Project Context

- **Project Title:** End-to-End Deep Learning for Medical Test Result Prediction
- **Project Objective:** To build a Deep Neural Network (DNN) model using Keras for multi-class classification on the 'Test Results' column.
- **Dataset:** "Healthcare Dataset" from Kaggle. (Link: https://www.kaggle.com/datasets/prasad22/healthcare-dataset/data)
- **Target Column:** Test Results (has 3 categories: 'Normal', 'Abnormal', 'Inconclusive').
- **Key Technologies:** Python, Pandas, NumPy, Matplotlib, Seaborn, Scikit-learn, TensorFlow (Keras).

Part 0: Environment Setup

In this initial section, we prepare our digital workspace. This involves importing all necessary libraries for data manipulation, visualization, and deep learning, as well as configuring notebook settings for optimal display and reproducibility.

0.1. Import Core Libraries

```
# Data Manipulation
import pandas as pd
import numpy as np

# Visualization
import matplotlib.pyplot as plt
import seaborn as sns

# Deep Learning
import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, Dropout

# Machine Learning Utilities
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, OneHotEncoder,
LabelEncoder
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
from sklearn.metrics import classification_report, confusion_matrix
```

0.2. Configuration and Helper Functions

```
# Set visualization style
sns.set_style('whitegrid')

# Set pandas options to display all columns
pd.set_option('display.max_columns', None)

# Set random seeds for reproducibility
```

```
np.random.seed(42)
tf.random.set_seed(42)
```

Part 1: Data Loading & Initial Inspection

Here, we will load the dataset and perform a high-level "first look" to grasp its structure, size, and content.

1.1. Load Dataset

```
# Load the dataset from the provided URL into a pandas DataFrame
# This dataset is hosted on my GitHub, so we can read it directly
using the raw content URL.
df =
pd.read_csv('https://raw.githubusercontent.com/LatiefDataVisionary/
healthcare-test-results-prediction/refs/heads/main/data/raw/
healthcare_dataset.csv')
```

1.2. Initial Inspection

Display the first 10 rows of the DataFrame to get a glimpse of the data

```
df.head(10)

                 Name  Age  Gender Blood Type Medical Condition  \
0        Bobby JacksOn   30    Male         B-            Cancer
1         LesLie TErRy   62    Male         A+           Obesity
2          DaNnY sMitH   76  Female         A-           Obesity
3         andrEw waTtS   28  Female         O+          Diabetes
4        adrIENNE bEll   43  Female        AB+            Cancer
5         EMILY JOHNSOn  36    Male         A+            Asthma
6        edwArD EDWaRDs  21  Female        AB-          Diabetes
7   CHrisTInA MARtinez   20  Female         A+            Cancer
8       JASmINe aGuIlaR  82    Male        AB+            Asthma
9     ChRISTopher BerG   58  Female        AB-            Cancer

  Date of Admission            Doctor                    Hospital  \
0        2024-01-31     Matthew Smith             Sons and Miller
1        2019-08-20   Samantha Davies                     Kim Inc
2        2022-09-22  Tiffany Mitchell                    Cook PLC
3        2020-11-18       Kevin Wells    Hernandez Rogers and Vang,
4        2022-09-19    Kathleen Hanna                 White-White
5        2023-12-20     Taylor Newton              Nunez-Humphrey
6        2020-11-03       Kelly Olson             Group Middleton
7        2021-12-28    Suzanne Thomas  Powell Robinson and Valdez,
8        2020-07-01    Daniel Ferguson                Sons Rich and
9        2021-05-23        Heather Day               Padilla-Walker

  Insurance Provider  Billing Amount  Room Number Admission Type  \
0         Blue Cross    18856.281306          328         Urgent
1           Medicare    33643.327287          265      Emergency
2              Aetna    27955.096079          205      Emergency
3           Medicare    37909.782410          450       Elective
4              Aetna    14238.317814          458         Urgent
5   UnitedHealthcare    48145.110951          389         Urgent
6           Medicare    19580.872345          389      Emergency
7              Cigna    45820.462722          277      Emergency
8              Cigna    50119.222792          316       Elective
9   UnitedHealthcare    19784.631062          249       Elective

  Discharge Date   Medication  Test Results
0     2024-02-02  Paracetamol        Normal
1     2019-08-26    Ibuprofen  Inconclusive
2     2022-10-07      Aspirin        Normal
3     2020-12-18    Ibuprofen      Abnormal
4     2022-10-09   Penicillin      Abnormal
5     2023-12-24    Ibuprofen        Normal
6     2020-11-15  Paracetamol  Inconclusive
7     2022-01-07  Paracetamol  Inconclusive
8     2020-07-14      Aspirin      Abnormal
9     2021-06-22  Paracetamol  Inconclusive
```

Display concise summary of the DataFrame, including data types and non-null values

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 55500 entries, 0 to 55499
Data columns (total 15 columns):
 #   Column              Non-Null Count  Dtype  
---  ------              --------------  -----  
 0   Name                55500 non-null  object 
 1   Age                 55500 non-null  int64  
 2   Gender              55500 non-null  object 
 3   Blood Type          55500 non-null  object 
 4   Medical Condition   55500 non-null  object 
 5   Date of Admission   55500 non-null  object 
 6   Doctor              55500 non-null  object 
 7   Hospital            55500 non-null  object 
 8   Insurance Provider  55500 non-null  object 
 9   Billing Amount      55500 non-null  float64
 10  Room Number         55500 non-null  int64  
 11  Admission Type      55500 non-null  object 
 12  Discharge Date      55500 non-null  object 
 13  Medication          55500 non-null  object 
 14  Test Results        55500 non-null  object 
dtypes: float64(1), int64(2), object(12)
memory usage: 6.4+ MB
```

Display the dimensions (number of rows and columns) of the DataFrame

```
df.shape
```

```
(55500, 15)
```

Inspect Unique Values in Each Column

```
for col in df.columns:
    unique_values = df[col].unique()
    print(f"Unique values in column '{col}': \n\t{unique_values}\n")
```

```
Unique values in column 'Name':
	['Bobby JacksOn' 'LesLie TErRy' 'DaNnY sMitH' ... 'LiSa sIMPsoN'
 'RoGER farRELl' 'kaTheRIne WeBSTer']

Unique values in column 'Age':
	[30 62 76 28 43 36 21 20 82 58 72 38 75 68 44 46 63 34 67 48 59
73 51 23
 78 25 33 26 70 57 74 81 49 65 31 22 77 42 24 84 55 40 83 18 27 19 29
61
 80 60 35 79 53 69 47 85 52 37 50 32 54 45 66 39 56 64 71 41 88 17 87
86
 15 16 13 14 89]

Unique values in column 'Gender':
	['Male' 'Female']

Unique values in column 'Blood Type':
	['B-' 'A+' 'A-' 'O+' 'AB+' 'AB-' 'B+' 'O-']

Unique values in column 'Medical Condition':
	['Cancer' 'Obesity' 'Diabetes' 'Asthma' 'Hypertension'
'Arthritis']

Unique values in column 'Date of Admission':
	['2024-01-31' '2019-08-20' '2022-09-22' ... '2019-05-31' '2023-
10-12'
 '2021-03-14']

Unique values in column 'Doctor':
	['Matthew Smith' 'Samantha Davies' 'Tiffany Mitchell' ...
'Deborah Sutton'
 'Mary Bartlett' 'Alec May']

Unique values in column 'Hospital':
	['Sons and Miller' 'Kim Inc' 'Cook PLC' ... 'Guzman Jones and
Graves,'
 'and Williams, Brown Mckenzie' 'Moreno Murphy, Griffith and']
```

```
Unique values in column 'Insurance Provider':
     ['Blue Cross' 'Medicare' 'Aetna' 'UnitedHealthcare' 'Cigna']

Unique values in column 'Billing Amount':
     [18856.28130598 33643.32728658 27955.09607884 ...  8441.14706442
 34934.2841126   8926.28593733]

Unique values in column 'Room Number':
     [328 265 205 450 458 389 277 316 249 394 288 134 309 182 465 114
449 260
 115 295 327 119 109 162 401 157 223 293 371 108 245 494 285 228 481
212
 113 272 478 196 418 410 300 211 413 138 456 234 492 180 250 296 330
405
 306 333 244 325 378 468 368 263 489 241 231 377 407 135 131 102 255
422
 320 273 395 152 321 428 482 268 120 318 144 226 459 208 227 402 442
425
 373 290 361 251 440 414 424 307 476 388 326 178 177 302 130 430 133
104
 408 376 331 275 480 233 384 380 310 406 213 427 500 451 485 267 154
466
 453 261 167 179 490 258 483 202 198 308 278 103 400 192 128 238 136
218
 348 486 147 126 314 271 341 498 168 189 438 286 266 392 156 315 322
184
 472 398 435 174 137 111 464 117 493 183 471 164 356 497 421 488 317
247
 158 242 151 221 359 370 141 343 319 121 166 397 186 299 101 142 181
282
 350 262 210 391 195 214 409 279 243 106 467 176 287 124 352 165 347
354
 225 357 140 404 426 236 194 188 415 185 358 390 112 283 439 123 469
230
 171 484 256 365 452 172 197 110 437 419 416 461 431 105 313 385 116
386
 175 270 338 360 252 215 434 374 217 366 118 387 237 355 364 169 301
463
 382 232 455 462 393 423 264 289 342 292 146 193 148 441 199 216 132
475
 436 403 433 206 207 375 159 304 349 396 445 276 298 129 209 420 324
443
 254 470 346 496 448 280 335 411 200 312 305 345 145 203 362 454 191
339
 477 219 412 379 340 170 190 363 491 487 334 125 332 224 204 323 248
297
 311 201 143 107 303 329 122 337 457 274 246 294 161 336 383 187 229
291
 155 173 353 281 446 399 479 429 150 253 149 369 220 127 153 474 372
381
 473 351 259 257 367 222 460 447 495 344 163 139 444 284 499 432 269
160
 240 239 417 235]

Unique values in column 'Admission Type':
      ['Urgent' 'Emergency' 'Elective']

Unique values in column 'Discharge Date':
      ['2024-02-02' '2019-08-26' '2022-10-07' ... '2019-05-09' '2024-
05-31'
 '2024-06-06']

Unique values in column 'Medication':
      ['Paracetamol' 'Ibuprofen' 'Aspirin' 'Penicillin' 'Lipitor']

Unique values in column 'Test Results':
      ['Normal' 'Inconclusive' 'Abnormal']
```

Check for missing values

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

```
Name                  0
Age                   0
Gender                0
Blood Type            0
Medical Condition     0
Date of Admission     0
Doctor                0
Hospital              0
Insurance Provider    0
Billing Amount        0
Room Number           0
Admission Type        0
Discharge Date        0
Medication            0
Test Results          0
dtype: int64
```

Check for duplicate rows

```
df.duplicated().sum()
```

```
np.int64(534)
```

1.3. Statistical Summary

Display statistical summary of the DataFrame, including descriptive statistics for all columns

```
display(df.describe(include='all'))
```

```
                 Name           Age Gender Blood Type Medical Condition
\
count           55500  55500.000000  55500      55500             55500
unique          49992           NaN      2          8                 6
top       DAvId muNoZ           NaN   Male         A-         Arthritis
freq                3           NaN  27774       6969              9308
mean              NaN     51.539459    NaN        NaN               NaN
std               NaN     19.602454    NaN        NaN               NaN
min               NaN     13.000000    NaN        NaN               NaN
25%               NaN     35.000000    NaN        NaN               NaN
50%               NaN     52.000000    NaN        NaN               NaN
75%               NaN     68.000000    NaN        NaN               NaN
max               NaN     89.000000    NaN        NaN               NaN

       Date of Admission         Doctor    Hospital Insurance Provider
\
count              55500          55500       55500              55500
unique              1827          40341       39876                  5
top           2024-03-16  Michael Smith   LLC Smith              Cigna
freq                  50             27          44              11249
mean                 NaN            NaN         NaN                NaN
std                  NaN            NaN         NaN                NaN
min                  NaN            NaN         NaN                NaN
25%                  NaN            NaN         NaN                NaN
50%                  NaN            NaN         NaN                NaN
75%                  NaN            NaN         NaN                NaN
max                  NaN            NaN         NaN                NaN
```

```
        Billing Amount   Room Number Admission Type Discharge Date
Medication  \
count     55500.000000  55500.000000          55500          55500
55500
unique             NaN           NaN              3           1856
5
top                NaN           NaN       Elective     2020-03-15
Lipitor
freq               NaN           NaN          18655             53
11140
mean      25539.316097    301.134829            NaN            NaN
NaN
std       14211.454431    115.243069            NaN            NaN
NaN
min       -2008.492140    101.000000            NaN            NaN
NaN
25%       13241.224652    202.000000            NaN            NaN
NaN
50%       25538.069376    302.000000            NaN            NaN
NaN
75%       37820.508436    401.000000            NaN            NaN
NaN
max       52764.276736    500.000000            NaN            NaN
NaN

       Test Results
count         55500
unique            3
top        Abnormal
freq          18627
mean            NaN
std             NaN
min             NaN
25%             NaN
50%             NaN
75%             NaN
max             NaN
```

Part 2: Exploratory Data Analysis (EDA)

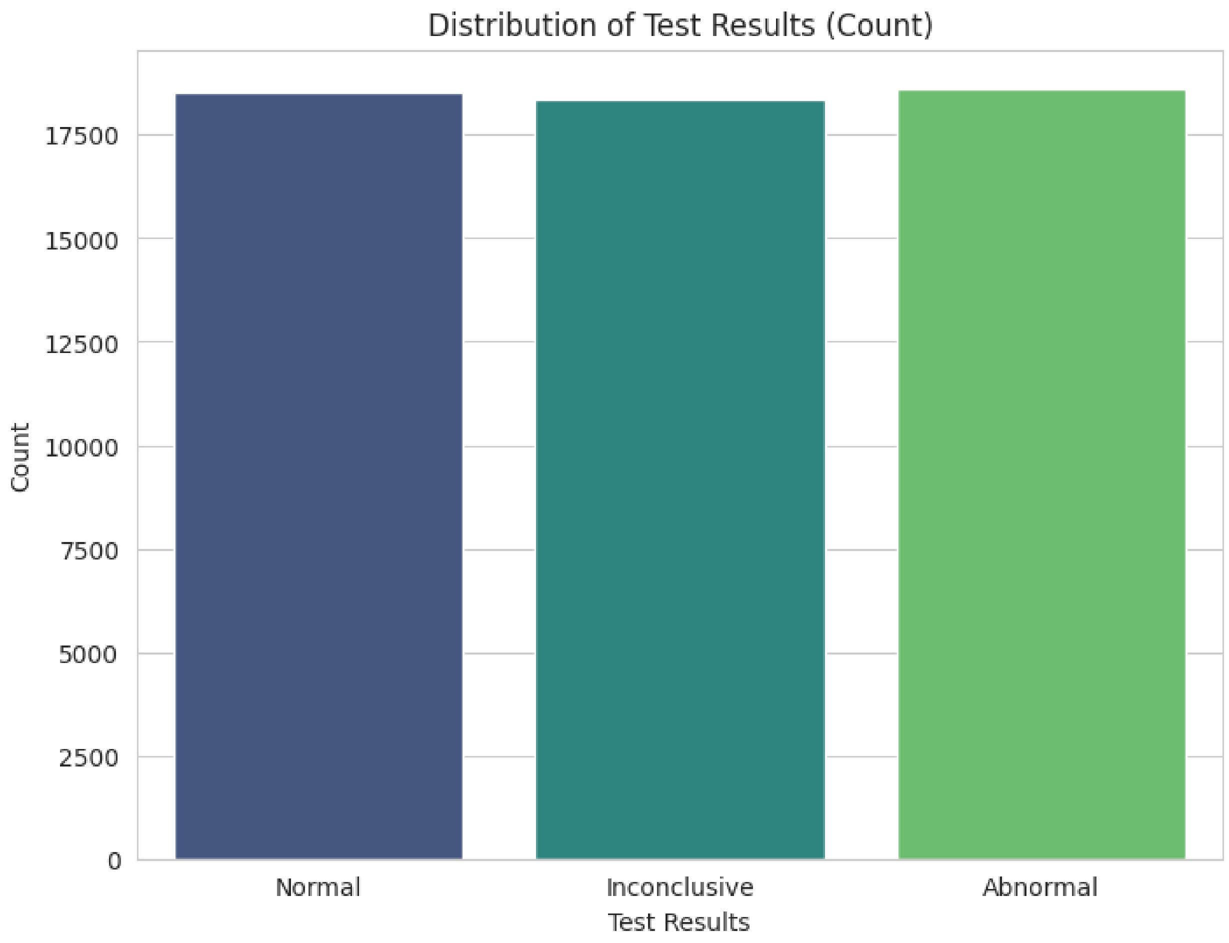
Through visualization and statistical analysis, we aim to uncover patterns, identify anomalies, and understand the relationships between different variables and our target variable, Test Results.

2.1. Target Variable Analysis

Create a countplot to visualize the distribution of the target variable 'Test Results'

```
plt.figure(figsize=(8, 6))
sns.countplot(data=df, x='Test Results', palette='viridis')
plt.title('Distribution of Test Results (Count)')
plt.xlabel('Test Results')
plt.ylabel('Count')
plt.show()
```

```
/tmp/ipython-input-29353002.py:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `x` variable to `hue` and set
`legend=False` for the same effect.

  sns.countplot(data=df, x='Test Results', palette='viridis')
```



Calculate and display the distribution of the target variable (count and percentage)

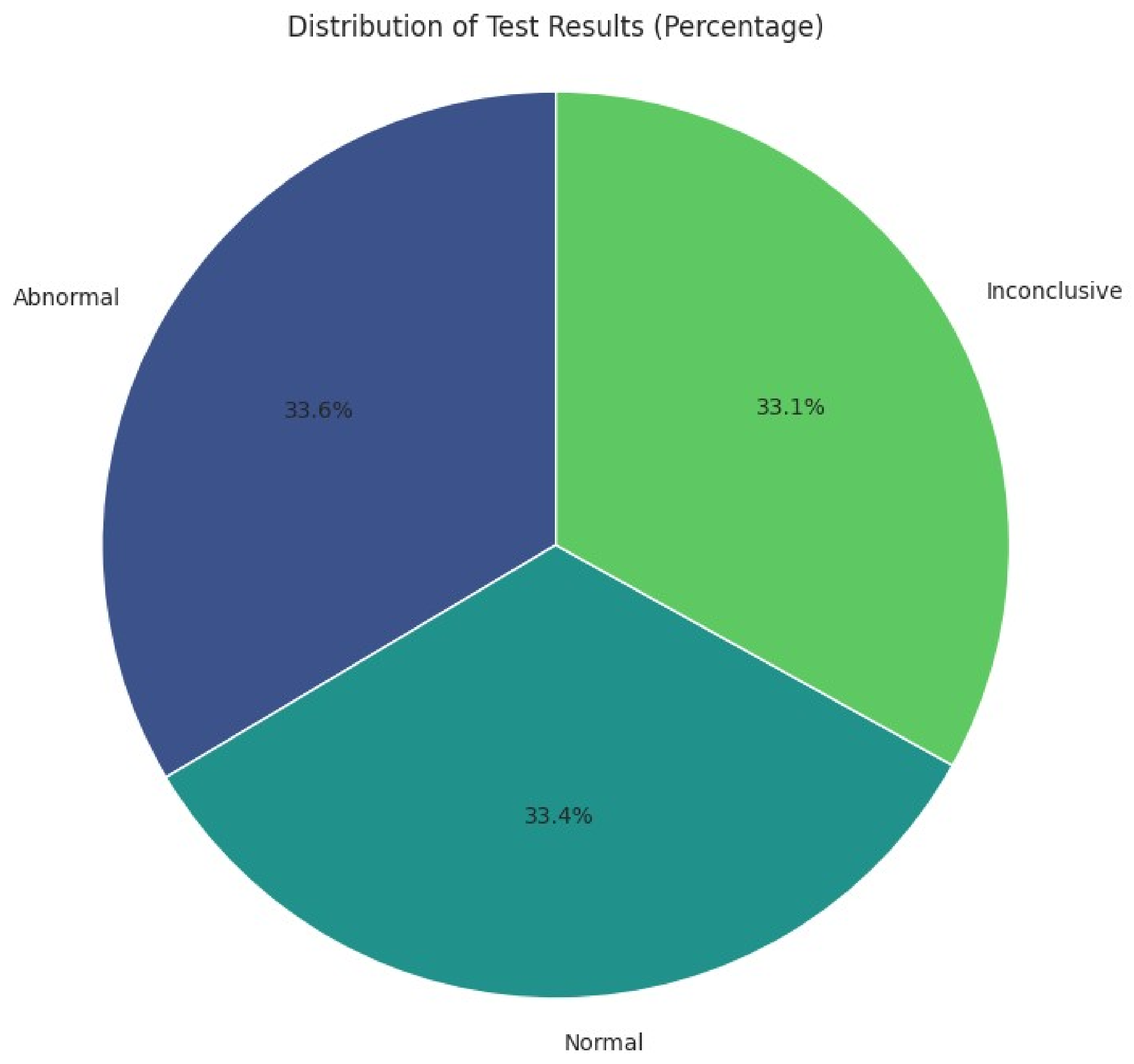
```
target_distribution = df['Test Results'].value_counts().reset_index()
target_distribution.columns = ['Test Results', 'Count']
target_distribution['Percentage (%)'] =
round(target_distribution['Count'] / len(df) * 100, 2)
```

```
print("\nDistribution of Test Results:")
display(target_distribution)
```

```
Distribution of Test Results:

   Test Results  Count  Percentage (%)
0      Abnormal  18627           33.56
1        Normal  18517           33.36
2  Inconclusive  18356           33.07
```

Create a pie plot to visualize the distribution of the target variable

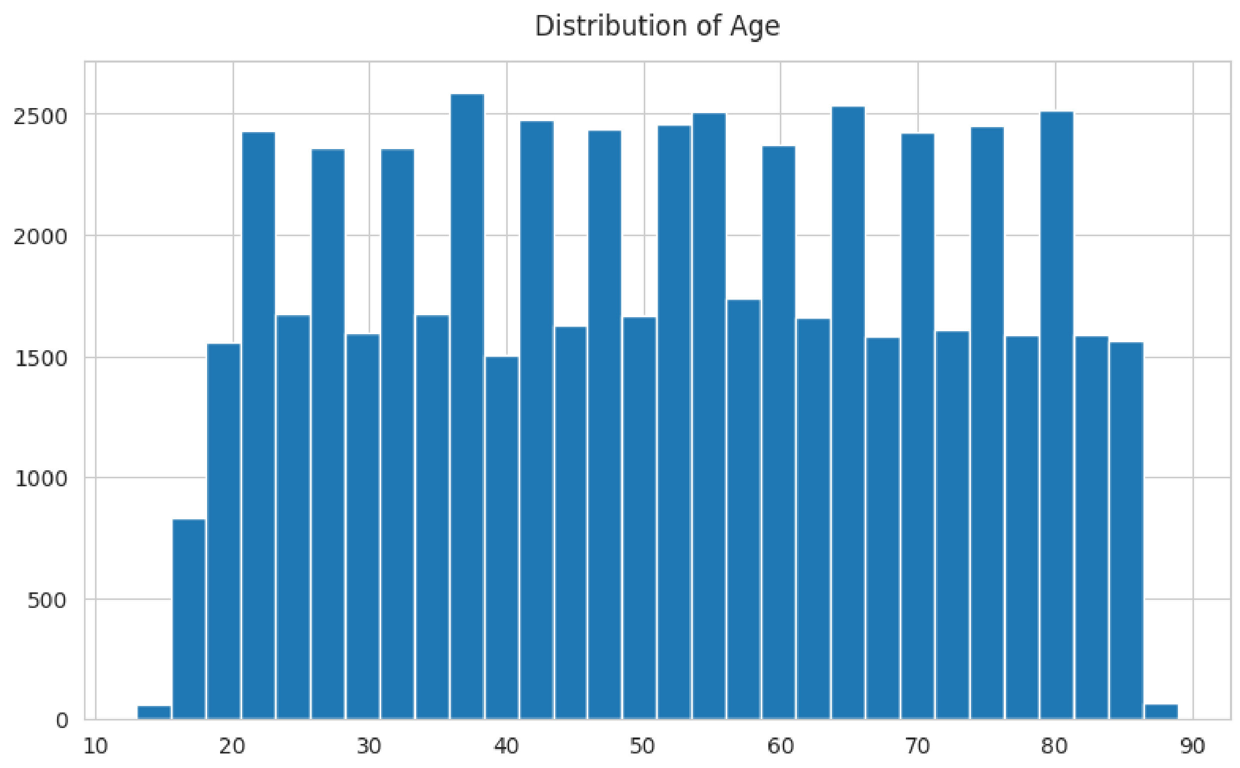
```
plt.figure(figsize=(8, 8))
plt.pie(target_distribution['Count'], labels=target_distribution['Test
Results'], autopct='%1.1f%%', startangle=90,
colors=sns.color_palette('viridis', len(target_distribution)))
plt.title('Distribution of Test Results (Percentage)')
plt.axis('equal') # Equal aspect ratio ensures that pie is drawn as a
circle.
plt.show()
```

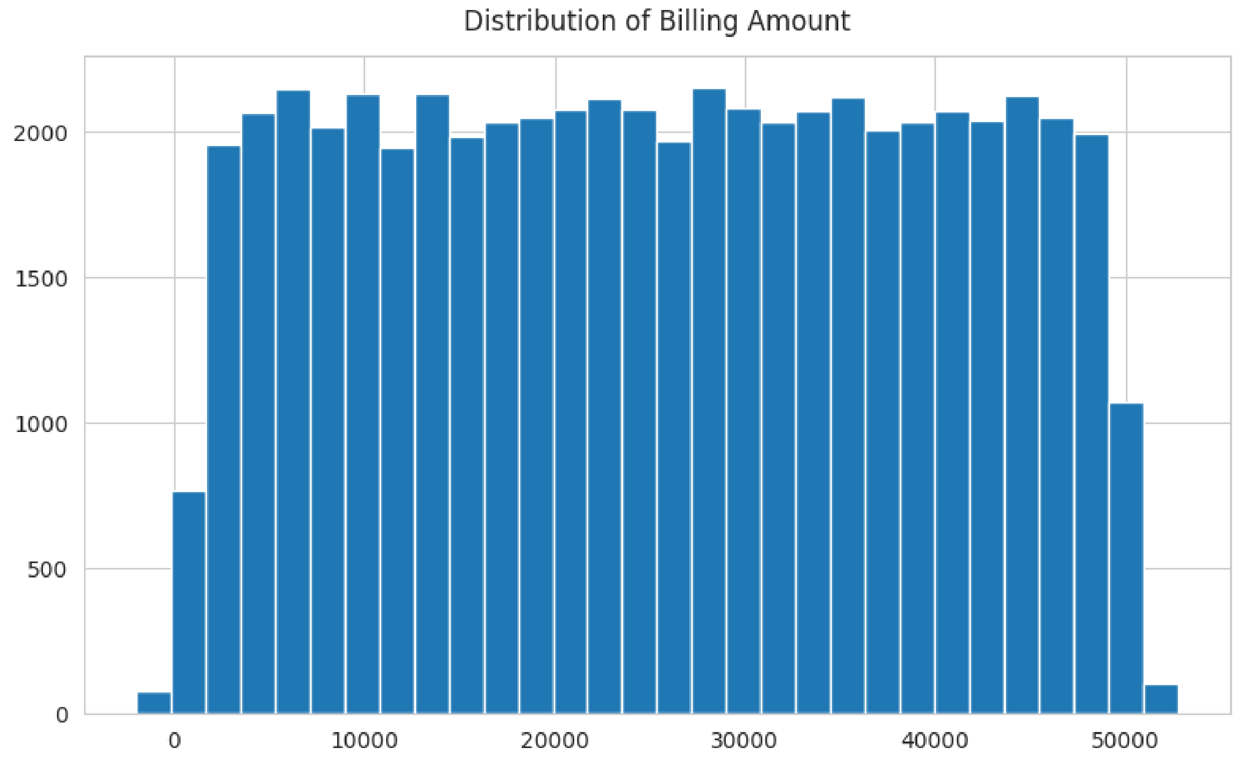


2.2. Univariate Analysis

Analyze the distribution of numerical features (Age, Billing Amount)

```python
numerical_features = ['Age', 'Billing Amount']
for col in numerical_features:
  df[col].hist(figsize=(8, 5), bins=30)
  plt.title(f'Distribution of {col}', y=1.02)
  plt.tight_layout()
  plt.show()
```

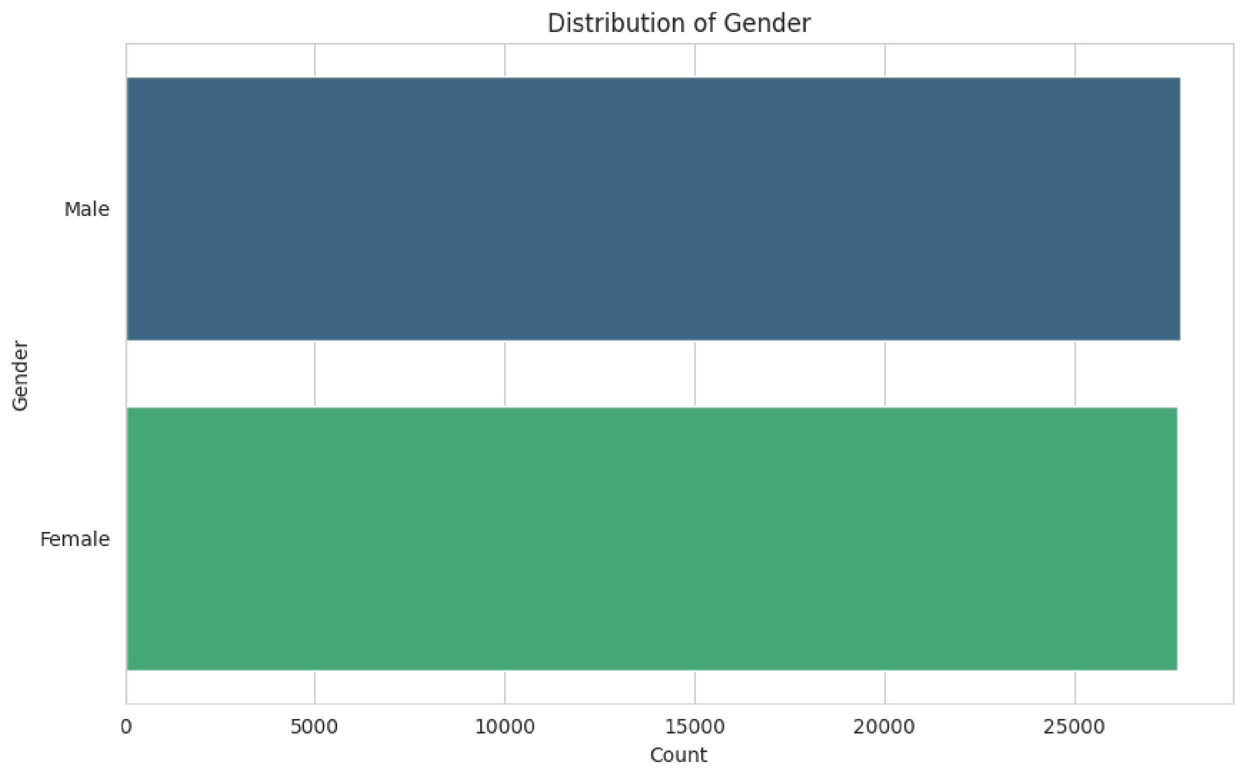




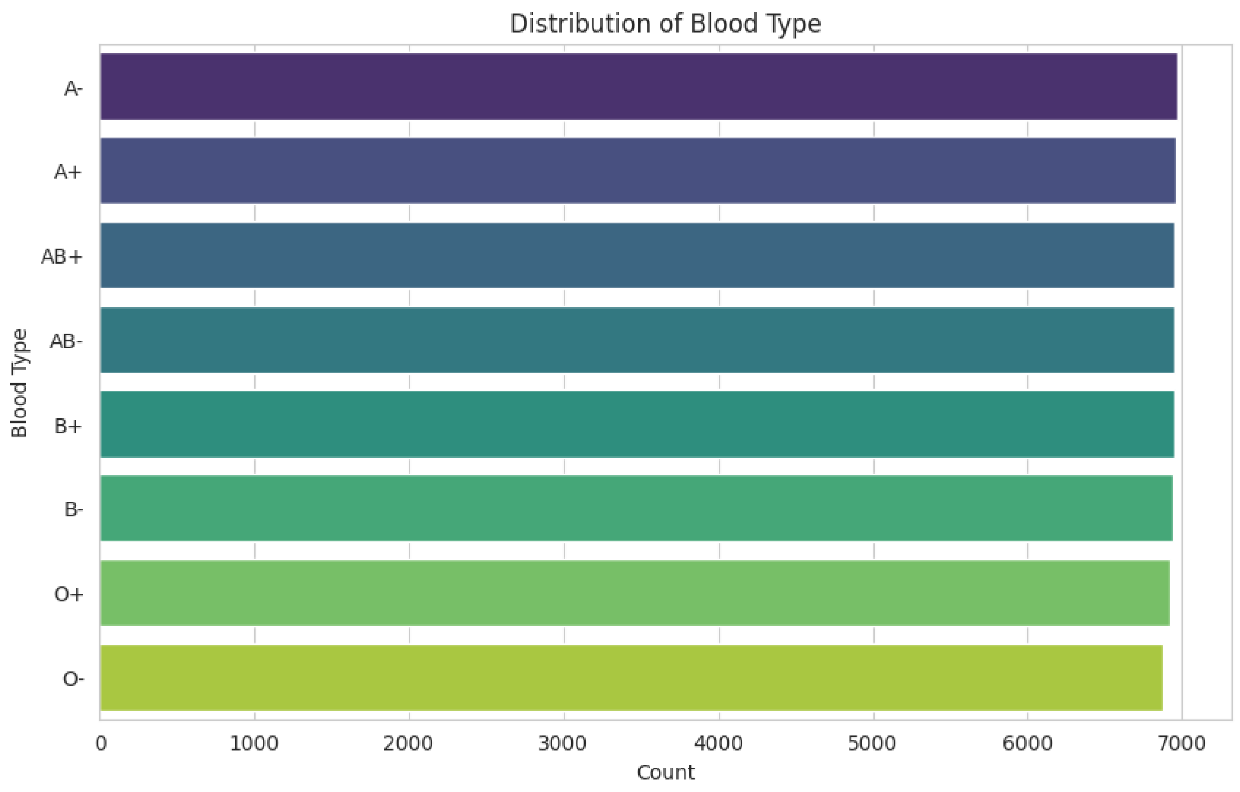
Analyze the distribution of key categorical features

```
# Analyze the distribution of all relevant categorical features
# Exclude 'Test Results' as it's the target variable analyzed
separately
# Exclude columns identified as irrelevant in Part 3 ('Name',
'Doctor', 'Hospital')
# Exclude date columns which were engineered into 'Length of Stay'
all_categorical_cols =
df.select_dtypes(include='object').columns.tolist()
relevant_categorical_features = [col for col in all_categorical_cols
if col not in ['Test Results', 'Name', 'Doctor', 'Hospital', 'Date of
Admission', 'Discharge Date']]

# Plot distribution for each relevant categorical feature individually
for col in relevant_categorical_features:
    plt.figure(figsize=(10, 6)) # Adjust figure size for individual
plots
    sns.countplot(data=df, y=col, palette='viridis',
order=df[col].value_counts().index) # Order by count
    plt.title(f'Distribution of {col}')
    plt.xlabel('Count')
    plt.ylabel(col)
    plt.show()
```

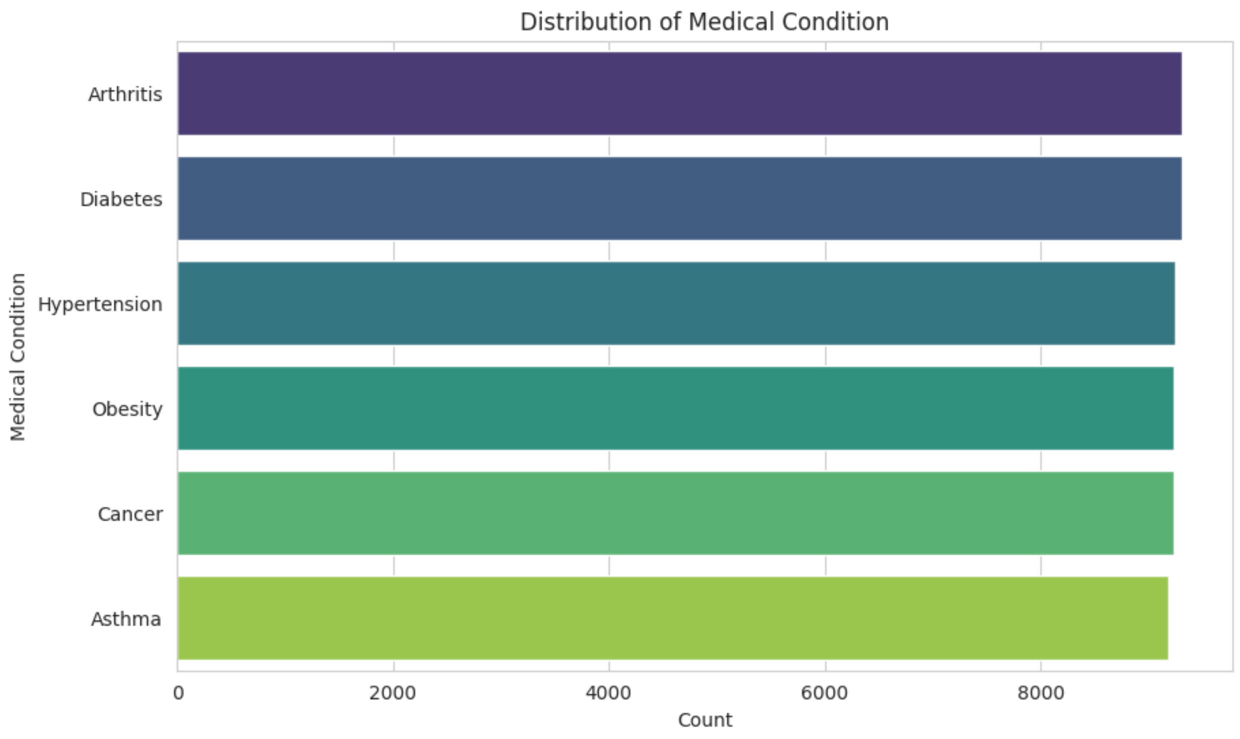
```
/tmp/ipython-input-3154795450.py:11: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `y` variable to `hue` and set
`legend=False` for the same effect.

  sns.countplot(data=df, y=col, palette='viridis',
order=df[col].value_counts().index) # Order by count
```



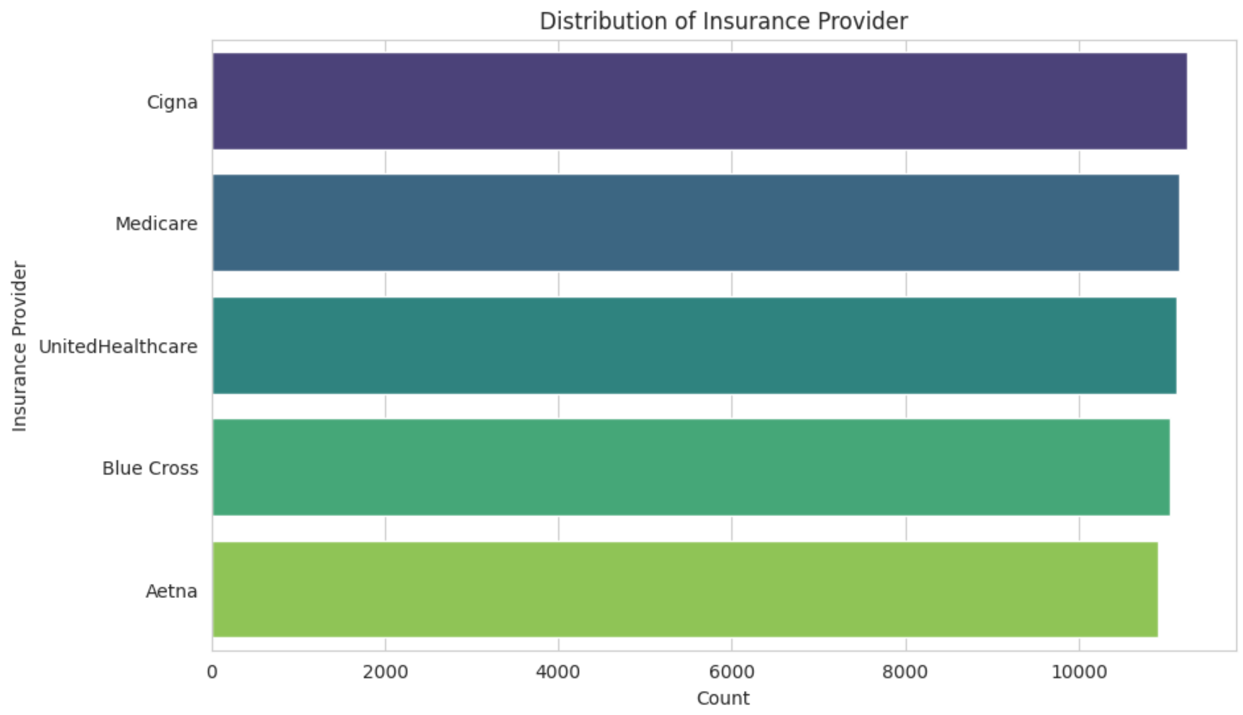
```
/tmp/ipython-input-3154795450.py:11: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `y` variable to `hue` and set
`legend=False` for the same effect.

  sns.countplot(data=df, y=col, palette='viridis',
order=df[col].value_counts().index) # Order by count
```



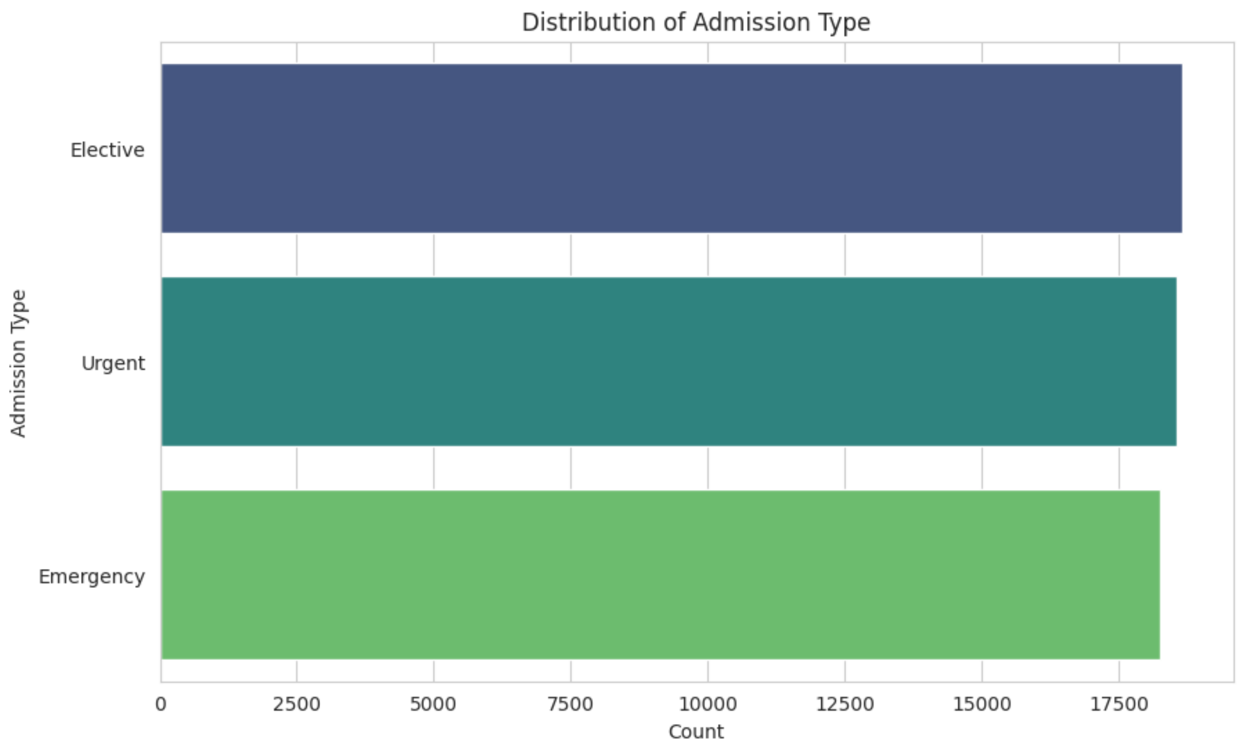
```
/tmp/ipython-input-3154795450.py:11: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `y` variable to `hue` and set
`legend=False` for the same effect.

  sns.countplot(data=df, y=col, palette='viridis',
order=df[col].value_counts().index) # Order by count
```



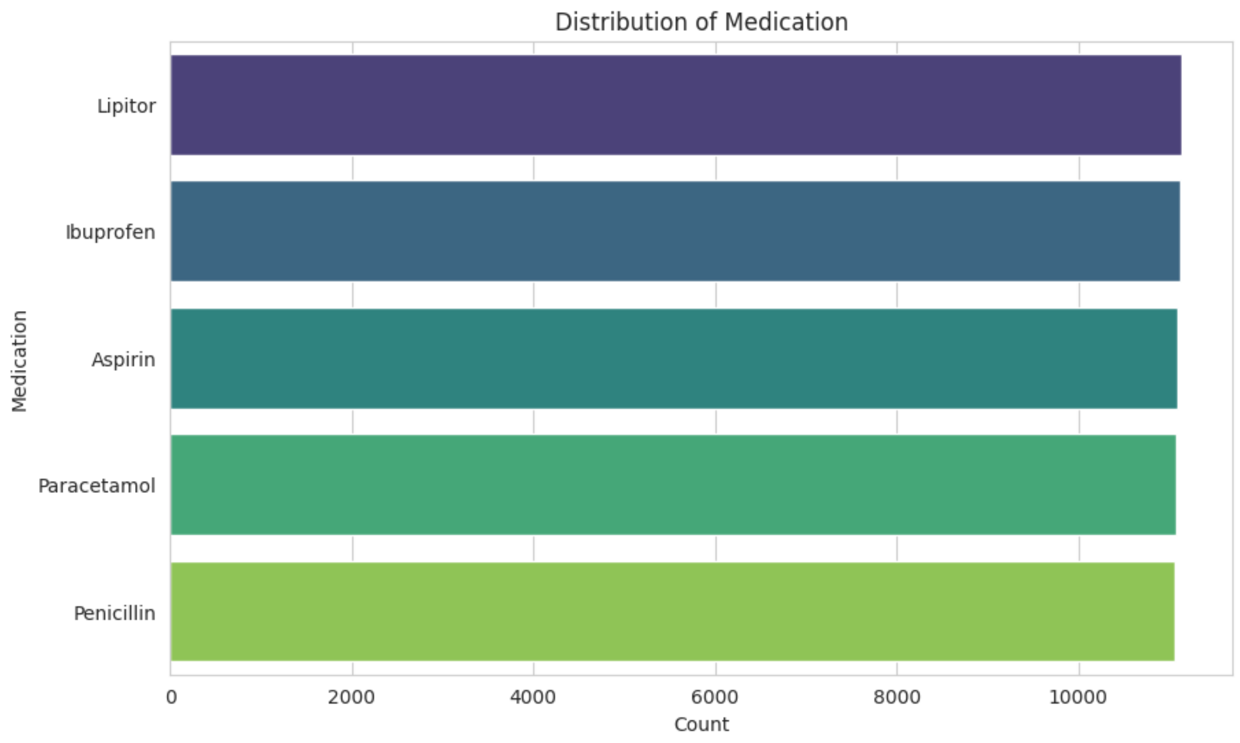
```
/tmp/ipython-input-3154795450.py:11: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `y` variable to `hue` and set
`legend=False` for the same effect.

  sns.countplot(data=df, y=col, palette='viridis',
order=df[col].value_counts().index) # Order by count
```



```
/tmp/ipython-input-3154795450.py:11: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `y` variable to `hue` and set
`legend=False` for the same effect.

  sns.countplot(data=df, y=col, palette='viridis',
order=df[col].value_counts().index) # Order by count
```



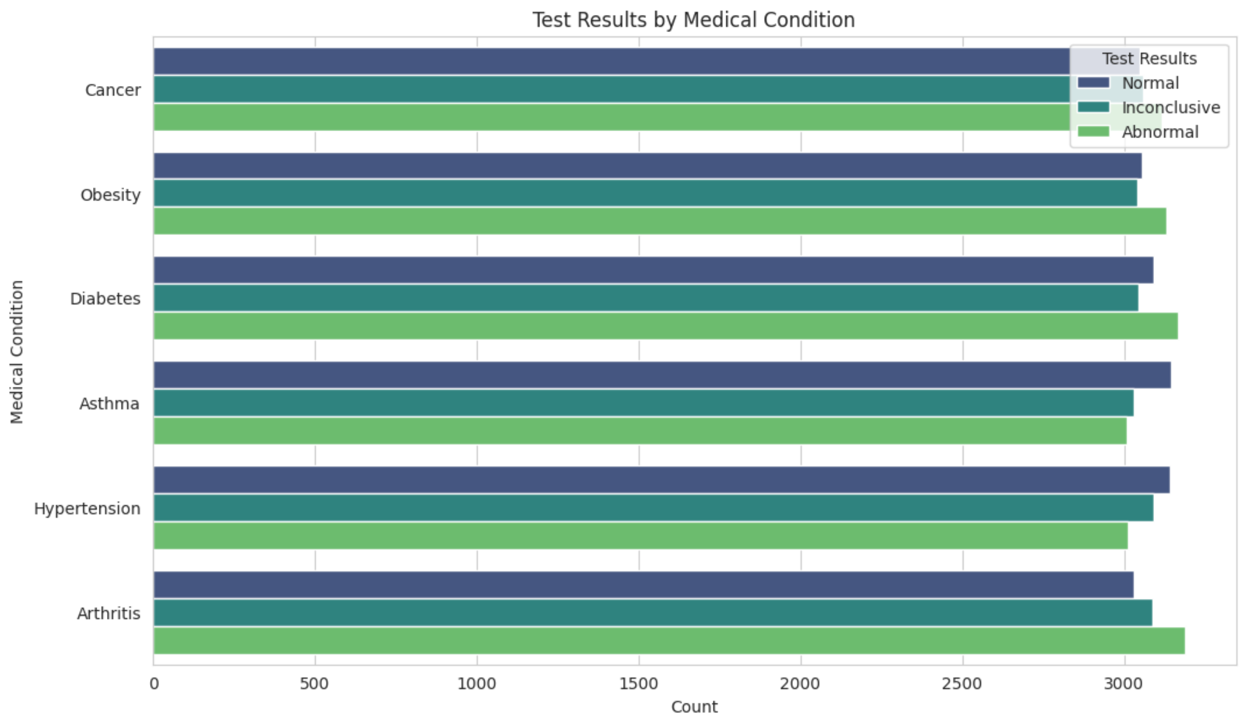
```
/tmp/ipython-input-3154795450.py:11: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `y` variable to `hue` and set
`legend=False` for the same effect.

  sns.countplot(data=df, y=col, palette='viridis',
order=df[col].value_counts().index) # Order by count
```



2.3. Bivariate Analysis

Analyze the relationship between 'Medical Condition' and 'Test Results'

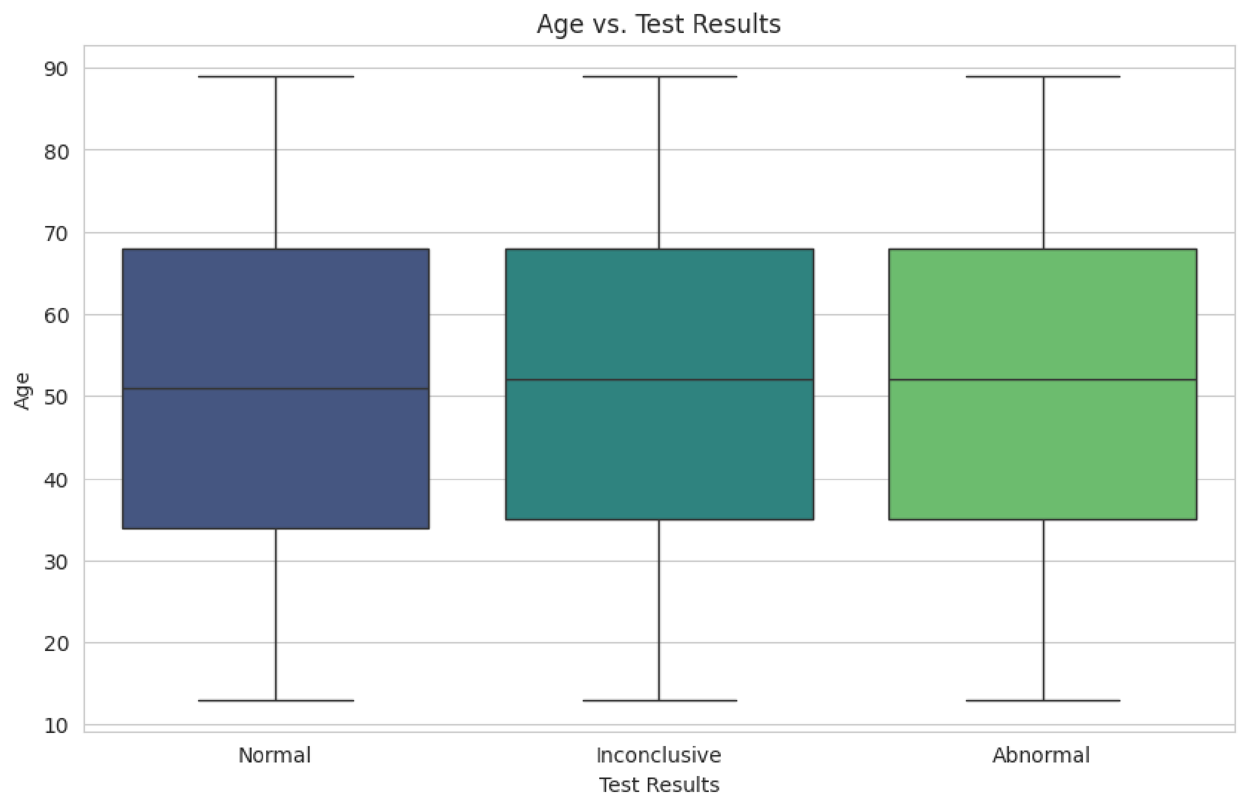
```
plt.figure(figsize=(12, 7))
sns.countplot(data=df, y='Medical Condition', hue='Test Results',
palette='viridis')
plt.title('Test Results by Medical Condition')
plt.xlabel('Count')
plt.ylabel('Medical Condition')
plt.show()
```



Analyze the relationship between 'Age' and 'Test Results' using a boxplot

```
plt.figure(figsize=(10, 6))
sns.boxplot(data=df, x='Test Results', y='Age', palette='viridis')
plt.title('Age vs. Test Results')
plt.xlabel('Test Results')
plt.ylabel('Age')
plt.show()
```

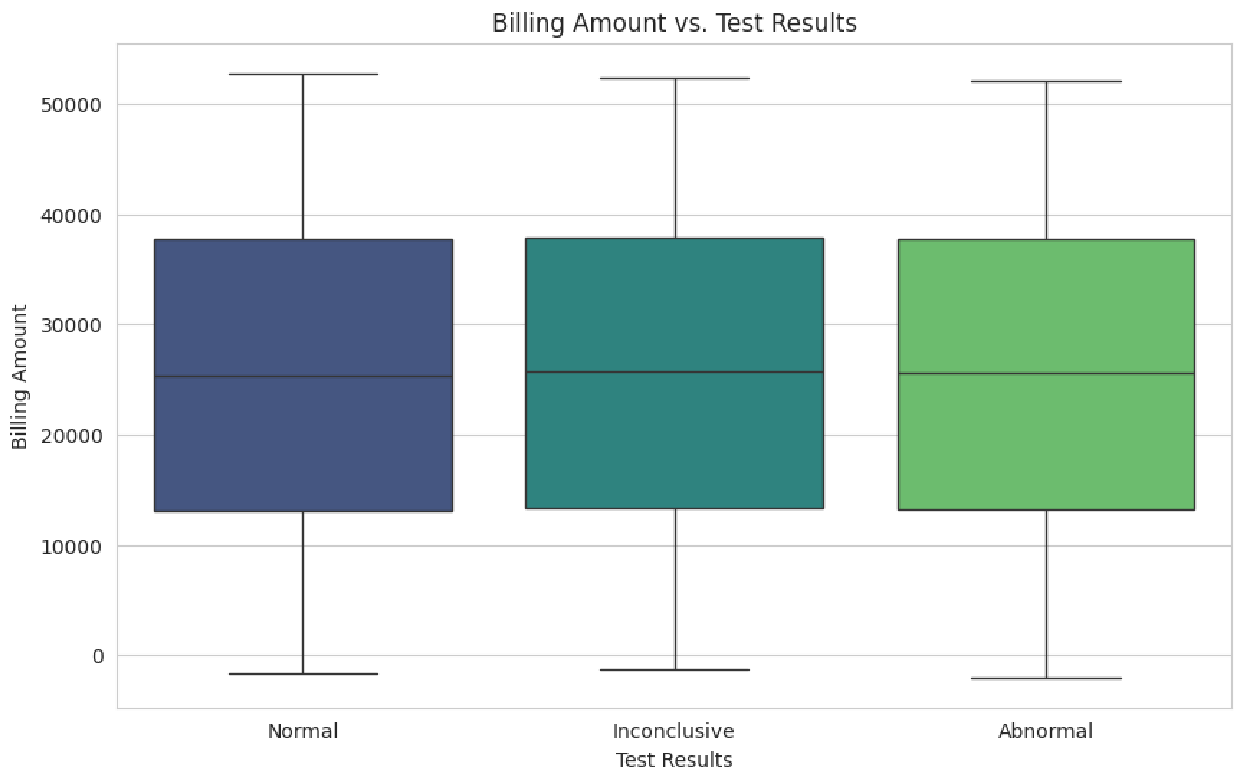
```
/tmp/ipython-input-3623247868.py:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `x` variable to `hue` and set
`legend=False` for the same effect.

  sns.boxplot(data=df, x='Test Results', y='Age', palette='viridis')
```



Analyze the relationship between 'Billing Amount' and 'Test Results' using a boxplot

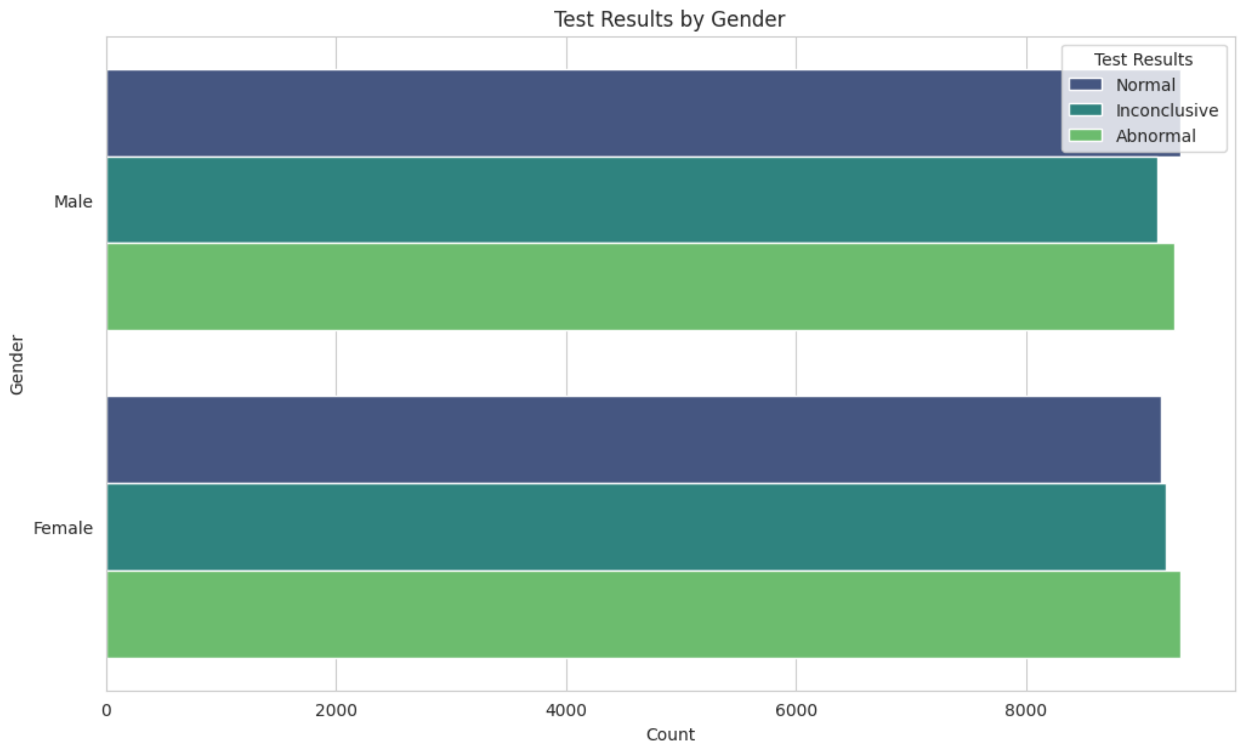
```
plt.figure(figsize=(10, 6))
sns.boxplot(data=df, x='Test Results', y='Billing Amount',
palette='viridis')
plt.title('Billing Amount vs. Test Results')
plt.xlabel('Test Results')
plt.ylabel('Billing Amount')
plt.show()
```

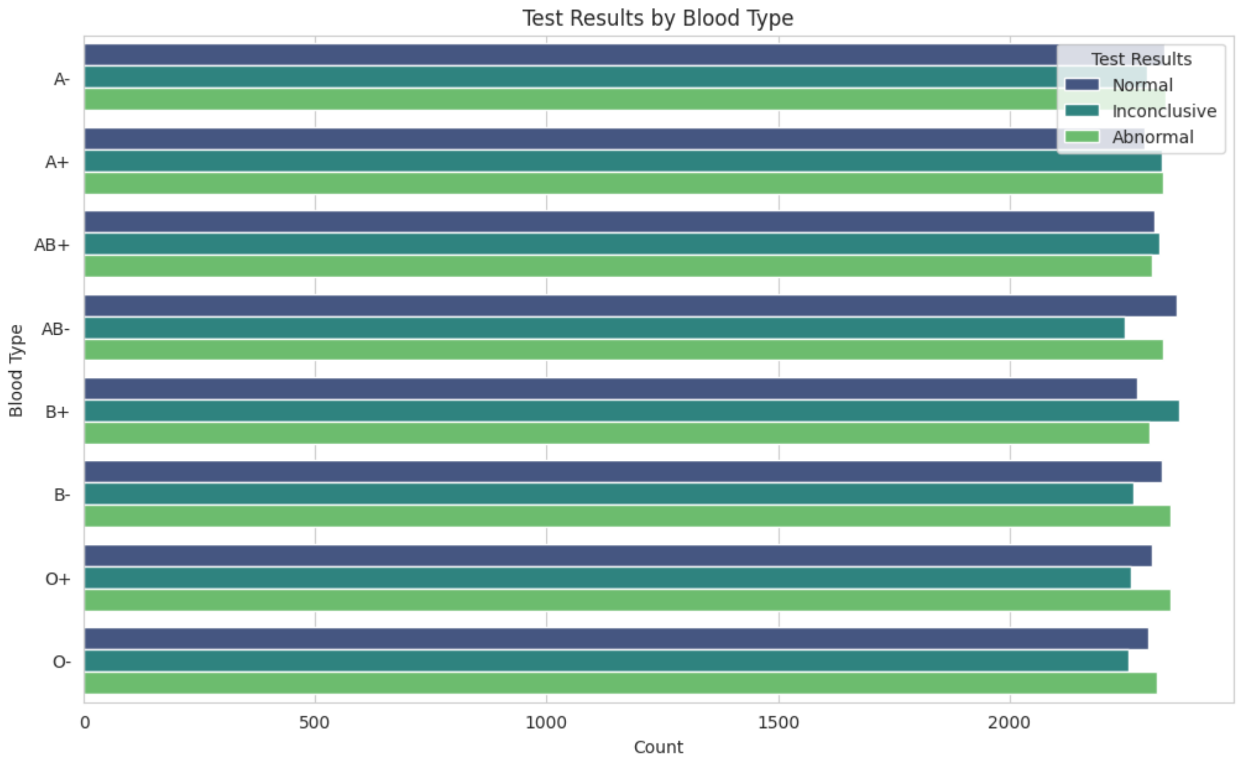
```
/tmp/ipython-input-3016713708.py:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be
removed in v0.14.0. Assign the `x` variable to `hue` and set
`legend=False` for the same effect.

  sns.boxplot(data=df, x='Test Results', y='Billing Amount',
palette='viridis')
```

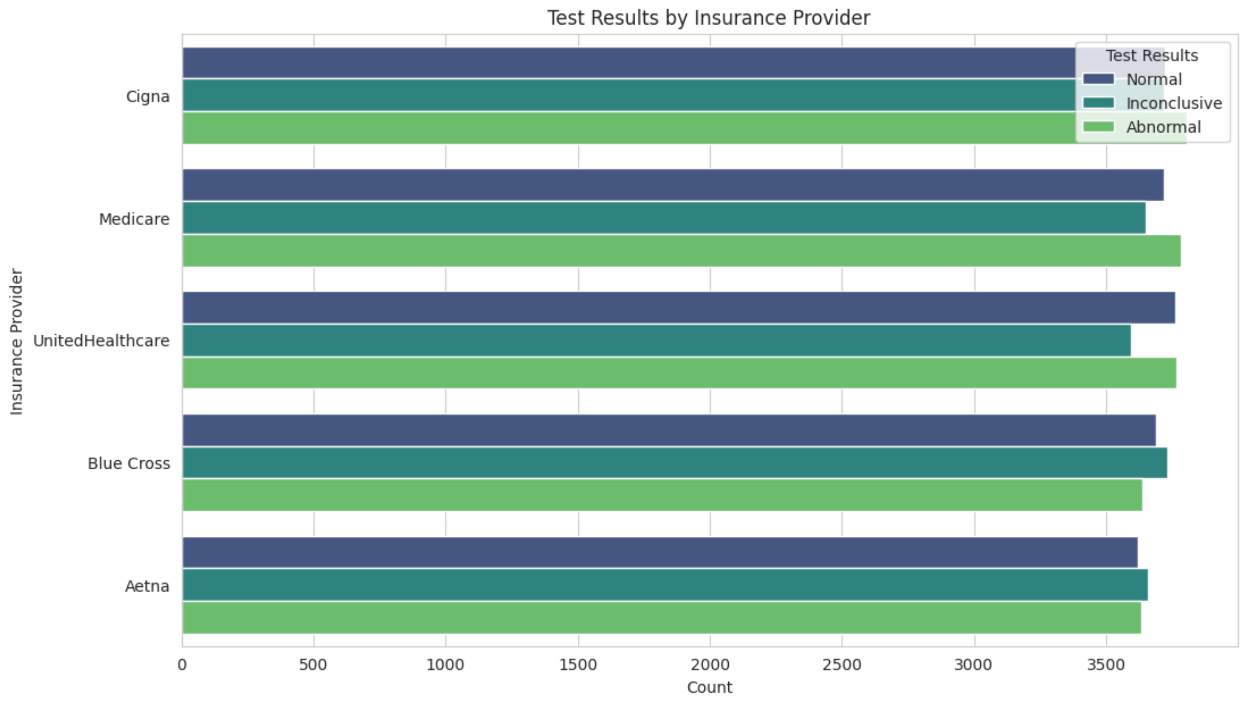


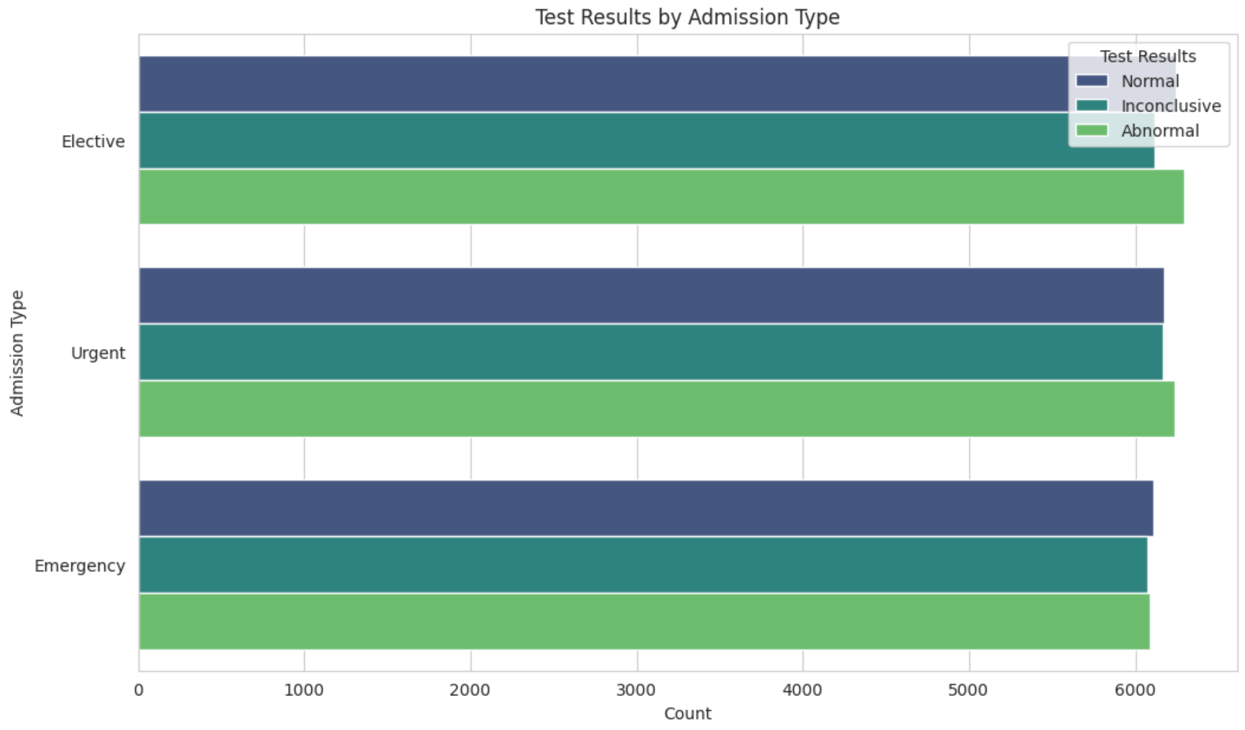
Analyze the relationship between other relevant categorical features and 'Test Results'

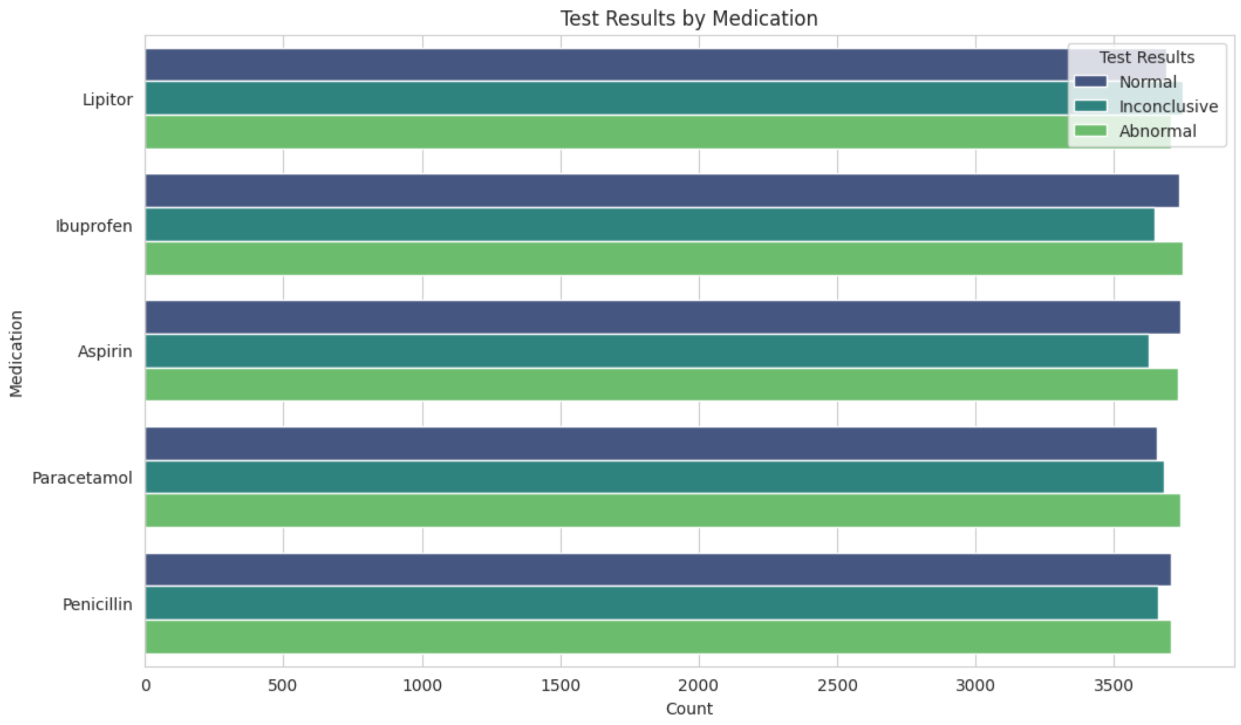
```
relevant_categorical_features_for_bivariate = ['Gender', 'Blood Type',
'Insurance Provider', 'Admission Type', 'Medication']

for col in relevant_categorical_features_for_bivariate:
    plt.figure(figsize=(12, 7))
    sns.countplot(data=df, y=col, hue='Test Results',
palette='viridis', order=df[col].value_counts().index)
    plt.title(f'Test Results by {col}')
    plt.xlabel('Count')
    plt.ylabel(col)
    plt.show()
```


Test Results by Gender
Test Results
Normal
Inconclusive
Abnormal
Male
Female
Gender
0
2000
4000
6000
8000
Count

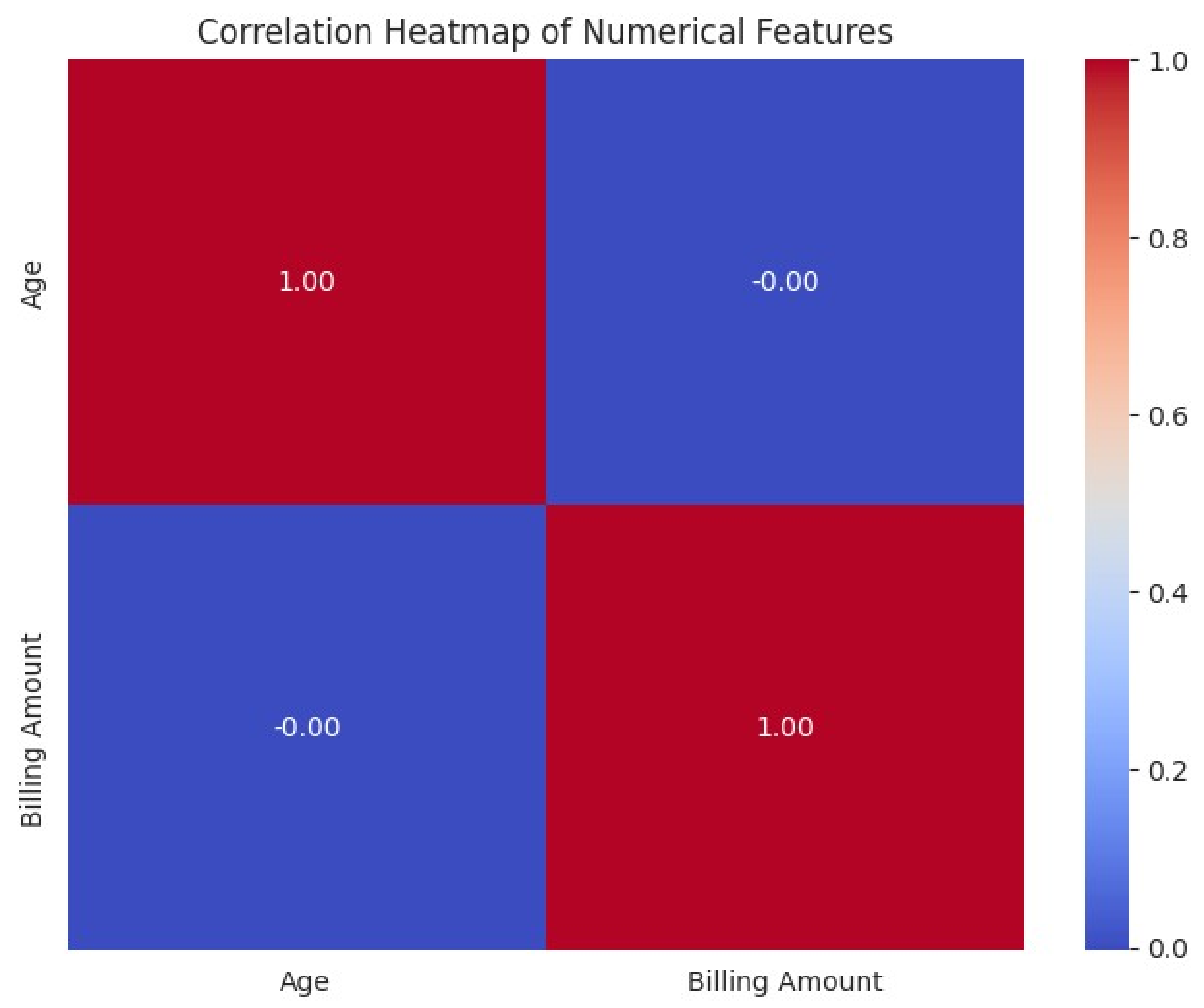

Test Results by Blood Type
Test Results
Normal
Inconclusive
Abnormal
A-
A+
AB+
AB-
B+
B-
O+
O-
Blood Type
0
500
1000
1500
2000
Count


Test Results by Insurance Provider
Test Results
Normal
Inconclusive
Abnormal
Cigna
Medicare
UnitedHealthcare
Blue Cross
Aetna
Insurance Provider
0
500
1000
1500
2000
2500
3000
3500
Count


Test Results by Admission Type
Test Results
Normal
Inconclusive
Abnormal
Elective
Urgent
Emergency
Admission Type
0
1000
2000
3000
4000
5000
6000
Count



```python
# Create a heatmap to visualize the correlation matrix of numerical
features
# Include 'Length of Stay' if it exists after Feature Engineering
(Part 3)
numerical_features_for_corr = ['Age', 'Billing Amount']
if 'Length of Stay' in df.columns:
    numerical_features_for_corr.append('Length of Stay')

plt.figure(figsize=(8, 6))
correlation_matrix = df[numerical_features_for_corr].corr()
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm',
fmt=".2f")
plt.title('Correlation Heatmap of Numerical Features')
plt.show()
```

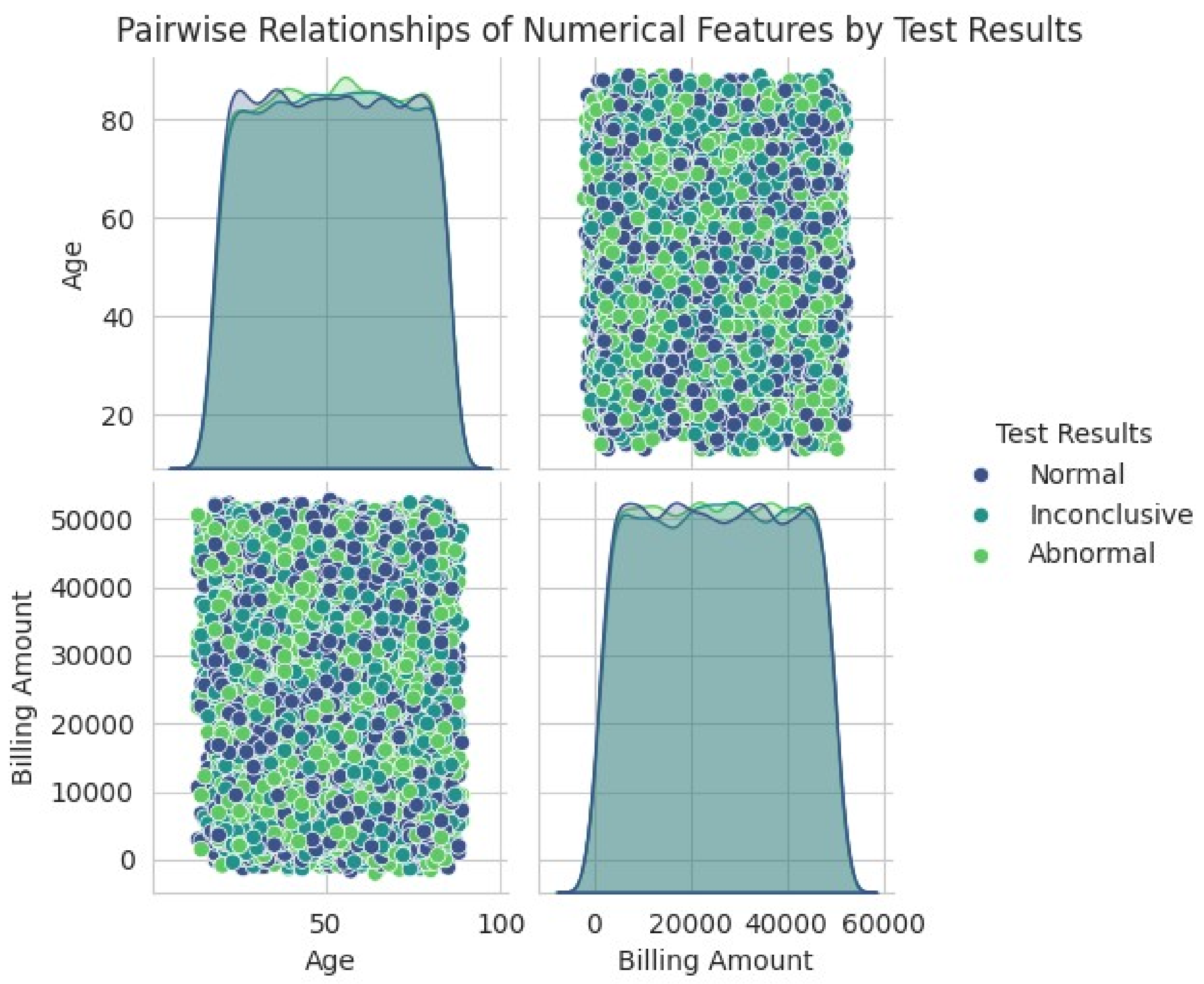


2.4. Multivariate Analysis

Here, we explore the relationships among multiple variables simultaneously to uncover more complex patterns or interactions.

```
# Explore relationships between numerical features, colored by the
target variable
# Include 'Length of Stay' if it was created in Feature Engineering
numerical_features_for_pairplot = ['Age', 'Billing Amount']
if 'Length of Stay' in df.columns:
    numerical_features_for_pairplot.append('Length of Stay')

# Add the target variable to the list for the pairplot
pairplot_cols = numerical_features_for_pairplot + ['Test Results']

# Create a pair plot to visualize pairwise relationships colored by
the target variable
# This helps to see if combinations of numerical features show
different patterns for different test results
```

```
sns.pairplot(df[pairplot_cols], hue='Test Results', palette='viridis')
plt.suptitle('Pairwise Relationships of Numerical Features by Test
Results', y=1.02)
plt.show()
```



Part 3: Data Preprocessing & Feature Engineering

This crucial section focuses on cleaning, transforming, and enriching the data to create a high-quality, model-ready feature set.

3.1. Data Cleaning

Check for duplicate rows

```
print(f"Number of duplicate rows before dropping:
{df.duplicated().sum()}")

Number of duplicate rows before dropping: 534
```

Drop duplicate rows

```
df.drop_duplicates(inplace=True)
print(f"Number of duplicate rows after dropping:
{df.duplicated().sum()}")

Number of duplicate rows after dropping: 0
```

Define and drop irrelevant columns that are unlikely to contribute to the model

```
irrelevant_cols = ['Name', 'Doctor', 'Hospital']
df.drop(columns=irrelevant_cols, inplace=True)
print(f"\nDropped irrelevant columns: {irrelevant_cols}")
print(f"DataFrame shape after dropping columns: {df.shape}")


Dropped irrelevant columns: ['Name', 'Doctor', 'Hospital']
DataFrame shape after dropping columns: (54966, 12)
```

3.2. Feature Engineering

Convert date columns to datetime objects

```
df['Date of Admission'] = pd.to_datetime(df['Date of Admission'])
df['Discharge Date'] = pd.to_datetime(df['Discharge Date'])
```

Calculate 'Length of Stay' in days

```
df['Length of Stay'] = (df['Discharge Date'] - df['Date of
Admission']).dt.days
```

Drop the original date columns as 'Length of Stay' is a more useful feature

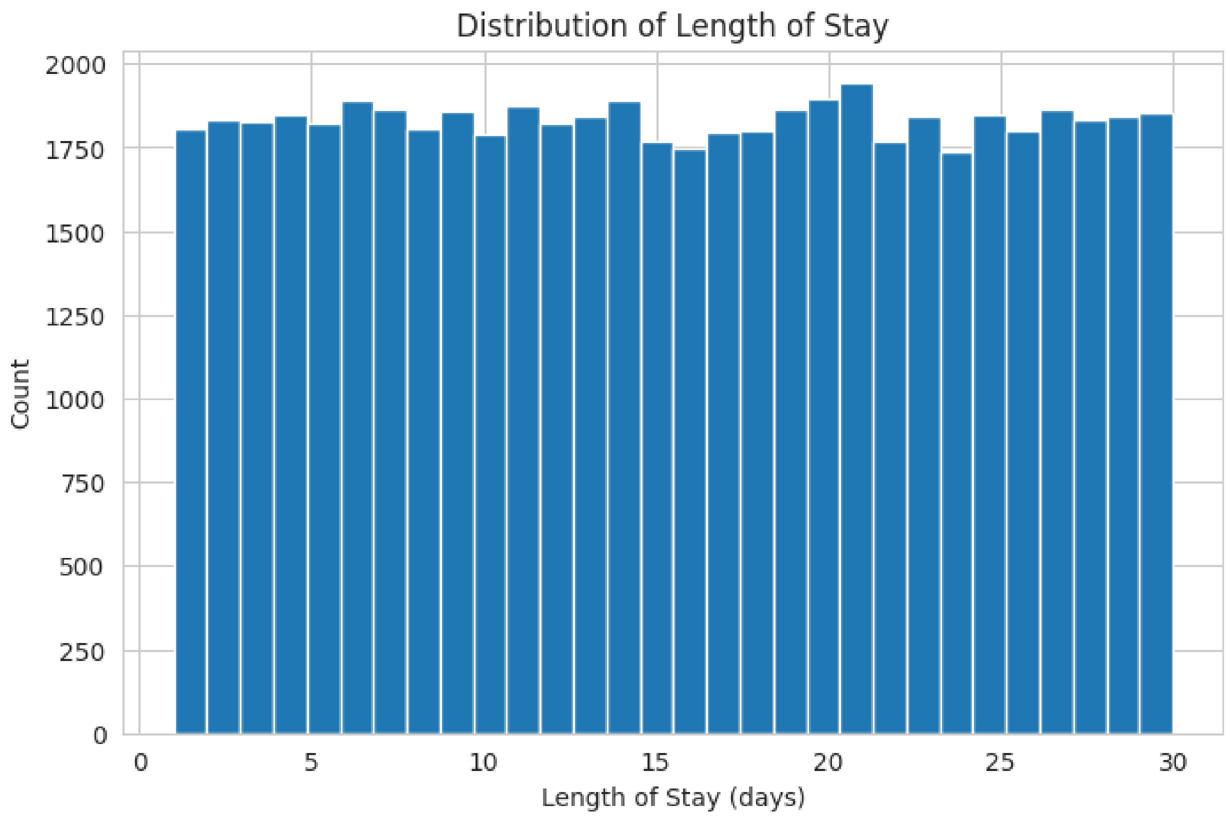
```
df.drop(columns=['Date of Admission', 'Discharge Date'], inplace=True)

print("\nCreated 'Length of Stay' feature and dropped original date
columns.")
display(df[['Length of Stay']].head())


Created 'Length of Stay' feature and dropped original date columns.

   Length of Stay
0               2
1               6
2              15
3              30
4              20
```

```
df['Length of Stay'].describe()
```

```
count    54966.000000
mean        15.499290
std          8.661471
min          1.000000
25%          8.000000
50%         15.000000
75%         23.000000
max         30.000000
Name: Length of Stay, dtype: float64
```

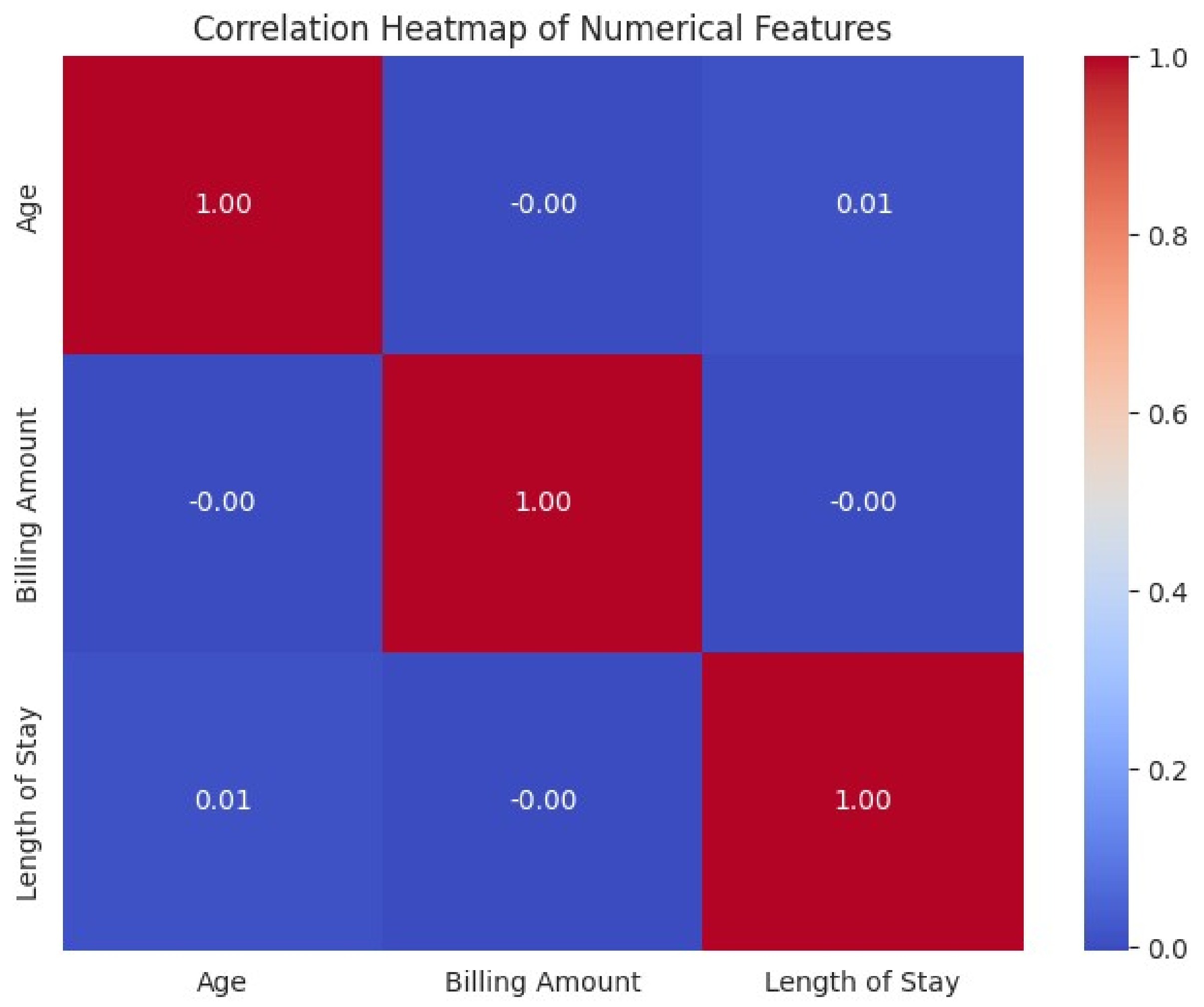
Plot the distribution of 'Length of Stay'

```
plt.figure(figsize=(8, 5))
df['Length of Stay'].hist(bins=30)
plt.title('Distribution of Length of Stay')
plt.xlabel('Length of Stay (days)')
plt.ylabel('Count')
plt.show()
```



```
# Create a heatmap to visualize the correlation matrix of numerical
features
```

```
# Include 'Length of Stay'
numerical_features_for_corr = ['Age', 'Billing Amount', 'Length of
Stay']

plt.figure(figsize=(8, 6))
correlation_matrix = df[numerical_features_for_corr].corr()
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm',
fmt=".2f")
plt.title('Correlation Heatmap of Numerical Features')
plt.show()
```



3.3. Column Separation

```
# Separate features (X) and target (y)
# The target variable 'Test Results' will be encoded separately
X = df.drop(columns=['Test Results'])
y = df['Test Results'] # Keep original target column for now before
encoding
```

```
# Identify numerical and categorical columns in the features (X)
# Exclude the target variable from these lists
numerical_cols = X.select_dtypes(include=np.number).columns.tolist()
categorical_cols = X.select_dtypes(include='object').columns.tolist()

print(f"\nFeatures (X) shape: {X.shape}")
print(f"Target (y) shape: {y.shape}")
print(f"\nNumerical columns in X: {numerical_cols}")
print(f"Categorical columns in X: {categorical_cols}")


Features (X) shape: (54966, 10)
Target (y) shape: (54966,)

Numerical columns in X: ['Age', 'Billing Amount', 'Room Number',
'Length of Stay']
Categorical columns in X: ['Gender', 'Blood Type', 'Medical
Condition', 'Insurance Provider', 'Admission Type', 'Medication']
```

3.4. Preprocessing (Manual Steps)

```
# Apply Label Encoding to the target variable 'Test Results'
# This converts the categorical target variable into numerical labels
(0, 1, 2)
label_encoder = LabelEncoder()
y_encoded = label_encoder.fit_transform(y)

# Display the mapping of original labels to encoded labels
print("Mapping of Test Results labels:")
for i, label in enumerate(label_encoder.classes_):
    print(f"{label}: {i}")

Mapping of Test Results labels:
Abnormal: 0
Inconclusive: 1
Normal: 2

# Create preprocessing pipelines for numerical and categorical
features
# Numerical features will be scaled using StandardScaler
numerical_transformer = StandardScaler()

# Categorical features will be one-hot encoded
# handle_unknown='ignore' handles unseen categories during prediction
(important for robust pipelines)
categorical_transformer = OneHotEncoder(handle_unknown='ignore')

# Create a ColumnTransformer to apply different transformations to
different columns
# 'remainder='passthrough'' means non-specified columns will be kept
(though we've separated all)
```

```
preprocessor = ColumnTransformer(
    transformers=[
        ('num', numerical_transformer, numerical_cols),
        ('cat', categorical_transformer, categorical_cols)])

# Apply the preprocessing transformations to the features (X)
# The output will be a NumPy array
X_processed = preprocessor.fit_transform(X)

# Convert the processed features back to a pandas DataFrame for easier
inspection if needed
# This step is optional but can be helpful for debugging
# Get feature names after one-hot encoding
onehot_feature_names =
preprocessor.named_transformers_['cat'].get_feature_names_out(categori
cal_cols)
all_feature_names = numerical_cols + list(onehot_feature_names)
X_processed_df = pd.DataFrame(X_processed, columns=all_feature_names)

print("\nShape of features after preprocessing:")
print(X_processed.shape)

print("\nFirst 5 rows of processed features (NumPy array):")
print(X_processed[:5])

print("\nFirst 5 encoded target labels:")
print(y_encoded[:5])
```

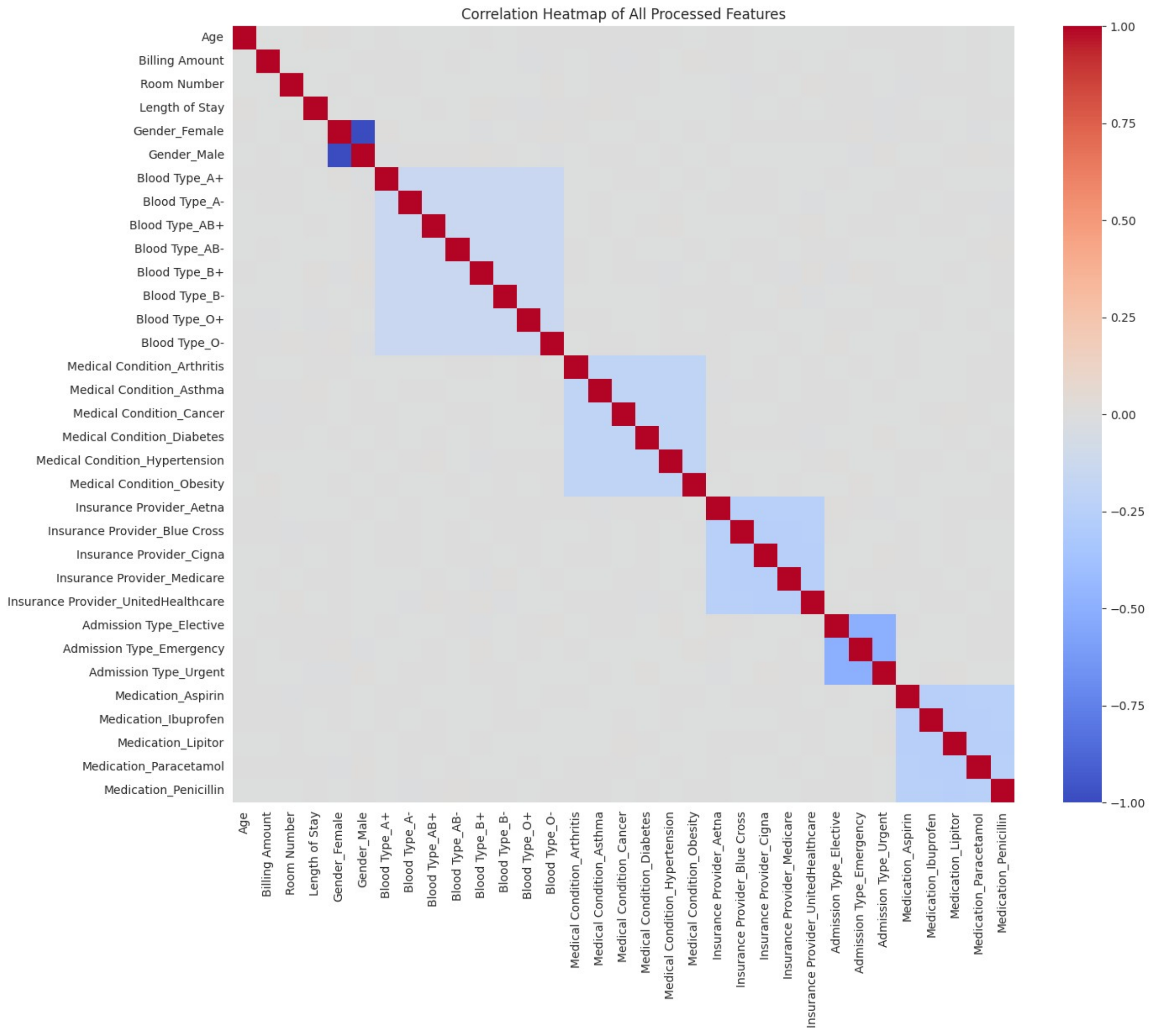
```
Shape of features after preprocessing:
(54966, 33)

First 5 rows of processed features (NumPy array):
[[-1.09842669 -0.47071319  0.23325037 -1.558559    0.          1.
   0.          0.          0.          0.          0.          1.
   0.          0.          0.          0.          1.          0.
   0.          0.          0.          1.          0.          0.
   0.          0.          0.          1.          0.          0.
   0.          1.          0.        ]
 [ 0.5337698   0.57002119 -0.31351977 -1.09673947  0.          1.
   1.          0.          0.          0.          0.          0.
   0.          0.          0.          0.          0.          0.
   0.          1.          0.          0.          0.          1.
   0.          0.          1.          0.          0.          1.
   0.          0.          0.        ]
 [ 1.24785577  0.16967499 -0.83425322 -0.05764552  1.          0.
   0.          1.          0.          0.          0.          0.
   0.          0.          0.          0.          0.          0.
   0.          1.          1.          0.          0.          0.
   0.          0.          1.          0.          1.          0.
   0.          0.          0.        ]
 [-1.20043897  0.87030068  1.29207507  1.67417772  1.          0.
   0.          0.          0.          0.          0.          0.
   1.          0.          0.          0.          0.          1.
   0.          0.          0.          0.          0.          1.
   0.          1.          0.          0.          0.          1.
   0.          0.          0.        ]
 [-0.43534686 -0.79573235  1.36150619  0.51962889  1.          0.
   0.          0.          1.          0.          0.          0.
   0.          0.          0.          0.          1.          0.
   0.          0.          1.          0.          0.          0.
   0.          0.          0.          1.          0.          0.
   0.          0.          1.        ]]

First 5 encoded target labels:
[2 1 2 0 0]
```

Correlation Heatmap of All Processed Features

Let's visualize the correlation matrix of all features after preprocessing (scaling and encoding) to explore potential linear relationships between them.

```
# Calculate the correlation matrix for all processed features
# Convert X_processed (NumPy array) back to DataFrame to retain column
names for heatmap
# Need to get the feature names correctly after ColumnTransformer
try:
    # Get feature names after one-hot encoding from the preprocessor
    onehot_feature_names =
preprocessor.named_transformers_['cat'].get_feature_names_out(categori
cal_cols)
    all_feature_names = numerical_cols + list(onehot_feature_names)
    X_processed_df_for_corr = pd.DataFrame(X_processed,
columns=all_feature_names)
except AttributeError:
    # Fallback if get_feature_names_out is not available (e.g., older
sklearn versions)
    print("Could not retrieve detailed feature names from
preprocessor. Using generic names.")
    X_processed_df_for_corr = pd.DataFrame(X_processed)


correlation_matrix_processed = X_processed_df_for_corr.corr()

# Plot the heatmap
plt.figure(figsize=(15, 12)) # Adjust figure size for better
readability with many features
sns.heatmap(correlation_matrix_processed, annot=False,
cmap='coolwarm', fmt=".2f") # annot=False due to potentially many
```

```
features
plt.title('Correlation Heatmap of All Processed Features')
plt.show()

# Optional: Display correlation values for a specific feature, e.g.,
with a target encoding (if we had one for features)
# Or with the numerical features as a starting point
# print("\nCorrelation of features with 'Age' (example):")
#
display(correlation_matrix_processed['Age'].sort_values(ascending=Fals
e))
```



Observation on Correlation Heatmap:

The correlation heatmap of all processed features (including scaled numerical features and one-hot encoded categorical features) shows generally very low correlation values between different features. This observation, combined with the model's low predictive performance, strongly supports the hypothesis that this dataset may be **synthetic** and **not reflect real-world relationships between the features and the target variable**. Meaningful linear (and potentially non-linear) patterns that a model could learn from appear to be largely absent or very weak in this dataset.

Part 4: Model Preparation □

This section prepares the data for the deep learning model by separating features and the target variable, and splitting the dataset into training and testing sets.

4.1 & 4.2. Define Features/Target & Split Data

```
# X_processed was created and scaled/encoded in the previous step
# y_encoded was created and label encoded in the previous step

# Split the data into training and testing sets
# test_size=0.2 means 20% of the data will be used for testing
# stratify=y_encoded ensures that the proportion of the target
variable is the same in both training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_processed,
y_encoded, test_size=0.2, stratify=y_encoded, random_state=42)

print(f"Shape of X_train: {X_train.shape}")
print(f"Shape of X_test: {X_test.shape}")
print(f"Shape of y_train: {y_train.shape}")
print(f"Shape of y_test: {y_test.shape}")
```

```
Shape of X_train: (43972, 33)
Shape of X_test: (10994, 33)
Shape of y_train: (43972,)
Shape of y_test: (10994,)
```

Part 5: Deep Learning Model Architecture

Here, we define the blueprint of our neural network using Keras, carefully choosing layers, neurons, and activation functions.

5.1. Build the Model

```
# Get the number of features for the input layer
input_shape = X_train.shape[1]

# Get the number of classes for the output layer
num_classes = len(label_encoder.classes_) # Using the label_encoder
from Part 3.4

# Build the Sequential model
model = Sequential([
    # Input layer: Defines the input shape based on the number of
features
    tf.keras.layers.InputLayer(input_shape=(input_shape,)),
    # First Dense layer with 128 neurons and ReLU activation
    Dense(128, activation='relu'),
    # Dropout layer for regularization, dropping 30% of neurons
    Dropout(0.3),
    # Second Dense layer with 64 neurons and ReLU activation
    Dense(64, activation='relu'),
    # Another Dropout layer
    Dropout(0.3),
    # Output layer with number of neurons equal to the number of
classes and softmax activation for multi-class classification
    Dense(num_classes, activation='softmax')
])
```

```
/usr/local/lib/python3.12/dist-packages/keras/src/layers/core/
input_layer.py:27: UserWarning: Argument `input_shape` is deprecated.
Use `shape` instead.
  warnings.warn(
```

5.2. Compile the Model

```
# Compile the model
# optimizer='adam' is a popular choice for deep learning models
# loss='sparse_categorical_crossentropy' is suitable for multi-class
classification with integer labels
# metrics=['accuracy'] to monitor the accuracy during training
model.compile(optimizer='adam',
              loss='sparse_categorical_crossentropy',
              metrics=['accuracy'])
```

5.3. Model Summary

```
# Print the summary of the model architecture
model.summary()
```

```
Model: "sequential_2"

┏━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━┳━━━━━━━━━━━━━━━━━━━━━━━━━┳━━━━━━━━━━
━━━━━┓
┃ Layer (type)                     ┃ Output Shape            ┃
Param # ┃
┡━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━╇━━━━━━━━━━━━━━━━━━━━━━━━━╇━━━━━━━━━━
━━━━━┩
│ dense_6 (Dense)                  │ (None, 128)             │
4,352 │
├──────────────────────────────────┼─────────────────────────┼──────────
─────┤
│ dropout_4 (Dropout)              │ (None, 128)             │
0 │
```

```
├──────────────────────────────────┼─────────────────────────┼──────────
──────┤
│ dense_7 (Dense)                  │ (None, 64)              │
8,256 │
├──────────────────────────────────┼─────────────────────────┼──────────
──────┤
│ dropout_5 (Dropout)              │ (None, 64)              │
0 │
├──────────────────────────────────┼─────────────────────────┼──────────
──────┤
│ dense_8 (Dense)                  │ (None, 3)               │
195 │
└──────────────────────────────────┴─────────────────────────┴──────────
──────┘

 Total params: 12,803 (50.01 KB)

 Trainable params: 12,803 (50.01 KB)

 Non-trainable params: 0 (0.00 B)
```

Part 6: Model Training & Evaluation

We train our model on the training data and then rigorously evaluate its performance on the unseen test data.

6.1. Training

```
# Train the model using the training data
# history variable will store the training process metrics
history = model.fit(X_train, y_train,
                    epochs=20,          # Number of training iterations
                    batch_size=32,      # Number of samples per
gradient update
                    validation_data=(X_test, y_test)) # Data to
evaluate the model after each epoch

Epoch 1/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 8s 5ms/step - accuracy: 0.3412 - loss:
1.1061 - val_accuracy: 0.3366 - val_loss: 1.0987
Epoch 2/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 4s 3ms/step - accuracy: 0.3426 - loss:
1.0985 - val_accuracy: 0.3290 - val_loss: 1.0991
Epoch 3/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 5s 4ms/step - accuracy: 0.3428 - loss:
1.0984 - val_accuracy: 0.3297 - val_loss: 1.0994
Epoch 4/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 4s 3ms/step - accuracy: 0.3474 - loss:
1.0981 - val_accuracy: 0.3322 - val_loss: 1.0988
Epoch 5/20
```

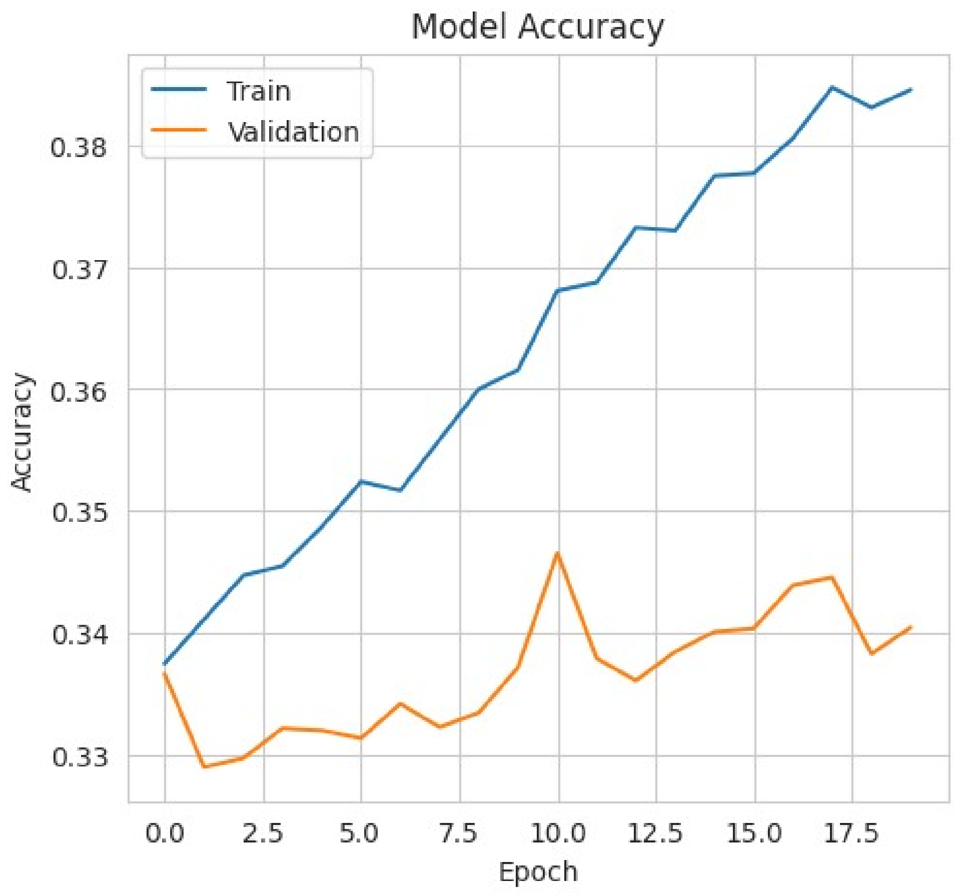
```
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 5s 3ms/step - accuracy: 0.3464 - loss:
1.0979 - val_accuracy: 0.3320 - val_loss: 1.0993
Epoch 6/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 7s 5ms/step - accuracy: 0.3521 - loss:
1.0970 - val_accuracy: 0.3314 - val_loss: 1.0994
Epoch 7/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 9s 4ms/step - accuracy: 0.3511 - loss:
1.0967 - val_accuracy: 0.3342 - val_loss: 1.0995
Epoch 8/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 4s 3ms/step - accuracy: 0.3572 - loss:
1.0957 - val_accuracy: 0.3323 - val_loss: 1.0999
Epoch 9/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 6s 4ms/step - accuracy: 0.3616 - loss:
1.0948 - val_accuracy: 0.3335 - val_loss: 1.1009
Epoch 10/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 5s 3ms/step - accuracy: 0.3609 - loss:
1.0947 - val_accuracy: 0.3372 - val_loss: 1.1000
Epoch 11/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 5s 3ms/step - accuracy: 0.3656 - loss:
1.0929 - val_accuracy: 0.3466 - val_loss: 1.1007
Epoch 12/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 6s 4ms/step - accuracy: 0.3652 - loss:
1.0924 - val_accuracy: 0.3379 - val_loss: 1.1005
Epoch 13/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 10s 3ms/step - accuracy: 0.3694 - loss:
1.0922 - val_accuracy: 0.3361 - val_loss: 1.1015
Epoch 14/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 5s 3ms/step - accuracy: 0.3711 - loss:
1.0904 - val_accuracy: 0.3385 - val_loss: 1.1024
Epoch 15/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 5s 3ms/step - accuracy: 0.3741 - loss:
1.0901 - val_accuracy: 0.3401 - val_loss: 1.1020
Epoch 16/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 5s 4ms/step - accuracy: 0.3786 - loss:
1.0885 - val_accuracy: 0.3404 - val_loss: 1.1024
Epoch 17/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 9s 3ms/step - accuracy: 0.3720 - loss:
1.0879 - val_accuracy: 0.3439 - val_loss: 1.1022
Epoch 18/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 6s 4ms/step - accuracy: 0.3809 - loss:
1.0859 - val_accuracy: 0.3446 - val_loss: 1.1045
Epoch 19/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 4s 3ms/step - accuracy: 0.3807 - loss:
1.0864 - val_accuracy: 0.3383 - val_loss: 1.1027
Epoch 20/20
1375/1375 ━━━━━━━━━━━━━━━━━━━━ 7s 4ms/step - accuracy: 0.3799 - loss:
1.0853 - val_accuracy: 0.3405 - val_loss: 1.1028
```

6.2. Visualizing History

Plot training & validation accuracy values

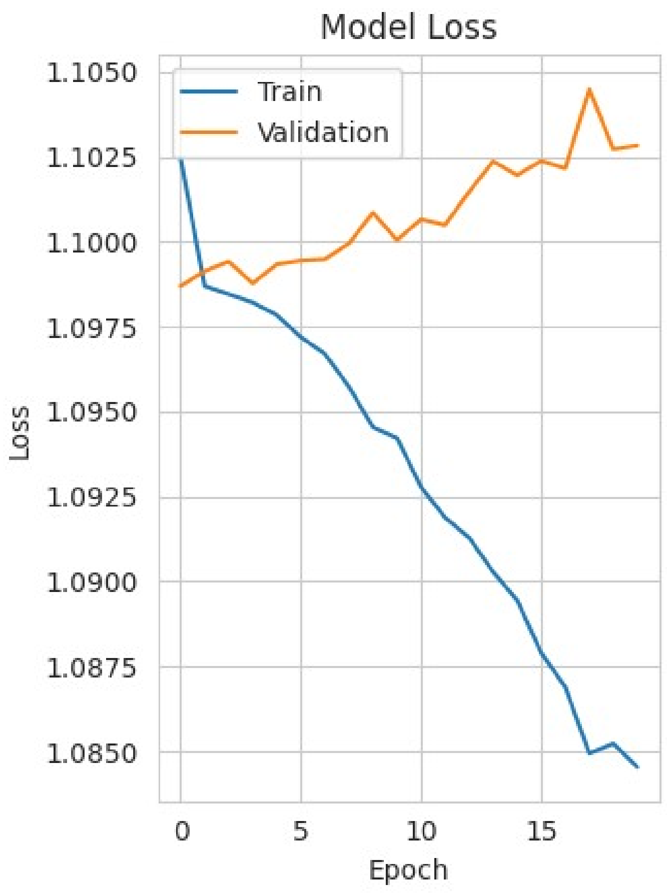
```
plt.figure(figsize=(12, 5))
plt.subplot(1, 2, 1)
plt.plot(history.history['accuracy'])
plt.plot(history.history['val_accuracy'])
plt.title('Model Accuracy')
plt.ylabel('Accuracy')
plt.xlabel('Epoch')
plt.legend(['Train', 'Validation'], loc='upper left')
```

```
<matplotlib.legend.Legend at 0x7f481e7380b0>
```



Plot training & validation loss values

```
plt.subplot(1, 2, 2)
plt.plot(history.history['loss'])
plt.plot(history.history['val_loss'])
plt.title('Model Loss')
plt.ylabel('Loss')
plt.xlabel('Epoch')
plt.legend(['Train', 'Validation'], loc='upper left')

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

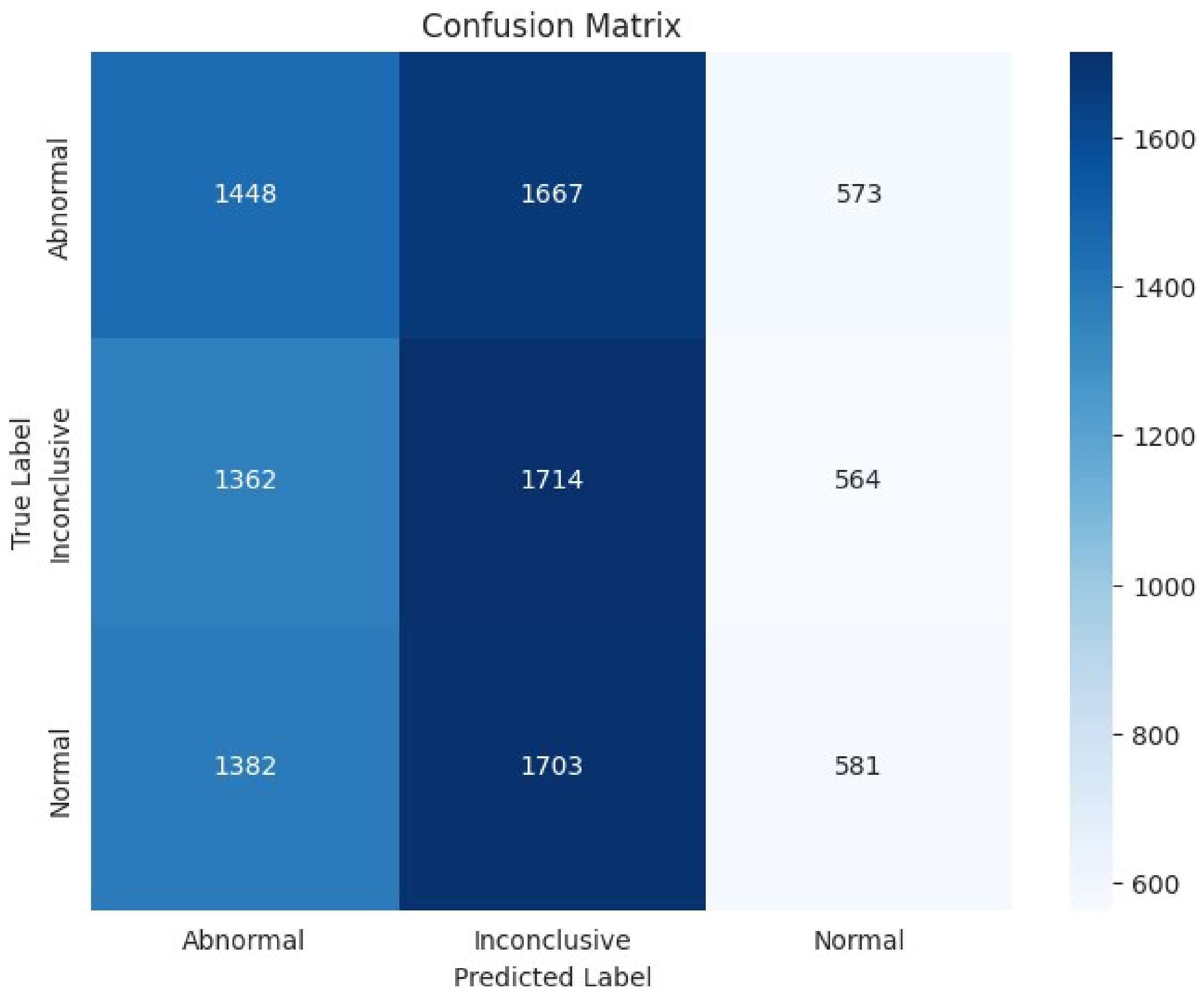


6.3. Evaluation

```
# Make predictions on the test data
y_pred_prob = model.predict(X_test)

344/344 ━━━━━━━━━━━━━━━━━━━━ 1s 1ms/step

# Convert predicted probabilities to class labels by selecting the
class with the highest probability
y_pred = np.argmax(y_pred_prob, axis=1)

# Print the classification report to show precision, recall, f1-score,
and support for each class
print("Classification Report:")
print(classification_report(y_test, y_pred,
target_names=label_encoder.classes_))
```

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

    Abnormal       0.35      0.39      0.37      3688
Inconclusive       0.34      0.47      0.39      3640
      Normal       0.34      0.16      0.22      3666

    accuracy                           0.34     10994
   macro avg       0.34      0.34      0.33     10994
weighted avg       0.34      0.34      0.33     10994
```

```python
# Compute the confusion matrix
cm = confusion_matrix(y_test, y_pred)

# Plot the confusion matrix using a heatmap for better visualization
plt.figure(figsize=(8, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
xticklabels=label_encoder.classes_,
yticklabels=label_encoder.classes_)
plt.title('Confusion Matrix')
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.show()
```



Part 7: Conclusion & Model Saving

In this final section, we summarize the key findings from our end-to-end Deep Learning project for medical test result prediction, discuss the model's performance in the context of the data, and save the resulting artifacts (trained model and processed data) for future use.

7.1. Comprehensive Conclusion

Throughout this project, we embarked on building a Deep Neural Network (DNN) model using Keras to predict medical test results ('Normal', 'Abnormal', 'Inconclusive') based on a healthcare dataset.

We began by setting up the environment and loading the dataset, performing an initial inspection that revealed the dataset's structure, data types, and the presence of duplicate entries but no missing values. Univariate analysis showed the distribution of individual features, including the target variable, which was relatively balanced across its three classes. Bivariate and multivariate analyses, including correlation heatmaps and pair plots, were conducted to explore relationships between features and the target.

A significant observation from the correlation heatmap of all processed features was the consistently low correlation values between almost all pairs of features. This finding is crucial because it suggests a lack of strong linear relationships within the dataset. Coupled with the model's performance, this strongly supports the hypothesis that the dataset, as discussed in external forums (like Kaggle), might be synthetically generated and may not accurately reflect real-world medical data patterns or predictive relationships.

In the data preprocessing phase, we successfully handled duplicate rows, removed irrelevant identifier columns ('Name', 'Doctor', 'Hospital'), and engineered a useful 'Length of Stay' feature from the admission and discharge dates. Categorical features were prepared using One-Hot Encoding, and numerical features were scaled using StandardScaler. The target variable was Label Encoded for compatibility with the model's loss function.

The Deep Neural Network model was designed with several dense layers and dropout for regularization. However, despite the standard preprocessing and a reasonable model architecture, the training and evaluation results showed low accuracy (around 34% on the test set), only slightly better than random chance (33.3%) for a 3-class problem. The training history plots indicated that the model struggled to learn meaningful patterns, with validation accuracy and loss showing limited improvement.

The low performance, despite these standard steps, reinforces the conclusion drawn from the EDA: the inherent structure or lack of strong predictive signals within this specific dataset appears to be the primary limiting factor, rather than issues with the model implementation itself. While hyperparameter tuning or alternative architectures could be explored, the fundamental data characteristics suggest that significant improvements might be challenging if the dataset truly lacks strong underlying patterns.

In conclusion, this project successfully demonstrates the end-to-end process of building a deep learning model for classification, including data loading, EDA, preprocessing, model definition, training, and evaluation. However, it also highlights the critical importance of data quality and the presence of meaningful patterns for achieving high predictive performance in machine learning tasks. The results obtained are likely a reflection of the dataset's nature rather than a failure of the modeling approach itself.

7.2. Save Trained Model

```
# Save the trained Keras model to a file in the native Keras format
model.save('medical_test_classifier.keras')

print("Trained model saved successfully as
'medical_test_classifier.keras'")
```

```
Trained model saved successfully as 'medical_test_classifier.keras'
```

7.3. Save Processed Dataset

```
# Convert processed features (NumPy array) back to DataFrame for
saving
# We need the column names for clarity when saving
try:
    onehot_feature_names =
preprocessor.named_transformers_['cat'].get_feature_names_out(categori
cal_cols)
    all_feature_names = numerical_cols + list(onehot_feature_names)
    X_processed_df_to_save = pd.DataFrame(X_processed,
columns=all_feature_names)
except AttributeError:
    print("Could not retrieve detailed feature names from
preprocessor. Saving processed features with generic names.")
    X_processed_df_to_save = pd.DataFrame(X_processed)

# Save the processed features and encoded target to CSV files
X_processed_df_to_save.to_csv('X_processed.csv', index=False)
y_encoded.dump('y_encoded.pkl') # Saving NumPy array using dump

print("\nProcessed features saved to 'X_processed.csv'")
print("Encoded target saved to 'y_encoded.pkl'")
```

```
Processed features saved to 'X_processed.csv'
Encoded target saved to 'y_encoded.pkl'
```