project-health-deterioration-model

June 12, 2025

1 0. Setup and Configuration

Step 1: Install Core Dependencies

Install all required Python packages for AI-powered feature engineering, modeling, and NLP tasks.

```
[1]: # Install Core Dependencies
     !pip install -q numpy pandas matplotlib seaborn scikit-learn xgboost␣
       ↪transformers imbalanced-learn tqdm
```

Step 2: Set Working Directory

All generated data files (e.g., raw outputs, datasets, summaries) will be saved to this path for clarity and version control.

```
[2]: # Set Working Directory in Colab/Drive
     import os
     my_file_path = "/content/drive/MyDrive/UM Data Science Course Information/
       ↪WQD7005/Assignment Project/"
     os.makedirs(my_file_path, exist_ok=True)
```

Step 3: Authenticate Hugging Face

plan to access transformer models (e.g., MiniLM, BERT-tiny), login to Hugging Face Hub is required.

```
[3]: # Setup Hugging Face Token
     from huggingface_hub import notebook_login
     notebook_login()
```

```
VBox(children=(HTML(value='<center> <img\nsrc=https://huggingface.co/front/
  ↪assets/huggingface_logo-noborder.sv…
```

Step 4: Securely Load Azure API Credentials

Using secrets.json avoids hardcoding sensitive information. This supports secure API usage and easier sharing of my notebook.

```
[4]: # Securely Load Azure API Credentials
     # Azure endpoint and keys
     import json
```

```python
# Load secrets.json after upload
secrets_file = os.path.join(my_file_path, "secrets.json")
if os.path.exists(secrets_file):
    with open(secrets_file, "r") as f:
        secrets = json.load(f)

endpoint = secrets["AZURE_ENDPOINT"]
subscription_key = secrets["AZURE_KEY"]
```

Step 5: Configure Azure OpenAI Client and Define GPT Prompt Wrapper

This step sets up the Azure OpenAI client and defines a reusable function for sending prompts to GPT-4o, enabling automated clinical text generation and interpretation.

[5]:
```python
# Import Supporting Libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from datetime import datetime, timedelta
from openai import AzureOpenAI
import random
import time

# Configure Azure OpenAI Client
api_version = "2024-12-01-preview"
deployment = "gpt-4o"
client = AzureOpenAI(
    api_version=api_version,
    azure_endpoint=endpoint,
    api_key=subscription_key,
)
# Prompt execution wrapper for reuse
def model_prompt(prompt, system_prompt="Act as a professional clinicians.",␣
 ↪temperature=0.7, max_tokens=4096):
    response = client.chat.completions.create(
        model=deployment,
        messages=[
            {"role": "system", "content": system_prompt},
            {"role": "user", "content": prompt}
        ],
        max_tokens=max_tokens,
        temperature=temperature,
    )
    return response.choices[0].message.content
```

Step 6: Single Sample Data Generation via GPT (Validation Prompt)

To verify the response structure of GPT-4o by generating a realistic single-patient daily monitoring record, ensuring the output conforms to expected JSON schema for later batch generation.

```
[6]: # Single Sample Data Generation via model
data_prompt = """
Generate a single, realistic patient monitoring record for one randomly␣
 ↪selected adult patient.

Provide the following fields:
- oxygen_saturation (in %)
- heart_rate (in bpm)
- temperature (in °C)
- blood_pressure (systolic/diastolic, e.g. "120/80")
- weight (in kg)
- blood_glucose (in mg/dL)

At the end, include a brief clinical_note (1-2 sentences, max 30 words)␣
 ↪summarizing the patient status based on the values above. Use professional␣
 ↪clinical tone with realistic variation (e.g. stable, recovering, mild␣
 ↪concerns).

Output as a valid JSON object with keys:
oxygen_saturation, heart_rate, temperature, blood_pressure, weight,␣
 ↪blood_glucose, clinical_note.

Constraints:
- Only output one JSON object.
- No markdown or explanation.
- Include realistic variation across different health conditions (e.g. fatigue,␣
 ↪post-op, dietary changes, stress).
- Ensure all fields are complete, no missing values.
"""

print(model_prompt(data_prompt))
```

```
{
  "oxygen_saturation": 95,
  "heart_rate": 88,
  "temperature": 37.6,
  "blood_pressure": "130/85",
  "weight": 75,
  "blood_glucose": 145,
  "clinical_note": "Patient exhibits mild tachycardia and elevated blood
glucose, likely related to dietary factors. Vital signs are stable overall, with
no immediate concerns requiring intervention."
}
```

2 1. Dataset Simulation and Feature Engineering

Since a synthetic patient dataset with labeled **note_status** was already generated and preprocessed in the previous assignment, so this section focuses on loading the prepared dataset, checking basic data structure, verifying label quality, and ensuring readiness for AI-driven feature engineering and modeling.

Step 1: Load Preprocessed Dataset

Load the previously prepared patient dataset containing all required features and labels.

[7]:
```python
import pandas as pd

# Load preprocessed dataset from previous assignment
df = pd.read_csv(my_file_path + "preprocessing_generate_patient_dataset.csv")

# Display basic info and preview
print(df.info())
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 6501 entries, 0 to 6500
Data columns (total 12 columns):
 #   Column                     Non-Null Count  Dtype  
---  ------                     --------------  -----  
 0   patient_id                 6501 non-null   object 
 1   timestamp                  6501 non-null   object 
 2   clinical_note              6501 non-null   object 
 3   temperature_zscore         6501 non-null   float64
 4   heart_rate_zscore          6501 non-null   float64
 5   blood_glucose_zscore       6501 non-null   float64
 6   oxygen_saturation_zscore   6501 non-null   float64
 7   systolic_bp_zscore         6501 non-null   float64
 8   diastolic_bp_zscore        6501 non-null   float64
 9   weight_zscore              6501 non-null   float64
 10  note_status                6501 non-null   object 
 11  note_status_encoded        6501 non-null   int64  
dtypes: float64(7), int64(1), object(4)
memory usage: 609.6+ KB
None
```

[8]:
```python
print(df.head())
```

```
  patient_id   timestamp                                      clinical_note  \
0      P0001  2025-01-01  Patient stable post-surgery. Vitals within nor…
1      P0001  2025-01-02  Mildly elevated heart rate and temperature. Mo…
2      P0001  2025-01-03  Temperature trending upward. Possible low-grad…
3      P0001  2025-01-04  Temperature stabilizing. Patient reports impro…
4      P0001  2025-01-05  Patient showing signs of steady recovery. Vita…
```

```
   temperature_zscore  heart_rate_zscore  blood_glucose_zscore  \
0            0.360442           0.256585             -0.617148
1            1.089682           0.881403             -0.438365
2            2.548162           1.506221             -0.736337
3            1.818922           0.673130             -0.140392
4            0.725062           0.048312             -0.855527

   oxygen_saturation_zscore  systolic_bp_zscore  diastolic_bp_zscore  \
0                  0.029323            1.034085             0.690185
1                 -0.785334            1.423315             1.208257
2                 -1.599992            1.812545             1.726329
3                 -0.785334            1.423315             1.467293
4                  0.029323            0.644855             0.690185

   weight_zscore note_status  note_status_encoded
0      -0.633036      Stable                    3
1      -0.734106  Recovering                    2
2      -0.784640  Recovering                    2
3      -0.835175      Stable                    3
4      -0.835175  Recovering                    2
```

```
[9]: print(df.describe())
```

```
       temperature_zscore  heart_rate_zscore  blood_glucose_zscore  \
count        6.501000e+03       6.501000e+03          6.501000e+03
mean        -5.744674e-15      -5.027683e-17          3.541237e-16
std          1.000077e+00       1.000077e+00          1.000077e+00
min         -3.285759e+00      -3.075779e+00         -2.107011e+00
25%         -7.334186e-01      -5.765064e-01         -8.555265e-01
50%         -4.178464e-03      -1.599609e-01         -2.595813e-01
75%          3.604416e-01       6.731301e-01          9.323091e-01
max          6.923603e+00       6.088221e+00          4.627169e+00

       oxygen_saturation_zscore  systolic_bp_zscore  diastolic_bp_zscore  \
count              6.501000e+03        6.501000e+03         6.501000e+03
mean               3.319364e-15        2.972891e-16        -1.141065e-15
std                1.000077e+00        1.000077e+00         1.000077e+00
min               -6.487937e+00       -3.247445e+00        -3.713428e+00
25%               -7.853344e-01       -9.120650e-01        -8.640312e-01
50%                2.932316e-02       -1.336051e-01        -8.692311e-02
75%                8.439807e-01        6.448548e-01         6.901850e-01
max                2.473296e+00        6.288689e+00         5.352834e+00

       weight_zscore  note_status_encoded
count   6.501000e+03          6501.000000
mean   -7.290140e-16             2.432241
std     1.000077e+00             0.677030
min    -2.704969e+00             0.000000
```

```
25%   -6.835706e-01            2.000000
50%    4.918627e-02            3.000000
75%    2.765936e-01            3.000000
max    5.431159e+00            3.000000
```

Step 2: Data Structure and Integrity Check

Check data types, confirm absence of missing values, and review main variables.

```
[10]: # Check data info and missing values
print(df.info())
print(df.isnull().sum())
```

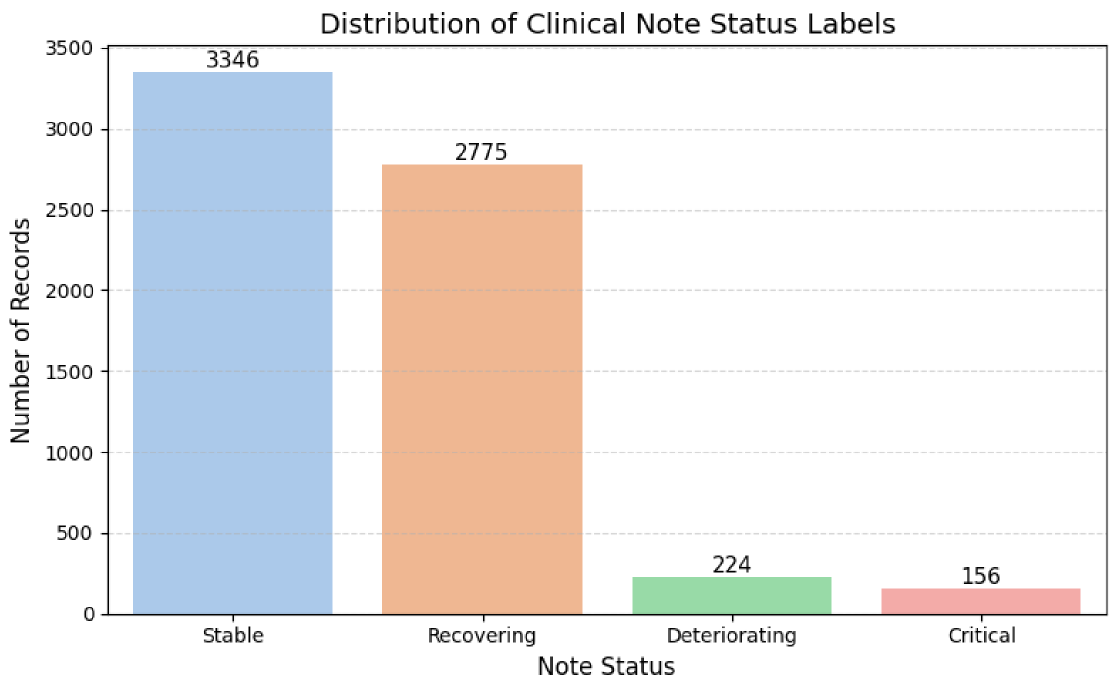
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 6501 entries, 0 to 6500
Data columns (total 12 columns):
 #   Column                     Non-Null Count  Dtype
---  ------                     --------------  -----
 0   patient_id                 6501 non-null   object
 1   timestamp                  6501 non-null   object
 2   clinical_note              6501 non-null   object
 3   temperature_zscore         6501 non-null   float64
 4   heart_rate_zscore          6501 non-null   float64
 5   blood_glucose_zscore       6501 non-null   float64
 6   oxygen_saturation_zscore   6501 non-null   float64
 7   systolic_bp_zscore         6501 non-null   float64
 8   diastolic_bp_zscore        6501 non-null   float64
 9   weight_zscore              6501 non-null   float64
 10  note_status                6501 non-null   object
 11  note_status_encoded        6501 non-null   int64
dtypes: float64(7), int64(1), object(4)
memory usage: 609.6+ KB
None
patient_id                  0
timestamp                   0
clinical_note               0
temperature_zscore          0
heart_rate_zscore           0
blood_glucose_zscore        0
oxygen_saturation_zscore    0
systolic_bp_zscore          0
diastolic_bp_zscore         0
weight_zscore               0
note_status                 0
note_status_encoded         0
dtype: int64
```

Step 3: Check Label Distribution

Review the distribution of the clinical status label (note_status) to ensure it is suitable for modeling.

[11]:
```
import matplotlib.pyplot as plt
import seaborn as sns

plt.figure(figsize=(8, 5))
ax = sns.countplot(
    data=df,
    x="note_status",
    order=df["note_status"].value_counts().index,
    palette="pastel"
)

plt.title("Distribution of Clinical Note Status Labels", fontsize=14)
plt.xlabel("Note Status", fontsize=12)
plt.ylabel("Number of Records", fontsize=12)
plt.grid(axis="y", linestyle="--", alpha=0.5)
plt.tight_layout()

# Add count labels on each bar
for p in ax.patches:
    count = int(p.get_height())
    ax.annotate(f"{count}", (p.get_x() + p.get_width() / 2, p.get_height()),
                ha="center", va="bottom", fontsize=11, color="black")

plt.show()
```

```
<ipython-input-11-1115314961>:5: FutureWarning:

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

  ax = sns.countplot(
```



Step 4: Standardize Note Status Label Encoding

Map the clinical status label (note_status) to standardized integer codes: 0 for Stable, 1 for Recovering, 2 for Deteriorating, and 3 for Critical. Replace the existing note_status_encoded with these values for consistency in downstream modeling.

[12]:
```
# Define standardized label mapping
note_status_mapping = {
    "Stable": 0,
    "Recovering": 1,
    "Deteriorating": 2,
    "Critical": 3
}

# Apply mapping to the note_status column and overwrite note_status_encoded
df['note_status_encoded'] = df['note_status'].map(note_status_mapping)

# Preview mapping results
print(df[['note_status', 'note_status_encoded']].head())
print(df['note_status_encoded'].value_counts().sort_index())
```

```
  note_status  note_status_encoded
0      Stable                    0
1  Recovering                    1
2  Recovering                    1
3      Stable                    0
```

```
4  Recovering                        1
note_status_encoded
0     3346
1     2775
2      224
3      156
Name: count, dtype: int64
```

Summary

The preprocessed patient dataset has been successfully loaded and validated. All core variables, including vital sign z-scores, clinical notes, and coded clinical status labels, are present with no missing values. The distribution of the "note_status" label has been visualized, revealing the class imbalance issue that will be addressed in the modeling phase. After confirming the dataset structure and quality, we are ready for AI-driven NLP feature engineering and predictive modeling.

3 2. NLP Feature Engineering

Step 1: Sentiment Analysis on Clinical Notes

Extract sentiment label and score from each clinical note using a transformer-based sentiment analysis model.

[13]:
```python
from transformers import pipeline
from tqdm import tqdm
import pandas as pd

sentiment_pipe = pipeline("sentiment-analysis",␣
↪model="distilbert-base-uncased-finetuned-sst-2-english")

def get_sentiment(text):
    result = sentiment_pipe(text[:512])[0]
    return pd.Series([result['label'], result['score']])

tqdm.pandas(desc="Sentiment Analysis")
df[['sentiment_label', 'sentiment_score']] = df['clinical_note'].
↪progress_apply(get_sentiment)
```

```
/usr/local/lib/python3.11/dist-packages/huggingface_hub/utils/_auth.py:94:
UserWarning:
The secret `HF_TOKEN` does not exist in your Colab secrets.
To authenticate with the Hugging Face Hub, create a token in your settings tab
(https://huggingface.co/settings/tokens), set it as secret in your Google Colab
and restart your session.
You will be able to reuse this secret in all of your notebooks.
Please note that authentication is recommended but still optional to access
public models or datasets.
  warnings.warn(
config.json:   0%|          | 0.00/629 [00:00<?, ?B/s]

model.safetensors:   0%|          | 0.00/268M [00:00<?, ?B/s]

tokenizer_config.json:   0%|          | 0.00/48.0 [00:00<?, ?B/s]

vocab.txt:   0%|          | 0.00/232k [00:00<?, ?B/s]

Device set to use cuda:0
Sentiment Analysis:   0%|          | 2/6501 [00:00<32:08,  3.37it/s]You seem to
be using the pipelines sequentially on GPU. In order to maximize efficiency
please use a dataset
Sentiment Analysis: 100%|      | 6501/6501 [00:31<00:00, 207.38it/s]
```

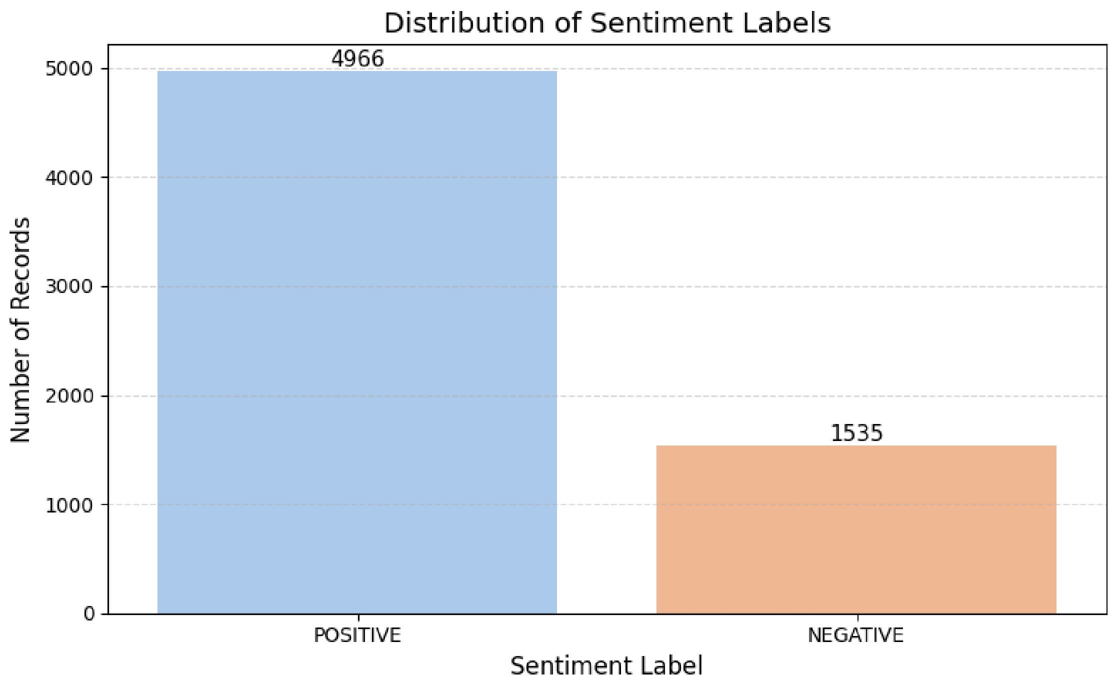
[14]:
```
# Preview sentiment features
print(df[['sentiment_label', 'sentiment_score']].head())
```

```
  sentiment_label  sentiment_score
0        POSITIVE         0.996446
1        NEGATIVE         0.970783
2        POSITIVE         0.873627
3        NEGATIVE         0.983538
4        POSITIVE         0.990160
```

[15]:
```
import matplotlib.pyplot as plt
import seaborn as sns

plt.figure(figsize=(8, 5))
ax = sns.countplot(
    data=df,
    x="sentiment_label",
    order=df["sentiment_label"].value_counts().index,
    palette="pastel"
)

plt.title("Distribution of Sentiment Labels", fontsize=14)
plt.xlabel("Sentiment Label", fontsize=12)
plt.ylabel("Number of Records", fontsize=12)
plt.grid(axis="y", linestyle="--", alpha=0.5)
plt.tight_layout()

# Add count labels on each bar
for p in ax.patches:
    count = int(p.get_height())
    ax.annotate(f"{count}", (p.get_x() + p.get_width() / 2, p.get_height()),
                ha="center", va="bottom", fontsize=11, color="black")

plt.show()
```

```
<ipython-input-15-2054194357>:5: FutureWarning:
```

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

  ax = sns.countplot(
```



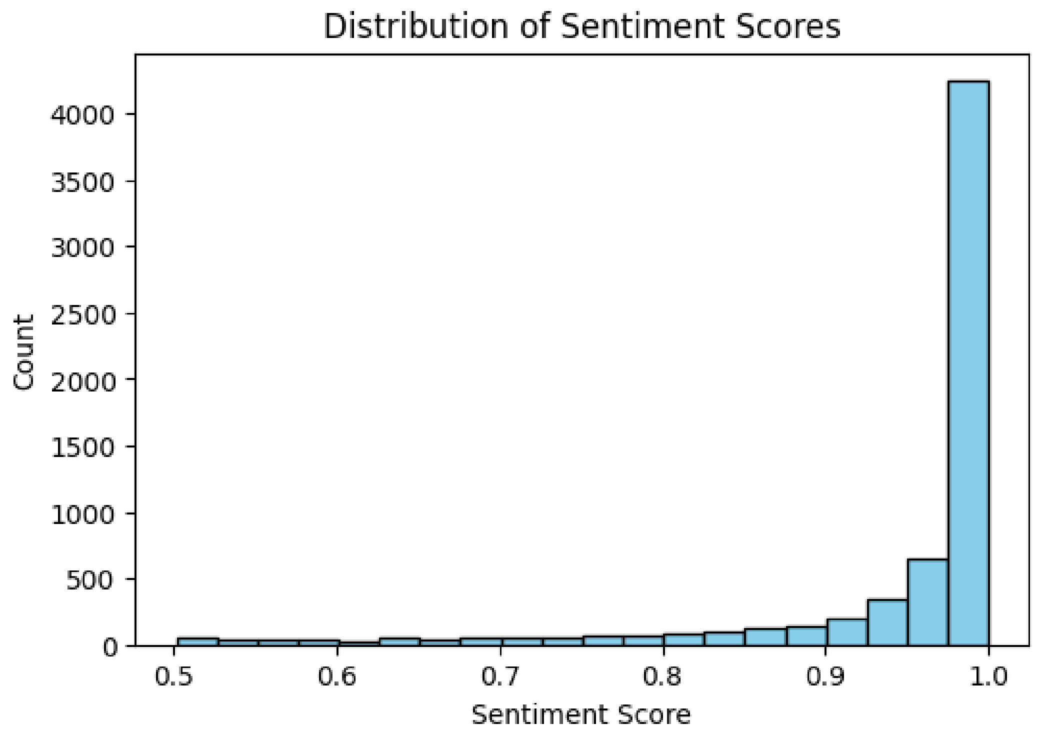
To check for ambiguous clinical notes, I analyze the distribution of sentiment scores. Scores near 0.5 suggest uncertainty, while scores closer to 0 or 1 indicate confident classification.

[16]:
```
# Count the number of potential "neutral" cases (sentiment_score between 0.4␣
↪and 0.6)
neutral_count = ((df['sentiment_score'] >= 0.4) & (df['sentiment_score'] <= 0.
↪6)).sum()
total = len(df)
percent_neutral = 100 * neutral_count / total

print(f"Potential 'neutral' cases (score between 0.4 and 0.6): {neutral_count}␣
↪({percent_neutral:.2f}%)")
```

```
Potential 'neutral' cases (score between 0.4 and 0.6): 184 (2.83%)
```

[17]:
```
# Visualize the distribution of sentiment scores for all clinical notes
import matplotlib.pyplot as plt
```

```
plt.figure(figsize=(6,4))
plt.hist(df['sentiment_score'], bins=20, color='skyblue', edgecolor='black')
plt.title("Distribution of Sentiment Scores")
plt.xlabel("Sentiment Score")
plt.ylabel("Count")
plt.show()
```



[18]:
```
# Preview random samples of "neutral" sentiment cases
neutral_samples = df[(df['sentiment_score'] >= 0.4) & (df['sentiment_score'] <=␣
↪0.6)].sample(5)
print(neutral_samples[['clinical_note', 'note_status','sentiment_label',␣
↪'sentiment_score']])
```

```
                                          clinical_note note_status  \
4410  Patient stable, no new concerns. Encouraged fu…      Stable
571   Patient nearing full recovery. Vitals returnin…  Recovering
5778  Patient continues to recover well. No signs of…  Recovering
6114  Stable clinical course. Patient ambulating ind…      Stable
6229  Patient stable with no significant changes; vi…      Stable

     sentiment_label  sentiment_score
4410        POSITIVE         0.536394
571         NEGATIVE         0.510942
```

```
5778        POSITIVE         0.519754
6114        NEGATIVE         0.522406
6229        POSITIVE         0.575101
```

The sentiment scores are strongly polarized, with very few notes falling in the ambiguous range (0.4–0.6). Only 2.8% of clinical notes show unclear sentiment, confirming that binary sentiment labels are appropriate for this dataset.

Step 2: Encode Sentiment Labels

Convert the sentiment labels into binary numeric values for downstream modeling. Encode sentiment labels as binary values (1=POSITIVE, 0=NEGATIVE) for model input.

[19]:
```
# Encode sentiment label as binary (POSITIVE=1, NEGATIVE=0)
df['sentiment_label_encoded'] = df['sentiment_label'].map({'POSITIVE': 1,␣
 ↪'NEGATIVE': 0})

# Preview encoded results
print(df[['sentiment_label', 'sentiment_label_encoded']].head())
print(df['sentiment_label_encoded'].value_counts())
```

```
  sentiment_label  sentiment_label_encoded
0        POSITIVE                        1
1        NEGATIVE                        0
2        POSITIVE                        1
3        NEGATIVE                        0
4        POSITIVE                        1
sentiment_label_encoded
1    4966
0    1535
Name: count, dtype: int64
```

Step 3: Generate MiniLM Embeddings for Clinical Notes

Convert each clinical note into a dense vector using the MiniLM model, creating numerical features that capture the semantic meaning of the text.

[20]:
```
from transformers import AutoTokenizer, AutoModel
import torch
import numpy as np
from tqdm import tqdm

# Load MiniLM model and tokenizer
tokenizer = AutoTokenizer.from_pretrained("sentence-transformers/
 ↪all-MiniLM-L6-v2")
model = AutoModel.from_pretrained("sentence-transformers/all-MiniLM-L6-v2")

# Function to get mean-pooled sentence embedding
def get_embedding(text):
    inputs = tokenizer(text[:512], return_tensors="pt", truncation=True,␣
  ↪padding=True, max_length=64)
    with torch.no_grad():
        emb = model(**inputs).last_hidden_state.mean(dim=1).squeeze().cpu().
  ↪numpy()
    return emb

# Generate embeddings with progress bar
embeddings = []
for note in tqdm(df['clinical_note'], desc="Generating MiniLM Embeddings"):
    embeddings.append(get_embedding(note))
embeddings = np.vstack(embeddings)
```

```
tokenizer_config.json:   0%|          | 0.00/350 [00:00<?, ?B/s]

vocab.txt:   0%|          | 0.00/232k [00:00<?, ?B/s]

tokenizer.json:   0%|          | 0.00/466k [00:00<?, ?B/s]

special_tokens_map.json:   0%|          | 0.00/112 [00:00<?, ?B/s]

config.json:   0%|          | 0.00/612 [00:00<?, ?B/s]

model.safetensors:   0%|          | 0.00/90.9M [00:00<?, ?B/s]

Generating MiniLM Embeddings: 100%|     | 6501/6501 [00:59<00:00,
109.11it/s]
```

[21]:
```
# Convert to DataFrame and merge with main df
embeddings_df = pd.DataFrame(embeddings, columns=[f'embedding_{i+1}' for i in␣
  ↪range(embeddings.shape[1])])
df = pd.concat([df.reset_index(drop=True), embeddings_df], axis=1)

# Preview embedding features
print(embeddings_df.shape)
print(embeddings_df.head())
```

```
(6501, 384)
   embedding_1  embedding_2  embedding_3  embedding_4  embedding_5  \
0    -0.002227     0.054226    -0.198225     0.007124    -0.314499
1     0.049453     0.058550     0.163853     0.278248    -0.112794
2    -0.074871    -0.096136     0.306630     0.355880     0.115569
3    -0.002369    -0.074267     0.152957     0.536647    -0.151257
4     0.005790     0.035201     0.092588     0.339710    -0.237124

   embedding_6  embedding_7  embedding_8  embedding_9  embedding_10  …  \
0    -0.064337    -0.051729     0.139015    -0.080340     -0.160634  …
1    -0.140065    -0.007666     0.156703    -0.058688     -0.029590  …
2    -0.017233     0.000656     0.174866    -0.035941      0.209080  …
3    -0.057069     0.056320    -0.003020    -0.189366      0.162416  …
```

```
4     0.011571    -0.100337     0.100693    -0.095893     -0.358720  …

   embedding_375  embedding_376  embedding_377  embedding_378  embedding_379  \
0      -0.185589       0.169756       0.236088       0.006934       0.170186
1      -0.494870       0.072143      -0.035751       0.089070       0.000560
2      -0.375889      -0.122558      -0.029090       0.086142      -0.097378
3      -0.586711      -0.131158       0.086496       0.063815       0.236612
4      -0.379787       0.157074      -0.139231       0.180917      -0.043465

   embedding_380  embedding_381  embedding_382  embedding_383  embedding_384
0       0.059771       0.004493       0.054284       0.086865      -0.191795
1       0.226057       0.091370      -0.274222      -0.128617       0.189073
2       0.088276      -0.063335      -0.246799      -0.399010       0.108029
3       0.215968      -0.039085      -0.395321      -0.270403       0.138713
4      -0.022627       0.010339       0.045971       0.056790      -0.261534

[5 rows x 384 columns]
```

4 3. Feature and Target Assignment

Step 1: Select Features for Modeling

Combine structured vital signs, sentiment analysis features, and MiniLM embeddings to form the initial input feature set.

[22]:
```python
# List of structured vital sign features
vital_features = [
    'temperature_zscore', 'heart_rate_zscore', 'blood_glucose_zscore',
    'oxygen_saturation_zscore', 'systolic_bp_zscore', 'diastolic_bp_zscore',␣
  ↪'weight_zscore'
]

# NLP features (sentiment + embeddings)
nlp_features = ['sentiment_label_encoded', 'sentiment_score'] +␣
  ↪[f'embedding_{i+1}' for i in range(embeddings_df.shape[1])]

# Combine all features for model input
feature_cols = vital_features + nlp_features
X = df[feature_cols]
print("Feature matrix shape:", X.shape)
```

```
Feature matrix shape: (6501, 393)
```

Step 2: Define Target Variable

Set the encoded clinical status label as the prediction target for multi-class classification.

[23]:
```python
# Target variable (multi-class clinical status)
y = df['note_status_encoded']
```

```
print("Target distribution:\n", y.value_counts().sort_index())
```

```
Target distribution:
 note_status_encoded
0    3346
1    2775
2     224
3     156
Name: count, dtype: int64
```

5 4. Train-Test Split

Step 1: Split the Dataset

Split the dataset into training and test sets, stratifying by the target variable to maintain class distribution.

[24]:
```
from sklearn.model_selection import train_test_split

# 80% for training, 20% for testing, stratified by class
X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.2, random_state=42, stratify=y
)

print("Training set shape:", X_train.shape)
print("Test set shape:", X_test.shape)
print("Training target distribution:\n", y_train.value_counts().sort_index())
print("Test target distribution:\n", y_test.value_counts().sort_index())
```

```
Training set shape: (5200, 393)
Test set shape: (1301, 393)
Training target distribution:
 note_status_encoded
0    2676
1    2220
2     179
3     125
Name: count, dtype: int64
Test target distribution:
 note_status_encoded
0    670
1    555
2     45
3     31
Name: count, dtype: int64
```

6 5. Class Imbalance Handling (SMOTE)

Step 1: Balance the Training Set with SMOTE

Apply SMOTE to the training set to generate synthetic minority samples and balance class distribution. The process may take some time for high-dimensional data.

[25]:
```python
from imblearn.over_sampling import SMOTE
from collections import Counter
import time
from tqdm import tqdm

# Optional: label mapping for pretty output
note_status_mapping = {0: "Stable", 1: "Recovering", 2: "Deteriorating", 3:␣
 ↪"Critical"}

# Print original class distribution (with labels)
print("Original training class distribution:")
for k, v in Counter(y_train).items():
    print(f"  {note_status_mapping[k]} ({k}): {v}")

# Start timer
start = time.time()

# Run SMOTE with overall progress feel
print("Applying SMOTE to balance classes...")
for _ in tqdm(range(1), desc="SMOTE Oversampling"):
    sm = SMOTE(random_state=42)
    X_train_bal, y_train_bal = sm.fit_resample(X_train, y_train)

# End timer
end = time.time()
print(f"SMOTE completed in {end-start:.2f} seconds.")
```

```
Original training class distribution:
  Stable (0): 2676
  Recovering (1): 2220
  Critical (3): 125
  Deteriorating (2): 179
Applying SMOTE to balance classes…

SMOTE Oversampling: 100%|      | 1/1 [00:00<00:00,  6.16it/s]

SMOTE completed in 0.16 seconds.
```

[26]:
```python
# Print balanced class distribution (with labels)
print("Balanced training class distribution:")
for k, v in Counter(y_train_bal).items():
    print(f"  {note_status_mapping[k]} ({k}): {v}")

print("Balanced training set shape:", X_train_bal.shape)
```

```
Balanced training class distribution:
  Stable (0): 2676
  Recovering (1): 2676
  Critical (3): 2676
  Deteriorating (2): 2676
Balanced training set shape: (10704, 393)
```

7 6. Model Development and Evaluation

Step 1: Step 1: Define the Traditional Model Evaluation Function

Define a general-purpose evaluation function for traditional models, reporting metrics, confusion matrix, and classification report.

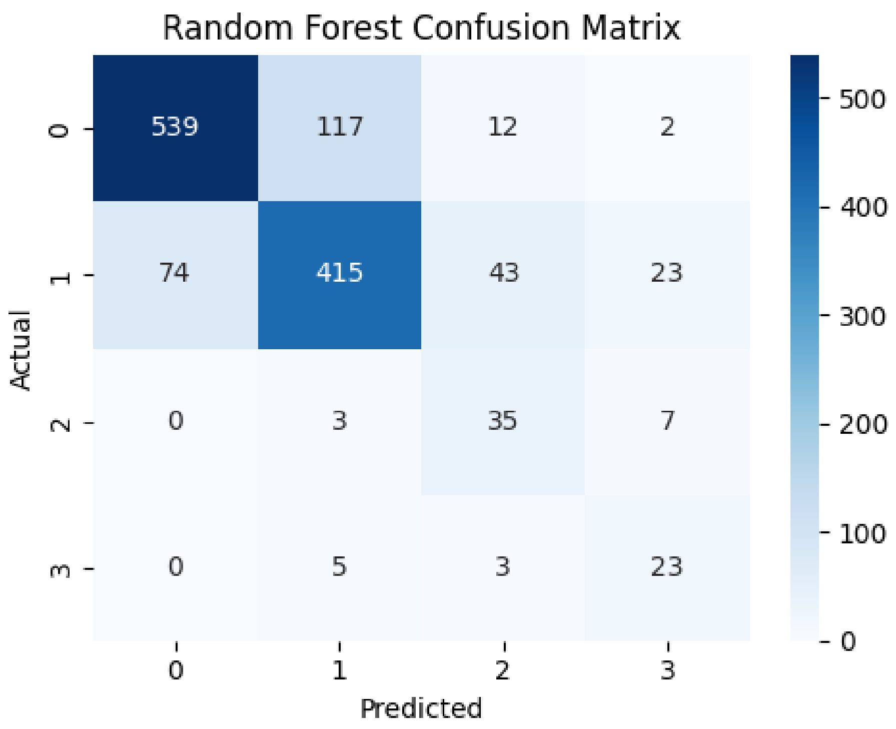
[27]:
```
def evaluate_model(model, X_train, y_train, X_test, y_test, model_name="Model"):
    """
    Evaluate a classification model with standard metrics and visualize the␣
↪confusion matrix.
    Returns a summary dictionary for results table, including raw evaluation␣
↪artifacts for LLM analysis.
    """
    from sklearn.metrics import (
        accuracy_score, f1_score, precision_score, recall_score,
        classification_report, confusion_matrix
    )
    import matplotlib.pyplot as plt
    import seaborn as sns

    # Predict
    y_pred = model.predict(X_test)
    y_train_pred = model.predict(X_train)

    # Metrics
    acc = accuracy_score(y_test, y_pred)
    f1_macro = f1_score(y_test, y_pred, average="macro")
    prec_macro = precision_score(y_test, y_pred, average="macro")
    recall_macro = recall_score(y_test, y_pred, average="macro")

    # Confusion matrix
    cm = confusion_matrix(y_test, y_pred)

    # Print results
    print(f"\n===== {model_name} Evaluation =====")
    print(f"Accuracy: {acc:.4f} | Macro F1: {f1_macro:.4f} | Precision:␣
↪{prec_macro:.4f} | Recall: {recall_macro:.4f}")

    plt.figure(figsize=(5, 4))
    sns.heatmap(cm, annot=True, cmap="Blues", fmt="d")
    plt.title(f"{model_name} Confusion Matrix")
    plt.xlabel("Predicted")
    plt.ylabel("Actual")
    plt.tight_layout()
    plt.show()

    print("\nClassification Report:")
    print(classification_report(y_test, y_pred, digits=3))

    # Add these for LLM-friendly result summaries
    cm_list = cm.tolist()  # For JSON/prompt/LLM
    report_dict = classification_report(y_test, y_pred, digits=3,␣
↪output_dict=True)  # For AI parsing
    report_str = classification_report(y_test, y_pred, digits=3)  # For human␣
↪reading

    # Return summary dict
    return {
        "Model": model_name,
        "Test F1": round(f1_macro, 4),
        "Accuracy": round(acc, 4),
        "Precision": round(prec_macro, 4),
        "Recall": round(recall_macro, 4),
        "Confusion Matrix": cm_list,
        "Classification Report (dict)": report_dict,
        "Classification Report (str)": report_str
    }
```

Step 2: Train and Evaluate Random Forest

Train a Random Forest classifier. Evaluate its test set performance using key metrics and visualize the confusion matrix.

[28]:
```
import warnings
warnings.filterwarnings('ignore')
from sklearn.ensemble import RandomForestClassifier

results_list = []

# Train Random Forest on balanced training set
rf = RandomForestClassifier(
    n_estimators=300,
    max_depth=10,
    min_samples_split=8,
    min_samples_leaf=4,
    max_features='sqrt',
    class_weight='balanced',
    random_state=42,
    n_jobs=-1
)
rf.fit(X_train_bal, y_train_bal)

# Evaluate model performance on test set
rf_results = evaluate_model(rf, X_train_bal, y_train_bal, X_test, y_test,␣
  ↪model_name="Random Forest")
results_list.append(rf_results)
```

```
===== Random Forest Evaluation =====
Accuracy: 0.7779 | Macro F1: 0.6601 | Precision: 0.6106 | Recall: 0.7680
```



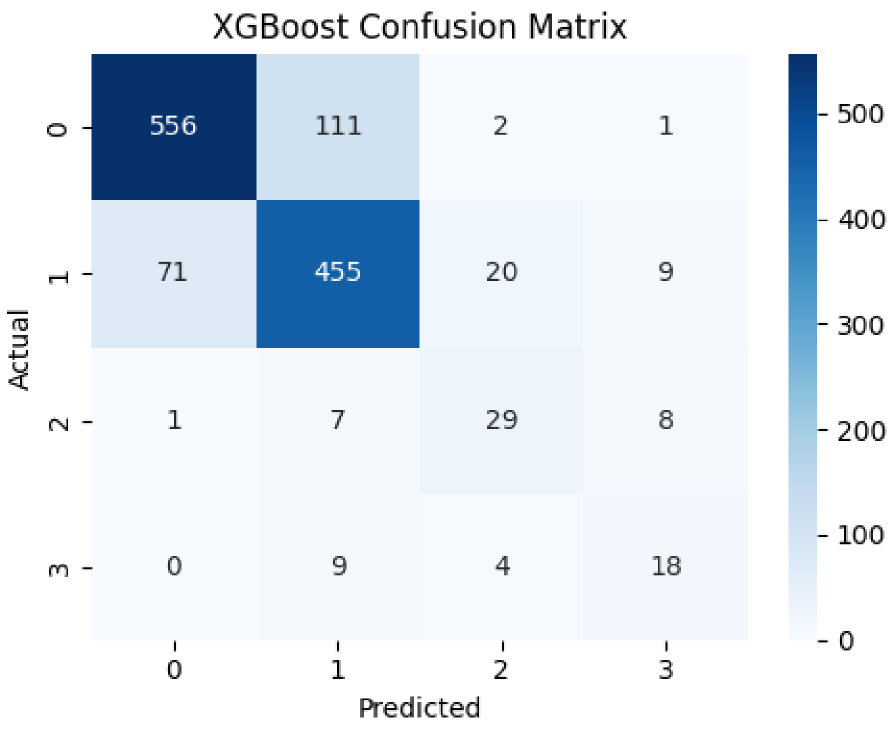
```
Classification Report:
              precision    recall  f1-score   support

           0      0.879     0.804     0.840       670
           1      0.769     0.748     0.758       555
           2       0.376     0.778     0.507        45
           3       0.418     0.742     0.535        31

    accuracy                           0.778      1301
   macro avg       0.611     0.768     0.660      1301
weighted avg       0.804     0.778     0.786      1301
```

Step 3: Train and Evaluate XGBoost

Train an XGBoost classifier using the same features and balanced data. Evaluate its performance using the same metrics for fair comparison.

[29]:
```python
from xgboost import XGBClassifier

# Train XGBoost on balanced training set
xgb = XGBClassifier(
    n_estimators=300,
    max_depth=6,
    learning_rate=0.07,
    subsample=0.8,
    colsample_bytree=0.8,
    min_child_weight=6,
    gamma=2,
    use_label_encoder=False,
    eval_metric='mlogloss',
    random_state=42,
    n_jobs=-1
)
xgb.fit(X_train_bal, y_train_bal)

# Evaluate model performance on test set
xgb_results = evaluate_model(xgb, X_train_bal, y_train_bal, X_test, y_test,␣
 ↪model_name="XGBoost")
results_list.append(xgb_results)
```

```
===== XGBoost Evaluation =====
Accuracy: 0.8132 | Macro F1: 0.6936 | Precision: 0.6736 | Recall: 0.7187
```



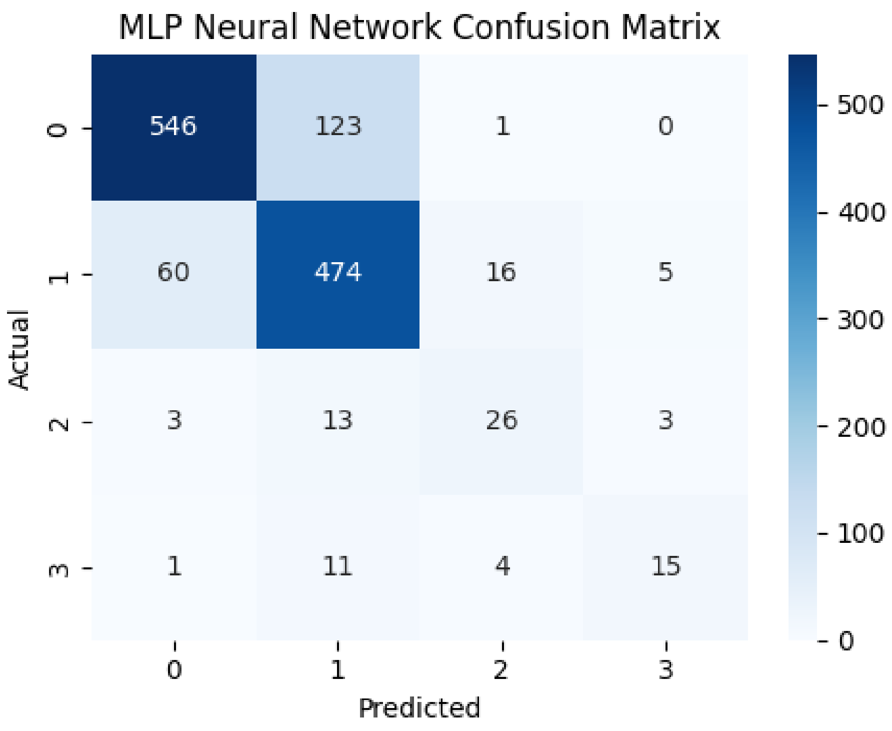
```
Classification Report:
              precision    recall  f1-score   support

           0      0.885     0.830     0.857       670
           1      0.782     0.820     0.800       555
           2      0.527     0.644     0.580        45
           3      0.500     0.581     0.537        31

    accuracy                          0.813      1301
   macro avg      0.674     0.719     0.694      1301
weighted avg      0.820     0.813     0.815      1301
```

Step 4: Train and Evaluate MLP Neural Network

Train a Multi-Layer Perceptron (MLP) neural network. Evaluate and visualize its classification performance.

[30]:
```
from sklearn.neural_network import MLPClassifier

# Train Multi-layer Perceptron on balanced training set
mlp = MLPClassifier(
    hidden_layer_sizes=(128, 64),
    activation='relu',
    solver='adam',
    alpha=0.01,
    batch_size=64,
    learning_rate_init=0.002,
    max_iter=200,
    early_stopping=True,
    random_state=42
)
mlp.fit(X_train_bal, y_train_bal)

# Evaluate model performance on test set
mlp_results = evaluate_model(mlp, X_train_bal, y_train_bal, X_test, y_test,␣
 ↪model_name="MLP Neural Network")
results_list.append(mlp_results)
```

```
===== MLP Neural Network Evaluation =====
Accuracy: 0.8155 | Macro F1: 0.6950 | Precision: 0.7159 | Recall: 0.6827
```



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

           0      0.895     0.815     0.853       670
           1       0.763     0.854     0.806       555
           2       0.553     0.578     0.565        45
           3       0.652     0.484     0.556        31

    accuracy                           0.816      1301
   macro avg       0.716     0.683     0.695      1301
weighted avg       0.821     0.816     0.816      1301
```

Step 5: Define the Transformer Model Evaluation Function

Define a specialized evaluation function for transformer-based models, capturing all metrics and artifacts needed for LLM-assisted interpretation.

[31]:
```python
from sklearn.model_selection import train_test_split

# Split data into train and test sets
train_texts, test_texts, train_labels_raw, test_labels_raw = train_test_split(
    df["clinical_note"].tolist(),
    df["note_status"].tolist(),
    test_size=0.2,
    random_state=42
)

# Manual label mapping for strict order: 0=Stable, 1=Recovering,␣
↪2=Deteriorating, 3=Critical
status2id = {
    "Stable": 0,
    "Recovering": 1,
    "Deteriorating": 2,
    "Critical": 3
}
id2status = {v: k for k, v in status2id.items()}

# Map original labels to integer labels
train_labels = [status2id[x] for x in train_labels_raw]
test_labels  = [status2id[x] for x in test_labels_raw]

print("Label mapping:", status2id)
print("Train label unique values:", set(train_labels))
print("Test label unique values:", set(test_labels))
```

```
Label mapping: {'Stable': 0, 'Recovering': 1, 'Deteriorating': 2, 'Critical': 3}
Train label unique values: {0, 1, 2, 3}
Test label unique values: {0, 1, 2, 3}
```

[32]:
```python
import numpy as np
from sklearn.metrics import (
    accuracy_score, f1_score, precision_score, recall_score, confusion_matrix,␣
  ↪classification_report
)
import matplotlib.pyplot as plt
import seaborn as sns

def evaluate_transformer_model(y_true, y_pred, model_name="Model",␣
  ↪target_names=None):
    """
    Evaluate a transformer model's predictions and print confusion matrix and␣
  ↪metrics.
    Returns summary dictionary for results table, including confusion matrix␣
  ↪and classification report.
    """
    acc = accuracy_score(y_true, y_pred)
    f1_macro = f1_score(y_true, y_pred, average="macro")
    prec_macro = precision_score(y_true, y_pred, average="macro")
    recall_macro = recall_score(y_true, y_pred, average="macro")

    cm = confusion_matrix(y_true, y_pred)

    print(f"\n===== {model_name} Evaluation =====")
    print(f"Accuracy: {acc:.4f} | Macro F1: {f1_macro:.4f} | Precision:␣
  ↪{prec_macro:.4f} | Recall: {recall_macro:.4f}")

    plt.figure(figsize=(5, 4))
    sns.heatmap(cm, annot=True, cmap="Blues", fmt="d")
    plt.title(f"{model_name} Confusion Matrix")
    plt.xlabel("Predicted")
    plt.ylabel("Actual")
    plt.tight_layout()
    plt.show()

    # Classification reports
    report_dict = classification_report(y_true, y_pred,␣
  ↪target_names=target_names, digits=3, output_dict=True)
    report_str = classification_report(y_true, y_pred,␣
  ↪target_names=target_names, digits=3)
    print("\nClassification Report:")
    print(report_str)

    return {
        "Model": model_name,
        "Test F1": round(f1_macro, 4),
        "Accuracy": round(acc, 4),
        "Precision": round(prec_macro, 4),
        "Recall": round(recall_macro, 4),
        "Confusion Matrix": cm.tolist(),                # <-- For saving or LLM␣
↪prompt
        "Classification Report (dict)": report_dict,    # <-- For LLM, code,␣
↪summary
        "Classification Report (str)": report_str       # <-- For direct prompt/
↪human reading
    }
```

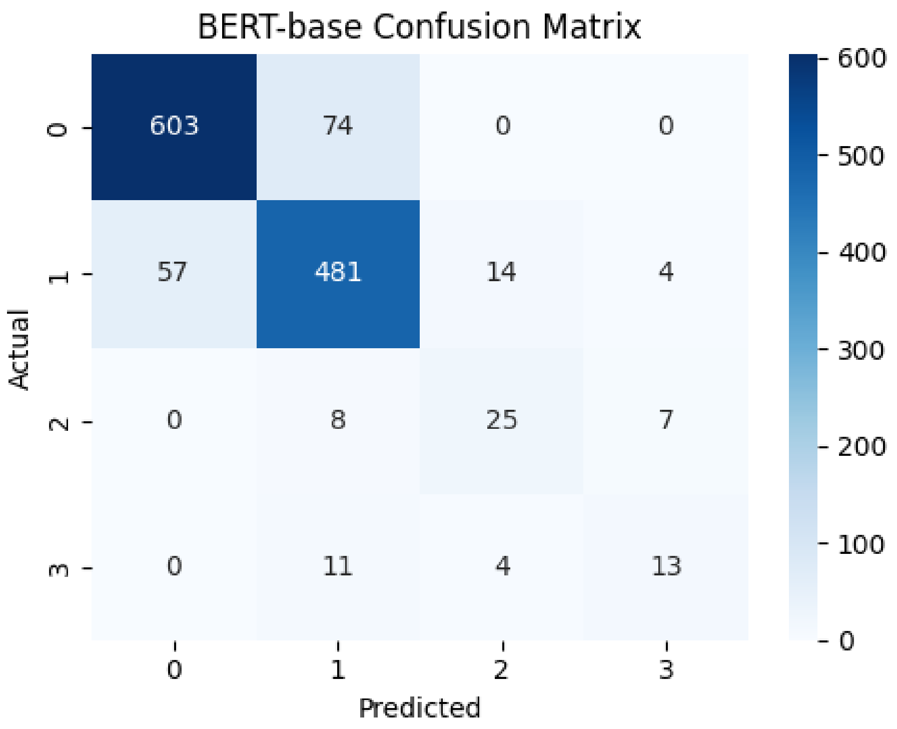
[33]:
```
from transformers import AutoTokenizer, AutoModelForSequenceClassification,␣
↪Trainer, TrainingArguments
from datasets import Dataset
import os

os.environ["WANDB_DISABLED"] = "true"  # Disable external logging

def train_and_predict_transformer(model_ckpt, train_texts, train_labels,␣
↪test_texts, test_labels, model_name="Transformer"):
    # 1. Load tokenizer and model
    tokenizer = AutoTokenizer.from_pretrained(model_ckpt)
    model = AutoModelForSequenceClassification.from_pretrained(model_ckpt,␣
↪num_labels=4)

    # 2. Tokenize texts
    train_encodings = tokenizer(train_texts, truncation=True, padding=True)
    test_encodings = tokenizer(test_texts, truncation=True, padding=True)

    train_dataset = Dataset.from_dict({**train_encodings, "label":␣
↪train_labels})
    test_dataset = Dataset.from_dict({**test_encodings, "label": test_labels})

    # 3. Training arguments
    training_args = TrainingArguments(
        output_dir="./results",
        per_device_train_batch_size=8,
        per_device_eval_batch_size=8,
        num_train_epochs=5,
        learning_rate=2e-5,
        weight_decay=0.01,
        warmup_ratio=0.1,
        logging_dir="./logs",
        logging_strategy="epoch",
        save_strategy="no",
        report_to="none"
    )
    # 4. Train
    trainer = Trainer(
        model=model,
        args=training_args,
        train_dataset=train_dataset,
        eval_dataset=test_dataset
    )
    trainer.train()

    # 5. Predict
    preds = trainer.predict(test_dataset)
    y_pred = np.argmax(preds.predictions, axis=1)
    return y_pred
```

Step 6: Train and Evaluate BERT-base Transformer

Fine-tune a BERT-base transformer on clinical note text for health status prediction. Evaluate its test performance with standard metrics and confusion matrix.

```
[34]: target_names = ['Stable', 'Recovering', 'Deteriorating', 'Critical']

# 1. BERT-base-uncased
bert_pred = train_and_predict_transformer("bert-base-uncased", train_texts,␣
 ↪train_labels, test_texts, test_labels, model_name="BERT-base")
results_list.append(evaluate_transformer_model(test_labels, bert_pred,␣
 ↪"BERT-base", target_names=target_names))
```

```
tokenizer_config.json:   0%|          | 0.00/48.0 [00:00<?, ?B/s]

config.json:   0%|          | 0.00/570 [00:00<?, ?B/s]

vocab.txt:   0%|          | 0.00/232k [00:00<?, ?B/s]

tokenizer.json:   0%|          | 0.00/466k [00:00<?, ?B/s]

model.safetensors:   0%|          | 0.00/440M [00:00<?, ?B/s]

Some weights of BertForSequenceClassification were not initialized from the
model checkpoint at bert-base-uncased and are newly initialized:
['classifier.bias', 'classifier.weight']
You should probably TRAIN this model on a down-stream task to be able to use it
for predictions and inference.

<IPython.core.display.HTML object>

<IPython.core.display.HTML object>


===== BERT-base Evaluation =====
Accuracy: 0.8624 | Macro F1: 0.7139 | Precision: 0.7187 | Recall: 0.7113
```



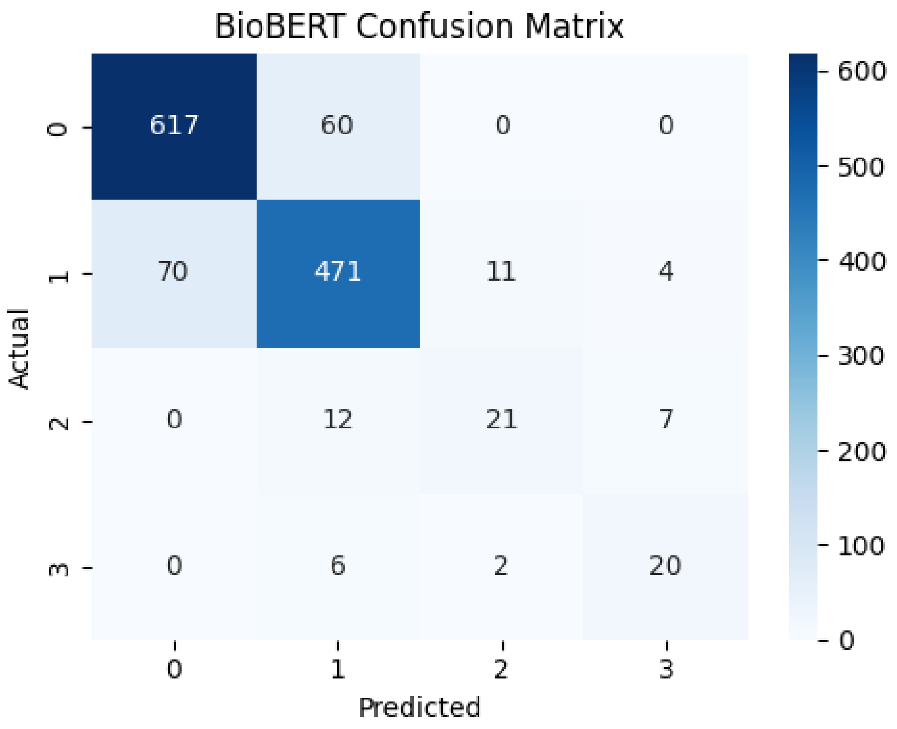
```
Classification Report:
              precision    recall  f1-score   support

      Stable      0.914     0.891     0.902       677
  Recovering      0.838     0.865     0.851       556
Deteriorating     0.581     0.625     0.602        40
     Critical     0.542     0.464     0.500        28

     accuracy                         0.862      1301
    macro avg     0.719     0.711     0.714      1301
 weighted avg     0.863     0.862     0.862      1301
```

Step 7: Train and Evaluate BioBERT Transformer

Fine-tune a BioBERT transformer model on the same prediction task. Assess its results using identical metrics for comparison.

[35]:
```
# 2. BioBERT
biobert_pred = train_and_predict_transformer("dmis-lab/biobert-base-cased-v1.
↪1", train_texts, train_labels, test_texts, test_labels, model_name="BioBERT")
results_list.append(evaluate_transformer_model(test_labels, biobert_pred,␣
↪"BioBERT", target_names=target_names))
```

```
config.json:   0%|          | 0.00/313 [00:00<?, ?B/s]

vocab.txt:   0%|          | 0.00/213k [00:00<?, ?B/s]

pytorch_model.bin:   0%|          | 0.00/436M [00:00<?, ?B/s]

model.safetensors:   0%|          | 0.00/436M [00:00<?, ?B/s]

Some weights of BertForSequenceClassification were not initialized from the
model checkpoint at dmis-lab/biobert-base-cased-v1.1 and are newly initialized:
['classifier.bias', 'classifier.weight']
You should probably TRAIN this model on a down-stream task to be able to use it
for predictions and inference.
Asking to truncate to max_length but no maximum length is provided and the model
has no predefined maximum length. Default to no truncation.

<IPython.core.display.HTML object>

<IPython.core.display.HTML object>


===== BioBERT Evaluation =====
Accuracy: 0.8678 | Macro F1: 0.7507 | Precision: 0.7547 | Recall: 0.7494
```



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

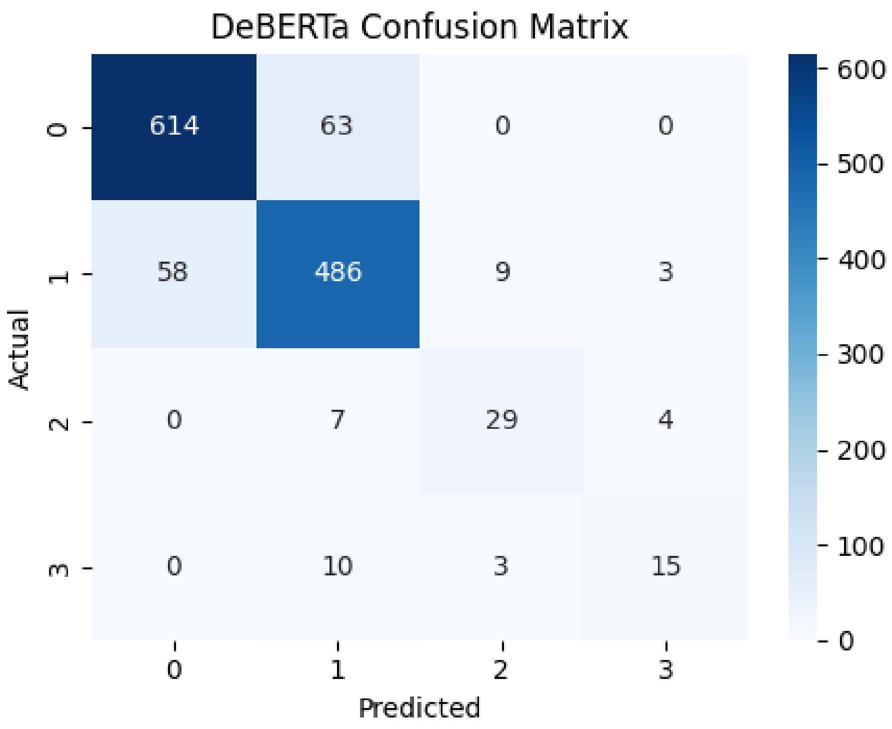
```
       Stable      0.898     0.911     0.905       677
   Recovering      0.858     0.847     0.852       556
Deteriorating      0.618     0.525     0.568        40
     Critical      0.645     0.714     0.678        28

     accuracy                          0.868      1301
    macro avg      0.755     0.749     0.751      1301
 weighted avg      0.867     0.868     0.867      1301
```

Step 8: Train and Evaluate DeBERTa Transformer

Fine-tune a DeBERTa transformer model for the multi-class classification task. Evaluate and compare its predictive performance.

[36]:
```
# 3. DeBERTa
deberta_pred = train_and_predict_transformer("microsoft/deberta-base",␣
 ↪train_texts, train_labels, test_texts, test_labels, model_name="DeBERTa")
results_list.append(evaluate_transformer_model(test_labels, deberta_pred,␣
 ↪"DeBERTa", target_names=target_names))
```

```
tokenizer_config.json:   0%|          | 0.00/52.0 [00:00<?, ?B/s]

config.json:   0%|          | 0.00/474 [00:00<?, ?B/s]

vocab.json:   0%|          | 0.00/899k [00:00<?, ?B/s]

merges.txt:   0%|          | 0.00/456k [00:00<?, ?B/s]

pytorch_model.bin:   0%|          | 0.00/559M [00:00<?, ?B/s]

Some weights of DebertaForSequenceClassification were not initialized from the
model checkpoint at microsoft/deberta-base and are newly initialized:
['classifier.bias', 'classifier.weight', 'pooler.dense.bias',
'pooler.dense.weight']
You should probably TRAIN this model on a down-stream task to be able to use it
for predictions and inference.
Asking to truncate to max_length but no maximum length is provided and the model
has no predefined maximum length. Default to no truncation.

<IPython.core.display.HTML object>

model.safetensors:   0%|          | 0.00/559M [00:00<?, ?B/s]

<IPython.core.display.HTML object>


===== DeBERTa Evaluation =====
Accuracy: 0.8793 | Macro F1: 0.7732 | Precision: 0.7904 | Recall: 0.7604
```



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

       Stable      0.914     0.907     0.910       677
   Recovering      0.859     0.874     0.866       556
Deteriorating      0.707     0.725     0.716        40
     Critical      0.682     0.536     0.600        28

     accuracy                          0.879      1301
    macro avg      0.790     0.760     0.773      1301
 weighted avg      0.879     0.879     0.879      1301
```

Step 9: Summarize and Compare All Model Results

Aggregate all results into a summary table for direct comparison across all traditional and transformer-based models.

[37]:
```python
import pandas as pd

summary_df = pd.DataFrame(results_list)
display(summary_df)
```

```
                   Model  Test F1  Accuracy  Precision  Recall  \
0       Random Forest   0.6601    0.7779     0.6106  0.7680
1             XGBoost   0.6936    0.8132     0.6736  0.7187
2  MLP Neural Network   0.6950    0.8155     0.7159  0.6827
3           BERT-base   0.7139    0.8624     0.7187  0.7113
4             BioBERT   0.7507    0.8678     0.7547  0.7494
5             DeBERTa   0.7732    0.8793     0.7904  0.7604

                                 Confusion Matrix  \
0  [[539, 117, 12, 2], [74, 415, 43, 23], [0, 3, …
1  [[556, 111, 2, 1], [71, 455, 20, 9], [1, 7, 29…
2  [[546, 123, 1, 0], [60, 474, 16, 5], [3, 13, 2…
3  [[603, 74, 0, 0], [57, 481, 14, 4], [0, 8, 25,…
4  [[617, 60, 0, 0], [70, 471, 11, 4], [0, 12, 21…
5  [[614, 63, 0, 0], [58, 486, 9, 3], [0, 7, 29, …

                         Classification Report (dict)  \
0  {'0': {'precision': 0.8792822185970636, 'recal…
1  {'0': {'precision': 0.8853503184713376, 'recal…
2  {'0': {'precision': 0.8950819672131147, 'recal…
3  {'Stable': {'precision': 0.9136363636363637, '…
4  {'Stable': {'precision': 0.8981077147016011, '…
5  {'Stable': {'precision': 0.9136904761904762, '…

                          Classification Report (str)
0                precision    recall  f1-score   …
1                precision    recall  f1-score   …
2                precision    recall  f1-score   …
3                 precision    recall  f1-score   …
4                 precision    recall  f1-score   …
5                 precision    recall  f1-score   …
```

8 7. LLM-Assisted Model Interpretation and Reporting

Leverage a Large Language Model (LLM) such as GPT-4o to automatically interpret, compare, and summarize the predictive performance of all evaluated models. This enables objective, human-readable scientific reporting and evidence-based model selection.

Step 1: Prepare the Model Performance Summary Table

Convert the pandas summary table of all model results into a markdown-formatted string for easier consumption by an LLM.

[38]:
```python
# Select key columns for summary and convert to markdown for LLM input
summary_table_text = summary_df[["Model", "Test F1", "Accuracy", "Precision",␣
 ↪"Recall"]].to_markdown(index=False)
```

Step 2: Define an Expert Prompt for the LLM

Write an instruction prompt that asks the LLM to analyze and summarize the model comparison table with scientific rigor and clarity.

[39]:
```
LLM_SUMMARY_PROMPT = """
You are an expert data scientist. Below is a summary table reporting key test␣
↪set performance metrics (Test F1, Accuracy, Precision, Recall) for six␣
↪machine learning models (three traditional and three transformer-based) on a␣
↪multi-class clinical status prediction task.

Summary Table (test set results):

{summary_table}

Instructions:
1. Compare the performance of traditional machine learning models (Random␣
↪Forest, XGBoost, MLP Neural Network) with transformer-based models␣
↪(BERT-base, BioBERT, DeBERTa), citing specific metrics and models by name.
2. Identify the best-performing model(s) and justify your conclusion with␣
↪numerical evidence.
3. Discuss interesting trends, weaknesses, or trade-offs, such as class␣
↪imbalance, computational resources, and overfitting risks.
4. Briefly comment on each model's practicality for clinical deployment,␣
↪considering real-world resource or interpretability constraints.
5. Suggest one area for further improvement or future research.
6. Conclude with a clear, formal academic recommendation (1-2 sentences).

Write your summary in concise, formal, and academic English, suitable for a␣
↪scientific report. Use bullet points if appropriate for clarity.
"""
```

Step 3: Format and Compose the Final Prompt

Insert the model performance table into the prompt template for LLM processing.

[40]:
```
# Merge the prompt with the actual model performance table
final_prompt = LLM_SUMMARY_PROMPT.format(summary_table=summary_table_text)
```

Step 4: Generate an Expert Summary via LLM

Send the formatted prompt to your LLM API (e.g., Azure, OpenAI GPT-4o) and print the summary for reporting.

[41]:
```
# Call your LLM (replace with your actual LLM function, e.g., OpenAI/Azure call)
llm_response = model_prompt(final_prompt, system_prompt="You are an expert␣
↪clinical data scientist. Write in academic style.")

# Output the summary for inclusion in your report
print(llm_response)
```

```
### Comparative Analysis of Model Performance
```

```
- **Traditional Machine Learning Models**:
  - Random Forest achieved a Test F1 score of 0.6601, Accuracy of 0.7779,
Precision of 0.6106, and Recall of 0.768. While demonstrating relatively strong
Recall, its lower Precision indicates a higher likelihood of false positives.
  - XGBoost outperformed Random Forest with a Test F1 score of 0.6936, Accuracy
of 0.8132, Precision of 0.6736, and Recall of 0.7187, achieving a more balanced
performance across metrics.
  - The Multi-Layer Perceptron (MLP) Neural Network showed marginal improvement
over XGBoost with a Test F1 score of 0.695, Accuracy of 0.8155, Precision of
0.7159, and Recall of 0.6827, excelling particularly in Precision but reflecting
slightly diminished Recall.

- **Transformer-Based Models**:
  - BERT-base demonstrated substantial performance enhancements over traditional
models, achieving a Test F1 score of 0.7139, Accuracy of 0.8624, Precision of
0.7187, and Recall of 0.7113. It balanced Precision and Recall effectively while
improving overall classification accuracy.
  - BioBERT further improved upon BERT-base, yielding a Test F1 score of 0.7507,
Accuracy of 0.8678, Precision of 0.7547, and Recall of 0.7494. This model
demonstrated superior performance across all metrics, indicating its domain-
specific optimization for clinical text.
  - DeBERTa emerged as the best-performing model, with a Test F1 score of
0.7732, Accuracy of 0.8793, Precision of 0.7904, and Recall of 0.7604. It
offered the highest Accuracy and Test F1 score, suggesting its robust capability
for multi-class clinical status prediction.

### Best-Performing Model
- DeBERTa is the best-performing model, as evidenced by its highest Test F1
score (0.7732), Accuracy (0.8793), and Precision (0.7904), alongside competitive
Recall (0.7604). This superior performance demonstrates its ability to minimize
false positives and false negatives while achieving high predictive reliability.

### Trends, Weaknesses, and Trade-Offs
- **Performance Trends**: Transformer-based models consistently outperform
traditional machine learning models across all metrics, highlighting their
ability to capture complex linguistic and contextual features in clinical data.
- **Trade-Offs**: While traditional models such as Random Forest are
computationally inexpensive and interpretable, their predictive performance is
comparatively lower. Transformer-based models, while highly accurate, require
extensive computational resources and may risk overfitting in smaller datasets
due to their complexity.
- **Class Imbalance**: Recall values for traditional models are relatively high,
indicating their sensitivity to minority classes. However, transformer-based
models balance Recall and Precision effectively, reducing bias toward specific
classes.

### Practicality for Clinical Deployment
```

- **Random Forest**: Its interpretability and low computational requirements make it suitable for resource-constrained settings but less applicable for complex tasks requiring higher accuracy.
- **XGBoost and MLP**: These models balance computational efficiency and predictive reliability, making them practical for moderate-resource environments, albeit with limitations in handling nuanced clinical data.
- **Transformer-Based Models**: While BioBERT and DeBERTa offer superior predictive performance, their high computational demands may restrict deployment in settings with limited hardware. Additionally, their black-box nature limits interpretability, which is critical for clinical decision-making.

### Future Research Directions
- Further exploration of model interpretability in transformer-based architectures is essential to enhance clinical adoption. Techniques such as attention visualization or post-hoc explainability methods can bridge the gap between performance and practical utility.

### Recommendation
DeBERTa is recommended for multi-class clinical status prediction tasks where predictive accuracy is paramount and computational resources are sufficient. For resource-constrained environments, XGBoost or MLP may be considered as viable alternatives.