```
In [1]: import pandas as pd
        import numpy as np
        import matplotlib.pyplot as plt
        import seaborn as sns
In [2]: df = pd.read csv("clean.csv")
        df.head()
Out[2]:
              SEQN RIAGENDR RIDAGEYR RIDRETH3 DMDBORN4 DMDEDUC2 INDFMPIR
        0 109290.0
                           2.0
                                     68.0
                                                4.0
                                                             1.0
                                                                        5.0
                                                                                  5.0
         1 109290.0
                           2.0
                                     68.0
                                                4.0
                                                             1.0
                                                                        5.0
                                                                                  5.0
         2 109290.0
                           2.0
                                     68.0
                                                4.0
                                                             1.0
                                                                        5.0
                                                                                  5.0
        3 109290.0
                           2.0
                                     68.0
                                                4.0
                                                             1.0
                                                                        5.0
                                                                                  5.0
        4 109300.0
                           2.0
                                     54.0
                                                6.0
                                                            2.0
                                                                        5.0
                                                                                  5.0
        5 rows × 65 columns
In [3]: df.columns
Out[3]: Index(['SEQN', 'RIAGENDR', 'RIDAGEYR', 'RIDRETH3', 'DMDBORN4', 'DMDEDUC2',
                'INDFMPIR', 'DR1TKCAL', 'DR1TPROT', 'DR1TCARB', 'DR1TSUGR', 'DR1TFIB
         Ε',
                'DR1TTFAT', 'DR1TSFAT', 'DR1TCHOL', 'DR1TALCO', 'DR1TCAFF', 'DR1TSOD
         Ι',
                'DR1TPOTA', 'DR2TKCAL', 'DR2TPROT', 'DR2TCARB', 'DR2TSUGR', 'DR2TFIB
         Ε',
                'DR2TTFAT', 'DR2TSFAT', 'DR2TCHOL', 'DR2TALCO', 'DR2TCAFF', 'DR2TSOD
         Ι',
                'DR2TPOTA', 'BPXOSY1', 'BPXODI1', 'BPXOSY2', 'BPXODI2', 'BPXOSY3',
                'BPXODI3', 'BPXOPLS1', 'BPXOPLS2', 'BPXOPLS3', 'BMXWT', 'BMXHT',
                'BMXBMI', 'BMXWAIST', 'LBXIN', 'LBXGLU', 'LBXTR', 'LBDLDL', 'LBDHD
         D',
                'LBXHSCRP', 'PHAFSTHR', 'PAQ605', 'PAQ620', 'PAQ635', 'PAQ650',
                'PAQ665', 'RXDUSE', 'RXDDRUG', 'RXDDRGID', 'RXDRSC1', 'BPQ020',
                'DIQ010', 'DBQ700', 'DBQ197', 'HIQ011'],
               dtype='object')
In [4]: columns_to_drop = [
            # Day 1 dietary variables
            'DR1TPROT', 'DR1TCARB', 'DR1TCHOL', 'DR1TALCO',
             'DR1TCAFF', 'DR1TSODI', 'DR1TPOTA',
            # Day 2 dietary variables
             'DR2TPROT', 'DR2TCARB', 'DR2TCHOL', 'DR2TALCO',
            'DR2TCAFF', 'DR2TSODI', 'DR2TPOTA',
            # Weight and height
            'BMXWT', 'BMXHT',
```

```
# Blood pressure pulse readings
    'BPXOPLS1', 'BPXOPLS2', 'BPXOPLS3',

# Drug metadata
    'RXDDRGID', 'RXDRSC1',

    'SEQN', 'LBDLDL', 'RIDAGEYR', 'RIDRETH3', 'DMDBORN4', 'DMDEDUC2', 'PHAFS
    'PAQ665', 'BPQ020', 'DIQ010', 'HIQ011'
]
df.drop(columns=columns_to_drop, inplace=True)
```

Feature Engineering

Clinical Risk Indicators (Metabolic Syndrome Flags)

```
In [5]: # Obesity based on waist circumference (gender-specific)
        df['flag\_obese'] = ((df['RIAGENDR'] == 1) & (df['BMXWAIST'] > 102)) | \
                            ((df['RIAGENDR'] == 2) \& (df['BMXWAIST'] > 88))
        # Elevated blood pressure
        df['avg_sys'] = df[['BPXOSY1', 'BPXOSY2', 'BPXOSY3']].mean(axis=1)
        df['avg_dia'] = df[['BPXODI1', 'BPXODI2', 'BPXODI3']].mean(axis=1)
        df['flag_high_bp'] = (df['avg_sys'] >= 130) | (df['avg_dia'] >= 85)
        # Elevated fasting glucose
        df['flag_high_glucose'] = df['LBXGLU'] >= 100
        # Elevated triglycerides
        df['flag_high_triglycerides'] = df['LBXTR'] >= 150
        # Low HDL cholesterol (gender-specific)
        df['flag_low_hdl'] = ((df['RIAGENDR'] == 1) & (df['LBDHDD'] < 40)) | \</pre>
                              ((df['RIAGENDR'] == 2) & (df['LBDHDD'] < 50))
        # HOMA-TR
        df['HOMA_IR'] = (df['LBXIN'] * df['LBXGLU']) / 405
        df['flag homa ir'] = df['HOMA IR'] > 2.5
```

Derived Metabolic Syndrome Target

Lifestyle Feature Engineering

```
In [7]: # Average Daily Intake
    df['avg_kcal'] = df[['DR1TKCAL', 'DR2TKCAL']].mean(axis=1)
    df['avg_sugar'] = df[['DR1TSUGR', 'DR2TSUGR']].mean(axis=1)
    df['avg_fat'] = df[['DR1TTFAT', 'DR2TTFAT']].mean(axis=1)
    df['avg_fiber'] = df[['DR1TFIBE', 'DR2TFIBE']].mean(axis=1)
```

```
# Change in Intake
 df['delta kcal'] = df['DR2TKCAL'] - df['DR1TKCAL']
 df['delta sugar'] = df['DR2TSUGR'] - df['DR1TSUGR']
 df['delta_fat'] = df['DR2TTFAT'] - df['DR1TTFAT']
 # Binary Flags for Intake Reduction
 df['reduced calories'] = df['delta kcal'] < -100</pre>
 df['reduced sugar'] = df['delta sugar'] < -10</pre>
 # Likely Dieting (Overweight + trying to lose weight + reduced intake)
 df['likely dieting'] = (
     (df['BMXBMI'] >= 25) &
     df['reduced calories'] &
     df['DBQ700'].eq(1)
 # Eating Out Behavior
 df['eats out often'] = df['DBQ197'].isin([1, 2]) # every day / most days
 df['eats_out_rarely'] = df['DBQ197'].isin([4, 5]) # 1-2x/week or never
 # Physical Activity
 df['physically_active'] = (
     df[['PAQ605', 'PAQ620', 'PAQ635', 'PAQ650']].isin([1]).any(axis=1)
 df['activity_score'] = df[['PAQ605', 'PAQ620', 'PAQ635', 'PAQ650']].applymar
 # Lifestyle Effort Score
 df['lifestyle_effort'] = (
     df['likely_dieting'].astype(int)
     + df['eats out rarely'].astype(int)
     + df['delta_kcal'].apply(lambda x: 1 if x < 0 else 0) # decreased calor
     + df['delta_sugar'].apply(lambda x: 1 if x < 0 else 0) # decreased sugar
     + df['physically active'].astype(int) # NEW: physical activity
/var/folders/z1/w_njtpr52ss65yn2_5wp9xfm0000gn/T/ipykernel_51747/814351403.p
y:31: FutureWarning: DataFrame.applymap has been deprecated. Use DataFrame.m
ap instead.
  df['activity_score'] = df[['PAQ605', 'PAQ620', 'PAQ635', 'PAQ650']].applym
```

```
ap(lambda x: 1 if x == 1 else 0).sum(axis=1)
```

Med Class Variable

```
In [8]: met syn drugs = [
            # Diabetes-related
            'METFORMIN', 'INSULIN', 'GLIPIZIDE', 'GLYBURIDE', 'PIOGLITAZONE', 'SITAG
            'EMPAGLIFLOZIN', 'DAPAGLIFLOZIN', 'CANAGLIFLOZIN', 'LINAGLIPTIN', 'LIRAG
            'EXENATIDE', 'SEMAGLUTIDE', 'GLIMEPIRIDE',
            # Hypertension
            'LISINOPRIL', 'LOSARTAN', 'AMLODIPINE', 'METOPROLOL', 'RAMIPRIL', 'FUROS
            'HYDROCHLOROTHIAZIDE', 'VALSARTAN', 'BISOPROLOL', 'SPIRONOLACTONE', 'DIL
            # Cholesterol
```

```
'ATORVASTATIN', 'ROSUVASTATIN', 'SIMVASTATIN', 'PRAVASTATIN', 'PITAVASTA
            'EZETIMIBE', 'FENOFIBRATE', 'GEMFIBROZIL', 'FENOFIBRIC ACID', 'NIACIN',
        1
        # Clean and classify each record
        def classify meds(drug str):
            if pd.isna(drug_str) or drug_str.strip().upper() in ['NONE', 'NO MEDICAT
                return 'None'
            # Clean and split into list
            drugs = [d.strip().upper() for d in drug_str.split(';')]
            has_met_syn = any(any(med in drug for med in met_syn_drugs) for drug in
            has_non_met_syn = any(not any(med in drug for med in met_syn_drugs) for
            if has_met_syn and has_non_met_syn:
                return 'Both MetSyn + Other'
            elif has_met_syn:
                return 'MetSyn-related'
            elif has non met syn:
                return 'Other'
            else:
                return 'None'
        # Apply to your column
        df['med_class'] = df['RXDDRUG'].astype(str).apply(classify_meds)
In [9]: # 1 corresponds to using medication
        # 2 corresponds to not using medication
```

Income Level Variable

```
Out[11]: Index(['RIAGENDR', 'INDFMPIR', 'DR1TKCAL', 'DR1TSUGR', 'DR1TFIBE', 'DR1TTFA
          Т',
                  'DR1TSFAT', 'DR2TKCAL', 'DR2TSUGR', 'DR2TFIBE', 'DR2TTFAT', 'DR2TSFA
          Т',
                  'BPXOSY1', 'BPXODI1', 'BPXOSY2', 'BPXODI2', 'BPXOSY3', 'BPXODI3',
                  'BMXBMI', 'BMXWAIST', 'LBXIN', 'LBXGLU', 'LBXTR', 'LBDHDD', 'LBXHSCR
          Ρ',
                  'PAQ605', 'PAQ620', 'PAQ635', 'PAQ650', 'RXDUSE', 'RXDDRUG', 'DBQ70
          0',
                  'DBQ197', 'flag_obese', 'avg_sys', 'avg_dia', 'flag_high_bp',
                  'flag_high_glucose', 'flag_high_triglycerides', 'flag_low_hdl',
                  'HOMA_IR', 'flag_homa_ir', 'met_syndrome_count',
                  'has_metabolic_syndrome', 'avg_kcal', 'avg_sugar', 'avg_fat', 'avg_fiber', 'delta_kcal', 'delta_sugar', 'delta_fat',
                  'reduced_calories', 'reduced_sugar', 'likely_dieting', 'eats_out_oft
          en',
                  'eats_out_rarely', 'physically_active', 'activity_score',
                  'lifestyle_effort', 'med_class', 'income_level'],
                 dtype='object')
```

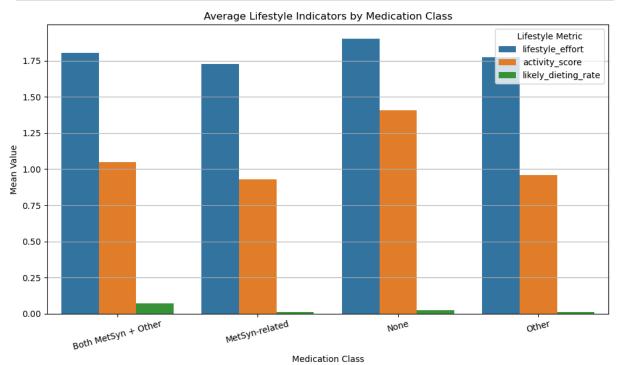
EDA

Do people on meds show differences in effort or health outcomes compared to those not on meds?

```
In [12]: df.groupby('med_class')[['lifestyle_effort', 'activity_score', 'likely_dieti'
                               lifestyle_effort activity_score likely_dieting
Out[12]:
                   med_class
          Both MetSyn + Other
                                     1.804878
                                                   1.048780
                                                                  0.073171
               MetSyn-related
                                     1.728976
                                                   0.928880
                                                                  0.011533
                         None
                                     1.904219
                                                   1.405929
                                                                 0.023945
                        Other
                                     1.775388
                                                   0.958241
                                                                 0.013603
```

```
In [13]: df['likely_dieting_numeric'] = df['likely_dieting'].astype(int)
# Calculate means grouped by medication class
grouped_means = df.groupby('med_class')[['lifestyle_effort', 'activity_score
grouped_means = grouped_means.rename(columns={'likely_dieting_numeric': 'lik
# Melt for plotting
melted = pd.melt(grouped_means, id_vars='med_class', var_name='Metric', valu
# Plotting
plt.figure(figsize=(10, 6))
sns.barplot(data=melted, x='med_class', y='Mean Value', hue='Metric')
plt.title('Average Lifestyle Indicators by Medication Class')
plt.ylabel('Mean Value')
plt.xlabel('Medication Class')
plt.xticks(rotation=15)
plt.tight_layout()
```

```
plt.legend(title='Lifestyle Metric')
plt.grid(axis='y')
plt.show()
```



Those who don't take medication have slightly higher lifestyle_effort and activity_score, but other than that the values for lifestyle_effort, activity_score, and likely_dieting_rate are generally around the same. Overall however, the averages for all of these are quite low, the highest average of lifestyle_effort is slightly over 1.75 and for those who aren't taking medicine, same for activity_score is between 1.25 and 1.50, which is also for those who aren't taking medicine. Then the highest average for likely_dieting_rate is well under 0.25 and it is for those who are taking medicine for metabolic syndrome and other.

Who is healthy without medication?

```
In [14]: # Number of people not taking medication and are healthy
    df[(df['med_class'] == 'None') & (df['has_metabolic_syndrome'] == False)].sh

Out[14]: (528, 62)

In [15]: # Number of people not taking medication and are healthy
    df[(df['med_class'] == 'None') & (df['has_metabolic_syndrome'] == True)].sha

Out[15]: (349, 62)

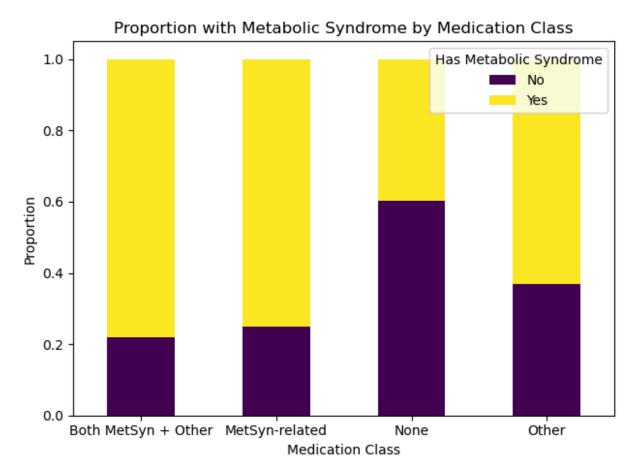
In [16]: # Number of people taking medication and are not healthy
    df[(df['med_class'] == 'MetSyn-related') & (df['has_metabolic_syndrome'] ==

Out[16]: (1561, 62)
```

```
In [17]: df[(df['med_class'] == 'MetSyn-related') & (df['has_metabolic_syndrome'] ==
Out[17]: (520, 62)
```

Metabolic syndrome vs med_class

```
In [18]: df.groupby('med_class')['has_metabolic_syndrome'].value_counts(normalize=Tru
Out[18]: med class
                               has_metabolic_syndrome
          Both MetSyn + Other
                               True
                                                          0.780488
                               False
                                                          0.219512
          MetSyn-related
                               True
                                                          0.750120
                               False
                                                          0.249880
         None
                               False
                                                          0.602052
                               True
                                                          0.397948
          0ther
                               True
                                                          0.632395
                               False
                                                          0.367605
          Name: proportion, dtype: float64
In [19]: # Get normalized proportions
         met_syn_dist = df.groupby('med_class')['has_metabolic_syndrome'].value_count
         # Plot as stacked bar
         met syn dist.plot(kind='bar', stacked=True, colormap='viridis')
         plt.title('Proportion with Metabolic Syndrome by Medication Class')
         plt.ylabel('Proportion')
         plt.xlabel('Medication Class')
         plt.legend(title='Has Metabolic Syndrome', labels=['No', 'Yes'])
         plt.xticks(rotation=0)
         plt.tight layout()
         plt.show()
```



the None medication class has the lowest proportion for those who have metabolic syndrome and the highest proportion for those who don't have metabolic syndrome. For the rest who do take any kind of medication, it shows that they are all similiar in that only 1/3 at the most don't have metabolic syndrome, and that the rest of the proportion do.

Does med_class improve prediction?

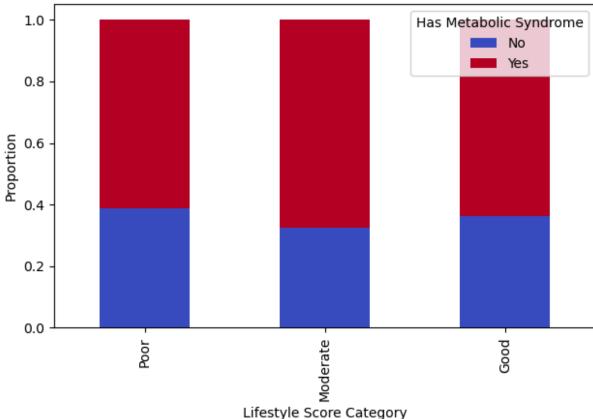
This project explores how well lifestyle and behavior predict metabolic syndrome in comparison to models that also include medication use. While medication is usually prescribed after diagnosis, and thus expected to correlate with the presence of metabolic syndrome, our goal is to understand its added predictive value. Through exploratory analysis and predictive modeling, we examine whether individuals on medications differ in their health outcomes and efforts compared to those who are not. Ultimately, we assess whether lifestyle-based indicators alone are strong enough for predictive modeling, reinforcing prevention-focused strategies.

```
# Plot
lifestyle_met_syn.plot(kind='bar', stacked=True, colormap='coolwarm')
plt.title('Metabolic Syndrome Prevalence by Lifestyle Category')
plt.ylabel('Proportion')
plt.xlabel('Lifestyle Score Category')
plt.legend(title='Has Metabolic Syndrome', labels=['No', 'Yes'])
plt.tight_layout()
plt.show()
```

/var/folders/z1/w_njtpr52ss65yn2_5wp9xfm0000gn/T/ipykernel_51747/2994981896. py:7: FutureWarning: The default of observed=False is deprecated and will be changed to True in a future version of pandas. Pass observed=False to retain current behavior or observed=True to adopt the future default and silence th is warning.

lifestyle_met_syn = df.groupby('lifestyle_bin')['has_metabolic_syndrome'].
value counts(normalize=True).unstack()





Surprisingly, the proportions generally seem the same, about 40% or slightly less of those with poor, moderate, or good lifestyles don't have metabolic syndrome, and the rest do.

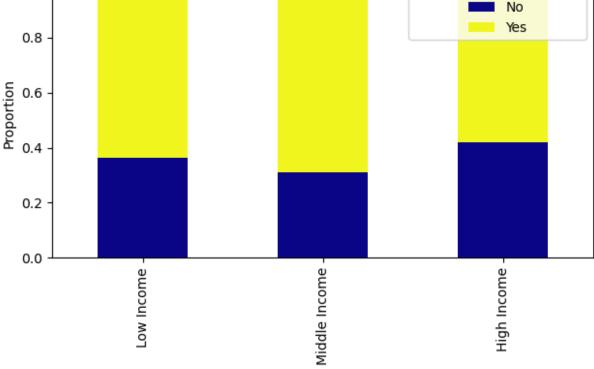
```
income_met_syn = df.groupby('income_level')['has_metabolic_syndrome'].value_
# Plot
income_met_syn.plot(kind='bar', stacked=True, colormap='plasma')
plt.title('Metabolic Syndrome Prevalence by Income Level')
plt.ylabel('Proportion')
plt.xlabel('Income Level (based on PIR)')
plt.legend(title='Has Metabolic Syndrome', labels=['No', 'Yes'])
plt.tight layout()
plt.show()
```

/var/folders/z1/w_njtpr52ss65yn2_5wp9xfm0000gn/T/ipykernel_51747/3630438039. py:7: FutureWarning: The default of observed=False is deprecated and will be changed to True in a future version of pandas. Pass observed=False to retain current behavior or observed=True to adopt the future default and silence th is warning.

income_met_syn = df.groupby('income_level')['has_metabolic_syndrome'].valu e counts(normalize=True).unstack()

Metabolic Syndrome Prevalence by Income Level



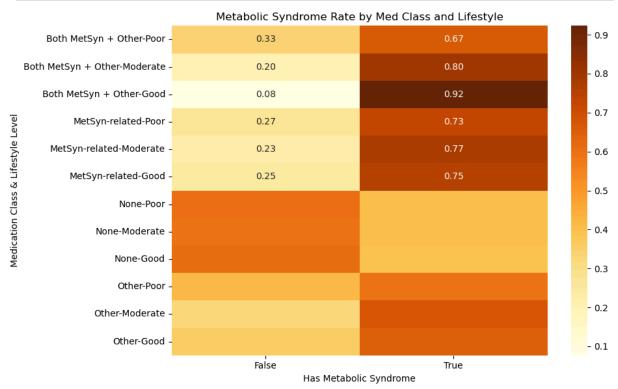


Income Level (based on PIR)

The same pattern is noticed across income levels, 40% or less of the proportion doesn't have metabolic syndrome while the rest do, and this is for low, middle, and high income individuals.

```
In [22]: # Cross-tab counts
         cross_tab = pd.crosstab([df['med_class'], df['lifestyle_bin']],
                                  df['has_metabolic_syndrome'],
                                  normalize='index')
```

```
# Plot as heatmap
plt.figure(figsize=(10,6))
sns.heatmap(cross_tab, annot=True, fmt=".2f", cmap='YlOrBr')
plt.title('Metabolic Syndrome Rate by Med Class and Lifestyle')
plt.xlabel('Has Metabolic Syndrome')
plt.ylabel('Medication Class & Lifestyle Level')
plt.tight_layout()
plt.show()
```

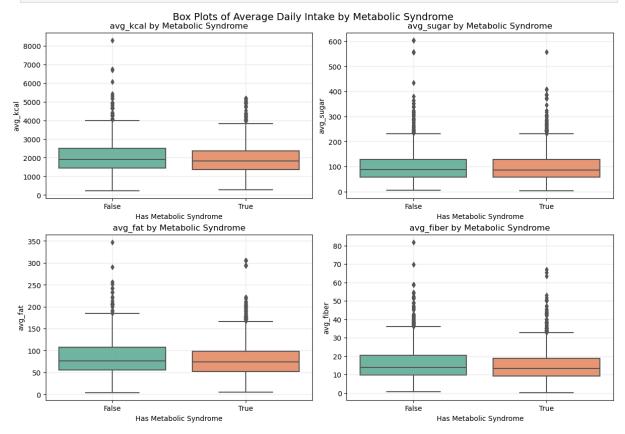


the cross tab is pretty much a mix of the previous plots and has simlar results

Does med_class improve prediction?

```
ax.grid(alpha=0.2)

plt.suptitle("Box Plots of Average Daily Intake by Metabolic Syndrome", y=1.
plt.savefig("boxplots_avg_intake.png", dpi=300, bbox_inches='tight')
plt.show()
```



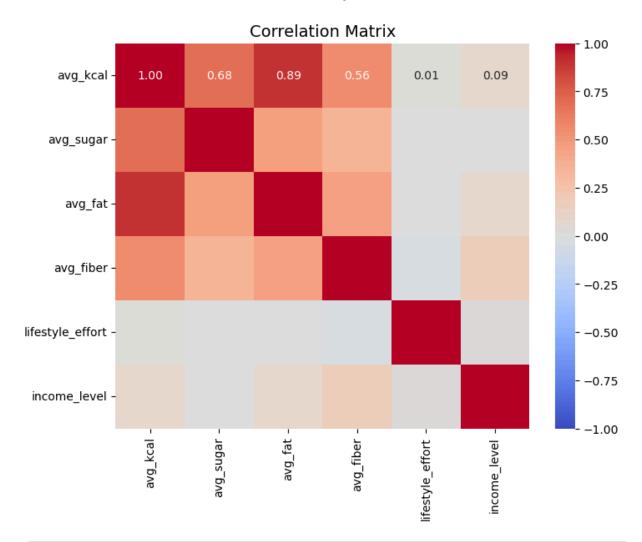
In [64]: df[df['has_metabolic_syndrome'] == True][avg_vars].describe()

Out[64]:		avg_kcal	avg_sugar	avg_fat	avg_fiber
	count	3941.000000	3941.000000	3941.000000	3941.000000
	mean	1906.121670	97.676370	79.839429	14.805379
	std	776.213294	57.399837	38.797628	7.921685
	min	283.500000	4.055000	5.105000	0.200000
	25%	1358.000000	57.595000	52.665000	9.250000
	50%	1833.500000	86.920000	74.560000	13.200000
	75%	2365.500000	127.990000	98.225000	18.750000
	max	5175.500000	556.920000	305.295000	67.100000

In [65]: df[df['has_metabolic_syndrome'] == False][avg_vars].describe()

Out[65]: avg_kcal avg_sugar avg_fat avg_fiber **count** 2219.000000 2219.000000 2219.000000 2219.000000 mean 2045.445020 100.574351 83.949349 15.957346 std 847.757015 63.069199 40.286931 9.313710 min 227.000000 6.120000 3.950000 0.650000 25% 1451.250000 57.825000 56.050000 9.650000 50% 1913.000000 88.095000 76.710000 13.900000 2491.000000 75% 128.655000 107.865000 20.300000 max 8313.000000 604.345000 347.585000 81.900000

```
numeric_df = df[['avg_kcal', 'avg_sugar', 'avg_fat', 'avg_fiber',
In [50]:
                          'lifestyle_effort', 'income_level']].copy()
         # Mapping income levels
         income_mapping = {'Low Income': 0, 'Middle Income': 1, 'High Income': 2}
         numeric_df['income_level'] = numeric_df['income_level'].map(income_mapping).
         # Pearson correlation
         corr_matrix = numeric_df.corr(method='pearson')
         # Simple heatmap
         plt.figure(figsize=(8, 6))
         sns.heatmap(
             corr_matrix,
             annot=True,
                            # show correlation values
             fmt=".2f",
                            # two decimal places
             cmap="coolwarm", # color palette
             vmin=-1, vmax=1 # correlation range
         plt.title("Correlation Matrix", fontsize=14)
         plt.savefig("correlation_matrix.png", dpi=300, bbox_inches='tight')
         plt.show()
```



In [34]: numeric_df.corr(method='pearson')

Out[34]:

:		avg_kcal	avg_sugar	avg_fat	avg_fiber	lifestyle_effort	income_le
	avg_kcal	1.000000	0.680347	0.892725	0.556251	0.008749	0.085
	avg_sugar	0.680347	1.000000	0.464911	0.348755	0.000237	0.001
	avg_fat	0.892725	0.464911	1.000000	0.448292	-0.002858	0.078
	avg_fiber	0.556251	0.348755	0.448292	1.000000	-0.045648	0.169
	lifestyle_effort	0.008749	0.000237	-0.002858	-0.045648	1.000000	0.023
	income_level	0.085876	0.001470	0.078461	0.169010	0.023422	1.000

In []: