Data Cleaning

```
In [32]:
          # Machine Learning
          from sklearn. model selection import train test split
          from sklearn.preprocessing import StandardScaler
          from sklearn.linear model import Ridge
          from sklearn.metrics import r2 score
          from sklearn.linear model import LogisticRegression
          import numpy as np
          import pandas as pd
          import matplotlib
          import matplotlib.pyplot as plt
          import seaborn as sns
          from sklearn.utils import resample
          from sklearn import metrics
          from scipy. stats import norm
          from scipy. stats import t
          from scipy import stats as st
          from sklearn. decomposition import PCA
          from sklearn. feature selection import VarianceThreshold
          from sklearn. feature selection import SelectKBest
          from sklearn. feature selection import chi2
          from sklearn. feature selection import SelectFromModel
          from sklearn.svm import LinearSVC
          from sklearn. feature selection import SelectKBest, f classif
          from sklearn.ensemble import RandomForestClassifier
          from sklearn import sym
          from sklearn.utils import shuffle
          import matplotlib.pyplot as plt
          from sklearn. metrics import precision recall curve
          from sklearn. metrics import plot confusion matrix
          from sklearn. metrics import confusion matrix
          import matplotlib.pyplot as plt
```

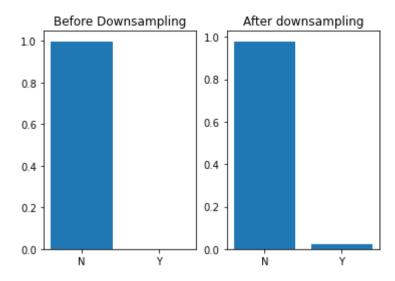
```
In [33]:  # take a look at our dataset
    import pandas as pd
    df2020 = pd. read_csv ('2020Anencephaly.csv')

df = df2020
```

```
print(df['CA ANEN']. value counts())
df = df. drop(['F CIGS 0', 'F CIGS 1', 'F CIGS 2', 'F CIGS 3', 'MRTERR', 'MRTERR.1', 'RESTATUS', 'F TOBACO', 'BFACIL', 'DWgt R'], axis
df. head()
df['IP GON'] = df['IP GON']. map(\{'Y': 1, 'N': 0, 'U': 0\})
df['IP SYPH'] = df['IP SYPH']. map(\{'Y': 1, 'N': 0, 'U': 0\})
df['IP CHLAM'] = df['IP CHLAM']. map(\{'Y': 1, 'N': 0, 'U': 0\})
df['IP HEPB'] = df['IP HEPB']. map(\{'Y': 1, 'N': 0, 'U': 0\})
df['IP HEPC'] = df['IP HEPC'], map(\{'Y': 1, 'N': 0, 'U': 0\})
df['RF PDIAB'] = df['RF PDIAB']. map(\{'Y': 1, 'N': 0, 'U': 0\})
df['RF GDIAB'] = df['RF GDIAB']. map(\{'Y': 1, 'N': 0, 'U': 0\})
df['RF INFTR'] = df['RF INFTR']. map(\{"Y": 1, "N": 0, "U": 0\})
df['RF FEDRG'] = df['RF FEDRG']. map(\{'Y': 1, 'N': 0, 'U': 0, 'X': 0\})
df['CA ANEN'] = df['CA ANEN']. map({'Y': 1, 'N': 0, 'U': 0})
df = df. dropna()
df = df. astype('int')
df = df [(df ['CIG 0']!= 99)]
df = df \lceil (df \lceil 'CIG 1' \rceil != 99) \rceil
df = df [(df ['CIG 2'] != 99)]
df = df [(df ['CIG 3'] != 99)]
df = df [(df ['PRIORLIVE'] != 99)]
df = df [(df ['PRIORDEAD'] != 99)]
df = df [(df ['PRIORTERM'] != 99)]
df = df [(df ['ILLB R'] != 999)]
df = df [(df ['ILOP R'] != 999)]
df = df [(df ['ILP R'] != 999)]
df = df [(df ['ILP R'] != 999)]
df = df[(df['BMI'] != 99.9)]
df = df [(df ['PWgt R'] != 999)]
df = df [(df ['FAGECOMB'] != 99)]
df. loc[df["ILLB R"] == 888, "ILLB R"] = 0
df. loc[df["ILOP R"] == 888. "ILOP R"] = 0
df. loc[df["ILP R"] == 888, "ILP R"] = 0
df save for causal = df
false data = df[df['CA ANEN'] == 0]
positive data = df[df['CA ANEN'] == 1]
false data downsample = resample (false data,
             replace=True.
             n samples=10000,
             random state=42)
```

```
df resample2020 = pd. concat([false data downsample, positive data])
df resample2020. reset index(drop=True, inplace=True)
print(df2020['CA ANEN'].value counts()[0], df2020['CA ANEN'].value counts()[1])
x1 = np. array(["N", "Y"])
v1 = np. array([df2020]'CA ANEN']. value counts()[0] / len(df2020['CA ANEN']),
                df2020['CA ANEN']. value counts()[1] / len(df2020['CA ANEN'])])
plt. subplot (1, 2, 1)
plt. bar (x1, y1)
plt. title ('Before Downsampling')
print(df resample2020['CA ANEN']. value counts()[0], df resample2020['CA ANEN']. value counts()[1])
x2 = np. array(["N", "Y"])
y2 = np. array([df resample2020['CA ANEN']. value counts()[0] / len(df resample2020['CA ANEN']),
                df resample2020 ['CA ANEN'], value counts() [1] / len(df resample2020 ['CA ANEN'])])
plt. subplot (1, 2, 2)
plt. bar (x2, y2)
plt. title('After downsampling')
plt. show()
N
     3614329
U
        5165
```

N 3614329 U 5165 Y 332 Name: CA_ANEN, dtype: int64 3614329 5165 10000 213

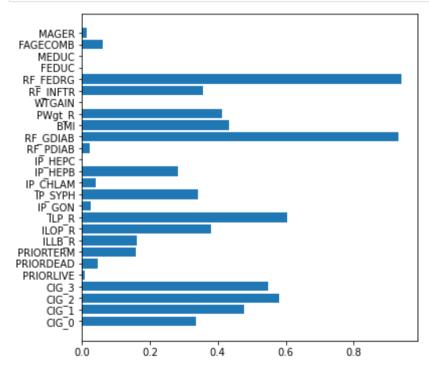


```
In [34]:
           df2017 = pd. read csv ('2017Anencephaly.csv')
           df = df2017
           print(df['CA ANEN']. value counts())
           df = df. drop(['F CIGS 0', 'F CIGS 1', 'F CIGS 2', 'F CIGS 3', 'MRTERR', 'MRTERR.1', 'RESTATUS', 'F TOBACO', 'BFACIL', 'DWgt R'], axis
           df. head()
           df['IP GON'] = df['IP GON']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df['IP SYPH'] = df['IP SYPH']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df['IP CHLAM'] = df['IP CHLAM']. map({'Y': 1, 'N': 0, 'U': 0})
           df['IP HEPB'] = df['IP HEPB']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df['IP HEPC'] = df['IP HEPC']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df['RF PDIAB'] = df['RF PDIAB']. map({'Y': 1, 'N': 0, 'U': 0})
           df['RF GDIAB'] = df['RF GDIAB']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df['RF INFTR'] = df['RF INFTR']. map(\{"Y": 1, "N": 0, "U": 0\})
           df['RF FEDRG'] = df['RF FEDRG']. map(\{'Y': 1, 'N': 0, 'U': 0, 'X': 0\})
           df['CA ANEN'] = df['CA ANEN']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df = df. dropna()
           df = df. astype('int')
           df = df [(df ['CIG O'] != 99)]
           df = df [(df ['CIG 1'] != 99)]
           df = df [(df ['CIG 2'] != 99)]
           df = df[(df['CIG 3'] != 99)]
           df = df \lceil (df \lceil PRIORLIVE' \rceil != 99) \rceil
           df = df \lceil (df \lceil PRIORDEAD' \rceil != 99) \rceil
           df = df[(df['PRIORTERM'] != 99)]
           df = df \lceil (df \rceil' ILLB R' \rceil != 999) \rceil
```

```
df = df \lceil (df \lceil 'ILOP R' \rceil != 999) \rceil
           df = df[(df['ILP R'] != 999)]
           df = df \lceil (df \lceil 'ILP R' \rceil != 999) \rceil
           df = df \lceil (df \lceil BMI' \rceil != 99.9) \rceil
           df = df \lceil (df \lceil PWgt R' \rceil != 999) \rceil
           df = df [(df ['FAGECOMB'] != 99)]
           df. loc[df["ILLB R"] == 888, "ILLB R"] = 0
           df. loc[df["ILOP R"] == 888. "ILOP R"] = 0
           df. loc[df["ILP R"] == 888, "ILP R"] = 0
           false data = df[df['CA ANEN'] == 0]
           positive data = df[df['CA ANEN'] == 1]
           false data downsample = resample (false data,
                         replace=True,
                         n samples=10000.
                         random state=42)
           df resample2017 = pd. concat([false data downsample, positive data])
           df resample2017. reset index (drop=True, inplace=True)
          N
                3859385
          U
                   4937
          Y
                    432
          Name: CA ANEN, dtype: int64
In [35]:
           df2018 = pd. read csv ('2018Anencephaly.csv')
           df = df2018
           print(df['CA ANEN']. value counts())
           df = df. drop(['F CIGS 0', 'F CIGS 1', 'F CIGS 2', 'F CIGS 3', 'MRTERR', 'MRTERR.1', 'RESTATUS', 'F TOBACO', 'BFACIL', 'DWgt R'], axis
           df. head()
           df['IP GON'] = df['IP GON']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df['IP SYPH'] = df['IP SYPH']. map({'Y': 1, 'N': 0, 'U': 0})
           df['IP CHLAM'] = df['IP CHLAM']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df['IP HEPB'] = df['IP HEPB']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df['IP HEPC'] = df['IP HEPC']. map({'Y': 1, 'N': 0, 'U': 0})
           df['RF PDIAB'] = df['RF PDIAB']. map({'Y': 1, 'N': 0, 'U': 0})
           df['RF GDIAB'] = df['RF GDIAB']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df['RF INFTR'] = df['RF INFTR']. map(\{"Y": 1, "N": 0, "U": 0\})
           df['RF FEDRG'] = df['RF FEDRG']. map(\{'Y': 1, 'N': 0, 'U': 0, 'X': 0\})
           df['CA ANEN'] = df['CA ANEN']. map(\{'Y': 1, 'N': 0, 'U': 0\})
           df = df. dropna()
           df = df. astype('int')
           df = df[(df['CIG O'] != 99)]
```

```
df = df \lceil (df \lceil 'CIG 1' \rceil != 99) \rceil
           df = df[(df['CIG 2'] != 99)]
           df = df \lceil (df \lceil 'CIG 3' \rceil != 99) \rceil
           df = df[(df['PRIORLIVE'] != 99)]
           df = df[(df['PRIORDEAD'] != 99)]
           df = df[(df['PRIORTERM'] != 99)]
           df = df [(df ['ILLB R'] != 999)]
           df = df [(df ['ILOP R'] != 999)]
           df = df [(df ['ILP R'] != 999)]
           df = df [(df ['ILP R'] != 999)]
           df = df [(df ['BMI'] != 99.9)]
           df = df [(df ['PWgt R'] != 999)]
           df = df [(df | FAGECOMB'] != 99)]
           df. loc[df["ILLB R"] == 888, "ILLB R"] = 0
           df. loc[df["ILOP R"] == 888, "ILOP R"] = 0
           df. loc[df["ILP R"] == 888, "ILP R"] = 0
           false data = df[df['CA ANEN'] == 0]
           positive data = df[df['CA ANEN'] == 1]
           false data downsample = resample (false data,
                         replace=True,
                         n samples=5000,
                         random state=42)
           df resample2018 = pd.concat([false data downsample, positive data])
           df resample2018. reset index (drop=True, inplace=True)
               3795073
                   6107
          U
                    354
          Name: CA ANEN, dtype: int64
In [36]:
           df resample = pd. concat([df resample2020, df resample2018, df resample2017])
In [66]:
           df resample = shuffle(df resample)
```

T-test



Logistic Regression

```
In [68]: | print(df resample['CA ANEN']. value counts()[0], df resample['CA ANEN']. value counts()[1])
          25000 750
In [69]:
           # seprate train and val
           train features = df resample.iloc[:, :-1]
           train labels = df resample.iloc[:, -1]
           feature names = train features.columns
           X train, X valAndTest, y train, y valAndTest = train test split(train features, train labels, test size=0.5, random state=42)
           X val, X test, y val, y test = train test split(X valAndTest, y valAndTest, test size=0.5, random state=42)
           scaler = StandardScaler().fit(X train)
           X train = scaler. transform(X train)
           X \text{ val} = \text{scaler. transform}(X \text{ val})
           X test = scaler. transform(X test)
In [120...
           bestModel = None
           bestRecall = - float('inf')
           bestFeatureSelection = None
           bestPrecision = 0
           bestRecall = 0
           bestF1 = 0
           bestKValue = 0
           k arr = []
           recall arr = []
           for bestK in range (X train. shape [1]-1, 5, -1):
               s = SelectKBest(f classif, k=bestK)
               X train new = s. fit transform(X train, y train)
               X val new = s. transform(X val)
               clf = LogisticRegression(solver='lbfgs', max_iter=300, class_weight = 'balanced').fit(np.array(X_train_new,
                                                                                                                   dtype = np. float64),
                                                                                                         np. array (y train, dtype=np. float64))
               y hat = np. dot(X val new, clf. coef . T) + clf. intercept
               # rmse = np. sqrt(np. mean(np. square(y val - y hat)))
               y \text{ hat}[y \text{ hat} >= 0.01] = 1
               y hat[y hat < 0.01] = 0
               temp = np. array(y val)
               true positive = 0
               false positive = 0
               false negative = 0
               true negative = 0
```

```
for i in range(len(y hat)):
        if v hat[i] == 1 and temp[i] == 1:
            true positive += 1
        elif y hat[i] == 1 and temp[i] == 0:
           false positive += 1
        elif v hat[i] == 0 and temp[i] == 1:
            false negative += 1
        else:
            true negative += 1
   Precision = true positive / (true positive + false positive)
    Recall = true positive / (true positive + false negative)
    F1 = 2 * Precision * Recall / (Precision + Recall)
    k arr. append (bestK)
   recall arr. append (Recall)
    #print(Recall)
    if bestRecall < Recall:
        bestModel = clf
        bestRecall = Recall
        bestFeatureSelection = s
        bestPrecision = Precision
        bestRecall = Recall
        bestF1 = F1
        bestKValue = bestK
print("true positive:", true_positive, "false_positive:", false_positive,
      "false negative:", false negative, "true negative:", true negative)
print("Best Precision: ", bestPrecision)
print("Best Recall: ", bestRecall)
print("Best F1: ", bestF1)
print("clf", bestModel)
print("bestK", bestKValue)
indexs = bestFeatureSelection.scores .argsort()[-bestKValue:][::-1]
important factor = []
for index in indexs:
    important factor.append(1[index])
print(important factor)
plt. plot (k arr, recall arr)
```

```
plt. title ('Recalls with Different Feature Selection for Logistic Regression')
plt. xlabel ('number of features')
plt. vlabel('recalls')
plt. show()
true positive: 95 false positive: 2362 false negative: 80 true negative: 3900
Best Precision: 0.03929594760540319
Best Recall: 0.5485714285714286
Best F1: 0.07333842627960274
clf LogisticRegression(class weight='balanced', max iter=300)
bestK 9
['WTGAIN', 'MEDUC', 'FEDUC', 'PRIORLIVE', 'CIG O', 'PRIORDEAD', 'CIG 3', 'IP HEPC', 'MAGER']
   Recalls with Different Feature Selection for Logistic Regression
  0.55
  0.54
  0.53
  0.52
S 0.51
  0.50
  0.49
  0.48
  0.47
           7.5
                 10.0
                       12.5 15.0
                                  17.5
                                         20.0
                                               22.5
                                                     25.0
```

number of features

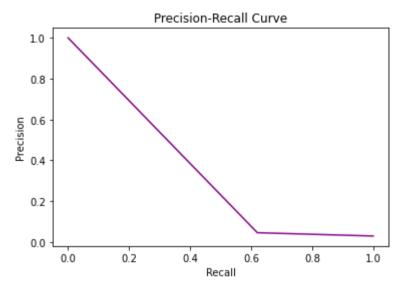
```
In [121... X_test_new = bestFeatureSelection.fit_transform(X_test, y_test)

y_hat = np. dot(X_test_new, bestModel.coef_.T) + bestModel.intercept_
y_hat[y_hat >= 0.01] = 1
y_hat[y_hat < 0.01] = 0
temp = np. array(y_test)

precision, recall, thresholds = precision_recall_curve(y_test, y_hat)

#create precision recall curve
fig, ax = plt.subplots()
ax.plot(recall, precision, color='purple')</pre>
```

```
#add axis labels to plot
ax. set title('Precision-Recall Curve')
ax. set ylabel('Precision')
ax. set xlabel('Recall')
#display plot
plt. show()
true positive = 0
false positive = 0
false negative = 0
true negative = 0
for i in range(len(y hat)):
    if y hat [i] == 1 and temp[i] == 1:
        true positive += 1
    elif v hat[i] == 1 and temp[i] == 0:
        false positive += 1
   elif v hat [i] == 0 and temp [i] == 1:
       false negative += 1
    else:
        true negative += 1
print ("true positive:", true positive, "false positive:", false positive, "false negative:",
     false negative, "true negative:", true negative)
Precision = true positive / (true positive + false positive)
Recall = true positive / (true positive + false negative)
F1 = 2 * Precision * Recall / (Precision + Recall)
print("Best Precision: ", Precision)
print("Best Recall: ", Recall)
print("Best F1: ",F1)
metrics.plot roc curve(bestModel, X test new, y test)
```



true positive: 116 false positive: 2447 false negative: 71 true negative: 3804

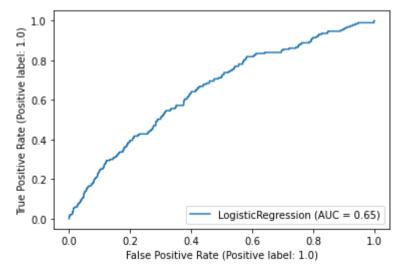
Best Precision: 0.04525946156847444 Best Recall: 0.6203208556149733 Best F1: 0.084363636363635

C:\anaconda3\envs\cs590w\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function plot_roc_curve is deprecated; Function:func:`plot_roc_curve` is deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:`sklearn.metric.RocCurveDisplay.from predictions` or :meth:`sklearn.metric.RocCurveDisplay.from estimator`.

warnings.warn(msg, category=FutureWarning)

<sklearn.metrics._plot.roc_curve.RocCurveDisplay at Ox1dldcea9ca0>





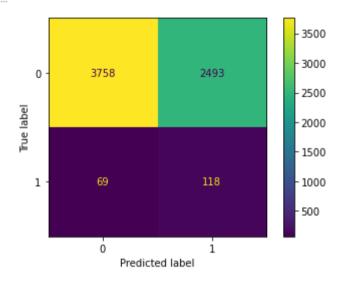
```
In [122...
```

```
plot_confusion_matrix(bestModel, X_test_new, y_test)
```

C:\anaconda3\envs\cs590w\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function plot_confusion_matrix is deprecate ed; Function `plot_confusion_matrix` is deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: ConfusionMatrixDi splay.from_predictions or ConfusionMatrixDisplay.from_estimator.

warnings.warn(msg, category=FutureWarning)

Out[122... <sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x1d1ddadc790>

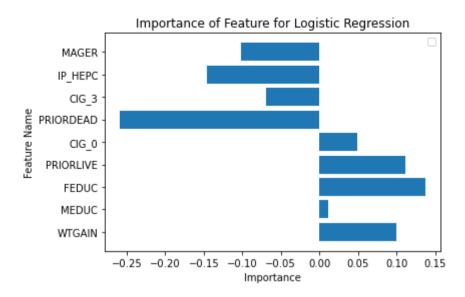


```
In [123...
    plt. barh(important_factor, bestModel.coef_[0].T)
    plt. legend()

plt. xlabel('Importance')
    plt. ylabel('Feature Name')
    plt. title('Importance of Feature for Logistic Regression')

plt. show()
```

No artists with labels found to put in legend. Note that artists whose label start with an underscore are ignored when legend() is called with no argument.



Random Forest:

```
In [88]: # seprate train and val
# df_resample = shuffle(df_resample)
train_features = df_resample.iloc[:, :-1]
train_labels = df_resample.iloc[:, -1]
feature_names = train_features.columns
X_train, X_valAndTest, y_train, y_valAndTest = train_test_split(train_features, train_labels, test_size=0.5, random_state=42)
X_val, X_test, y_val, y_test = train_test_split(X_valAndTest, y_valAndTest, test_size=0.5, random_state=42)
scaler = StandardScaler().fit(X_train)
X_train = scaler.transform(X_train)
X_val = scaler.transform(X_val)
X_test = scaler.transform(X_test)
In [90]: hestModel = None
```

```
bestModel = None
bestRecall = - float('inf')
bestFeatureSelection = None
bestPrecision = 0
bestRecall = 0
bestFl = 0
bestKValue = 0
k_arr = []
```

```
recall arr = []
for bestK in range (X train. shape [1]-1, 5, -1):
    s = SelectKBest(f classif, k=bestK)
    X train new = s. fit transform(X train, y train)
    X \text{ val new} = s. \operatorname{transform}(X \text{ val})
    clf = RandomForestClassifier(max depth=10, random state=42, class weight = 'balanced')
    clf. fit (X train new, y train)
    y hat = clf. predict(X val new)
    # rmse = np.sqrt(np.mean(np.square(y val - y hat)))
    y \text{ hat}[y \text{ hat} >= 0.01] = 1
    y \text{ hat } [y \text{ hat } < 0.01] = 0
    temp = np. array(y val)
    true positive = 0
    false positive = 0
    false negative = 0
    true negative = 0
    for i in range(len(y hat)):
        if y hat[i] == 1 and temp[i] == 1:
             true positive += 1
        elif v hat [i] == 1 and temp [i] == 0:
            false positive += 1
        elif v hat [i] == 0 and temp [i] == 1:
             false negative += 1
        else:
             true negative += 1
    #
    Precision = true positive / (true positive + false positive)
    Recall = true positive / (true positive + false negative)
   F1 = 2 * Precision * Recall / (Precision + Recall)
    k arr. append (bestK)
    recall arr. append (Recall)
    #print(Recall)
    if bestRecall < Recall:
        bestModel = clf
        bestRecall = Recall
        bestFeatureSelection = s
        bestPrecision = Precision
        bestRecall = Recall
        bestF1 = F1
```

```
bestKValue = bestK
  print ("true positive:", true positive, "false positive:", false positive, "false negative:", false negative; "true negative:", true negative: ", true negat
  print("Best Precision: ", bestPrecision)
  print("Best Recall: ", bestRecall)
  print("Best F1: ", bestF1)
  print("clf", bestModel)
  print("bestK". bestKValue)
  indexs = bestFeatureSelection.scores .argsort()[-bestKValue:][::-1]
  important factor = []
  for index in indexs:
                important factor.append(1[index])
  print(important factor)
  plt. plot (k arr, recall arr)
  plt. title ('Recalls with Different Feature for Random Forest')
  plt. xlabel ('number of features')
  plt. ylabel('recalls')
  plt. show()
true positive: 25 false positive: 620 false negative: 150 true negative: 5642
Best Precision: 0.04793756967670011
Best Recall: 0.24571428571428572
```

Best F1: 0.08022388059701492

bestK 8

clf RandomForestClassifier(class weight='balanced', max depth=10, random state=42)

['WTGAIN', 'MEDUC', 'FEDUC', 'PRIORLIVE', 'CIG O', 'PRIORDEAD', 'CIG 3', 'IP HEPC']

Recalls with Different Feature for Random Forest 0.24 0.22 0.20 0.16 0.14 0.12 7.5 10.0 12.5 15.0 17.5 20.0 22.5 25.0 number of features

```
In [76]:
          X test new = bestFeatureSelection.fit transform(X test, y test)
          X val new = bestFeatureSelection.fit transform(X val, y val)
          X train new = bestFeatureSelection.fit transform(X train, y train)
          bestRecall = - float('inf')
          bestDepth = -1
          depths = []
          recalls = []
          for i in range (2, 15):
               tempModel = RandomForestClassifier(max depth=i, random state=42, class weight = 'balanced')
               tempModel.fit(X_train_new, y_train)
               y hat = tempModel.predict(X val new)
               y hat[y hat >= 0.01] = 1
               y \text{ hat}[y \text{ hat } < 0.01] = 0
               tn, fp, fn, tp = confusion matrix(y val, y hat).ravel()
               currRecall = tp / (tp + fn)
               if bestRecal1 < currRecal1:</pre>
                   bestModel = tempModel
                   bestDepth = i
               depths. append(i)
              recalls. append (currRecall)
          fig = plt. figure()
```

```
plt. plot (depths, recalls)
fig. suptitle ('Random Forest Depth vs. Recall', fontsize=20)
plt. xlabel ('depth', fontsize=18)
plt.ylabel('recall', fontsize=16)
bestModel = RandomForestClassifier(max depth=2, random state=42, class weight = 'balanced')
bestModel.fit(X train new, y train)
y hat = bestModel.predict(X test new)
precision, recall, thresholds = precision recall curve(y test, y hat)
#create precision recall curve
fig, ax = plt. subplots()
ax. plot(recall, precision, color='purple')
#add axis labels to plot
ax. set title('Precision-Recall Curve')
ax. set ylabel('Precision')
ax. set xlabel('Recall')
#display plot
plt. show()
y \text{ hat}[y \text{ hat} >= 0.01] = 1
y hat[y hat < 0.01] = 0
temp = np. array(y test)
true positive = 0
false positive = 0
false negative = 0
true negative = 0
for i in range(len(y hat)):
    if y hat [i] == 1 and temp[i] == 1:
        true positive += 1
    elif y hat [i] == 1 and temp [i] == 0:
        false positive += 1
    elif y hat[i] == 0 and temp[i] == 1:
        false negative += 1
    else:
        true negative += 1
print("true positive:", true positive,
```

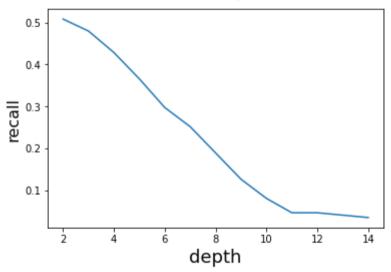
```
"false_positive:", false_positive,
    "false_negative:", false_negative,
    "true_negative:", true_negative)

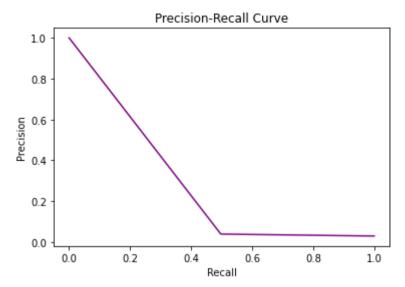
Precision = true_positive / (true_positive + false_positive)
Recall = true_positive / (true_positive + false_negative)
F1 = 2 * Precision * Recall / (Precision + Recall)

print("Best Precision: ", Precision)
print("Best Recall: ", Recall)
print("Best F1: ", F1)

metrics. plot_roc_curve(bestModel, X_test_new, y_test)
```

Random Forest Depth vs. Recall





true positive: 93 false positive: 2313 false negative: 94 true negative: 3938

Best Precision: 0.03865336658354115 Best Recall: 0.49732620320855614

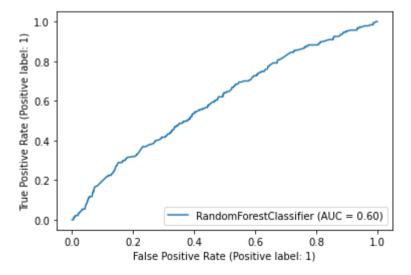
Best F1: 0.0717315850366371

C:\anaconda3\envs\cs590w\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function plot roc curve is deprecated; Fun ction: func: plot roc curve is deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth: sklearn.metric.Roc CurveDisplay.from predictions or :meth: sklearn.metric.RocCurveDisplay.from estimator.

warnings.warn(msg, category=FutureWarning)

<sklearn.metrics. plot.roc curve.RocCurveDisplay at Ox1d1ddde4cd0>

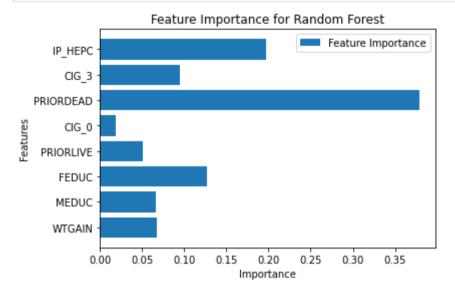
Out[76]:



```
In [77]:    plt. barh(important_factor, bestModel. feature_importances_, label="Feature Importance")
    plt. legend()

    plt. xlabel('Importance')
    plt. ylabel('Features')
    plt. title('Feature Importance for Random Forest')

    plt. show()
```

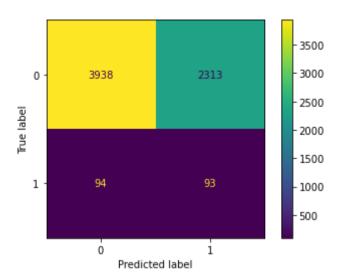


Out[78]:

```
In [78]: plot_confusion_matrix(bestModel, X_test_new, y_test)
```

C:\anaconda3\envs\cs590w\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function plot_confusion_matrix is deprecate ed; Function `plot_confusion_matrix` is deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: ConfusionMatrixDisplay.from_predictions or ConfusionMatrixDisplay.from_estimator.

warnings.warn(msg, category=FutureWarning)
<sklearn.metrics. plot.confusion matrix.ConfusionMatrixDisplay at 0x1d1deec8550>



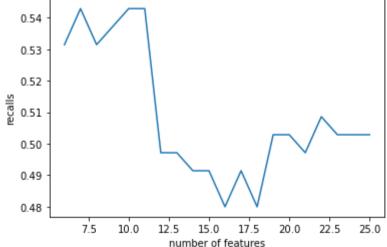
SVM + linear

```
In [109... # seprate train and val
# df_resample = shuffle(df_resample)
train_features = df_resample.iloc[:, :-1]
train_labels = df_resample.iloc[:, -1]
feature_names = train_features.columns
X_train, X_valAndTest, y_train, y_valAndTest = train_test_split(train_features, train_labels, test_size=0.5, random_state=42)
X_val, X_test, y_val, y_test = train_test_split(X_valAndTest, test_size=0.5, random_state=42)
scaler = StandardScaler().fit(X_train)
X_train = scaler.transform(X_train)
X_val = scaler.transform(X_val)
X_test = scaler.transform(X_test)
In [110... bestModel = Name
```

```
bestModel = None
bestRecall = - float('inf')
bestFeatureSelection = None
bestPrecision = 0
bestRecall = 0
bestF1 = 0
bestKValue = 0
k_arr = []
recall_arr = []
```

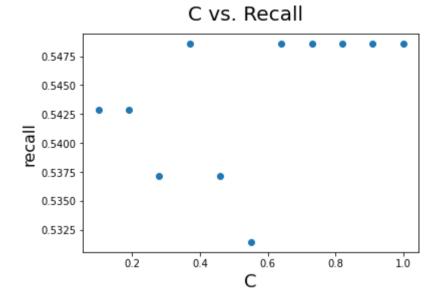
```
for bestK in range (X train. shape [1]-1, 5, -1):
    s = SelectKBest(f classif, k=bestK)
   X train new = s. fit transform(X train, y train)
   X val new = s. transform(X val)
   clf = svm. SVC(C=3, kernel='linear', class weight = 'balanced')
    clf. fit (X train new, y train)
    y hat = clf. predict(X val new)
    # rmse = np. sqrt (np. mean (np. square (y val - y hat)))
   y hat[y hat >= 0.01] = 1
   y \text{ hat}[y \text{ hat } < 0.01] = 0
    temp = np. array(y val)
    true positive = 0
    false positive = 0
    false negative = 0
    true negative = 0
   for i in range(len(y hat)):
        if y \text{ hat}[i] == 1 \text{ and } temp[i] == 1:
            true positive += 1
        elif v hat [i] == 1 and temp [i] == 0:
            false positive += 1
        elif v hat[i] == 0 and temp[i] == 1:
            false negative += 1
        else:
            true negative += 1
    # print("true positive:", true positive, "false positive;", false positive, "false negative:", false negative;",
   Precision = true positive / (true positive + false positive)
    Recall = true positive / (true positive + false negative)
   F1 = 2 * Precision * Recall / (Precision + Recall)
   k arr. append (bestK)
   recall arr. append (Recall)
    #print (Recall)
   if bestRecall < Recall:
        bestModel = clf
        bestRecall = Recall
        bestFeatureSelection = s
        bestPrecision = Precision
        bestRecall = Recall
        bestF1 = F1
        bestKValue = bestK
```

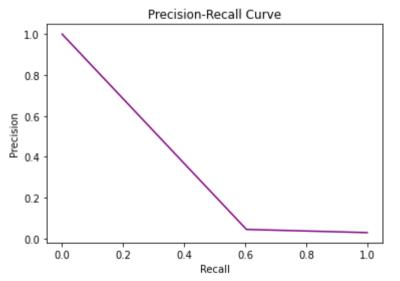
```
print("Best Precision: ", bestPrecision)
print("Best Recall: ", bestRecall)
print("Best F1: ", bestF1)
print("clf", bestModel)
print("bestK", bestKValue)
indexs = bestFeatureSelection.scores .argsort()[-bestKValue:][::-1]
important factor = []
 for index in indexs:
     important factor.append(1[index])
print(important factor)
plt. plot(k arr, recall arr)
 plt. title ('Recalls with Different Feature Selection for SVM with Linear Kernel')
 plt. xlabel ('number of features')
plt. ylabel('recalls')
 plt. show()
Best Precision: 0.03772835583796664
Best Recall: 0.5428571428571428
Best F1: 0.07055328629780913
clf SVC(C=3, class weight='balanced', kernel='linear')
bestK 11
['WTGAIN', 'MEDUC', 'FEDUC', 'PRIORLIVE', 'CIG O', 'PRIORDEAD', 'CIG 3', 'IP HEPC', 'MAGER', 'RF PDIAB', 'CIG 1']
  Recalls with Different Feature Selection for SVM with Linear Kernel
  0.54
```



```
In [119...
           X train new = bestFeatureSelection. transform(X train)
           X val new = bestFeatureSelection.transform(X val)
           bestRecall = - float('inf')
           bestDepth = -1
           Cs = []
           recalls = []
           Cs = np. 1inspace (0.1, 1, 11)
           for c val in Cs:
               tempModel = svm. SVC(C=c val, kernel='linear', class weight = 'balanced')
               tempModel.fit(X train new, y train)
               y hat = tempModel.predict(X val new)
               y \text{ hat}[y \text{ hat} >= 0.01] = 1
               y \text{ hat } [y \text{ hat } < 0.01] = 0
               tn, fp, fn, tp = confusion matrix(y val, y hat).ravel()
               currRecall = tp / (tp + fn)
               if bestRecall < currRecall:
                   bestModel = tempModel
                   bestDepth = i
               recalls. append (currRecall)
           fig = plt. figure()
           plt. scatter (Cs, recalls)
           fig. suptitle ('C vs. Recall', fontsize=20)
           plt. xlabel ('C', fontsize=18)
           plt. vlabel ('recall', fontsize=16)
           X test new = bestFeatureSelection.fit transform(X test, y test)
           y hat = bestModel.predict(X test new)
           precision, recall, thresholds = precision_recall curve(y test, y hat)
           #create precision recall curve
           fig, ax = plt. subplots()
           ax. plot (recall, precision, color='purple')
           #add axis labels to plot
           ax. set title ('Precision-Recall Curve')
           ax. set ylabel('Precision')
```

```
ax. set xlabel('Recall')
#display plot
plt. show()
y \text{ hat}[y \text{ hat} >= 0.01] = 1
y \text{ hat}[y \text{ hat } < 0.01] = 0
temp = np. array(y test)
true positive = 0
false positive = 0
false negative = 0
true negative = 0
for i in range(len(y hat)):
    if y hat [i] == 1 and temp[i] == 1:
        true positive += 1
    elif v hat[i] == 1 and temp[i] == 0:
        false positive += 1
    elif v hat[i] == 0 and temp[i] == 1:
        false negative += 1
    else:
        true negative += 1
print("true positive:", true positive,
      "false positive:", false positive,
      "false negative:", false negative,
      "true negative:", true negative)
Precision = true positive / (true positive + false positive)
Recall = true positive / (true positive + false negative)
F1 = 2 * Precision * Recall / (Precision + Recall)
print("Best Precision: ", Precision)
print("Best Recall: ", Recall)
print("Best F1: ", F1)
metrics.plot roc curve (bestModel, X test new, y test)
```





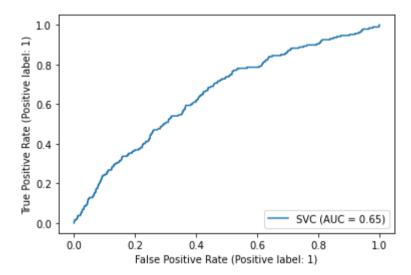
true_positive: 113 false_positive: 2421 false_negative: 74 true_negative: 3830

Best Precision: 0.04459352801894238 Best Recall: 0.6042780748663101 Best F1: 0.08305769937522971

C:\anaconda3\envs\cs590w\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function plot_roc_curve is deprecated; Function:func: plot_roc_curve is deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth: sklearn.metric.Roc

CurveDisplay.from_predictions` or :meth:`sklearn.metric.RocCurveDisplay.from_estimator`. warnings.warn(msg, category=FutureWarning)
<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x1d1dd3878e0>

Out[119...

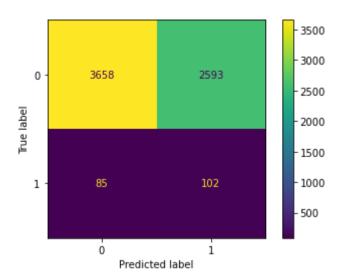


In [113... plot_confusion_matrix(bestModel, X_test_new, y_test)

C:\anaconda3\envs\cs590w\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function plot_confusion_matrix is deprecated; Function `plot_confusion_matrix` is deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: ConfusionMatrixDisplay.from predictions or ConfusionMatrixDisplay.from estimator.

warnings.warn(msg, category=FutureWarning)

Out[113... <sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x1d1de74bfa0>



SVM + rbf

```
bestModel = None
bestRecall = - float('inf')
bestFeatureSelection = None
bestPrecision = 0
bestRecall = 0
bestF1 = 0
bestKValue = 0
bestTP = 0
bestFP = 0
```

```
bestTN = 0
bestFN = 0
x val saved = None
y val saved = None
X val new = None
k arr = []
recall arr = []
for bestK in range (X train. shape [1]-1, 5, -1):
    s = SelectKBest(f classif, k=bestK)
   X train new = s. fit transform(X train, y train)
    X val new = s. transform(X val)
    clf = svm. SVC(C=0.62, kernel='rbf', class weight = 'balanced')
    clf. fit(X train new, y train)
    y hat = clf. predict(X val new)
    # rmse = np. sqrt (np. mean (np. square (y val - y hat)))
   y \text{ hat}[y \text{ hat} >= 0.1] = 1
   y hat[y hat < 0.1] = 0
    temp = np. array(y val)
    true positive = 0
    false positive = 0
    false negative = 0
    true negative = 0
    for i in range(len(y hat)):
        if y hat [i] == 1 and temp[i] == 1:
            true positive += 1
        elif v hat [i] == 1 and temp [i] == 0:
            false positive += 1
        elif v hat [i] == 0 and temp [i] == 1:
            false negative += 1
        else:
            true negative += 1
    # print("true positive:", true positive, "false positive:", false positive, "false negative:", false negative;",
    Precision = true positive / (true positive + false positive)
    Recall = true positive / (true positive + false negative)
    F1 = 2 * Precision * Recall / (Precision + Recall)
    k arr. append (bestK)
    recall arr. append (Recall)
```

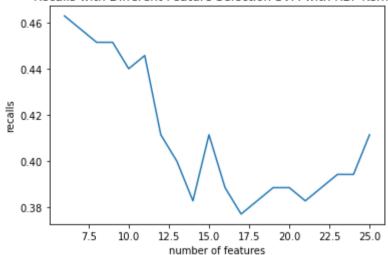
```
#print(Recall)
    if bestRecall < Recall:
        bestModel = clf
        bestRecall = Recall
        bestFeatureSelection = s
        bestPrecision = Precision
        bestRecall = Recall
        bestF1 = F1
        bestKValue = bestK
        bestTP = true positive
        bestFP = false positive
        bestFN = false negative
        bestTN = true negative
    \#if\ bestK == 5:
        \#x val saved = x val new
        #y val saved = y hat
print ("true positive:", bestTP, "false positive:", bestFP, "false negative:", bestFN, "true negative:", bestTN)
print("Best Precision: ", bestPrecision)
print("Best Recall: ", bestRecall)
print("Best F1: ", bestF1)
print("clf", bestModel)
print("bestK", bestKValue)
indexs = bestFeatureSelection.scores .argsort()[-bestKValue:][::-1]
important factor = []
for index in indexs:
    important factor.append(1[index])
print(important factor)
plt. plot (k arr, recall arr)
plt. title ('Recalls with Different Feature Selection SVM with RBF Kernel')
plt. xlabel ('number of features')
plt. ylabel('recalls')
plt. show()
```

true_positive: 81 false_positive: 1989 false_negative: 94 true_negative: 4273 Best Precision: 0.0391304347826087

Best Recall: 0.46285714285714286

```
Best F1: 0.07216035634743877
clf SVC(C=0.62, class_weight='balanced')
bestK 6
['WTGAIN', 'MEDUC', 'FEDUC', 'PRIORLIVE', 'CIG 0', 'PRIORDEAD']
```

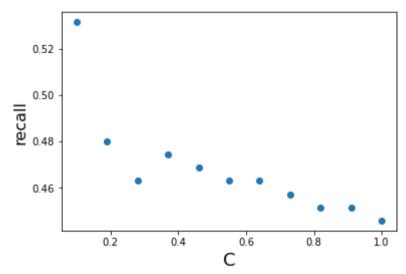
Recalls with Different Feature Selection SVM with RBF Kernel

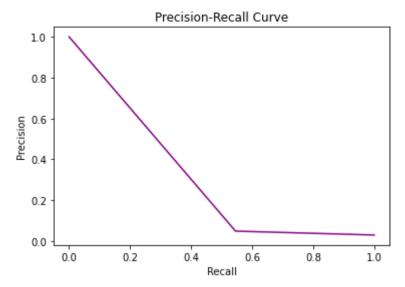


```
In [117...
          X train new = bestFeatureSelection. transform(X train)
           X val new = bestFeatureSelection.transform(X val)
           X test new = bestFeatureSelection.transform(X test)
           C_S = []
           recalls = []
           Cs = np. linspace (0.1, 1, 11)
           for c val in Cs:
               tempModel = svm. SVC(C=c val, kernel='rbf', class weight = 'balanced')
               tempModel.fit(X train new, y train)
               y hat = tempModel.predict(X val new)
              y hat[y hat >= 0.01] = 1
              y hat[y hat < 0.01] = 0
               tn, fp, fn, tp = confusion_matrix(y_val, y_hat).ravel()
               currRecall = tp / (tp + fn)
               if bestRecall < currRecall:</pre>
```

```
bestModel = tempModel
        bestDepth = i
   recalls. append (currRecall)
fig = plt. figure()
plt. scatter (Cs, recalls)
fig. suptitle ('SVM rbf C vs. Recall', fontsize=20)
plt.xlabel('C', fontsize=18)
plt. vlabel ('recall', fontsize=16)
y hat = bestModel.predict(X test new)
precision, recall, thresholds = precision recall curve(y test, y hat)
#create precision recall curve
fig, ax = plt. subplots()
ax. plot(recall, precision, color='purple')
#add axis labels to plot
ax. set title('Precision-Recall Curve')
ax. set ylabel('Precision')
ax. set xlabel('Recall')
#display plot
plt. show()
y \text{ hat}[y \text{ hat} >= 0.01] = 1
y hat[y hat < 0.01] = 0
temp = np. array(y test)
true positive = 0
false positive = 0
false negative = 0
true negative = 0
for i in range(len(y hat)):
    if y hat [i] == 1 and temp[i] == 1:
        true positive += 1
    elif y hat[i] == 1 and temp[i] == 0:
        false positive += 1
    elif y_hat[i] == 0 and temp[i] == 1:
        false negative += 1
    else:
        true negative += 1
```

SVM rbf C vs. Recall





true positive: 102 false positive: 2015 false negative: 85 true negative: 4236

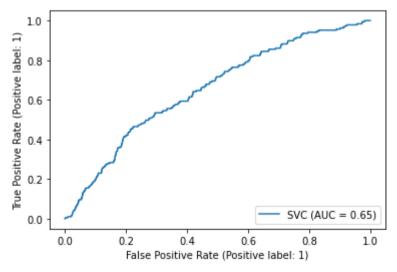
Best Precision: 0.048181388757675955 Best Recall: 0.54545454545454 Best F1: 0.08854166666666666

C:\anaconda3\envs\cs590w\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function plot_roc_curve is deprecated; Function :func:`plot_roc_curve` is deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: :meth:`sklearn.metric.RocCurveDisplay.from predictions` or :meth:`sklearn.metric.RocCurveDisplay.from estimator`.

warnings.warn(msg, category=FutureWarning)

<sklearn.metrics._plot.roc_curve.RocCurveDisplay at 0x1d1de783490>





```
In [118...
```

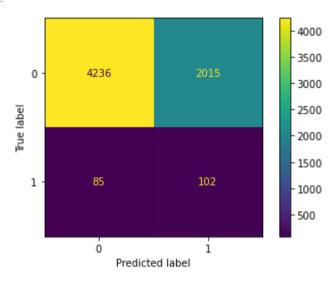
```
plot_confusion_matrix(bestModel, X_test_new, y_test)
```

C:\anaconda3\envs\cs590w\lib\site-packages\sklearn\utils\deprecation.py:87: FutureWarning: Function plot_confusion_matrix is deprecate ed; Function `plot_confusion_matrix` is deprecated in 1.0 and will be removed in 1.2. Use one of the class methods: ConfusionMatrixDi splay.from_predictions or ConfusionMatrixDisplay.from_estimator.

warnings.warn(msg, category=FutureWarning)

<sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x1d1def27c70>





DAG Analysis

```
In [160...
```

```
X = df_resample.iloc[:, :-1]
y = df_resample.iloc[:, -1]
```

In [161...

```
1 = df. columns. values. tolist()
print(1)
```

['CIG_O', 'CIG_1', 'CIG_2', 'CIG_3', 'PRIORLIVE', 'PRIORDEAD', 'PRIORTERM', 'ILLB_R', 'ILOP_R', 'IP_R', 'IP_GON', 'IP_SYPH', 'IP_CHL AM', 'IP_HEPB', 'IP_HEPC', 'RF_PDIAB', 'RF_GDIAB', 'BMI', 'PWgt_R', 'WTGAIN', 'RF_INFTR', 'RF_FEDRG', 'FEDUC', 'MEDUC', 'FAGECOMB', 'MAGER', 'CA ANEN']

WTGAIN DAG

```
In [ ]:
         from sklearn.linear model import LinearRegression
         exposure = "WTGAIN" # change for your exposure
         outcome = "CA ANEN"
         df = df save for causal
         df DAG unadjusted = df[[exposure, outcome]].dropna()
         model = LinearRegression(). fit(np. array(df DAG unadjusted[exposure], dtype=np. float64). reshape(-1, 1),
                                                       np. array(df DAG unadjusted['CA ANEN'], dtype=np. float64))
         beta = model.coef [0]
         odds ratio = np. exp(beta)
         print("The odds ratio for unadjusted association is", odds ratio)
         positive data = df DAG unadjusted[df DAG unadjusted['CA ANEN'] == 1]
         positive data = positive data. drop(columns=['CA ANEN'])
         false data = df DAG unadjusted[df DAG unadjusted['CA ANEN'] == 0]
         false data = false data. drop(columns=['CA ANEN'])
         print("# of positive data", len(positive data))
         print("# of false data", len(false data))
         print("# of total population", len(df))
         results = st. ttest ind(a=false data, b=positive data, equal var=False, alternative='two-sided')
         print(" - statistics = {}". format(results. statistic))
         print(" - p-value = {}". format(results. pvalue))
         positive data = np. array (positive data)
         false data = np. array (false data)
         s1 = np. var(positive data, ddof = 1)
         s2 = np. var(false data, ddof = 1)
         n1 = len(positive data)
         n2 = 1en(false data)
         x1 mu = np. mean (positive data)
```

```
x2_mu = np. mean(false_data)
z = 1.96

sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
ci_1 = (x1_mu - x2_mu) - z * sp * np. sqrt(1/n1 + 1/n2)
ci_2 = (x1_mu - x2_mu) + z * sp * np. sqrt(1/n1 + 1/n2)
print("The 95% confidence interval is", [ci_1, ci_2])
```

Unadjusted Association

```
In [ ]:
         exposure = "WTGAIN" # change for your exposure
         variableMostConfident = "MAGER" # change for your variables
         outcome = "CA ANEN"
         df DAG limited adjustment = df[[exposure, variableMostConfident, outcome]].dropna()
         model = LinearRegression(). fit(np. array(df DAG limited adjustment.drop(columns=['CA ANEN'])),
                                                       np. array(df DAG limited adjustment['CA ANEN']))
         beta = model.coef [0]
         odds ratio = np. exp(beta)
         print("The odds ratio for Naïve adjusted association is", odds ratio)
         positive data = np. array(positive data)
         false data = np. array(false data)
         s1 = np. var(positive data, ddof = 1)
         s2 = np. var(false data, ddof = 1)
         n1 = len(positive data)
         n2 = 1en(false data)
         x1 mu = np. mean (positive data)
         x2 mu = np. mean(false data)
         z = 1.96
          sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
         ci 1 = (x1 mu - x2 mu) - z * sp * np. sqrt (1/n1 + 1/n2)
         ci 2 = (x1 mu - x2 mu) + z * sp * np. sqrt (1/n1 + 1/n2)
         print ("The 95% confidence level is", [ci 1, ci 2])
```

Fully Adjusted Association

In []: exposure = "WTGAIN" # change for your exposure outcome = "CA ANEN" # change based on your DAG df DAG limited adjustment = df[[exposure, 'MAGER', 'CIG 1', 'CIG 2', 'CIG 3', 'RF GDIAB', 'PWgt R', 'RF PDIAB', outcome]]. dropna() model = LinearRegression(). fit(np. array(df DAG limited adjustment.drop(columns=['CA ANEN'])), np. array(df DAG limited adjustment['CA ANEN'])) beta = model.coef [0] odds ratio = np. exp(beta) print ("The odds ratio for fully adjusted association is", odds ratio) positive data = np. array (positive data) false data = np. array (false data) s1 = np. var(positive data, ddof = 1)s2 = np. var(false data, ddof = 1) n1 = len(positive data) n2 = 1en(false data)x1 mu = np. mean (positive data) x2 mu = np. mean(false data) z = 1.96sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))ci 1 = (x1 mu - x2 mu) - z * sp * np. sqrt (1/n1 + 1/n2)ci 2 = (x1 mu - x2 mu) + z * sp * np. sqrt (1/n1 + 1/n2)print ("The 95% confidence level is", [ci 1, ci 2])

CIG_3 DAG

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In []: df = df_save_for_causal
    exposure = "CIG_3"  # change for your exposure
    outcome = "CA_ANEN"

# change based on your DAG
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df DAG limited adjustment = df[[exposure, 'CIG O', 'IP HEPC', 'WTGAIN', 'IP HEPB', 'IP SYPH', 'IP CHLAM', 'RF INFTR', 'RF GDIAB', 'MEDU
model = LinearRegression(). fit(np. array(df DAG limited adjustment.drop(columns=['CA ANEN'])),
                                              np. array(df DAG limited adjustment['CA ANEN']))
beta = model.coef [0]
odds ratio = np. exp(beta)
print ("The odds ratio for fully adjusted association is", odds ratio)
positive data = np. array (positive data)
false data = np. array (false data)
print ("# of positive data", len (positive data))
print("# of false data", len(false data))
print("# of total population", len(df))
s1 = np. var(positive data, ddof = 1)
s2 = np. var(false data, ddof = 1)
n1 = len(positive data)
n2 = 1en(false data)
x1 mu = np. mean (positive data)
x2_{mu} = np. mean(false data)
z = 1.96
sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
ci 1 = (x1 mu - x2 mu) - z * sp * np. sqrt (1/n1 + 1/n2)
ci 2 = (x1 mu - x2 mu) + z * sp * np. sqrt (1/n1 + 1/n2)
print ("The 95% confidence level is", [ci 1, ci 2])
```

```
s1 = np. var(positive_data, ddof = 1)
s2 = np. var(false_data, ddof = 1)
n1 = len(positive_data)
n2 = len(false_data)
x1_mu = np. mean(positive_data)
x2_mu = np. mean(false_data)
z = 1.96

sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
ci_1 = (x1_mu - x2_mu) - z * sp * np. sqrt(1/n1 + 1/n2)
ci_2 = (x1_mu - x2_mu) + z * sp * np. sqrt(1/n1 + 1/n2)
print("The 95% confidence level is", [ci_1, ci_2])
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```
In [ ]:
         exposure = "CIG 3" # change for your exposure
         outcome = "CA ANEN"
         df DAG unadjusted = df[[exposure, outcome]].dropna()
         model = LinearRegression(). fit(np. array(df DAG unadjusted[exposure], dtype=np. float64). reshape(-1,1),
                                                       np. array (df DAG unadjusted ['CA ANEN'], dtype=np. float64))
         beta = model.coef [0]
         odds ratio = np. exp(beta)
         print("The odds ratio for unadjusted association is", odds ratio)
         positive data = df DAG unadjusted[df DAG unadjusted['CA ANEN'] == 1]
         positive data = positive data. drop(columns=['CA ANEN'])
         false data = df DAG unadjusted[df DAG unadjusted['CA ANEN'] == 0]
         false data = false data. drop(columns=['CA ANEN'])
         results = st. ttest ind(a=false data, b=positive data, equal var=False, alternative='two-sided')
         print(" - statistics = {}". format(results. statistic))
         print(" - p-value = {}". format(results. pvalue))
         positive data = np. array (positive data)
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```
false_data = np. array(false_data)
s1 = np. var(positive_data, ddof = 1)
s2 = np. var(false_data, ddof = 1)
n1 = len(positive_data)
n2 = len(false_data)
x1_mu = np. mean(positive_data)
x2_mu = np. mean(false_data)
z = 1.96

sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
ci_1 = (x1_mu - x2_mu) - z * sp * np. sqrt(1/n1 + 1/n2)
ci_2 = (x1_mu - x2_mu) + z * sp * np. sqrt(1/n1 + 1/n2)
print("The 95% confidence level is", [ci_1, ci_2])
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RF_PDIAB

```
false data = false data. drop(columns=['CA ANEN'])
, , ,
print("# of positive data", len(positive data))
print("# of false data", len(false data))
print ("# of total population", len(df))
results = st. ttest ind(a=false data, b=positive data, equal var=False, alternative='two-sided')
print(" - statistics = {}". format(results. statistic))
print(" - p-value = {}". format(results. pvalue))
positive data = np. array (positive data)
false data = np. array (false data)
s1 = np. var(positive data, ddof = 1)
s2 = np. var(false data, ddof = 1)
n1 = len(positive data)
n2 = 1en(false data)
x1 mu = np. mean (positive data)
x2 mu = np. mean(false data)
z = 1.96
sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
ci 1 = (x1 mu - x2 mu) - z * sp * np. sqrt (1/n1 + 1/n2)
ci 2 = (x1 mu - x2 mu) + z * sp * np. sqrt (1/n1 + 1/n2)
print ("The 95% confidence level is", [ci 1, ci 2])
```

```
false_data = np. array(false_data)
s1 = np. var(positive_data, ddof = 1)
s2 = np. var(false_data, ddof = 1)
n1 = len(positive_data)
n2 = len(false_data)
x1_mu = np. mean(positive_data)
x2_mu = np. mean(false_data)
z = 1.96

sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
ci_1 = (x1_mu - x2_mu) - z * sp * np. sqrt(1/n1 + 1/n2)
ci_2 = (x1_mu - x2_mu) + z * sp * np. sqrt(1/n1 + 1/n2)
print("The 95% confidence level is", [ci_1, ci_2])
```

```
In [ ]:
          exposure = "RF PDIAB" # change for your exposure
         outcome = "CA ANEN"
          # change based on your DAG
         df DAG limited adjustment = df[[exposure, 'CIG O', 'IP HEPC', 'WTGAIN', 'IP HEPB', 'IP SYPH', 'IP CHLAM', 'RF INFTR', 'MEDUC', 'FEDUC',
          model = LogisticRegression(max iter=1e6). fit(np. array(df DAG limited adjustment. drop(columns=['CA ANEN'])),
                                                       np. array(df DAG limited adjustment['CA ANEN']))
          beta = model. coef [0, 0]
          odds ratio = np. exp(beta)
          print ("The odds ratio for fully adjusted association is", odds ratio)
         positive data = np. array(positive data)
          false data = np. array(false data)
          s1 = np. var(positive data, ddof = 1)
         s2 = np. var(false data, ddof = 1)
          n1 = len(positive data)
          n2 = 1en(false data)
         x1 mu = np. mean (positive data)
          x2 mu = np. mean(false data)
          z = 1.96
          sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
         ci 1 = (x1 mu - x2 mu) - z * sp * np. sqrt (1/n1 + 1/n2)
          ci 2 = (x1 mu - x2 mu) + z * sp * np. sqrt (1/n1 + 1/n2)
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print("The 95% confidence level is", [ci_1, ci_2])
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IP_HEPB

```
In [ ]:
         df = df save for causal
          exposure = "IP HEPB" # change for your exposure
         outcome = "CA ANEN"
         df DAG unadjusted = df[[exposure, outcome]].dropna()
          model = LogisticRegression (max iter=1e6). fit (np. array (df DAG unadjusted[exposure], dtype=np. float64). reshape (-1, 1),
                                                       np. array (df DAG unadjusted ['CA ANEN'], dtype=np. float64))
          beta = model.coef [0, 0]
          odds ratio = np. exp(beta)
          print ("The odds ratio for unadjusted association is", odds ratio)
         print("positive: ", len(df DAG unadjusted[df DAG unadjusted[exposure] == 1]))
         print("negative: ", len(df DAG unadjusted[df DAG unadjusted[exposure] == 0]))
          positive data = df DAG unadjusted[df DAG unadjusted['CA ANEN'] == 1]
          positive data = positive data. drop(columns=['CA ANEN'])
         false_data = df_DAG_unadjusted[df_DAG_unadjusted['CA ANEN'] == 0]
         false data = false data. drop(columns=['CA ANEN'])
         print("# of positive data", len(positive data))
         print("# of false data", len(false data))
          print ("# of total population", len(df))
         results = st. ttest ind(a=false data, b=positive data, equal var=False, alternative='two-sided')
         print(" - statistics = {}". format(results. statistic))
```

```
print(" - p-value = {}". format(results. pvalue))
positive data = np. array(positive data)
false data = np. array(false data)
s1 = np. var(positive data, ddof = 1)
s2 = np. var(false data, ddof = 1)
n1 = len(positive data)
n2 = 1en(false data)
x1 mu = np. mean (positive data)
x2 mu = np. mean(false data)
z = 1.96
sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
ci 1 = (x1 mu - x2 mu) - z * sp * np. sqrt (1/n1 + 1/n2)
ci 2 = (x1 mu - x2 mu) + z * sp * np. sqrt (1/n1 + 1/n2)
print ("The 95% confidence level is", [ci 1, ci 2])
exposure = "IP HEPB" # change for your exposure
variableMostConfident = "CIG 0" # change for your variables
outcome = "CA ANEN"
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```
In [ ]:
         df DAG limited adjustment = df[[exposure, variableMostConfident, outcome]].dropna()
         model = LogisticRegression(max iter=1e6). fit(np. array(df DAG limited adjustment. drop(columns=['CA ANEN'])),
                                                       np. array(df DAG limited adjustment['CA ANEN']))
         beta = model.coef[0, 0]
         odds ratio = np. exp(beta)
         print("The odds ratio for Naïve adjusted association is", odds ratio)
         positive data = np. array (positive data)
         false data = np. array(false data)
         s1 = np. var(positive data, ddof = 1)
         s2 = np. var(false data, ddof = 1)
         n1 = len(positive data)
         n2 = 1en(false data)
         x1 mu = np. mean (positive data)
         x2 mu = np. mean(false data)
         z = 1.96
         sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
```

```
print("The 95% confidence level is", [ci 1, ci 2])
In [ ]:
         exposure = "IP HEPB" # change for your exposure
         outcome = "CA ANEN"
         # change based on your DAG
         df DAG limited adjustment = df[[exposure, 'CIG O', 'RF INFTR', 'MEDUC', 'FEDUC', 'RF PDIAB', 'RF GDIAB', outcome]]. dropna()
         model = LogisticRegression(max iter=1e6). fit(np. array(df DAG limited adjustment. drop(columns=['CA ANEN'])),
                                                       np. array(df DAG limited adjustment['CA ANEN']))
         beta = model.coef [0, 0]
         odds ratio = np. exp(beta)
         print ("The odds ratio for fully adjusted association is", odds ratio)
         positive data = np. array(positive data)
         false data = np. array(false data)
         s1 = np. var(positive data, ddof = 1)
         s2 = np. var(false data, ddof = 1)
         n1 = len(positive data)
         n2 = 1en(false data)
         x1 mu = np. mean (positive data)
         x2 mu = np. mean(false data)
         z = 1.96
         sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
         ci 1 = (x1 mu - x2 mu) - z * sp * np. sqrt (1/n1 + 1/n2)
         ci 2 = (x1 mu - x2 mu) + z * sp * np. sqrt (1/n1 + 1/n2)
         print ("The 95% confidence level is", [ci 1, ci 2])
In [ ]:
         1 = df. columns. values. tolist()
         for i in range (1en(1)-1):
```

 $ci_1 = (x1_mu - x2_mu) - z * sp * np. sqrt(1/n1 + 1/n2)$ $ci_2 = (x1_mu - x2_mu) + z * sp * np. sqrt(1/n1 + 1/n2)$

```
exposure = 1[i]
outcome = "CA ANEN"
df DAG unadjusted = df[[exposure, outcome]]. dropna()
model = LogisticRegression (max iter=1e6). fit (np. array (df DAG unadjusted exposure, dtype=np. float64). reshape (-1,1),
                                              np. array (df DAG unadjusted ['CA ANEN'], dtype=np. float64))
beta = model.coef [0, 0]
odds ratio = np. exp(beta)
print(1[i], "The odds ratio for unadjusted association is", odds ratio)
, , ,
positive data = df DAG unadjusted[df DAG unadjusted['CA ANEN'] == 1]
positive data = positive data.drop(columns=['CA ANEN'])
false data = df DAG unadjusted[df DAG unadjusted['CA ANEN'] == 0]
false data = false data.drop(columns=['CA ANEN'])
results = st.ttest ind(a=false data, b=positive data, equal var=False, alternative='two-sided')
print(" - statistics = {}".format(results.statistic))
print(" - p-value = {}".format(results.pvalue))
positive data = np. array (positive data)
false data = np. array(false data)
s1 = np. var(positive data, ddof = 1)
s2 = np. var(false data, ddof = 1)
n1 = len(positive data)
n2 = len(false data)
x1 mu = np. mean(positive data)
x2 mu = np. mean(false data)
z = 1.96
sp = np. sqrt(((n1-1)*s1**2+(n2-1)*s2**2)/(n1+n2-2))
ci 1 = (x1 mu - x2 mu) - z * sp * np. sqrt (1/n1 + 1/n2)
ci 2 = (x1 mu - x2 mu) + z * sp * np. sqrt (1/n1 + 1/n2)
print ("The 95% confidence level is", [ci 1, ci 2])
```

```
CIG 1 The odds ratio for unadjusted association is 0.9987017088165707
CIG 2 The odds ratio for unadjusted association is 1.0110606003368303
CIG 3 done
PRIORLIVE The odds ratio for unadjusted association is 1.1947840524182531
PRIORDEAD The odds ratio for unadjusted association is 1.3387372490209957 -> to do
PRIORTERM The odds ratio for unadjusted association is 1.1713297909526108
ILLB R The odds ratio for unadjusted association is 1.002104084704455
ILOP R The odds ratio for unadjusted association is 1.0016633028289226
ILP R The odds ratio for unadjusted association is 0.9995076020172732
IP GON The odds ratio for unadjusted association is 0.7461448009317625
IP SYPH The odds ratio for unadjusted association is 0.8191542650408749
IP CHLAM The odds ratio for unadjusted association is 1.0596617578968939
IP HEPB done
IP HEPC The odds ratio for unadjusted association is 1.2267542819334163
RF PDIAB done
RF GDIAB The odds ratio for unadjusted association is 0.9533819751478366
BMI The odds ratio for unadjusted association is 1.011010932399839
PWgt R The odds ratio for unadjusted association is 1.0005549689713746
WTGAIN done
RF INFTR The odds ratio for unadjusted association is 0.9222551027523305
RF FEDRG The odds ratio for unadjusted association is 0.7522220620267115
FEDUC The odds ratio for unadjusted association is 0.8616172656186928
MEDUC The odds ratio for unadjusted association is 0.828819665402354
FAGECOMB The odds ratio for unadjusted association is 0.99375851582722
MAGER The odds ratio for unadjusted association is 1.0005779591583988
, , ,
```