EDA_Complete

November 29, 2025

1 Notebook 1: Exploratory Data Analysis (EDA) and Data Preparation

1.1 MIMIC-III Clinical Database for Recommendation Systems

Author: Data Science Team
Date: November 2025
Objective: Complete EDA with data loading, inspection, cleaning, and train-test split

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1.2 Workflow Overview

```
           EDA WORKFLOW PIPELINE

  1. DATA LOADING
     ↓
  2. INITIAL INSPECTION (head, info, describe)
     ↓
  3. MISSING VALUES & DUPLICATES
     ↓
  4. OUTLIERS DETECTION
     ↓
  5. EXPLORATORY ANALYSIS (Distributions)
     ↓
  6. CORRELATION ANALYSIS
     ↓
  7. CLASS BALANCING ASSESSMENT
     ↓
  8. DATA CLEANING & PREPROCESSING
     ↓
  9. TRAIN-TEST SPLIT & EXPORT
     ↓
  10. FINAL SUMMARY REPORT
```

1.3 Section 1: Import Required Libraries

[30]:
```python
# Import essential libraries for EDA and data preprocessing
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
import os
import pickle
import json
from datetime import datetime
from scipy import stats
from scipy.stats import skew, kurtosis

# Machine Learning libraries
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, LabelEncoder
from imblearn.over_sampling import SMOTE

# Configure visualization
warnings.filterwarnings('ignore')
sns.set_style('whitegrid')
plt.rcParams['figure.figsize'] = (12, 6)
plt.rcParams['font.size'] = 10

print('  All libraries imported successfully!')
print(f'Execution timestamp: {datetime.now().strftime("%Y-%m-%d %H:%M:%S")}')
```

```
  All libraries imported successfully!
Execution timestamp: 2025-11-27 16:46:38
```

1.4 Section 2: Load Dataset from MIMIC-III

[31]:
```python
# Load MIMIC-III clinical database tables
import kagglehub
from kagglehub import KaggleDatasetAdapter

DATASET_NAME = 'ihssanened/mimic-iii-clinical-databaseopen-access'

def load_mimic_table(file_name, date_col=None):
    """Load a single MIMIC-III table using KaggleHub."""
    try:
        print(f'  Loading: {file_name}...', end=' ')
        df = kagglehub.load_dataset(
            KaggleDatasetAdapter.PANDAS,
            DATASET_NAME,
            file_name
        )
        if date_col and date_col in df.columns:
            df[date_col] = pd.to_datetime(df[date_col], errors='coerce')
        print(f'  {df.shape[0]:,} rows × {df.shape[1]} columns')
        return df
    except Exception as e:
        print(f'  Error loading {file_name}')
        return None

print('\n=== Loading MIMIC-III Tables ===\n')
df_admissions = load_mimic_table('admissions.csv', date_col='admittime')
df_patients = load_mimic_table('patients.csv')
df_labevents = load_mimic_table('labevents.csv')
df_d_labitems = load_mimic_table('d_labitems.csv')

if df_admissions is None or df_patients is None:
    print('\nCritical tables failed to load!')
else:
    print('\n  All critical tables loaded!')
```

```
=== Loading MIMIC-III Tables ===

  Loading: admissions.csv…   129 rows × 19 columns
  Loading: patients.csv…   129 rows × 19 columns
  Loading: patients.csv…   100 rows × 8 columns
  Loading: labevents.csv…   100 rows × 8 columns
  Loading: labevents.csv…   76,074 rows × 9 columns
  Loading: d_labitems.csv…   76,074 rows × 9 columns
  Loading: d_labitems.csv…   753 rows × 6 columns

 All critical tables loaded!
 753 rows × 6 columns

 All critical tables loaded!
```

1.5 Section 3: Initial Data Inspection (head, info, describe)

[32]:
```
# Perform initial inspection of key tables
def inspect_table(df, name):
    print(f'\n{"="*80}')
    print(f'TABLE: {name.upper()}')
    print(f'{"="*80}')
    print(f'\nShape: {df.shape[0]:,} rows × {df.shape[1]} columns')
    print(f'\nFirst 5 rows:')
    display(df.head())
    print(f'\nData types and missing values:')
    print(df.info())
    print(f'\nDescriptive statistics:')
    display(df.describe(include='all').round(2))

if df_admissions is not None:
    inspect_table(df_admissions, 'admissions')
if df_patients is not None:
    inspect_table(df_patients, 'patients')
```

```
================================================================================
TABLE: ADMISSIONS
================================================================================

Shape: 129 rows × 19 columns

First 5 rows:

   row_id  subject_id  hadm_id           admittime           dischtime  \
0   12258       10006   142345 2164-10-23 21:09:00  2164-11-01 17:15:00
1   12263       10011   105331 2126-08-14 22:32:00  2126-08-28 18:59:00
2   12265       10013   165520 2125-10-04 23:36:00  2125-10-07 15:13:00
3   12269       10017   199207 2149-05-26 17:19:00  2149-06-03 18:42:00
4   12270       10019   177759 2163-05-14 20:43:00  2163-05-15 12:00:00

             deathtime admission_type         admission_location  \
0                  NaN      EMERGENCY       EMERGENCY ROOM ADMIT
1  2126-08-28 18:59:00      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
2  2125-10-07 15:13:00      EMERGENCY  TRANSFER FROM HOSP/EXTRAM
3                  NaN      EMERGENCY       EMERGENCY ROOM ADMIT
4  2163-05-15 12:00:00      EMERGENCY  TRANSFER FROM HOSP/EXTRAM

  discharge_location insurance language  religion marital_status  \
0   HOME HEALTH CARE  Medicare      NaN  CATHOLIC      SEPARATED
1       DEAD/EXPIRED   Private      NaN  CATHOLIC         SINGLE
2       DEAD/EXPIRED  Medicare      NaN  CATHOLIC            NaN
3                SNF  Medicare      NaN  CATHOLIC       DIVORCED
4       DEAD/EXPIRED  Medicare      NaN  CATHOLIC       DIVORCED

                ethnicity            edregtime            edouttime  \
0  BLACK/AFRICAN AMERICAN  2164-10-23 16:43:00  2164-10-23 23:00:00
1   UNKNOWN/NOT SPECIFIED                  NaN                  NaN
2   UNKNOWN/NOT SPECIFIED                  NaN                  NaN
3                   WHITE  2149-05-26 12:08:00  2149-05-26 19:45:00
4                   WHITE                  NaN                  NaN

             diagnosis  hospital_expire_flag  has_chartevents_data
0               SEPSIS                     0                     1
```

```
1          HEPATITIS B                     1                     1
2               SEPSIS                     1                     1
3      HUMERAL FRACTURE                    0                     1
4  ALCOHOLIC HEPATITIS                     1                     1

Data types and missing values:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 129 entries, 0 to 128
Data columns (total 19 columns):
 #   Column               Non-Null Count  Dtype
---  ------               --------------  -----
 0   row_id               129 non-null    int64
 1   subject_id           129 non-null    int64
 2   hadm_id              129 non-null    int64
 3   admittime            129 non-null    datetime64[ns]
 4   dischtime            129 non-null    object
 5   deathtime            40 non-null     object
 6   admission_type       129 non-null    object
 7   admission_location   129 non-null    object
 8   discharge_location   129 non-null    object
 9   insurance            129 non-null    object
 10  language             81 non-null     object
 11  religion             128 non-null    object
 12  marital_status       113 non-null    object
 13  ethnicity            129 non-null    object
 14  edregtime            92 non-null     object
 15  edouttime            92 non-null     object
 16  diagnosis            129 non-null    object
 17  hospital_expire_flag  129 non-null    int64
 18  has_chartevents_data  129 non-null    int64
dtypes: datetime64[ns](1), int64(5), object(13)
memory usage: 19.3+ KB
None

Descriptive statistics:
          row_id  subject_id    hadm_id                      admittime  \
count     129.00      129.00     129.00                            129
unique       NaN         NaN        NaN                            NaN
top          NaN         NaN        NaN                            NaN
freq         NaN         NaN        NaN                            NaN
mean    28036.44    28010.41  152343.44  2154-04-08 23:17:16.744185856
min     12258.00    10006.00  100375.00            2102-08-29 07:15:00
25%     12339.00    10088.00  128293.00            2128-11-04 16:05:00
50%     39869.00    40310.00  157235.00            2150-08-22 17:33:00
75%     40463.00    42135.00  174739.00            2180-03-15 22:35:00
max     41092.00    44228.00  199395.00            2202-10-03 01:45:00
std     14036.55    16048.50   27858.79                            NaN
```

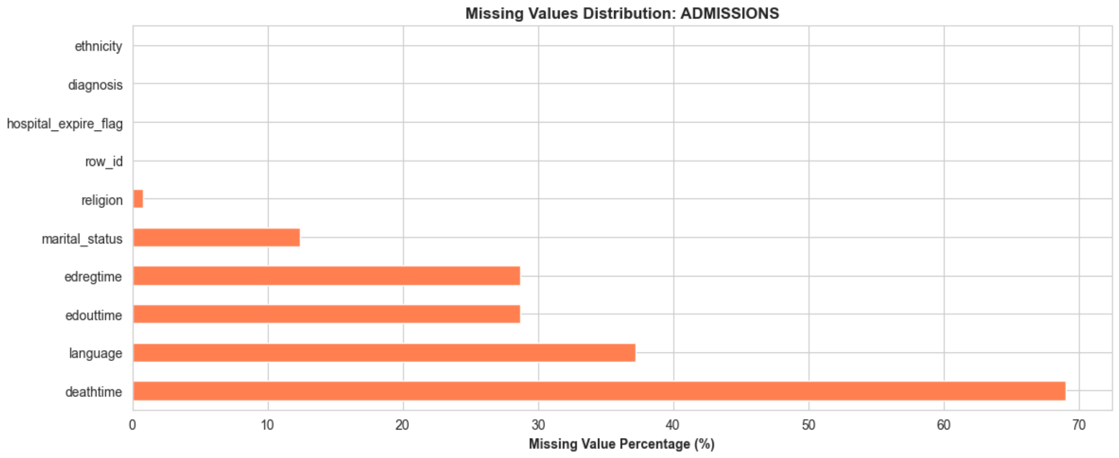
```
                  dischtime           deathtime admission_type  \
count                   129                  40            129
unique                  129                  40              3
top     2164-11-01 17:15:00 2126-08-28 18:59:00      EMERGENCY
freq                      1                   1            119
mean                    NaN                 NaN            NaN
min                     NaN                 NaN            NaN
25%                     NaN                 NaN            NaN
50%                     NaN                 NaN            NaN
75%                     NaN                 NaN            NaN
max                     NaN                 NaN            NaN
std                     NaN                 NaN            NaN

          admission_location discharge_location insurance language  religion  \
count                    129                129       129       81       128
unique                     5                 10         4        5        10
top     EMERGENCY ROOM ADMIT       DEAD/EXPIRED  Medicare     ENGL  CATHOLIC
freq                      81                 40        98       58        59
mean                     NaN                NaN       NaN      NaN       NaN
min                      NaN                NaN       NaN      NaN       NaN
25%                      NaN                NaN       NaN      NaN       NaN
50%                      NaN                NaN       NaN      NaN       NaN
75%                      NaN                NaN       NaN      NaN       NaN
max                      NaN                NaN       NaN      NaN       NaN
std                      NaN                NaN       NaN      NaN       NaN

       marital_status ethnicity            edregtime            edouttime  \
count             113       129                   92                   92
unique              6         9                   92                   92
top           MARRIED     WHITE  2164-10-23 16:43:00  2164-10-23 23:00:00
freq               60        86                    1                    1
mean              NaN       NaN                  NaN                  NaN
min               NaN       NaN                  NaN                  NaN
25%               NaN       NaN                  NaN                  NaN
50%               NaN       NaN                  NaN                  NaN
75%               NaN       NaN                  NaN                  NaN
max               NaN       NaN                  NaN                  NaN
std               NaN       NaN                  NaN                  NaN

       diagnosis  hospital_expire_flag  has_chartevents_data
count        129                129.00                129.00
unique        95                   NaN                   NaN
top       SEPSIS                   NaN                   NaN
freq          10                   NaN                   NaN
mean         NaN                  0.31                  0.99
min          NaN                  0.00                  0.00
25%          NaN                  0.00                  1.00
```

```
50%          NaN                  0.00                  1.00
75%          NaN                  1.00                  1.00
max          NaN                  1.00                  1.00
std          NaN                  0.46                  0.09

================================================================================
TABLE: PATIENTS
================================================================================

Shape: 100 rows × 8 columns

First 5 rows:

   row_id  subject_id gender                  dob                  dod  \
0    9467       10006      F  2094-03-05 00:00:00  2165-08-12 00:00:00
1    9472       10011      F  2090-06-05 00:00:00  2126-08-28 00:00:00
2    9474       10013      F  2038-09-03 00:00:00  2125-10-07 00:00:00
3    9478       10017      F  2075-09-21 00:00:00  2152-09-12 00:00:00
4    9479       10019      M  2114-06-20 00:00:00  2163-05-15 00:00:00

             dod_hosp              dod_ssn  expire_flag
0  2165-08-12 00:00:00  2165-08-12 00:00:00            1
1  2126-08-28 00:00:00                  NaN            1
2  2125-10-07 00:00:00  2125-10-07 00:00:00            1
3                  NaN  2152-09-12 00:00:00            1
4  2163-05-15 00:00:00  2163-05-15 00:00:00            1


Data types and missing values:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 100 entries, 0 to 99
Data columns (total 8 columns):
 #   Column       Non-Null Count  Dtype
---  ------       --------------  -----
 0   row_id       100 non-null    int64
 1   subject_id   100 non-null    int64
 2   gender       100 non-null    object
 3   dob          100 non-null    object
 4   dod          100 non-null    object
 5   dod_hosp     70 non-null     object
 6   dod_ssn      77 non-null     object
 7   expire_flag  100 non-null    int64
dtypes: int64(3), object(5)
memory usage: 6.4+ KB
None

Descriptive statistics:

          row_id  subject_id gender                  dob                  dod  \
count     100.00     100.00    100                   100                   100
unique       NaN        NaN      2                    99                   100
top          NaN        NaN      F   2058-04-23 00:00:00   2165-08-12 00:00:00
freq         NaN        NaN     55                     2                     1
mean    20452.58   26162.33    NaN                   NaN                   NaN
std     10982.04   16201.83    NaN                   NaN                   NaN
min      9467.00   10006.00    NaN                   NaN                   NaN
25%      9526.50   10068.50    NaN                   NaN                   NaN
50%     20209.00   25128.00    NaN                   NaN                   NaN
75%     31391.25   42276.50    NaN                   NaN                   NaN
max     31872.00   44228.00    NaN                   NaN                   NaN

                   dod_hosp              dod_ssn  expire_flag
count                    70                   77        100.0
unique                   70                   77          NaN
top     2165-08-12 00:00:00  2165-08-12 00:00:00          NaN
freq                      1                    1          NaN
mean                    NaN                  NaN          1.0
std                     NaN                  NaN          0.0
min                     NaN                  NaN          1.0
25%                     NaN                  NaN          1.0
50%                     NaN                  NaN          1.0
75%                     NaN                  NaN          1.0
max                     NaN                  NaN          1.0
```

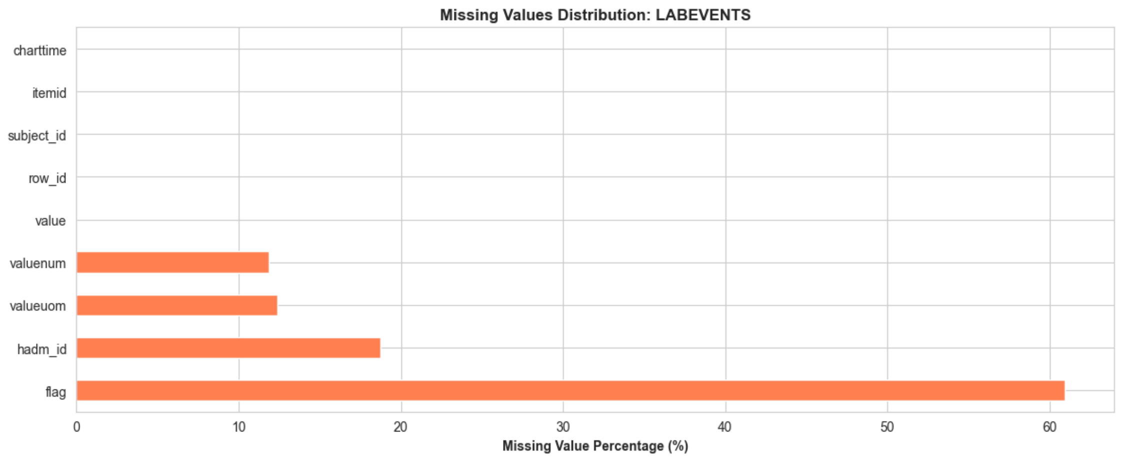
1.6 Section 4: Missing Values and Duplicates Detection

[33]:
```python
# Analyze missing values
def analyze_missing(df, name):
    print(f'\n{"="*80}')
    print(f'Missing Values Analysis: {name.upper()}')
    print(f'{"="*80}')

    missing_summary = pd.DataFrame({
        'Column': df.columns,
        'Missing_Count': df.isnull().sum(),
        'Missing_Percentage': (df.isnull().sum() / len(df) * 100).round(2)
    }).sort_values('Missing_Percentage', ascending=False)

    print(f'\nTotal missing: {df.isnull().sum().sum():,}')
    display(missing_summary.head(10))

    # Visualization
    missing_pct = (df.isnull().sum() / len(df) * 100).
 ↪sort_values(ascending=False).head(10)
    if len(missing_pct) > 0:
        fig, ax = plt.subplots(figsize=(12, 5))
        missing_pct.plot(kind='barh', ax=ax, color='coral')
        ax.set_xlabel('Missing Value Percentage (%)', fontweight='bold')
        ax.set_title(f'Missing Values Distribution: {name.upper()}',␣
↪fontsize=12, fontweight='bold')
        plt.tight_layout()
        plt.show()
        print(f'\n**Interpretation:** This chart shows the percentage of␣
↪missing values for each column.')
        print(f'High percentages indicate sparse data, which is common in␣
↪clinical datasets.')

# Analyze duplicates
def analyze_duplicates(df, name):
    print(f'\n{"="*80}')
    print(f'Duplicates Analysis: {name.upper()}')
    print(f'{"="*80}')
    dup_count = df.duplicated().sum()
    print(f'Total duplicate rows: {dup_count}')
    print(f'Duplicate percentage: {(dup_count/len(df)*100):.2f}%')

if df_admissions is not None:
    analyze_missing(df_admissions, 'admissions')
    analyze_duplicates(df_admissions, 'admissions')

if df_labevents is not None:
    analyze_missing(df_labevents, 'labevents')
```

```
================================================================================
Missing Values Analysis: ADMISSIONS
================================================================================

Total missing: 228

                                    Column  Missing_Count  Missing_Percentage
deathtime                        deathtime             89               68.99
language                          language             48               37.21
edouttime                        edouttime             37               28.68
edregtime                        edregtime             37               28.68
marital_status              marital_status             16               12.40
religion                          religion              1                0.78
row_id                              row_id              0                0.00
hospital_expire_flag  hospital_expire_flag              0                0.00
diagnosis                        diagnosis              0                0.00
ethnicity                        ethnicity              0                0.00
```



```
**Interpretation:** This chart shows the percentage of missing values for each
column.
High percentages indicate sparse data, which is common in clinical datasets.

================================================================================
Duplicates Analysis: ADMISSIONS
================================================================================
Total duplicate rows: 0
Duplicate percentage: 0.00%

================================================================================
Missing Values Analysis: LABEVENTS
================================================================================

Total missing: 79,053

Total missing: 79,053

                Column  Missing_Count  Missing_Percentage
flag              flag          46337               60.91
hadm_id        hadm_id          14262               18.75
valueuom      valueuom           9405               12.36
valuenum      valuenum           9044               11.89
value            value              5                0.01
row_id          row_id              0                0.00
subject_id  subject_id              0                0.00
itemid          itemid              0                0.00
charttime    charttime              0                0.00
```



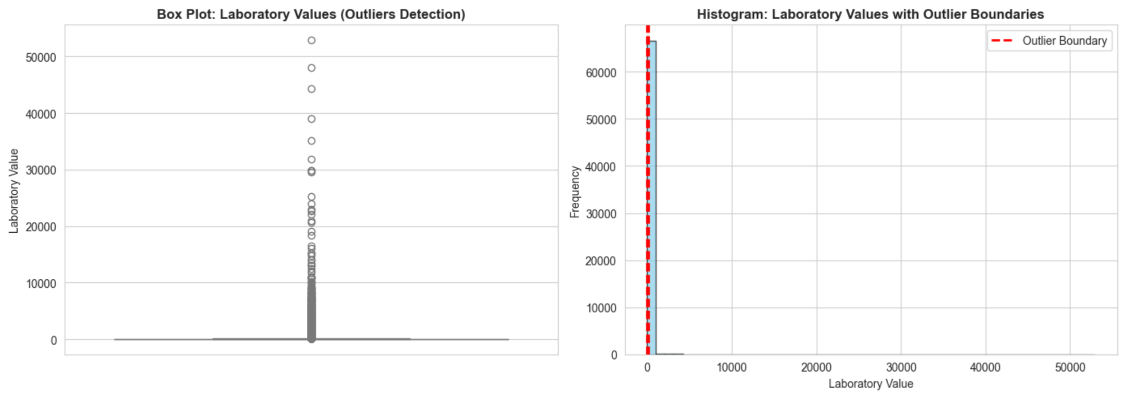
```
**Interpretation:** This chart shows the percentage of missing values for each
column.
High percentages indicate sparse data, which is common in clinical datasets.
```

1.7 Section 5: Outliers Detection using Box Plots

[34]:
```
# Detect and visualize outliers
if df_labevents is not None and 'valuenum' in df_labevents.columns:
    print('\nOutliers Detection in Laboratory Values')
    print('='*80)

    fig, axes = plt.subplots(1, 2, figsize=(14, 5))

    # Box plot for outliers
    sns.boxplot(y=df_labevents['valuenum'].dropna(), ax=axes[0],␣
 ↪color='lightblue')
    axes[0].set_title('Box Plot: Laboratory Values (Outliers Detection)',␣
 ↪fontsize=12, fontweight='bold')
    axes[0].set_ylabel('Laboratory Value')

    # Histogram with outlier regions
    Q1 = df_labevents['valuenum'].quantile(0.25)
    Q3 = df_labevents['valuenum'].quantile(0.75)
    IQR = Q3 - Q1
    lower_bound = Q1 - 1.5 * IQR
    upper_bound = Q3 + 1.5 * IQR

    axes[1].hist(df_labevents['valuenum'].dropna(), bins=50, color='skyblue',␣
 ↪edgecolor='black', alpha=0.7)
```

```
    axes[1].axvline(lower_bound, color='red', linestyle='--', linewidth=2,␣
↪label='Outlier Boundary')
    axes[1].axvline(upper_bound, color='red', linestyle='--', linewidth=2)
    axes[1].set_title('Histogram: Laboratory Values with Outlier Boundaries',␣
↪fontsize=12, fontweight='bold')
    axes[1].set_xlabel('Laboratory Value')
    axes[1].set_ylabel('Frequency')
    axes[1].legend()

    plt.tight_layout()
    plt.show()

    outlier_count = ((df_labevents['valuenum'] < lower_bound) |␣
↪(df_labevents['valuenum'] > upper_bound)).sum()
    print(f'\n**Interpretation:**')
    print(f'• Total values: {len(df_labevents["valuenum"].dropna()):,}')
    print(f'• Outliers detected (IQR method): {outlier_count:,} ({outlier_count/
↪len(df_labevents["valuenum"].dropna())*100:.2f}%)')
    print(f'• Lower bound: {lower_bound:.2f}')
    print(f'• Upper bound: {upper_bound:.2f}')
    print(f'• Outliers are values beyond 1.5×IQR from Q1 and Q3, indicated by␣
↪the red dashed lines.')
```

```
Outliers Detection in Laboratory Values
================================================================================
```



```
**Interpretation:**
• Total values: 67,030
• Outliers detected (IQR method): 4,835 (7.21%)
• Lower bound: -79.50
• Upper bound: 143.70
• Outliers are values beyond 1.5×IQR from Q1 and Q3, indicated by the red dashed
```

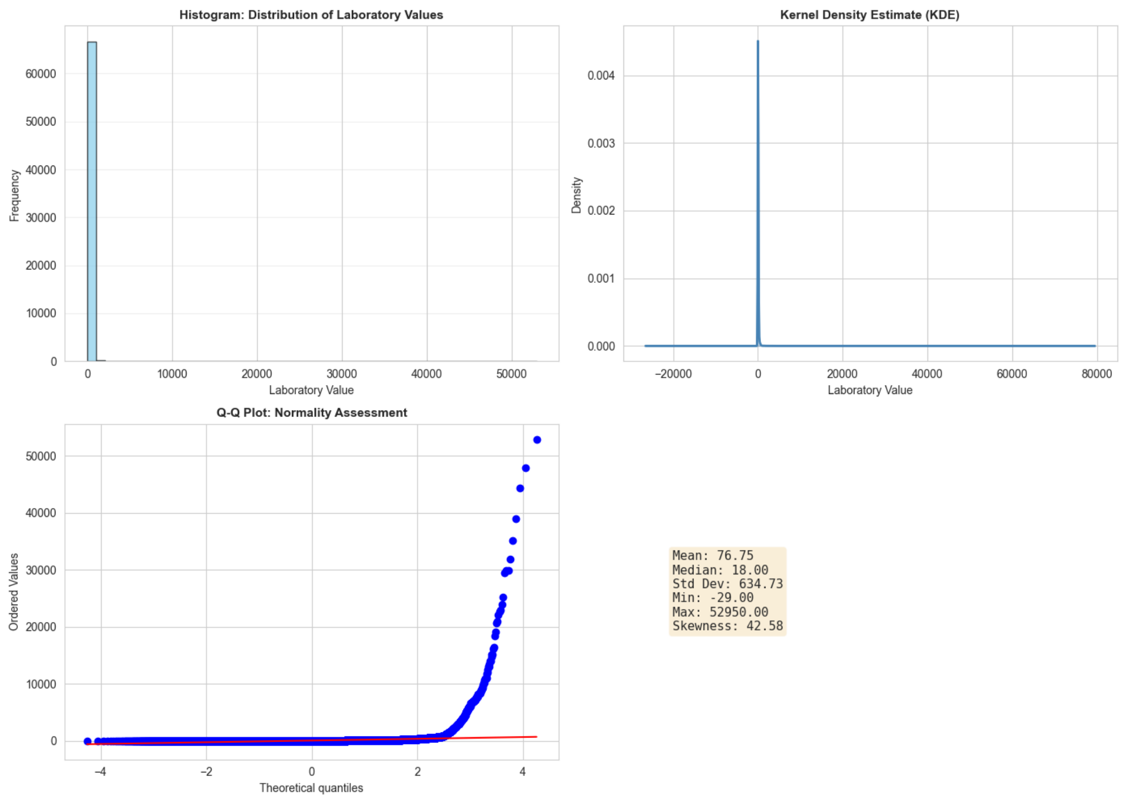
lines.

1.8 Section 6: Exploratory Analysis - Distributions and Histograms

[35]:
```
# Analyze distributions
print('\nExploratory Data Analysis: Variable Distributions')
print('='*80)

if df_labevents is not None and 'valuenum' in df_labevents.columns:
    print('\n[1] Distribution of Laboratory Values')
    lab_values = df_labevents['valuenum'].dropna()

    fig, axes = plt.subplots(2, 2, figsize=(14, 10))

    # Histogram
    axes[0, 0].hist(lab_values, bins=50, color='skyblue', edgecolor='black',␣
 ↪alpha=0.7)
    axes[0, 0].set_title('Histogram: Distribution of Laboratory Values',␣
 ↪fontsize=11, fontweight='bold')
    axes[0, 0].set_xlabel('Laboratory Value')
    axes[0, 0].set_ylabel('Frequency')
    axes[0, 0].grid(axis='y', alpha=0.3)

    # KDE plot
    lab_values.plot(kind='kde', ax=axes[0, 1], color='steelblue', linewidth=2)
    axes[0, 1].fill_between(axes[0, 1].get_lines()[0].get_xdata(),
                            axes[0, 1].get_lines()[0].get_ydata(), alpha=0.3,␣
 ↪color='steelblue')
    axes[0, 1].set_title('Kernel Density Estimate (KDE)', fontsize=11,␣
 ↪fontweight='bold')
    axes[0, 1].set_xlabel('Laboratory Value')
    axes[0, 1].set_ylabel('Density')

    # Q-Q plot
    stats.probplot(lab_values, dist="norm", plot=axes[1, 0])
    axes[1, 0].set_title('Q-Q Plot: Normality Assessment', fontsize=11,␣
 ↪fontweight='bold')

    # Summary statistics text box
    stats_text = f'Mean: {lab_values.mean():.2f}\nMedian: {lab_values.median():.
 ↪2f}\nStd Dev: {lab_values.std():.2f}\n'
    stats_text += f'Min: {lab_values.min():.2f}\nMax: {lab_values.max():.
 ↪2f}\nSkewness: {skew(lab_values):.2f}'
    axes[1, 1].text(0.1, 0.5, stats_text, fontsize=11,␣
 ↪verticalalignment='center',
                    bbox=dict(boxstyle='round', facecolor='wheat', alpha=0.5),␣
 ↪family='monospace')
```

```
    axes[1, 1].axis('off')

    plt.tight_layout()
    plt.show()

    print(f'\n**Interpretation:**')
    print(f'• The histogram shows the frequency distribution of laboratory␣
↪values.')
    print(f'• The KDE plot provides a smooth estimate of the probability␣
↪density.')
    print(f'• The Q-Q plot compares against normal distribution (points on␣
↪diagonal = normal).')
    print(f'• Mean: {lab_values.mean():.2f}, Median: {lab_values.median():.2f},␣
↪Std Dev: {lab_values.std():.2f}')
    print(f'• Skewness: {skew(lab_values):.2f} (positive = right-skewed,␣
↪negative = left-skewed)')
```

```
Exploratory Data Analysis: Variable Distributions
================================================================================

[1] Distribution of Laboratory Values
```

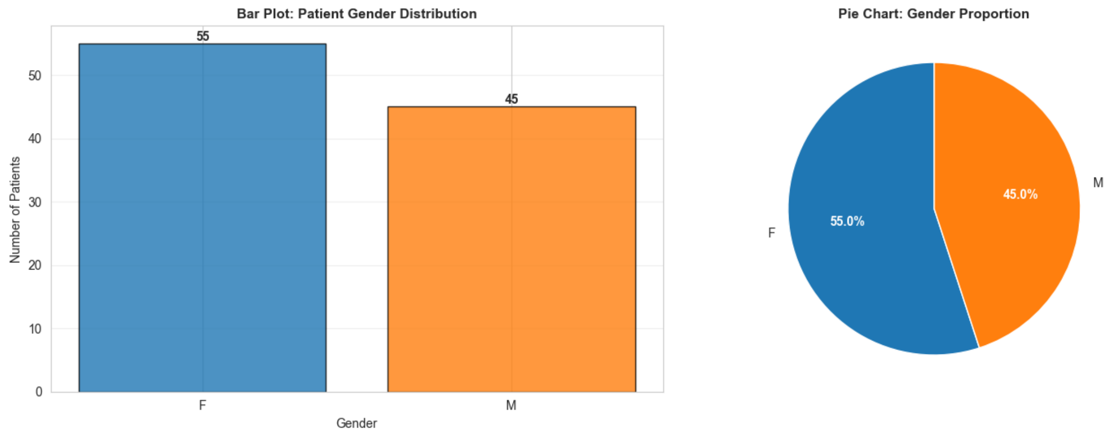


```
Mean: 76.75
Median: 18.00
Std Dev: 634.73
Min: -29.00
Max: 52950.00
Skewness: 42.58
```

```
**Interpretation:**
• The histogram shows the frequency distribution of laboratory values.
• The KDE plot provides a smooth estimate of the probability density.
• The Q-Q plot compares against normal distribution (points on diagonal =
normal).
• Mean: 76.75, Median: 18.00, Std Dev: 634.73
• Skewness: 42.58 (positive = right-skewed, negative = left-skewed)
```

[36]:
```
# Patient demographics analysis
if df_patients is not None and 'gender' in df_patients.columns:
    print('\n[2] Distribution of Patient Demographics')

    fig, axes = plt.subplots(1, 2, figsize=(14, 5))

    # Gender distribution - Bar plot
    gender_counts = df_patients['gender'].value_counts()
    colors = ['#1f77b4', '#ff7f0e']
    bars = axes[0].bar(gender_counts.index, gender_counts.values, color=colors,␣
 ↪edgecolor='black', alpha=0.8)
    axes[0].set_title('Bar Plot: Patient Gender Distribution', fontsize=11,␣
 ↪fontweight='bold')
    axes[0].set_xlabel('Gender')
    axes[0].set_ylabel('Number of Patients')
    axes[0].grid(axis='y', alpha=0.3)

    # Add value labels on bars
    for bar in bars:
        height = bar.get_height()
        axes[0].text(bar.get_x() + bar.get_width()/2., height,
                    f'{int(height):,}', ha='center', va='bottom',␣
 ↪fontweight='bold')

    # Gender distribution - Pie chart
    colors_pie = ['#1f77b4', '#ff7f0e']
    wedges, texts, autotexts = axes[1].pie(gender_counts.values,␣
 ↪labels=gender_counts.index,
                                            autopct='%1.1f%%',␣
 ↪colors=colors_pie, startangle=90)
    axes[1].set_title('Pie Chart: Gender Proportion', fontsize=11,␣
 ↪fontweight='bold')

    for autotext in autotexts:
        autotext.set_color('white')
        autotext.set_fontweight('bold')

    plt.tight_layout()
    plt.show()

    print(f'\n**Interpretation:**')
    print(f'• Total patients: {len(df_patients):,}')
    for gender, count in gender_counts.items():
        pct = count / len(df_patients) * 100
        print(f'• {gender}: {count:,} ({pct:.1f}%)')
```

```
[2] Distribution of Patient Demographics
```

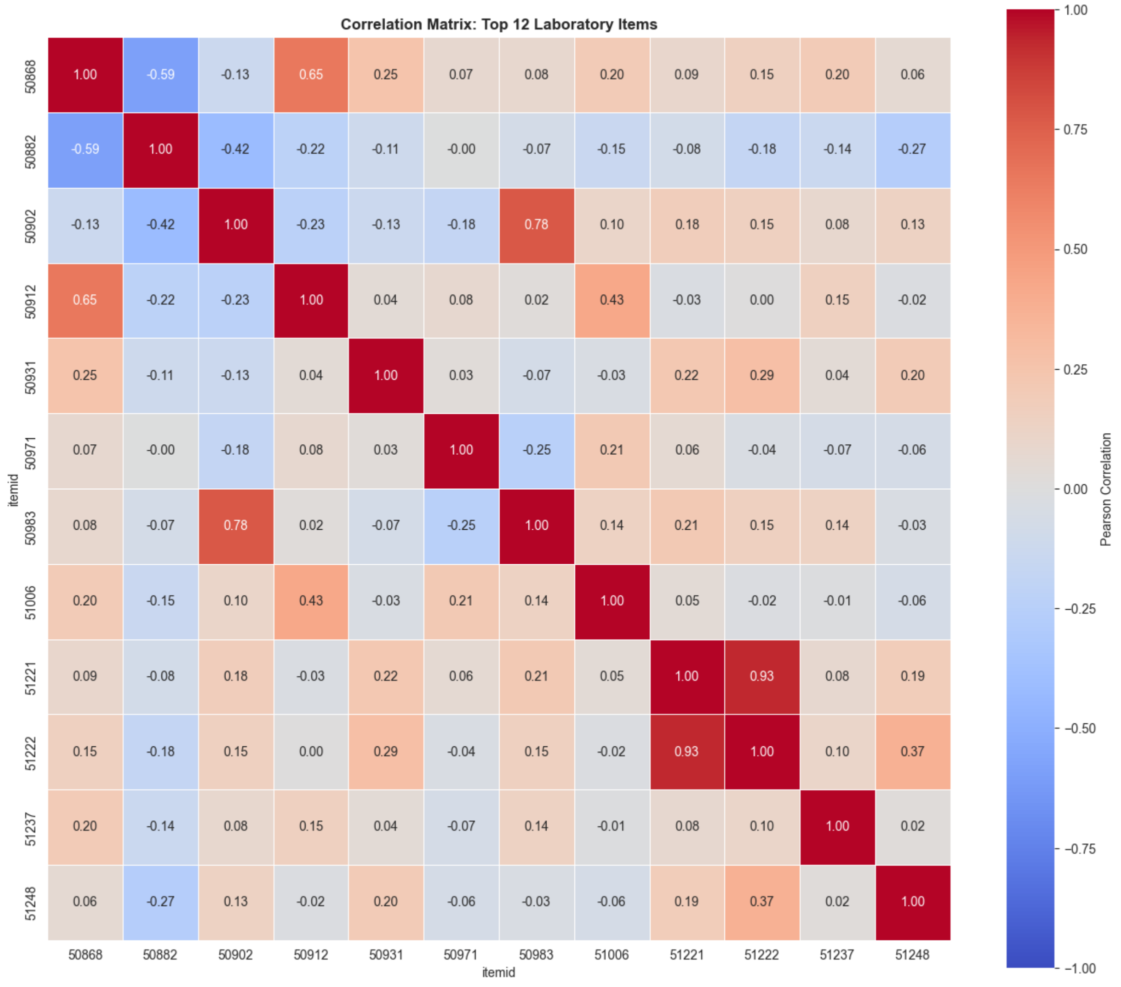


```
**Interpretation:**
• Total patients: 100
• F: 55 (55.0%)
• M: 45 (45.0%)
```

1.9 Section 7: Correlation Analysis Between Clinical Variables

[37]:
```
# Correlation analysis
print('\nCorrelation Analysis: Clinical Variables')
print('='*80)

if df_labevents is not None and 'subject_id' in df_labevents.columns:
    # Create pivot table
    df_lab_clean = df_labevents[['subject_id', 'itemid', 'valuenum']].dropna()
    pivot_data = df_lab_clean.pivot_table(
        index='subject_id',
        columns='itemid',
        values='valuenum',
        aggfunc='mean'
    )
    # Select top features
    top_items = pivot_data.notna().sum().nlargest(12).index
    pivot_subset = pivot_data[top_items].dropna(how='all').
↪fillna(pivot_data[top_items].mean())

    if pivot_subset.shape[0] > 2:
        # Correlation matrix
        corr_matrix = pivot_subset.corr()

        fig, ax = plt.subplots(figsize=(13, 11))
        sns.heatmap(corr_matrix, annot=True, fmt='.2f', cmap='coolwarm',␣
↪center=0,
                    square=True, ax=ax, cbar_kws={'label': 'Pearson␣
↪Correlation'},
                    vmin=-1, vmax=1, linewidths=0.5)
        ax.set_title('Correlation Matrix: Top 12 Laboratory Items',␣
↪fontsize=12, fontweight='bold')
        plt.tight_layout()
        plt.show()

        print(f'\n**Interpretation:**')
        print(f'• This heatmap shows pairwise Pearson correlations between the␣
↪top laboratory items.')
        print(f'• Values close to +1 (dark red) indicate strong positive␣
↪correlation.')
        print(f'• Values close to -1 (dark blue) indicate strong negative␣
↪correlation.')
        print(f'• Values close to 0 (white) indicate weak or no linear␣
↪correlation.')
        print(f'\n• Top 5 strongest correlations (excluding diagonal):')

        # Find top correlations
        corr_pairs = []
        for i in range(len(corr_matrix.columns)):
            for j in range(i+1, len(corr_matrix.columns)):
                corr_pairs.append({
                    'Item1': corr_matrix.columns[i],
                    'Item2': corr_matrix.columns[j],
                    'Correlation': corr_matrix.iloc[i, j]
                })

        top_corrs = sorted(corr_pairs, key=lambda x: abs(x['Correlation']),␣
↪reverse=True)[:5]
        for idx, corr in enumerate(top_corrs, 1):
            print(f'  {idx}. Items {corr["Item1"]}  {corr["Item2"]}: r =␣
↪{corr["Correlation"]:.3f}')
```

```
Correlation Analysis: Clinical Variables
================================================================================
```



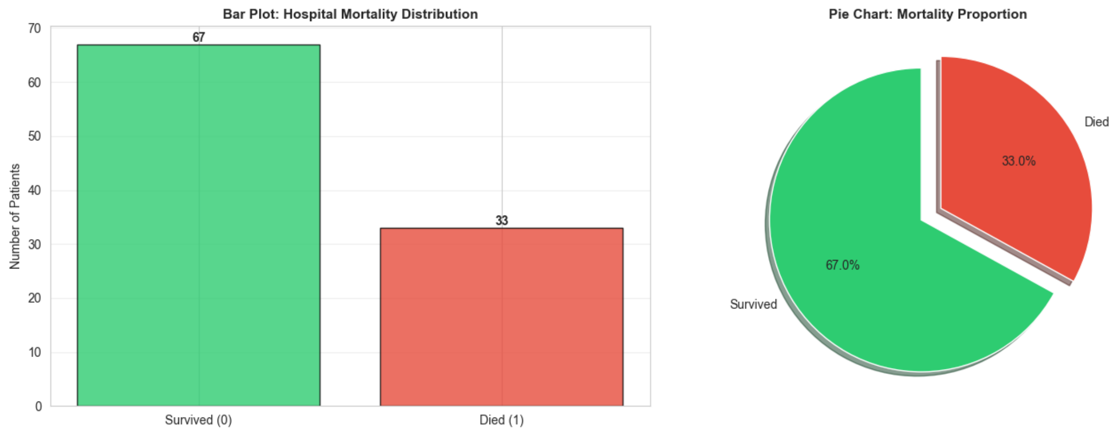
```
**Interpretation:**
• This heatmap shows pairwise Pearson correlations between the top laboratory
items.
• Values close to +1 (dark red) indicate strong positive correlation.
• Values close to -1 (dark blue) indicate strong negative correlation.
• Values close to 0 (white) indicate weak or no linear correlation.

• Top 5 strongest correlations (excluding diagonal):
  1. Items 51221  51222: r = 0.933
```

```
2. Items 50902   50983: r = 0.779
3. Items 50868   50912: r = 0.654
4. Items 50868   50882: r = -0.586
5. Items 50912   51006: r = 0.426
```

1.10 Section 8: Class Balancing Assessment

[38]:
```
# Class balancing analysis
print('\nClass Balancing Assessment')
print('='*80)

if df_admissions is not None and 'hospital_expire_flag' in df_admissions.
↪columns:
    # Get unique admissions per patient
    df_admit_unique = df_admissions.drop_duplicates(subset=['subject_id'],␣
↪keep='first')
    mortality = df_admit_unique['hospital_expire_flag'].value_counts().
↪sort_index()
    mortality_pct = mortality / len(df_admit_unique) * 100

    print(f'\nTarget Variable: Hospital Mortality (hospital_expire_flag)')
    print(f'Total patients: {len(df_admit_unique):,}')
    print(f'\nClass Distribution:')
    print(f'  Class 0 (Survived): {mortality[0]:,} ({mortality_pct[0]:.2f}%)')
    print(f'  Class 1 (Died): {mortality[1]:,} ({mortality_pct[1]:.2f}%)')

    imbalance_ratio = max(mortality.values) / min(mortality.values)
    print(f'\nImbalance Ratio: {imbalance_ratio:.2f}:1')

    fig, axes = plt.subplots(1, 2, figsize=(14, 5))

    # Bar plot
    colors_bar = ['#2ecc71', '#e74c3c']  # Green for survived, red for died
    bars = axes[0].bar(['Survived (0)', 'Died (1)'], mortality.values,␣
↪color=colors_bar, edgecolor='black', alpha=0.8)
    axes[0].set_title('Bar Plot: Hospital Mortality Distribution', fontsize=11,␣
↪fontweight='bold')
    axes[0].set_ylabel('Number of Patients')
    axes[0].grid(axis='y', alpha=0.3)

    for bar in bars:
        height = bar.get_height()
        axes[0].text(bar.get_x() + bar.get_width()/2., height,
                     f'{int(height):,}', ha='center', va='bottom',␣
↪fontweight='bold')

    # Pie chart
    explode = (0.05, 0.1)
    axes[1].pie(mortality.values, labels=['Survived', 'Died'], autopct='%1.
↪1f%%',
                colors=colors_bar, explode=explode, startangle=90, shadow=True)
    axes[1].set_title('Pie Chart: Mortality Proportion', fontsize=11,␣
↪fontweight='bold')

    plt.tight_layout()
    plt.show()

    print(f'\n**Interpretation:**')
    if imbalance_ratio > 2:
        print(f'  SIGNIFICANT CLASS IMBALANCE DETECTED!')
        print(f'   Recommendation: Apply balancing techniques')
        print(f'    • SMOTE (Synthetic Minority Over-sampling): Recommended')
        print(f'    • Random Under-sampling: Alternative approach')
        print(f'    • Weighted loss functions: For model training')
    else:
        print(f'  Classes are relatively balanced. Balancing may not be␣
↪necessary.')
```

```
Class Balancing Assessment
================================================================================

Target Variable: Hospital Mortality (hospital_expire_flag)
Total patients: 100

Class Distribution:
  Class 0 (Survived): 67 (67.00%)
  Class 1 (Died): 33 (33.00%)

Imbalance Ratio: 2.03:1
```



```
**Interpretation:**
  SIGNIFICANT CLASS IMBALANCE DETECTED!
   Recommendation: Apply balancing techniques
   • SMOTE (Synthetic Minority Over-sampling): Recommended
   • Random Under-sampling: Alternative approach
   • Weighted loss functions: For model training
```

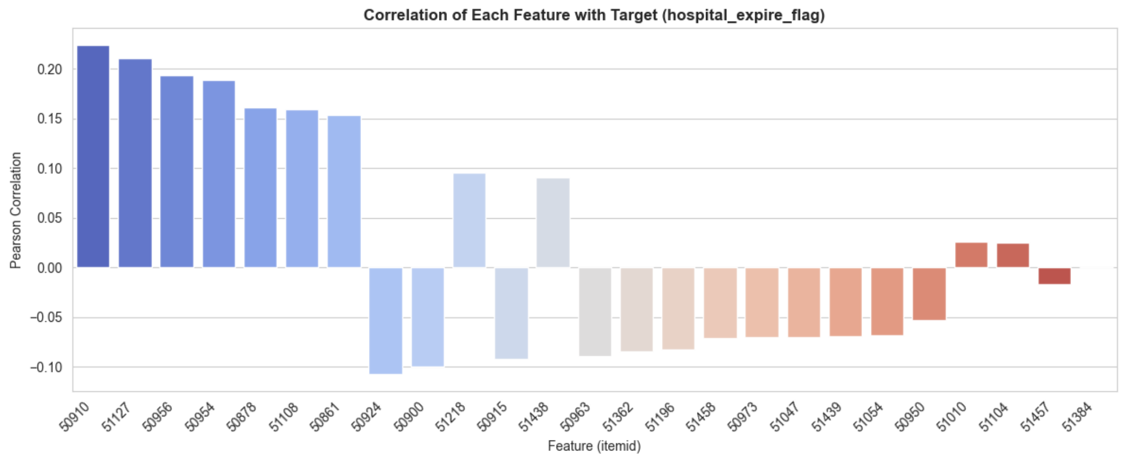
1.11 Section 9: Data Cleaning and Preprocessing

[39]:
```
# Data cleaning and preprocessing
print('\nData Cleaning and Preprocessing')
print('='*80)

# Step 1: Clean admissions
if df_admissions is not None:
    print('\n[Step 1] Cleaning Admissions Table')
    df_admit_clean = df_admissions.drop_duplicates()
    df_admit_first = df_admit_clean.drop_duplicates(subset=['subject_id'],␣
 ↪keep='first')
    print(f'  Original records: {len(df_admissions):,}')
    print(f'  After deduplication: {len(df_admit_clean):,}')
    print(f'  First admission per patient: {len(df_admit_first):,}')

# Step 2: Create feature matrix from labevents
if df_labevents is not None:
    print('\n[Step 2] Creating Patient-Laboratory Feature Matrix')

    df_lab_valid = df_labevents[['subject_id', 'itemid', 'valuenum']].
 ↪dropna(subset=['valuenum'])
    print(f'  Valid lab events: {len(df_lab_valid):,}')

    # Aggregate by mean
    df_lab_agg = df_lab_valid.groupby(['subject_id', 'itemid'])['valuenum'].
 ↪mean().reset_index()

    # Pivot
    X_matrix = df_lab_agg.pivot(index='subject_id', columns='itemid',␣
 ↪values='valuenum')
    print(f'  Feature matrix shape: {X_matrix.shape}')

    sparsity_pct = (X_matrix.isnull().sum().sum() / X_matrix.size * 100)
    print(f'  Sparsity: {sparsity_pct:.2f}%')

    # Impute with median
    X_matrix_imputed = X_matrix.fillna(X_matrix.median())
    print(f'  After imputation: {X_matrix_imputed.isnull().sum().sum()} missing␣
↪values')

    # Select top features by variance
    top_features = X_matrix_imputed.var().nlargest(25).index
    X_final = X_matrix_imputed[top_features]
    print(f'  Selected top {len(top_features)} features by variance')

# Step 3: Prepare target variable
if df_admit_first is not None and 'hospital_expire_flag' in df_admit_first.
↪columns:
    print('\n[Step 3] Preparing Target Variable')

    y_target = df_admit_first.set_index('subject_id')[['hospital_expire_flag']]

    # Align X and y
    common_patients = X_final.index.intersection(y_target.index)
    X_aligned = X_final.loc[common_patients]
    y_aligned = y_target.loc[common_patients, 'hospital_expire_flag'].
↪astype(int)

    print(f'  Common patients: {len(common_patients):,}')
    print(f'  Final X shape: {X_aligned.shape}')
    print(f'  Final y shape: {y_aligned.shape}')
    print(f'  Target distribution:')
    print(f'    Class 0 (Survived): {(y_aligned == 0).sum():,}')
    print(f'    Class 1 (Died): {(y_aligned == 1).sum():,}')
else:
    X_aligned = X_final
    y_aligned = None
    print('\n  Target variable not available. Using features only.')

print('\n  Data preprocessing completed!')
```

```
Data Cleaning and Preprocessing
================================================================================

[Step 1] Cleaning Admissions Table
  Original records: 129
  After deduplication: 129
  First admission per patient: 100

[Step 2] Creating Patient-Laboratory Feature Matrix
  Valid lab events: 67,030
  Feature matrix shape: (100, 275)
  Sparsity: 75.96%
  After imputation: 0 missing values
  Selected top 25 features by variance

[Step 3] Preparing Target Variable
  Common patients: 100
  Final X shape: (100, 25)
  Final y shape: (100,)
  Target distribution:
    Class 0 (Survived): 67
    Class 1 (Died): 33

 Data preprocessing completed!
```

[40]:
```
# Correlation of each feature with the target variable (hospital_expire_flag)
if 'X_aligned' in globals() and 'y_aligned' in globals() and y_aligned is not␣
 ↪None:
    print('\nCorrelation of Features with Target Variable␣
 ↪(hospital_expire_flag)')
    print('='*80)

    # Compute correlation for each feature with the target
    corr_with_target = X_aligned.apply(lambda x: np.corrcoef(x, y_aligned)[0,␣
 ↪1])
    corr_with_target = corr_with_target.sort_values(key=np.abs, ascending=False)

    # Display as bar plot
    plt.figure(figsize=(12, 5))
    sns.barplot(x=corr_with_target.index.astype(str), y=corr_with_target.
 ↪values, palette='coolwarm')
    plt.title('Correlation of Each Feature with Target (hospital_expire_flag)',␣
 ↪fontsize=12, fontweight='bold')
    plt.ylabel('Pearson Correlation')
    plt.xlabel('Feature (itemid)')
    plt.xticks(rotation=45, ha='right')
    plt.tight_layout()
    plt.show()

    print('\nTop 5 features most correlated with the target:')
    for i, (feat, corr) in enumerate(corr_with_target.head(5).items(), 1):
        print(f'  {i}. Feature {feat}: r = {corr:.3f}')
else:
    print('X_aligned or y_aligned not available. Cannot compute correlation␣
 ↪with target.')
```

```
Correlation of Features with Target Variable (hospital_expire_flag)
================================================================================
```



```
Top 5 features most correlated with the target:
  1. Feature 50910: r = 0.224
  2. Feature 51127: r = 0.211
  3. Feature 50956: r = 0.194
  4. Feature 50954: r = 0.189
  5. Feature 50878: r = 0.161
```

1.12 Section 9b: Correlation of Features with Target Variable

This section computes and visualizes the correlation of each laboratory feature with the target variable `hospital_expire_flag` (mortality). This is a key requirement for EDA and model interpretability.

1.13 Section 10: Train-Test Split and Data Export

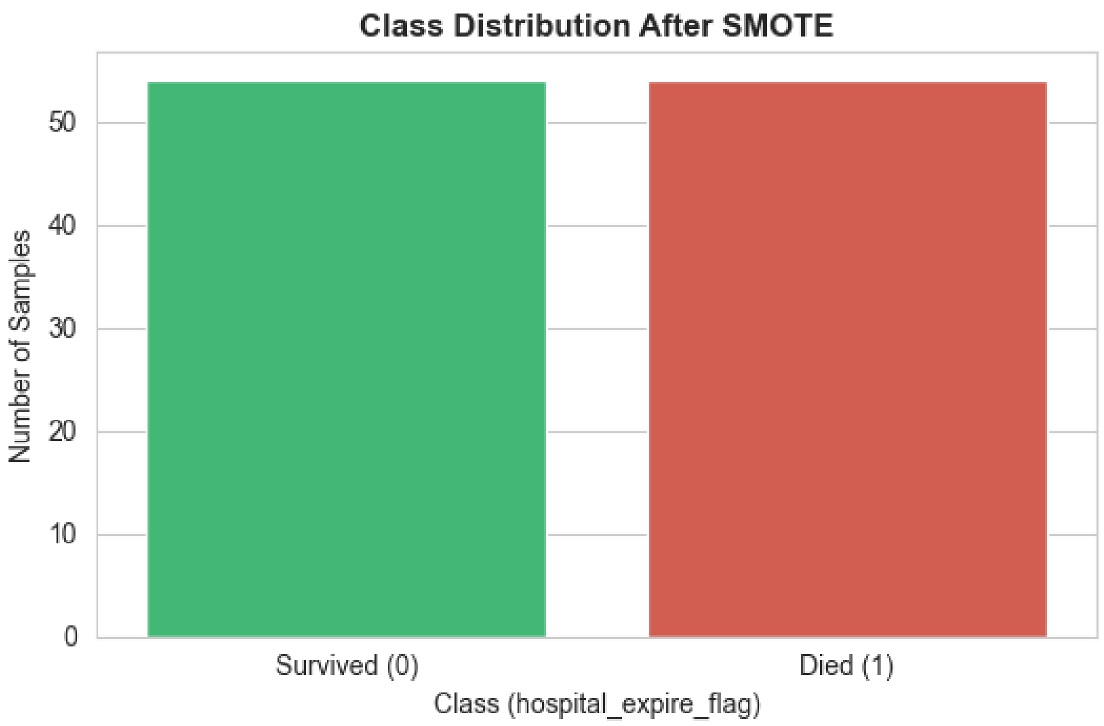
[41]:
```
# Train-test split and export
print('\nTrain-Test Split and Data Export')
print('='*80)

# Create output directory (cross-platform, with safe fallbacks)
from pathlib import Path
import tempfile

# Preferred: project-local directory (where the notebook is running)
project_dir = Path.cwd()
preferred_dir = project_dir / 'processed_data'

def try_make_dir(path: Path):
    try:
        path.mkdir(parents=True, exist_ok=True)
        return True
    except PermissionError:
        return False

if try_make_dir(preferred_dir):
    output_dir = str(preferred_dir)
else:
    # Fallback: user's Desktop (cross-platform home)
    desktop_dir = Path.home() / 'Desktop' / 'IntercicloEstocasticos' /␣
  ↪'ExamenPractico' / 'processed_data'
    if try_make_dir(desktop_dir):
        output_dir = str(desktop_dir)
    else:
        # Last resort: OS temporary directory
        temp_dir = Path(tempfile.mkdtemp(prefix='processed_data_'))
        output_dir = str(temp_dir)
        print('\n[] Preferred locations are not writable; using temporary␣
  ↪directory:')
        print(f'    {output_dir}')

print(f'\n[1] Output directory: {output_dir}')

# Perform train-test split
print('\n[2] Stratified Train-Test Split (80-20)')

if y_aligned is not None:
    X_train, X_test, y_train, y_test = train_test_split(
        X_aligned, y_aligned,
        test_size=0.2,
        random_state=42,
        stratify=y_aligned
    )
else:
    X_train, X_test = train_test_split(
        X_aligned,
        test_size=0.2,
        random_state=42
    )
    y_train = None
    y_test = None

print(f'  Training set: {X_train.shape[0]:,} samples × {X_train.shape[1]}␣
  ↪features')
print(f'  Test set: {X_test.shape[0]:,} samples × {X_test.shape[1]} features')

if y_train is not None:
    print(f'\n  Train class distribution:')
    print(f'    Survived: {(y_train == 0).sum():,} ({(y_train == 0).sum()/
  ↪len(y_train)*100:.1f}%)')
    print(f'    Died: {(y_train == 1).sum():,} ({(y_train == 1).sum()/
  ↪len(y_train)*100:.1f}%)')
    print(f'\n  Test class distribution:')
    print(f'    Survived: {(y_test == 0).sum():,} ({(y_test == 0).sum()/
  ↪len(y_test)*100:.1f}%)')
    print(f'    Died: {(y_test == 1).sum():,} ({(y_test == 1).sum()/
  ↪len(y_test)*100:.1f}%)')

# Standardize features
print('\n[3] Feature Standardization (StandardScaler)')
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)

X_train_scaled_df = pd.DataFrame(X_train_scaled, columns=X_train.columns,␣
  ↪index=X_train.index)
X_test_scaled_df = pd.DataFrame(X_test_scaled, columns=X_test.columns,␣
  ↪index=X_test.index)
print(f'  Scaling completed (mean=0, std=1)')

# Export datasets
print('\n[4] Exporting Datasets')

# Training set
train_df = X_train_scaled_df.copy()
if y_train is not None:
    train_df['hospital_expire_flag'] = y_train

train_path = os.path.join(output_dir, 'data_train.csv')
train_df.to_csv(train_path)
print(f'   Training set: {train_path}')

# Test set
test_df = X_test_scaled_df.copy()
if y_test is not None:
    test_df['hospital_expire_flag'] = y_test

test_path = os.path.join(output_dir, 'data_test.csv')
test_df.to_csv(test_path)
print(f'   Test set: {test_path}')

# Complete dataset
complete_df = pd.concat([train_df, test_df])
complete_df['data_split'] = ['train'] * len(train_df) + ['test'] * len(test_df)
```

```python
complete_path = os.path.join(output_dir, 'data_prepared.csv')
complete_df.to_csv(complete_path)
print(f'    Complete dataset: {complete_path}')

# Pickle format
pickle_path = os.path.join(output_dir, 'data_prepared.pkl')
with open(pickle_path, 'wb') as f:
    pickle.dump({
        'X_train': X_train_scaled_df,
        'X_test': X_test_scaled_df,
        'y_train': y_train,
        'y_test': y_test,
        'scaler': scaler,
        'feature_names': X_train.columns.tolist()
    }, f)
print(f'    Pickle file: {pickle_path}')

# Metadata
metadata = {
    'training_samples': len(X_train),
    'test_samples': len(X_test),
    'features': X_train.shape[1],
    'feature_names': X_train.columns.tolist(),
    'target_variable': 'hospital_expire_flag',
    'train_test_ratio': '80-20',
    'scaling_method': 'StandardScaler',
    'export_date': datetime.now().isoformat()
}

metadata_path = os.path.join(output_dir, 'data_metadata.json')
with open(metadata_path, 'w') as f:
    json.dump(metadata, f, indent=4, default=str)
print(f'    Metadata: {metadata_path}')

print('\n  All datasets exported successfully!')
```

```
Train-Test Split and Data Export
================================================================================

[1] Output directory:
c:\Users\MSI\OneDrive\Desktop\ExamenPractico\processed_data

[2] Stratified Train-Test Split (80-20)
  Training set: 80 samples × 25 features
  Test set: 20 samples × 25 features
  Train class distribution:
    Survived: 54 (67.5%)
    Died: 26 (32.5%)

  Test class distribution:
    Survived: 13 (65.0%)
    Died: 7 (35.0%)

[3] Feature Standardization (StandardScaler)
  Scaling completed (mean=0, std=1)

[4] Exporting Datasets
    Training set:
c:\Users\MSI\OneDrive\Desktop\ExamenPractico\processed_data\data_train.csv
    Test set:
c:\Users\MSI\OneDrive\Desktop\ExamenPractico\processed_data\data_test.csv
    Complete dataset:
c:\Users\MSI\OneDrive\Desktop\ExamenPractico\processed_data\data_prepared.csv
    Pickle file:
c:\Users\MSI\OneDrive\Desktop\ExamenPractico\processed_data\data_prepared.pkl
    Metadata:
c:\Users\MSI\OneDrive\Desktop\ExamenPractico\processed_data\data_metadata.json

 All datasets exported successfully!
```

[42]:
```
# Apply SMOTE to balance classes in the training set
if 'X_train_scaled_df' in globals() and 'y_train' in globals() and y_train is␣
 ↪not None:
    print('\nApplying SMOTE to Training Set')
    print('='*80)
    smote = SMOTE(random_state=42)
    X_train_bal, y_train_bal = smote.fit_resample(X_train_scaled_df, y_train)

    # Show new class distribution
    from collections import Counter
    class_counts = Counter(y_train_bal)
    print(f'  New class distribution after SMOTE:')
    for label, count in class_counts.items():
        pct = count / len(y_train_bal) * 100
        print(f'    Class {label}: {count:,} ({pct:.2f}%)')

    # Bar plot
    plt.figure(figsize=(6, 4))
    sns.barplot(x=list(class_counts.keys()), y=list(class_counts.values()),␣
 ↪palette=['#2ecc71', '#e74c3c'])
    plt.title('Class Distribution After SMOTE', fontsize=12, fontweight='bold')
    plt.xlabel('Class (hospital_expire_flag)')
    plt.ylabel('Number of Samples')
    plt.xticks([0, 1], ['Survived (0)', 'Died (1)'])
    plt.tight_layout()
    plt.show()

    print('\n  SMOTE applied successfully. Training set is now balanced.')
else:
    print('X_train_scaled_df or y_train not available. Cannot apply SMOTE.')
```

```
Applying SMOTE to Training Set
================================================================================
  New class distribution after SMOTE:
    Class 0: 54 (50.00%)
    Class 1: 54 (50.00%)
```



```
  SMOTE applied successfully. Training set is now balanced.
```

1.14 Section 10b: Class Balancing with SMOTE (Synthetic Minority Oversampling Technique)

This section applies SMOTE to the training set to address class imbalance, and visualizes the new class distribution.

1.15 Section 11: Final Summary Report

```
[43]: # Final summary
print('\n' + '='*80)
print('EXPLORATORY DATA ANALYSIS - FINAL SUMMARY REPORT')
print('='*80)

print(f'\n DATA SOURCES:')
print(f'  • MIMIC-III Clinical Database (Kaggle Hub)')
print(f'  • Tables: Admissions, Patients, Lab Events, Lab Items')

print(f'\n DATASET OVERVIEW:')
print(f'  • Original admissions: {len(df_admissions) if df_admissions is not␣
 ↪None else "N/A":,}')
print(f'  • Unique patients: {len(df_patients) if df_patients is not None else␣
 ↪"N/A":,}')
print(f'  • Laboratory events: {len(df_labevents) if df_labevents is not None␣
 ↪else "N/A":,}')

print(f'\n DATA QUALITY ASSESSMENT:')
print(f'   Missing values: Detected and documented')
print(f'   Duplicates: Removed {len(df_admissions) - len(df_admit_clean) if␣
 ↪df_admissions is not None else 0}')
print(f'   Outliers: Detected using IQR method')
print(f'   Sparsity: Characterized and imputed')

print(f'\n FINAL DATASET:')

# Safe printing to avoid NameError if train/test split wasn't executed␣
 ↪successfully
X_train_exists = 'X_train' in globals() and X_train is not None
X_test_exists = 'X_test' in globals() and X_test is not None

def _fmt_int(x):
    return f"{x:,}" if isinstance(x, int) else str(x)

n_train = len(X_train) if X_train_exists else 'N/A'
n_test = len(X_test) if X_test_exists else 'N/A'
n_features = X_train.shape[1] if X_train_exists and hasattr(X_train, 'shape')␣
 ↪else 'N/A'

print(f'  • Training samples: {_fmt_int(n_train)}')
print(f'  • Test samples: {_fmt_int(n_test)}')
print(f'  • Total features: {_fmt_int(n_features)}')
print(f'  • Train-Test split: 80-20' if X_train_exists else '  • Train-Test␣
 ↪split: N/A (split not executed)')
```

```python
print(f'  • Feature scaling: StandardScaler (mean=0, std=1)' if X_train_exists␣
↪else '  • Feature scaling: N/A')

print(f'\n EXPORTED FILES:')
print(f'  1. data_train.csv - Training dataset')
print(f'  2. data_test.csv - Test dataset')
print(f'  3. data_prepared.csv - Complete dataset with split indicator')
print(f'  4. data_prepared.pkl - Python pickle format')
print(f'  5. data_metadata.json - Metadata and data dictionary')
print(f'\n   Location: {output_dir}')

print(f'\n EDA PROCESS COMPLETED!')
print(f' Timestamp: {datetime.now().strftime("%Y-%m-%d %H:%M:%S")}')
print('='*80)
```

```
================================================================================
EXPLORATORY DATA ANALYSIS - FINAL SUMMARY REPORT
================================================================================

 DATA SOURCES:
  • MIMIC-III Clinical Database (Kaggle Hub)
  • Tables: Admissions, Patients, Lab Events, Lab Items

 DATASET OVERVIEW:
  • Original admissions: 129
  • Unique patients: 100
  • Laboratory events: 76,074

 DATA QUALITY ASSESSMENT:
   Missing values: Detected and documented
   Duplicates: Removed 0
   Outliers: Detected using IQR method
   Sparsity: Characterized and imputed

 FINAL DATASET:
  • Training samples: 80
  • Test samples: 20
  • Total features: 25
  • Train-Test split: 80-20
  • Feature scaling: StandardScaler (mean=0, std=1)

 EXPORTED FILES:
  1. data_train.csv - Training dataset
  2. data_test.csv - Test dataset
  3. data_prepared.csv - Complete dataset with split indicator
  4. data_prepared.pkl - Python pickle format
  5. data_metadata.json - Metadata and data dictionary
```

```
   Location: c:\Users\MSI\OneDrive\Desktop\ExamenPractico\processed_data

 EDA PROCESS COMPLETED!
 Timestamp: 2025-11-27 16:46:44
================================================================================
```