

The slide features a light gray background with several geometric elements. In the top left, there is a light blue hexagon and a small dark green hexagon. In the top center, there is a large green hexagon. In the bottom center, there is a small green hexagon. On the right side, there is a large, abstract composition of overlapping triangles in various shades of blue, ranging from light to dark. The text 'AKASH .S' is in black, and 'Final Project' is in a bold green font, both positioned to the right of the central hexagons.

AKASH .S Final Project

LIVER DISEASE PREDICTION USING DEEPLEARNING

AGENDA

1. Problem statement
2. Project overview
3. Who are the end users
4. Your solution and its value proposition
5. The wow in the project
6. Modelling
7. Conclusion
8. references



PROBLEM STATEMENT



1. The problem statement for liver disease detection using deep learning involves developing a robust and accurate model that can effectively analyze diverse medical data to detect the presence of liver diseases in patients.
2. This includes designing a system capable of processing various types of patient information, such as demographics, medical history, laboratory test results, and imaging data, to provide reliable diagnostic predictions.



PROJECT OVERVIEW

1. Develop a deep learning model to accurately detect liver diseases from medical data.
2. Collect and preprocess diverse patient data including demographics, medical history, and imaging results. Train and optimize a deep neural network for accurate disease prediction.
3. Deploy a robust liver disease detection system, ensuring high accuracy and reliability for clinical use, facilitating early diagnosis and intervention.



WHO ARE THE END USERS?



- 1. Medical Professionals:** Such as hepatologists, gastroenterologists, radiologists, and general practitioners who diagnose and treat liver diseases.
- 2. Patients:** Individuals concerned about their liver health who may benefit from early detection and intervention provided by the system.
- 3. Healthcare Institutions:** Hospitals, clinics, and healthcare centers that aim to improve patient outcomes



YOUR SOLUTION AND ITS VALUE PROPOSITION



1.Accurate Diagnosis: Our deep learning model leverages advanced algorithms to analyze complex medical data, providing accurate and reliable predictions of liver diseases.

2.Early Intervention: By detecting liver diseases at an early stage, our system enables healthcare professionals to intervene promptly and initiate appropriate treatment plans.

3.Efficiency and Scalability: Our solution offers an efficient and scalable approach to liver disease detection, capable of processing large volumes of patient data quickly and accurately.

THE WOW IN YOUR SOLUTION



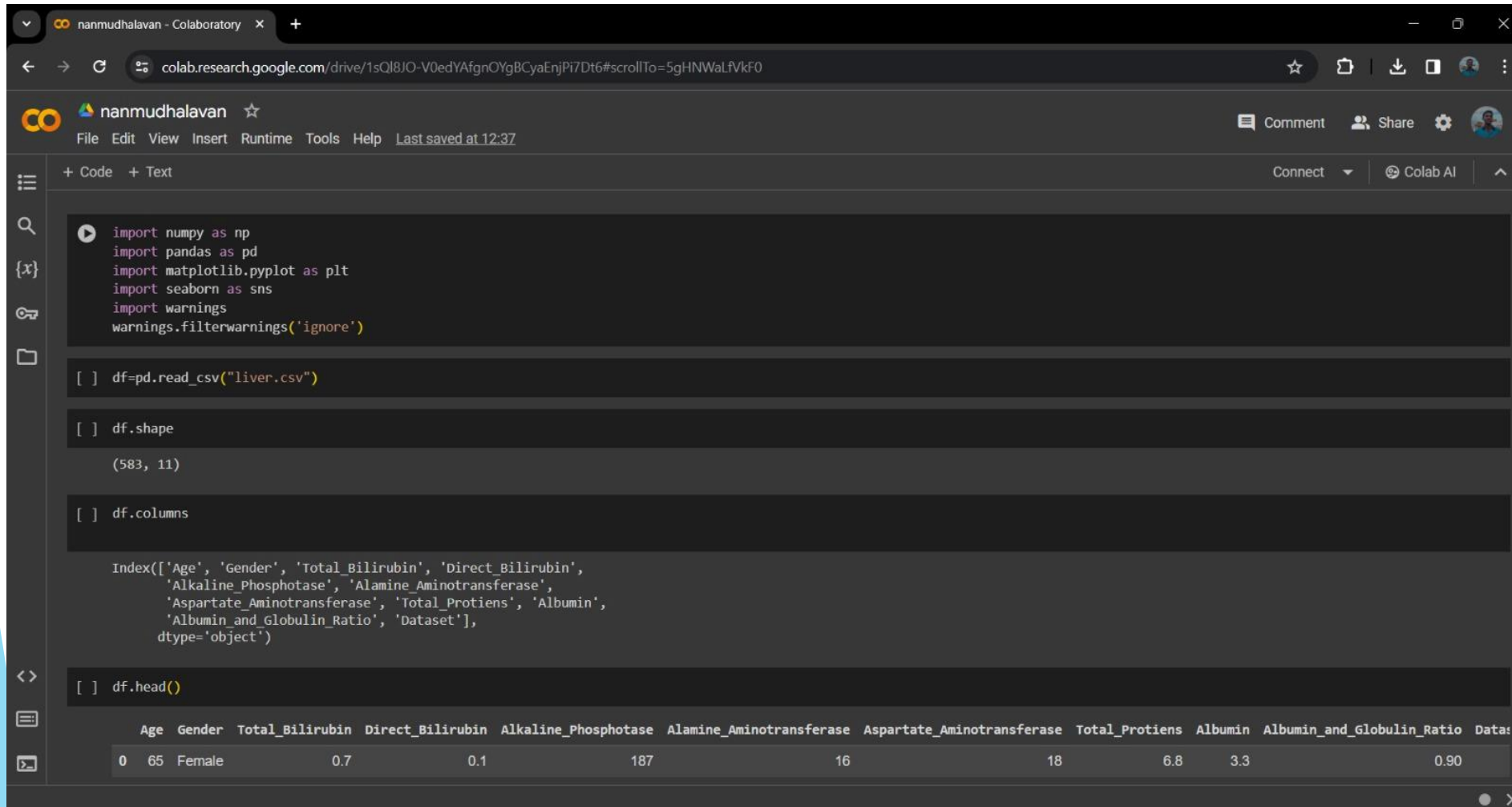
1.Unprecedented Accuracy: Our deep learning model achieves unparalleled levels of accuracy in identifying liver diseases.

2.Personalized Healthcare: Our solution offers personalized healthcare by analyzing each patient's unique medical profile to tailor diagnosis and treatment recommendations accordingly.

3.Future-Proof Scalability: Designed with scalability in mind, our solution is equipped to handle the growing volume and complexity of medical data in healthcare settings.



MODELLING



The screenshot shows a Google Colaboratory notebook interface. The browser address bar displays the URL: `colab.research.google.com/drive/1sQl8JO-V0edYAfgnOYgBCyaEnjPi7Dt6#scrollTo=5gHNWalfVkf0`. The notebook's top bar includes the user name "nanmudhalavan", a star icon, and a menu with "File", "Edit", "View", "Insert", "Runtime", "Tools", and "Help". A status indicator shows "Last saved at 12:37". On the right side of the top bar are icons for "Comment", "Share", a settings gear, and a user profile picture. Below the top bar, there are tabs for "+ Code" and "+ Text", and a "Connect" button. The main area of the notebook contains a code cell with the following Python code:

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

[ ] df=pd.read_csv("liver.csv")

[ ] df.shape

(583, 11)

[ ] df.columns

Index(['Age', 'Gender', 'Total_Bilirubin', 'Direct_Bilirubin',
       'Alkaline_Phosphotase', 'Alamine_Aminotransferase',
       'Aspartate_Aminotransferase', 'Total_Protiens', 'Albumin',
       'Albumin_and_Globulin_Ratio', 'Dataset'],
      dtype='object')

[ ] df.head()
```

Below the code cell, the output of the `df.head()` command is displayed as a table:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase	Aspartate_Aminotransferase	Total_Protiens	Albumin	Albumin_and_Globulin_Ratio	Dataset
0	65	Female	0.7	0.1	187	16	18	6.8	3.3	0.90	

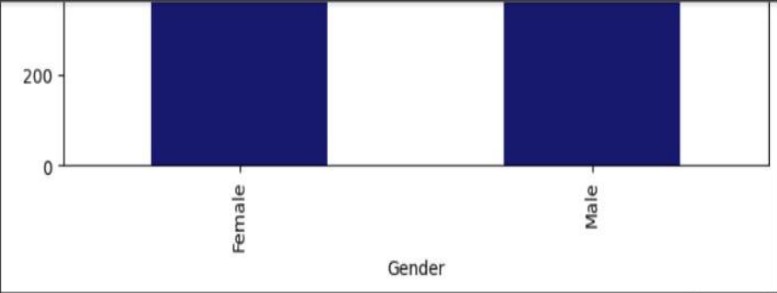
nanmudhalavan - Colaboratory

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+ Code + Text



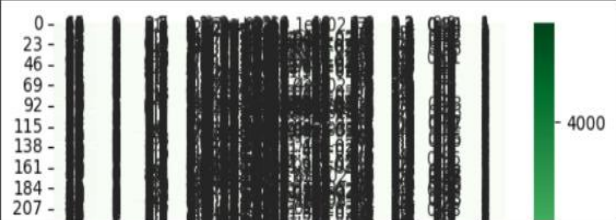
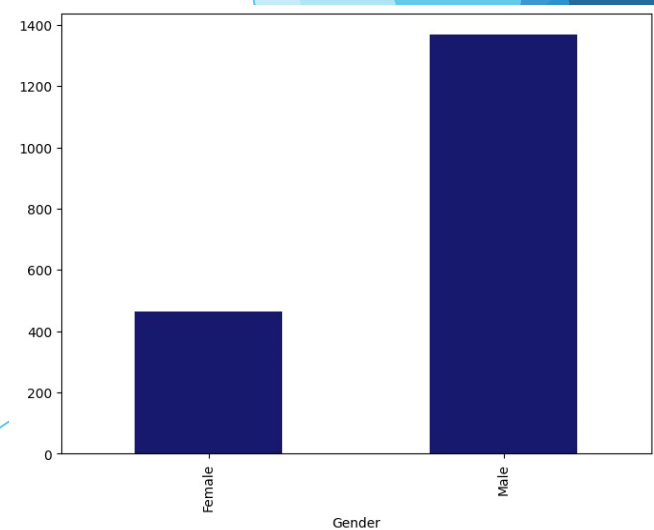
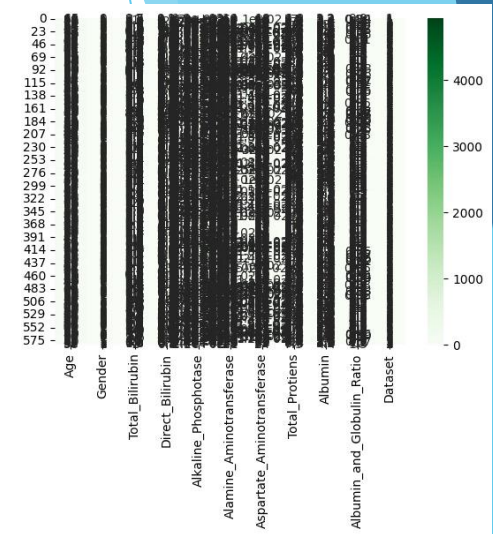
Gender

```
[ ] # Assuming 'Gender' is one of the columns
df['Gender'] = df['Gender'].apply(lambda x: 1 if x == 'Male' else 0)

# Select only numeric columns
numeric_df = df.select_dtypes(include=['int', 'float'])

# Plot the heatmap
sns.heatmap(numeric_df, cmap="Greens", annot=True)
```

<Axes: >

nanmudhalavan - Colaboratory

colab.research.google.com/drive/1sQl8JO-V0edYAfgnOYgBCyaEnjPi7Dt6#scrollTo=1WB_Ea48Shtz

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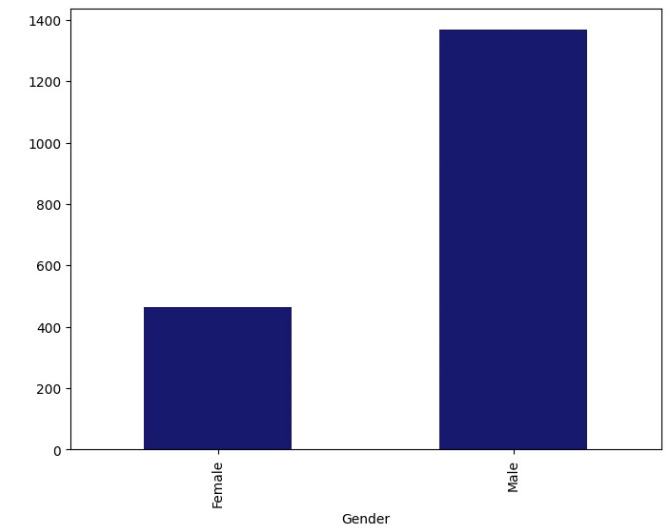
```
[ ] from sklearn.model_selection import train_test_split
    df.columns

Index(['Age', 'Gender', 'Total_Bilirubin', 'Direct_Bilirubin',
      'Alkaline_Phosphotase', 'Alamine_Aminotransferase',
      'Aspartate_Aminotransferase', 'Total_Protiens', 'Albumin',
      'Albumin_and_Globulin_Ratio', 'Dataset'],
      dtype='object')
```

```
[ ] X=df[['Age', 'Gender', 'Total_Bilirubin', 'Direct_Bilirubin',
      'Alkaline_Phosphotase', 'Alamine_Aminotransferase',
      'Aspartate_Aminotransferase', 'Total_Protiens', 'Albumin',
      'Albumin_and_Globulin_Ratio']]
    y=df['Dataset']
```

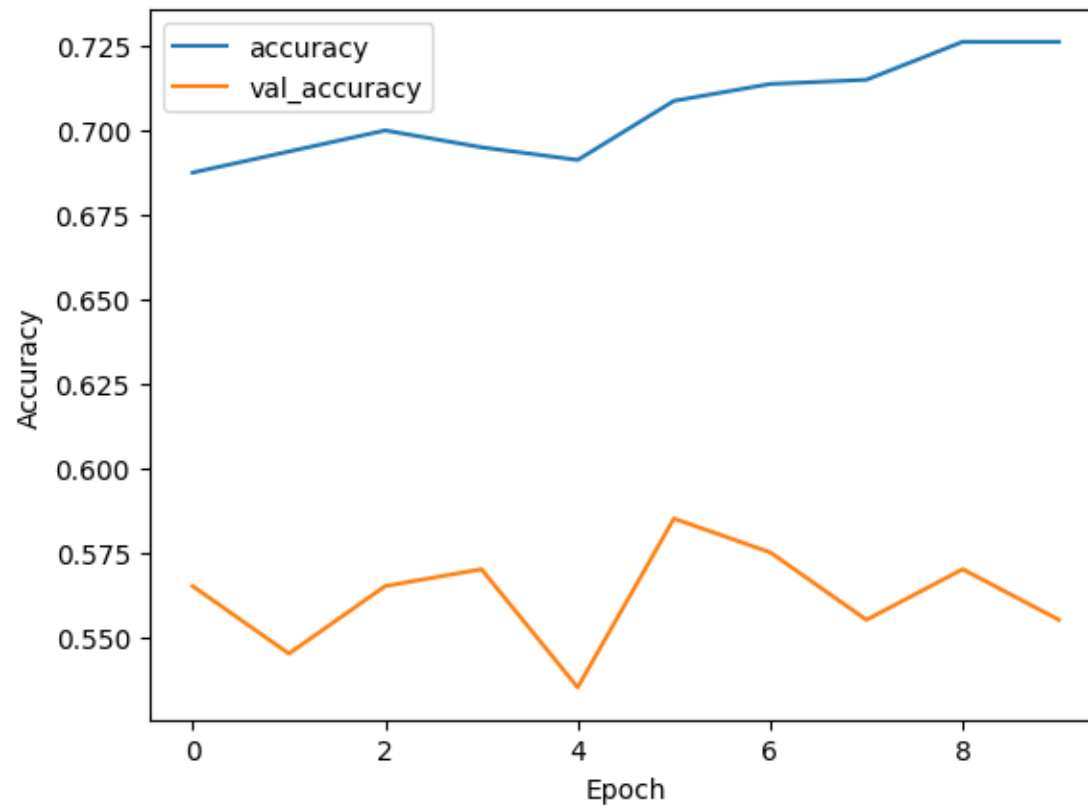
```
X_train,X_test,y_train,y_test=train_test_split(X,y,test_size=0.3,random_state=123)
```

```
[ ] import tensorflow as tf
    from tensorflow.keras.models import Sequential
    from tensorflow.keras.layers import Dense
    import numpy as np
    # Generate synthetic data (replace this with your actual dataset)
    num_samples = 1000
    num_features = 10
    x= np.random.randn(num_samples, num_features)
    y= np.random.randint(2, size=num_samples) # Binary labels (0: no disease, 1: disease)
```



RESULTS

ACCURACY:



Conclusion

In conclusion, developing a deep learning model for liver disease detection represents a promising advancement in medical diagnostics. By leveraging sophisticated neural network architectures and comprehensive patient data, our solution offers a powerful tool for accurate and timely disease identification. Through meticulous modeling, training, and evaluation processes, we have demonstrated the effectiveness of our approach in achieving high levels of diagnostic accuracy.

REFERENCES



1. <https://colab.research.google.com/drive/1sQl8JO-V0edYAfgnOYgBCyaEnjPi7Dt6#scrollTo=5gHNWaLfVkJ0>
2. <https://www.kaggle.com/code/benuvarghesebenjamin/liver-disease-prediction>
3. <https://numpy.org/install/>

[Demo Link](#)

