Exploratory Data Analysis
Digital Assignment

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Import necessary libraries

```
[1] import pandas as pd
    import numpy as np
    import seaborn as sns
    import matplotlib.pyplot as plt
    from sklearn.ensemble import RandomForestClassifier
    from sklearn.model_selection import train_test_split
    from sklearn.metrics import classification_report, confusion_matrix
```

Load the dataset

```
df = pd.read_csv("HepatitisCdata.csv")
df.head()
```

	Unnamed: 0	Category	Age	Sex	ALB	ALP	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
0	1	0=Blood Donor	32	m	38.5	52.5	7.7	22.1	7.5	6.93	3.23	106.0	12.1	69.0
1	2	0=Blood Donor	32	m	38.5	70.3	18.0	24.7	3.9	11.17	4.80	74.0	15.6	76.5
2	3	0=Blood Donor	32	m	46.9	74.7	36.2	52.6	6.1	8.84	5.20	86.0	33.2	79.3
3	4	0=Blood Donor	32	m	43.2	52.0	30.6	22.6	18.9	7.33	4.74	80.0	33.8	75.7
4	5	0=Blood Donor	32	m	39.2	74.1	32.6	24.8	9.6	9.15	4.32	76.0	29.9	68.7

Delete numbers column

```
[3] df = df.iloc[:, 1:]
    df.head()
```

	Category	Age	Sex	ALB	ALP	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
0	0=Blood Donor	32	m	38.5	52.5	7.7	22.1	7.5	6.93	3.23	106.0	12.1	69.0
1	0=Blood Donor	32	m	38.5	70.3	18.0	24.7	3.9	11.17	4.80	74.0	15.6	76.5
2	0=Blood Donor	32	m	46.9	74.7	36.2	52.6	6.1	8.84	5.20	86.0	33.2	79.3
3	0=Blood Donor	32	m	43.2	52.0	30.6	22.6	18.9	7.33	4.74	80.0	33.8	75.7
4	0=Blood Donor	32	m	39.2	74.1	32.6	24.8	9.6	9.15	4.32	76.0	29.9	68.7

Display basic information about the dataset

```
[4] print("Basic Information:")
    print(df.info())
```

```
Basic Information:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 615 entries, 0 to 614
Data columns (total 13 columns):
 #   Column    Non-Null Count  Dtype
---  ------    --------------  -----
 0   Category  615 non-null    object
 1   Age       615 non-null    int64
 2   Sex       615 non-null    object
 3   ALB       614 non-null    float64
 4   ALP       597 non-null    float64
 5   ALT       614 non-null    float64
 6   AST       615 non-null    float64
 7   BIL       615 non-null    float64
 8   CHE       615 non-null    float64
 9   CHOL      605 non-null    float64
 10  CREA      615 non-null    float64
 11  GGT       615 non-null    float64
 12  PROT      614 non-null    float64
dtypes: float64(10), int64(1), object(2)
memory usage: 62.6+ KB
None
```

Find duplicate values

```
[5] duplicate_count = df.duplicated().sum()
    print(f"\nNumber of duplicate rows: {duplicate_count}")
```

```
Number of duplicate rows: 0
```

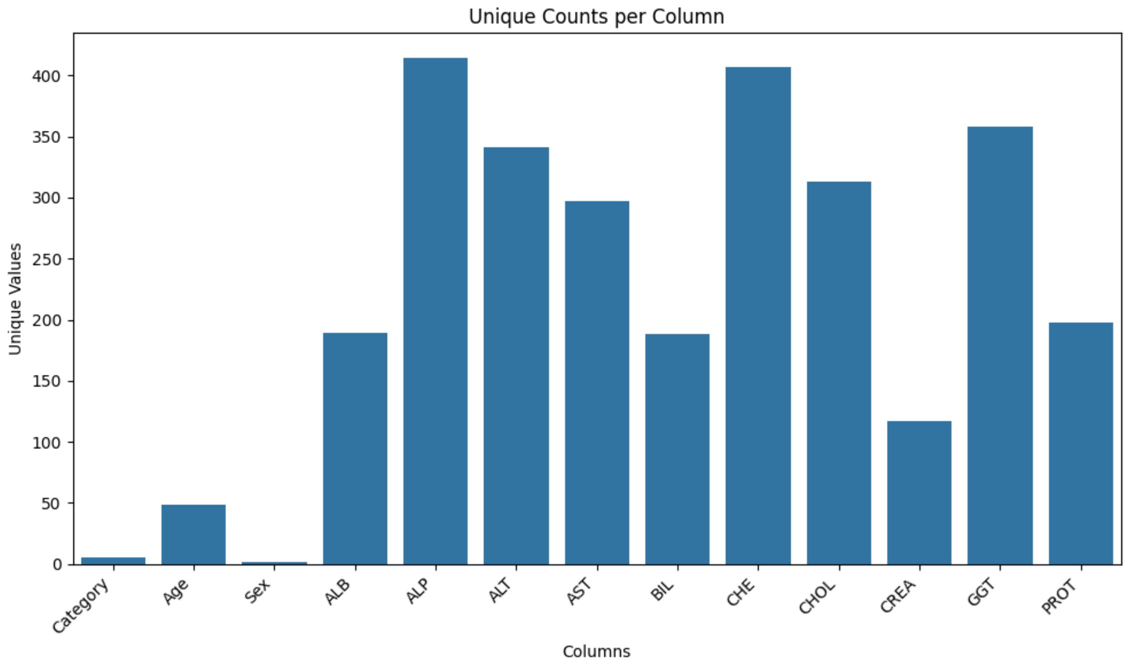
No of unique values in each column

```
[6] print("\nUnique values in each column:")
    for col in df.columns:
        print(f"{col}: {df[col].nunique()}")
```

```
Unique values in each column:
Category: 5
Age: 49
Sex: 2
ALB: 189
ALP: 414
ALT: 341
AST: 297
BIL: 188
CHE: 407
CHOL: 313
CREA: 117
GGT: 358
PROT: 198
```

Visualize unique counts

```
[7] unique_counts = df.nunique()
    plt.figure(figsize=(10, 6))
    sns.barplot(x=unique_counts.index, y=unique_counts.values)
    plt.xticks(rotation=45, ha="right")
    plt.title("Unique Counts per Column")
    plt.ylabel("Unique Values")
    plt.xlabel("Columns")
    plt.tight_layout()
    plt.show()
```



Find null values

```
[8] print("Null values in each column:")
    df.isnull().sum()
```

Null values in each column:

	0
Category	0
Age	0
Sex	0
ALB	1
ALP	18
ALT	1
AST	0
BIL	0
CHE	0
CHOL	10
CREA	0
GGT	0
PROT	1

dtype: int64

Replace null values

```
[9] from sklearn.impute import KNNImputer
    imputer = KNNImputer(n_neighbors= 5)
    numeric_df = df.select_dtypes(include='float64')
    imputed_df = imputer.fit_transform(numeric_df)
    imputed_df = pd.DataFrame(imputed_df ,columns=numeric_df.columns)
    df[numeric_df.columns] = imputed_df
    df.isna().sum()
```

	0
Category	0
Age	0
Sex	0
ALB	0
ALP	0
ALT	0
AST	0
BIL	0
CHE	0
CHOL	0
CREA	0
GGT	0
PROT	0

dtype: int64

Check data types

```
[10] print("\nData types of the columns:")
     print(df.dtypes)
```

```
Data types of the columns:
Category     object
Age           int64
Sex          object
ALB         float64
ALP         float64
ALT         float64
AST         float64
BIL         float64
CHE         float64
CHOL        float64
CREA        float64
GGT         float64
PROT        float64
dtype: object
```

Filter the data

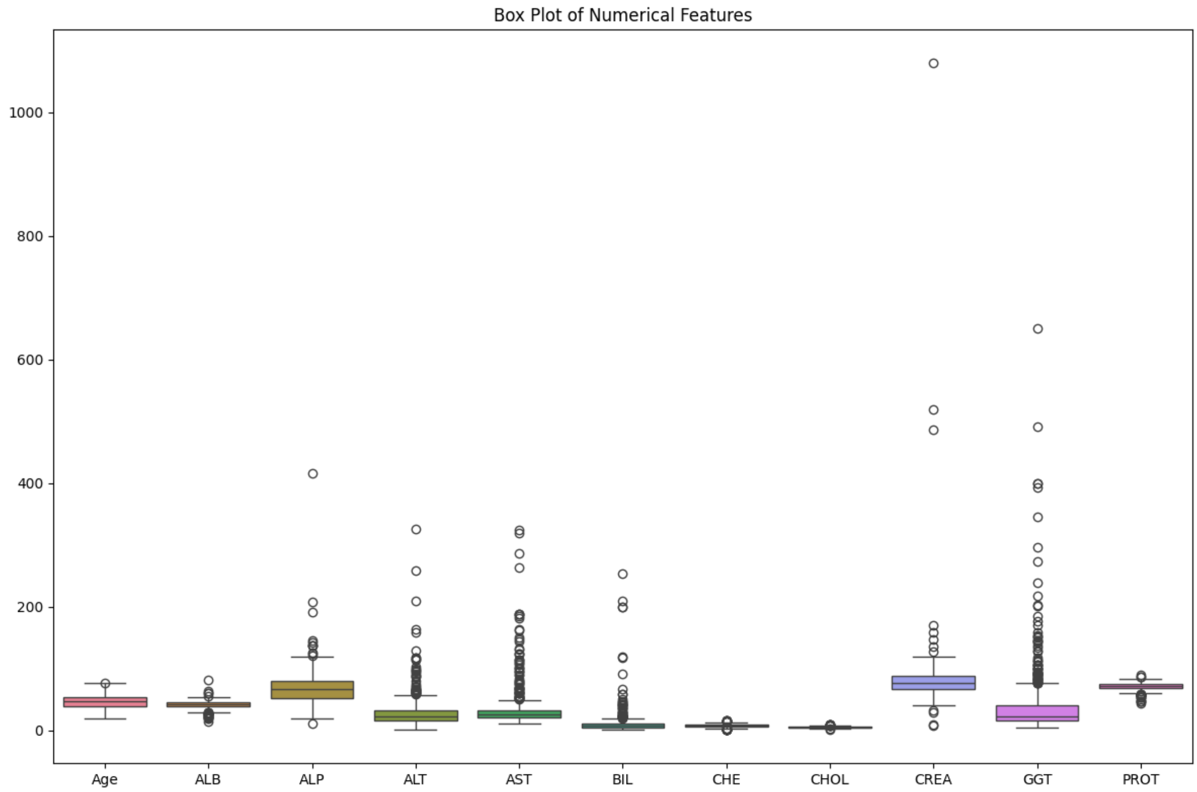
```
[11] filtered_data = df[df["Category"] == "1=Hepatitis"]
     print("\nFiltered data (Category = 1=Hepatitis):")
     filtered_data.head()
```

[11] Filtered data (Category = 1=Hepatitis):

	Category	Age	Sex	ALB	ALP	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
540	1=Hepatitis	38	m	45.0	56.30	28.02	33.1	7.0	9.58	6.00	77.9	18.9	63.0
541	1=Hepatitis	19	m	41.0	64.22	87.00	67.0	12.0	7.55	3.90	62.0	65.0	75.0
542	1=Hepatitis	23	m	47.0	19.10	38.90	164.2	17.0	7.09	3.20	79.3	90.4	70.1
543	1=Hepatitis	25	m	42.0	38.20	63.30	187.7	14.0	6.00	4.28	66.9	40.2	70.5
544	1=Hepatitis	27	m	45.0	27.50	10.50	37.8	10.0	8.77	3.20	55.2	35.9	74.5

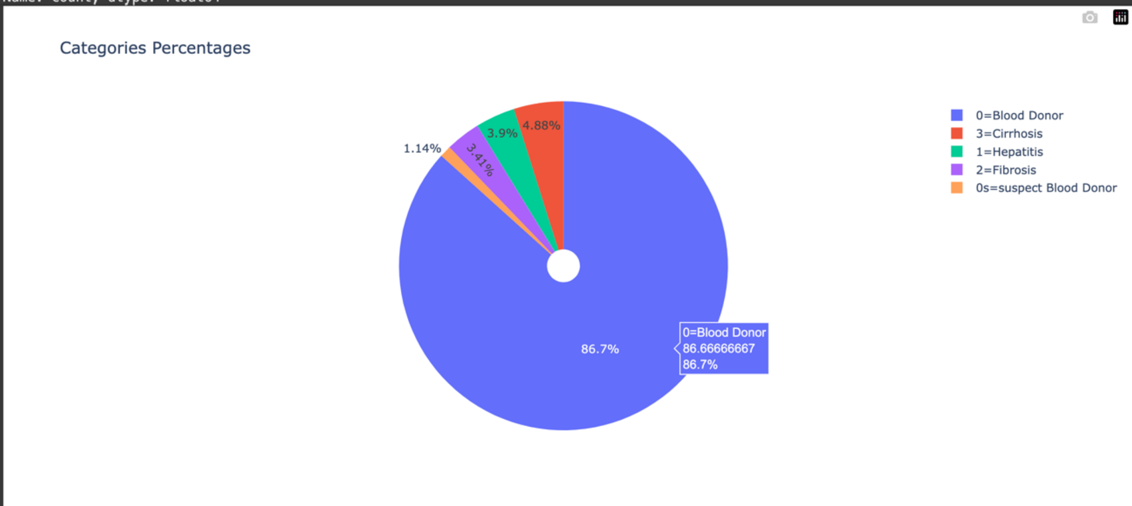
Univariate Analysis

```
[12] plt.figure(figsize=(12, 8))
     sns.boxplot(data=df.select_dtypes(include=[np.number]))
     plt.title("Box Plot of Numerical Features")
     plt.tight_layout()
     plt.show()
```



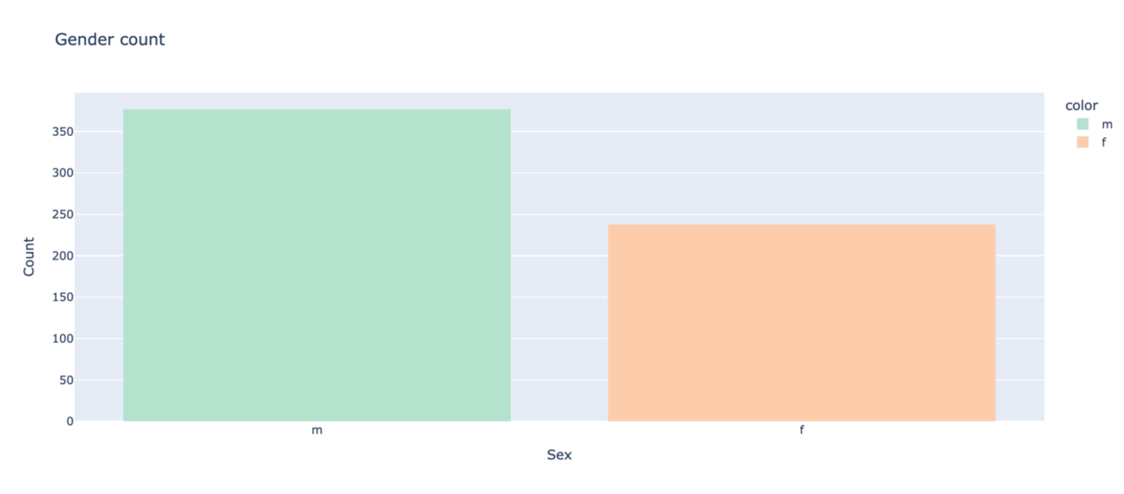

```
[13] import plotly.graph_objects as go
     cat_count = df.Category.value_counts()
     cat_percentage = (cat_count / cat_count.sum()) *100
     print(cat_percentage)

     labels = cat_percentage.index
     values = cat_percentage.values
     fig = go.Figure(data=[go.Pie(labels=labels , values=values , hole =.1)])
     fig.update_layout(title = "Categories Percentages")
     fig.show()
```

```
Category
0=Blood Donor            86.666667
3=Cirrhosis               4.878049
1=Hepatitis               3.902439
2=Fibrosis                3.414634
0s=suspect Blood Donor    1.138211
Name: count, dtype: float64
```



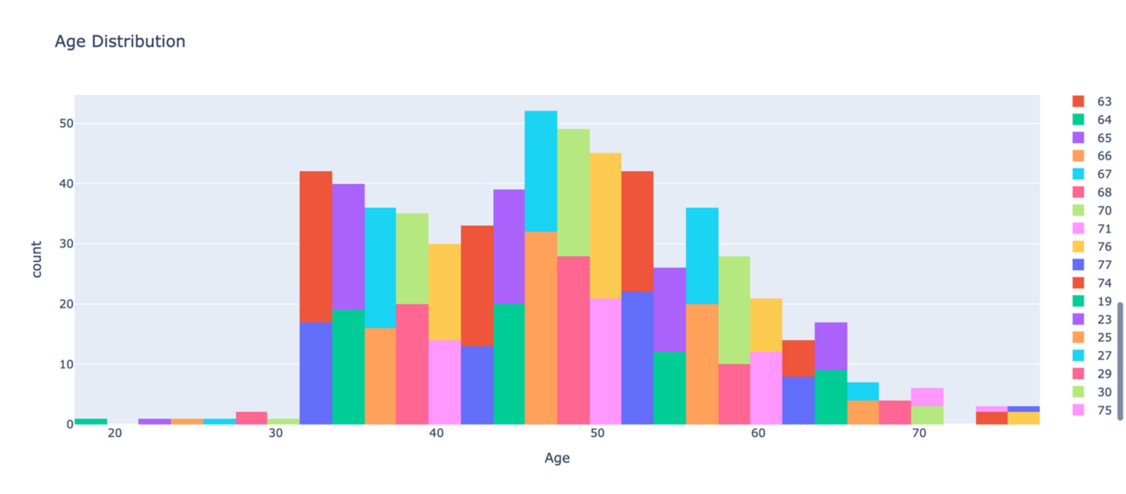

```
[14] import plotly.express as px
     values = df.Sex.value_counts().values
     labels = df.Sex.value_counts().index
     px.bar(df,
            x=labels,
            y= values,
            color=labels,
            color_discrete_sequence=px.colors.qualitative.Pastel2,
            title= "Gender count",
            labels = {"x" : "Sex" , "y" : "Count"},
            )
```

[14]




```
[15] from plotly.offline import iplot
     iplot(px.histogram(
         df,
         x = "Age",
         title= "Age Distribution",
         color = "Age"
     ))
```

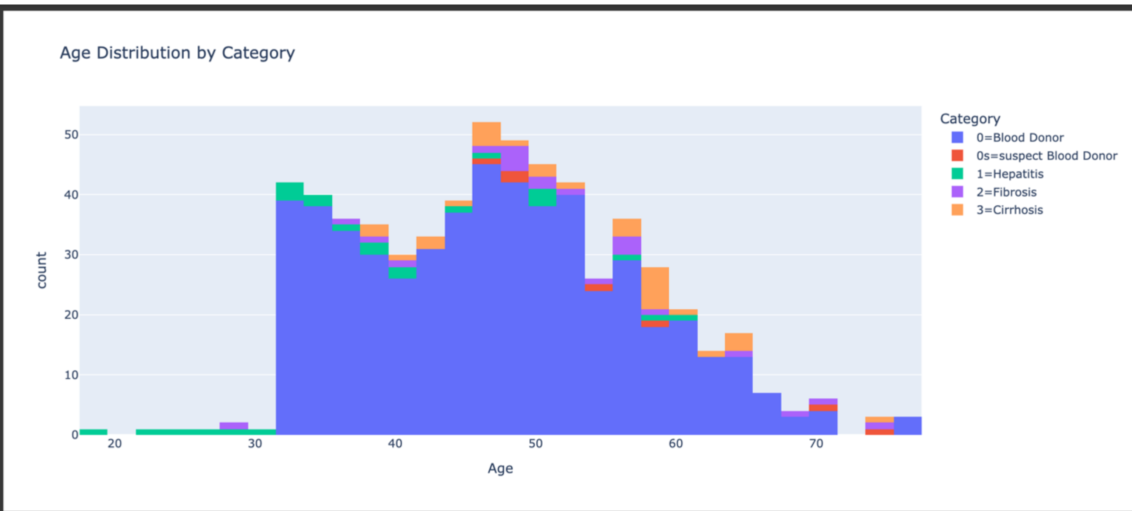
[15]



Bivariate Analysis

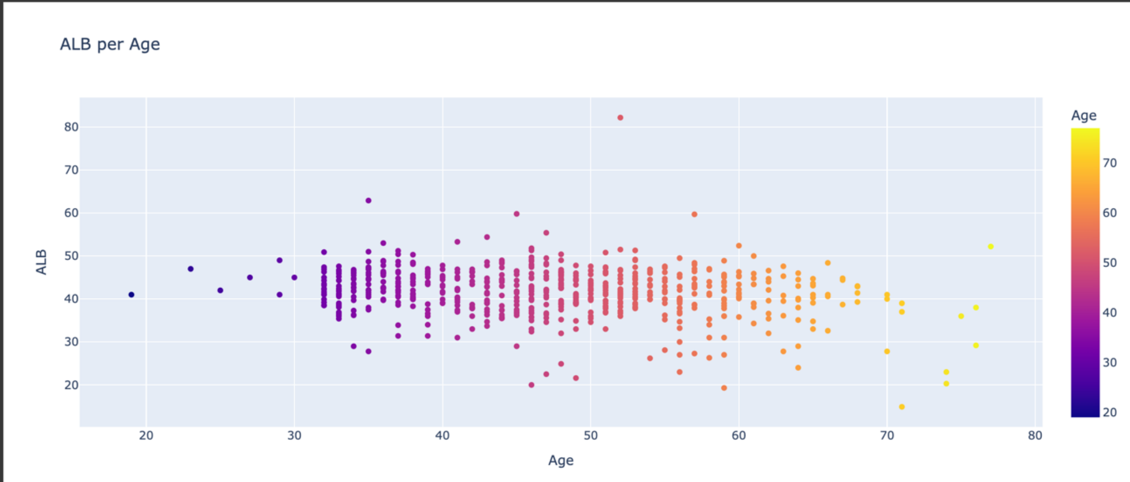
```
[16] iplot(
         px.histogram(
             df,
             x = "Age",
             color = "Category",
             title= "Age Distribution by Category",
         )
     )
```

[16]

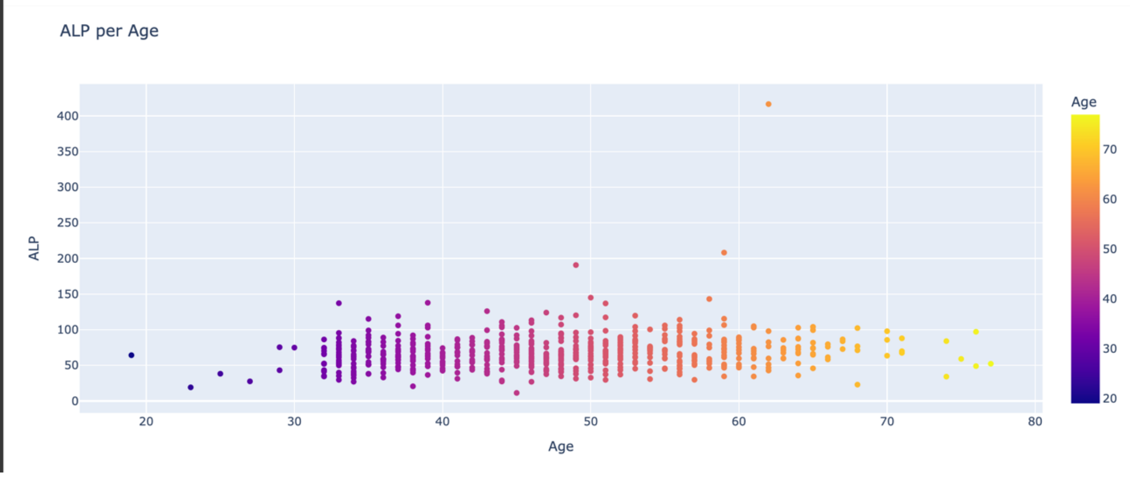


[17]

```python
for i, bio_mark in enumerate(df.select_dtypes(include='float64')):
    iplot(
        px.scatter(df,x= 'Age', y = bio_mark, color = "Age", title= f"{bio_mark} per Age"))
```

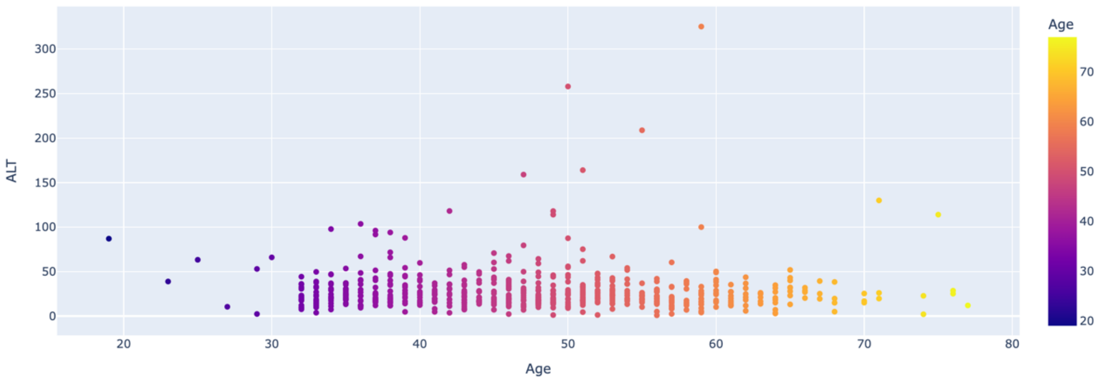


[17]

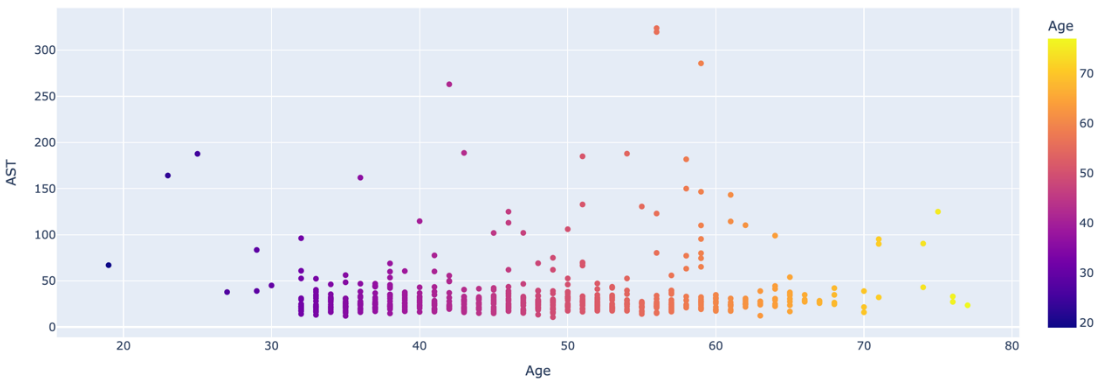


[17]

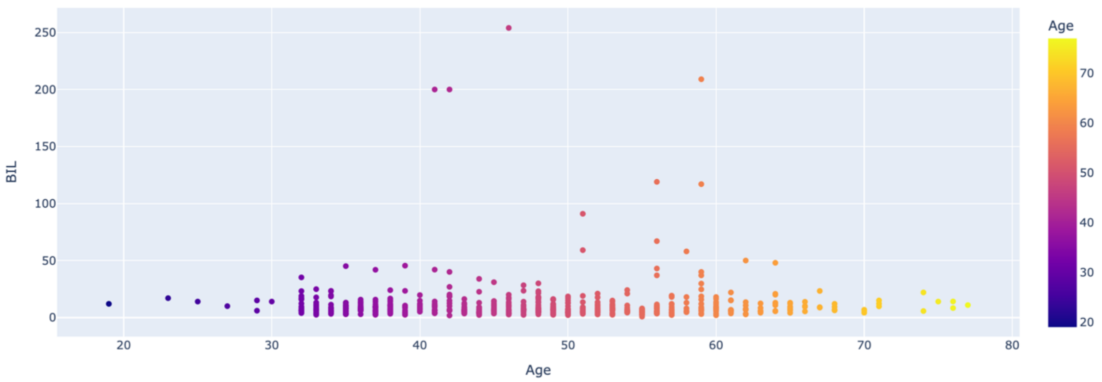
ALT per Age



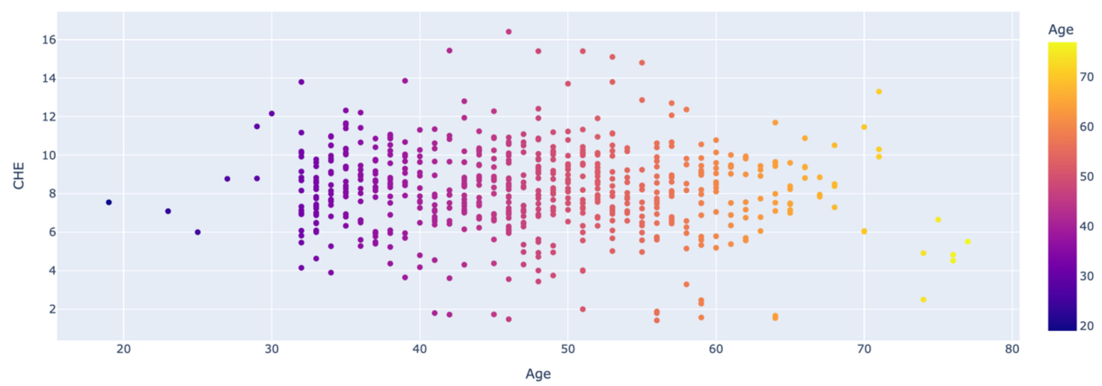
AST per Age

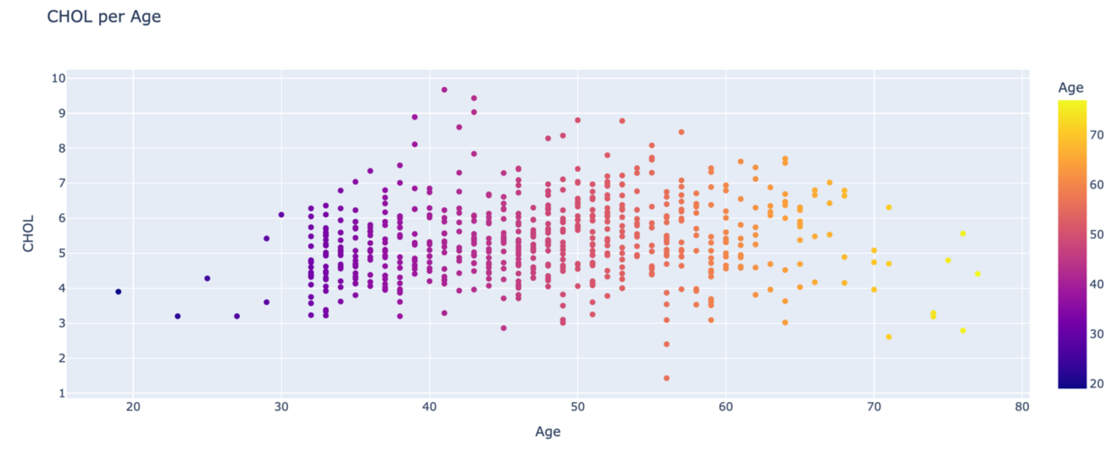


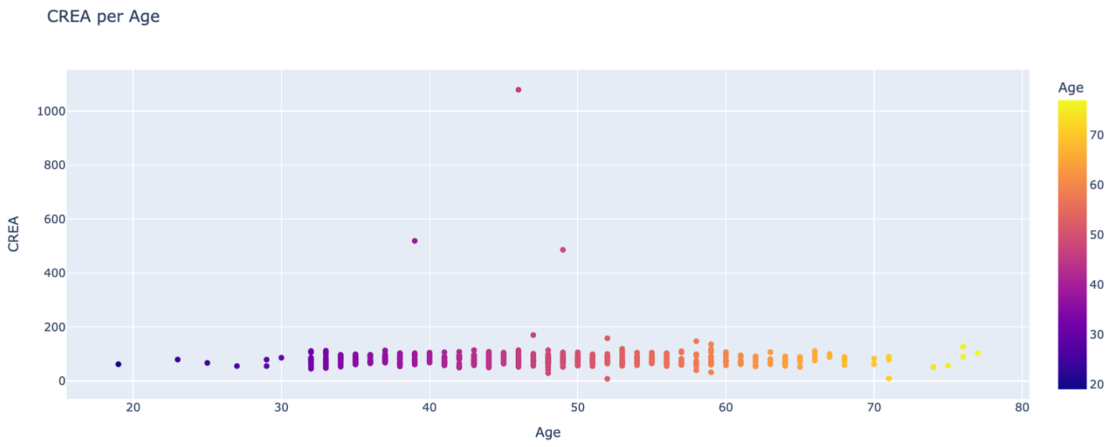
BIL per Age

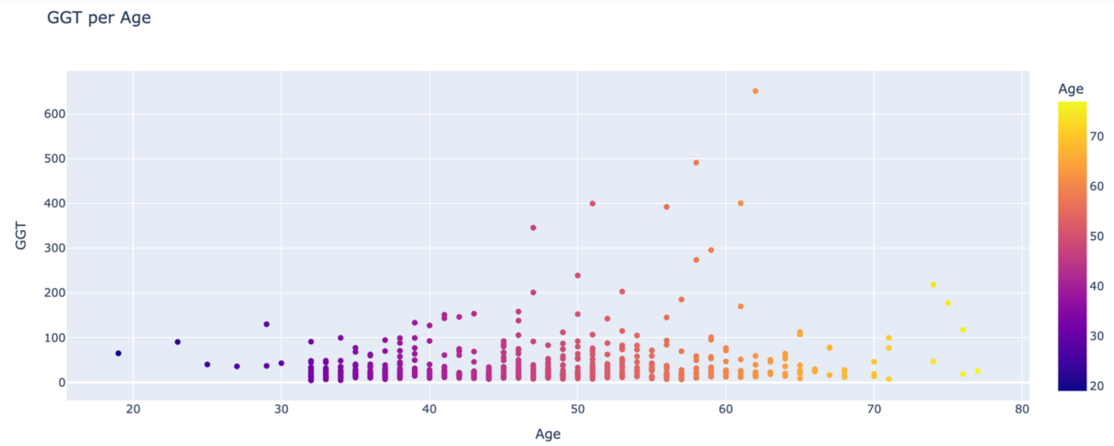


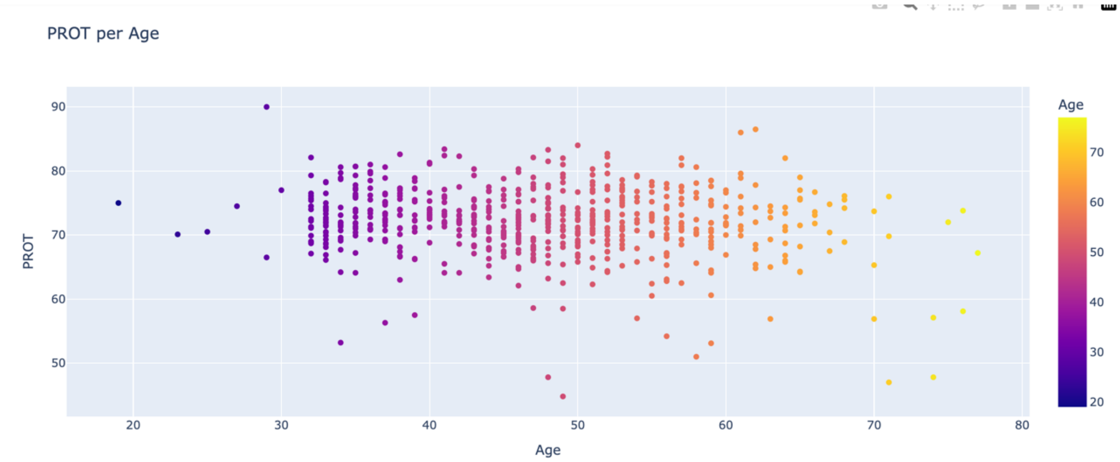
CHE per Age




CHOL per Age
CHOL
10
9
8
7
6
5
4
3
2
1
20
30
40
50
60
70
80
Age
Age
70
60
50
40
30
20

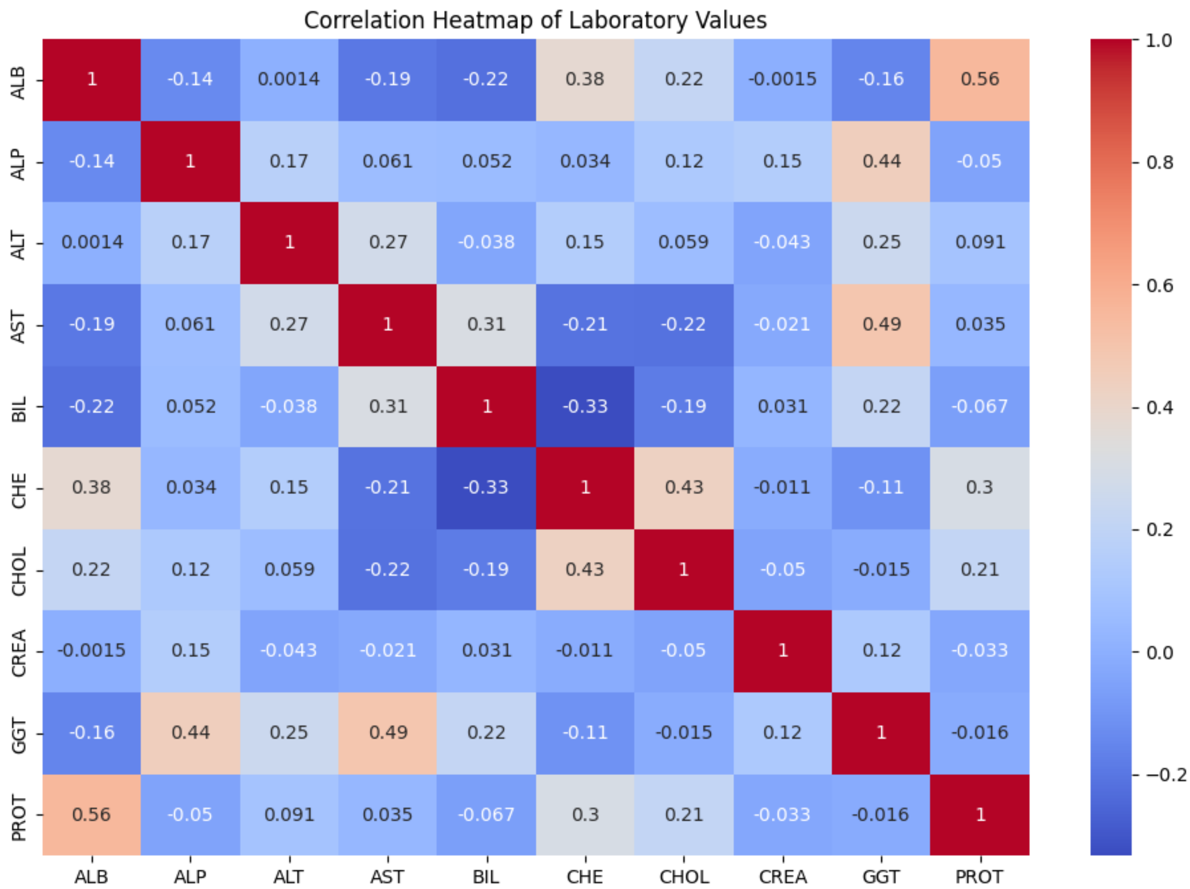

CREA per Age
CREA
1000
800
600
400
200
0
20
30
40
50
60
70
80
Age
Age
70
60
50
40
30
20


GGT per Age
GGT
600
500
400
300
200
100
0
20
30
40
50
60
70
80
Age
Age
70
60
50
40
30
20


PROT per Age
PROT
90
80
70
60
50
20
30
40
50
60
70
80
Age
Age
70
60
50
40
30
20

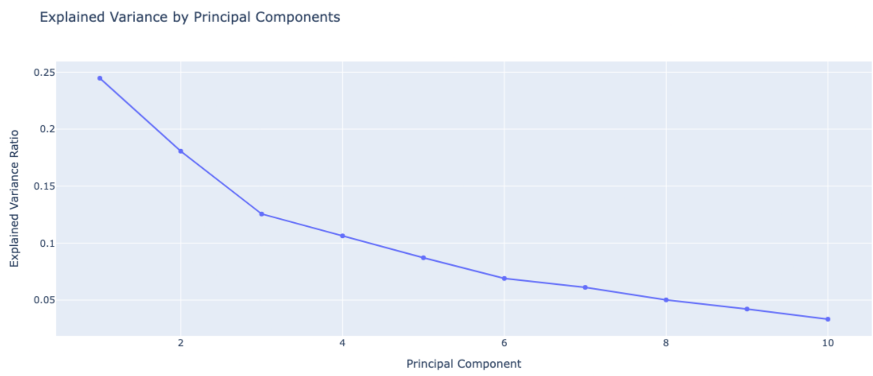
Multivariate Analysis

```python
[18] plt.figure(figsize=(12, 8))
     sns.heatmap(df[['ALB', 'ALP', 'ALT', 'AST', 'BIL', 'CHE', 'CHOL', 'CREA', 'GGT', 'PROT']].corr(), annot=True, cmap='coolwarm')
     plt.title('Correlation Heatmap of Laboratory Values')
     plt.show()
```



PCA Analysis

```python
[19] from sklearn.decomposition import PCA
     from sklearn.preprocessing import StandardScaler

     df_numeric = df.select_dtypes(include='float64')
     scalar = StandardScaler()
     df_scaled = scalar.fit_transform(df_numeric)
     pca = PCA()
     pca_result = pca.fit_transform(df_scaled)
     fig = go.Figure()

     fig.add_trace(go.Scatter(x=list(range(1, len(pca.explained_variance_ratio_) + 1)),
                              y=pca.explained_variance_ratio_,
                              mode='lines+markers',
                              name='Explained Variance Ratio'))

     fig.update_layout(title='Explained Variance by Principal Components',
                       xaxis_title='Principal Component',
                       yaxis_title='Explained Variance Ratio',
                       )
     fig.show()
```



Random Forest Model

Label Encoding

```
[20] from sklearn.preprocessing import LabelEncoder

     Label_pre = LabelEncoder()
     data_cols=df.select_dtypes(exclude=['int','float']).columns
     label_col =list(data_cols)
     df[label_col]= df[label_col].apply(lambda col:Label_pre.fit_transform(col))
```

```
[21] df.head()
```

	Category	Age	Sex	ALB	ALP	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
0	0	32	1	38.5	52.5	7.7	22.1	7.5	6.93	3.23	106.0	12.1	69.0
1	0	32	1	38.5	70.3	18.0	24.7	3.9	11.17	4.80	74.0	15.6	76.5
2	0	32	1	46.9	74.7	36.2	52.6	6.1	8.84	5.20	86.0	33.2	79.3
3	0	32	1	43.2	52.0	30.6	22.6	18.9	7.33	4.74	80.0	33.8	75.7
4	0	32	1	39.2	74.1	32.6	24.8	9.6	9.15	4.32	76.0	29.9	68.7

Splitting features and target

```
[22] x = df.drop("Category", axis=1)
     y = df["Category"]
```

```
[23] x.shape,y.shape
```

```
((615, 12), (615,))
```

Train Test Split

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

     X_train, X_test, y_train, y_test = train_test_split(x, y, test_size=0.2, random_state=42)

     print("Rows and columns of training data X_train:", X_train.shape)
     print("Rows and columns of testing data X_test:", X_test.shape)
```

```
Rows and columns of training data X_train: (492, 12)
Rows and columns of testing data X_test: (123, 12)
```

SMOTE to balance data

```
[26] from imblearn.over_sampling import SMOTE
     smote = SMOTE(k_neighbors=2, random_state=42)
     X_train_res, y_train_res = smote.fit_resample(X_train, y_train)

     print("Class distribution after SMOTE:")
     print(pd.Series(y_train_res).value_counts())
```

```
Class distribution after SMOTE:
Category
0    437
3    437
4    437
2    437
1    437
Name: count, dtype: int64
```

Model Creation

```
[27] rf_model = RandomForestClassifier(random_state=42)
     rf_model.fit(X_train_res, y_train_res)
```

```
RandomForestClassifier
RandomForestClassifier(random_state=42)
```

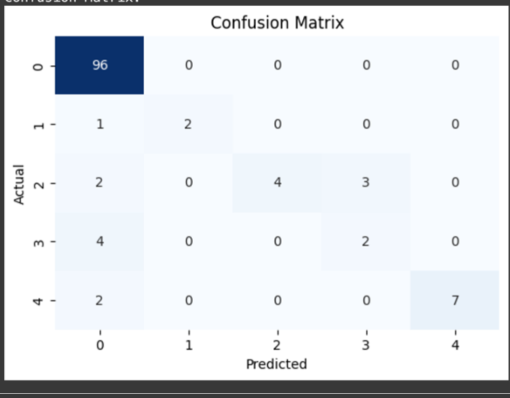
Evaluate the model

```
[28] y_pred = rf_model.predict(X_test)
     print("Classification Report:")
     print(classification_report(y_test, y_pred))
```

```
Classification Report:
              precision    recall  f1-score   support

           0       0.91      1.00      0.96        96
           1       1.00      0.67      0.80         3
           2       1.00      0.44      0.62         9
           3       0.40      0.33      0.36         6
           4       1.00      0.78      0.88         9

    accuracy                           0.90       123
   macro avg       0.86      0.64      0.72       123
weighted avg       0.90      0.90      0.89       123
```

```
[29] print("Confusion Matrix:")
     cm = confusion_matrix(y_test, y_pred)
     plt.figure(figsize=(6, 4))
     sns.heatmap(cm, annot=True, fmt="d", cmap="Blues", cbar=False)
     plt.title("Confusion Matrix")
     plt.xlabel("Predicted")
     plt.ylabel("Actual")
     plt.show()
```

```
Confusion Matrix:
```



Random Forest Model Accuracy - 90%