

▼ Project Wine

Group 4

Team Members:

Gabriella Rosal Calit, Sebastian Bonifasi Sanchez, Priya Khullar, KC Kim

```
%matplotlib inline

import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import statsmodels.api as sm

from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import scale
from sklearn.model_selection import train_test_split, cross_val_score, RepeatedKFold, GridSearchCV
from sklearn.linear_model import LinearRegression, Ridge, RidgeCV, Lasso, LassoCV, ElasticNet, ElasticNetCV
from sklearn.metrics import mean_squared_error
from numpy import mean
from numpy import std
from numpy import absolute

wine_data = pd.read_csv("winequality-red.csv")
X = wine_data.drop("quality", axis=1)
y = wine_data["quality"]
```

▼ Ordinary Least Squares (OLS)

```
wineQuality = wine_data
wineQuality
```

	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	densi
0	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.997
1	7.8	0.880	0.00	2.6	0.098	25.0	67.0	0.996
2	7.8	0.760	0.04	2.3	0.092	15.0	54.0	0.997
3	11.2	0.280	0.56	1.9	0.075	17.0	60.0	0.998
4	7.4	0.700	0.00	1.9	0.076	11.0	34.0	0.997
...	...	...	...	...	...	...	...	...
1594	6.2	0.600	0.08	2.0	0.090	32.0	44.0	0.994
1595	5.9	0.550	0.10	2.2	0.062	39.0	51.0	0.995
1596	6.3	0.510	0.13	2.3	0.076	29.0	40.0	0.995
1597	5.9	0.645	0.12	2.0	0.075	32.0	44.0	0.995
1598	6.0	0.310	0.47	3.6	0.067	18.0	42.0	0.995

1599 rows x 12 columns



```
wineQuality.sort_values('quality', inplace=True)

# Added a constant to the independent variables
X_ols = sm.add_constant(X)
model = sm.OLS(y, X_ols)
results = model.fit()

print(results.summary())
```

## OLS Regression Results

=====						
Dep. Variable:	quality	R-squared:	0.361			
Model:	OLS	Adj. R-squared:	0.356			
Method:	Least Squares	F-statistic:	81.35			
Date:	Tue, 02 May 2023	Prob (F-statistic):	1.79e-145			
Time:	23:42:46	Log-Likelihood:	-1569.1			
No. Observations:	1599	AIC:	3162.			
Df Residuals:	1587	BIC:	3227.			
Df Model:	11					
Covariance Type:	nonrobust					
=====						
	coef	std err	t	P> t	[0.025	0.975]
-----						
const	21.9652	21.195	1.036	0.300	-19.607	63.538
fixed acidity	0.0250	0.026	0.963	0.336	-0.026	0.076
volatile acidity	-1.0836	0.121	-8.948	0.000	-1.321	-0.846
citric acid	-0.1826	0.147	-1.240	0.215	-0.471	0.106
residual sugar	0.0163	0.015	1.089	0.276	-0.013	0.046
chlorides	-1.8742	0.419	-4.470	0.000	-2.697	-1.052
free sulfur dioxide	0.0044	0.002	2.009	0.045	0.000	0.009
total sulfur dioxide	-0.0033	0.001	-4.480	0.000	-0.005	-0.002
density	-17.8812	21.633	-0.827	0.409	-60.314	24.551
pH	-0.4137	0.192	-2.159	0.031	-0.789	-0.038
sulphates	0.9163	0.114	8.014	0.000	0.692	1.141
alcohol	0.2762	0.026	10.429	0.000	0.224	0.328
=====						
Omnibus:	27.376	Durbin-Watson:	1.757			
Prob(Omnibus):	0.000	Jarque-Bera (JB):	40.965			
Skew:	-0.168	Prob(JB):	1.27e-09			
Kurtosis:	3.708	Cond. No.	1.13e+05			
=====						

## Notes:

- [1] Standard Errors assume that the covariance matrix of the errors is correctly specified.  
 [2] The condition number is large, 1.13e+05. This might indicate that there are strong multicollinearity or other numerical problems.

```
#Baseline Model
regression = LinearRegression()
regression.fit(X,y)
first_model = (mean_squared_error(y_true=y, y_pred=regression.predict(X)))
print(first_model)

0.41676716722125007
```

```
#Coefficients_OLS
coef_dict_baseline = {}
for coef, feat in zip(regression.coef_, X.columns) :
    coef_dict_baseline[feat] = coef
coef_dict_baseline

{'fixed acidity': 0.024990552675656412,
 'volatile acidity': -1.083590258692188,
 'citric acid': -0.1825639484061993,
 'residual sugar': 0.01633126976610759,
 'chlorides': -1.8742251580848106,
 'free sulfur dioxide': 0.0043613333090892215,
 'total sulfur dioxide': -0.0032645797031345403,
 'density': -17.88116383506437,
 'pH': -0.4136531438094561,
 'sulphates': 0.9163344127157658,
 'alcohol': 0.27619769922229687}
```

## ▼ Ridge Regression

Calculating the cross-validation errors for each alphas with Ridge Regression

```
alphas = np.arange(0.1,1.01,0.01)
errors = np.zeros(len(alphas))
i = 0

for alpha in alphas:
    L2_cv = RidgeCV(alphas=[alpha], cv=10, scoring='neg_mean_squared_error').fit(X,y)
    errors[i] = -L2_cv.best_score_
    i += 1
```

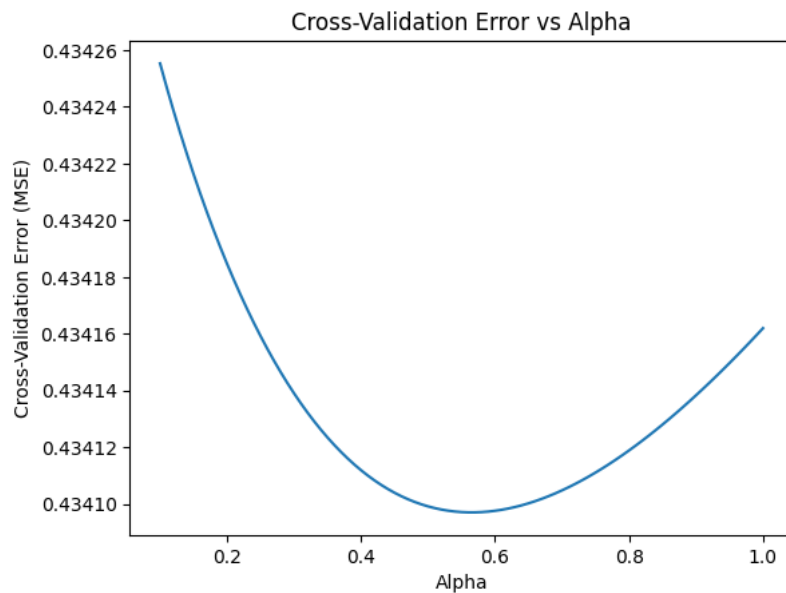
errors

```
array([0.43425534, 0.43424685, 0.43423872, 0.43423093, 0.43422347,
       0.43421631, 0.43420944, 0.43420285, 0.43419653, 0.43419048,
       0.43418468, 0.43417912, 0.4341738 , 0.4341687 , 0.43416384,
       0.43415918, 0.43415475, 0.43415051, 0.43414648, 0.43414264,
       0.43413898, 0.43413552, 0.43413223, 0.43412912, 0.43412618,
       0.4341234 , 0.43412079, 0.43411833, 0.43411603, 0.43411388,
       0.43411188, 0.43411001, 0.43410829, 0.4341067 , 0.43410525,
       0.43410392, 0.43410272, 0.43410165, 0.43410069, 0.43409985,
       0.43409912, 0.43409851, 0.434098 , 0.4340976 , 0.43409731,
       0.43409711, 0.43409701, 0.43409701, 0.43409711, 0.43409729,
       0.43409756, 0.43409793, 0.43409837, 0.4340989 , 0.43409951,
       0.4341002 , 0.43410097, 0.43410181, 0.43410272, 0.43410371,
       0.43410477, 0.43410589, 0.43410709, 0.43410834, 0.43410966,
       0.43411105, 0.43411249, 0.43411399, 0.43411555, 0.43411717,
       0.43411884, 0.43412056, 0.43412234, 0.43412417, 0.43412605,
       0.43412797, 0.43412995, 0.43413197, 0.43413403, 0.43413614,
       0.43413829, 0.43414048, 0.43414272, 0.43414499, 0.43414731,
       0.43414966, 0.43415205, 0.43415447, 0.43415693, 0.43415942,
       0.43416195])
```

Plotting the alphas vs cross-validation errors

```
plt.plot(alphas, errors)
plt.xlabel("Alpha")
plt.ylabel("Cross-Validation Error (MSE)")
plt.title("Cross-Validation Error vs Alpha")
```

```
Text(0.5, 1.0, 'Cross-Validation Error vs Alpha')
```



The Optimal Coefficients for Lasso Regression

```
L2_cv = RidgeCV(alphas=alphas, cv=10, scoring='neg_mean_squared_error').fit(X,y)
L2_coef = pd.Series(L2_cv.coef_, index=X.columns)
L2_coef
```

```
fixed acidity      0.011715
volatile acidity  -1.105811
citric acid       -0.196327
residual sugar     0.008078
chlorides         -1.539256
free sulfur dioxide 0.004489
total sulfur dioxide -0.003248
density          -0.033193
pH               -0.461639
sulphates         0.844934
alcohol           0.296391
dtype: float64
```

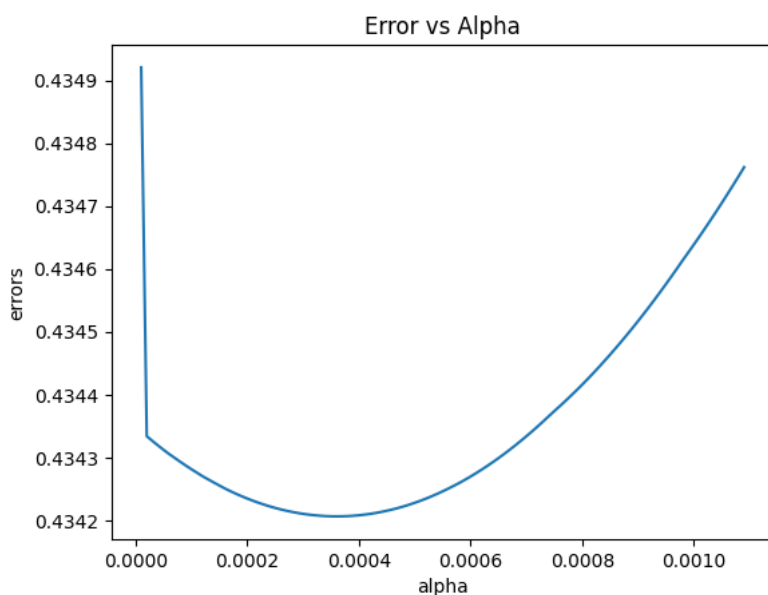
## ▼ Lasso Regression

```
#plot alpha vs cross validation error
lasso = Lasso(max_iter = 10000)
errors = []
alpha2= np.arange(0.00001, 0.0011, 0.00001)

for alpha in alpha2:
    Lasso_Graph = LassoCV(alphas=[alpha], cv=10).fit(X,y)
    errors += [np.mean(Lasso_Graph.mse_path_)]
print (errors)

plt.plot(alpha2, errors)
plt.xlabel('alpha')
plt.ylabel('errors')
plt.title("Error vs Alpha")

[0.4349207254891259, 0.4343337029859756, 0.43432629719924093, 0.43431910937
Text(0.5, 1.0, 'Error vs Alpha')
```



```
#table of coeff
L1_cv = LassoCV(alphas=alpha2, cv=10).fit(X,y)
L1_coef = pd.Series(L1_cv.coef_, index=X.columns)
L1_coef
```

```
fixed acidity      0.009732
volatile acidity  -1.088788
citric acid       -0.158843
residual sugar     0.007936
chlorides         -1.669697
free sulfur dioxide 0.004549
total sulfur dioxide -0.003293
density           -0.000000
pH                -0.453641
sulphates          0.854297
alcohol            0.293931
dtype: float64
```

## ▼ Elastic Net

```
# Define the pipeline
pipe = Pipeline([
    ('scaler', StandardScaler()),
    ('elastic', ElasticNet())])
```

```

# Define the grid search
search = GridSearchCV(
    estimator=pipe,
    param_grid={
        'elastic__alpha': np.logspace(-5, 2, 8),
        'elastic__l1_ratio': [0.2, 0.4, 0.6, 0.8]
    },
    scoring='neg_mean_squared_error',
    n_jobs=1,
    refit=True,
    cv=10
)

search.fit(X,y)
print(search.best_params_)
print(abs(search.best_score_))

    {'elastic__alpha': 0.01, 'elastic__l1_ratio': 0.8}
    0.43420396645297565

model_elastic = ElasticNet(alpha=0.01, l1_ratio=0.8)
model_elastic.fit(X,y)
second_model_elastic = (mean_squared_error(y_true=y, y_pred=model_elastic.predict(X)))
print(second_model_elastic)

    0.4300141899744741

ENet = ElasticNetCV(cv=10, l1_ratio=0.8).fit(X,y)
ENet.alpha_

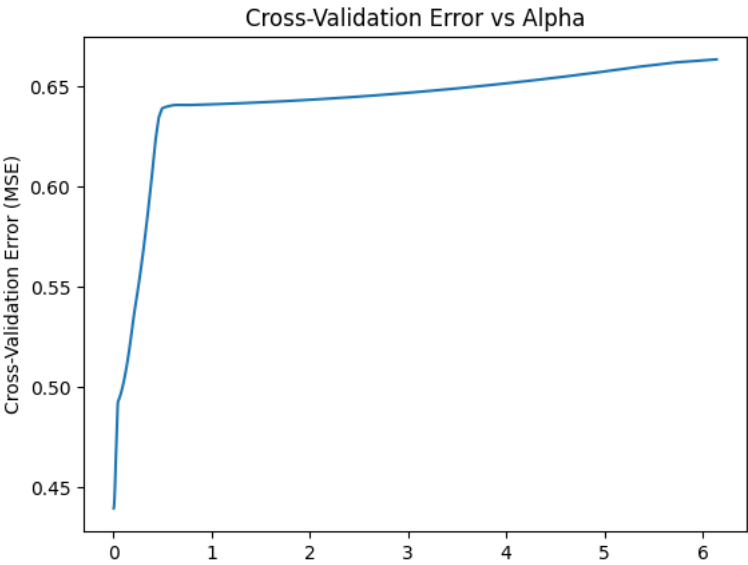
    0.006142702345626427

pd.Series(ENet.coef_, index=X.columns)

    fixed acidity      0.030865
    volatile acidity  -0.956373
    citric acid        -0.000000
    residual sugar     0.000000
    chlorides          -0.000000
    free sulfur dioxide 0.004852
    total sulfur dioxide -0.003083
    density            -0.000000
    pH                 -0.000000
    sulphates          0.514888
    alcohol            0.302855
    dtype: float64

plt.plot(ENet.alphas_, np.mean(ENet.mse_path_,axis=1))
plt.xlabel('Alpha (a+b)') #a = L1 parameter, b = L2 parameter
plt.ylabel("Cross-Validation Error (MSE)")
plt.title("Cross-Validation Error vs Alpha")
plt.show()

```



✓ 0s completed at 4:43 PM

