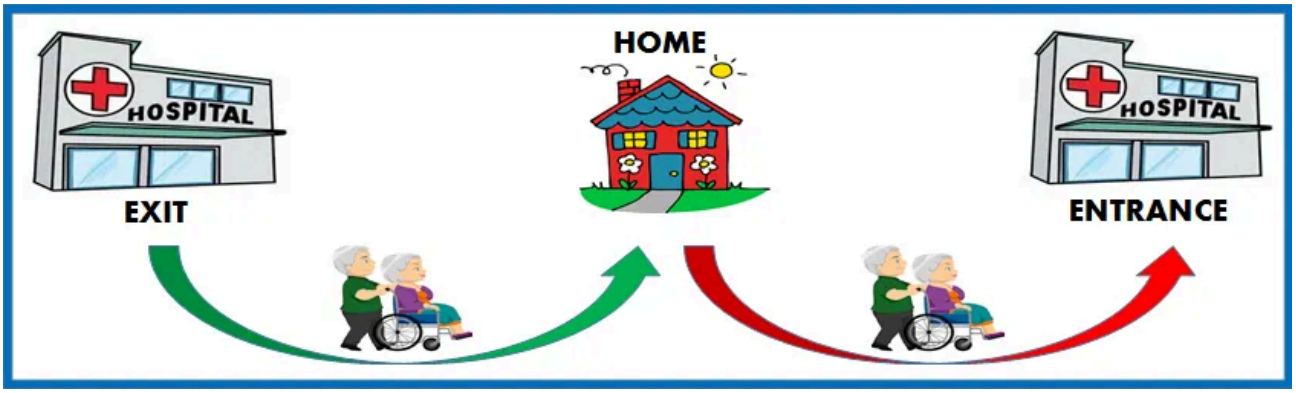
```
from google.colab import drive
drive.mount('/content/gdrive')
```

```
Mounted at /content/gdrive
```

Capstone Project: Predicting Hospital Readmission Risk in Diabetic Patients



Double-click (or enter) to edit

Import Libraries

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.impute import SimpleImputer
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, confusion_matrix, classificat
```

Load and Explore Data

```
data = pd.read_csv("/content/gdrive/MyDrive/diabetic_data.csv")
```

```
# Display basic info
print("Dataset Shape:", data.shape)
print("\nColumns:\n", data.columns.tolist())
print("\nPreview:\n", data.head())
```

```
Dataset Shape: (17469, 50)

Columns:
 ['encounter_id', 'patient_nbr', 'race', 'gender', 'age', 'weight', 'admis

Preview:
    encounter_id  patient_nbr             race  gender      age weight  \
0       2278392      8222157        Caucasian  Female   [0-10)      ?
1        149190     55629189        Caucasian  Female  [10-20)      ?
2         64410     86047875  AfricanAmerican  Female  [20-30)      ?
3        500364     82442376        Caucasian    Male  [30-40)      ?
4         16680     42519267        Caucasian    Male  [40-50)      ?

   admission_type_id  discharge_disposition_id  admission_source_id  \
0                  6                        25                    1
1                  1                         1                    7
2                  1                         1                    7
3                  1                         1                    7
4                  1                         1                    7

   time_in_hospital  ... citoglipton insulin  glyburide-metformin  \
0                 1  ...          No      No                   No
1                 3  ...          No      Up                   No
2                 2  ...          No      No                   No
3                 2  ...          No      Up                   No
4                 1  ...          No  Steady                   No

   glipizide-metformin  glimepiride-pioglitazone  metformin-rosiglitazone
0                   No                        No                       No
1                   No                        No                       No
2                   No                        No                       No
3                   No                        No                       No
4                   No                        No                       No

   metformin-pioglitazone  change diabetesMed readmitted
0                      No      No          No         NO
1                      No      Ch         Yes        >30
2                      No      No         Yes         NO
3                      No      Ch         Yes         NO
4                      No      Ch         Yes         NO

[5 rows x 50 columns]
```

Data cleaning

```
# Replace '?' with NaN
data.replace('?', np.nan, inplace=True)
```

```
# Drop columns that are not useful for prediction
data.drop(['encounter_id', 'patient_nbr', 'weight', 'payer_code', 'medica

# Check how many missing values remain
print("\nMissing values per column:\n", data.isnull().sum())
```

```
Missing values per column:
 race                      291
gender                       0
age                          0
admission_type_id            0
discharge_disposition_id     0
admission_source_id          0
time_in_hospital             0
num_lab_procedures           0
num_procedures               0
num_medications              0
number_outpatient            0
number_emergency             0
number_inpatient             0
diag_1                       7
diag_2                     104
diag_3                     498
number_diagnoses             0
max_glu_serum            15754
A1Cresult                14213
metformin                    0
repaglinide                  0
nateglinide                  0
chlorpropamide               0
glimepiride                  0
acetohexamide                0
glipizide                    0
glyburide                    0
tolbutamide                  0
pioglitazone                 0
rosiglitazone                0
acarbose                     0
miglitol                     0
troglitazone                 0
tolazamide                   0
examide                      0
citoglipton                  0
insulin                      0
glyburide-metformin          0
glipizide-metformin          0
glimepiride-pioglitazone     0
metformin-rosiglitazone      0
metformin-pioglitazone       0
change                       0
diabetesMed                  0
readmitted                   0
dtype: int64
/tmp/ipython-input-1993658940.py:2: FutureWarning: Downcasting behavior in
```

```
data.replace('?', np.nan, inplace=True)
```

Feature Engineering

```
# Convert target variable 'readmitted' into binary
# '<30' and '>30' = 1 (readmitted), 'NO' = 0 (not readmitted)
data['readmitted'] = data['readmitted'].replace({'NO': 0, '<30': 1, '>30'

# Encode all categorical (string) columns
label_encoder = LabelEncoder()
categorical_cols = data.select_dtypes(include=['object']).columns

for col in categorical_cols:
    data[col] = label_encoder.fit_transform(data[col].astype(str))

    print("Categorical columns encoded:", list(categorical_cols))
```

```
Categorical columns encoded: ['race', 'gender', 'age', 'diag_1', 'diag_2',
Categorical columns encoded: ['race', 'gender', 'age', 'diag_1', 'diag_2',
Categorical columns encoded: ['race', 'gender', 'age', 'diag_1', 'diag_2',
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Categorical columns encoded: ['race', 'gender', 'age', 'diag_1', 'diag_2',
```

```
/tmp/ipython-input-136016837.py:3: FutureWarning: Downcasting behavior in
  data['readmitted'] = data['readmitted'].replace({'NO': 0, '<30': 1, '>30
```

Handle Missing Values and Scale Data

```
# Fill missing values with the most frequent value
imputer = SimpleImputer(strategy='most_frequent')
data_imputed = pd.DataFrame(imputer.fit_transform(data), columns=data.colu

# Scale numeric features
scaler = StandardScaler()
X = data_imputed.drop('readmitted', axis=1)
y = data_imputed['readmitted']
X_scaled = scaler.fit_transform(X)

print("After preprocessing, data shape:", X_scaled.shape)
```

```
After preprocessing, data shape: (17469, 44)
```

Train-Test Split

```
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size

print("Training set size:", X_train.shape)
print("Testing set size:", X_test.shape)
```

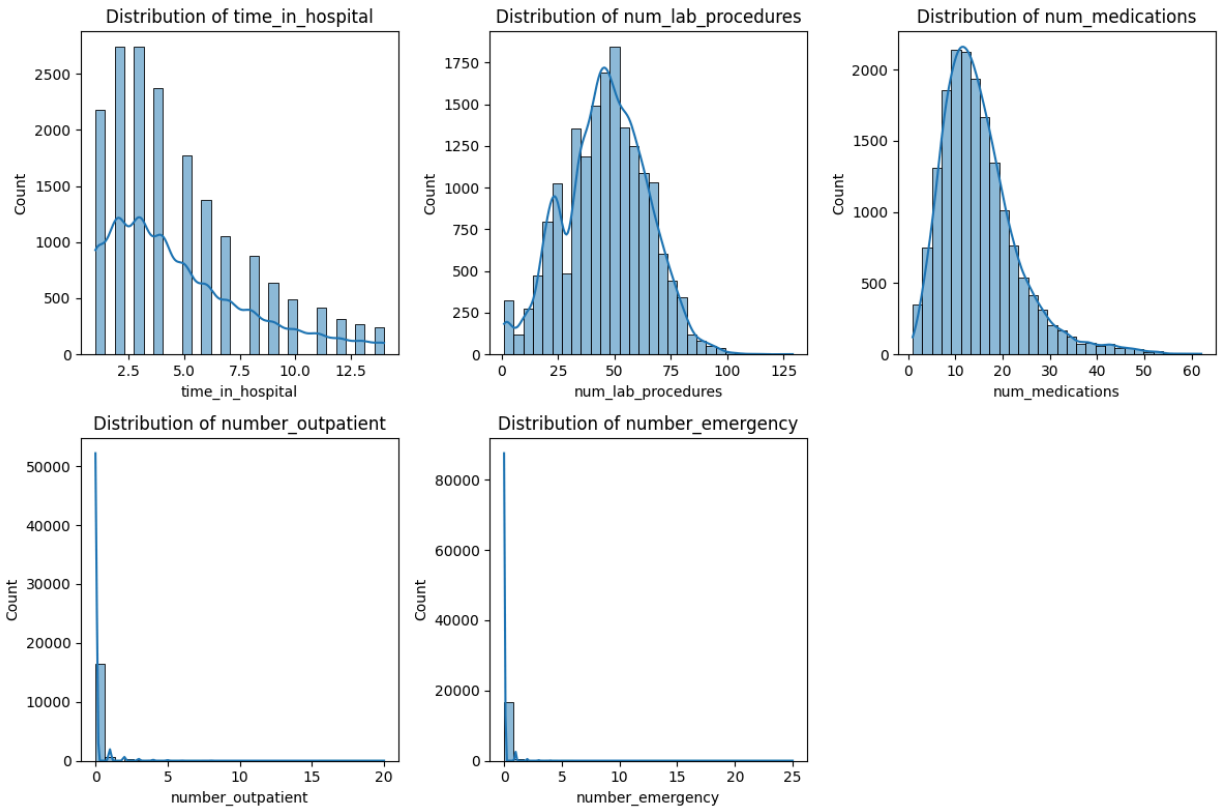
```
Training set size: (13975, 44)
Testing set size: (3494, 44)
```

Feature Scaling

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

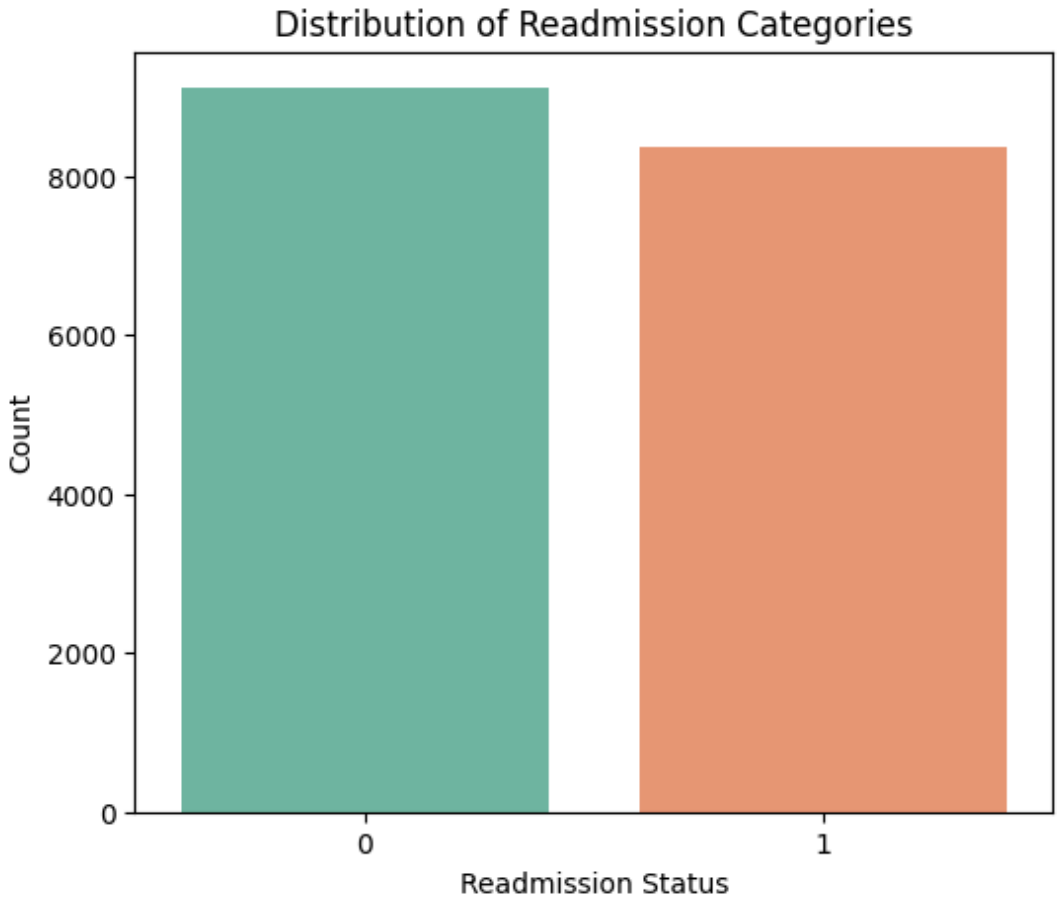
```
import matplotlib.pyplot as plt
import seaborn as sns

num_cols = ['time_in_hospital', 'num_lab_procedures', 'num_medications',

plt.figure(figsize=(12,8))
```

```
for i, col in enumerate(num_cols, 1):
    plt.subplot(2, 3, i)
    sns.histplot(data[col], bins=30, kde=True)
    plt.title(f'Distribution of {col}')
plt.tight_layout()
plt.show()
```

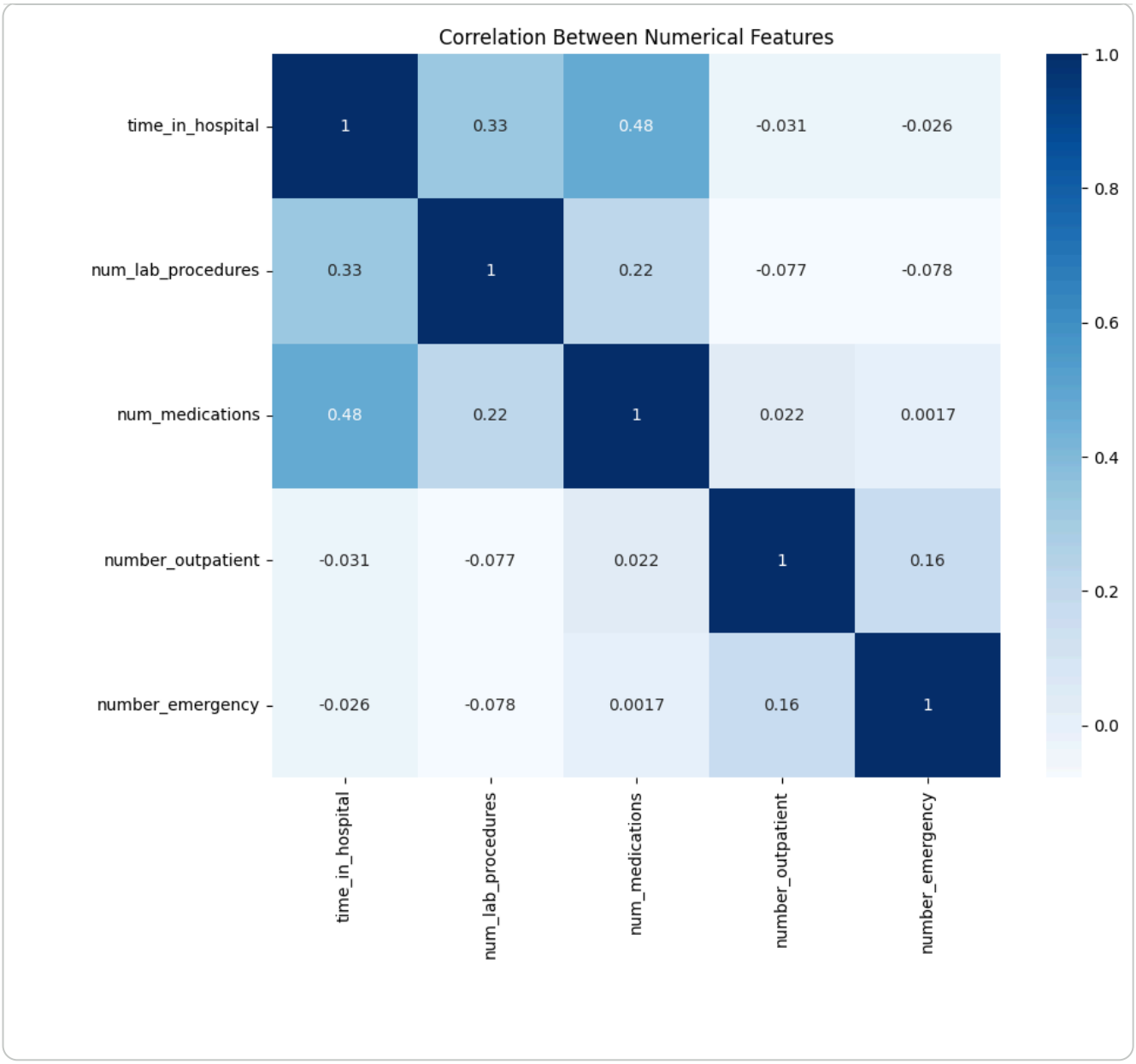



```
plt.figure(figsize=(6,5))
sns.countplot(x='readmitted', data=data, palette='Set2')
plt.title('Distribution of Readmission Categories')
plt.xlabel('Readmission Status')
plt.ylabel('Count')
plt.show()
```

```
/tmp/ipython-input-1917754014.py:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be remove

  sns.countplot(x='readmitted', data=data, palette='Set2')
```

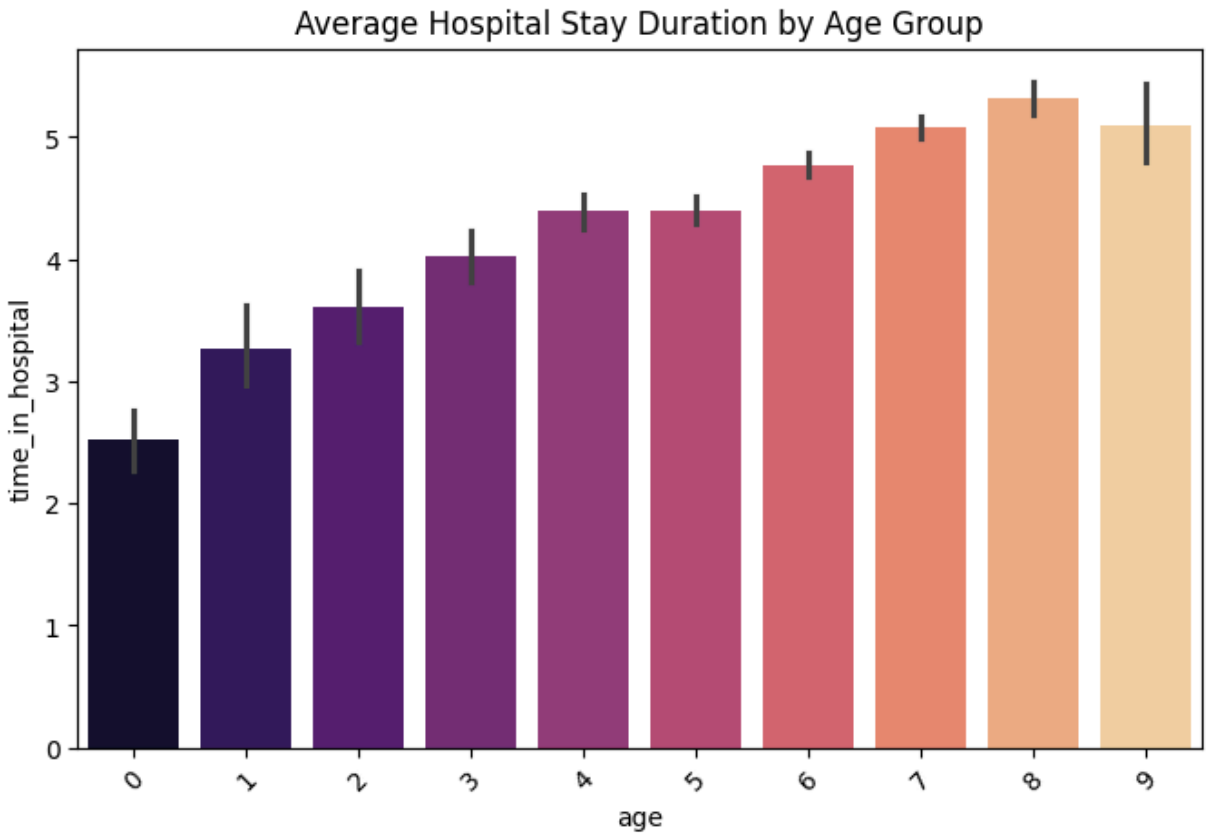



```
plt.figure(figsize=(10,8))
sns.heatmap(data[num_cols].corr(), annot=True, cmap='Blues')
plt.title('Correlation Between Numerical Features')
plt.show()
```




```
plt.figure(figsize=(8,5))
sns.barplot(x='age', y='time_in_hospital', data=data, palette='magma')
plt.title('Average Hospital Stay Duration by Age Group')
plt.xticks(rotation=45)
plt.show()
```

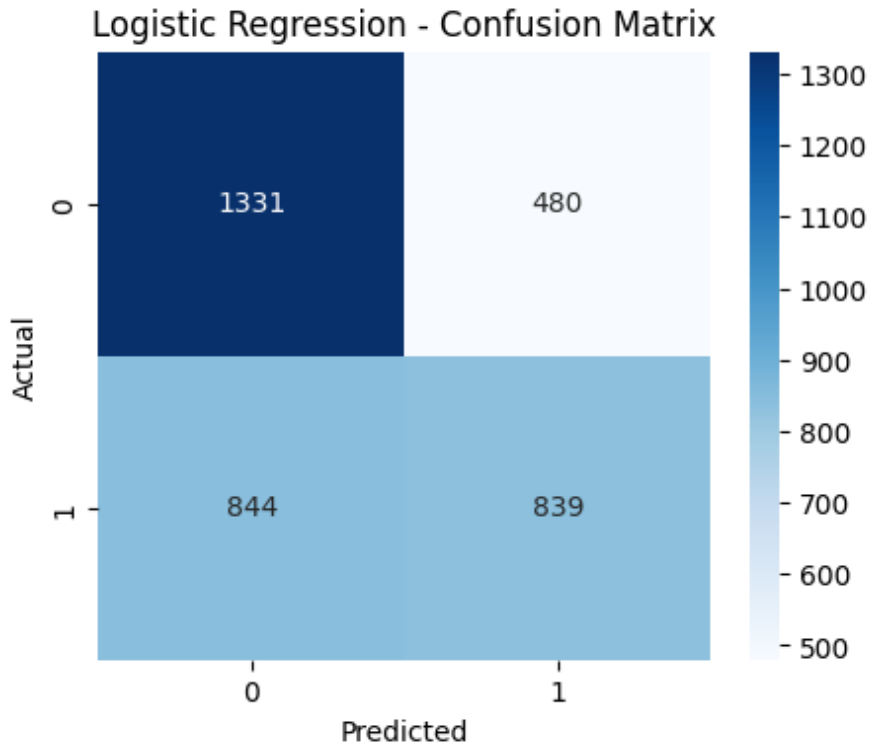
```
/tmp/ipython-input-4067393693.py:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be remove

  sns.barplot(x='age', y='time_in_hospital', data=data, palette='magma')
```



Logistic Regression

```
log_model = LogisticRegression(max_iter=2000)
log_model.fit(X_train, y_train)

y_pred_log = log_model.predict(X_test)

print("Logistic Regression Accuracy:", accuracy_score(y_test, y_pred_log)
print("\nClassification Report:\n", classification_report(y_test, y_pred_

# Confusion Matrix
plt.figure(figsize=(5,4))
sns.heatmap(confusion_matrix(y_test, y_pred_log), annot=True, fmt='d', cm
plt.title("Logistic Regression - Confusion Matrix")
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.show()
```

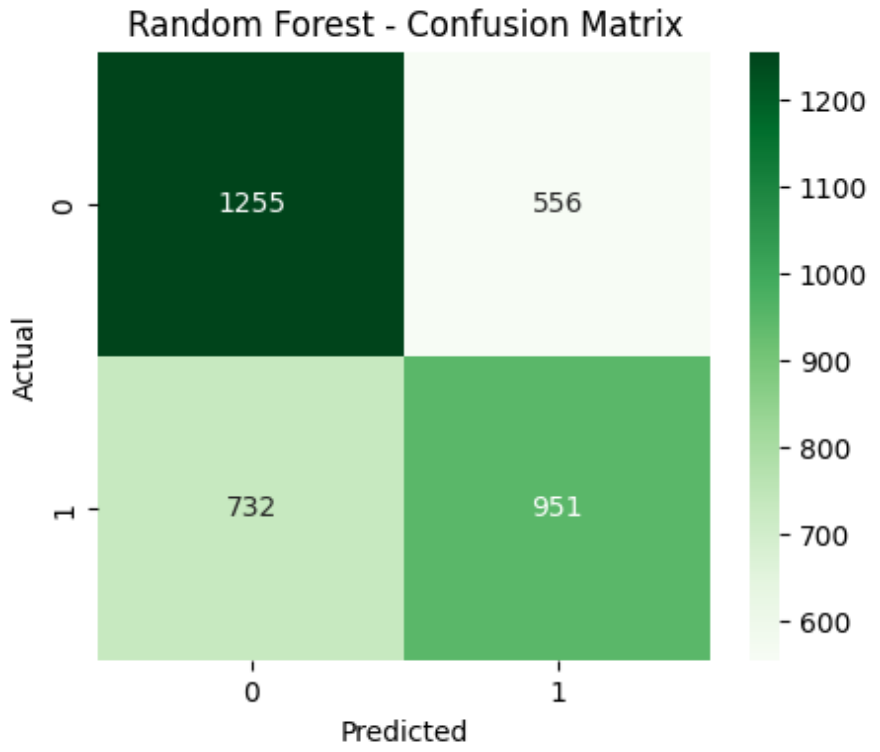
```
Logistic Regression Accuracy: 0.6210646823125358

Classification Report:
              precision    recall  f1-score   support

           0       0.61      0.73      0.67      1811
           1       0.64      0.50      0.56      1683

    accuracy                           0.62      3494
   macro avg       0.62      0.62      0.61      3494
weighted avg       0.62      0.62      0.62      3494
```



Random Forest Classifier

```
rf_model = RandomForestClassifier(n_estimators=200, random_state=42)
rf_model.fit(X_train, y_train)

y_pred_rf = rf_model.predict(X_test)

print("Random Forest Accuracy:", accuracy_score(y_test, y_pred_rf))
print("\nClassification Report:\n", classification_report(y_test, y_pred_

plt.figure(figsize=(5,4))
sns.heatmap(confusion_matrix(y_test, y_pred_rf), annot=True, fmt='d', cma
plt.title("Random Forest - Confusion Matrix")
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.show()
```

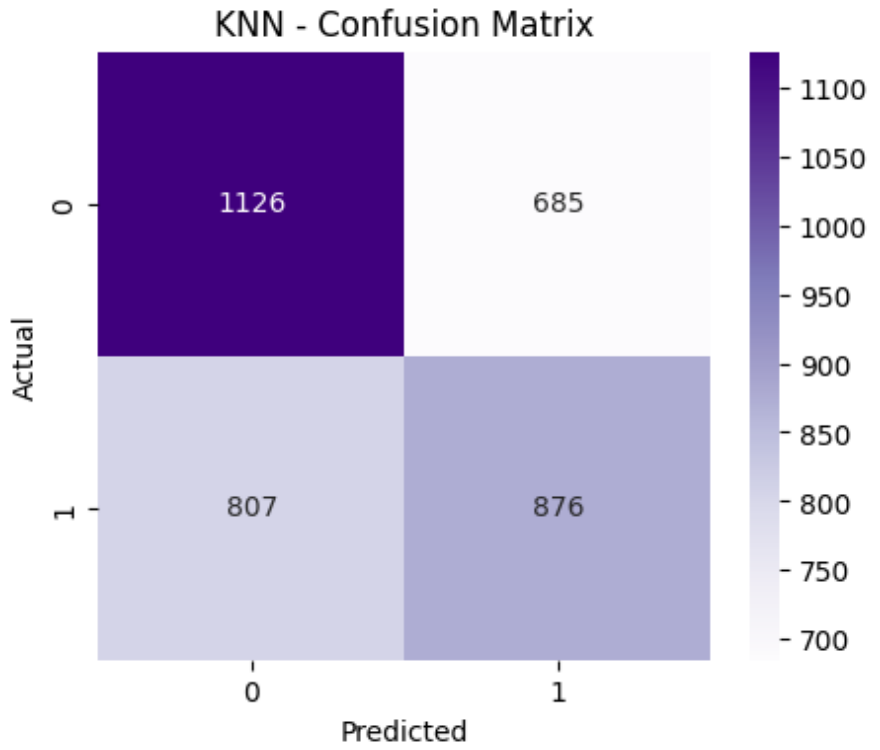
```
Random Forest Accuracy: 0.6313680595306239

Classification Report:
              precision    recall  f1-score   support

           0       0.63      0.69      0.66      1811
           1       0.63      0.57      0.60      1683

    accuracy                           0.63      3494
   macro avg       0.63      0.63      0.63      3494
weighted avg       0.63      0.63      0.63      3494
```



K-Nearest Neighbors

```
knn_model = KNeighborsClassifier(n_neighbors=5)
knn_model.fit(X_train, y_train)

y_pred_knn = knn_model.predict(X_test)

print("KNN Accuracy:", accuracy_score(y_test, y_pred_knn))
print("\nClassification Report:\n", classification_report(y_test, y_pred_

plt.figure(figsize=(5,4))
sns.heatmap(confusion_matrix(y_test, y_pred_knn), annot=True, fmt='d', cm
plt.title("KNN - Confusion Matrix")
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.show()
```

```
KNN Accuracy: 0.5729822552947911

Classification Report:
              precision    recall  f1-score   support

           0       0.58      0.62      0.60      1811
           1       0.56      0.52      0.54      1683

    accuracy                           0.57      3494
   macro avg       0.57      0.57      0.57      3494
weighted avg       0.57      0.57      0.57      3494
```

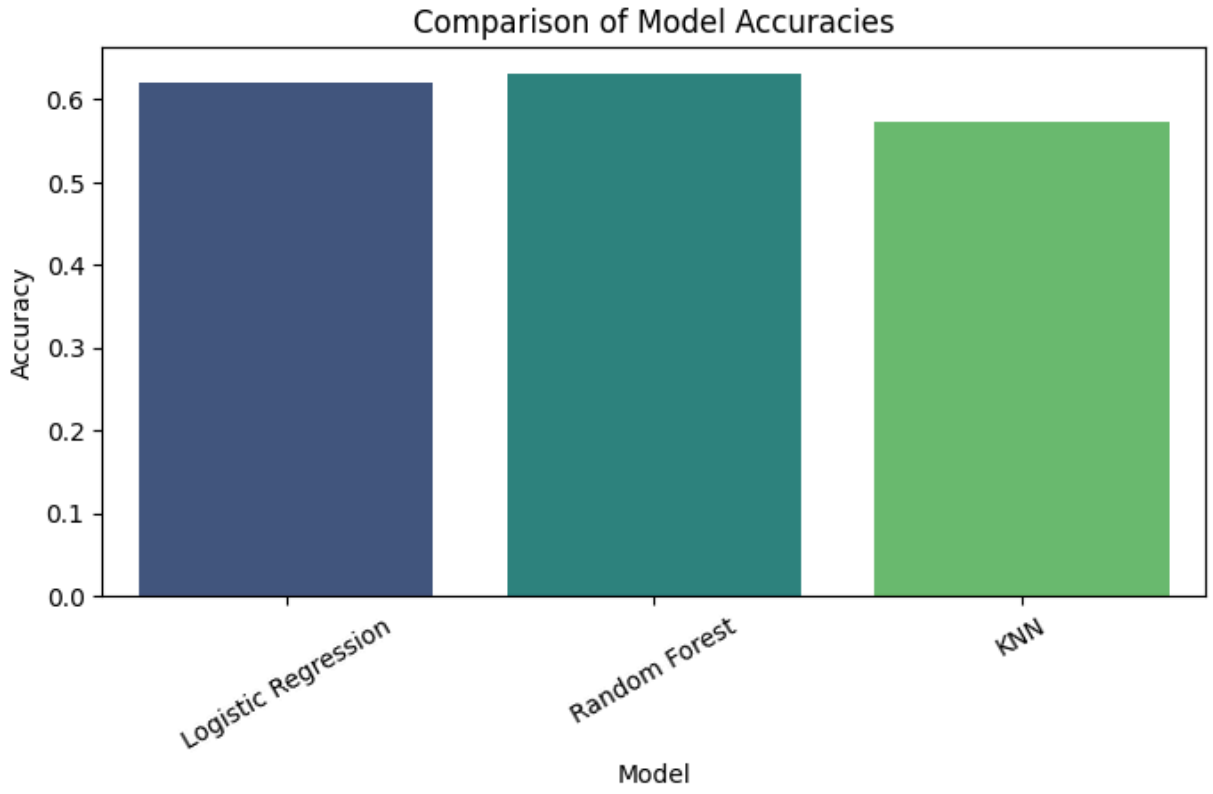


Compare All Models

```
model_results = {
      "Model": ["Logistic Regression", "Random Forest", "KNN"],
       "Accuracy": [
         accuracy_score(y_test, y_pred_log),
         accuracy_score(y_test, y_pred_rf),
         accuracy_score(y_test, y_pred_knn)
                     ]
                    }
results_df = pd.DataFrame(model_results)
print("\n\n FINAL MODEL PERFORMANCE")
print(results_df)

plt.figure(figsize=(8,4))
sns.barplot(x="Model", y="Accuracy", data=results_df, palette="viridis")
plt.title("Comparison of Model Accuracies")
```

```
plt.xticks(rotation=30)
plt.show()
```

```
 FINAL MODEL PERFORMANCE
                 Model  Accuracy
0  Logistic Regression  0.621065
1        Random Forest  0.631368
2                  KNN  0.572982
/tmp/ipython-input-268332014.py:14: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be remove

  sns.barplot(x="Model", y="Accuracy", data=results_df, palette="viridis")
```




```
print("\nFINAL CONCLUSION:")
print("Random Forest performed the best and is recommended for predicting
```

```
FINAL CONCLUSION:
Random Forest performed the best and is recommended for predicting readmis
```

```
import numpy as np

feature_importances = rf_model.feature_importances
```