0.000	23.000	32.000	110.00
Insulin	2000.0	80.25400	111.180534	0.000	0.000	40.000	130.000	744.00
BMI	2000.0	32.19300	8.149901	0.000	27.375	32.300	36.800	80.60
DiabetesPedigreeFunction	2000.0	0.47093	0.323553	0.078	0.244	0.376	0.624	2.42
Age	2000.0	33.09050	11.786423	21.000	24.000	29.000	40.000	81.00
Outcome	2000.0	0.34200	0.474498	0.000	0.000	0.000	1.000	1.00

In [ ]:
```
# Returns true for a column having null values, else false
df.isnull().any()
```

Out[13]:
```
Pregnancies                 False
Glucose                     False
BloodPressure               False
SkinThickness               False
Insulin                     False
BMI                         False
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

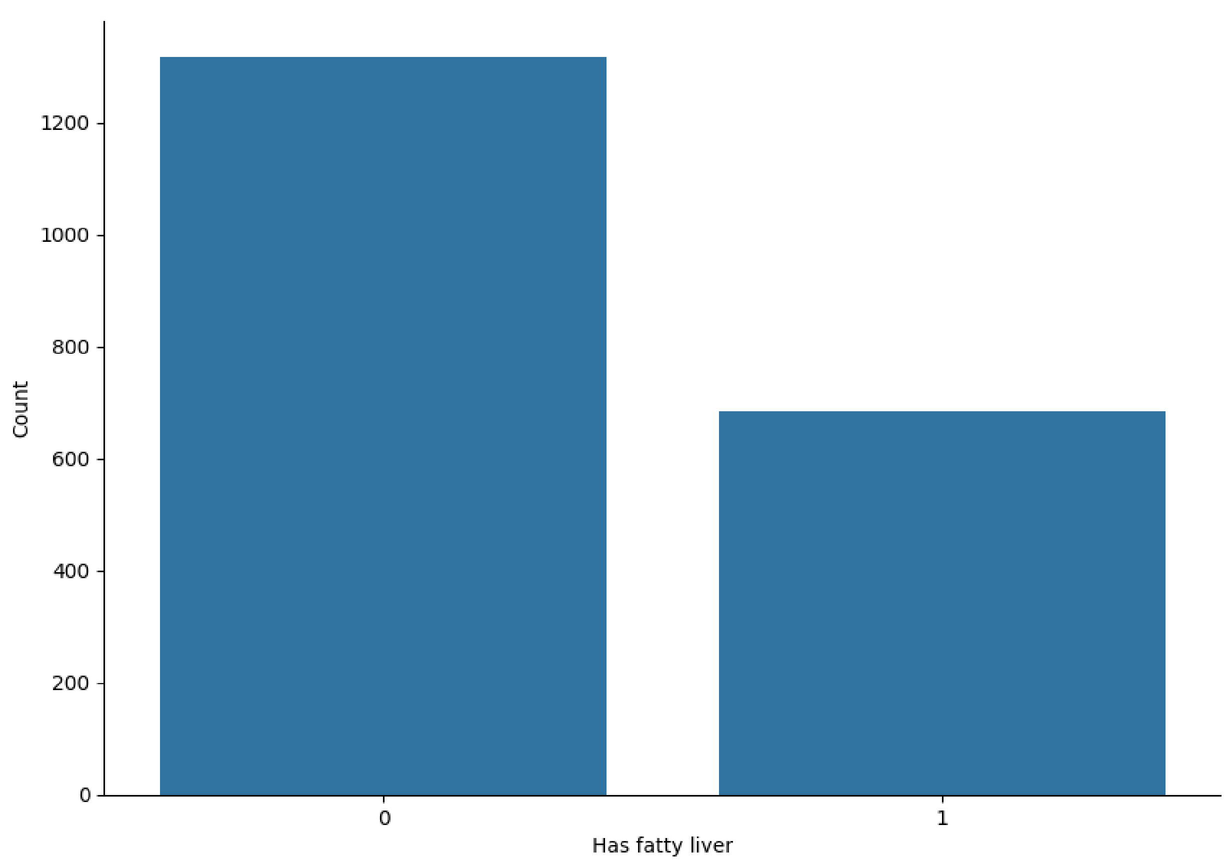
In [ ]:
```
df = df.rename(columns={'DiabetesPedigreeFunction':'DPF'})
df.head()
```

Out[14]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DPF	Age	Outcome
0	2	138	62	35	0	33.6	0.127	47	1
1	0	84	82	31	125	38.2	0.233	23	0
2	0	145	0	0	0	44.2	0.630	31	1
3	0	135	68	42	250	42.3	0.365	24	1
4	1	139	62	41	480	40.7	0.536	21	0

In [ ]:
```
# Importing essential libraries for visualization
import matplotlib.pyplot as plt
import seaborn as sns
```

In [ ]:
```
# Plotting the Outcomes based on the number of dataset entries
plt.figure(figsize=(10,7))
sns.countplot(x='Outcome', data=df)

# Removing the unwanted spines
plt.gca().spines['top'].set_visible(False)
plt.gca().spines['right'].set_visible(False)

# Headings
plt.xlabel('Has fatty liver')
plt.ylabel('Count')

plt.show()
```

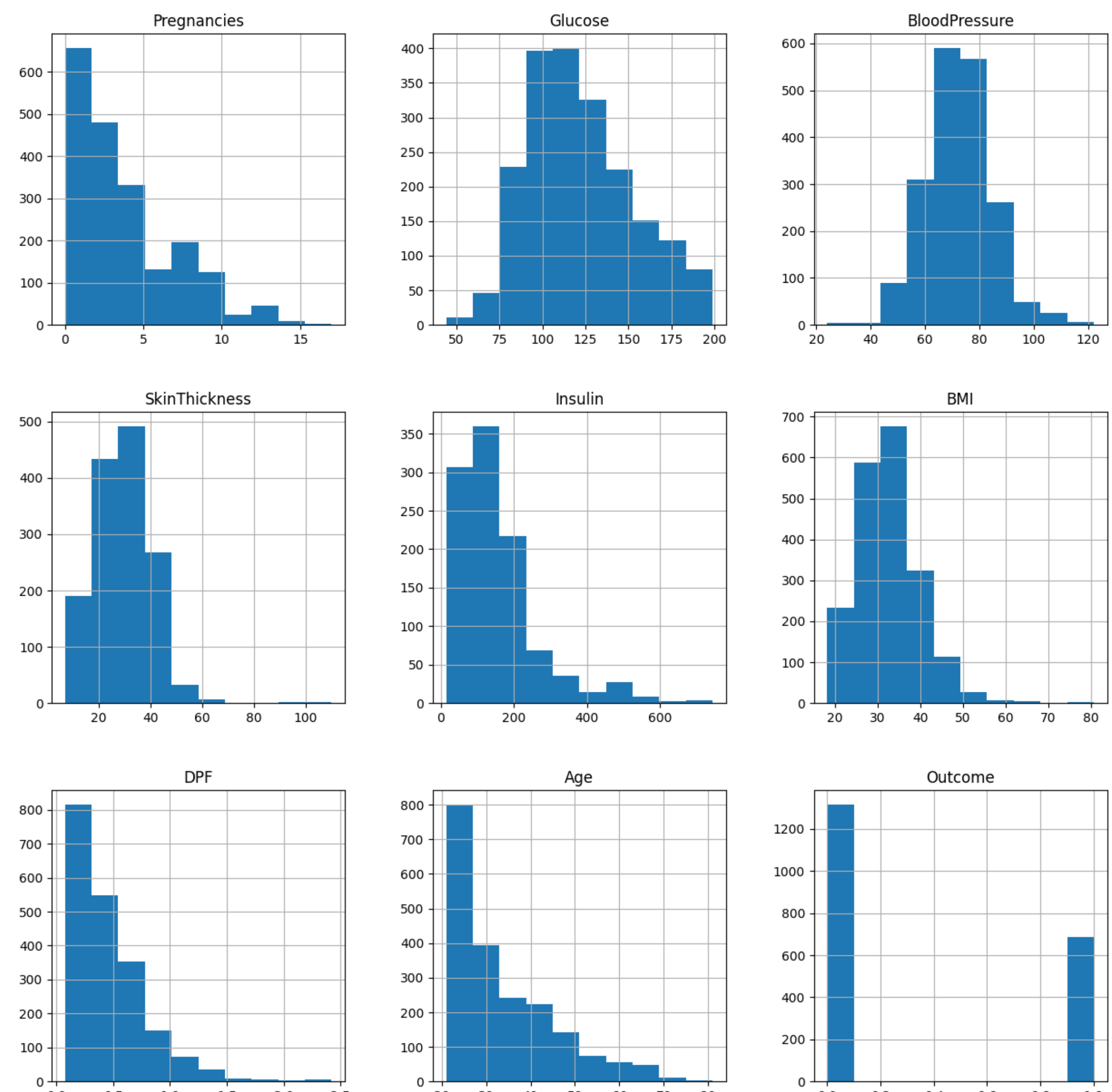


2. Data preprocessing & cleaning

In [ ]:
```
# Replacing the 0 values from ['Glucose','BloodPressure','SkinThickness','I
df_copy = df.copy(deep=True)
df_copy[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']] = df_c
df_copy.isnull().sum()
```

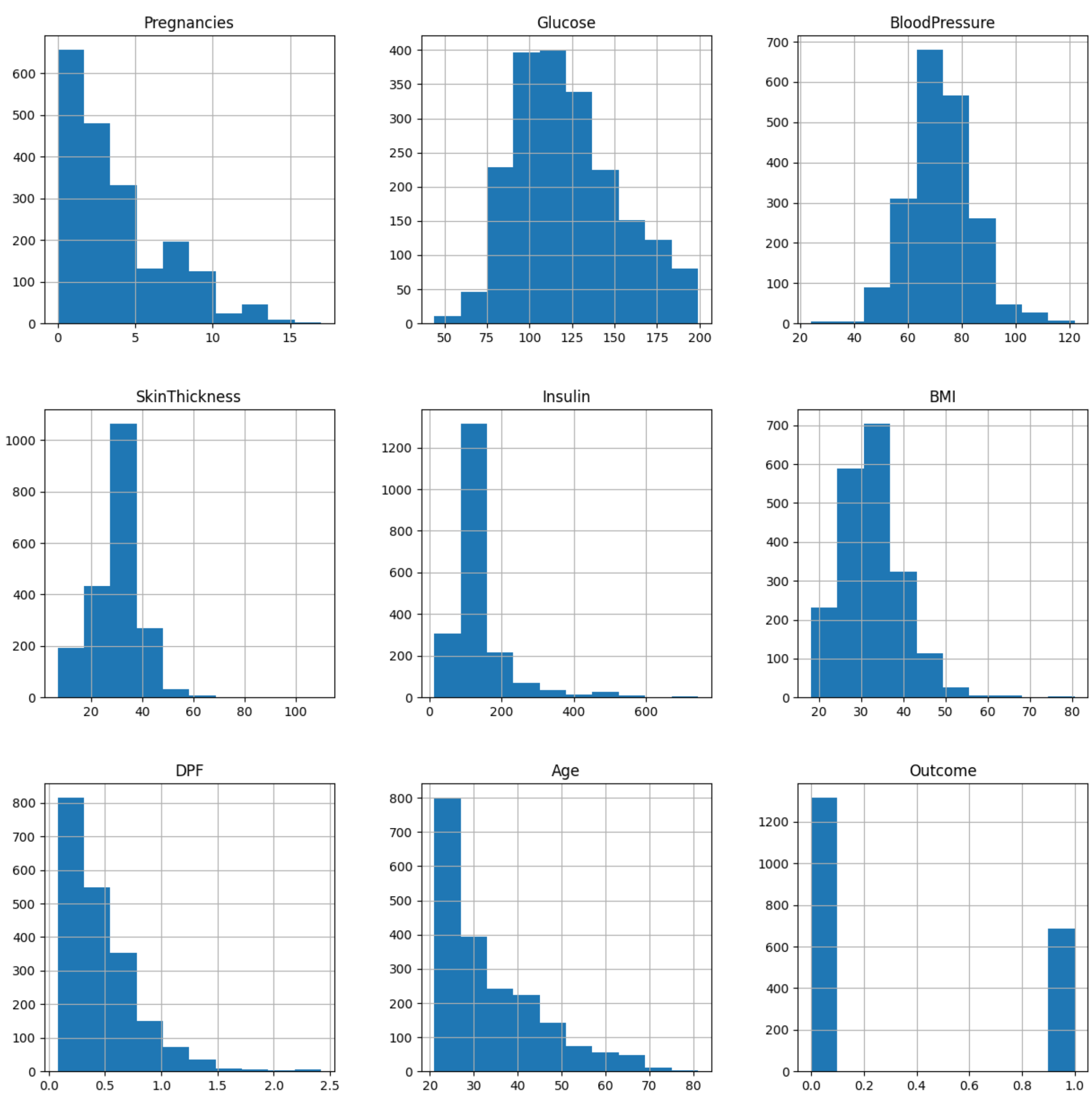
Out[17]:
```
Pregnancies        0
Glucose           13
BloodPressure     90
SkinThickness    573
Insulin          956
BMI               28
DPF                0
Age                0
Outcome            0
dtype: int64
```

In [ ]:
```
# To fill these Nan values the data distribution needs to be understood
# Plotting histogram of dataset before replacing NaN values
p = df_copy.hist(figsize = (15,15))
```



```
In [ ]: # Replacing NaN value by mean, median depending upon distribution
        """ If there is normal(Gaws) or symmetric distribution, replacement by mean
        is better."""

        # If there are outliers, median is better.

        # Replacing by mean
        df_copy['Glucose'].fillna(df_copy['Glucose'].mean(), inplace=True)
        df_copy['BloodPressure'].fillna(df_copy['BloodPressure'].mean(), inplace=Tr
        df_copy['SkinThickness'].fillna(df_copy['SkinThickness'].mean(), inplace=Tr
        df_copy['BMI'].fillna(df_copy['BMI'].mean(), inplace=True)

        #Replacing by median.
        df_copy['Pregnancies'].fillna(df_copy['Pregnancies'].median(), inplace=True
        df_copy['Insulin'].fillna(df_copy['Insulin'].median(), inplace=True)
        df_copy['DPF'].fillna(df_copy['DPF'].median(), inplace=True)
        df_copy['Age'].fillna(df_copy['Age'].median(), inplace=True)
```

```
In [ ]:
        # Plotting histogram of dataset after replacing NaN values

        p = df_copy.hist(figsize = (15,15))
```




```
In [ ]: df_copy.isnull().sum()

Out[21]: Pregnancies       0
         Glucose           0
         BloodPressure     0
         SkinThickness     0
         Insulin           0
         BMI               0
         DPF               0
         Age               0
         Outcome           0
         dtype: int64
```

Prediction about feature importance

The problem is non-linear and each feature importance needs specialized knowledge in the field of medicine or related sciences. However, Features with high variance are likely to be important, as they capture more information about the data.

In [ ]:
```python
feature_variance = df.var()
print(feature_variance)
```

```
Pregnancies          10.930053
Glucose            1028.397392
BloodPressure       368.191425
SkinThickness       259.314432
Insulin           12361.111040
BMI                  66.420881
DPF                   0.104686
Age                 138.919770
Outcome               0.225149
dtype: float64
```

3. Split dataset to test & train data

In [ ]:
```python
# split and standard the data in this place
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

X, y = df_copy[["Pregnancies" , "Glucose" , "BloodPressure" , "SkinThicknes

# Split into train and test
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, ra

# Standardization
sc = StandardScaler()
sc.fit(X_train)
X_train_scaled = sc.transform(X_train)
X_test_scaled = sc.transform(X_test)
```

4. ANN model design

In [ ]:
```python
#create nueral network model in kears/tensorflow in this place

import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense
import keras

model = Sequential()
model.add(Dense(8, activation='relu', input_dim=8))  # Input layer
model.add(Dense(17, activation='tanh'))
model.add(Dense(35, activation='tanh'))
model.add(Dense(35, activation='tanh'))
model.add(Dense(17, activation='tanh'))
model.add(Dense(1, activation='sigmoid'))  # Output layer (binary classific
```

5. Model Training & evaluation

In [ ]:
```
# optimizer and learning rate selection
#optimizer = tf.keras.optimizers.Adam(learning_rate=0.001)

model.compile(optimizer='Adam', loss='binary_crossentropy', metrics=['accur

# Train the model
model.fit(X_train_scaled, y_train, epochs=300, batch_size=64)

# Storing training steps and epochs in order to plot in the future
history = model.fit(X_train_scaled, y_train, epochs=300, batch_size=64, val
```

```
Epoch 1/300
25/25 [==============================] - 1s 3ms/step - loss: 0.5885 - acc
uracy: 0.6756
Epoch 2/300
25/25 [==============================] - 0s 3ms/step - loss: 0.5161 - acc
uracy: 0.7400
Epoch 3/300
25/25 [==============================] - 0s 3ms/step - loss: 0.4968 - acc
uracy: 0.7469
Epoch 4/300
25/25 [==============================] - 0s 3ms/step - loss: 0.4828 - acc
uracy: 0.7600
Epoch 5/300
25/25 [==============================] - 0s 3ms/step - loss: 0.4746 - acc
uracy: 0.7619
Epoch 6/300
25/25 [==============================] - 0s 3ms/step - loss: 0.4649 - acc
uracy: 0.7731
Epoch 7/300
```

Evaluation

In [ ]:
```
# evaluation your model in this place
from sklearn.metrics import confusion_matrix, classification_report, accura

threshold = 0.5
y_pred = model.predict(X_test_scaled)
y_pred_binary = (y_pred > threshold).astype(int)

# Confusion matrix
matrix = confusion_matrix(y_test, y_pred_binary)
matrix
```

```
13/13 [==============================] - 0s 2ms/step
```

Out[521]:
```
array([[248,   5],
       [  0, 147]])
```

In [ ]:
```
# Classification report
target_names = ['class 1', 'class 2']
print(classification_report(y_test, y_pred_binary, target_names=target_name
```

```
              precision    recall  f1-score   support

     class 1       1.00      0.98      0.99       253
     class 2       0.97      1.00      0.98       147

    accuracy                           0.99       400
   macro avg       0.98      0.99      0.99       400
weighted avg       0.99      0.99      0.99       400
```

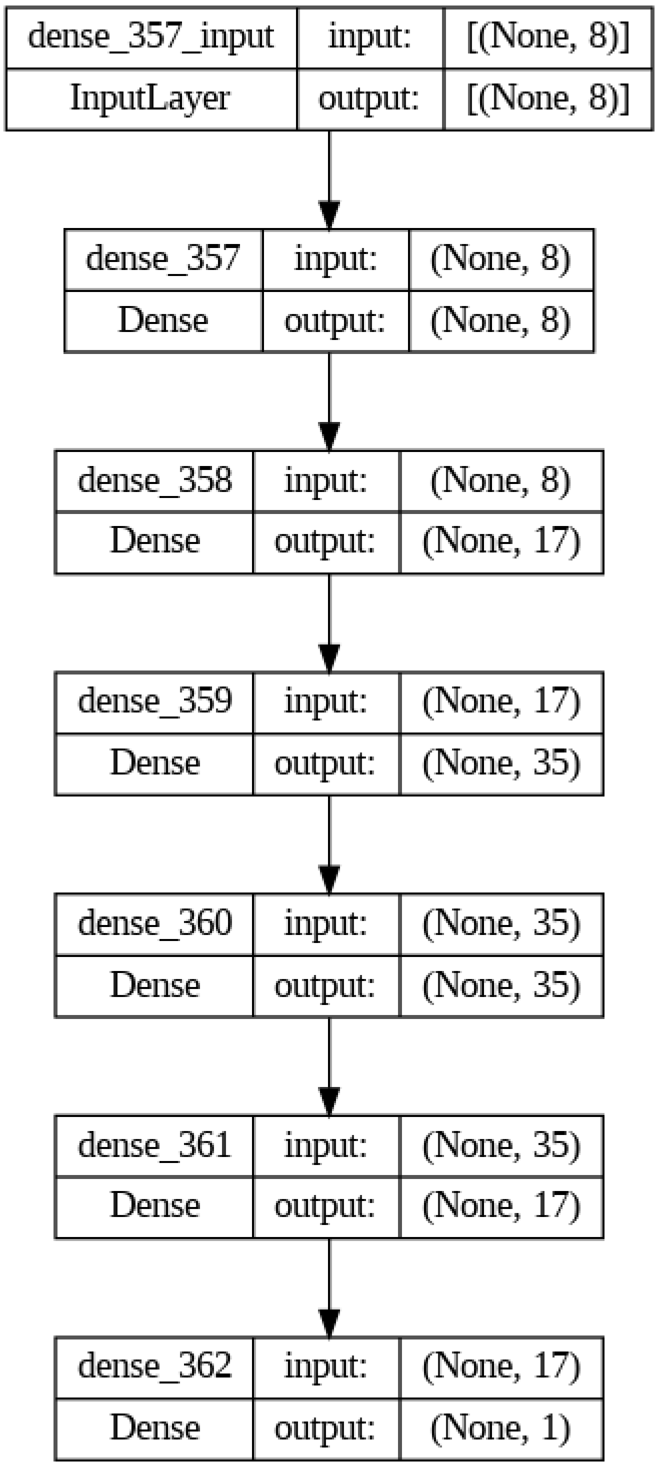
In [ ]:
```
# Overall accuracy score

accuracy = accuracy_score(y_test, y_pred_binary)
accuracy
```

Out[523]:
```
0.9875
```

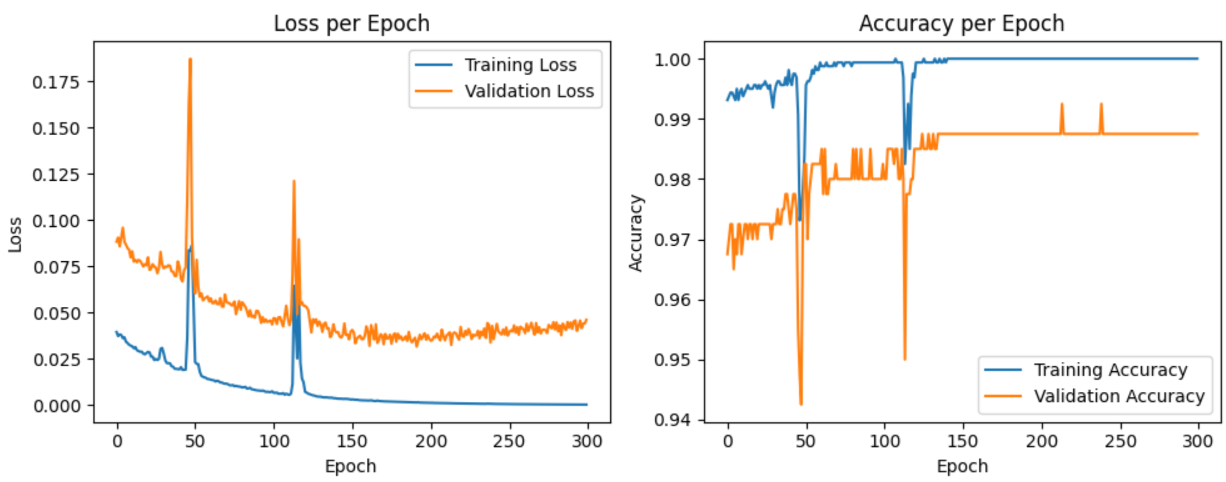
Visualization

In [ ]:
```
keras.utils.plot_model(model, to_file='model.png', show_shapes=True, show_l
```

Out[526]:



In [ ]:
```
# Loss per epoch plot
plt.figure(figsize=(10, 4))
plt.subplot(1, 2, 1)
plt.plot(history.history['loss'], label='Training Loss')
plt.plot(history.history['val_loss'], label='Validation Loss')
plt.xlabel('Epoch')
plt.ylabel('Loss')
plt.title('Loss per Epoch')
plt.legend()

# Accuracy per epoch plot
plt.subplot(1, 2, 2)
plt.plot(history.history['accuracy'], label='Training Accuracy')
plt.plot(history.history['val_accuracy'], label='Validation Accuracy')
plt.xlabel('Epoch')
plt.ylabel('Accuracy')
plt.title('Accuracy per Epoch')
plt.legend()

plt.tight_layout()
plt.show()
```



6. Prediction

In [ ]:
```
# Creating a function for prediction
def predict_diabetes(Pregnancies, Glucose, BloodPressure, SkinThickness, In
    preg = int(Pregnancies)
    glucose = float(Glucose)
    bp = float(BloodPressure)
    st = float(SkinThickness)
    insulin = float(Insulin)
    bmi = float(BMI)
    dpf = float(DPF)
    age = int(Age)

    x = [[preg, glucose, bp, st, insulin, bmi, dpf, age]]
    x = sc.transform(x)
    prediction = model.predict(x)
    binary_prediction = (y_pred > 0.5).astype(int)
    return binary_prediction
```

In [ ]:
```
# Prediction 1 // this sample didnt have fatty liver
# Input sequence: Pregnancies, Glucose, BloodPressure, SkinThickness, Insul
prediction = predict_diabetes(2, 81, 72, 15, 76, 30.1, 0.547, 25)[0]
if prediction:
  print('Oops! You have fatty liver.')
else:
  print("Great! You don't have fatty liver.")
```

```
1/1 [==============================] - 0s 27ms/step
Oops! You have fatty liver.

/usr/local/lib/python3.10/dist-packages/sklearn/base.py:439: UserWarning:
X does not have valid feature names, but StandardScaler was fitted with f
eature names
  warnings.warn(
```

7. Wrong prediction and suggestions for improvement (false negetive/positive).

Confusion matrix visualize the performance of the algorithm and represents the reliability of the model in prediction. In this problem, false negetive is more critical.

By implementing some of the strategies below, the values in the confusion matrix can be improved and the number of wrong predictions may be reduced.

1. Collect and preprocess high-quality large datasets.
2. Hyperparameters tuning.
3. Cross validation.
4. Study about choosing a different value of threshold.

8. Callbacks APIs (EarlyStopping & ModelCheckpoint)

According to developer's documentation, a callback is an object that can perform actions at various stages of training. These stages and point are:

1. At the start and end of training
2. At the start and end of each epoch
3. At the start and end of each batch
4. At the start and end of testing or prediction

One of its applications is hyperparameter tuning such as finding the optimum learning rate or activation function.

There are many callbacks available. These APIs are listed below.

1. Base Callback class
2. ModelCheckpoint
3. BackupAndRestore
4. TensorBoard
5. EarlyStopping
6. LearningRateScheduler
7. ReduceLROnPlateau
8. RemoteMonitor
9. LambdaCallback
10. TerminateOnNaN
11. CSVLogger
12. ProgbarLogger
13. SwapEMAWeights

It's also possible to create custom callbacks APIs(objects).

ModelCheckpoint

This callback is used to save the state of a model's training or its weight metrics at any point of training. They can be loaded later to continue the training from the state saved.

EarlyStopping

This API Stops training when the objective function or monitored metric has stopped improving. For example if the loss function is assumed as the objective function, it has to get minimized.