PROJECT
PROSTATE CANCER
PREDICTION

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NEURAL NETWORK MODEL FOR PROSTATE CANCER PREDICTION

Project Introduction

Prostate canceris a major healthconcern for men, and early identification of risk factors plays an important role in diagnosis and treatment planning. Clinical measurements such as tumor volume, prostate size, PSA levels, and Gleason score are commonly used by doctors to assess the progression and severity of prostate cancer. However, interpreting these medical variables together can be challenging due to complex relationships among them.

In this project, we use a Neural Network (NN) model to predict prostate cancer severity using a structured medical dataset containing 97 patient samples and 10 clinical features. These features include several log-transformed measurements that represent tumor characteristics and biochemical markers:

- **lcavol** – log cancer volume
- **lweight** – log prostate weight
- **age** – patient's age
- **lbph** – log of benign prostatic hyperplasia
- **svi** – seminal vesicle invasion (0 = no, 1 = yes)
- **lcp** – log capsular penetration
- **gleason** – Gleason score (cancer aggressiveness)
- **pgg45** – percentage of Gleason patterns 4 or 50
- **lpsa** – log PSA (prostate-specific antigen)
- **target** – final cancer severity class label

  1 = cancer present / higher severity

  0 = low-risk or no cancer

These features represent a combination of laboratory tests, biopsy results, and patient- specific clinical markers. Because medical data is often non-linear and multidimensional, a neural network is an ideal model to learn hidden patterns and distinguish between benign and cancerous outcomes effectively.

The main objectives of this project are:

- Perform Exploratory Data Analysis (EDA) to understand the patterns and distribution of clinical features.
  Preprocess the data by handling missing values, encoding, and feature scaling.
- Build and train a simple feed-forward Neural Network using TensorFlow/Keras.
- Evaluate model performance using accuracy, loss curves.
- This project demonstrates how deep learning techniques can support medical decision-making by providing insights and predictions based on clinical data

IMPORT REQUIRED LIBRARIES

```
import numpy as np import pandas as pd
import matplotlib.pyplot as plt import
seaborn as sns

from sklearn.model_selection import train_test_split from sklearn.preprocessing import
LabelEncoder, OneHotEncoder, StandardScaler


from tensorflow.keras.models import Sequential from
tensorflow.keras.optimizers import Adam from
tensorflow.keras.layers import Dense, Dropout from
tensorflow.keras.callbacks import EarlyStopping
```

LOAD THE DATASET

```
df = pd.read_csv('/content/drive/MyDrive/prostate.csv')
```

```
df.head()
```

	lcavol	lweight	age	lbph	svi	lcp	gleason	pgg45	lpsa	train
0	-0.579818	2.769459	50	-1.386294	0	-1.386294	6	0	-0.430783	True
1	-0.994252	3.319626	58	-1.386294	0	-1.386294	6	0	-0.162519	True
2	-0.510826	2.691243	74	-1.386294	0	-1.386294	7	20	-0.162519	True
3	-1.203973	3.282789	58	-1.386294	0	-1.386294	6	0	-0.162519	True
4	0.751416	3.432373	62	-1.386294	0	-1.386294	6	0	0.371564	True

```
df.tail()
```

	lcavol	lweight	age	lbph	svi	lcp	gleason	pgg45	lpsa	train
92	2.830268	3.876396	68	-1.386294	1	1.321756	7	60	4.385147	True
93	3.821004	3.896909	44	-1.386294	1	2.169054	7	40	4.684443	True
94	2.907447	3.396185	52	-1.386294	1	2.463853	7	10	5.143124	False
95	2.882564	3.773910	68	1.558145	1	1.558145	7	80	5.477509	True
96	3.471966	3.974998	68	0.438255	1	2.904165	7	20	5.582932	False

```
df.shape
```

(97, 10)

```
df.info()
```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 97 entries, 0 to 96
Data columns (total 10 columns):

	Column	Non-Null Count	Dtype
0	lcavol	97 non-null	float64
1	lweight	97 non-null	float64
2	age	97 non-null	int64
3	lbph	97 non-null	float64
4	svi	97 non-null	int64
5	lcp	97 non-null	float64
6	gleason	97 non-null	int64
7	pgg45	97 non-null	int64
8	lpsa	97 non-null	float64
9	train	97 non-null	bool

dtypes: bool(1), float64(5), int64(4)
memory usage: 7.0 KB

EXPLORATORY DATA ANALYSIS (EDA)

```
# Encode the boolean values : True - 1 & False - 0
df['train'] = df['train'].astype(int)
```

```
# Rename the columns to 'Target' df =
df.rename(columns={'train': 'target'})
```

```
df['target'].value_counts()
```

TARGET	COUNT
1	67
0	30

DTYPE: INT64

TARGET VARIABLE (1 = CANCER PRESENCE/SEVERITY, 0 = NO/LOW-RISK CANCER)

```
df
```

	LCAVOL	LWEIGHT	AGE	LBPH	SVI	LCP	GLEASON	PGG45	LPSA	TARGET
0	-0.579818	2.769459	50	-1.386294	0	-1.386294	6	0	-0.430783	1
1	-0.994252	3.319626	58	-1.386294	0	-1.386294	6	0	-0.162519	1
2	-0.510826	2.691243	74	-1.386294	0	-1.386294	7	20	-0.162519	1
3	-1.203973	3.282789	58	-1.386294	0	-1.386294	6	0	-0.162519	1
4	0.751416	3.432373	62	-1.386294	0	-1.386294	6	0	0.371564	1
...	...	...	...	...	...	...	...	...	...	...
92	2.830268	3.876396	68	-1.386294	1	1.321756	7	60	4.385147	1
93	3.821004	3.896909	44	-1.386294	1	2.169054	7	40	4.684443	1
94	2.907447	3.396185	52	-1.386294	1	2.463853	7	10	5.143124	0
95	2.882564	3.773910	68	1.558145	1	1.558145	7	80	5.477509	1
96	3.471966	3.974998	68	0.438255	1	2.904165	7	20	5.582932	0

97 rows × 10 columns

```
df.describe()
```

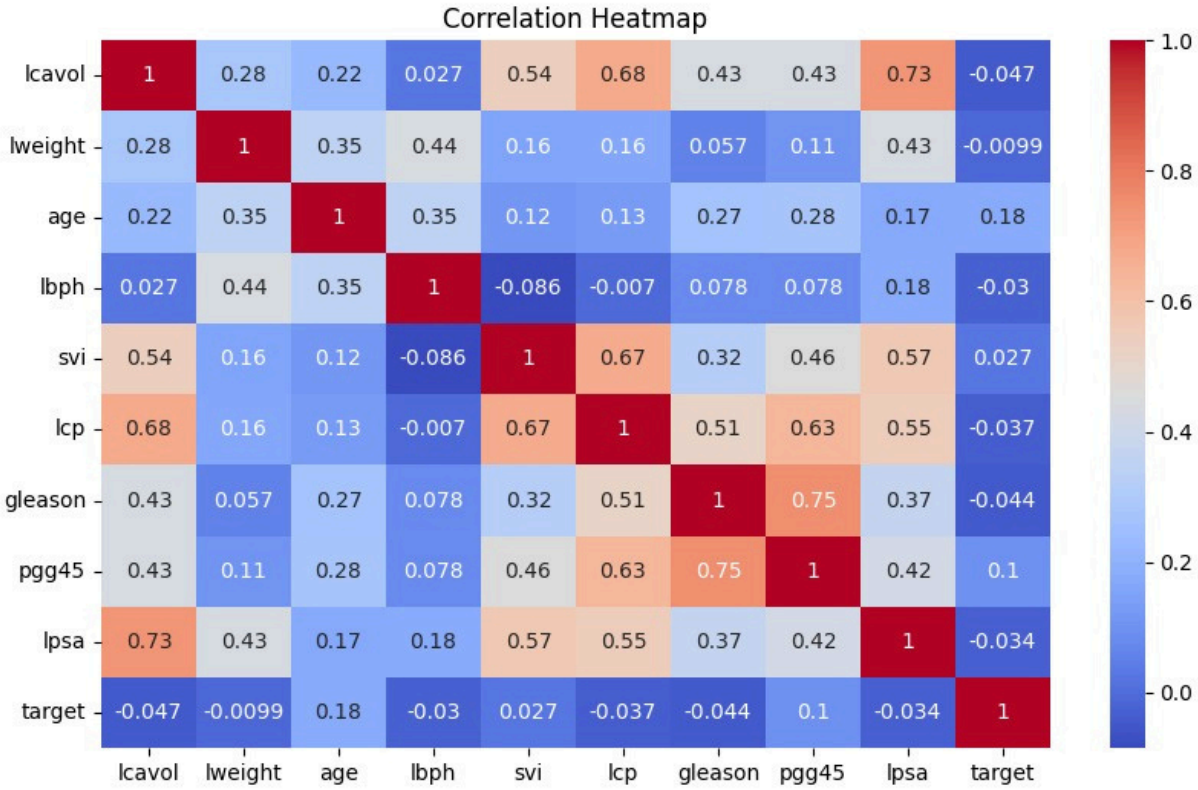
	lcavol	lweight	age	lbph	svi	lcp	gleason	pg
count	97.000000	97.000000	97.000000	97.000000	97.000000	97.000000	97.000000	97.000
mean	1.350010	3.628943	63.865979	0.100356	0.216495	-0.179366	6.752577	24.381
std	1.178625	0.428411	7.445117	1.450807	0.413995	1.398250	0.722134	28.204
min	-1.347074	2.374906	41.000000	-1.386294	0.000000	-1.386294	6.000000	0.000
25%	0.512824	3.375880	60.000000	-1.386294	0.000000	-1.386294	6.000000	0.000
50%	1.446919	3.623007	65.000000	0.300105	0.000000	-0.798508	7.000000	15.000
75%	2.127041	3.876396	68.000000	1.558145	0.000000	1.178655	7.000000	40.000
max	3.821004	4.780383	79.000000	2.326302	1.000000	2.904165	9.000000	100.000

```
df.isnull().sum()
```

	0
lcavol	0
lweight	0
age	0
lbph	0
svi	0
lcp	0
gleason	0
pgg45	0
lpsa	0
target	0

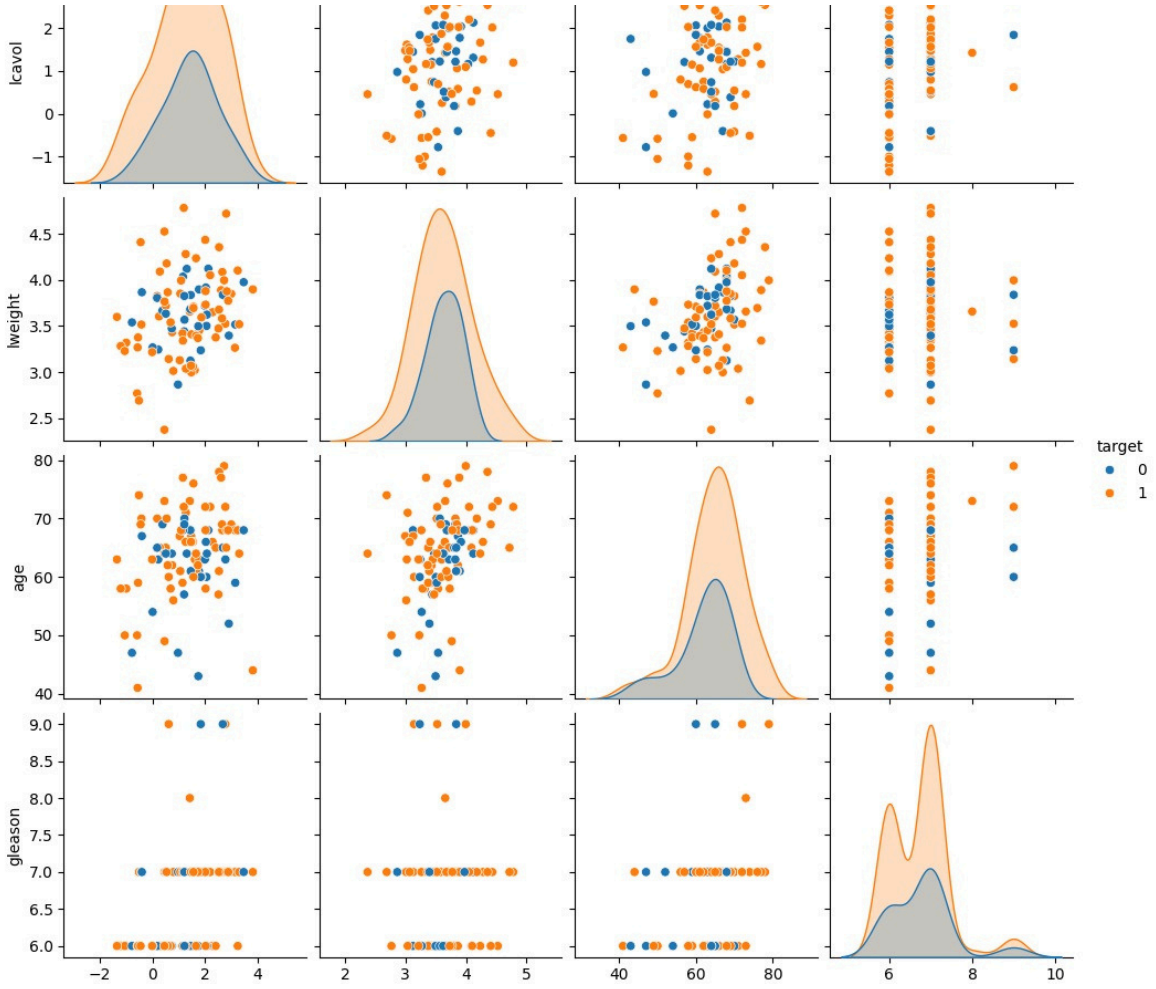
dtype: int64

```
# Correlation Heatmap plt.figure(figsize=(10, 6))
sns.heatmap(df.corr(), annot=True, cmap='coolwarm')
plt.title('Correlation Heatmap') plt.show()
```



Pairplot

```
sns.pairplot(df,vars=["lcavol","lweight",'age','gleason'], hue="target") plt.show()
```



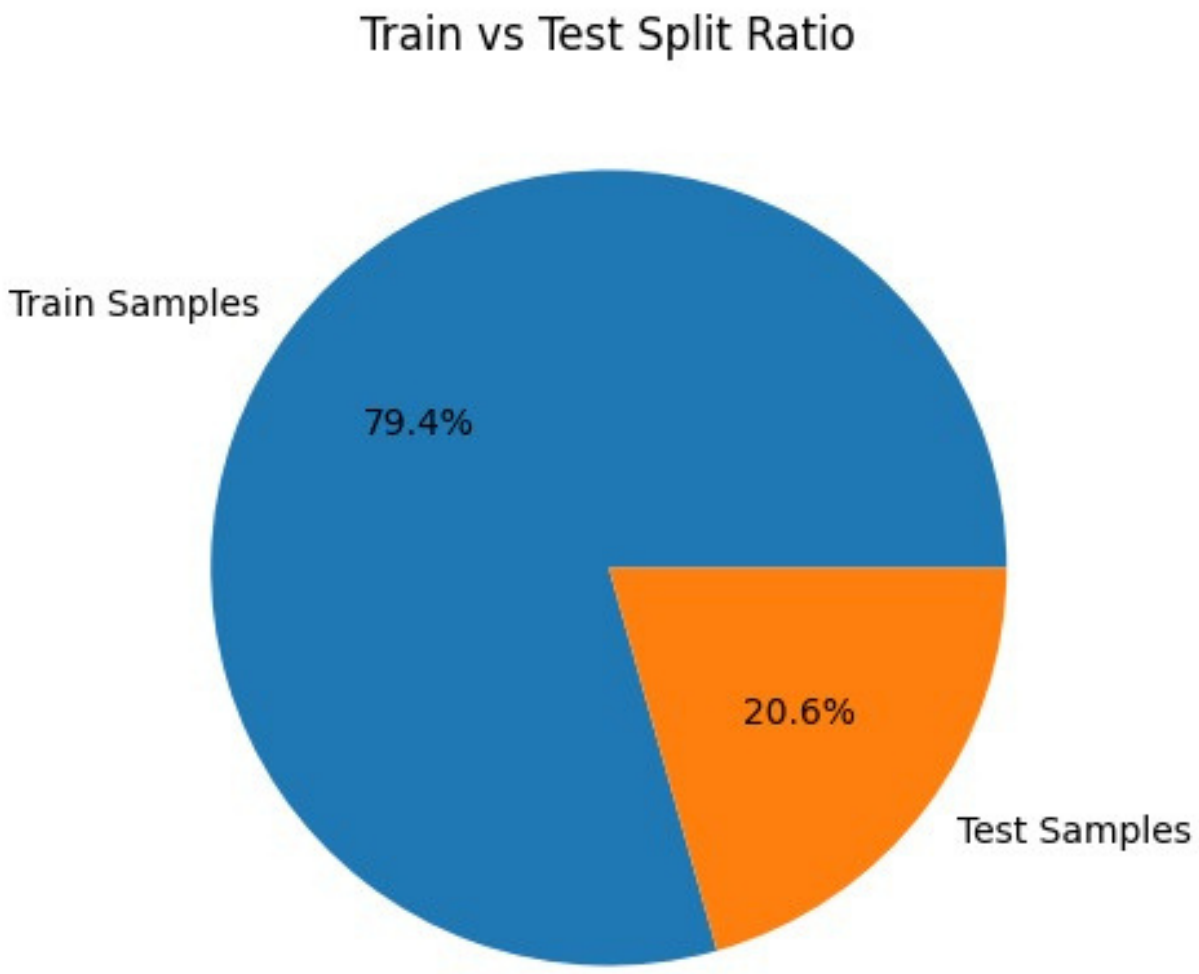
Train-Test Split

```
X = df.drop('target', axis=1) y =
df['target']
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_sta
```

```
plt.figure(figsize=(5,5)) sizes = [len(X_train), len(X_test)]
labels = ['Train Samples', 'Test Samples']

plt.pie(sizes, labels=labels, autopct='%1.1f%%')
plt.title("Train vs Test Split Ratio")
plt.show()
```



Feature Scaling

```
scaler = StandardScaler() X_train =
scaler.fit_transform(X_train) X_test =
scaler.transform(X_test)
```

BUILDING THE MODEL

```
model = Sequential([
  Dense(128, activation='relu', input_shape=(X_train.shape[1],)),  # First layer
  Dropout(0.2),                                                    # Dropout to prevent overfitting
  Dense(64, activation='relu'),                                    # Second layer
  Dropout(0.2),                                                    # Dropout
  Dense(32, activation='relu'),                                    # Third layer
  Dropout(0.1),                                                    # Light dropout
  Dense(1, activation='sigmoid')                                   # Output (binary)
])
```

```
/usr/local/lib/python3.12/dist-packages/keras/src/layers/core/dense.py:93: UserWarni
ng: Do not pass an `input_shape`/`input_dim` argument to a layer. When using Sequent
ial models, prefer using an `Input(shape)` object as the first layer in the model in
stead.
super().__init__(activity_regularizer=activity_regularizer, **kwargs)
```

Compile the model

```
model.compile(optimizer='adam',loss='binary_crossentropy',metrics=['accuracy'])
```

Train the model

```
early_stop = EarlyStopping(monitor='val_loss', patience=20, restore_best_weights=Tr

history = model.fit(X_train, y_train,epochs=40,batch_size=16,validation_split=0.2,c
```

```
Epoch 1/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 2s 75ms/step - accuracy: 0.5787 - loss: 0.6832 - val_accura
cy: 0.8125 - val_loss: 0.6213
Epoch 2/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 24ms/step - accuracy: 0.6215 - loss: 0.6412 - val_accura
cy: 0.8125 - val_loss: 0.5978
Epoch 3/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 21ms/step - accuracy: 0.6037 - loss: 0.6526 - val_accura
cy: 0.8125 - val_loss: 0.5842
Epoch 4/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 21ms/step - accuracy: 0.6685 - loss: 0.6501 - val_accura
cy: 0.8125 - val_loss: 0.5643
Epoch 5/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 37ms/step - accuracy: 0.6516 - loss: 0.6076 - val_accura
cy: 0.8125 - val_loss: 0.5451
Epoch 6/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 66ms/step - accuracy: 0.6099 - loss: 0.6351 - val_accura
cy: 0.8125 - val_loss: 0.5299
Epoch 7/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 113ms/step - accuracy: 0.6456 - loss: 0.6090 - val_accur
acy: 0.8125 - val_loss: 0.5143
Epoch 8/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 1s 109ms/step - accuracy: 0.6224 - loss: 0.6026 - val_accur
acy: 0.8125 - val_loss: 0.5031
Epoch 9/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 1s 151ms/step - accuracy: 0.6849 - loss: 0.5471 - val_accur
acy: 0.8125 - val_loss: 0.4948
Epoch 10/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 60ms/step - accuracy: 0.6477 - loss: 0.5974 - val_accura
cy: 0.8125 - val_loss: 0.4933
Epoch 11/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 96ms/step - accuracy: 0.5769 - loss: 0.6355 - val_accura
cy: 0.8125 - val_loss: 0.5004
Epoch 12/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 84ms/step - accuracy: 0.6310 - loss: 0.5988 - val_accura
cy: 0.8125 - val_loss: 0.5041
Epoch 13/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 84ms/step - accuracy: 0.6685 - loss: 0.5483 - val_accura
cy: 0.8125 - val_loss: 0.5065
Epoch 14/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 89ms/step - accuracy: 0.6456 - loss: 0.5661 - val_accura
cy: 0.8125 - val_loss: 0.5089
Epoch 15/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 78ms/step - accuracy: 0.6370 - loss: 0.5832 - val_accura
cy: 0.8125 - val_loss: 0.5123
Epoch 16/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 76ms/step - accuracy: 0.6918 - loss: 0.5166 - val_accura
cy: 0.8125 - val_loss: 0.5158
Epoch 17/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 93ms/step - accuracy: 0.6400 - loss: 0.5909 - val_accura
cy: 0.7500 - val_loss: 0.5266
Epoch 18/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 1s 67ms/step - accuracy: 0.6885 - loss: 0.5353 - val_accura
cy: 0.7500 - val_loss: 0.5329
Epoch 19/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 51ms/step - accuracy: 0.7070 - loss: 0.5380 - val_accura
```

```
cy: 0.7500 - val_loss: 0.5387
Epoch 20/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 55ms/step - accuracy: 0.6861 - loss: 0.5206 - val_accura
cy: 0.7500 - val_loss: 0.5483
Epoch 21/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 49ms/step - accuracy: 0.7367 - loss: 0.4812 - val_accura
cy: 0.7500 - val_loss: 0.5551
Epoch 22/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 51ms/step - accuracy: 0.6674 - loss: 0.5120 - val_accura
cy: 0.6250 - val_loss: 0.5653
Epoch 23/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 37ms/step - accuracy: 0.7531 - loss: 0.4652 - val_accura
cy: 0.6250 - val_loss: 0.5699
Epoch 24/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 58ms/step - accuracy: 0.7135 - loss: 0.4584 - val_accura
cy: 0.6250 - val_loss: 0.5764
Epoch 25/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 63ms/step - accuracy: 0.8023 - loss: 0.4312 - val_accura
cy: 0.6875 - val_loss: 0.5859
Epoch 26/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 76ms/step - accuracy: 0.7263 - loss: 0.5296 - val_accura
cy: 0.6875 - val_loss: 0.5982
Epoch 27/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 70ms/step - accuracy: 0.6933 - loss: 0.4829 - val_accura
cy: 0.6875 - val_loss: 0.6012
Epoch 28/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 38ms/step - accuracy: 0.7925 - loss: 0.4421 - val_accura
cy: 0.6875 - val_loss: 0.6150
Epoch 29/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 80ms/step - accuracy: 0.7481 - loss: 0.4494 - val_accura
cy: 0.6875 - val_loss: 0.6222
Epoch 30/40
4/4 ━━━━━━━━━━━━━━━━━━━━ 0s 54ms/step - accuracy: 0.8722 - loss: 0.4013 - val_accura
cy: 0.6875 - val_loss: 0.6308
```

Evaluate the Model on Test Data

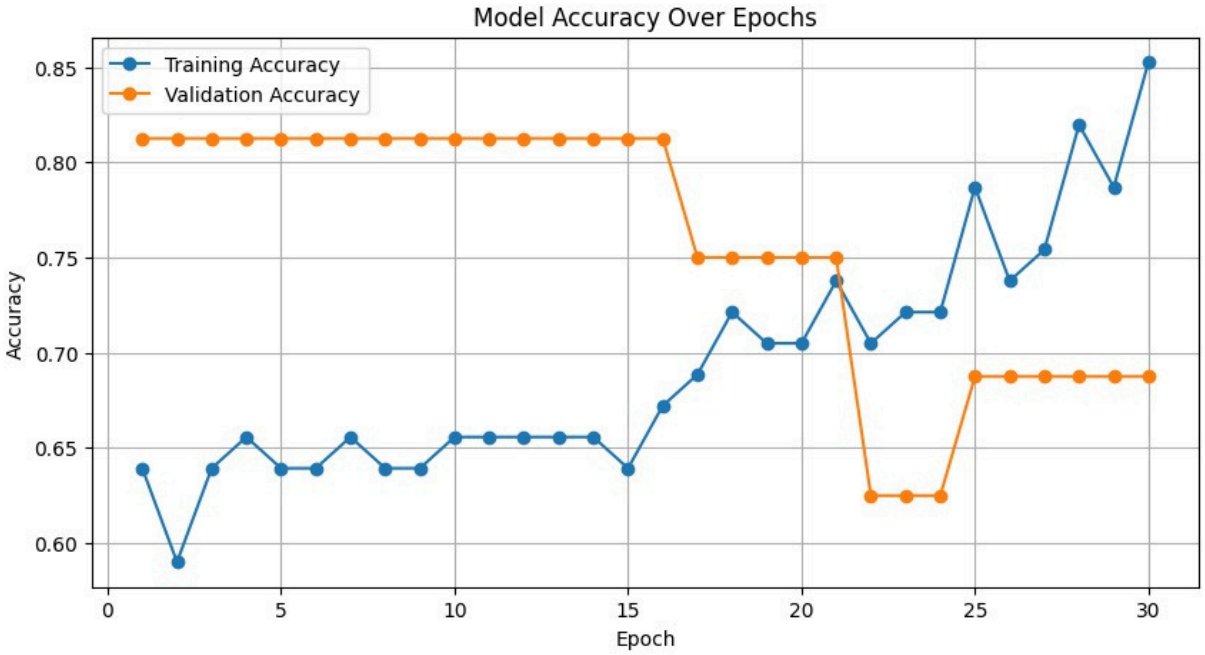
```
# Evaluate model on unseen test data
test_loss, test_accuracy = model.evaluate(X_test, y_test, verbose=1)

print("Test Accuracy:", test_accuracy)
print("Test Loss:", test_loss)
```

```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 458ms/step - accuracy: 0.7500 - loss: 0.6806
Test Accuracy: 0.75
Test Loss: 0.6805676221847534
```

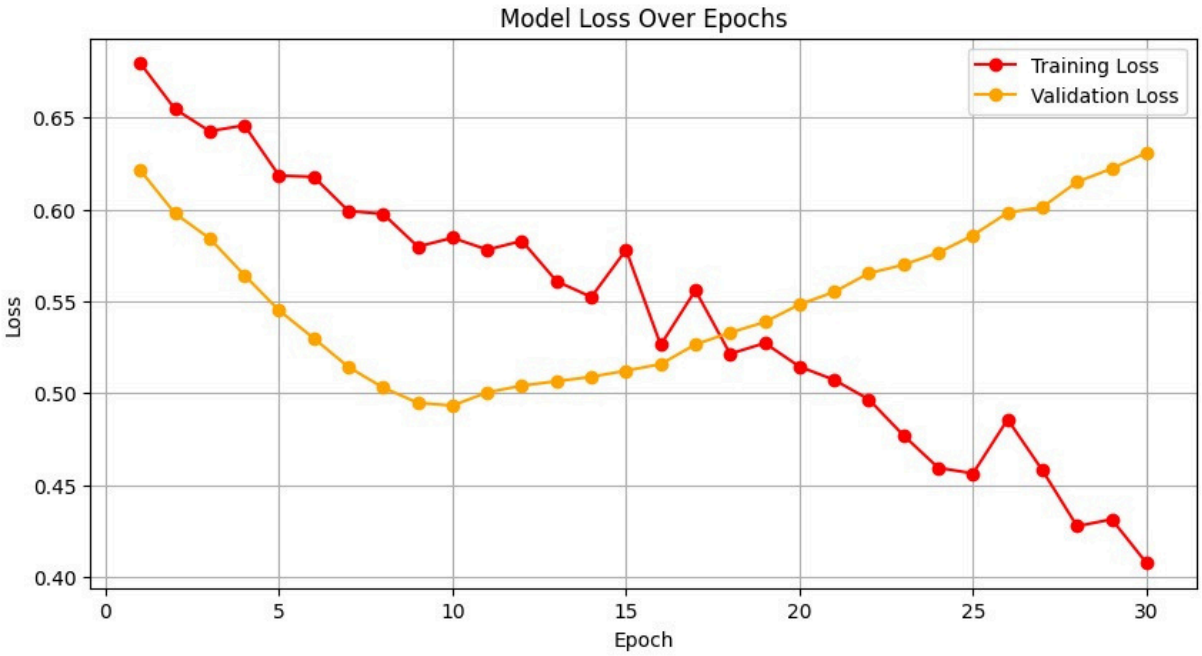
AccuracyCurve

```
plt.figure(figsize=(10, 5))
epochs = range(1, len(history.history['accuracy']) + 1)
plt.plot(epochs, history.history['accuracy'], label='Training Accuracy', marker='o')
plt.plot(epochs, history.history['val_accuracy'], label='Validation Accuracy', marker='o')
plt.title('Model Accuracy Over Epochs')
plt.xlabel('Epoch')
plt.ylabel('Accuracy')
plt.legend()
plt.grid(True)
plt.show()
```



Loss Curve

```
plt.figure(figsize=(10, 5))
epochs = range(1, len(history.history['loss']) + 1)
plt.plot(epochs, history.history['loss'], label='Training Loss', marker='o', color='red')
plt.plot(epochs, history.history['val_loss'], label='Validation Loss', marker='o', color='orange')
plt.title('Model Loss Over Epochs')
plt.xlabel('Epoch')
plt.ylabel('Loss')
plt.legend()
plt.grid(True)
plt.show()
```



Conclusion

Overall,this projectshows that a neural network can help predict prostate cancer severity using simple medical measurements. Even though we used a small dataset, the model still reached about 75% accuracy, which means it is able to correctly classify many patient cases. This proves that machine learning can support doctors by giving early insights, but the results can become even better if we use a larger dataset, balance the classes, or test more advanced models. In short, this project is a good starting point for using AI in prostate cancer prediction, and there is clear potential for improvement in future work.