Prediction model

July 28, 2025

0.1 1. Setup & Data Load

Load libraries, set constants (random seed, paths), and read the CSV.

[1]:
```python
import os
from pathlib import Path
import numpy as np
import pandas as pd

RANDOM_STATE = 42
DATA_PATH = "C:/Users/USER/anxiety-risk-api/data/anxiety.csv"

plots_dir = Path("plots")
plots_dir.mkdir(exist_ok=True)

df = pd.read_csv(DATA_PATH)
df.head()
```

[1]:
```
   Age  Gender Occupation  Sleep Hours  Physical Activity (hrs/week)  \
0   29  Female     Artist          6.0                           2.7
1   46   Other      Nurse          6.2                           5.7
2   64    Male      Other          5.0                           3.7
3   20  Female  Scientist          5.8                           2.8
4   49  Female      Other          8.2                           2.3

   Caffeine Intake (mg/day)  Alcohol Consumption (drinks/week) Smoking  \
0                       181                                 10     Yes
1                       200                                  8     Yes
2                       117                                  4      No
3                       360                                  6     Yes
4                       247                                  4     Yes

  Family History of Anxiety  Stress Level (1-10)  Heart Rate (bpm)  \
0                        No                   10               114
1                       Yes                    1                62
2                       Yes                    1                91
3                        No                    4                86
4                        No                    1                98
```

```
   Breathing Rate (breaths/min)  Sweating Level (1-5) Dizziness Medication  \
0                            14                     4        No        Yes   
1                            23                     2       Yes         No   
2                            28                     3        No         No   
3                            17                     3        No         No   
4                            19                     4       Yes        Yes   

   Therapy Sessions (per month) Recent Major Life Event  Diet Quality (1-10)  \
0                             3                     Yes                    7   
1                             2                      No                    8   
2                             1                     Yes                    1   
3                             0                      No                    1   
4                             1                      No                    3   

   Anxiety Level (1-10)  
0                   5.0  
1                   3.0  
2                   1.0  
3                   2.0  
4                   1.0  
```

0.2 2. Feature Engineering

Add interaction terms and bucketed categories you designed earlier.
This can reveal non-linear relationships and make class boundaries easier to learn.

[2]:
```
# Interactions / ratios
df['sleep_stress_int']    = df['Sleep Hours'] * df['Stress Level (1-10)']
df['caffeine_per_sleep']  = df['Caffeine Intake (mg/day)'] / df['Sleep Hours']
df['alc_per_activity']    = df['Alcohol Consumption (drinks/week)'] /␣
 ↪(df['Physical Activity (hrs/week)'] + 1e-3)
df['therapy_efficiency']  = df['Therapy Sessions (per month)'] / (df['Stress␣
 ↪Level (1-10)'] + 1e-3)

# Composite scores
df['unhealthy_score'] = (
    (df['Smoking'] == 'Yes').astype(int)
  + (df['Alcohol Consumption (drinks/week)'] > 7).astype(int)
  + (df['Caffeine Intake (mg/day)'] > 400).astype(int)
)
df['symptom_severity'] = (
    (df['Dizziness'] == 'Yes').astype(int)
  + df['Sweating Level (1-5)']
  + (df['Recent Major Life Event'] != 'None').astype(int)
)
```

```
df['diet_activity_int'] = df['Diet Quality (1-10)'] * df['Physical Activity (hrs/
↪week)']

# Buckets
df['age_group']    = pd.cut(df['Age'], bins=[0,25,35,50,100],␣
↪labels=['<25','25-35','35-50','50+'])
df['sleep_cat']    = pd.cut(df['Sleep Hours'], bins=[0,6,8,24], labels=['Short␣
↪(<6h)','Normal (6-8h)','Long (>8h)'])
df['activity_cat']= pd.cut(df['Physical Activity (hrs/week)'],␣
↪bins=[-1,2,5,100], labels=['Low','Moderate','High'])

df.head()
```

[2]:
```
   Age  Gender Occupation  Sleep Hours  Physical Activity (hrs/week)  \
0   29  Female     Artist          6.0                           2.7
1   46   Other      Nurse          6.2                           5.7
2   64    Male      Other          5.0                           3.7
3   20  Female  Scientist          5.8                           2.8
4   49  Female      Other          8.2                           2.3

   Caffeine Intake (mg/day)  Alcohol Consumption (drinks/week) Smoking  \
0                       181                                 10     Yes
1                       200                                  8     Yes
2                       117                                  4      No
3                       360                                  6     Yes
4                       247                                  4     Yes

  Family History of Anxiety  Stress Level (1-10)  ...  sleep_stress_int  \
0                        No                   10  ...              60.0
1                       Yes                    1  ...               6.2
2                       Yes                    1  ...               5.0
3                        No                    4  ...              23.2
4                        No                    1  ...               8.2

   caffeine_per_sleep  alc_per_activity therapy_efficiency unhealthy_score  \
0           30.166667          3.702332           0.299970               2
1           32.258065          1.403263           1.998002               2
2           23.400000          1.080789           0.999001               0
3           62.068966          2.142092           0.000000               1
4           30.121951          1.738375           0.999001               1

   symptom_severity diet_activity_int  age_group      sleep_cat  activity_cat
0                 5              18.9      25-35    Short (<6h)      Moderate
1                 4              45.6      35-50  Normal (6-8h)          High
2                 4               3.7        50+    Short (<6h)      Moderate
3                 4               2.8        <25    Short (<6h)      Moderate
4                 6               6.9      35-50     Long (>8h)      Moderate
```

[5 rows x 29 columns]

0.3 3. Target Binning (Low / Medium / High)

Convert the 1–10 anxiety score into 3 ordered categories to combat sparsity and class imbalance.

[3]:
```python
from sklearn.preprocessing import LabelEncoder

BIN_BOUNDS  = [0, 3, 7, 10]            # (0,3] Low, (3,7] Medium, (7,10] High
BIN_LABELS  = ['Low','Medium','High']

df['anxiety_bin'] = pd.cut(df['Anxiety Level (1-10)'],
                           bins=BIN_BOUNDS, labels=BIN_LABELS,
                           include_lowest=True, right=True)

le = LabelEncoder()
y = le.fit_transform(df['anxiety_bin'])

# Drop original/derived target cols from features
X = pd.get_dummies(df.drop(['Anxiety Level (1-10)', 'anxiety_bin'], axis=1),
                   drop_first=True).apply(pd.to_numeric)

y[:5], le.classes_
```

[3]:
```
(array([2, 1, 1, 1, 1]), array(['High', 'Low', 'Medium'], dtype=object))
```

0.4 4. Train/Test Split

Use a stratified split so each class proportion is maintained in train & test.

[4]:
```python
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.2, stratify=y, random_state=RANDOM_STATE
)

# Handy integer ids for classes
hi_id = np.where(le.classes_=='High')[0][0]
lo_id = np.where(le.classes_=='Low')[0][0]
me_id = np.where(le.classes_=='Medium')[0][0]

len(X_train), len(X_test)
```

[4]:
```
(8800, 2200)
```

0.5 5. Global Benchmark

Compare multiple model variants via 5-fold CV on **macro-F1**:

- LR / RF / XGB
- With and without `class_weight='balanced'`
- With SMOTE & BorderlineSMOTE (oversampling)
- **StandardScaler** only in LR pipelines (trees don't need scaling)

Pick the best by mean macro-F1.

[5]:
```
from sklearn.preprocessing import StandardScaler
from sklearn.pipeline import Pipeline
from imblearn.pipeline import Pipeline as ImbPipeline
from imblearn.over_sampling import SMOTE, BorderlineSMOTE

from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from xgboost import XGBClassifier
from sklearn.model_selection import cross_val_score

variants = {
    'LR (base)': Pipeline([
        ('scaler', StandardScaler()),
        ('lr', LogisticRegression(multi_class='multinomial', solver='lbfgs',
                                  max_iter=2000, random_state=RANDOM_STATE))
    ]),
    'RF (base)': RandomForestClassifier(n_estimators=200,␣
↪random_state=RANDOM_STATE),
    'XGB (base)': XGBClassifier(use_label_encoder=False, eval_metric='mlogloss',␣
↪random_state=RANDOM_STATE),

    'LR (balanced)': Pipeline([
        ('scaler', StandardScaler()),
        ('lr', LogisticRegression(multi_class='multinomial', solver='lbfgs',
                                  class_weight='balanced', max_iter=2000,␣
↪random_state=RANDOM_STATE))
    ]),
    'RF (balanced)': RandomForestClassifier(n_estimators=200,␣
↪class_weight='balanced', random_state=RANDOM_STATE),

    'LR + SMOTE': ImbPipeline([
        ('smote', SMOTE(random_state=RANDOM_STATE)),
        ('scaler', StandardScaler()),
        ('lr', LogisticRegression(multi_class='multinomial', solver='lbfgs',
                                  max_iter=2000, random_state=RANDOM_STATE))
    ]),
    'RF + SMOTE': ImbPipeline([
        ('smote', SMOTE(random_state=RANDOM_STATE)),
        ('rf', RandomForestClassifier(n_estimators=200,␣
↪random_state=RANDOM_STATE))
```

```python
    ]),
    'XGB + SMOTE': ImbPipeline([
        ('smote', SMOTE(random_state=RANDOM_STATE)),
        ('xgb', XGBClassifier(use_label_encoder=False, eval_metric='mlogloss',␣
↪random_state=RANDOM_STATE))
    ]),

    'LR + BSMOTE': ImbPipeline([
        ('bsmote', BorderlineSMOTE(random_state=RANDOM_STATE)),
        ('scaler', StandardScaler()),
        ('lr', LogisticRegression(multi_class='multinomial', solver='lbfgs',
                                  max_iter=2000, random_state=RANDOM_STATE))
    ]),
    'RF + BSMOTE': ImbPipeline([
        ('bsmote', BorderlineSMOTE(random_state=RANDOM_STATE)),
        ('rf', RandomForestClassifier(n_estimators=200,␣
↪random_state=RANDOM_STATE))
    ]),
    'XGB + BSMOTE': ImbPipeline([
        ('bsmote', BorderlineSMOTE(random_state=RANDOM_STATE)),
        ('xgb', XGBClassifier(use_label_encoder=False, eval_metric='mlogloss',␣
↪random_state=RANDOM_STATE))
    ])
}

cv_results = {}
for name, model in variants.items():
    scores = cross_val_score(model, X_train, y_train,
                             cv=5, scoring='f1_macro', n_jobs=-1)
    cv_results[name] = (scores.mean(), scores.std())

cv_df = (pd.DataFrame(cv_results, index=['mean','std']).T
         .sort_values('mean', ascending=False))
cv_df
```

[5]:

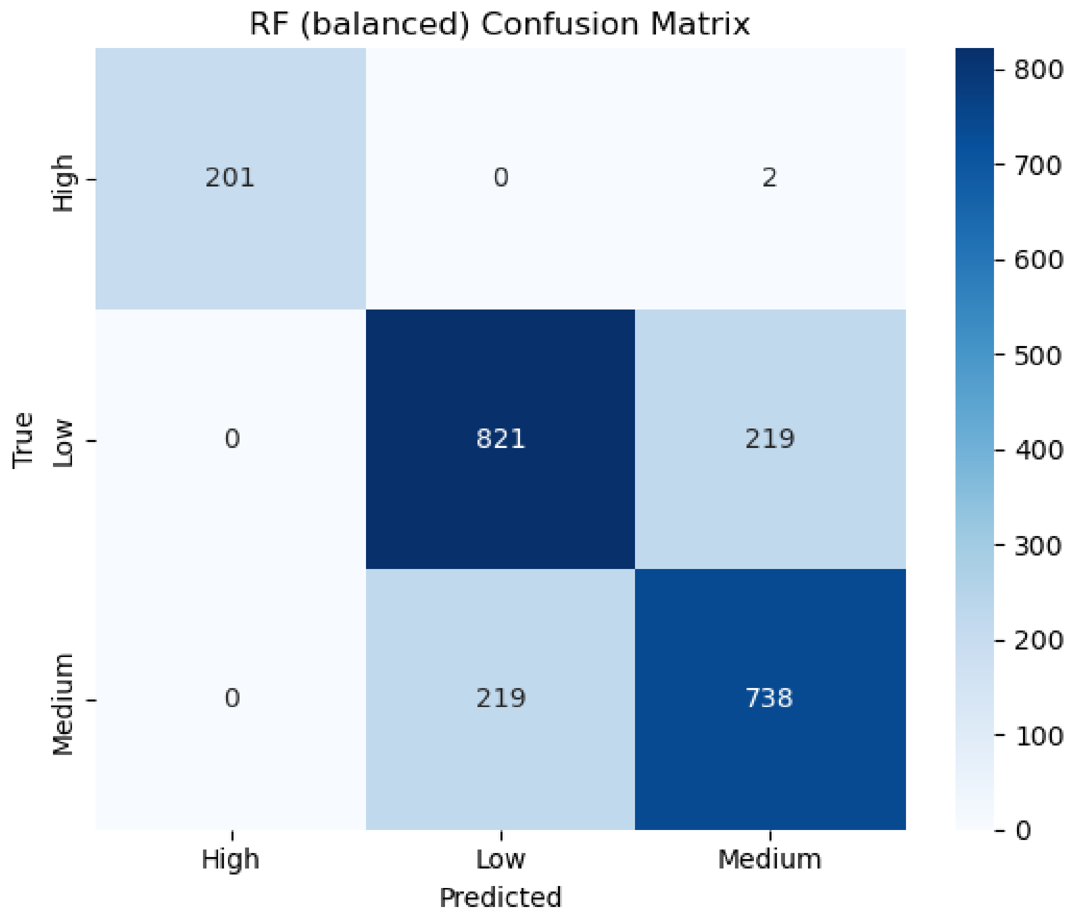
	mean	std
RF (balanced)	0.845616	0.007463
RF + SMOTE	0.845177	0.006085
RF + BSMOTE	0.845059	0.005716
RF (base)	0.844704	0.005433
LR (base)	0.843253	0.008198
LR + SMOTE	0.840373	0.008587
LR + BSMOTE	0.839609	0.009977
LR (balanced)	0.836242	0.009739
XGB + SMOTE	0.833341	0.007265
XGB + BSMOTE	0.833042	0.006517
XGB (base)	0.830181	0.006430

0.6 6. Test Evaluation

Fit the best variant on the full training set, evaluate on the test set, and plot a confusion matrix.

[6]:
```
from sklearn.metrics import f1_score, accuracy_score, classification_report,␣
↪confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt

best_name = cv_df.index[0]
best_model = variants[best_name].fit(X_train, y_train)

y_pred = best_model.predict(X_test)

print(f"Best variant: {best_name}")
print(f"Test macro-F1: {f1_score(y_test, y_pred, average='macro'):.3f}")
print(f"Test accuracy: {accuracy_score(y_test, y_pred):.3f}\n")
print("Classification Report:\n",
      classification_report(le.inverse_transform(y_test),
                            le.inverse_transform(y_pred),
                            digits=3))

cm = confusion_matrix(y_test, y_pred, labels=[hi_id, lo_id, me_id])
plt.figure(figsize=(6,5))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=['High','Low','Medium'],
            yticklabels=['High','Low','Medium'])
plt.xlabel('Predicted'); plt.ylabel('True')
plt.title(f'{best_name} Confusion Matrix')
plt.tight_layout()
plt.savefig(plots_dir/'cm_best.png')
plt.show()
```

```
Best variant: RF (balanced)
Test macro-F1: 0.852
Test accuracy: 0.800

Classification Report:
               precision    recall  f1-score   support

        High      1.000     0.990     0.995       203
         Low      0.789     0.789     0.789      1040
      Medium      0.770     0.771     0.770       957

    accuracy                          0.800      2200
   macro avg      0.853     0.850     0.852      2200
weighted avg      0.800     0.800     0.800      2200
```



0.7 7. Hierarchical Model

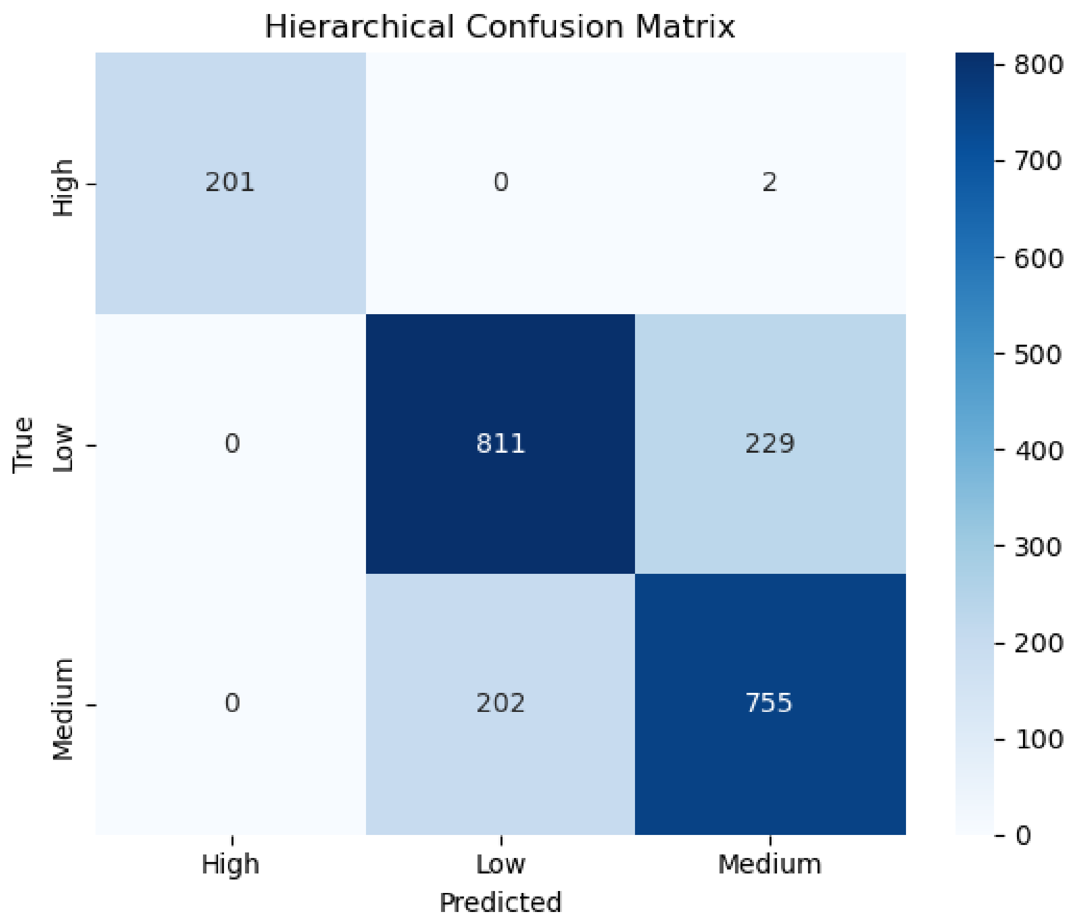
Use the best model twice: 1. Stage 1: High vs Not-High
2. Stage 2: Low vs Medium (on remaining samples)

Evaluate whether it actually improves Low/Medium F1.

[7]:
```
from sklearn.base import clone

# Stage 1: High vs Rest
y_hi = (y_train == hi_id).astype(int)
clf_hi = clone(best_model)
clf_hi.fit(X_train, y_hi)

# Stage 2: Low vs Medium
mask_lm = (y_train != hi_id)
y_lm = (y_train[mask_lm] == lo_id).astype(int)
clf_lm = clone(best_model)
clf_lm.fit(X_train[mask_lm], y_lm)
```

```
# Predict
p_hi = clf_hi.predict(X_test)
pred_final = np.full(len(X_test), me_id)
pred_final[p_hi == 1] = hi_id
idx_rest = np.where(p_hi == 0)[0]
pred_final[idx_rest] = np.where(clf_lm.predict(X_test.iloc[idx_rest])==1, lo_id,␣
↪me_id)

# Evaluate
macro_all = f1_score(y_test, pred_final, average='macro')
lm_mask   = np.isin(y_test, [lo_id, me_id])
macro_lm  = f1_score(y_test[lm_mask], pred_final[lm_mask], average='macro')

print(f"Hierarchical -> Macro-F1(all): {macro_all:.3f} | Macro-F1(L+M):␣
↪{macro_lm:.3f}\n")
print("Classification Report (hierarchical):\n",
      classification_report(le.inverse_transform(y_test),
                            le.inverse_transform(pred_final),
                            digits=3))

cm_h = confusion_matrix(y_test, pred_final, labels=[hi_id, lo_id, me_id])
plt.figure(figsize=(6,5))
sns.heatmap(cm_h, annot=True, fmt='d', cmap='Blues',
            xticklabels=['High','Low','Medium'],
            yticklabels=['High','Low','Medium'])
plt.xlabel('Predicted'); plt.ylabel('True')
plt.title('Hierarchical Confusion Matrix')
plt.tight_layout()
plt.savefig(plots_dir/'cm_hier.png')
plt.show()
```

```
Hierarchical -> Macro-F1(all): 0.854 | Macro-F1(L+M): 0.784

Classification Report (hierarchical):
               precision    recall  f1-score   support

        High      1.000     0.990     0.995       203
         Low      0.801     0.780     0.790      1040
      Medium      0.766     0.789     0.777       957

    accuracy                          0.803      2200
   macro avg      0.855     0.853     0.854      2200
weighted avg      0.804     0.803     0.803      2200
```



0.8 Conclusion

- **Best single model:** `RandomForestClassifier` with `class_weight = "balanced"`
  - **Test macro-F1:** 0.852|**Accuracy:** 0.800
  - **Class “High”** is essentially perfect (F1 = 0.995; only 2 misclassifications).
  - **Main confusion:** “Low” “Medium” (219 swaps each way).
- **Hierarchical model (High vs Rest → Low vs Medium):**
  - **Macro-F1 (all):** 0.854 (↑ +0.002)|**Accuracy:** 0.803
  - **Macro-F1 on Low & Medium:** 0.784 (very close to the flat model)
  - Slight reduction of Medium→Low errors (202 vs 219) but an increase of Low→Medium (229 vs 219). Net gain is marginal.

Takeaway:
The flat RF model is simpler and already strong. The hierarchical approach adds complexity without a meaningful overall improvement. Unless you must prioritize one specific class (Low or Medium)

for business reasons, keep the single RF (balanced) pipeline.

Potential next steps: 1. Fine-tune class weights or probability thresholds if class-specific performance matters.
2. Prune or rework features that showed negative importance.
3. Test an ordinal model or regression-then-round as an alternative baseline.
4. Package the final pipeline (preprocessing + model) and log metrics for reproducibility.