Decomposition of Drug Substance Use on Health Dispositions

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2025-02-27

Preamble

Modules

In [1]:
```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import pyreadr
from random import random
from scipy.stats import chi2_contingency, skewnorm
import seaborn as sns
from sklearn.compose import ColumnTransformer
from sklearn.decomposition import PCA
from sklearn.ensemble import (
    GradientBoostingRegressor,
    RandomForestClassifier,
    RandomForestRegressor
)
from sklearn.feature_selection import SequentialFeatureSelector
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
from sklearn.metrics import (
    accuracy_score,
    classification_report,
    mean_absolute_error,
    mean_squared_error,
    r2_score
)
from sklearn.preprocessing import (
    LabelEncoder,
    MinMaxScaler,
    OneHotEncoder,
    OrdinalEncoder,
    PowerTransformer,
    QuantileTransformer
)
from statsmodels.stats.outliers_influence import variance_inflation_factor
```

Functions

In [2]:
```
def restrata_cat(cpd):
    i = random()
    for idx, x in cpd.items():
        if i > x:
            continue
        else:
            return idx
```

In [3]:
```
def restrata_num(mean, std, bounds = None, skew = 0):
    while True:
        x = skewnorm.rvs(a= skew, size= 1)[0]
        x = (x * std) + mean
        if bounds:
            if (x >= bounds[0]) and (x <= bounds[1]):
                return x
            else:
                continue
        else:
            return x
```

Imports

In [4]:
```
inread = pyreadr.read_r(".data/NSDUH_2023.Rdata")
```

Mining & Preprocessing

Subset features to information pertinent to reseach and analysis hypotheses. Research focuses on physical & mental health quality, drug dependencies, and recent drug uses. Most features utilized are recoded versions of original survey questions, as recoded by survey providers to create consistent, reliable, and viable data points.

Several features are not applicable to minors, which sources the primary reason for excluding them from final analysis. Segmentation analysis by respondent generation will be used to evaluate any necessary grouping or facetting in the report's findings.

In [5]:
```
subset = [
  # DEMOGRAPHICS
  # Variable                     Name                              Data Type     Pre
  # ---------------------------------------------------------------------------------
    'AGE3',                    # age                               cat int
    'IRSEX',                   # gender                            cat int
    'SEXIDENT22',              # sexual identity                   cat int
    'IRMARIT',                 # marital status                    cat int
    'IREDUHIGHST2',            # education level                   ord int
    'EDUSCHLGO',               # in-school status                  cat int
    'IRWRKSTAT',               # employment status                 cat int
  # 'MILSTAT',                 # military status                   cat int       Rem
    'ANYHLTI2',                # healthcare status                 cat int
    'GOVTPROG',                # income assistance status          cat int
    'INCOME',                  # annual income                     ord int
    'POVERTY3',                # poverty status                     ord int

  # HEALTH
  # Variable                    Name                                 Data Type
  # ----------------------------------------------------------------------------------
    'HEALTH',                  # health condition                   ord int
    'BMI2',                    # BMI                                float 9-69
    'KSSLR6MON',               # psych distress score               int 1-24
    'AMIPY',                   # any mental illness -yr             bool

  # DRUG USE
  # Variable                    Name                                 Data Type     Ris
  # ----------------------------------------------------------------------------------
    'IRPMNICDEP',              # nicotine dependence -yr            bool
    'IRMJFM',                  # pot freq use -mth                  int 1-30      1
    'IRCOCFM',                 # cocaine freq use -mth              int 1-30      6
    'IRCRKFM',                 # crack freq use -mth                int 1-30      6
    'IRHERFM',                 # heroine freq use -mth              int 1-30      7
    'IRHALLUC30N',             # hallucinogens freq use -mth        int 1-30      2
    'IRINHAL30N',              # inhalants freq use -mth            int 1-30      3
    'IRMETHAM30N',             # meth freq use -mth                 int 1-30      5
    'IRPNRNM30FQ',             # painmed freq use -mth              int 1-30      8
    'IRTRQNM30FQ',             # tranqs freq use -mth               int 1-30      4
    'IRSTMNM30FQ',             # stims freq use -mth                int 1-30      5
    'IRSEDNM30FQ'              # sedatives freq use -mth            int 1-30      4
]

data = inread['puf2023_102124'][subset]
data = data[data['AGE3'] > 3]
```

Relabel features for readability.

```
In [6]: renames = {
                'AGE3': 'generation',
            'ANYHLTI2': 'health_insurance_flag',
                'BMI2': 'bmi',
           'EDUSCHLGO': 'education_flag',
            'GOVTPROG': 'income_assistance_flag',
              'HEALTH': 'health_level',
             'IRCOCFM': 'cocaine_use',
              'INCOME': 'annual_income',
             'IRCRKFM': 'crack_use',
        'IREDUHIGHST2': 'education_level',
         'IRHALLUC30N': 'hallucinogen_use',
             'IRHERFM': 'heroine_use',
          'IRINHAL30N': 'inhalant_use',
             'IRMARIT': 'marital',
         'IRMETHAM30N': 'amphetamine_use',
              'IRMJFM': 'marajuana_use',
          'IRPMNICDEP': 'nicotine_dependence_flag',
         'IRPNRNM30FQ': 'opioid_use',
         'IRSEDNM30FQ': 'sedative_use',
               'IRSEX': 'gender',
         'IRSTMNM30FQ': 'stimulant_use',
           'IRWRKSTAT': 'employment',
     'IRTRQNM30FQ': 'tranquilizer_use',
       'KSSLR6MON': 'psychological_distress',
#        'MILSTAT': 'military_service',
        'POVERTY3': 'poverty_level',
      'SEXIDENT22': 'sexuality',
           'AMIPY': 'mental_illness_flag'
}

data = data.rename(columns= renames)
```

Recoding

Recoding variables from system codes to readable elements. Some overwriting recoding has been done to retain usability of some features, and is annotated accordingly.

Recode Edits:

1. Annual Income was grouped into survey ranges; groups are being populated to maintain uniform distributions within each band to allow smoother normalization in model preprocessing efforts.
2. Slight deviations of 0-3 years were made when switching age buckets to generations and ages were grouped into the generation which majority-mapped to the applicable range.

In [7]:
```
# recoding
recodes = {
    'education_flag': {
         1: 'True',
         2: 'False',
        11: 'True'
    },
    'education_level': {        # effective US grade level
         1: 5,
         2: 6,
         3: 7,
         4: 8,
         5: 9,
         6: 10,
         7: 11,
         8: 12,
         9: 12,
        10: 13,
        11: 14
    },
    'employment': {
         1: 'Full Employment',
         2: 'Partial Employment',
         3: 'Unemployed',
         4: pd.NA,
        99: pd.NA
    },
    'gender': {
        1: 'Male',
        2: 'Female'
    },
    'generation': {              # see recode note 2
         1: 'A',
         2: 'Z',
         3: 'Zillennial',
         4: 'Zillennial',
         5: 'Zillennial',
         6: 'Zillennial',
         7: 'Millennial',
         8: 'Millennial',
         9: 'Xennial',
        10: 'X',
        11: 'Baby Boomer'
    },
    'health_insurance_flag': {
        1: 'True',
        2: 'False'
    },
    'health_level': {
        1: 5,
        2: 4,
        3: 3,
        4: 2,
        5: 1
    },
    'income_assistance_flag': {
        1: 'True',
        2: 'False'
    },
    'marital': {
        None: 'Single',
           1: 'Married',
           2: 'Widowed',
           3: 'Divorced',
           4: 'Single'

    },
    'nicotine_dependence_flag': {
        0: 'False',
        1: 'True'
    },
    'poverty_level': {
        1: 'Below',
        2: 'Baseline',
        3: 'Above'
    },
    'sexuality': {
        1: 'Heterosexual',
        2: 'Homosexual',
        3: 'Bisexual'
    },
    'mental_illness_flag': {
        0: 'False',
        1: 'True'
    }
}

for c in recodes:
    mapper = recodes[c]
    data[c] = data[c].map(mapper)
```

`Drug Use` fields have 90-series codes referring to insufficient, bad, or non-applicable data. Features with such values are recoded to no use for conservative utility of the fields and biases against the hypothesis to increate the threshold of positive analysis results.

In [8]:
```
reranges = [
    'amphetamine_use',
    'cocaine_use',
    'crack_use',
    'hallucinogen_use',
    'heroine_use',
    'inhalant_use',
    'marajuana_use',
    'opioid_use',
    'sedative_use',
    'stimulant_use',
    'tranquilizer_use'
]

for c in reranges:
    data[c] = data[c].apply(lambda x: 0 if x > 30 else x)
```

Clean datatypes

In [9]:
```
data['education_level'] = data['education_level'].astype(float)
data['annual_income'] = data['annual_income'].astype(float)
```

Missing at Random Analysis

Several features show missing data. Missing at Random (MAR) analyses are done to reduce inter-dependency analysis and feature size for the model selection stages. Dependency is tested via Chi-Squared tests at the α = 0.05 level.

In [10]:
```
data.isnull().sum()
```

```
Out[10]: generation                  0
         gender                      0
         sexuality                4956
         marital                     0
         education_level             0
         education_flag           1688
         employment              13444
         health_insurance_flag    1740
         income_assistance_flag      0
         annual_income               0
         poverty_level              11
         health_level               14
         bmi                      1964
         psychological_distress      0
         mental_illness_flag         0
         nicotine_dependence_flag    0
         marajuana_use               0
         cocaine_use                 0
         crack_use                   0
         heroine_use                 0
         hallucinogen_use            0
         inhalant_use                0
         amphetamine_use             0
         opioid_use                  0
         tranquilizer_use            0
         stimulant_use               0
         sedative_use                0
         dtype: int64
```

```
In [11]: data_missing = data.isna()
colset = []

for i in range(len(data_missing.columns)):
    for j in range(i, len(data_missing.columns)):
        combo = sorted([data_missing.columns[i], data_missing.columns[j]])
        if combo[0] == combo[1]:
            continue
        if combo not in colset:
            colset.append(combo)

missing_tests = []
for a, b in colset:
    contingency = pd.crosstab(data_missing[a], data_missing[b])
    chi2, p, dof, expected = chi2_contingency(contingency)
    if p < .05:
        result = 'Dependent'
    else:
        result = 'Independent'
    if dof > 0:
        missing_tests.append(
            (a, b, round(p, 4), result)
    )

cross_missing = pd.DataFrame(missing_tests, columns= ['feature_a', 'feature_b', 'p_
cross_missing = cross_missing[cross_missing['dependency'] == 'Dependent']
cross_missing = cross_missing.sort_values(['p_value', 'feature_a', 'feature_b']).re
cross_missing
```

Out[11]:

	feature_a	feature_b	p_value	dependency
0	bmi	education_flag	0.0000	Dependent
1	bmi	employment	0.0000	Dependent
2	bmi	health_insurance_flag	0.0000	Dependent
3	bmi	health_level	0.0000	Dependent
4	bmi	sexuality	0.0000	Dependent
5	education_flag	employment	0.0000	Dependent
6	education_flag	health_insurance_flag	0.0000	Dependent
7	education_flag	health_level	0.0000	Dependent
8	education_flag	sexuality	0.0000	Dependent
9	employment	sexuality	0.0000	Dependent
10	health_insurance_flag	health_level	0.0000	Dependent
11	health_insurance_flag	sexuality	0.0000	Dependent
12	health_level	sexuality	0.0000	Dependent
13	employment	health_insurance_flag	0.0316	Dependent

We can see the dependency tests show 7 features dependent on each other in some combination. Preliminary EDA revealed other features that were revoked in report refinement (i.e. `military_service`) and others have a real world relationship we expect some dependency on (i.e. `employment` and `health_insurance_flag`). Results indicate the majority of these nulls can be restratified with appropriate filling scalers and transformations, while the `employment` and `health_insurance_flag` pair may not be applicable due to them not assuredly be MAR given the confidence bounds of the test.

Null Cleanup & Restrata

This is done only on previously-identified applicable fields (or on fields that did not result in the MAR analysis) that can be reasonably expected to not impact clustering or predictive analysis and is not done on fields with high null content.

In [12]:

```
restratas_cat = [
    'education_flag',
    'health_insurance_flag',
    'health_level',
    'psychological_distress',
    'sexuality'
]
```

```
for c in restratas_cat:
    a = data[c].value_counts(normalize= True)
    cpd = a.sort_index().cumsum()
    data[c] = data[c].apply(lambda x: x if pd.notna(x) else restrata_cat(cpd))
```

In [13]:
```
restratas_num = [
    'bmi'
]

for c in restratas_num:
    a, b = data[c].min(), data[c].max()
    m, d, s = data[c].mean(), data[c].std(), data[c].skew()
    data[c] = data[c].apply(lambda x: x if pd.notna(x) else restrata_num(m, d, boun
```

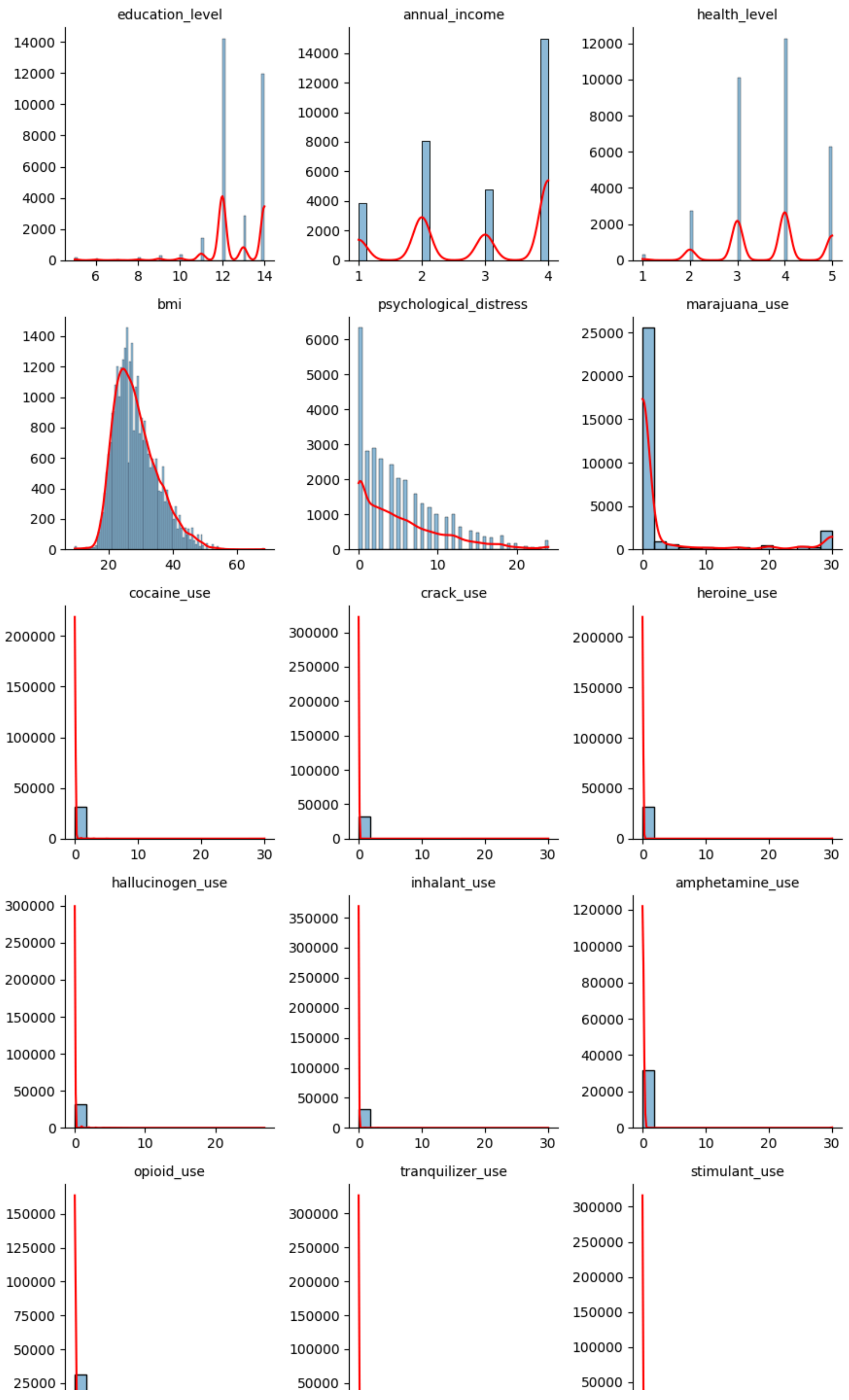
All remaining nulls are dropped to create the final cleaned dataset for modeling purposes.

In [14]:
```
data_clean = data.dropna()
data_clean.shape
```

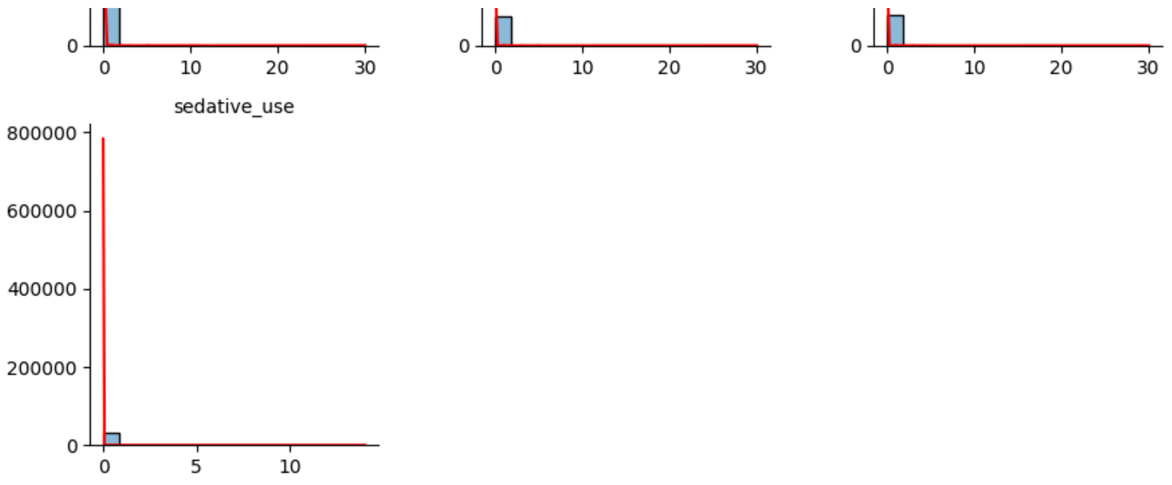
Out[14]:
```
(31683, 27)
```

Distribution Analysis

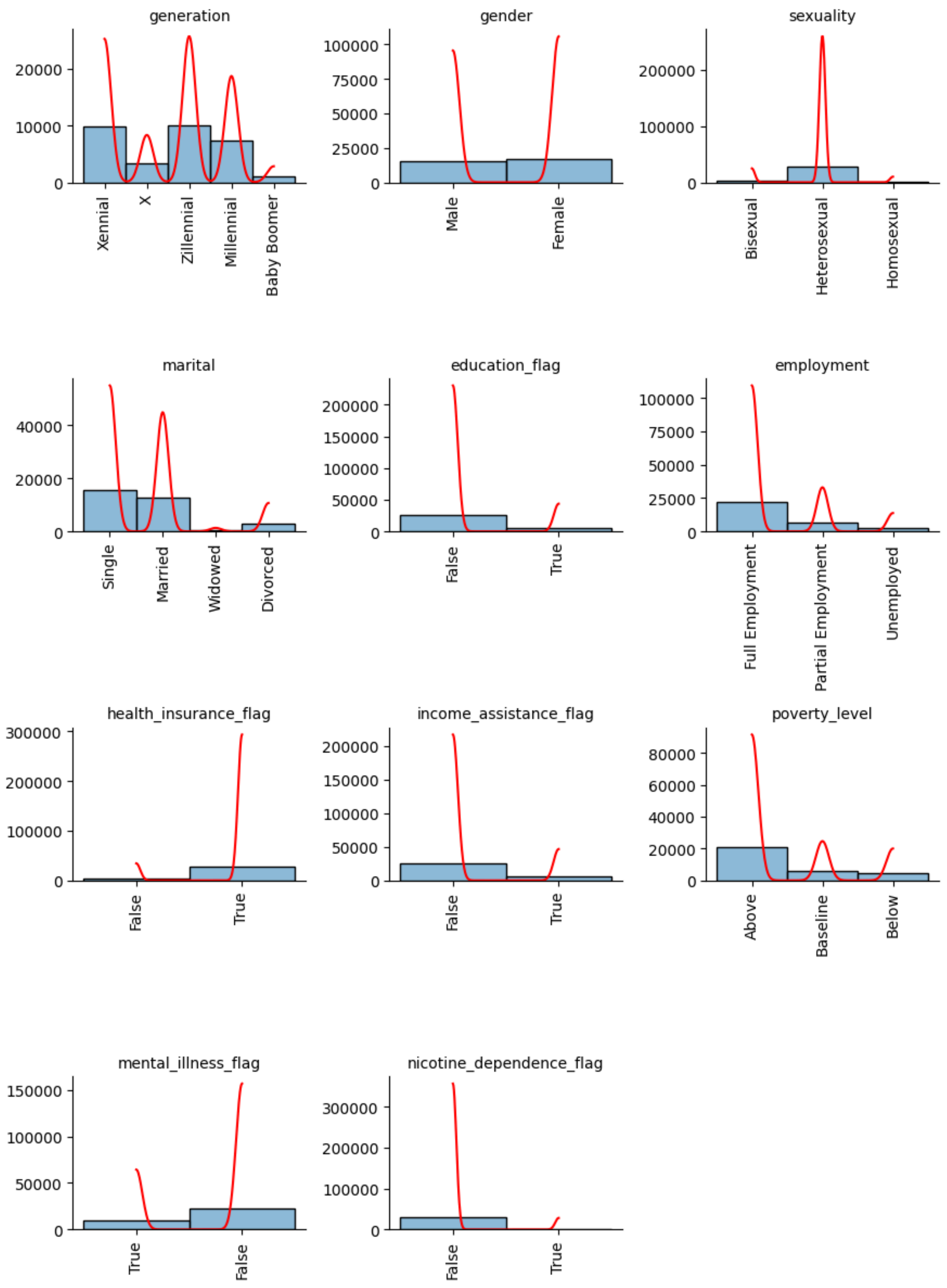
In [15]:
```
cols_nums = data_clean.select_dtypes(include= 'number').columns.tolist()
df_melt = data_clean[cols_nums].melt(
    var_name= 'col',
    value_name='val'
)

g = sns.FacetGrid(
    df_melt,
    col= 'col',
    col_wrap= 3,
    sharex= False,
    sharey= False
)
g.map(
    sns.histplot,
    'val',
    kde= True
).add_legend()

for ax in g.axes.flat:
    for line in ax.lines:
        line.set_color('red')


g.set_axis_labels('', '')
g.set_titles("{col_name}")
g.tight_layout()
plt.show()
```



education_level
annual_income
health_level
bmi
psychological_distress
marajuana_use
cocaine_use
crack_use
heroine_use
hallucinogen_use
inhalant_use
amphetamine_use
opioid_use
tranquilizer_use
stimulant_use



In [16]:
```python
cols_cats = data_clean.select_dtypes(exclude= 'number').columns.tolist()
df_melt = data_clean[cols_cats].melt(
    var_name= 'col',
    value_name='val'
)

g = sns.FacetGrid(
    df_melt,
    col='col',
    col_wrap= 3,
    sharex= False,
    sharey= False
)
g.map(
    sns.histplot,
    'val',
    kde= True
).add_legend()

for ax in g.axes.flat:
    for label in ax.get_xticklabels():
        label.set_rotation(90)
    for line in ax.lines:
        line.set_color('red')

# Adjust layout
g.set_axis_labels('', '')
g.set_titles("{col_name}")
g.tight_layout()
plt.show()
```



Scaling and Preprocessing

Distribution analysis shows the majority of features are not applicable to standard transformations for modeling. Drug use fields were chosen to apply `PowerTransformation` in order to handle the heavily skewed data creating outlier and distortion. Each modeling section creates its transformations applicable to the model subsets.

Performancce was evaluated in some model applications on the transformations used in liew of `PowerTransformation` with negligible-to-marginally negative results over the selected distribution. Those results are not shown here for concision.

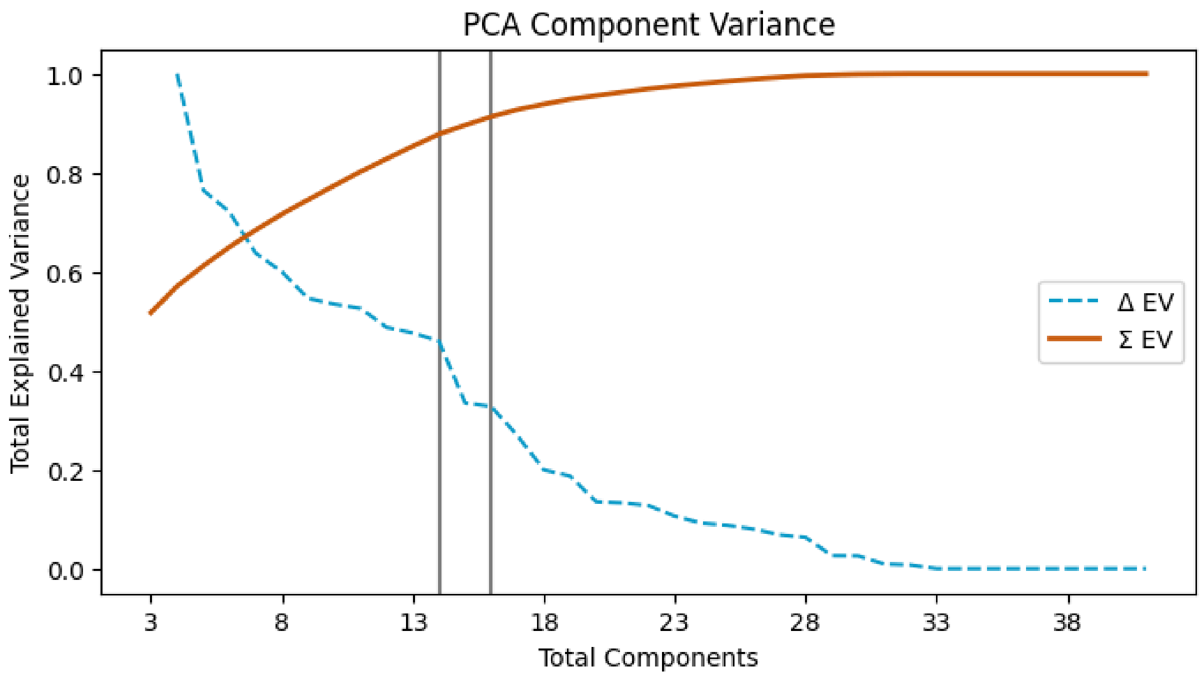
In [17]:
```
cols_minmax = [
   'bmi'
]

cols_onehot = [
    'education_flag',
    'employment',
    'gender',
    'health_insurance_flag',
    'income_assistance_flag',
    'marital',
    'mental_illness_flag',
    'nicotine_dependence_flag',
    'poverty_level',
    'sexuality'
]

cols_ordinal = [
    'generation'
]

cols_poweryeo = [
    'amphetamine_use',
    'cocaine_use',
    'crack_use' ,
    'hallucinogen_use',
    'heroine_use',
    'inhalant_use',
    'marajuana_use',
    'opioid_use',
    'psychological_distress',
    'sedative_use',
    'stimulant_use',
    'tranquilizer_use'
]

cols_quantnorm = [
    'education_level',
    'health_level'
]

cols_quantuni = [
   'annual_income'
]
```

Principal Component Analysis

The goal of this PCA is to try and identify key features that heavily-classify the data. Outputs from the PCA will be used to see if the highest-classifying features can be used to accurately and simply classify the data in other models.

In [18]:
```
# preprocess transformations
tf_minmax = MinMaxScaler()
tf_onehot = OneHotEncoder()
tf_ordinal = OrdinalEncoder()
tf_poweryeo = PowerTransformer(method= 'yeo-johnson')
tf_quantnorm = QuantileTransformer(output_distribution= 'normal')
tf_quantuni = QuantileTransformer(output_distribution= 'uniform')

preprocessor = ColumnTransformer(
    transformers=[
        ('tf1', tf_minmax, cols_minmax),
        ('tf2', tf_onehot, cols_onehot),
        ('tf3', tf_ordinal, cols_ordinal),
        ('tf5', tf_poweryeo, cols_poweryeo),
        ('tf6', tf_quantnorm, cols_quantnorm),
        ('tf7', tf_quantuni, cols_quantuni)
    ]
)

data_processed = preprocessor.fit_transform(data_clean)

# explained variances
evr = []
for n in range(3, len(preprocessor.get_feature_names_out())):
    model_pca = PCA(n_components= n)
    pca_fit = model_pca.fit(data_processed)
    evr.append((n, sum(model_pca.explained_variance_ratio_)))
```

In [19]:
```
z = []
for i, (x, y) in enumerate(evr):
    if i == len(evr) - 1:
        continue
    z.append(evr[i + 1][1] - y)

z = z / max(z)
x, y = zip(*evr)

plt.figure(figsize= (8, 4))
plt.axvline(x= 14, color= 'gray')
plt.axvline(x= 16, color= 'gray')
plt.plot(
    x[1:], z,
    linestyle= '--',
    color= '#0c9bc9',
    label= 'Δ EV'
)
plt.plot(
    x, y,
    linestyle= '-',
    color= '#c95b0c',
    linewidth= 2,
    label= 'Σ EV'
)
plt.xticks(np.arange(3, max(x) + 1, 5))
plt.xlabel('Total Components')
plt.ylabel('Total Explained Variance')
plt.title('PCA Component Variance')
plt.legend(loc= 'center right')
plt.show()
```



In [20]:
```
oc = [14, 16]
for i in oc:
    model_pca = PCA(n_components= i)
    pca_fit = model_pca.fit(data_processed)
    oev = sum(model_pca.explained_variance_ratio_)
    print(f"Optimal Explained Variance of {oev:.4f} with {i} Components")
```

```
Optimal Explained Variance of 0.8782 with 14 Components
Optimal Explained Variance of 0.9136 with 16 Components
```

In [21]:
```
pca_feature_names = preprocessor.get_feature_names_out()
pca_top_components = model_pca.components_[:max(oc)]
pca_components = pd.DataFrame()

for i, component in enumerate(pca_top_components):
    sorted_feature_idx = np.argsort(np.abs(component))[::-1]
    sorted_feature_names = preprocessor.get_feature_names_out()[sorted_feature_idx]
    sorted_loadings = component[sorted_feature_idx]

    row = dict(zip(sorted_feature_names, sorted_loadings))
    pca_components = pd.concat(
        [pca_components, pd.DataFrame([row])],
        ignore_index= True
    )
```

Borda Influence Scores

Results showed 16 component vectors the optimal total variance coverage. To determine which features have the highest influence over the components, we will use weighted borda summations where each subsequent component vector has a linearly devalued weight and the borda score values of each vector are calculated. The lower the weighted score, the more value it contributed to the explained variance within each component vector.

In [22]:
```
pca_compranks = pca_components.T.abs().rank(method= 'dense', ascending= False)
for i in pca_compranks.columns:
    pca_compranks[i] = pca_compranks[i] * (16 - i)
borda_scores = round(pca_compranks.sum(axis= 1) / 16, 1)
borda_scores.sort_values(ascending= True)[:10]
```

Out[22]:
```
tf5__marajuana_use               58.3
tf3__generation                  65.9
tf5__psychological_distress      69.1
tf5__amphetamine_use             79.6
tf5__cocaine_use                 84.6
tf5__opioid_use                  85.8
tf5__heroine_use                 92.2
tf5__tranquilizer_use           101.4
tf5__crack_use                  101.8
tf5__hallucinogen_use           103.7
dtype: float64
```

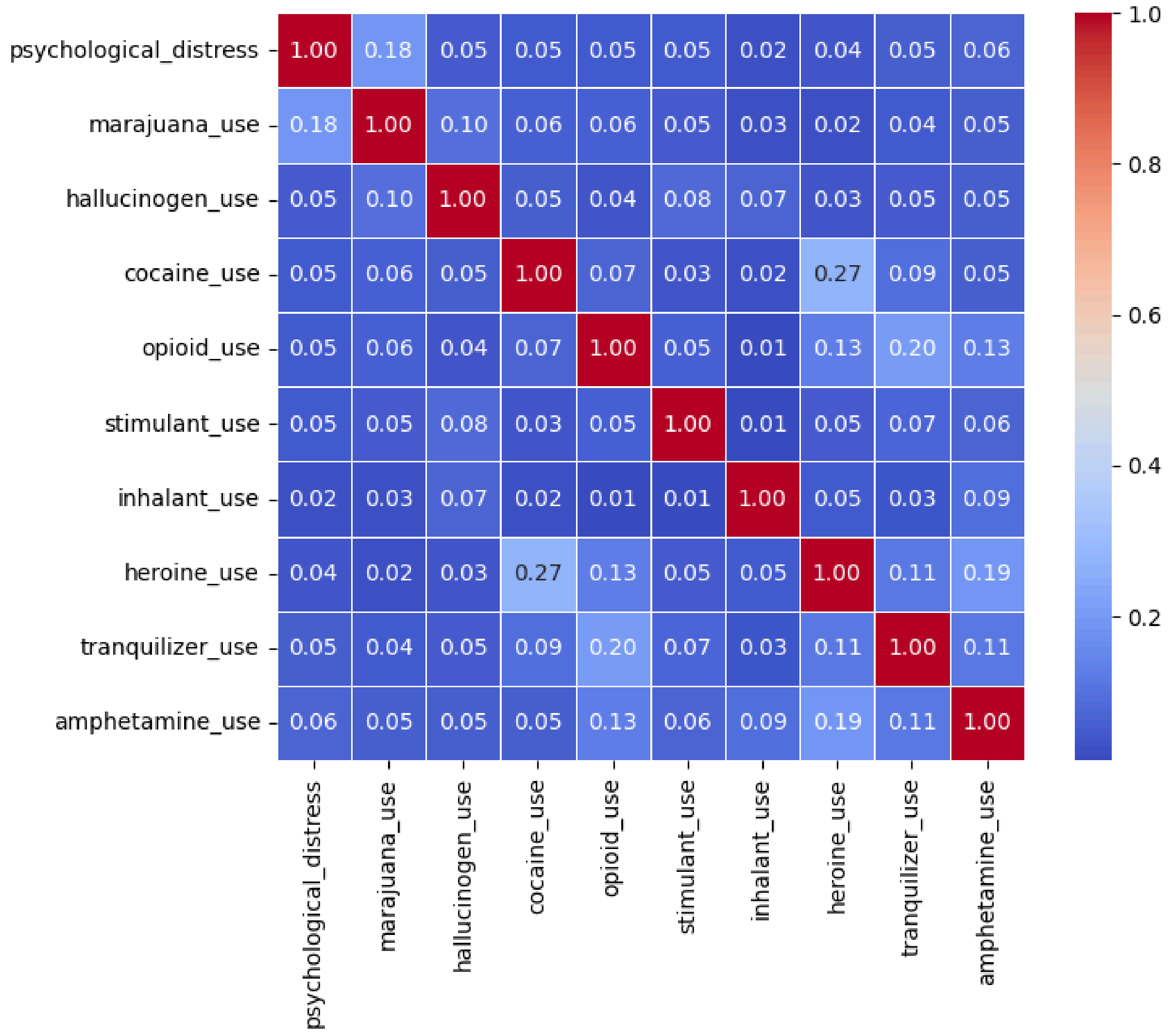
Multicolinearity

The downside is a potential concern of multicolinearity or intra-dependence, which will be evaluated next utilizing a variance inflation factor analysis.

In [23]:
```
mc_cols = [
    'psychological_distress',
    'marajuana_use',
    'hallucinogen_use',
    'cocaine_use',
    'opioid_use',
    'stimulant_use',
    'inhalant_use',
    'heroine_use',
    'tranquilizer_use',
    'amphetamine_use'
]
correlation_matrix = data[mc_cols].corr()

vif_data = pd.DataFrame()
vif_data['feature_name'] = data[mc_cols].columns
vif_data['vif_score'] = [variance_inflation_factor(data[mc_cols].values, i) for i i

print("\nVariance Inflation Factor (VIF):\n", vif_data)
```

```
Variance Inflation Factor (VIF):
              feature_name  vif_score
0  psychological_distress   1.180237
1           marajuana_use   1.182923
2        hallucinogen_use   1.028839
3             cocaine_use   1.094480
4              opioid_use   1.071641
5           stimulant_use   1.020335
6            inhalant_use   1.014413
7             heroine_use   1.137491
8        tranquilizer_use   1.067827
9         amphetamine_use   1.074707
```

In [24]:
```python
plt.figure(figsize= (8, 6))
sns.heatmap(
    correlation_matrix,
    annot= True,
    cmap= 'coolwarm',
    fmt= '.2f',
    linewidths= 0.5,
    square= True
)
plt.show()
```



	psychological_distress	marajuana_use	hallucinogen_use	cocaine_use	opioid_use	stimulant_use	inhalant_use	heroine_use	tranquilizer_use	amphetamine_use
psychological_distress	1.00	0.18	0.05	0.05	0.05	0.05	0.02	0.04	0.05	0.06
marajuana_use	0.18	1.00	0.10	0.06	0.06	0.05	0.03	0.02	0.04	0.05
hallucinogen_use	0.05	0.10	1.00	0.05	0.04	0.08	0.07	0.03	0.05	0.05
cocaine_use	0.05	0.06	0.05	1.00	0.07	0.03	0.02	0.27	0.09	0.05
opioid_use	0.05	0.06	0.04	0.07	1.00	0.05	0.01	0.13	0.20	0.13
stimulant_use	0.05	0.05	0.08	0.03	0.05	1.00	0.01	0.05	0.07	0.06
inhalant_use	0.02	0.03	0.07	0.02	0.01	0.01	1.00	0.05	0.03	0.09
heroine_use	0.04	0.02	0.03	0.27	0.13	0.05	0.05	1.00	0.11	0.19
tranquilizer_use	0.05	0.04	0.05	0.09	0.20	0.07	0.03	0.11	1.00	0.11
amphetamine_use	0.06	0.05	0.05	0.05	0.13	0.06	0.09	0.19	0.11	1.00

Fortunately all features showed negligible correlation rates and low VIF scores, meaning all features are independently and collectively viable influencers to the analysis.

Prediction Models: **Health Level**

Challenge: `Health Level` is a respondent-percieved status on their overall health disposition, with 1-5 representing bad to great. Can this be directly imputed from given data? Can it be imputed specifically from drug use and addiction statuses?

Full Featureset

In [25]:
```
# preprocess transformers
tf_minmax = MinMaxScaler()
tf_onehot = OneHotEncoder()
tf_ordinal = OrdinalEncoder()
tf_poweryeo = PowerTransformer(method= 'yeo-johnson')
tf_quantnorm = QuantileTransformer(output_distribution= 'normal')
tf_quantuni = QuantileTransformer(output_distribution= 'uniform')

# pipeline
preprocessor = ColumnTransformer(
    transformers=[
        ('tf1', tf_minmax, cols_minmax),
        ('tf2', tf_onehot, cols_onehot),
        ('tf3', tf_ordinal, cols_ordinal),
        ('tf5', tf_poweryeo, cols_poweryeo),
        ('tf6', tf_quantnorm, [x for x in cols_quantnorm if x != 'health_level']),
        ('tf7', tf_quantuni, cols_quantuni)
    ]
)

# datasplit
X_train, X_test, y_train, y_test = train_test_split(
    data_clean.drop(columns= 'health_level'),
    data_clean['health_level'],
    train_size= .2,
    random_state= 13
)

# apply fit transformations
X_train_scaled = preprocessor.fit_transform(X_train)
X_test_scaled = preprocessor.transform(X_test)
```

Logistic Classifier

In [26]:
```
model = LogisticRegression(random_state= 13, max_iter= 1000)
model.fit(X_train_scaled, y_train)

y_pred = model.predict(X_test_scaled)
y_pred_train = model.predict(X_train_scaled)
```

```
acc = accuracy_score(y_train, y_pred_train)

print(f"Overall Train Accuracy: {acc:.4f}")

acc = accuracy_score(y_test, y_pred)
mae = mean_absolute_error(y_test, y_pred)

print(f"Overall Test Accuracy: {acc:.4f}")
print(f"Mean Absolute Error: {mae:.4f}")
```

```
Overall Train Accuracy: 0.4575
Overall Test Accuracy: 0.4477
Mean Absolute Error: 0.6364
```

Logistic Forward Selection

In [27]:
```
model = LogisticRegression(max_iter= 500, random_state= 13)
sfs = SequentialFeatureSelector(
    model,
    n_features_to_select= 'auto',
    direction= 'forward',
    cv= 5
)
sfs.fit(X_train_scaled, y_train)

selected_features = sfs.get_support(indices= True)
X_train_selected = X_train_scaled[:, selected_features]
X_test_selected = X_test_scaled[:, selected_features]
model.fit(X_train_selected, y_train)

y_pred = model.predict(X_test_selected)
y_pred_train = model.predict(X_train_selected)

acc = accuracy_score(y_train, y_pred_train)

print(f"Overall Train Accuracy: {acc:.4f}")

acc = accuracy_score(y_test, y_pred)
mae = mean_absolute_error(y_test, y_pred)

print(f"Overall Test Accuracy: {acc:.4f}")
print(f"Mean Absolute Error: {mae:.4f}")
print("\nClassification Report:\n", classification_report(y_test, y_pred))
```

```
Overall Train Accuracy: 0.4566
Overall Test Accuracy: 0.4481
Mean Absolute Error: 0.6342

Classification Report:
              precision    recall  f1-score   support

         1.0       0.17      0.00      0.01       229
         2.0       0.20      0.00      0.00      2175
         3.0       0.44      0.45      0.45      8068
         4.0       0.45      0.73      0.56      9792
         5.0       0.46      0.11      0.18      5083

    accuracy                           0.45     25347
   macro avg       0.34      0.26      0.24     25347
weighted avg       0.43      0.45      0.39     25347
```

In [28]:
```
preprocessor.get_feature_names_out()[selected_features]
```

Out[28]:
```
array(['tf1__bmi', 'tf2__education_flag_False',
       'tf2__education_flag_True', 'tf2__employment_Unemployed',
       'tf2__marital_Divorced', 'tf2__marital_Married',
       'tf2__nicotine_dependence_flag_False',
       'tf2__nicotine_dependence_flag_True', 'tf2__sexuality_Homosexual',
       'tf3__generation', 'tf5__amphetamine_use', 'tf5__crack_use',
       'tf5__hallucinogen_use', 'tf5__heroine_use', 'tf5__inhalant_use',
       'tf5__marajuana_use', 'tf5__psychological_distress',
       'tf5__sedative_use', 'tf5__stimulant_use', 'tf6__education_level'],
      dtype=object)
```

Random Forest

In [29]:
```
model = RandomForestRegressor(n_estimators= 50, random_state= 13)
model.fit(X_train_scaled, y_train)

y_pred = model.predict(X_test_scaled)
y_pred_train = model.predict(X_train_scaled)

r2 = r2_score(y_train, y_pred_train)

print(f"Train R² Score: {r2:.4f}")

mae = mean_absolute_error(y_test, y_pred)
r2 = r2_score(y_test, y_pred)

print(f"Test R² Score: {r2:.4f}")
print(f"Mean Absolute Error: {mae:.4f}")
```

```
Train R² Score: 0.8710
Test R² Score: 0.1186
Mean Absolute Error: 0.6909
```

Gradient Booster

```
In [30]: model = GradientBoostingRegressor(n_estimators= 50, learning_rate=0.1, max_depth=3,
         model.fit(X_train_scaled, y_train)
         y_pred = model.predict(X_test_scaled)

         r2 = r2_score(y_train, y_pred_train)
         print(f"Train R² Score: {r2:.4f}")

         r2 = r2_score(y_test, y_pred)
         mse = mean_squared_error(y_test, y_pred)

         print(f"Test R² Score: {r2:.4f}")
         print(f"Mean Squared Error: {mse:.4f}")
```

```
Train R² Score: 0.8710
Test R² Score: 0.1879
Mean Squared Error: 0.6848
```

Drug Use Sub-Featureset

```
In [31]: drug_subset = [
             'mental_illness_flag',
             'nicotine_dependence_flag',
             'amphetamine_use',
             'cocaine_use',
             'crack_use' ,
             'hallucinogen_use',
             'heroine_use',
             'inhalant_use',
             'marajuana_use',
             'opioid_use',
             'sedative_use',
             'stimulant_use',
             'tranquilizer_use',
             'health_level'
         ]
```

```
In [32]: data_clean_subset1 = data_clean[drug_subset]
         tf_onehot = OneHotEncoder(drop= 'first')
         tf_poweryeo = PowerTransformer(method= 'yeo-johnson')

         preprocessor = ColumnTransformer(
             transformers=[
                 ('tf2', tf_onehot, [
                     'mental_illness_flag',
                     'nicotine_dependence_flag'
                 ]),
                 ('tf5', tf_poweryeo, [
                     'amphetamine_use',
                     'cocaine_use',
                     'crack_use' ,
                     'hallucinogen_use',
                     'heroine_use',
                     'inhalant_use',
                     'marajuana_use',
                     'opioid_use',
                     'sedative_use',
                     'stimulant_use',
                     'tranquilizer_use'
                 ])
             ]
         )

         X_train, X_test, y_train, y_test = train_test_split(
             data_clean_subset1.drop(columns= 'health_level'),
             data_clean_subset1['health_level'],
             train_size= .2,
             random_state= 13
         )

         X_train_scaled = preprocessor.fit_transform(X_train)
         X_test_scaled = preprocessor.transform(X_test)
```

Logistic Classifier

In [33]:
```
model = LogisticRegression(random_state= 13, max_iter= 1000)
model.fit(X_train_scaled, y_train)
y_pred = model.predict(X_test_scaled)
y_pred_train = model.predict(X_train_scaled)

acc = accuracy_score(y_train, y_pred_train)

print(f"Overall Train Accuracy: {acc:.4f}")

acc = accuracy_score(y_test, y_pred)
mae = mean_absolute_error(y_test, y_pred)

print(f"Overall Test Accuracy: {acc:.4f}")
print(f"Mean Absolute Error: {mae:.4f}")
```

```
Overall Train Accuracy: 0.4217
Overall Test Accuracy: 0.4086
Mean Absolute Error: 0.6752
```

Generation Predictor

In [34]:
```
generation_subset = [
    'generation',
    'mental_illness_flag',
    'nicotine_dependence_flag',
    'amphetamine_use',
    'cocaine_use',
    'crack_use' ,
    'hallucinogen_use',
    'heroine_use',
    'inhalant_use',
    'marajuana_use',
    'opioid_use',
    'sedative_use',
    'stimulant_use',
    'tranquilizer_use'
]
```

Random Forest

In [35]:

```
data_clean_subset2 = data_clean[generation_subset].copy()
tf_poweryeo = PowerTransformer(method= 'yeo-johnson')

label_encoder = LabelEncoder()
data_clean_subset2['generation'] = \
    label_encoder.fit_transform(data_clean_subset2['generation'])
data_clean_subset2['mental_illness_flag'] = \
    data_clean_subset2['mental_illness_flag'].map({'True': 1, 'False': 0})
data_clean_subset2['nicotine_dependence_flag'] = \
    data_clean_subset2['nicotine_dependence_flag'].map({'True': 1, 'False': 0})
data_clean_subset2[[
    'amphetamine_use',
    'cocaine_use',
    'crack_use' ,
    'hallucinogen_use',
    'heroine_use',
    'inhalant_use',
    'marajuana_use',
    'opioid_use',
    'sedative_use',
    'stimulant_use',
    'tranquilizer_use'
]] = tf_poweryeo.fit_transform(data_clean_subset2[[
    'amphetamine_use',
    'cocaine_use',
    'crack_use' ,
    'hallucinogen_use',
    'heroine_use',
    'inhalant_use',
    'marajuana_use',
    'opioid_use',
    'sedative_use',
    'stimulant_use',
    'tranquilizer_use'
]])

X = data_clean_subset2.drop(columns=['generation'])
y = data_clean_subset2['generation']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size= 0.2, random_st
model = RandomForestClassifier(n_estimators= 50, random_state= 13)

model.fit(X_train, y_train)

y_pred = model.predict(X_test)
y_pred_train = model.predict(X_train)

r2 = accuracy_score(y_train, y_pred_train)
print(f"Overall Train Accuracy: {r2:.4f}")

r2 = accuracy_score(y_test, y_pred)
```

```
mae = mean_absolute_error(y_test, y_pred)

print(f"Overall Test Accuracy: {r2:.4f}")
print(f"Mean Absolute Error: {mae:.4f}")
```

```
Overall Train Accuracy: 0.3743
Overall Test Accuracy: 0.3618
Mean Absolute Error: 1.0642
```

Support Vector Machines

In [36]:
```
model = SVC(kernel='rbf', C= 1.0, gamma= 'scale', random_state= 13)
model.fit(X_train, y_train)

y_pred = model.predict(X_test)
y_pred_train = model.predict(X_train)

acc = accuracy_score(y_train, y_pred_train)
print(f"Overall Train Accuracy: {acc:.4f}")

acc = accuracy_score(y_test, y_pred)
mae = mean_absolute_error (y_test, y_pred)

cr = classification_report(y_test, y_pred, target_names= label_encoder.classes_, ze
print(f"Overall Test Accuracy: {acc:.4f}")
print(f"Mean Absolute Error: {mae:.4f}")
print(f"\nClassification Report:\n{cr}")
```

```
Overall Train Accuracy: 0.3649
Overall Test Accuracy: 0.3617
Mean Absolute Error: 1.0704

Classification Report:
              precision    recall  f1-score   support

 Baby Boomer       1.00      0.00      0.00       208
  Millennial       0.22      0.02      0.03      1437
           X       0.00      0.00      0.00       648
     Xennial       0.35      0.67      0.46      2024
  Zillennial       0.39      0.45      0.42      2020

    accuracy                           0.36      6337
   macro avg       0.39      0.23      0.18      6337
weighted avg       0.32      0.36      0.29      6337
```

Conclusion

PCA was successfull in reducing the dimensions of our data, with explained variances in excess of 90% distribution. Component vectors showed the drug usage features have the highest consistent influence. This is an expected and positive result because it shows consistent viability of the drug usage data in classifying survey respondents. Integrity validations will be needed to ensure there is no dependency factor within these features because the usage of them is not assuredly mutually exclusive. Multicolinearity analysis later showd these dependencies were not an issue, supporting the integrity of the PCA results.

Overall, even though PCA was successfull, analysis around the drug use data yielded unusable predictive models. Health Levels were modeled with subpar results and accuracies ranging between sub-random chance (20%) and 50%. Efforts to identify generational classifications were even less successfull.

The mixed results of this report show poor modeling efficacy on the entire collection of respondents. Post-analysis research on other peer journals with the survey data show different methodologies on focused demographic subsets had more informative results. Most analysis focused on adolescents, gender, and the rise in opioid use as time-series analysis over several survey report years;[1] [2] other reports were able to expand and compare the survey responses to comparable clinical analysis.[3]

^1. National Estimates of Marijuana Use and Related Indicators http://dx.doi.org/10.15585/mmwr.ss6511a1

^2. Gender and prescription opioids: Findings from the National Survey on Drug Use and Health https://doi.org/10.1016/j.addbeh.2010.06.018

^3. A clinical validation of the National Survey on Drug Use and Health Assessment of Substance Use Disorders https://doi.org/10.1016/j.addbeh.2007.12.007