About The Wrapping Method. • It to predict to predict the target variable on the basis randomly selective features and those will give us better prediction assumme that this features combination bettter is best for us. But it having drawbacks that is nothing but is computationally very expensive than filter method. But Perform the better than filter method. It is not always recommended to the higher dimensional datasets. Types Of Wrapping Methods. Foreward Step Selection.(Recurssive) Backward Step Selection.(Recurssive) Exhaustive Feature Selection (Subset Selection) In the Filter Method we do not use the machine learning algorithm but in the wrapper we use the machine learning algorithm while selecting Features. **Foreward Step Selection.** In this Foreward Step Selection method start to use the feature from intial level there we will use feature first time then it will possible and random combination with other feature to make the better the prediction. Select the best feature combination. **Backward Step Selection.** In this feature selection techique we generally initialized with the all features then step by step removing the features which are not so much putting the information to predict the best possible outcome. **Exhaustive Feature Selection** It is uses all posiible combination all features. It requires Massive Comutational Power. Let's Start With Machine Learning import pandas as pd import numpy as np import matplotlib.pyplot as plt import seaborn as sns import warnings warnings.filterwarnings('ignore') from sklearn.preprocessing import StandardScaler from sklearn.metrics import accuracy score, confusion matrix, classification report from sklearn.model selection import train test split from mlxtend.feature selection import SequentialFeatureSelector as SFS data = pd.read csv('Wine.csv') data.head() Alcohol Malic Acid Ash Ash_Alcanity Magnesium Total_Phenols Flavanoids **Nonflavanoid Phenols Proanthocyanins** Color_Intensity Hue 0 14.23 1.71 2.43 15.6 127 2.80 3.06 0.28 2.29 5.64 1.04 1.78 2.14 1 13.20 11.2 100 2.65 2.76 0.26 1.28 4.38 1.0 2 101 3.24 13.16 2.36 2.67 18.6 2.80 0.30 2.81 5.68 1.03 3 14.37 1.95 2.50 16.8 113 3.85 0.24 3.49 2.18 7.80 0.8 2.59 2.87 2.80 1.82 13.24 21.0 118 2.69 0.39 4.32 1.04 data.tail() Alcohol Malic_Acid Ash Ash_Alcanity Magnesium Total_Phenols Flavanoids Nonflavanoid_Phenols Proanthocyanins Color_Intensity F 0.52 173 13.71 5.65 2.45 20.5 95 1.68 0.61 1.06 7.7 (174 13.40 3.91 2.48 23.0 102 1.80 0.75 0.43 1.41 7.3 175 13.27 4.28 2.26 20.0 120 1.59 0.69 0.43 1.35 10.2 (176 13.17 2.59 2.37 20.0 120 1.65 0.68 0.53 1.46 9.3 (2.05 0.76 0.56 1.35 9.2 (177 14.13 4.10 2.74 24.5 96 data.columns 'Customer Segment'], dtype='object') data.nunique() Out[63]: Alcohol 133 Malic Acid 79 Ash 63 Ash Alcanity Magnesium Total Phenols 97 Flavanoids 132 Nonflavanoid_Phenols 39 Proanthocyanins 101 Color Intensity 132 Hue 78 OD280 122 Proline 121 Customer Segment 3 dtype: int64 In [64]: x = data.drop(columns=['Customer Segment']) y = data['Customer Segment'] x.shape, y.shape Out[65]: ((178, 13), (178,)) x train, x test, y train, y test = train test split(x,y,train size=0.80,random state=42,stratify=y) x train.shape,x test.shape ((142, 13), (36, 13)) from sklearn.ensemble import RandomForestClassifier sel = SFS(RandomForestClassifier(n estimators=100, criterion='gini', random state=42), k features=8, forward=True, f sel.fit(x train, y train) Out[70]: SequentialFeatureSelector(clone estimator=True, cv=4, estimator=RandomForestClassifier(bootstrap=True, ccp_alpha=0.0, class weight=None, criterion='gini', max depth=None, max features='auto', max leaf nodes=None, max samples=None, min impurity decrease=0.0, min_impurity_split=None, min_samples_leaf=1, min samples split=2, min weight fraction leaf=0.0, n estimators=100, n jobs=None, oob score=False, random state=42, verbose=0, warm start=False), floating=False, forward=True, k features=8, n jobs=1, pre_dispatch='2*n_jobs', scoring='accuracy', verbose=0) sel.k feature names Out[71]: ('Alcohol', 'Malic Acid', 'Ash Alcanity', 'Magnesium', 'Flavanoids', 'Proanthocyanins', 'Color Intensity', 'Hue') sel.k score 0.99305555555556 pd.DataFrame.from dict(sel.get metric dict()).T feature idx cv_scores avg_score feature_names ci bound std_dev std_err (Color_Intensity,) (9,)0.683333 0.090885 0.0566974 0.0327343 0.6388888888888888, 0.628... [0.88888888888888, 2 (6, 9)0.950992 (Flavanoids, Color_Intensity) 0.0574777 0.0358567 0.0207019 0.97222222222222, 0.971... [0.916666666666666, 1.0, (Magnesium, Flavanoids, 0.0582191 0.0363193 3 (4, 6, 9)0.964881 0.0209689 0.9428571428571428, ... Color_Intensity) [0.97222222222222, (Alcohol, Magnesium, Flavanoids, 0.0314903 0.0196449 4 (0, 4, 6, 9)0.972024 0.011342 Color_Intensity) [1.0, 0.972222222222222, (Alcohol, Magnesium, Flavanoids, 0.0225862 0.0140901 0.00813492 5 0.985913 (0, 4, 6, 8, 9)0.9714285714285714, ... Proanthocyani... (Alcohol, Malic_Acid, Magnesium, [1.0, 0.97222222222222, 0.985913 0.0225862 0.0140901 0.00813492 (0, 1, 4, 6, 8, 9)0.9714285714285714, ... Flavanoids, P... (0, 1, 4, 6, 8, 9, (Alcohol, Malic_Acid, Magnesium, [1.0, 0.97222222222222, 1.0, 1.0] 0.993056 0.0192809 0.0120281 0.00694444 Flavanoids, P... (0, 1, 3, 4, 6, 8, 9,(Alcohol, Malic_Acid, Ash_Alcanity, 0.0192809 0.0120281 0.00694444 [1.0, 0.97222222222222, 1.0, 1.0] 0.993056 Magnesium,... **Backward Selection Method** sel = SFS(RandomForestClassifier(n estimators=100,criterion='gini',random state=42),k features=8,forward=False, In [74]: sel.fit(x train, y train) Out[74]: SequentialFeatureSelector(clone estimator=True, cv=4, estimator=RandomForestClassifier(bootstrap=True, ccp alpha=0.0, class weight=None,

sbs = sel

('Alcohol', 'Malic Acid',

'Ash Alcanity', 'Magnesium', 'Total Phenols', 'Flavanoids', 'Color_Intensity')

sbs.k_score_

12

9

8

0.99305555555556

pd.DataFrame(sbs.get metric dict()).T

feature_idx

10, 11, 12)

10, 11)

11)

(0, 1, 2, 3, 4, 5, 6, 7, 8, 9,

(0, 1, 2, 3, 4, 5, 6, 7, 8, 9,

(0, 1, 2, 3, 4, 5, 6, 7, 9, 10,

(0, 1, 2, 3, 4, 5, 6, 7, 9)

(0, 1, 2, 3, 4, 5, 6, 9)

efs.fit(x_train,y_train)

Exhaustive Feature Selection.

10 (0, 1, 2, 3, 4, 5, 6, 7, 9, 10)

'Ash',

sbs.k feature names

verbose=0)

criterion='gini', max depth=None, max features='auto', max leaf nodes=None, max samples=None,

n estimators=100, n jobs=None, oob score=False, random state=42,

warm start=False),

verbose=0,

floating=False, forward=False, k features=8, n jobs=1,

pre dispatch='2*n_jobs', scoring='accuracy',

cv scores

[0.9722222222222,

[0.97222222222222,

[0.97222222222222,

0.97222222222222, 1.0, ...

0.97222222222222, 0.971...

0.97222222222222, 0.971...

[1.0, 0.9722222222222, 1.0, 1.0]

[1.0, 0.9722222222222, 1.0, 1.0]

from mlxtend.feature selection import ExhaustiveFeatureSelector as efs

avg_score

0.978968

0.978968

0.993056

0.986111

0.986111

0.993056

efs = efs(RandomForestClassifier(n estimators=100, criterion='gini', random state=42), min features=4, max features

min_impurity_decrease=0.0, min_impurity_split=None, min_samples_leaf=1, min samples split=2,

min weight fraction leaf=0.0,

feature_names

(Alcohol, Malic_Acid, Ash,

Ash_Alcanity, Magne...

Ash_Alcanity, Magne...

Ash_Alcanity, Magne...

Ash_Alcanity, Magne...

Ash_Alcanity, Magne...

Ash_Alcanity, Magne...

ci bound

0.0194714

0.0194714

0.0192809

0.0385617 0.0240563

std dev

0.0222636 0.0138889 0.00801875

0.0192809 0.0120281 0.00694444

0.012147 0.00701308

0.012147 0.00701308

0.0120281 0.00694444

std err

0.0138889