Predicting Hospital Readmissions for Diabetic Patients

Problem statement and justification for the proposed approach

Hospital readmissions are costly for both healthcare systems and patients, particularly for chronic conditions like diabetes.

- For patients: readmissions are stressful, costly, disruptive, and potentially dangerous, particularly for those managing chronic conditions like diabetes
- For hospitals and providers: readmissions carry significant financial consequences. In 2014, the Centers for Medicare & Medicaid Services (CMS) issued penalties to 2,610 hospitals for excessive 30-day readmissions under the Hospital Readmissions Reduction Program (HRRP). (Smith et al. 2021)
- Patients diagnosed with diabetes face even higher readmission rates, ranging from 14.4% to 22.7%, compared to the general population. (Smith et al. 2021)
- According to the Agency for Healthcare Research and Quality (AHRQ), a modest 5% reduction in readmissions could lead to fewer admissions per year, translating to over $1.2 billion in annual cost savings. (Smith et al. 2021)
- Reducing readmission rates is a key quality metric in value-based healthcare.

Given these clinical and financial stakes, the ability to accurately predict which diabetic patients are at high risk of readmission at the time of discharge is critical. Such insight would allow healthcare systems to proactively intervene with targeted follow-up care, care coordination, and risk mitigation strategies.

Proposed Approach

This project proposes a supervised machine learning solution trained on a rich dataset of real-world electronic health records (EHR) collected from over 130 U.S. hospitals between 1999–2008. Our goal is to:

- Develop a predictive model for 30-day readmission risk in diabetic patients.
- Ensure the model is interpretable and production ready supporting real-time clinical use.
- Enable providers to integrate the model into EHR workflows, identifying high-risk discharges and triggering appropriate post-discharge protocols such as early follow-up scheduling or care management outreach.

Predictive modeling enables hospitals to proactively identify high-risk patients at the time of discharge, rather than reacting after costly readmissions occur. Given the dataset's characteristics—including mixed data types (categorical and numeric), missing values, and class imbalance, we explore ensemble tree-based methods like XGBoost and CatBoost, which are particularly well-suited for high cardinality categorical features, and offer interpretability.

References:

Smith, J., Jones, A., et al. (2021). Explainable machine learning for hospital readmission prediction among diabetes patients. BMC Medical Informatics and Decision Making. https://doi.org/10.1186/s12911-021-01423-y

Data Understanding (EDA)

- Records from ~100,000 hospital encounters
- Target: Readmitted within 30 days (readmitted_binary)
- Mix of numeric (e.g., num_lab_procedures) and categorical (e.g., discharge_disposition_id, insulin) features

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from collections import Counter
from sklearn.model_selection import train_test_split
from sklearn.metrics import classification_report, confusion_matrix, roc_auc_score, roc_curv
from sklearn.metrics import precision_recall_curve, f1_score, accuracy_score
from catboost import CatBoostClassifier, Pool
import os
import warnings
import xgboost as xgb
warnings.filterwarnings('ignore')

def load_data(file_path):
    try:
        df = pd.read_csv(file_path)
        print("Data loaded successfully.")
        print(f"Dataset shape: {df.shape}")
        return df
    except FileNotFoundError:
        print(f"File not found: {file_path}")
        return None

# Load the diabetic readmission dataset
data_path = "diabetic_data.csv"
df = load_data(data_path)
```

```
print("\nCOLUMN DATA TYPES:")
print(df.dtypes.value_counts())

print("\nBASIC STATISTICS:")
print(df.describe())

df.head()
```

```
Data loaded successfully.
Dataset shape: (101766, 50)

COLUMN DATA TYPES:
object    37
int64     13
Name: count, dtype: int64

BASIC STATISTICS:
       encounter_id   patient_nbr  admission_type_id  \
count  1.017660e+05  1.017660e+05      101766.000000
mean   1.652016e+08  5.433040e+07           2.024006
std    1.026403e+08  3.869636e+07           1.445403
min    1.252200e+04  1.350000e+02           1.000000
25%    8.496119e+07  2.341322e+07           1.000000
50%    1.523890e+08  4.550514e+07           1.000000
75%    2.302709e+08  8.754595e+07           3.000000
max    4.438672e+08  1.895026e+08           8.000000

       discharge_disposition_id  admission_source_id  time_in_hospital  \
count             101766.000000        101766.000000     101766.000000
mean                   3.715642             5.754437          4.395987
std                    5.280166             4.064081          2.985108
min                    1.000000             1.000000          1.000000
25%                    1.000000             1.000000          2.000000
50%                    1.000000             7.000000          4.000000
75%                    4.000000             7.000000          6.000000
max                   28.000000            25.000000         14.000000

       num_lab_procedures  num_procedures  num_medications  number_outpatient  \
count       101766.000000   101766.000000    101766.000000      101766.000000
mean            43.095641        1.339730        16.021844           0.369357
std             19.674362        1.705807         8.127566           1.267265
min              1.000000        0.000000         1.000000           0.000000
25%             31.000000        0.000000        10.000000           0.000000
50%             44.000000        1.000000        15.000000           0.000000
75%             57.000000        2.000000        20.000000           0.000000
max            132.000000        6.000000        81.000000          42.000000
```

```
       number_emergency  number_inpatient  number_diagnoses
count     101766.000000     101766.000000     101766.000000
mean           0.197836          0.635566          7.422607
std            0.930472          1.262863          1.933600
min            0.000000          0.000000          1.000000
25%            0.000000          0.000000          6.000000
50%            0.000000          0.000000          8.000000
75%            0.000000          1.000000          9.000000
max           76.000000         21.000000         16.000000
```

```
   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
```

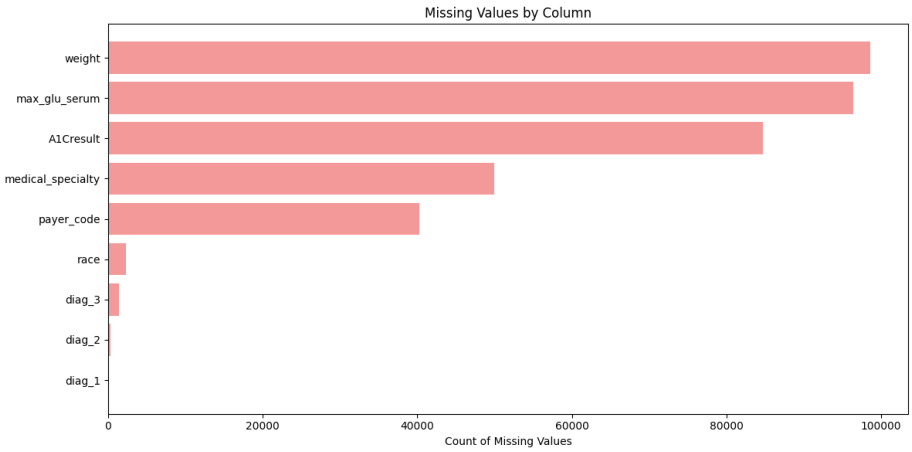
```
[5 rows x 50 columns]
```

Missing Values Analysis

```python
# ====================================
# MISSING VALUES ANALYSIS
# ====================================

def analyze_missing_values(df):
    """Comprehensive missing values analysis"""
    print("\n" + "="*50)
    print("MISSING VALUES ANALYSIS")
    print("="*50)

     # Replace '?' with np.nan for true missing value detection
    df = df.replace('?', np.nan).copy()

    # Calculate missing values
    missing_data = df.isnull().sum()
    missing_percent = 100 * missing_data / len(df)

    # Create missing values summary
    missing_summary = pd.DataFrame({
        'Column': missing_data.index,
        'Missing_Count': missing_data.values,
        'Missing_Percentage': missing_percent.values
    })
    missing_summary = missing_summary[missing_summary['Missing_Count'] > 0].sort_values('Mis

    # Display summary
    if missing_summary.empty:
        print("No missing values found in the dataset.")
    else:
        print("\nMissing Values Summary:")
        print(missing_summary.to_string(index=False))

        # Visualize missing values
        plt.figure(figsize=(12, 6))
        plt.barh(
            missing_summary['Column'],
            missing_summary['Missing_Count'],
            color='lightcoral', alpha=0.8
        )
        plt.xlabel('Count of Missing Values')
        plt.title('Missing Values by Column')
        plt.gca().invert_yaxis()  # Show largest at top
```

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

    return df, missing_summary

analyze_missing_values(df)
```

```
==================================================
MISSING VALUES ANALYSIS
==================================================

Missing Values Summary:
           Column  Missing_Count  Missing_Percentage
           weight          98569           96.858479
    max_glu_serum          96420           94.746772
        A1Cresult          84748           83.277322
medical_specialty          49949           49.082208
       payer_code          40256           39.557416
             race           2273            2.233555
           diag_3           1423            1.398306
           diag_2            358            0.351787
           diag_1             21            0.020636
```




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

```
101761     443847548    100162476  AfricanAmerican    Male  [70-80)    NaN
101762     443847782     74694222  AfricanAmerican  Female  [80-90)    NaN
101763     443854148     41088789        Caucasian    Male  [70-80)    NaN
101764     443857166     31693671        Caucasian  Female  [80-90)    NaN
101765     443867222    175429310        Caucasian    Male  [70-80)    NaN

        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
...                   ...                       ...                  ...
101761                  1                         3                    7
101762                  1                         4                    5
101763                  1                         1                    7
101764                  2                         3                    7
101765                  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
...                  ...  ...         ...     ...                  ...
101761                 3  ...          No    Down                   No
101762                 5  ...          No  Steady                   No
101763                 1  ...          No    Down                   No
101764                10  ...          No      Up                   No
101765                 6  ...          No      No                   No

        glipizide-metformin  glimepiride-pioglitazone  \
0                        No                        No
1                        No                        No
2                        No                        No
3                        No                        No
4                        No                        No
...                     ...                       ...
101761                   No                        No
101762                   No                        No
101763                   No                        No
101764                   No                        No
101765                   No                        No

        metformin-rosiglitazone  metformin-pioglitazone  change diabetesMed  \
```

```
0                          No                    No      No          No
1                          No                    No      Ch         Yes
2                          No                    No      No         Yes
3                          No                    No      Ch         Yes
4                          No                    No      Ch         Yes
...                       ...                   ...     ...        ...
101761                     No                    No      Ch         Yes
101762                     No                    No      No         Yes
101763                     No                    No      Ch         Yes
101764                     No                    No      Ch         Yes
101765                     No                    No      No          No

       readmitted
0              NO
1             >30
2              NO
3              NO
4              NO
...           ...
101761        >30
101762         NO
101763         NO
101764         NO
101765         NO

[101766 rows x 50 columns],
               Column  Missing_Count  Missing_Percentage
5              weight          98569           96.858479
22      max_glu_serum          96420           94.746772
23          A1Cresult          84748           83.277322
11  medical_specialty          49949           49.082208
10         payer_code          40256           39.557416
2                race           2273            2.233555
20             diag_3           1423            1.398306
19             diag_2            358            0.351787
18             diag_1             21            0.020636)
```

Missing Values Analysis Notes

Weight, max_glu_serum, A1C_Result, payer_code, medical_speciality missing a large number of values and will need to be handled.

Target variable analysis

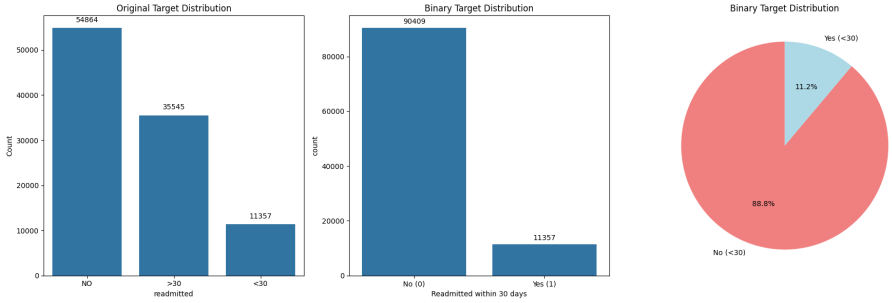
Analyzing the target variable, readmitted. Readmitted is a categorical variable with 3 levels: >30, <30, and NO. For value based care, we care if they are

readmitted within 30 days. So converting the target variable to a binary variable.

```
def analyze_target_variable(df, target_col='readmitted'):
    """Analyze the target variable distribution"""
    print("\n" + "="*50)
    print("TARGET VARIABLE ANALYSIS")
    print("="*50)

    # Original target variable distribution
    target_counts = df[target_col].value_counts()
    target_percentages = df[target_col].value_counts(normalize=True) * 100

    print("Original Target Variable Distribution:")
    for value in target_counts.index:
        print(f"  {value}: {target_counts[value]:,} ({target_percentages[value]:.2f}%)")

    # Create binary target: 1 for <30 (readmitted within 30 days), 0 for others
    df['readmitted_binary'] = (df[target_col] == '<30').astype(int)

    # Binary target distribution
    binary_counts = df['readmitted_binary'].value_counts()
    binary_percentages = df['readmitted_binary'].value_counts(normalize=True) * 100

    print("\nBinary Target Variable Distribution (Focus: <30 days):")
    print(f"  0 (NO or >30): {binary_counts[0]:,} ({binary_percentages[0]:.2f}%)")
    print(f"  1 (<30): {binary_counts[1]:,} ({binary_percentages[1]:.2f}%)")

    # Visualization
    fig, axes = plt.subplots(1, 3, figsize=(18, 6))

    # Original distribution
    sns.countplot(data=df, x=target_col, ax=axes[0])
    axes[0].set_title('Original Target Distribution')
    axes[0].set_ylabel('Count')
    for i, v in enumerate(target_counts.values):
        axes[0].text(i, v + 1000, str(v), ha='center', va='bottom')

    # Binary distribution
    sns.countplot(data=df, x='readmitted_binary', ax=axes[1])
    axes[1].set_title('Binary Target Distribution')
    axes[1].set_xlabel('Readmitted within 30 days')
    axes[1].set_xticklabels(['No (0)', 'Yes (1)'])
    for i, v in enumerate(binary_counts.values):
        axes[1].text(i, v + 1000, str(v), ha='center', va='bottom')

    # Pie chart for binary
```

```
    axes[2].pie(binary_counts.values, labels=['No (<30)', 'Yes (<30)'],
                autopct='%1.1f%%', startangle=90, colors=['lightcoral', 'lightblue'])
    axes[2].set_title('Binary Target Distribution')

    plt.tight_layout()
    plt.show()

    return target_counts, binary_counts

# Run target variable analysis
if df is not None:
    target_analysis, binary_analysis = analyze_target_variable(df)
```

```
==================================================
TARGET VARIABLE ANALYSIS
==================================================
Original Target Variable Distribution:
  NO: 54,864 (53.91%)
  >30: 35,545 (34.93%)
  <30: 11,357 (11.16%)

Binary Target Variable Distribution (Focus: <30 days):
  0 (NO or >30): 90,409 (88.84%)
  1 (<30): 11,357 (11.16%)
```



Target Variable Analysis Notes The dataset is severely imbalanced with only ~11% of the patients readmitted to the hospital within 30 days. Balancing techniques will need to be used to address this.

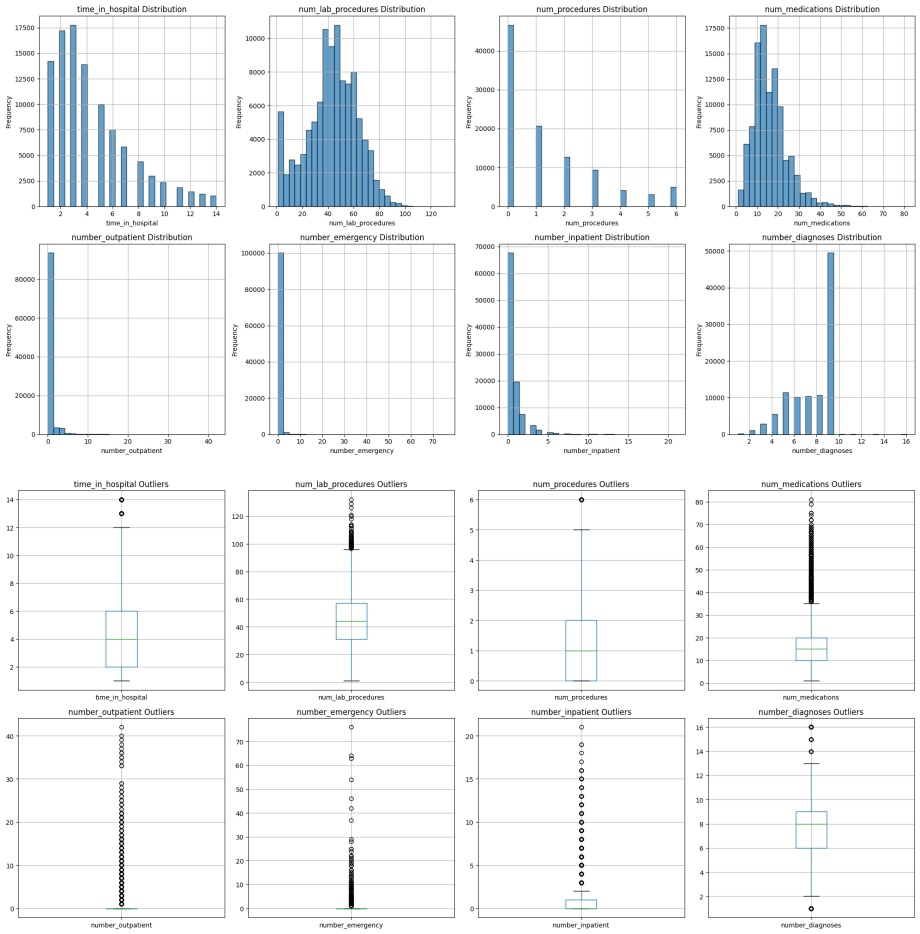
Numerical Features Analysis

```
def analyze_numerical_variables(df):
    """Analyze numerical variables for modeling insights"""
    print("\n" + "="*50)
    print("NUMERICAL VARIABLES ANALYSIS")
```

```
print("="*50)

# Identify numerical columns (exclude ID columns)
numerical_cols = df.select_dtypes(include=[np.number]).columns.tolist()
numerical_cols = [col for col in numerical_cols if 'id' not in col.lower() and 'nbr' not

print(f"Numerical columns ({len(numerical_cols)}): {numerical_cols}")

# Statistical summary
print("\nStatistical Summary:")
print(df[numerical_cols].describe().round(2))

# Distribution plots
n_cols = len(numerical_cols)
fig, axes = plt.subplots(2, 4, figsize=(20, 10))
axes = axes.ravel()

for i, col in enumerate(numerical_cols):
    if i < len(axes):
        df[col].hist(bins=30, ax=axes[i], alpha=0.7, edgecolor='black')
        axes[i].set_title(f'{col} Distribution')
        axes[i].set_xlabel(col)
        axes[i].set_ylabel('Frequency')

plt.tight_layout()
plt.show()

# Box plots for outlier detection
fig, axes = plt.subplots(2, 4, figsize=(20, 10))
axes = axes.ravel()

for i, col in enumerate(numerical_cols):
    if i < len(axes):
        df.boxplot(column=col, ax=axes[i])
        axes[i].set_title(f'{col} Outliers')

plt.tight_layout()
plt.show()

# Correlation matrix
plt.figure(figsize=(10, 8))
correlation_matrix = df[numerical_cols].corr()
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', center=0,
            square=True, fmt='.2f')
plt.title('Correlation Matrix of Numerical Variables')
plt.tight_layout()
```

```
    plt.show()

    return numerical_cols

# Run numerical analysis
if df is not None:
    numerical_features = analyze_numerical_variables(df)
```

```
==================================================
NUMERICAL VARIABLES ANALYSIS
==================================================
Numerical columns (9): ['time_in_hospital', 'num_lab_procedures', 'num_procedures', 'num_med

Statistical Summary:
       time_in_hospital  num_lab_procedures  num_procedures  num_medications  \
count         101766.00           101766.00       101766.00        101766.00
mean               4.40               43.10            1.34            16.02
std                2.99               19.67            1.71             8.13
min                1.00                1.00            0.00             1.00
25%                2.00               31.00            0.00            10.00
50%                4.00               44.00            1.00            15.00
75%                6.00               57.00            2.00            20.00
max               14.00              132.00            6.00            81.00

       number_outpatient  number_emergency  number_inpatient  \
count          101766.00         101766.00         101766.00
mean                0.37              0.20              0.64
std                 1.27              0.93              1.26
min                 0.00              0.00              0.00
25%                 0.00              0.00              0.00
50%                 0.00              0.00              0.00
75%                 0.00              0.00              1.00
max                42.00             76.00             21.00

       number_diagnoses  readmitted_binary
count         101766.00          101766.00
mean               7.42               0.11
std                1.93               0.31
min                1.00               0.00
25%                6.00               0.00
50%                8.00               0.00
75%                9.00               0.00
max               16.00               1.00
```


time_in_hospital Distribution
num_lab_procedures Distribution
num_procedures Distribution
num_medications Distribution
number_outpatient Distribution
number_emergency Distribution
number_inpatient Distribution
number_diagnoses Distribution
Frequency
time_in_hospital
num_lab_procedures
num_procedures
num_medications
number_outpatient
number_emergency
number_inpatient
number_diagnoses
time_in_hospital Outliers
num_lab_procedures Outliers
num_procedures Outliers
num_medications Outliers
number_outpatient Outliers
number_emergency Outliers
number_inpatient Outliers
number_diagnoses Outliers

Numerical Features Analysis Notes

- The target variable shows the strongest correlation with the following features (in descending order): number_inpatient, number_emergency, number_diagnoses, time_in_hospital, and num_medications.
- The length of hospital stay is typically short, with the majority of patients staying between 2 to 4 days.
- The number of inpatient visits is generally low, with the majority of patients having 0 to 2 visits
- The number of medications is between 10-20 with the majority of the patients.
- Most patients had no emergency visits recorded (number_emergency = 0).
- The number of diagnoses is commonly clustered around 6 to 8 diagnoses per patient.

Categorical Features Analysis

```
# Map some categorical variables to named categories for easier analysis

admission_type_map = {
    1: "Emergency",
    2: "Urgent",
    3: "Elective",
    4: "Newborn",
    5: "Not Available",
    6: "NULL",
    7: "Trauma Center",
    8: "Not Mapped"
}

df['admission_type'] = df['admission_type_id'].map(admission_type_map)

discharge_disposition_map = {
    1: "Discharged to home",
    2: "To-short-term-hospital",
    3: "To SNF",
    4: "To ICF",
    5: "To other inpatient care",
    6: "Home w/ HS",
    7: "Left AMA",
    8: "Home under IV provider",
    9: "Admitted inpatient",
    10: "Neonate to another hospital",
    11: "Expired",
    12: "Still patient",
    13: "Hospice / home",
    14: "Hospice / facility",
    15: "To Medicare swing bed",
    16: "To outpatient (other inst.)",
    17: "To outpatient (this inst.)",
    18: "NULL",
    19: "Expired at home (Medicaid)",
    20: "Expired in facility (Medicaid)",
    21: "Expired, unknown place",
    22: "To rehab facility",
    23: "To long-term care hospital",
    24: "To Medicaid-only nursing",
    25: "Not Mapped",
    26: "Unknown/Invalid",
    27: "To federal facility",
    28: "To psychiatric hospital",
```

```
    29: "To Critical Access Hospital"
}



df['discharge_disposition'] = df['discharge_disposition_id'].map(discharge_disposition_map)

# Admission Type Mapping
admission_source_map = {
    1: 'Physician Referral',
    2: 'Clinic Referral',
    3: 'HMO Referral',
    4: 'Transfer from hospital',
    5: 'Transfer from SNF',
    6: 'Transfer from other ',
    7: 'Emergency Room',
    8: 'Court/Law Enforcement',
    9: 'Not Available',
    10: 'Transfer from critical access ',
    11: 'Normal Delivery',
    12: 'Premature Delivery',
    13: 'Sick Baby',
    14: 'Extramural Birth',
    15: 'Not Available',
    17: 'NULL',
    18: 'Transfer from another HHA',
    19: 'Readmission to same HHA',
    20: 'Not Mapped',
    21: 'Unknown/Invalid',
    22: 'Transfer within same facility',
    23: 'Born inside hospital',
    24: 'Born outside hospital',
    25: 'Transfer from Ambulatory Surgery Center',
    26: 'Transfer from Hospice'
}

df['admission_source'] = df['admission_source_id'].map(admission_source_map)

# There are some dicharge dispositions that are not relevant to our analysis, including exp
exclude_discharge_ids = [11, 12, 13, 14, 19, 20, 21]

# Filter dataframe to exclude these discharge types
df = df[~df['discharge_disposition_id'].isin(exclude_discharge_ids)].copy()

# Diagnoses mapping and analysis
# The diagnoses columns have ICD 9 codes and its large set. Mapping them to few categories
# As defined in the paper, https://onlinelibrary.wiley.com/doi/10.1155/2014/781670, groupin
```

```python
import re
# Define the groups and their ICD code ranges as tuples (start, end)
# For simplicity, codes like 250.xx are treated as 250 to 250.99
# 'E' and 'V' codes handled separately

# We'll convert codes to float for numeric ranges, and handle E, V codes as special.

def icd9_to_group(code):
    if pd.isna(code):
        return 'Unknown'
    code = str(code).strip()

    # Handle E and V codes separately
    if code.startswith('E'):
        return 'External causes of injury and supplemental classification'
    if code.startswith('V'):
        return 'External causes of injury and supplemental classification'

    # Extract numeric part before decimal
    match = re.match(r'(\d+)(?:\.(\d+))?', code)
    if not match:
        return 'Other/Unknown'

    main_code = int(match.group(1))
    # decimal_part = match.group(2) # we might use if needed

    # Map ranges from your table:
    if (390 <= main_code <= 459) or main_code == 785:
        return 'Circulatory'
    elif (460 <= main_code <= 519) or main_code == 786:
        return 'Respiratory'
    elif (520 <= main_code <= 579) or main_code == 787:
        return 'Digestive'
    elif main_code == 250:
        return 'Diabetes'
    elif 800 <= main_code <= 999:
        return 'Injury'
    elif 710 <= main_code <= 739:
        return 'Musculoskeletal'
    elif (580 <= main_code <= 629) or main_code == 788:
        return 'Genitourinary'
    elif 140 <= main_code <= 239:
        return 'Neoplasms'
    elif main_code in [780, 781, 784] or (790 <= main_code <= 799):
        return 'Other symptoms, signs, and ill-defined conditions'
```

```
    elif (240 <= main_code <= 279) and main_code != 250:
        return 'Endocrine, nutritional, and metabolic diseases (excluding diabetes)'
    elif (680 <= main_code <= 709) or main_code == 782:
        return 'Skin and subcutaneous tissue diseases'
    elif 1 <= main_code <= 139:
        return 'Infectious and parasitic diseases'
    elif 290 <= main_code <= 319:
        return 'Mental disorders'
    elif 280 <= main_code <= 289:
        return 'Blood diseases'
    elif 320 <= main_code <= 359:
        return 'Nervous system diseases'
    elif 630 <= main_code <= 679:
        return 'Pregnancy complications'
    elif 360 <= main_code <= 389:
        return 'Sense organs diseases'
    elif 740 <= main_code <= 759:
        return 'Congenital anomalies'
    else:
        return 'Other/Unknown'

for col in ['diag_1', 'diag_2', 'diag_3']:
    df[col + '_group'] = df[col].apply(icd9_to_group)

# Example output check:
print(df[['diag_1', 'diag_1_group', 'diag_2', 'diag_2_group', 'diag_3', 'diag_3_group']].hea
```

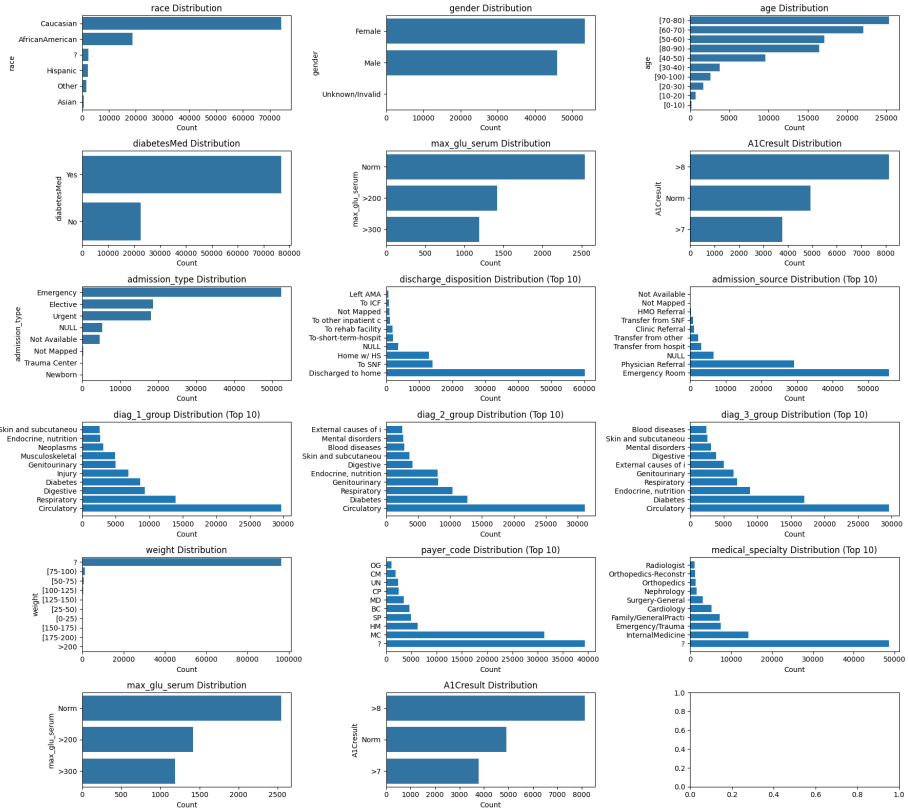
```
   diag_1                                      diag_1_group  diag_2  \
0  250.83                                          Diabetes       ?
1     276  Endocrine, nutritional, and metabolic diseases...  250.01
2     648                          Pregnancy complications     250
3       8              Infectious and parasitic diseases  250.43
4     197                                       Neoplasms     157

    diag_2_group diag_3                                      diag_3_group
0  Other/Unknown      ?                                     Other/Unknown
1       Diabetes    255  Endocrine, nutritional, and metabolic diseases...
2       Diabetes    V27  External causes of injury and supplemental cla...
3       Diabetes    403                                       Circulatory
4      Neoplasms    250                                          Diabetes
```

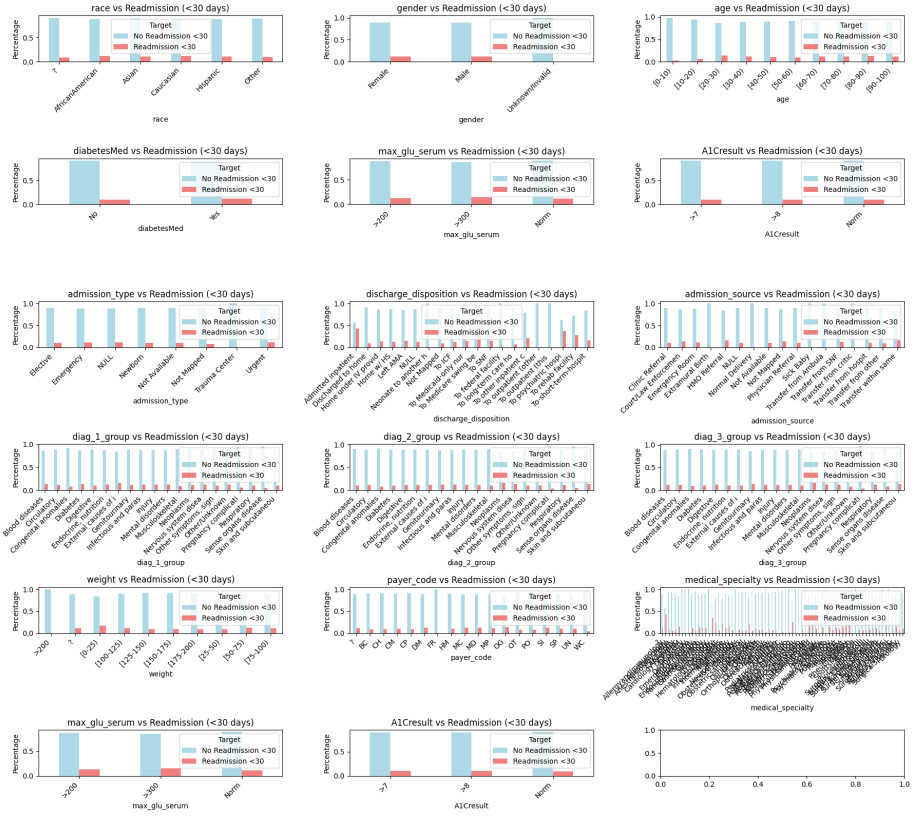
```
def analyze_categorical_variables(df, target_col='readmitted_binary'):
    """Analyze categorical variables for modeling insights"""
    print("\n" + "="*50)
    print("CATEGORICAL VARIABLES ANALYSIS")
    print("="*50)
```

```python
# Identify categorical columns (exclude target)
categorical_cols = df.select_dtypes(include=['object']).columns.tolist()
categorical_cols = [col for col in categorical_cols if col not in ['readmitted', target_

print(f"Categorical columns ({len(categorical_cols)}): {categorical_cols}")

# Analyze key categorical variables for modeling
key_categorical = ['race', 'gender', 'age', 'diabetesMed', 'max_glu_serum', 'A1Cresult',
'admission_source', 'diag_1_group', 'diag_2_group', 'diag_3_group', 'weight', 'payer_coo

# Distribution plots
fig, axes = plt.subplots(6, 3, figsize=(18, 16))
axes = axes.ravel()

for i, col in enumerate(key_categorical):
    if col in df.columns and i < len(axes):
        value_counts = df[col].value_counts()

        if len(value_counts) <= 15:  # Only plot if not too many categories
            sns.countplot(data=df, y=col, ax=axes[i], order=value_counts.index[:10])
            axes[i].set_title(f'{col} Distribution')
            axes[i].set_xlabel('Count')
        else:
            # For columns with many categories, show top 10
            top_values = value_counts.head(10)
            axes[i].barh(range(len(top_values)), top_values.values)
            axes[i].set_yticks(range(len(top_values)))
            axes[i].set_yticklabels(top_values.index)
            axes[i].set_title(f'{col} Distribution (Top 10)')
            axes[i].set_xlabel('Count')
                        # Truncate x-tick labels to 20 characters
            yticks = axes[i].get_yticklabels()
            axes[i].set_yticklabels([tick.get_text()[:20] for tick in yticks])


plt.tight_layout()
plt.show()

# Relationship with BINARY target variable (<30 days readmission)
fig, axes = plt.subplots(6, 3, figsize=(18, 16))
axes = axes.ravel()

for i, col in enumerate(key_categorical):
    if col in df.columns and i < len(axes):
        # Create crosstab showing readmission rates by category (binary)
        crosstab = pd.crosstab(df[col], df[target_col], normalize='index')
```

```
            crosstab.plot(kind='bar', ax=axes[i],
                          color=['lightblue', 'lightcoral'])
            axes[i].set_title(f'{col} vs Readmission (<30 days)')
            axes[i].set_xlabel(col)
            axes[i].set_ylabel('Percentage')
            axes[i].legend(['No Readmission <30', 'Readmission <30'], title='Target')
            axes[i].tick_params(axis='x', rotation=45)
            # Truncate x-tick labels to 20 characters
            xticks = axes[i].get_xticklabels()
            axes[i].set_xticklabels([tick.get_text()[:20] for tick in xticks], rotation=45,

    plt.tight_layout()
    plt.show()

    # Print unique values for modeling consideration
    print("\nUNIQUE VALUES IN KEY CATEGORICAL COLUMNS:")
    for col in key_categorical:
        if col in df.columns:
            unique_count = df[col].nunique()
            print(f"  {col}: {unique_count} unique values")
            if unique_count <= 10:
                print(f"    Values: {df[col].unique().tolist()}")

    return categorical_cols

# Run categorical analysis
if df is not None:
    categorical_features = analyze_categorical_variables(df)
```

```
==================================================
CATEGORICAL VARIABLES ANALYSIS
==================================================
Categorical columns (42): ['race', 'gender', 'age', 'weight', 'payer_code', 'medical_specia
```


race Distribution
Caucasian
AfricanAmerican
?
Hispanic
Other
Asian
race
0 10000 20000 30000 40000 50000 60000 70000
Count
gender Distribution
Female
Male
Unknown/Invalid
gender
0 10000 20000 30000 40000 50000
Count
age Distribution
[70-80)
[60-70)
[50-60)
[80-90)
[40-50)
[30-40)
[90-100)
[20-30)
[10-20)
[0-10)
age
0 5000 10000 15000 20000 25000
Count
diabetesMed Distribution
Yes
No
diabetesMed
0 10000 20000 30000 40000 50000 60000 70000 80000
Count
max_glu_serum Distribution
Norm
>200
>300
max_glu_serum
0 500 1000 1500 2000 2500
Count
A1Cresult Distribution
>8
Norm
>7
A1Cresult
0 1000 2000 3000 4000 5000 6000 7000 8000
Count
admission_type Distribution
Emergency
Elective
Urgent
NULL
Not Available
Not Mapped
Trauma Center
Newborn
admission_type
0 10000 20000 30000 40000 50000
Count
discharge_disposition Distribution (Top 10)
Left AMA
To ICF
Not Mapped
To other inpatient c
To rehab facility
To-short-term-hospit
NULL
Home w/ HS
To SNF
Discharged to home
0 10000 20000 30000 40000 50000 60000
Count
admission_source Distribution (Top 10)
Not Available
Not Mapped
HMO Referral
Transfer from SNF
Clinic Referral
Transfer from other
Transfer from hospit
NULL
Physician Referral
Emergency Room
0 10000 20000 30000 40000 50000
Count
diag_1_group Distribution (Top 10)
Skin and subcutaneou
Endocrine, nutrition
Neoplasms
Musculoskeletal
Genitourinary
Injury
Diabetes
Digestive
Respiratory
Circulatory
0 5000 10000 15000 20000 25000 30000
Count
diag_2_group Distribution (Top 10)
External causes of i
Mental disorders
Blood diseases
Skin and subcutaneou
Digestive
Endocrine, nutrition
Genitourinary
Respiratory
Diabetes
Circulatory
0 5000 10000 15000 20000 25000 30000
Count
diag_3_group Distribution (Top 10)
Blood diseases
Skin and subcutaneou
Mental disorders
Digestive
External causes of i
Genitourinary
Respiratory
Endocrine, nutrition
Diabetes
Circulatory
0 5000 10000 15000 20000 25000 30000
Count
weight Distribution
?
[75-100)
[50-75)
[100-125)
[125-150)
[25-50)
[0-25)
[150-175)
[175-200)
>200
weight
0 20000 40000 60000 80000 100000
Count
payer_code Distribution (Top 10)
OG
CM
UN
CP
MD
BC
SP
HM
MC
?
0 5000 10000 15000 20000 25000 30000 35000 40000
Count
medical_specialty Distribution (Top 10)
Radiologist
Orthopedics-Reconstr
Orthopedics
Nephrology
Surgery-General
Cardiology
Family/GeneralPracti
Emergency/Trauma
InternalMedicine
?
0 10000 20000 30000 40000 50000
Count
max_glu_serum Distribution
Norm
>200
>300
max_glu_serum
0 500 1000 1500 2000 2500
Count
A1Cresult Distribution
>8
Norm
>7
A1Cresult
0 1000 2000 3000 4000 5000 6000 7000 8000
Count
0.0 0.2 0.4 0.6 0.8 1.0
0.0 0.2 0.4 0.6 0.8 1.0




```
UNIQUE VALUES IN KEY CATEGORICAL COLUMNS:
  race: 6 unique values
    Values: ['Caucasian', 'AfricanAmerican', '?', 'Other', 'Asian', 'Hispanic']
  gender: 3 unique values
    Values: ['Female', 'Male', 'Unknown/Invalid']
  age: 10 unique values
    Values: ['[0-10)', '[10-20)', '[20-30)', '[30-40)', '[40-50)', '[50-60)', '[60-70)', '[7
  diabetesMed: 2 unique values
    Values: ['No', 'Yes']
  max_glu_serum: 3 unique values
    Values: [nan, '>300', 'Norm', '>200']
  A1Cresult: 3 unique values
    Values: [nan, '>7', '>8', 'Norm']
  admission_type: 8 unique values
    Values: ['NULL', 'Emergency', 'Urgent', 'Elective', 'Newborn', 'Not Available', 'Not Map
  discharge_disposition: 20 unique values
  admission_source: 17 unique values
  diag_1_group: 20 unique values
```

```
diag_2_group: 20 unique values
diag_3_group: 20 unique values
weight: 10 unique values
  Values: ['?', '[75-100)', '[50-75)', '[0-25)', '[100-125)', '[25-50)', '[125-150)', '[17
payer_code: 18 unique values
medical_specialty: 73 unique values
max_glu_serum: 3 unique values
  Values: [nan, '>300', 'Norm', '>200']
A1Cresult: 3 unique values
  Values: [nan, '>7', '>8', 'Norm']
```

Categorical Features Analysis notes

- The majority of patients are Caucasian, followed by African American and Hispanic.
- Most patients fall into older age groups, particularly those above middle age, which is consistent with the higher prevalence of diabetes among older adults.
- The most common admission type is emergency, indicating that many patients are entering the hospital due to acute or unplanned health events rather than scheduled care.
- A notably high proportion of readmitted patients were discharged to a Medicare swing bed, suggesting that patients transitioning to skilled nursing care may be at elevated risk for early readmission.
- Most Diagnosis codes are circulatory, diabetes related and respitory. With the readmitted population, neoplasms are common for secondary and third diagnosis.
- Most patients had A1C values >8, indicating poorly controlled diabetes, while the majority had normal maximum glucose serum levels

Medication Features analysis

There are many medication features that indicate whether a drug was prescribed to the patient or whether was change in dosage. Values: up if the dosage was increased during the encounter, down if the dosage was decreased, steady if the dosage did not change, and no if the drug was not prescribed. We will use only medications that have least 1000 patients to reduce noise.

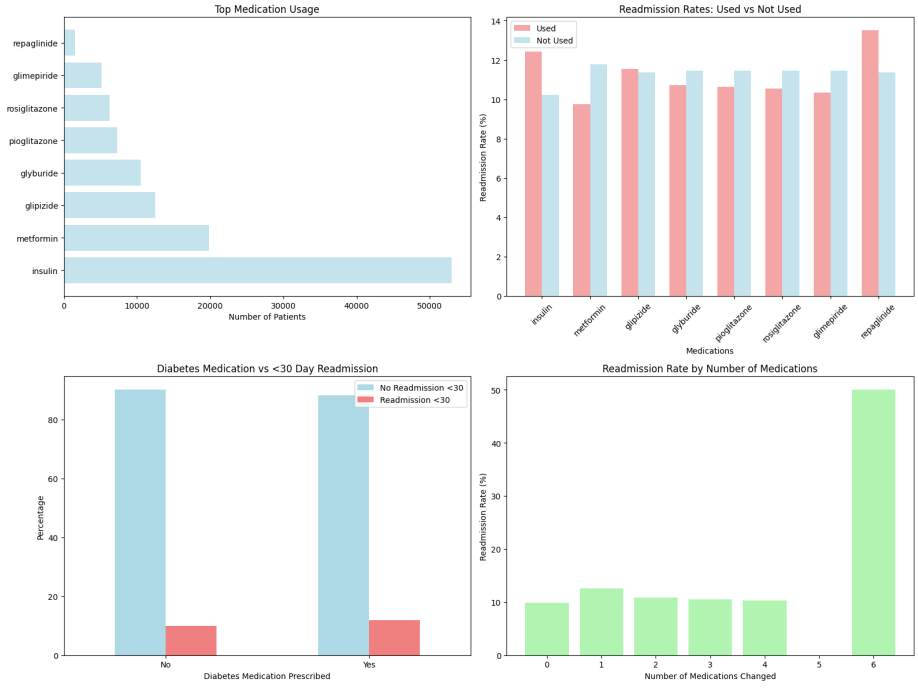
```python
def analyze_medications(df, target_col='readmitted_binary'):
    """Analyze diabetes medications for modeling insights"""
    print("\n" + "="*50)
    print("MEDICATION ANALYSIS")
    print("="*50)
```

```
# Identify medication columns
medication_cols = ['metformin', 'repaglinide', 'nateglinide', 'chlorpropamide',
                   'glimepiride', 'acetohexamide', 'glipizide', 'glyburide',
                   'tolbutamide', 'pioglitazone', 'rosiglitazone', 'acarbose',
                   'miglitol', 'troglitazone', 'tolazamide', 'examide',
                   'citoglipton', 'insulin']

# Count medication usage (any change from 'No')
medication_usage = {}
for med in medication_cols:
    if med in df.columns:
        usage_count = (df[med] != 'No').sum()
        medication_usage[med] = usage_count

# Sort by usage and filter medications with reasonable usage
sorted_meds = sorted(medication_usage.items(), key=lambda x: x[1], reverse=True)
top_meds = [(med, count) for med, count in sorted_meds if count > 1000]  # At least 100

print("Top Medication Usage (patients who received each medication):")
for med, count in top_meds:
    percentage = (count / len(df)) * 100
    print(f"  {med}: {count:,} patients ({percentage:.2f}%)")

# Medication vs readmission analysis
print(f"\nMedication Impact on <30 Day Readmission:")
med_impact = []
for med, count in top_meds:
    # Calculate readmission rates
    med_used = df[df[med] != 'No'][target_col].mean() * 100
    med_not_used = df[df[med] == 'No'][target_col].mean() * 100
    difference = med_used - med_not_used

    med_impact.append((med, med_used, med_not_used, difference))
    print(f"  {med}: Used {med_used:.1f}% vs Not Used {med_not_used:.1f}% (Diff: {differ

# Visualizations
fig, axes = plt.subplots(2, 2, figsize=(16, 12))

# Top medication usage
meds, counts = zip(*top_meds[:8])  # Top 8
axes[0,0].barh(meds, counts, color='lightblue', alpha=0.7)
axes[0,0].set_xlabel('Number of Patients')
axes[0,0].set_title('Top Medication Usage')

# Medication impact on readmission
meds_impact, used_rates, not_used_rates, differences = zip(*med_impact[:8])
```

```
    x = range(len(meds_impact))
    width = 0.35

    axes[0,1].bar([i - width/2 for i in x], used_rates, width, label='Used', alpha=0.7, colo
    axes[0,1].bar([i + width/2 for i in x], not_used_rates, width, label='Not Used', alpha=0
    axes[0,1].set_xlabel('Medications')
    axes[0,1].set_ylabel('Readmission Rate (%)')
    axes[0,1].set_title('Readmission Rates: Used vs Not Used')
    axes[0,1].set_xticks(x)
    axes[0,1].set_xticklabels(meds_impact, rotation=45)
    axes[0,1].legend()

    # Overall diabetes medication analysis
    if 'diabetesMed' in df.columns:
        diabetes_crosstab = pd.crosstab(df['diabetesMed'], df[target_col], normalize='index'
        diabetes_crosstab.plot(kind='bar', ax=axes[1,0], color=['lightblue', 'lightcoral'])
        axes[1,0].set_title('Diabetes Medication vs <30 Day Readmission')
        axes[1,0].set_xlabel('Diabetes Medication Prescribed')
        axes[1,0].set_ylabel('Percentage')
        axes[1,0].legend(['No Readmission <30', 'Readmission <30'])
        axes[1,0].tick_params(axis='x', rotation=0)

    # Medication count analysis
    df['med_count'] = 0
    for med in medication_cols:
        if med in df.columns:
            df['med_count'] += (df[med] != 'No').astype(int)

    med_count_crosstab = df.groupby('med_count')[target_col].mean() * 100
    axes[1,1].bar(med_count_crosstab.index, med_count_crosstab.values, color='lightgreen', a
    axes[1,1].set_xlabel('Number of Medications Changed')
    axes[1,1].set_ylabel('Readmission Rate (%)')
    axes[1,1].set_title('Readmission Rate by Number of Medications')

    plt.tight_layout()
    plt.show()

    return top_meds, med_impact

# Run medication analysis
if df is not None:
    medication_patterns, medication_impact = analyze_medications(df)
```

```
==================================================
MEDICATION ANALYSIS
```

```
==================================================
Top Medication Usage (patients who received each medication):
  insulin: 52,964 patients (53.32%)
  metformin: 19,844 patients (19.98%)
  glipizide: 12,531 patients (12.61%)
  glyburide: 10,523 patients (10.59%)
  pioglitazone: 7,255 patients (7.30%)
  rosiglitazone: 6,304 patients (6.35%)
  glimepiride: 5,122 patients (5.16%)
  repaglinide: 1,518 patients (1.53%)

Medication Impact on <30 Day Readmission:
  insulin: Used 12.4% vs Not Used 10.2% (Diff: +2.2%)
  metformin: Used 9.8% vs Not Used 11.8% (Diff: -2.0%)
  glipizide: Used 11.5% vs Not Used 11.4% (Diff: +0.2%)
  glyburide: Used 10.7% vs Not Used 11.5% (Diff: -0.7%)
  pioglitazone: Used 10.6% vs Not Used 11.4% (Diff: -0.8%)
  rosiglitazone: Used 10.5% vs Not Used 11.4% (Diff: -0.9%)
  glimepiride: Used 10.3% vs Not Used 11.4% (Diff: -1.1%)
  repaglinide: Used 13.5% vs Not Used 11.4% (Diff: +2.2%)
```



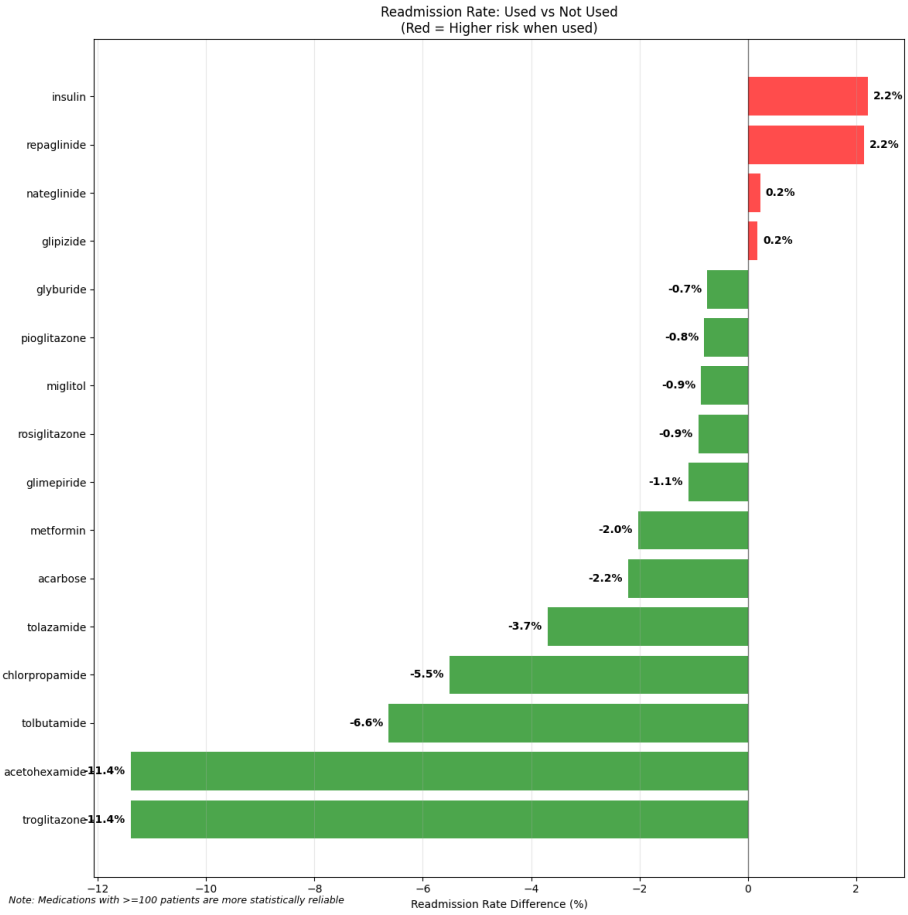

```
# ====================================
# MEDICATION READMISSION RATE DIFFERENCE CHART
# ====================================
```

```python
def create_medication_readmission_chart(df, target_col='readmitted_binary'):
    """Create medication readmission rate difference chart"""

    # Medication columns
    medication_cols = ['metformin', 'repaglinide', 'nateglinide', 'chlorpropamide',
                       'glimepiride', 'acetohexamide', 'glipizide', 'glyburide',
                       'tolbutamide', 'pioglitazone', 'rosiglitazone', 'acarbose',
                       'miglitol', 'troglitazone', 'tolazamide', 'examide',
                       'citoglipton', 'insulin']

    # Calculate readmission rate differences for ALL medications
    med_differences = []

    print("Medication Usage and Readmission Rate Analysis:")
    print("Note: Filter of >=100 patients recommended for statistical reliability")
    print("(Small sample sizes may show misleading differences)\n")

    for med in medication_cols:
        if med in df.columns:
            # Calculate usage for all medications
            used_count = (df[med] != 'No').sum()

            if used_count > 0:  # Only need at least 1 patient
                # Readmission rates
                med_used_rate = df[df[med] != 'No'][target_col].mean() * 100
                med_not_used_rate = df[df[med] == 'No'][target_col].mean() * 100
                difference = med_used_rate - med_not_used_rate

                # Track reliability status
                reliable = used_count >= 100

                med_differences.append((med, difference, used_count, reliable))
                print(f"{med}: {used_count:,} patients, difference: {difference:+.1f}%")

    # Sort by difference
    med_differences.sort(key=lambda x: x[1])

    # Prepare data for plotting
    medications, differences, counts, reliability = zip(*med_differences)

    # Create colors: red for positive (higher risk), green for negative (lower risk)
    colors = ['green' if diff < 0 else 'red' for diff in differences]

    # Create the chart
    plt.figure(figsize=(12, 12))
```

```
    bars = plt.barh(medications, differences, color=colors, alpha=0.7)

    # Formatting
    plt.xlabel('Readmission Rate Difference (%)')
    plt.title('Readmission Rate: Used vs Not Used\n(Red = Higher risk when used)')
    plt.axvline(x=0, color='black', linestyle='-', alpha=0.5, linewidth=1)
    plt.grid(True, alpha=0.3, axis='x')

    # Add value labels on bars
    for bar, diff, count, reliable in zip(bars, differences, counts, reliability):
        x_pos = diff + (0.1 if diff >= 0 else -0.1)
        plt.text(x_pos, bar.get_y() + bar.get_height()/2,
                f'{diff:.1f}%', ha='left' if diff >= 0 else 'right',
                va='center', fontweight='bold', fontsize=10)

    # Add note about statistical reliability
    plt.figtext(0.02, 0.02, "Note: Medications with >=100 patients are more statistically re
                fontsize=9, style='italic')

    plt.tight_layout()
    plt.show()

    reliable_count = sum(1 for r in reliability if r)
    unreliable_count = len(reliability) - reliable_count

    print(f"\nSummary: {reliable_count} medications with >=100 patients")
    print(f"         {unreliable_count} medications with <100 patients")

if df is not None:
    create_medication_readmission_chart(df)
```

```
Medication Usage and Readmission Rate Analysis:
Note: Filter of >=100 patients recommended for statistical reliability
(Small sample sizes may show misleading differences)

metformin: 19,844 patients, difference: -2.0%
repaglinide: 1,518 patients, difference: +2.2%
nateglinide: 689 patients, difference: +0.2%
chlorpropamide: 85 patients, difference: -5.5%
glimepiride: 5,122 patients, difference: -1.1%
acetohexamide: 1 patients, difference: -11.4%
glipizide: 12,531 patients, difference: +0.2%
glyburide: 10,523 patients, difference: -0.7%
tolbutamide: 21 patients, difference: -6.6%
pioglitazone: 7,255 patients, difference: -0.8%
rosiglitazone: 6,304 patients, difference: -0.9%
```

```
acarbose: 305 patients, difference: -2.2%
miglitol: 38 patients, difference: -0.9%
troglitazone: 3 patients, difference: -11.4%
tolazamide: 39 patients, difference: -3.7%
insulin: 52,964 patients, difference: +2.2%
```




```
Summary: 10 medications with >=100 patients
         6 medications with <100 patients
```

Medications Feature Analysis Notes We examined the 18 diabetes-related medication features to understand their prevalence and association with 30-day readmission. Key findings include:

- Insulin was the most common (53.3%), followed by Metformin (20%)
- Insulin users had a 12.4% readmission rate versus 10.2% for non-user, suggesting insulin dependant patients are at higher risk

- Metformin stood out for its protective association: users had a 9.8% readmission rate vs 11.8% for non-users
- Patients with more medications changed or prescribed tended to have slightly higher readmission rates, reflecting overall disease complexity and treatment intensity.

Data Understanding Analysis Summary

The dataset primarily consists of older adult patients, with a majority identifying as Caucasian and most hospital admissions occurring through emergency visits, reflecting acute health events. Key categorical features reveal that patients discharged to Medicare swing beds show elevated readmission rates, and common diagnoses include circulatory, diabetes-related, and respiratory conditions—with neoplasms more frequent in secondary or tertiary diagnoses among readmitted patients. Medication analysis highlights insulin as the most commonly prescribed drug (53.3%), with insulin users exhibiting higher readmission risk, while metformin use appears protective. Numerical features such as number of inpatient visits, emergency visits, total diagnoses, and medication count are strongly correlated with readmission risk. Most patients had short hospital stays (2–4 days), 0–2 prior inpatient visits, and typically managed 10–20 medications. Additionally, most patients had A1C values >8, indicating poorly controlled diabetes, while the majority had normal maximum glucose serum levels. These insights guided feature engineering and informed model design.

Data Preparation & Feature Engineering

Handling Missing Values

Weight, payer code, medical specialty have significant percentage of missing values. These are hard to be imputed for effective analysis so dropping those. For missing values of race, imputing them with "unknown". For missing values of diagnosis, imputing them "missing". For missing A1C result, imputing them with "No Test taken" and for missing max_glu_serum, imputing them with "No Test taken".

```
# ====================================
# COMPREHENSIVE MISSING VALUES HANDLING
# ====================================

def handle_missing_values_comprehensive(df):
    """Comprehensive missing values handling"""
    print("\n" + "="*50)
    print("COMPREHENSIVE MISSING VALUES HANDLING")
    print("="*50)

    # Replace '?' with np.nan for true missing value detection
    df = df.replace('?', np.nan).copy()
```

```
    # Drop columns with excessive missing values (>90%)
    columns_to_drop = ['payer_code', 'weight', 'medical_specialty']
    df.drop(columns=columns_to_drop, inplace=True, errors='ignore')
    print(f"Dropped columns: {columns_to_drop}")

    # Handle categorical missing values
    df['race'] = df['race'].fillna('Unknown')
    df['A1Cresult'] = df['A1Cresult'].replace({np.nan: 'No test', 'None': 'No test'})
    df['max_glu_serum'] = df['max_glu_serum'].replace({np.nan: 'No test', 'None': 'No test'}

    # Handle diagnosis missing values
    for col in ['diag_1', 'diag_2', 'diag_3']:
        df[col] = df[col].fillna('Missing')

    # Handle any remaining categorical missing values for modeling
    categorical_cols = df.select_dtypes(include=['object']).columns
    for col in categorical_cols:
        df[col] = df[col].fillna('Unknown').astype(str)

    # Handle numerical missing values
    numerical_cols = df.select_dtypes(include=[np.number]).columns
    for col in numerical_cols:
        if df[col].isnull().sum() > 0:
            df[col] = df[col].fillna(df[col].median())

    # Verify no missing values remain
    missing_after = df.isnull().sum()
    if missing_after.sum() > 0:
        print("WARNING: Still have missing values:")
        print(missing_after[missing_after > 0])
    else:
        print("All missing values handled successfully")

    return df

# Apply comprehensive missing value handling
df = handle_missing_values_comprehensive(df)
```

```
==================================================
COMPREHENSIVE MISSING VALUES HANDLING
==================================================
Dropped columns: ['payer_code', 'weight', 'medical_specialty']
All missing values handled successfully
```

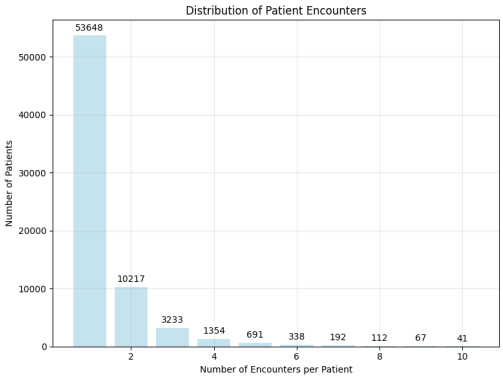
Handling Duplicates

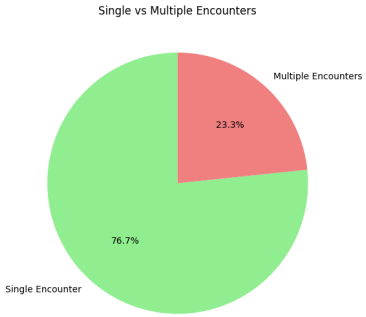
We want to see if there are multiple encounters for a patient. If there are, retain only the first encounter to avoid data leakage and ensure fair modeling, mimicking real-world use where future visits are unknown at prediction time.

```
def analyze_duplicates(df):
    print("\n" + "="*50)
    print("DUPLICATE ANALYSIS")
    print("="*50)

    # Check for exact duplicates
    duplicate_rows = df.duplicated().sum()
    print(f"Exact duplicate rows: {duplicate_rows:,}")

    # Check for duplicate patient encounters
    if 'patient_nbr' in df.columns:
        duplicate_patients = df['patient_nbr'].duplicated().sum()
        unique_patients = df['patient_nbr'].nunique()

        print(f"Duplicate patient numbers: {duplicate_patients:,}")
        print(f"Unique patients: {unique_patients:,}")
        print(f"Total encounters: {len(df):,}")
        print(f"Average encounters per patient: {len(df)/unique_patients:.2f}")

        # Patients with multiple encounters
        patient_encounters = df['patient_nbr'].value_counts()
        multiple_encounters = (patient_encounters > 1).sum()

        print(f"Patients with multiple encounters: {multiple_encounters:,}")
        print(f"Patients with single encounter: {unique_patients - multiple_encounters:,}")

        # Visualization
        fig, axes = plt.subplots(1, 2, figsize=(15, 6))

        # Distribution of encounters per patient
        encounter_dist = patient_encounters.value_counts().sort_index()
        encounter_dist_limited = encounter_dist.head(10)  # Show up to 10 encounters

        axes[0].bar(encounter_dist_limited.index, encounter_dist_limited.values,
                    color='lightblue', alpha=0.7)
        axes[0].set_xlabel('Number of Encounters per Patient')
        axes[0].set_ylabel('Number of Patients')
        axes[0].set_title('Distribution of Patient Encounters')
        axes[0].grid(True, alpha=0.3)
```

```
        # Add value labels on bars
        for i, v in enumerate(encounter_dist_limited.values):
            axes[0].text(encounter_dist_limited.index[i], v + max(encounter_dist_limited.val
                         str(v), ha='center', va='bottom')

        # Single vs Multiple encounters
        single_vs_multiple = [unique_patients - multiple_encounters, multiple_encounters]
        labels = ['Single Encounter', 'Multiple Encounters']

        axes[1].pie(single_vs_multiple, labels=labels, autopct='%1.1f%%',
                    colors=['lightgreen', 'lightcoral'], startangle=90)
        axes[1].set_title('Single vs Multiple Encounters')

        plt.tight_layout()
        plt.show()

        # Data quality summary
        print(f"\nDATA QUALITY SUMMARY:")
        if multiple_encounters > 0:
            multiple_pct = (multiple_encounters / unique_patients) * 100
            print(f"  {multiple_pct:.1f}% of patients have multiple encounters")

        if duplicate_rows > 0:
            print(f"  {duplicate_rows:,} exact duplicate rows found")
        else:
            print(f"  No exact duplicate rows found")

    return duplicate_rows, unique_patients if 'patient_nbr' in df.columns else None

# Run duplicate analysis
if df is not None:
    duplicates, unique_patients = analyze_duplicates(df)
```

```
==================================================
DUPLICATE ANALYSIS
==================================================
Exact duplicate rows: 0
Duplicate patient numbers: 29,352
Unique patients: 69,988
Total encounters: 99,340
Average encounters per patient: 1.42
Patients with multiple encounters: 16,340
Patients with single encounter: 53,648
```






```
DATA QUALITY SUMMARY:
  23.3% of patients have multiple encounters
  No exact duplicate rows found
```

```
if df is not None and unique_patients is not None:
    df = df.sort_values(by='encounter_id').drop_duplicates(subset='patient_nbr', keep='first
    print(f"\nFiltered dataset to first encounter for each patient. New row count: {len(df)
```

```
Filtered dataset to first encounter for each patient. New row count: 69,988
```

Handling Age Bins

Originally a categorical range (e.g., "[70–80)"), was converted to a numeric mid-point (e.g., 75) to support numerical modeling and allow for advanced transformations like high-risk flags.

```
# convert age to numeric for better analysis for ensemble models
age_map = {
    '[0-10)': 5,
    '[10-20)': 15,
    '[20-30)': 25,
    '[30-40)': 35,
    '[40-50)': 45,
    '[50-60)': 55,
    '[60-70)': 65,
    '[70-80)': 75,
    '[80-90)': 85,
    '[90-100)': 95
}

df['age_numeric'] = df['age'].map(age_map)

# Final dataset shape and summary
```

```python
if df is not None:
    print(f"\nFinal dataset shape: {df.shape}")
    print("Final dataset summary:")
    print(df.describe(include='all').transpose())
```

```
Final dataset shape: (69988, 55)
Final dataset summary:
                           count unique                top   freq  \
encounter_id             69988.0    NaN                NaN    NaN
patient_nbr              69988.0    NaN                NaN    NaN
race                       69988      6          Caucasian  52303
gender                     69988      3             Female  37239
age                        69988     10            [70-80)  17750
admission_type_id        69988.0    NaN                NaN    NaN
discharge_disposition_id 69988.0    NaN                NaN    NaN
admission_source_id      69988.0    NaN                NaN    NaN
time_in_hospital         69988.0    NaN                NaN    NaN
num_lab_procedures       69988.0    NaN                NaN    NaN
num_procedures           69988.0    NaN                NaN    NaN
num_medications          69988.0    NaN                NaN    NaN
number_outpatient        69988.0    NaN                NaN    NaN
number_emergency         69988.0    NaN                NaN    NaN
number_inpatient         69988.0    NaN                NaN    NaN
diag_1                     69988    695                414   5210
diag_2                     69988    724                250   4996
diag_3                     69988    757                250   8981
number_diagnoses         69988.0    NaN                NaN    NaN
max_glu_serum              69988      4            No test  66639
A1Cresult                  69988      4            No test  57142
metformin                  69988      4                 No  55083
repaglinide                69988      4                 No  69071
nateglinide                69988      4                 No  69497
chlorpropamide             69988      4                 No  69917
glimepiride                69988      4                 No  66290
acetohexamide              69988      2                 No  69987
glipizide                  69988      4                 No  60978
glyburide                  69988      4                 No  62212
tolbutamide                69988      2                 No  69971
pioglitazone               69988      4                 No  64722
rosiglitazone              69988      4                 No  65327
acarbose                   69988      3                 No  69788
miglitol                   69988      4                 No  69968
troglitazone               69988      2                 No  69985
tolazamide                 69988      2                 No  69958
examide                    69988      1                 No  69988
```

citoglipton	69988	1	No	69988	
insulin	69988	4	No	34266	
glyburide-metformin	69988	4	No	69492	
glipizide-metformin	69988	2	No	69981	
glimepiride-pioglitazone	69988	1	No	69988	
metformin-rosiglitazone	69988	2	No	69986	
metformin-pioglitazone	69988	2	No	69987	
change	69988	2	No	38491	
diabetesMed	69988	2	Yes	53304	
readmitted	69988	3	NO	41478	
readmitted_binary	69988.0	NaN	NaN	NaN	
admission_type	69988	8	Emergency	35479	
discharge_disposition	69988	20	Discharged to home	44322	
admission_source	69988	17	Emergency Room	37273	
diag_1_group	69988	20	Circulatory	21389	
diag_2_group	69988	20	Circulatory	22084	
diag_3_group	69988	20	Circulatory	20867	
age_numeric	69988.0	NaN	NaN	NaN	

	mean	std	min	\
encounter_id	156675883.288049	100390028.088346	12522.0	
patient_nbr	54947270.332428	39487774.890281	135.0	
race	NaN	NaN	NaN	
gender	NaN	NaN	NaN	
age	NaN	NaN	NaN	
admission_type_id	2.106933	1.509434	1.0	
discharge_disposition_id	3.412442	5.180297	1.0	
admission_source_id	5.636566	4.165507	1.0	
time_in_hospital	4.273318	2.934019	1.0	
num_lab_procedures	42.875836	19.894641	1.0	
num_procedures	1.425459	1.757036	0.0	
num_medications	15.665385	8.287305	1.0	
number_outpatient	0.279591	1.0641	0.0	
number_emergency	0.103904	0.511829	0.0	
number_inpatient	0.176273	0.601629	0.0	
diag_1	NaN	NaN	NaN	
diag_2	NaN	NaN	NaN	
diag_3	NaN	NaN	NaN	
number_diagnoses	7.224067	2.001286	1.0	
max_glu_serum	NaN	NaN	NaN	
A1Cresult	NaN	NaN	NaN	
metformin	NaN	NaN	NaN	
repaglinide	NaN	NaN	NaN	
nateglinide	NaN	NaN	NaN	
chlorpropamide	NaN	NaN	NaN	
glimepiride	NaN	NaN	NaN	

acetohexamide	NaN	NaN	NaN
glipizide	NaN	NaN	NaN
glyburide	NaN	NaN	NaN
tolbutamide	NaN	NaN	NaN
pioglitazone	NaN	NaN	NaN
rosiglitazone	NaN	NaN	NaN
acarbose	NaN	NaN	NaN
miglitol	NaN	NaN	NaN
troglitazone	NaN	NaN	NaN
tolazamide	NaN	NaN	NaN
examide	NaN	NaN	NaN
citoglipton	NaN	NaN	NaN
insulin	NaN	NaN	NaN
glyburide-metformin	NaN	NaN	NaN
glipizide-metformin	NaN	NaN	NaN
glimepiride-pioglitazone	NaN	NaN	NaN
metformin-rosiglitazone	NaN	NaN	NaN
metformin-pioglitazone	NaN	NaN	NaN
change	NaN	NaN	NaN
diabetesMed	NaN	NaN	NaN
readmitted	NaN	NaN	NaN
readmitted_binary	0.089787	0.285878	0.0
admission_type	NaN	NaN	NaN
discharge_disposition	NaN	NaN	NaN
admission_source	NaN	NaN	NaN
diag_1_group	NaN	NaN	NaN
diag_2_group	NaN	NaN	NaN
diag_3_group	NaN	NaN	NaN
age_numeric	65.442219	15.973697	5.0

	25%	50%	75%	max
encounter_id	81311511.0	143870568.0	215382904.5	443867222.0
patient_nbr	23342375.25	47985084.0	87498463.5	189502619.0
race	NaN	NaN	NaN	NaN
gender	NaN	NaN	NaN	NaN
age	NaN	NaN	NaN	NaN
admission_type_id	1.0	1.0	3.0	8.0
discharge_disposition_id	1.0	1.0	3.0	28.0
admission_source_id	1.0	7.0	7.0	25.0
time_in_hospital	2.0	3.0	6.0	14.0
num_lab_procedures	31.0	44.0	57.0	132.0
num_procedures	0.0	1.0	2.0	6.0
num_medications	10.0	14.0	20.0	81.0
number_outpatient	0.0	0.0	0.0	42.0
number_emergency	0.0	0.0	0.0	42.0
number_inpatient	0.0	0.0	0.0	12.0

diag_1	NaN	NaN	NaN	NaN
diag_2	NaN	NaN	NaN	NaN
diag_3	NaN	NaN	NaN	NaN
number_diagnoses	6.0	8.0	9.0	16.0
max_glu_serum	NaN	NaN	NaN	NaN
A1Cresult	NaN	NaN	NaN	NaN
metformin	NaN	NaN	NaN	NaN
repaglinide	NaN	NaN	NaN	NaN
nateglinide	NaN	NaN	NaN	NaN
chlorpropamide	NaN	NaN	NaN	NaN
glimepiride	NaN	NaN	NaN	NaN
acetohexamide	NaN	NaN	NaN	NaN
glipizide	NaN	NaN	NaN	NaN
glyburide	NaN	NaN	NaN	NaN
tolbutamide	NaN	NaN	NaN	NaN
pioglitazone	NaN	NaN	NaN	NaN
rosiglitazone	NaN	NaN	NaN	NaN
acarbose	NaN	NaN	NaN	NaN
miglitol	NaN	NaN	NaN	NaN
troglitazone	NaN	NaN	NaN	NaN
tolazamide	NaN	NaN	NaN	NaN
examide	NaN	NaN	NaN	NaN
citoglipton	NaN	NaN	NaN	NaN
insulin	NaN	NaN	NaN	NaN
glyburide-metformin	NaN	NaN	NaN	NaN
glipizide-metformin	NaN	NaN	NaN	NaN
glimepiride-pioglitazone	NaN	NaN	NaN	NaN
metformin-rosiglitazone	NaN	NaN	NaN	NaN
metformin-pioglitazone	NaN	NaN	NaN	NaN
change	NaN	NaN	NaN	NaN
diabetesMed	NaN	NaN	NaN	NaN
readmitted	NaN	NaN	NaN	NaN
readmitted_binary	0.0	0.0	0.0	1.0
admission_type	NaN	NaN	NaN	NaN
discharge_disposition	NaN	NaN	NaN	NaN
admission_source	NaN	NaN	NaN	NaN
diag_1_group	NaN	NaN	NaN	NaN
diag_2_group	NaN	NaN	NaN	NaN
diag_3_group	NaN	NaN	NaN	NaN
age_numeric	55.0	65.0	75.0	95.0

```
# save the cleaned dataset
df.to_csv('cleaned_diabetic_data.csv', index=False)
```

Feature Engineering

To enrich the model's ability to identify complex patterns in the data, we engineered several new features based on clinical intuition and correlations observed during EDA:

Utilization and Complexity Features

- total_visits: Sum of inpatient, outpatient, and emergency visits — a proxy for overall healthcare usage.
- med_complexity: Interaction of number of medications and number of diagnoses — capturing medical treatment intensity.
- stay_per_procedure: Average hospital stay length per procedure — indicating potential treatment efficiency or acuity.

Age-Related Risk

- high_risk_age: Binary flag for patients aged 75 and older, capturing increased vulnerability in elderly patients.

Hospital Intensity

- hospital_intensity: Sum of labs, procedures, and medications — measuring the extent of clinical interventions during hospitalization.

```
def create_enhanced_features(df):
    """Creating new features to enhance model predictive power"""
    print("="*50)
    print("FEATURE ENGINEERING")
    print("="*50)

    df_enhanced = df.copy()

    # Healthcare utilization patterns
    df_enhanced['total_visits'] = (df_enhanced['number_outpatient'] +
                                   df_enhanced['number_emergency'] +
                                   df_enhanced['number_inpatient'])

    # Medical complexity scores
    df_enhanced['med_complexity'] = (df_enhanced['num_medications'] *
                                     df_enhanced['number_diagnoses'])

    # Length of stay relative to procedures
    df_enhanced['stay_per_procedure'] = (df_enhanced['time_in_hospital'] /
                                         (df_enhanced['num_procedures'] + 1))

    # Age-based risk categories
    df_enhanced['high_risk_age'] = (df_enhanced['age_numeric'] >= 75).astype(int)
```

```
    # Hospital intensity score
    df_enhanced['hospital_intensity'] = (df_enhanced['num_lab_procedures'] +
                                         df_enhanced['num_procedures'] +
                                         df_enhanced['num_medications'])

    print(f"Enhanced features created. Dataset shape: {df_enhanced.shape}")
    return df_enhanced



# Step 1: Feature Engineering
df_enhanced = create_enhanced_features(df)
```

```
==================================================
FEATURE ENGINEERING
==================================================
Enhanced features created. Dataset shape: (69988, 60)
```

Feature Selection

To ensure high model performance and clinical relevance, features were carefully selected based on data quality, interpretability, and predictive value:

- Dropped features with high missingness: Columns such as payer_code, medical_specialty, and weight were removed due to excessive missing data, which could introduce noise or bias if imputed without strong justification.
- Diagnosis grouping for dimensionality reduction: The original ICD-9 diagnosis codes (diag_1, diag_2, diag_3) were mapped into clinically meaningful categories (e.g., Circulatory, Endocrine, Neoplasms) to reduce sparsity and improve interpretability.
- Targeted medication selection: Among the 18 diabetes-related medications, only those with sufficient patient representation and a meaningful difference in readmission outcomes were retained, namely, insulin, metformin, glipizide, glyburide, and pioglitazone.
- Filtered discharge dispositions: Dispositions indicating death or hospice care were excluded, as modeling readmission for these patients would be inappropriate.
- Enhanced features added: Aggregated features such as total_visits, med_complexity, and hospital_intensity were engineered to capture latent patterns of utilization, complexity, and risk.
- Avoided data leakage: Identifiers like encounter_id and patient_nbr, as well as repeated encounters, were excluded to ensure that the model would not inadvertently learn from future or externally leaked data.

```python
def prepare_feature_sets(df_enhanced):
    """Define and prepare feature sets for modeling"""

    # Numerical features (original + enhanced)
    numerical_features = [
        'time_in_hospital', 'num_lab_procedures', 'num_procedures',
        'num_medications', 'number_outpatient', 'number_emergency',
        'number_inpatient', 'number_diagnoses', 'age_numeric',
        # Enhanced numerical features
        'total_visits', 'med_complexity', 'stay_per_procedure',
        'hospital_intensity'
    ]

    # Categorical features (original + enhanced)
    categorical_features = [
        'race', 'gender', 'admission_type', 'discharge_disposition',
        'admission_source', 'diag_1_group', 'diag_2_group', 'diag_3_group',
        'diabetesMed', 'max_glu_serum', 'A1Cresult', 'change',
        'insulin', 'metformin', 'glipizide', 'glyburide', 'pioglitazone',
        'high_risk_age'  # Enhanced categorical
    ]

    # Combine all features
    feature_columns = numerical_features + categorical_features

    # Prepare feature matrix and target
    X = df_enhanced[feature_columns].copy()
    y = df_enhanced['readmitted_binary'].copy()

    print(f"Feature preparation complete")
    print(f"Total features: {len(feature_columns)}")
    print(f"Numerical: {len(numerical_features)}, Categorical: {len(categorical_features)}")
    print(f"Original class distribution: {Counter(y)}")

    return X, y, feature_columns

X, y, feature_columns = prepare_feature_sets(df_enhanced)
```

```
Feature preparation complete
Total features: 31
Numerical: 13, Categorical: 18
Original class distribution: Counter({0: 63704, 1: 6284})
```

Modeling

To predict 30-day hospital readmission among diabetic patients, we explored two state-of-the-art ensemble algorithms: XGBoost and CatBoost. Both models are gradient boosting frameworks known for their strong performance on structured tabular data, which aligns well with the nature of our dataset.

Handling Class Imbalance

The dataset is highly imbalanced, with only ~11% of samples labeled as positive (readmitted within 30 days). To address this:

For XGBoost, we used the scale_pos_weight parameter to penalize misclassification of the minority class proportionally.

For CatBoost, we used the class_weights parameter to assign more importance to the underrepresented readmission class during training.

Although, we experimented with SMOTE (Synthetic Minority Oversampling Technique) to synthetically generate new samples of the minority class, this approach led to degraded performance in preliminary experiments. These native techniques ensure that the model does not become biased toward the majority (non-readmitted) class and remains sensitive to high-risk patients.

XGBoost Model

We configured XGBoost with the following key parameters:

- n_estimators: 100 boosting rounds for iterative learning
- scale_pos_weight: Calculated as the ratio of negative to positive samples to counter class imbalance (readmissions are underrepresented)
- reg_alpha = 1, reg_lambda = 1: L1 and L2 regularization terms to reduce overfitting
- eval_metric: AUC (Area Under the ROC Curve), well-suited for imbalanced classification
- enable_categorical = True: Enabled native support for categorical features without one-hot encoding
- The dataset was split into training and testing sets (80/20), using stratified sampling to preserve the proportion of the minority class across both sets.
- Categorical features were automatically detected by selecting columns with data types object or category, and then explicitly cast to category type to allow XGBoost to natively handle categorical splits.

Threshold Optimization

To improve model performance on the minority class, we performed a threshold sweep across values from 0.2 to 0.5. The goal was to identify a threshold that

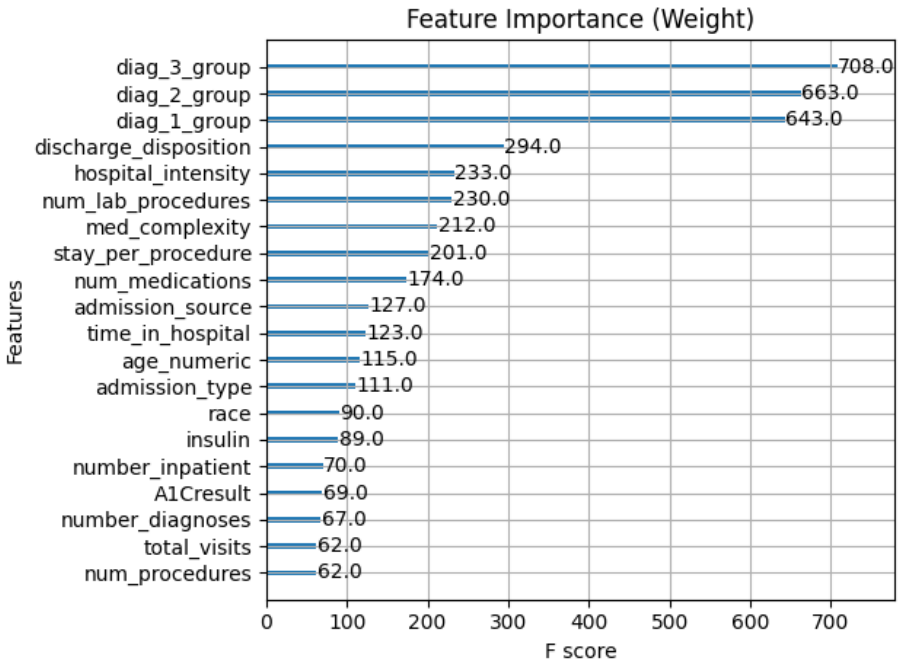
maximized the F1-score, which balances precision and recall. The best-performing threshold was used for final evaluation and prediction.

```
def train_xgboost_model(X_train, y_train, random_seed=42):

    scale_pos_weight = len(y_train[y_train == 0]) / len(y_train[y_train == 1])

    xgb_model = xgb.XGBClassifier(
        random_state=random_seed,
        eval_metric="auc",
        enable_categorical=True,
        reg_alpha=1,
        reg_lambda=1,
        n_estimators=100,
        scale_pos_weight=scale_pos_weight
    )

    # Fit the model
    xgb_model.fit(X_train, y_train)
    return xgb_model


   # Detect categorical features
cat_features = X.select_dtypes(include=['object', 'category']).columns.tolist()
print(f"Categorical features: {cat_features}")

X_categorized = X.copy()
for col in cat_features:
    X_categorized[col] = X_categorized[col].astype('category')

X_train, X_test, y_train, y_test = train_test_split(
        X_categorized, y, test_size=0.2, random_state=42, stratify=y
)
xgb_model = train_xgboost_model(X_train, y_train)

y_proba = xgb_model.predict_proba(X_test)[:, 1]
for threshold in [0.5, 0.4, 0.3, 0.2]:
    y_pred = (y_proba >= threshold).astype(int)
    print(f"\nThreshold: {threshold}")
    print(classification_report(y_test, y_pred))


# Compute AUC_ROC
roc_auc = roc_auc_score(y_test, y_proba)
print(f"\nAUC-ROC: {roc_auc:.4f}")
```

```python
# Feature importance
def plot_feature_importance(model, feature_names):
    """Plot feature importance for XGBoost model"""
    plt.figure(figsize=(12, 8))
    xgb.plot_importance(model, importance_type='weight', max_num_features=20)
    plt.title('Feature Importance (Weight)')
    plt.xlabel('F score')
    plt.ylabel('Features')
    plt.tight_layout()
    plt.show()

plot_feature_importance(xgb_model, feature_columns)
```

```
Categorical features: ['race', 'gender', 'admission_type', 'discharge_disposition', 'admissi

Threshold: 0.5
              precision    recall  f1-score   support

           0       0.92      0.80      0.86     12741
           1       0.14      0.32      0.19      1257

    accuracy                           0.76     13998
   macro avg       0.53      0.56      0.53     13998
weighted avg       0.85      0.76      0.80     13998


Threshold: 0.4
              precision    recall  f1-score   support

           0       0.93      0.65      0.76     12741
           1       0.12      0.49      0.19      1257

    accuracy                           0.63     13998
   macro avg       0.52      0.57      0.48     13998
weighted avg       0.86      0.63      0.71     13998


Threshold: 0.3
              precision    recall  f1-score   support

           0       0.93      0.47      0.62     12741
           1       0.11      0.66      0.19      1257

    accuracy                           0.48     13998
   macro avg       0.52      0.56      0.40     13998
weighted avg       0.86      0.48      0.58     13998
```

```
Threshold: 0.2
              precision    recall  f1-score   support

           0       0.94      0.29      0.45     12741
           1       0.10      0.81      0.18      1257

    accuracy                           0.34     13998
   macro avg       0.52      0.55      0.31     13998
weighted avg       0.86      0.34      0.42     13998


AUC-ROC: 0.6014

<Figure size 1200x800 with 0 Axes>
```



CatBoost Model

We configured CatBoost with the following key parameters:

- Iterations: 1000 boosting rounds with early stopping at 100 rounds
- Depth: 7: to capture moderate feature interactions
- Class Weights: [1, 5] to address class imbalance (readmission class is underrepresented)

- Metric: AUC (Area Under the ROC Curve), a suitable metric for imbalanced classification

The data was split into training and test sets (80/20) using stratified sampling to preserve class proportions.

Categorical features were automatically identified and passed to CatBoost, allowing the model to handle them natively.

Threshold Optimization Rather than using the default 0.5 classification threshold, we performed a threshold sweep from 0.1 to 0.9 to find the threshold that maximized the F1-score, which balances precision and recall. The optimal threshold was selected for final prediction.

```
from catboost import CatBoostClassifier
from sklearn.metrics import accuracy_score, f1_score, roc_auc_score, classification_report
from sklearn.model_selection import train_test_split
from collections import Counter
import numpy as np

def create_catboost_model_with_class_weights():
    """Create CatBoost model using class weights to handle imbalance"""
    print("\n" + "="*50)
    print("CATBOOST MODEL CONFIGURATION (Class Weights)")
    print("="*50)

    model = CatBoostClassifier(
        iterations=1000,
        learning_rate=0.1,
        depth=7,
        l2_leaf_reg=3,
        random_strength=1,
        eval_metric='AUC',
        early_stopping_rounds=100,
        task_type='CPU',
        random_seed=42,
        verbose=200,
        bootstrap_type='Bernoulli',
        subsample=0.8,
        colsample_bylevel=0.8,
        class_weights=[1, 5]  # Assumes class 0 is majority and class 1 is minority
    )

    print("CatBoost model configured with class weights")
    return model
```

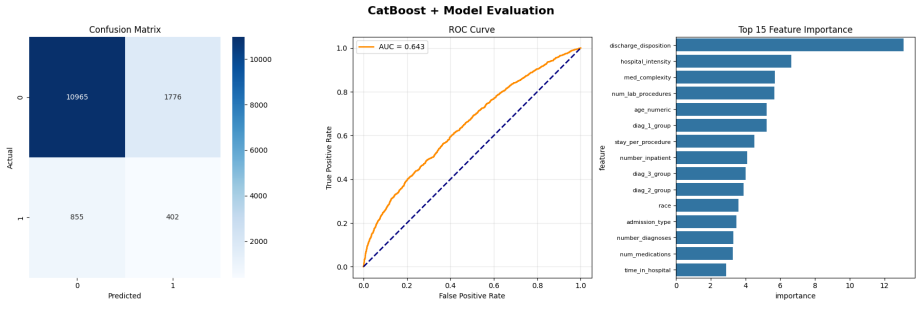
```python
def train_and_evaluate_model(X, y):
    print("\n" + "="*50)
    print("MODEL TRAINING AND EVALUATION")
    print("="*50)

    # Split data
    X_train, X_test, y_train, y_test = train_test_split(
        X, y, test_size=0.2, random_state=42, stratify=y
    )

    print(f"Training: {X_train.shape}, Test: {X_test.shape}")
    print(f"Train class distribution: {Counter(y_train)}")
    print(f"Test class distribution: {Counter(y_test)}")

    # Detect categorical features
    cat_features = X_train.select_dtypes(include=['object', 'category']).columns.tolist()
    print(f"Categorical features: {cat_features}")

    # Create and train model
    model = create_catboost_model_with_class_weights()

    print("\nTraining model...")
    model.fit(X_train, y_train, eval_set=(X_test, y_test), cat_features=cat_features, plot=F

    # Predictions
    y_pred_proba = model.predict_proba(X_test)[:, 1]

    # Threshold sweep
    print("\n" + "="*50)
    print("THRESHOLD SWEEP FOR OPTIMAL F1")
    print("="*50)
    best_f1, best_thresh = 0, 0.5
    for t in np.linspace(0.1, 0.9, 17):
        preds_t = (y_pred_proba > t).astype(int)
        f1 = f1_score(y_test, preds_t)
        print(f"Threshold {t:.2f} → F1-score: {f1:.4f}")
        if f1 > best_f1:
            best_f1, best_thresh = f1, t

    print(f"\n→ Optimal Threshold: {best_thresh:.2f} (F1={best_f1:.4f})")

    # Final predictions using best threshold
    final_preds = (y_pred_proba > best_thresh).astype(int)
    accuracy = accuracy_score(y_test, final_preds)
    auc = roc_auc_score(y_test, y_pred_proba)
```

```
    print(f"\n" + "="*40)
    print("FINAL MODEL PERFORMANCE @ OPTIMAL THRESHOLD")
    print("="*40)
    print(f"Accuracy:  {accuracy:.4f}")
    print(f"F1 Score:  {best_f1:.4f}")
    print(f"AUC-ROC:   {auc:.4f}")

    print(f"\nClassification Report:")
    print(classification_report(y_test, final_preds))

    return model, X_test, y_test, final_preds, y_pred_proba, best_thresh

def plot_model_results(y_test, y_pred, y_pred_proba, model, X):
    """Create evaluation plots without prediction distribution"""

    fig, axes = plt.subplots(1, 3, figsize=(18, 6))
    fig.suptitle('CatBoost + Model Evaluation', fontsize=16, fontweight='bold')

    # Confusion Matrix
    cm = confusion_matrix(y_test, y_pred)
    sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', ax=axes[0])
    axes[0].set_title('Confusion Matrix')
    axes[0].set_xlabel('Predicted')
    axes[0].set_ylabel('Actual')

    # ROC Curve
    fpr, tpr, _ = roc_curve(y_test, y_pred_proba)
    auc_score = roc_auc_score(y_test, y_pred_proba)
    axes[1].plot(fpr, tpr, color='darkorange', lw=2, label=f'AUC = {auc_score:.3f}')
    axes[1].plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
    axes[1].set_xlabel('False Positive Rate')
    axes[1].set_ylabel('True Positive Rate')
    axes[1].set_title('ROC Curve')
    axes[1].legend()
    axes[1].grid(True, alpha=0.3)

    # Feature Importance (top 15 for encoded features)
    feature_importance = model.get_feature_importance()
    importance_df = pd.DataFrame({
        'feature': X.columns,
        'importance': feature_importance
    }).sort_values('importance', ascending=False).head(15)

    sns.barplot(data=importance_df, y='feature', x='importance', ax=axes[2])
    axes[2].set_title('Top 15 Feature Importance')
    axes[2].tick_params(axis='y', labelsize=8)
```

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

    return importance_df
print("IMPLEMENTING CATBOOST SOLUTION with Threshold Sweep")


# Train and Evaluate Model with Threshold Sweep
model, X_test, y_test, final_preds, y_pred_proba, best_thresh = train_and_evaluate_model(X,

#  Visualization
importance_df = plot_model_results(y_test, final_preds, y_pred_proba, model, X)
```

```
IMPLEMENTING CATBOOST SOLUTION with Threshold Sweep

==================================================
MODEL TRAINING AND EVALUATION
==================================================
Training: (55990, 31), Test: (13998, 31)
Train class distribution: Counter({0: 50963, 1: 5027})
Test class distribution: Counter({0: 12741, 1: 1257})
Categorical features: ['race', 'gender', 'admission_type', 'discharge_disposition', 'admissi

==================================================
CATBOOST MODEL CONFIGURATION (Class Weights)
==================================================
CatBoost model configured with class weights

Training model...
0: test: 0.5648511 best: 0.5648511 (0) total: 29.9ms remaining: 29.8s
200: test: 0.6406323 best: 0.6434298 (177) total: 11.2s remaining: 44.6s
Stopped by overfitting detector  (100 iterations wait)

bestTest = 0.6434297734
bestIteration = 177

Shrink model to first 178 iterations.

==================================================
THRESHOLD SWEEP FOR OPTIMAL F1
==================================================
Threshold 0.10 → F1-score: 0.1655
Threshold 0.15 → F1-score: 0.1692
Threshold 0.20 → F1-score: 0.1791
```

```
Threshold 0.25 → F1-score: 0.1953
Threshold 0.30 → F1-score: 0.2099
Threshold 0.35 → F1-score: 0.2221
Threshold 0.40 → F1-score: 0.2341
Threshold 0.45 → F1-score: 0.2257
Threshold 0.50 → F1-score: 0.2040
Threshold 0.55 → F1-score: 0.1801
Threshold 0.60 → F1-score: 0.1576
Threshold 0.65 → F1-score: 0.1172
Threshold 0.70 → F1-score: 0.0663
Threshold 0.75 → F1-score: 0.0246
Threshold 0.80 → F1-score: 0.0047
Threshold 0.85 → F1-score: 0.0000
Threshold 0.90 → F1-score: 0.0000

→ Optimal Threshold: 0.40 (F1=0.2341)

========================================
FINAL MODEL PERFORMANCE @ OPTIMAL THRESHOLD
========================================
Accuracy:  0.8120
F1 Score:  0.2341
AUC-ROC:   0.6434

Classification Report:
              precision    recall  f1-score   support

           0       0.93      0.86      0.89     12741
           1       0.18      0.32      0.23      1257

    accuracy                           0.81     13998
   macro avg       0.56      0.59      0.56     13998
weighted avg       0.86      0.81      0.83     13998
```



Evaluation

We trained both XGBoost and CatBoost Models. The XGBoost model's AUC-ROC was approximately 0.60, indicating weaker discriminative ability compared to the CatBoost model. Feature importance analysis showed that the model relied heavily on the diagnosis group features (diag_1_group, diag_2_group, and diag_3_group). This over-reliance may have contributed to overfitting, as these variables appeared highly informative in training but did not generalize well to unseen data.

CatBoostModel Evaluation

At the optimal threshold 0.40, the model achieved overall accuracy of 81.2%. While accuracy is high, this metric is influenced by the large majority class. Precision for the positive class (patients readmitted within 30 days) was low at 18%, meaning many false positives. However, the recall was higher at 32%, indicating the model correctly identified nearly one-third of patients who actually were readmitted early. This tradeoff is common in imbalanced clinical datasets and highlights the challenge of reliably detecting the minority class.Nevertheless, identifying 32% of high-risk patients can be clinically valuable for targeted interventions and resource allocation.

The model's AUC-ROC was approximately 0.64, reflecting moderate discriminative ability. This indicates the model performs better than random guessing in distinguishing between patients who will or will not be readmitted within 30 days, but there is significant room for improvement to increase clinical utility.

Feature Importance Feature importance analysis revealed several influential predictors:

- Discharge disposition stood out as a top feature, likely reflecting post-acute care needs and patient stability at discharge, which are strongly linked to readmission risk.
- Hospital intensity, a composite measure combining procedures, labs, and medications, highlighted the complexity of inpatient care as a key driver of early return to the hospital.
- Medical complexity, calculated from the interaction of number of diagnoses and medications, also ranked highly, underscoring the burden of comorbid conditions in predicting readmission.
- Number of lab procedures served as a proxy for diagnostic activity or uncertainty, and was a strong indicator of patient acuity.
- Age (numeric), particularly for older patients, was associated with elevated risk, consistent with known challenges faced by elderly populations during care transitions.

- Primary diagnosis group (diag_1_group) added further clinical context, patients admitted for certain categories (e.g., circulatory, neoplasms, or infections) were more likely to be readmitted

Limitations

Data quality challenges such as missing values, particularly in weight, payer code, and medical specialty limited the feature set and may have constrained model performance. Although we explored synthetic oversampling techniques like SMOTE to address class imbalance, this approach led to worse performance in initial experiments and was therefore not pursued further.

Deployment Plan

```
# save the model and see its size
import joblib
model_filename = 'readmissiondiabetic_catboost.pkl'
joblib.dump(model, model_filename)
print(f"Model saved to {model_filename} with size {os.path.getsize(model_filename) / 1024:.2
```

```
Model saved to readmissiondiabetic_catboost.pkl with size 885.13 KB
```

```
# Inference run time
import time
import numpy as np

sample_input = X_test.iloc[0:1]  # single patient row

start_time = time.time()
_ =model.predict(sample_input)
inference_time_ms = (time.time() - start_time) * 1000
print(f"Inference time: {inference_time_ms:.2f} ms")
```

```
Inference time: 4.73 ms
```

Usage: Clinical Workflow Integration

The objective is to deploy the trained CatBoost model to predict whether a diabetic patient will be readmitted to the hospital within 30 days of discharge. This model is designed for real-time use at the point of discharge. As part of hospital workflow:

When a patient is being discharged, the model is automatically invoked to evaluate their risk of readmission. The risk score will be used to trigger follow-up protocols under a "High Risk" readmission flag, such as:

- Early follow-up appointment scheduling
- Care coordinator outreach or check-ins

- Enhanced medication adherence support
- Enrollment in telehealth or remote monitoring programs

As such the model will be invoked via an API that is integrated into an EHR like Epic, via FHIR-based SMART on FHIR integration.

Input

The API expects a POST request with a JSON payload of structured patient data at discharge, including:

```
{
  "gender": "Male",
  "age": "[70-80)",
  "admission_type_id": 1,
  "discharge_disposition_id": 1,
  "number_inpatient": 2,
  "number_emergency": 1,
  "number_diagnoses": 9,
  "A1Cresult": ">8",
  "insulin": "No",
  "diabetesMed": "Yes",
  ...
}
```

Output

The API will return

```
{
  "readmission_risk": 1,
  "probability": 0.78,
  "top_features": ["discharge_disposition", "insulin", "number_inpatient"]
}
```

The probability helps understand the readmission risk better and top features help explain why a patient is high risk

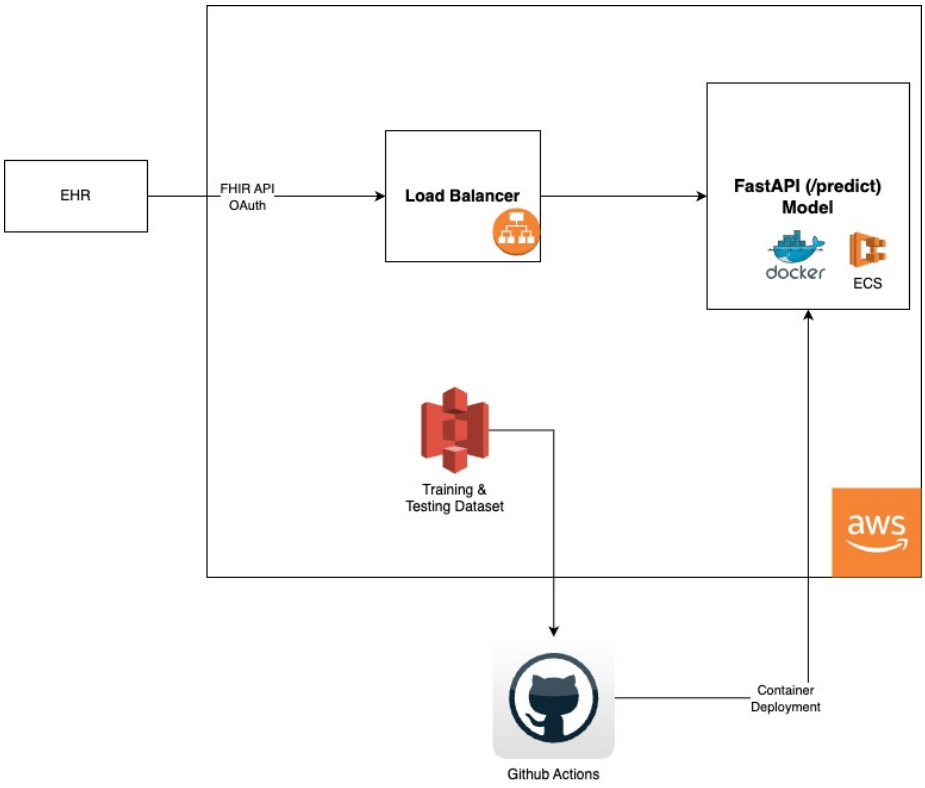
Architecture

We are choosing an AWS-based deployment strategy as our infrastructure already resides in the cloud.

Given the small size of the trained CatBoost model and its low inference latency (~6 ms), a FastAPI-based RESTful API is a lightweight, efficient, and maintainable deployment choice. This approach offers flexibility without the added complexity or cost of a fully managed service like SageMaker.

Key Components:

- Model: Trained CatBoost classifier with integrated feature preprocessing.
- Interface: RESTful API via FastAPI.
- Containerization: API and the model are packaged into a Docker container for portability and consistency across environments.
- Deployment Platform: Hosted on AWS ECS (Elastic Container Service) using Fargate, which provides serverless container orchestration with automatic scaling and no infrastructure management.
- Monitoring & Logging: CloudWatch logs and AWS X-Ray (optional) for tracing requests and monitoring inference latency.
- Networking: Deployed behind an Application Load Balancer with HTTPS support and authentication middleware (e.g., OAuth2/JWT) for secure access.
- S3: Used to store training and testing datasets



Model Deployment & Iteration

- The trained model is serialized using pickle and saved as a .pkl file.
- On application startup, the FastAPI app loads the model from disk using joblib or pickle.
- The API container includes all preprocessing logic to ensure consistency

with the training pipeline.

- CI/CD deployment using Docker + AWS ECS ensures that updates to the model or preprocessing can be redeployed seamlessly.

Future Enhancements

- Incorporate model drift detection and retraining pipeline using updated EHR data.
- Monitor real-world performance via outcome tracking (e.g., did flagged patients actually get readmitted?).
- Enable versioning to allow rollback/testing of new model iterations.

Security and Compliance

- All traffic is routed over HTTPS
- PHI data is minimized, BAA with AWS in place to protect any PHI Storage
- Model input/output payloads are encrypted in transit and at rest
- Access to the API is authenticated via OAuth2 or token-based mechanism
- Audit logging is enabled to track model requests and responses
- FHIR and HIPAA-aligned practices for healthcare interoperability and compliance

Discussion and conclusions

In this project, we developed predictive models to identify patients at risk of hospital readmission within 30 days, leveraging clinical, demographic, and treatment-related features. We addressed key data challenges such as missing values, class imbalance, and feature engineering to enhance model performance.

Our best-performing model, CatBoost with class weights, achieved an overall accuracy of 81.2% and an AUC-ROC of 0.64 at the optimal threshold of 0.40. While the precision for the positive class (early readmission) was modest at 18%, the recall of 32% indicates the model successfully identified nearly one-third of high-risk patients.

Missing data on variables such as patient weight remain a limitation. Although methods like SMOTE were tested to address imbalance, they did not improve performance in this context, highlighting the complexity of clinical data and the need for nuanced approaches.

The model is planned for deployment as a clinical decision support tool, integrated with the hospital's electronic health record system to provide real-time readmission risk scores at patient discharge, enabling timely and targeted interventions.

Overall, the model demonstrates potential as a decision support tool to identify patients at higher risk for early readmission, which could help healthcare providers allocate resources more effectively and tailor post-discharge care plans.

Future Directions

- Inclusion of longitudinal data to capture temporal patterns
- Enriching feature sets with additional clinical information, such as lab time series or clinical notes.
- Exploring stacking or blending of multiple models to improve robustness and predictive performance
- Developing imputation strategies or leveraging domain knowledge to better handle missing data (such as weight)