

# project\_1\_final\_combined

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## 0.1 Econ 412 Project 1

Alex Hong: 905857714

Gedian Wang: 705638831

Youssef Mahmoud: 905854027

Zachary DeBar: 705867064

### 0.1.1 Section 1: Classification

```
[1]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import sklearn
import seaborn as sns #visualization library
from sklearn.naive_bayes import GaussianNB
from sklearn.linear_model import LogisticRegression #problem will be solved
    ↳with scikit
from sklearn.metrics import accuracy_score
from sklearn import metrics
from sklearn.metrics import mean_squared_error
from sklearn.model_selection import train_test_split, LeaveOneOut, KFold,
    ↳cross_val_score
from sklearn.preprocessing import PolynomialFeatures
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis # LDA
from sklearn.discriminant_analysis import QuadraticDiscriminantAnalysis # QDA
from sklearn.neighbors import KNeighborsClassifier #(KNN)
from sklearn.metrics import confusion_matrix, classification_report,
    ↳precision_score
import statsmodels.api as sm
from IPython.core.pylabtools import figsize
import statsmodels.formula.api as smf
from patsy import dmatrices
from sklearn import datasets
%matplotlib inline
```

```
[2]: df1 = pd.read_csv('healthcare-dataset-stroke-data.csv')
df1
```

```
[2]:
```

	id	gender	age	hypertension	heart_disease	ever_married	\
0	9046	Male	67.0	0	1	Yes	
1	51676	Female	61.0	0	0	Yes	
2	31112	Male	80.0	0	1	Yes	
3	60182	Female	49.0	0	0	Yes	
4	1665	Female	79.0	1	0	Yes	
...	...	...	...	...	...	...	
5105	18234	Female	80.0	1	0	Yes	
5106	44873	Female	81.0	0	0	Yes	
5107	19723	Female	35.0	0	0	Yes	
5108	37544	Male	51.0	0	0	Yes	
5109	44679	Female	44.0	0	0	Yes	

	work_type	Residence_type	avg_glucose_level	bmi	smoking_status	\
0	Private	Urban	228.69	36.6	formerly smoked	
1	Self-employed	Rural	202.21	NaN	never smoked	
2	Private	Rural	105.92	32.5	never smoked	
3	Private	Urban	171.23	34.4	smokes	
4	Self-employed	Rural	174.12	24.0	never smoked	
...	...	...	...	...	...	
5105	Private	Urban	83.75	NaN	never smoked	
5106	Self-employed	Urban	125.20	40.0	never smoked	
5107	Self-employed	Rural	82.99	30.6	never smoked	
5108	Private	Rural	166.29	25.6	formerly smoked	
5109	Govt_job	Urban	85.28	26.2	Unknown	

	stroke
0	1
1	1
2	1
3	1
4	1
...	...
5105	0
5106	0
5107	0
5108	0
5109	0

[5110 rows x 12 columns]

```
[3]: df1.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 5110 entries, 0 to 5109
```

Data columns (total 12 columns):

#	Column	Non-Null Count	Dtype
0	id	5110 non-null	int64
1	gender	5110 non-null	object
2	age	5110 non-null	float64
3	hypertension	5110 non-null	int64
4	heart_disease	5110 non-null	int64
5	ever_married	5110 non-null	object
6	work_type	5110 non-null	object
7	Residence_type	5110 non-null	object
8	avg_glucose_level	5110 non-null	float64
9	bmi	4909 non-null	float64
10	smoking_status	5110 non-null	object
11	stroke	5110 non-null	int64

dtypes: float64(3), int64(4), object(5)

memory usage: 479.2+ KB

For our classification data, we chose to analyze patient data containing observations of stroke and other variables which may have been useful in predicting stroke before it occurred. This set originates from the World Health Organization. The variables are as follows:

- 1) id: unique identifier
- 2) gender: “Male”, “Female” or “Other”
- 3) age: age of the patient
- 4) hypertension: 0 if the patient doesn’t have hypertension, 1 if the patient has hypertension
- 5) heart\_disease: 0 if the patient has no heart diseases, 1 if the patient has a heart disease
- 6) ever\_married: “No” or “Yes”
- 7) work\_type: “children”, “Govt\_job”, “Never\_worked”, “Private” or “Self-employed”
- 8) Residence\_type: “Rural” or “Urban”
- 9) avg\_glucose\_level: average glucose level in blood
- 10) bmi: Body Mass Index
- 11) smoking\_status: “formerly smoked”, “never smoked”, “smokes” or “Unknown”\*
- 12) stroke: 1 if the patient suffered a stroke, 0 if patient has not suffered stroke \*Note: “Unknown” in smoking\_status means that the information is unavailable for this patient

```
[4]: df1['gender'] = df1['gender'].map({'Male':0, 'Female':1})
df1['ever_married'] = df1['ever_married'].map({'No':0, 'Yes':1})
```

```
df1['work_type'] = df1['work_type'].map({'Private':0, 'Self-employed':
    ↪1, 'Govt_job':2})
df1['Residence_type'] = df1['Residence_type'].map({'Urban':0, 'Rural':1})
df1['smoking_status'] = df1['smoking_status'].map({'never smoked':0, 'Unknown':
    ↪1, 'formerly smoked':2, 'smokes':3})
```

```
[5]: df1.update(df1['bmi'].fillna(value=df1['bmi'].mean(), inplace=True))
```

```
[6]: df1

df1_backup = df1
```

```
[7]: df1.corr()
```

```
[7]:
```

	id	gender	age	hypertension	heart_disease	\
id	1.000000	-0.001929	0.003538	0.003550	-0.001296	
gender	-0.001929	1.000000	0.027752	-0.021223	-0.085685	
age	0.003538	0.027752	1.000000	0.276398	0.263796	
hypertension	0.003550	-0.021223	0.276398	1.000000	0.108306	
heart_disease	-0.001296	-0.085685	0.263796	0.108306	1.000000	
ever_married	0.013690	0.030171	0.679125	0.164243	0.114644	
work_type	-0.014817	0.008759	0.190557	0.047113	0.024998	
Residence_type	0.001403	-0.006105	-0.014180	0.007913	-0.003092	
avg_glucose_level	0.001092	-0.054722	0.238171	0.174474	0.161857	
bmi	0.002999	0.025606	0.325942	0.160189	0.038899	
smoking_status	-0.001713	-0.067496	0.079205	0.012531	0.063138	
stroke	0.006388	-0.009081	0.245257	0.127904	0.134914	

	ever_married	work_type	Residence_type	avg_glucose_level	\
id	0.013690	-0.014817	0.001403	0.001092	
gender	0.030171	0.008759	-0.006105	-0.054722	
age	0.679125	0.190557	-0.014180	0.238171	
hypertension	0.164243	0.047113	0.007913	0.174474	
heart_disease	0.114644	0.024998	-0.003092	0.161857	
ever_married	1.000000	0.118094	-0.006261	0.155068	
work_type	0.118094	1.000000	-0.020416	0.022348	
Residence_type	-0.006261	-0.020416	1.000000	0.004946	
avg_glucose_level	0.155068	0.022348	0.004946	1.000000	
bmi	0.335705	0.006788	0.000120	0.168751	
smoking_status	0.085086	0.001486	-0.032112	0.025186	
stroke	0.108340	0.015050	-0.015458	0.131945	

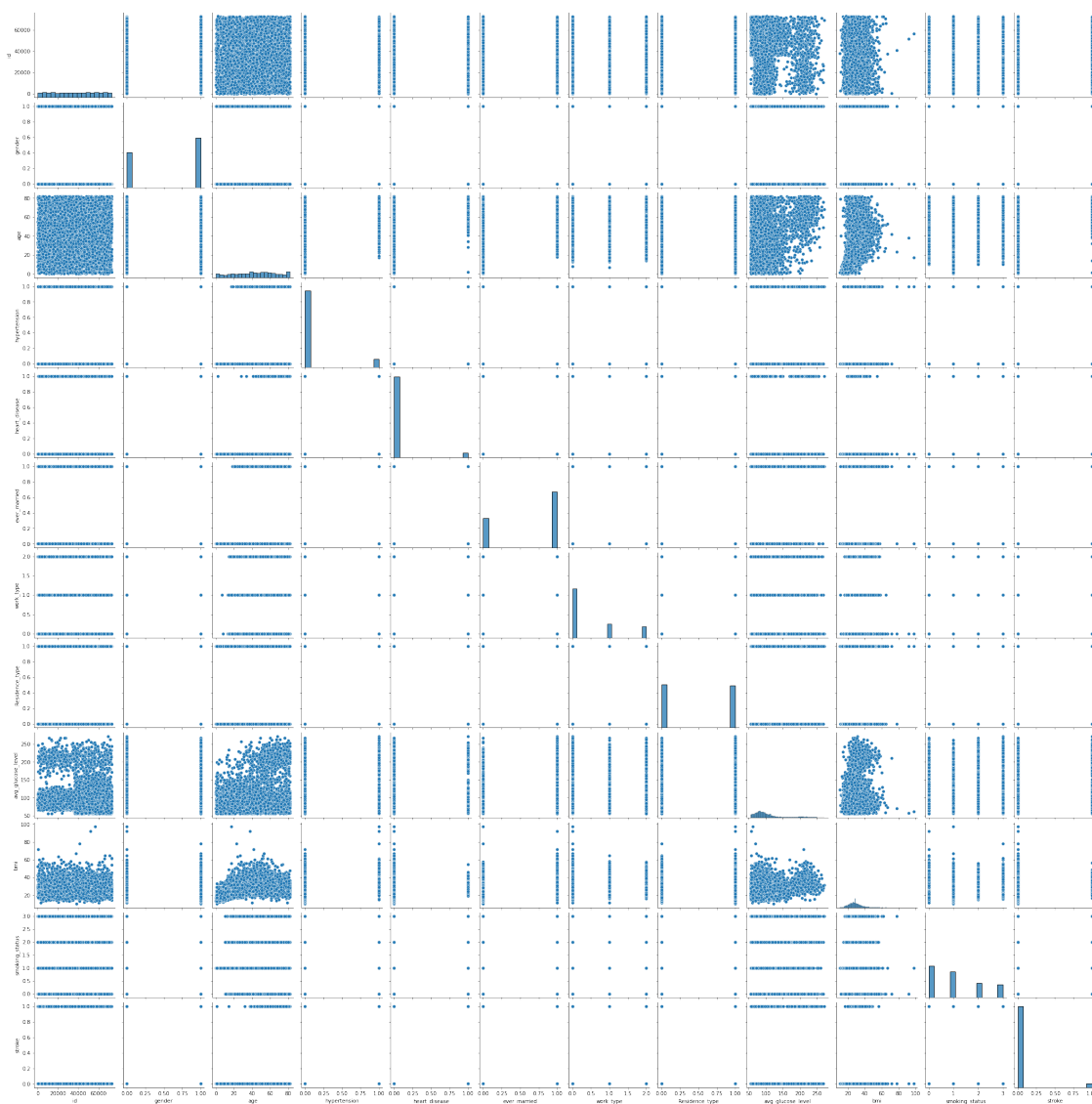
  

	bmi	smoking_status	stroke
id	0.002999	-0.001713	0.006388
gender	0.025606	-0.067496	-0.009081
age	0.325942	0.079205	0.245257
hypertension	0.160189	0.012531	0.127904

heart_disease	0.038899	0.063138	0.134914
ever_married	0.335705	0.085086	0.108340
work_type	0.006788	0.001486	0.015050
Residence_type	0.000120	-0.032112	-0.015458
avg_glucose_level	0.168751	0.025186	0.131945
bmi	1.000000	0.046660	0.038947
smoking_status	0.046660	1.000000	0.030682
stroke	0.038947	0.030682	1.000000

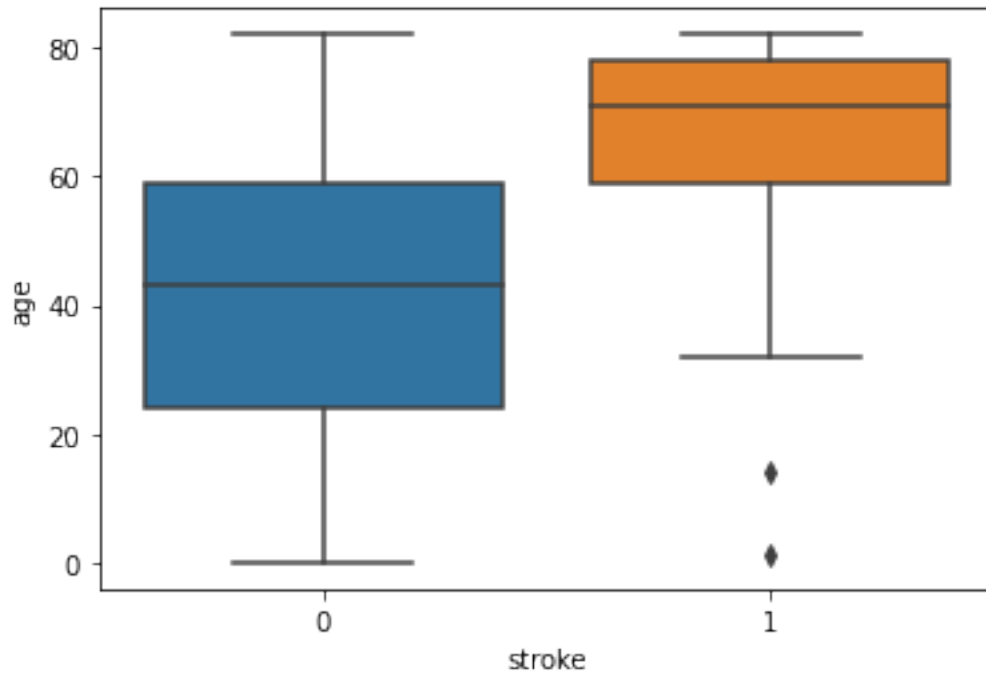
Based on the correlation plot, the variables age, hypertension, heart disease and average glucose level show the highest correlation with our dependent variable, stroke.

```
[8]: sns.pairplot(df1);
```



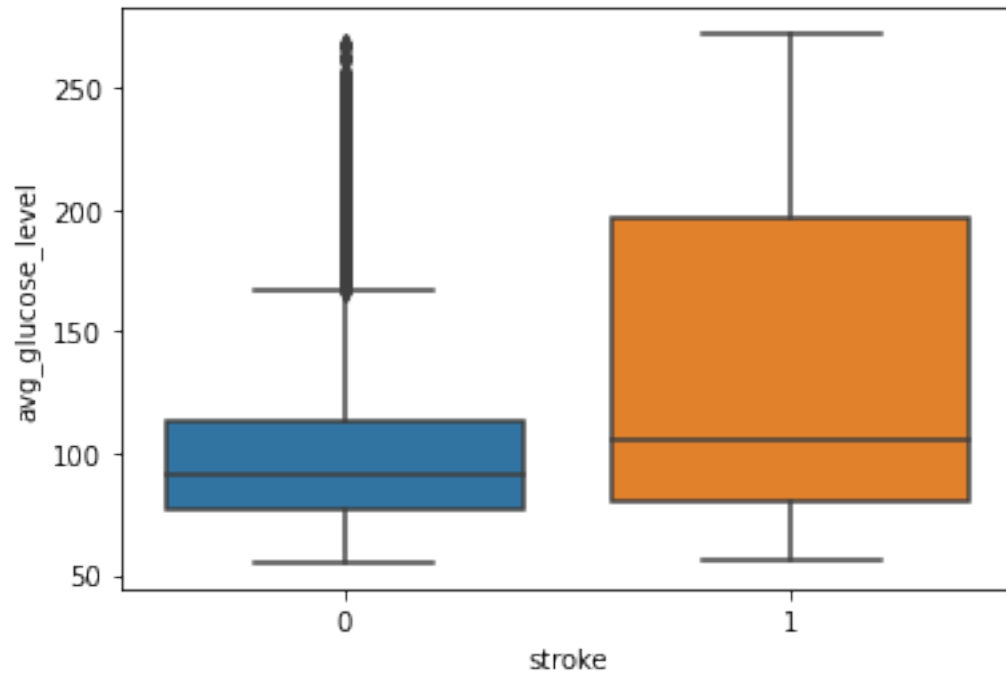
Based on the pairplots, the variable age implies that for ages below 40, the chance of getting a stroke is very low, but varies for ages above 40. The average glucose level shows a lot of variation so it is difficult to predict a pattern that shows the direction of the relationship with getting a stroke. The pairplots for hypertension and heart\_disease do not show any obvious implications. The BMI variable implies that when its value is under 20, it's unlikely to get a stroke.

```
[9]: sns.boxplot(x='stroke', y='age', data=df1);
```



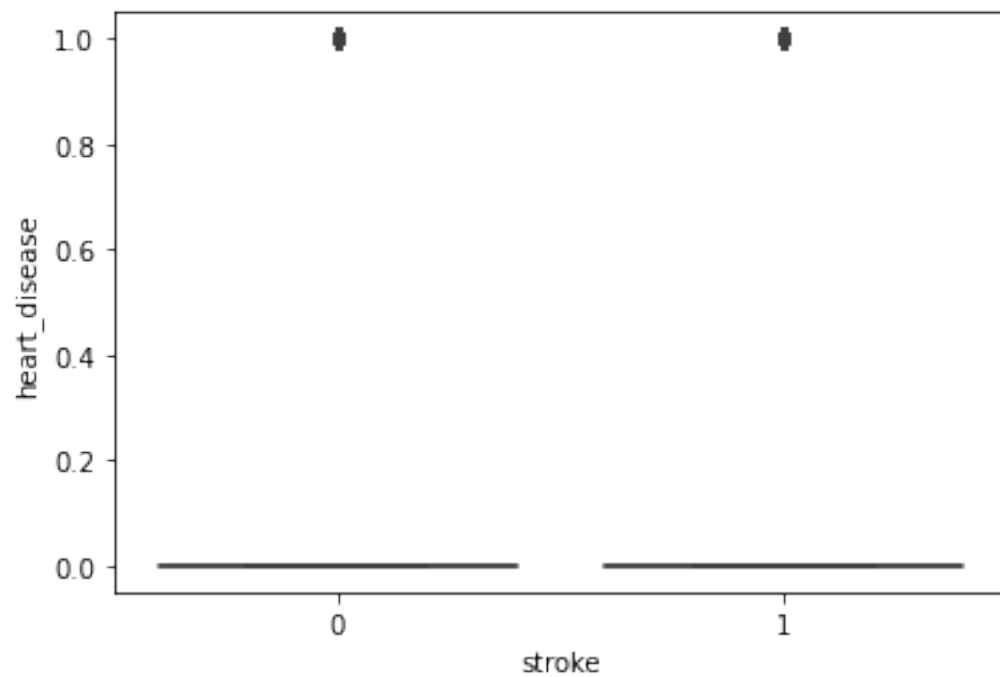
The boxplots support our previous conclusion that strokes are more likely to occur at higher ages.

```
[10]: sns.boxplot(x='stroke', y='avg_glucose_level', data=df1);
```

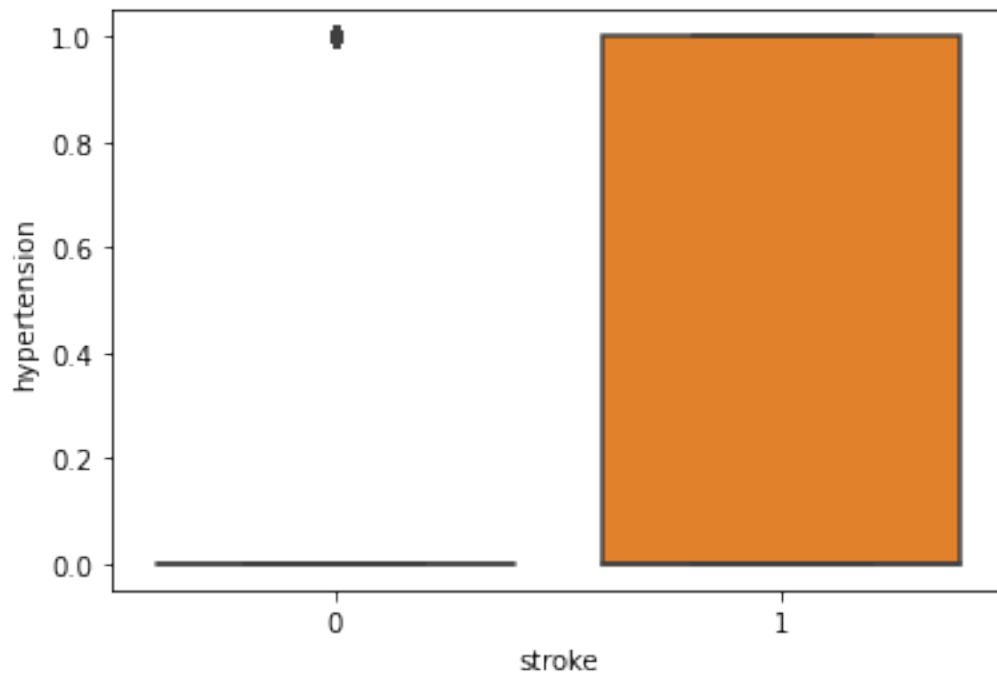


The boxplot implies that it is more likely for a stroke to occur as the average level of glucose rises.

```
[11]: sns.boxplot(x='stroke', y='heart_disease', data=df1);
```



```
[12]: sns.boxplot(x='stroke', y='hypertension', data=df1);
```



The boxplots for hypertension and heart disease are not informative because they are both binary variables, unlike age and average glucose level.

Now a logistic regression model will be run to finalize the choice of the best predictors

```
[13]: y, X = dmatrices('stroke ~ bmi + avg_glucose_level + age + smoking_status +
↳gender + ever_married + work_type + Residence_type + hypertension +
↳heart_disease', data=df1, return_type='dataframe')

logit = sm.Logit(y, X)
results_logit = logit.fit()
print(results_logit.summary())
```

Optimization terminated successfully.

Current function value: 0.176862

Iterations 9

#### Logit Regression Results

```
=====
Dep. Variable:          stroke    No. Observations:          4400
Model:                Logit      Df Residuals:              4389
Method:                MLE       Df Model:                  10
Date:                 Wed, 27 Apr 2022    Pseudo R-squ.:          0.1820
```



```

Time:                01:22:54    Log-Likelihood:          -778.19
converged:            True      LL-Null:                -951.29
Covariance Type:      nonrobust    LLR p-value:          2.570e-68

```

```

=====
=====

```

	coef	std err	z	P> z	[0.025
0.975]					
-----					
Intercept	-7.5923	0.579	-13.115	0.000	-8.727
-6.458					
bmi	0.0013	0.011	0.112	0.910	-0.021
0.024					
avg_glucose_level	0.0042	0.001	3.475	0.001	0.002
0.007					
age	0.0725	0.006	12.884	0.000	0.062
0.084					
smoking_status	0.1017	0.062	1.629	0.103	-0.021
0.224					
gender	-0.0359	0.142	-0.253	0.801	-0.314
0.243					
ever_married	-0.1764	0.225	-0.783	0.433	-0.618
0.265					
work_type	-0.1457	0.100	-1.464	0.143	-0.341
0.049					
Residence_type	-0.0887	0.139	-0.639	0.523	-0.361
0.183					
hypertension	0.3880	0.164	2.370	0.018	0.067
0.709					
heart_disease	0.2749	0.191	1.441	0.150	-0.099
0.649					

```

=====
=====

```

After performing initial logit regression across all variables, we found “age”, “avg\_glucose\_level”, and “hypertension” to be significant predictors of “stroke” outcome. We continued to develop our predictive models with these variables.

```

[14]: #Partitioning the dataset
df1_50 = df1[(df1['age']<=50)]
df1_82 = df1[(df1['age'] >50) & (df1['age'] <=82)]

```

```

[15]: lr = LogisticRegression()
# Training set
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
# Logistic Fit
mod = lr.fit(X,df1_50['stroke'])

```

```
[16]: # Testing Set
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

# Confusion matrix
conf_mat = confusion_matrix(df1_82['stroke'], lr.predict(X_test))
print(conf_mat)
#overall fraction of correct predictions
lr.score(X_test, df1_82['stroke'])
print('Accuracy =', lr.score(X_test, df1_82['stroke']))
```

```
[[1897    4]
 [ 226    0]]
Accuracy = 0.8918664786083685
```

```
[17]: #LDA
# Training set
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]

# LDA Fit
lda = LinearDiscriminantAnalysis()
lda.fit(X, df1_50['stroke'])
LinearDiscriminantAnalysis(n_components=None, priors=None, shrinkage=None,
                           solver='svd', store_covariance=False, tol=0.0001)
```

```
[17]: LinearDiscriminantAnalysis()
```

```
[18]: # Testing Set
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

# Confusion matrix
conf_mat = confusion_matrix(df1_82['stroke'], lda.predict(X_test))
print(conf_mat)
lda.score(X_test, df1_82['stroke'])
print('Accuracy =', lda.score(X_test, df1_82['stroke']))
```

```
[[1860   41]
 [ 212   14]]
Accuracy = 0.8810531264692054
```

```
[19]: #QDA
# Training set
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]

# QDA Fit
qda = QuadraticDiscriminantAnalysis()
qda.fit(X, df1_50['stroke'])
QuadraticDiscriminantAnalysis(priors=None, reg_param=0.0,
                              store_covariance=False, tol=0.0001)
```

```
[19]: QuadraticDiscriminantAnalysis()
```

```
[20]: # Testing Set
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

# Confusion matrix
conf_mat = confusion_matrix(df1_82['stroke'], qda.predict(X_test))
print(conf_mat)
qda.score(X_test, df1_82['stroke'])
print('Accuracy =', qda.score(X_test, df1_82['stroke']))
```

```
[[1529  372]
 [ 157   69]]
Accuracy = 0.7512929007992478
```

```
[21]: #KNN, n=1
# Training set
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]

# KNN Fit
nbrs = KNeighborsClassifier(n_neighbors=1)
nbrs.fit(X, df1_50['stroke'])
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                    metric_params=None, n_jobs=1, n_neighbors=1, p=2,
                    weights='uniform')
```

```
[21]: KNeighborsClassifier(n_jobs=1, n_neighbors=1)
```

```
[22]: # Testing Set
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

# Confusion matrix
conf_mat = confusion_matrix(df1_82['stroke'], nbrs.predict(X_test))
print(conf_mat)
nbrs.score(X_test, df1_82['stroke'])
print('Accuracy =', nbrs.score(X_test, df1_82['stroke']))
```

```
[[1824   77]
 [ 214   12]]
Accuracy = 0.8631875881523272
```

```
[23]: #KNN, n=2
# Training set
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]

# KNN Fit
nbrs2 = KNeighborsClassifier(n_neighbors=2)
nbrs2.fit(X, df1_50['stroke'])
```

```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=1, n_neighbors=2, p=2,
                     weights='uniform')
```

[23]: KNeighborsClassifier(n\_jobs=1, n\_neighbors=2)

```
[24]: # Testing Set
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

# Confusion matrix
conf_mat = confusion_matrix(df1_82['stroke'], nbrs2.predict(X_test))
print(conf_mat)
nbrs2.score(X_test, df1_82['stroke'])
print('Accuracy =', nbrs2.score(X_test, df1_82['stroke']))
```

```
[[1892    9]
 [ 225    1]]
Accuracy = 0.8899858956276445
```

```
[25]: #KNN,n=3
# Training set
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]

# KNN Fit
nbrs3 = KNeighborsClassifier(n_neighbors=3)
nbrs3.fit(X,df1_50['stroke'])
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=1, n_neighbors=3, p=2,
                     weights='uniform')
```

[25]: KNeighborsClassifier(n\_jobs=1, n\_neighbors=3)

```
[26]: # Testing Set
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

# Confusion matrix
conf_mat = confusion_matrix(df1_82['stroke'], nbrs3.predict(X_test))
print(conf_mat)
nbrs3.score(X_test, df1_82['stroke'])
print('Accuracy =', nbrs3.score(X_test, df1_82['stroke']))
```

```
[[1886   15]
 [ 222    4]]
Accuracy = 0.8885754583921015
```

```
[27]: #KNN,n=4
# Training set
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
```

```

# KNN Fit
nbrs4 = KNeighborsClassifier(n_neighbors=4)
nbrs4.fit(X,df1_50['stroke'])
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                    metric_params=None, n_jobs=1, n_neighbors=4, p=2,
                    weights='uniform')

```

[27]: KNeighborsClassifier(n\_jobs=1, n\_neighbors=4)

```

[28]: # Testing Set
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

# Confusion matrix
conf_mat = confusion_matrix(df1_82['stroke'], nbrs4.predict(X_test))
print(conf_mat)
nbrs4.score(X_test, df1_82['stroke'])
print('Accuracy =', nbrs4.score(X_test, df1_82['stroke']))

```

```

[[1901    0]
 [ 226    0]]
Accuracy = 0.8937470615890927

```

```

[29]: #KNN,n=5
# Training set
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]

# KNN Fit
nbrs5 = KNeighborsClassifier(n_neighbors=5)
nbrs5.fit(X,df1_50['stroke'])
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                    metric_params=None, n_jobs=1, n_neighbors=5, p=2,
                    weights='uniform')

```

[29]: KNeighborsClassifier(n\_jobs=1)

```

[30]: # Testing Set
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

# Confusion matrix
conf_mat = confusion_matrix(df1_82['stroke'], nbrs5.predict(X_test))
print(conf_mat)
nbrs5.score(X_test, df1_82['stroke'])
print('Accuracy =', nbrs5.score(X_test, df1_82['stroke']))

```

```

[[1901    0]
 [ 226    0]]
Accuracy = 0.8937470615890927

```

According to the accuracies of the models ran, KNN4 and KNN5 have the highest accuracy amongst all models. Both models had the same accuracy and confusion matrix, so we will use Bootstrap to find the model with lowest MSE.

### 0.1.2 Bootstrap Performance Evaluation

```
[31]: models_mse = []
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

for i in range(100):

    boot = sklearn.utils.resample(X, replace = False, n_samples = 2127,
    ↪random_state = i)
    boot_Y = sklearn.utils.resample(df1_50["stroke"], replace = False,
    ↪n_samples = 2127, random_state = i)
    lr.fit(boot, boot_Y)
    MSE = mean_squared_error(df1_82['stroke'], lr.predict(X_test))
    models_mse.append(MSE)
print("Bootstrapped MSE={}".format(sum(models_mse)/100))
```

Bootstrapped MSE=0.1310296191819465

The bootstrapped MSE for logistic regression is 0.13103.

```
[32]: models_mse = []
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

for i in range(100):

    boot = sklearn.utils.resample(X, replace = False, n_samples = 2127,
    ↪random_state = i)
    boot_Y = sklearn.utils.resample(df1_50["stroke"], replace = False,
    ↪n_samples = 2127, random_state = i)
    qda.fit(boot, boot_Y)
    MSE = mean_squared_error(df1_82['stroke'], qda.predict(X_test))
    models_mse.append(MSE)
print("Bootstrapped MSE={}".format(sum(models_mse)/100))
```

```
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:808: UserWarning: Variables are
collinear
    warnings.warn("Variables are collinear")
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: divide by zero
encountered in power
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-
```

```

packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: invalid value
encountered in multiply
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:836: RuntimeWarning: divide by zero
encountered in log
    u = np.asarray([np.sum(np.log(s)) for s in self.scalings_])
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:808: UserWarning: Variables are
collinear
    warnings.warn("Variables are collinear")
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: divide by zero
encountered in power
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: invalid value
encountered in multiply
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:836: RuntimeWarning: divide by zero
encountered in log
    u = np.asarray([np.sum(np.log(s)) for s in self.scalings_])
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:808: UserWarning: Variables are
collinear
    warnings.warn("Variables are collinear")
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: divide by zero
encountered in power
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: invalid value
encountered in multiply
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:836: RuntimeWarning: divide by zero
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    u = np.asarray([np.sum(np.log(s)) for s in self.scalings_])
C:\Users\Zachary DeBar\anaconda3\lib\site-
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collinear
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packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: divide by zero
encountered in power
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-

```

```

packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: invalid value
encountered in multiply
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:836: RuntimeWarning: divide by zero
encountered in log
    u = np.asarray([np.sum(np.log(s)) for s in self.scalings_])

Bootstrapped MSE=0.28128819934179583

C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:808: UserWarning: Variables are
collinear
    warnings.warn("Variables are collinear")
C:\Users\Zachary DeBar\anaconda3\lib\site-
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    u = np.asarray([np.sum(np.log(s)) for s in self.scalings_])
C:\Users\Zachary DeBar\anaconda3\lib\site-
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collinear
    warnings.warn("Variables are collinear")
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: divide by zero
encountered in power
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:833: RuntimeWarning: invalid value
encountered in multiply
    X2 = np.dot(Xm, R * (S ** (-0.5)))
C:\Users\Zachary DeBar\anaconda3\lib\site-
packages\sklearn\discriminant_analysis.py:836: RuntimeWarning: divide by zero
encountered in log
    u = np.asarray([np.sum(np.log(s)) for s in self.scalings_])

The bootstrapped MSE for QDA is 0.28129.

```

```

[33]: models_mse = []
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

```



```

for i in range(100):

    boot = sklearn.utils.resample(X, replace = False, n_samples = 2127,
    ↪random_state = i)
    boot_Y = sklearn.utils.resample(df1_50["stroke"], replace = False,
    ↪n_samples = 2127, random_state = i)
    lda.fit(boot, boot_Y)
    MSE = mean_squared_error(df1_82['stroke'], lda.predict(X_test))
    models_mse.append(MSE)
print("Bootstrapped MSE={}".format(sum(models_mse)/100))

```

Bootstrapped MSE=0.1445463093559004

The bootstrapped MSE for LDA is 0.14455.

```

[34]: models_mse = []
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

for i in range(100):

    boot = sklearn.utils.resample(X, replace = False, n_samples = 2127,
    ↪random_state = i)
    boot_Y = sklearn.utils.resample(df1_50["stroke"], replace = False,
    ↪n_samples = 2127, random_state = i)
    nbrs.fit(boot, boot_Y)
    MSE = mean_squared_error(df1_82['stroke'], nbrs.predict(X_test))
    models_mse.append(MSE)
print("Bootstrapped MSE={}".format(sum(models_mse)/100))

```

Bootstrapped MSE=0.1335731076633757

The bootstrapped MSE for KNN-1 is 0.13357.

```

[35]: models_mse = []
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

for i in range(100):

    boot = sklearn.utils.resample(X, replace = False, n_samples = 2127,
    ↪random_state = i)
    boot_Y = sklearn.utils.resample(df1_50["stroke"], replace = False,
    ↪n_samples = 2127, random_state = i)
    nbrs2.fit(boot, boot_Y)
    MSE = mean_squared_error(df1_82['stroke'], nbrs2.predict(X_test))
    models_mse.append(MSE)
print("Bootstrapped MSE={}".format(sum(models_mse)/100))

```

Bootstrapped MSE=0.10827456511518584

The bootstrapped MSE for KNN-2 is 0.10827.

```
[36]: models_mse = []
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

for i in range(100):

    boot = sklearn.utils.resample(X, replace = False, n_samples = 2127,
    ↪random_state = i)
    boot_Y = sklearn.utils.resample(df1_50["stroke"], replace = False,
    ↪n_samples = 2127, random_state = i)
    nbrs3.fit(boot, boot_Y)
    MSE = mean_squared_error(df1_82['stroke'], nbrs3.predict(X_test))
    models_mse.append(MSE)
print("Bootstrapped MSE={}".format(sum(models_mse)/100))
```

Bootstrapped MSE=0.10914433474377055

The bootstrapped MSE for KNN-3 is 0.109144.

```
[37]: models_mse = []
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

for i in range(100):

    boot = sklearn.utils.resample(X, replace = False, n_samples = 2127,
    ↪random_state = i)
    boot_Y = sklearn.utils.resample(df1_50["stroke"], replace = False,
    ↪n_samples = 2127, random_state = i)
    nbrs4.fit(boot, boot_Y)
    MSE = mean_squared_error(df1_82['stroke'], nbrs4.predict(X_test))
    models_mse.append(MSE)
print("Bootstrapped MSE={}".format(sum(models_mse)/100))
```

Bootstrapped MSE=0.10625293841090754

The bootstrapped MSE for KNN-4 is 0.10625.

```
[38]: models_mse = []
X = df1_50[['avg_glucose_level', 'age', 'hypertension']]
X_test = df1_82[['avg_glucose_level', 'age', 'hypertension']]

for i in range(100):

    boot = sklearn.utils.resample(X, replace = False, n_samples = 2127,
    ↪random_state = i)
```

```

boot_Y = sklearn.utils.resample(df1_50["stroke"], replace = False,
↪n_samples = 2127, random_state = i)
nbrs5.fit(boot, boot_Y)
MSE = mean_squared_error(df1_82['stroke'], nbrs5.predict(X_test))
models_mse.append(MSE)
print("Bootstrapped MSE={}".format(sum(models_mse)/100))

```

Bootstrapped MSE=0.10625293841090754

The bootstrapped MSE for KNN-5 is 0.10625.

Based on the results of our bootstrap analysis, KNN-4 and KNN-5 are the models which produce the minimized bootstrap Mean Square Error, both tied at 0.10625.

## 0.2 Section 2: Regularization

```

[39]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import sklearn
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import scale
from sklearn import model_selection
from sklearn.linear_model import LinearRegression, Ridge, RidgeCV, Lasso,
↪LassoCV, ElasticNet, ElasticNetCV
from sklearn.decomposition import PCA
from sklearn.cross_decomposition import PLSRegression
from sklearn.model_selection import KFold, cross_val_score
from sklearn.metrics import mean_squared_error
%matplotlib inline
plt.style.use('seaborn-white')

```

```

[40]: data = pd.read_csv('Movie_classification.csv')
data.index.name = 'movie'
data.info()

```

<class 'pandas.core.frame.DataFrame'>

RangeIndex: 506 entries, 0 to 505

Data columns (total 19 columns):

#	Column	Non-Null Count	Dtype
0	Marketing expense	506 non-null	float64
1	Production expense	506 non-null	float64
2	Multiplex coverage	506 non-null	float64
3	Budget	506 non-null	float64
4	Movie_length	506 non-null	float64
5	Lead_Actor_Rating	506 non-null	float64
6	Lead_Actress_rating	506 non-null	float64

```

7   Director_rating      506 non-null    float64
8   Producer_rating      506 non-null    float64
9   Critic_rating        506 non-null    float64
10  Trailer_views        506 non-null    int64
11  3D_available         506 non-null    object
12  Time_taken           494 non-null    float64
13  Twitter_hashtags     506 non-null    float64
14  Genre                506 non-null    object
15  Avg_age_actors       506 non-null    int64
16  Num_multiplex        506 non-null    int64
17  Collection           506 non-null    int64
18  Start_Tech_Oscar     506 non-null    int64
dtypes: float64(12), int64(5), object(2)
memory usage: 75.2+ KB

```

Our objective in analyzing this data is to identify if there is a functional prediction model to predict whether or not a film will qualify for an Oscar award, as indicated with the “Start\_Tech\_Oscar” variable.

Data source:

[https://www.kaggle.com/datasets/balakrishcodes/others?select=Movie\\_classification.csv](https://www.kaggle.com/datasets/balakrishcodes/others?select=Movie_classification.csv)

[41]: data

```

[41]:      Marketing expense  Production expense  Multiplex coverage  Budget \
movie
0          20.1264          59.62          0.462  36524.125
1          20.5462          69.14          0.531  35668.655
2          20.5458          69.14          0.531  39912.675
3          20.6474          59.36          0.542  38873.890
4          21.3810          59.36          0.542  39701.585
...          ...          ...          ...          ...
501         21.2526          78.86          0.427  36624.115
502         20.9054          78.86          0.427  33996.600
503         21.2152          78.86          0.427  38751.680
504         22.1918          78.86          0.427  37740.670
505         20.9482          78.86          0.427  33496.650

      Movie_length  Lead_ Actor_Rating  Lead_Actress_rating  Director_rating \
movie
0          138.7          7.825          8.095          7.910
1          152.4          7.505          7.650          7.440
2          134.6          7.485          7.570          7.495
3          119.3          6.895          7.035          6.920
4          127.7          6.920          7.070          6.815
...          ...          ...          ...          ...
501         142.6          8.680          8.775          8.620
502         150.2          8.780          8.945          8.770

```

503	164.5	8.830	8.970	8.855
504	162.8	8.730	8.845	8.800
505	154.3	8.640	8.880	8.680

	Producer_rating	Critic_rating	Trailer_views	3D_available	Time_taken \
movie					
0	7.995	7.94	527367	YES	109.60
1	7.470	7.44	494055	NO	146.64
2	7.515	7.44	547051	NO	147.88
3	7.020	8.26	516279	YES	185.36
4	7.070	8.26	531448	NO	176.48
...	...	...	...	...	...
501	8.970	6.80	492480	NO	186.96
502	8.930	7.80	482875	YES	132.24
503	9.010	7.80	532239	NO	109.56
504	8.845	6.80	496077	YES	158.80
505	8.790	6.80	518438	YES	205.60

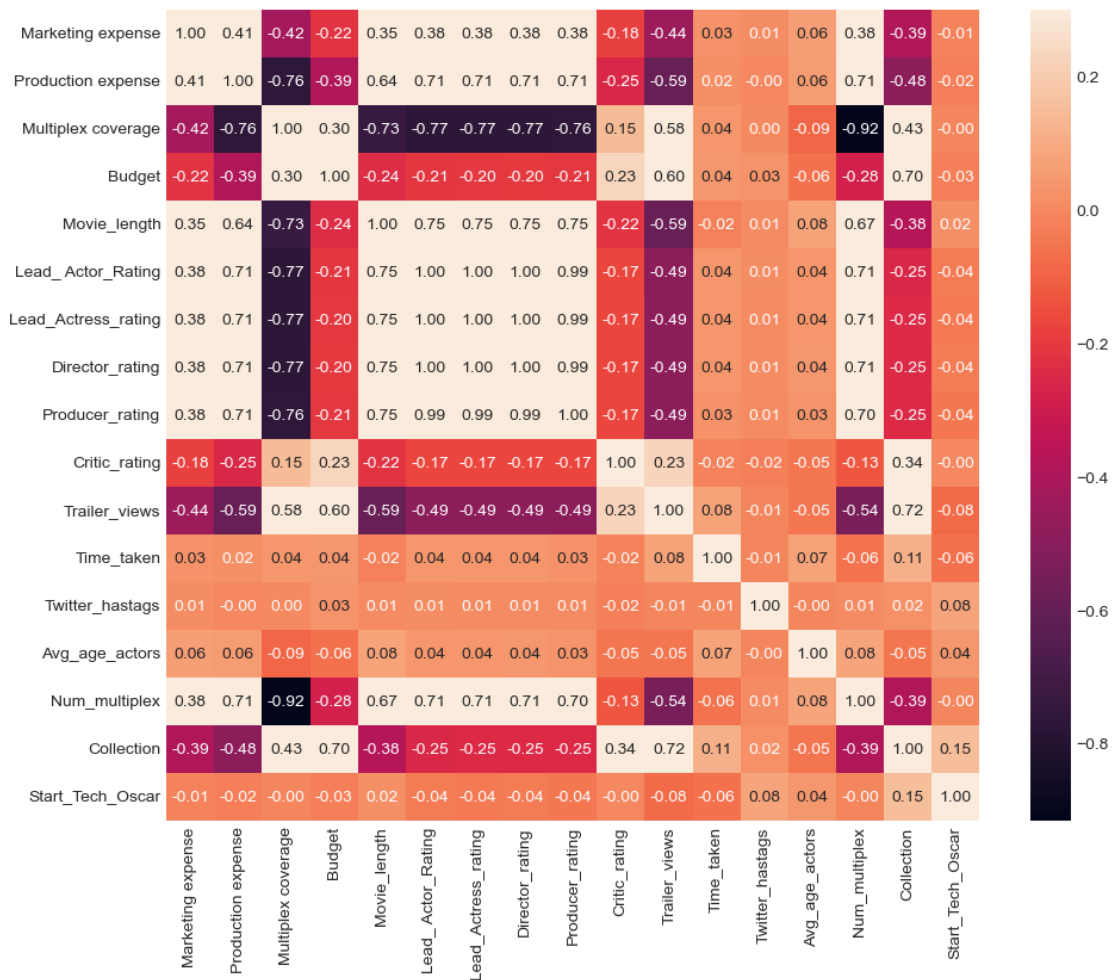
	Twitter_hastags	Genre	Avg_age_actors	Num_multiplex	Collection \
movie					
0	223.840	Thriller	23	494	48000
1	243.456	Drama	42	462	43200
2	2022.400	Comedy	38	458	69400
3	225.344	Drama	45	472	66800
4	225.792	Drama	55	395	72400
...	...	...	...	...	...
501	243.584	Action	27	561	44800
502	263.296	Action	20	600	41200
503	243.824	Comedy	31	576	47800
504	303.520	Comedy	47	607	44000
505	203.040	Comedy	45	604	38000

	Start_Tech_Oscar
movie	
0	1
1	0
2	1
3	1
4	1
...	...
501	0
502	0
503	0
504	0
505	0

[506 rows x 19 columns]

```
[42]: # Correlation plot

correlations = data.corr()          # 17*17 matrix of corr coefficients
plt.figure(figsize=(11, 9),dpi=100) # picture size
sns.heatmap(data = correlations,
            vmax=0.3,                # color depth
            annot=True,              # add number
            fmt=".2f",                # round digit
            annot_kws={'size':10})    # word size
plt.show()
```



This correlation plot allows us to visually identify all relationships between variables, ranging all the way from -0.92 (close to perfectly inverse) to 1, indicating several perfect connections variables.

```
[43]: # data cleaning
```

```

data = data.dropna() #_
↳ 506*19 - 494*19
dummies = pd.get_dummies(data[['3D_available']]) #_
↳ 494*2 - 1 or 0
data = data.drop(['3D_available'], axis=1) #_
↳ 494*18 - no 3D YES/NO
data = pd.concat([data, dummies[['3D_available_YES']]], axis=1) #_
↳ 494*19 - 3D 1 or 0

# split X and Y
newX = data.drop(['Start_Tech_Oscar', 'Genre'], axis = 1) #_
↳ 494*17
newY = data['Start_Tech_Oscar'] #_
↳ 494*1

# split train and test
X_train,X_test,y_train,y_test = sklearn.model_selection.train_test_split(
    newX, newY, test_size=0.3, random_state = 10)

```

[44]: *#Generate different values of alpha to fit different Ridge models*

```

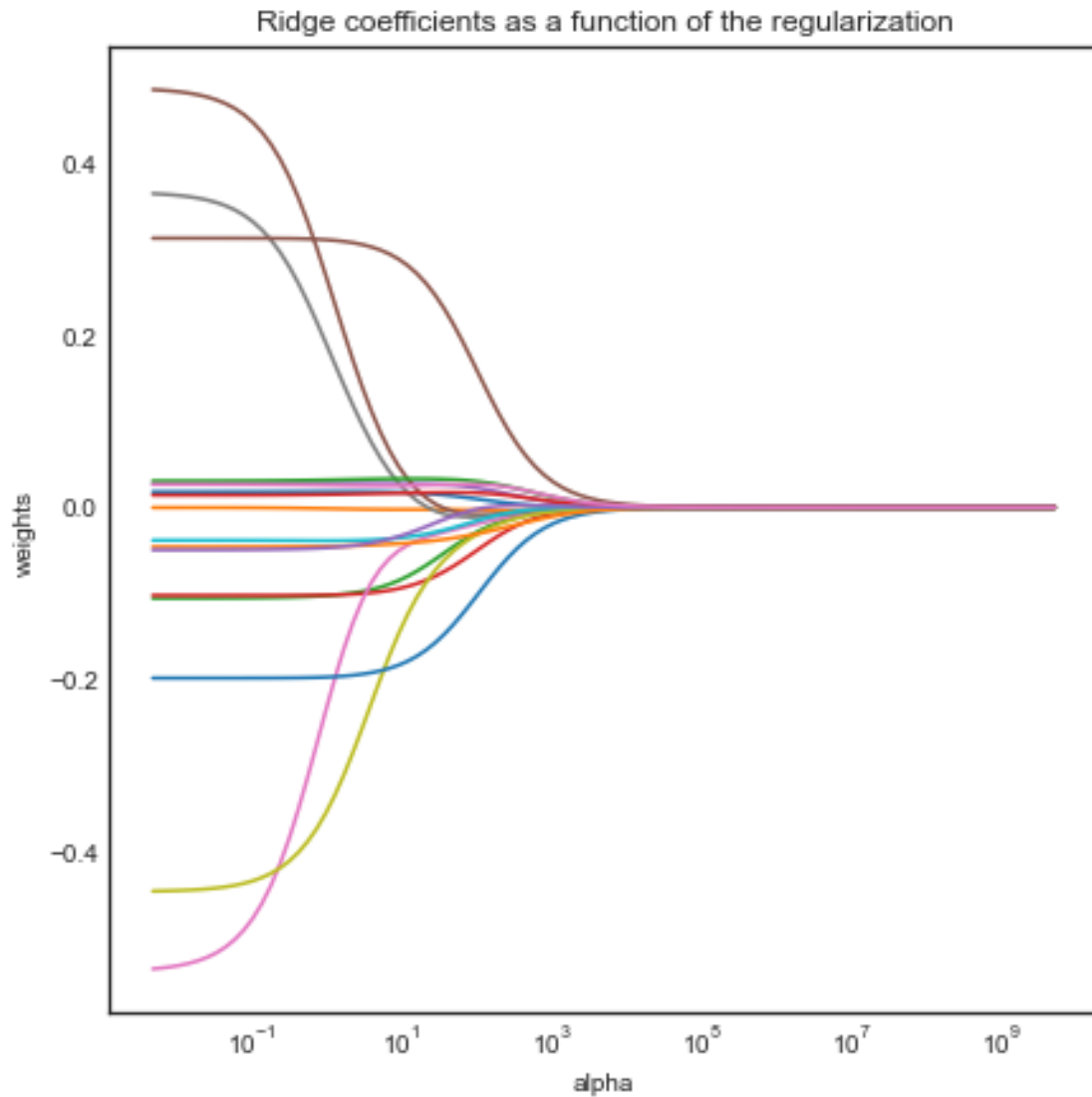
alphas = 10**np.linspace(10,-2,100)*0.5

ridge = Ridge()
coefs = []

for a in alphas:
    ridge.set_params(alpha=a)
    ridge.fit(scale(newX), newY)
    coefs.append(ridge.coef_)

plt.figure(figsize=(7, 7))
ax = plt.gca()
ax.plot(alphas, coefs)
ax.set_xscale('log')
#ax.set_xlim(ax.get_xlim()[::-1]) # reverse axis
plt.axis('tight')
plt.xlabel('alpha')
plt.ylabel('weights')
plt.title('Ridge coefficients as a function of the regularization');

```



```
[45]: scaler = StandardScaler().fit(X_train)
```

```
[46]: # Perform CV and figure out the best alpha
ridgecv = RidgeCV(alphas=alphas, scoring='neg_mean_squared_error')
ridgecv.fit(scale(X_train), y_train)
print('Ridge alpha =', ridgecv.alpha_)
```

Ridge alpha = 0.4348745013088917

```
[47]: # Estimate the Ridge Model using the best alpha
ridge2 = Ridge()
ridge2.set_params(alpha=0.4348745013088917)
ridge2.fit(scale(X_train), y_train)
```



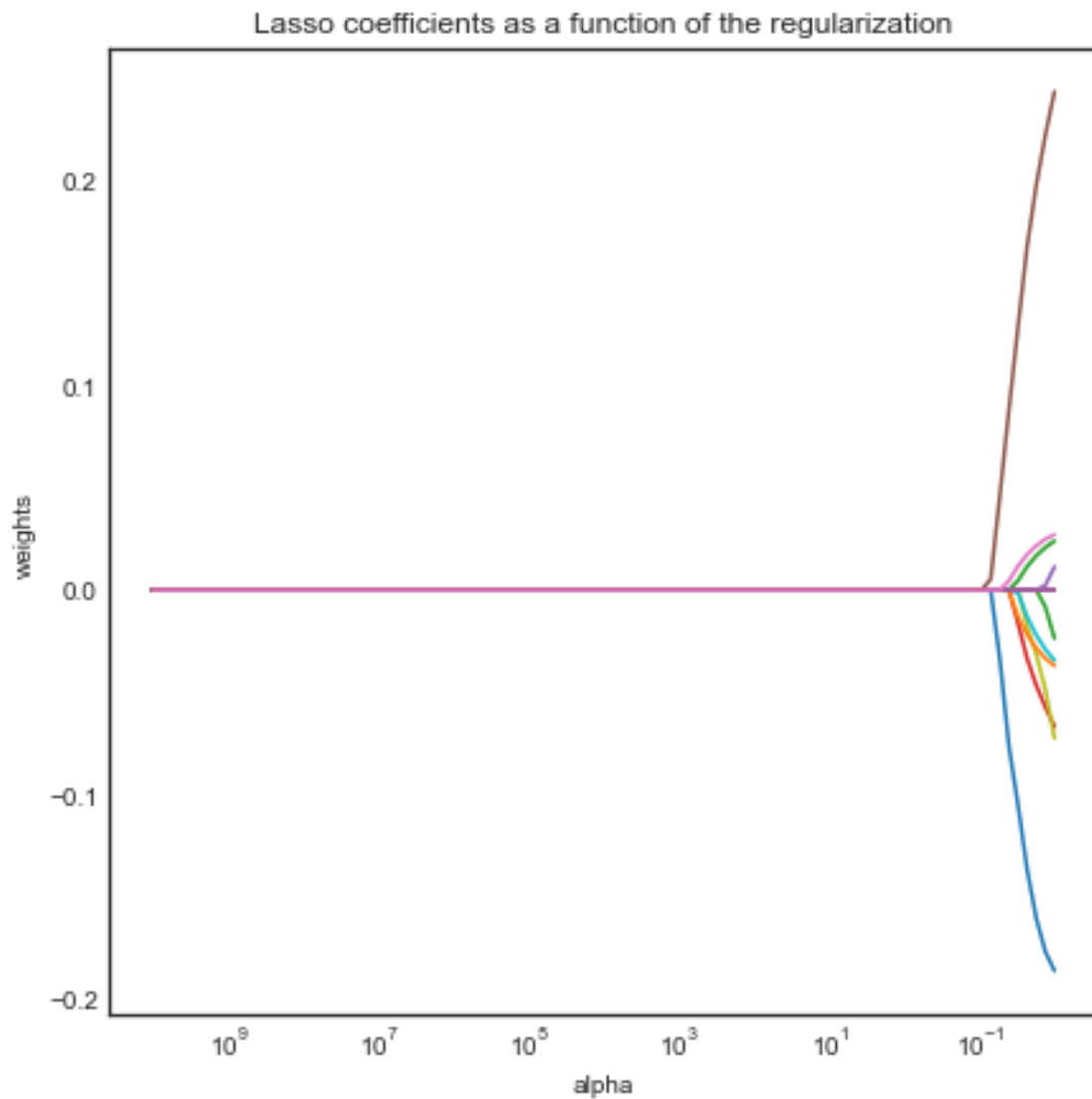
```
mean_squared_error(y_test, ridge2.predict(scale(X_test)))
print('MSE = ', mean_squared_error(y_test, ridge2.predict(scale(X_test))))
pd.Series(ridge2.coef_.flatten(), index=newX.columns)
```

MSE = 0.22884003850357437

```
[47]: Marketing expense      0.003978
      Production expense    -0.001698
      Multiplex coverage    -0.074519
      Budget                -0.093257
      Movie_length          0.036134
      Lead_Actor_Rating      0.682304
      Lead_Actress_rating    -0.480387
      Director_rating        0.251312
      Producer_rating        -0.583666
      Critic_rating          -0.045632
      Trailer_views          -0.214620
      Time_taken             -0.050685
      Twitter_hastags         0.028511
      Avg_age_actors         0.003928
      Num_multiplex          -0.018708
      Collection             0.300376
      3D_available_YES       0.038242
      dtype: float64
```

```
[48]: #LASSO
      # Generate different values of alpha to fit different Ridge models
      lasso = Lasso(max_iter=10000)
      coefs = []

      for a in alphas*2:
          lasso.set_params(alpha=a)
          lasso.fit(scale(X_train), y_train)
          coefs.append(lasso.coef_)
      plt.figure(figsize=(7, 7))
      ax = plt.gca()
      ax.plot(alphas*2, coefs)
      ax.set_xscale('log')
      ax.set_xlim(ax.get_xlim()[::-1]) # reverse axis
      plt.axis('tight')
      plt.xlabel('alpha')
      plt.ylabel('weights')
      plt.title('Lasso coefficients as a function of the regularization');
```



```
[49]: lasso_cv = LassoCV(alphas=None, cv=10, max_iter=10000)
lasso_cv.fit(scale(X_train), y_train.values.ravel())
```

```
[49]: LassoCV(cv=10, max_iter=10000)
```

```
[50]: lasso_cv.alpha_
```

```
[50]: 0.0017531554062430593
```

```
[51]: pd.Series(lasso_cv.coef_, index=newX.columns)
```

```
[51]: Marketing expense    -0.000000
      Production expense -0.000000
```

```

Multiplex coverage    -0.023622
Budget                -0.066727
Movie_length          0.011344
Lead_Actor_Rating     -0.000000
Lead_Actress_rating   -0.000000
Director_rating        -0.000000
Producer_rating        -0.072485
Critic_rating          -0.034419
Trailer_views         -0.186127
Time_taken            -0.037044
Twitter_hastags        0.023906
Avg_age_actors         0.000000
Num_multiplex          0.000000
Collection             0.243543
3D_available_YES       0.027096
dtype: float64

```

```

[52]: lasso.set_params(alpha=lassocv.alpha_)
lasso.fit(scale(X_train), y_train)
print('MSE = ',mean_squared_error(y_test, lasso.predict(scale(X_test))))

```

```
MSE = 0.22532078753761933
```

```

[53]: # Step 1: Use CV to get the best alpha
enetcv = ElasticNetCV(cv=10, max_iter=10000)
enetcv.fit(scale(X_train), y_train.values.ravel())

# Step 2: Estimate the model w/ best alpha
enet_best = ElasticNet(alpha=enetcv.alpha_)
enet_best.fit(scale(X_train), y_train)

# Step 3: Print model estimates
print(list(zip(enet_best.coef_, newX)))

# Step 4: Print Error Metrics

print('MSE',mean_squared_error(y_test, enetcv.predict(scale(X_test))))

```

```

[(0.003682700664003383, 'Marketing expense'), (0.00014356385080630177,
'Production expense'), (-0.07060803189691985, 'Multiplex coverage'),
(-0.09147593761157329, 'Budget'), (0.036190123531168815, 'Movie_length'),
(0.8817014400727423, 'Lead_Actor_Rating'), (-0.6586712782319618,
'Lead_Actress_rating'), (0.28172629499553775, 'Director_rating'),
(-0.6357448733243666, 'Producer_rating'), (-0.044269891266599734,
'Critic_rating'), (-0.2151420592866737, 'Trailer_views'),
(-0.050520714804323213, 'Time_taken'), (0.027043885410953518,
'Twitter_hastags'), (0.003844124090292974, 'Avg_age_actors'),
(-0.01566769360198046, 'Num_multiplex'), (0.29911219999780425, 'Collection'),

```

```
(0.038982620574758035, '3D_available_YES'])  
MSE 0.23172439193909705
```

```
C:\Users\Zachary DeBar\anaconda3\lib\site-  
packages\sklearn\linear_model\_coordinate_descent.py:530: ConvergenceWarning:  
Objective did not converge. You might want to increase the number of iterations.  
Duality gap: 1.8601542419681394, tolerance: 0.00857217391304348  
    model = cd_fast.enet_coordinate_descent(
```

```
[54]: #PCA  
  
pca = PCA()  
X_reduced = pca.fit_transform(scale(newX))  
  
print(pca.components_.shape) # Loadings  
pd.DataFrame(pca.components_.T).loc[:4,:5]
```

```
(17, 17)
```

```
[54]:
```

	0	1	2	3	4	5
0	-0.185507	-0.152768	-0.130542	0.006585	0.014600	0.090904
1	-0.305953	-0.060285	-0.020739	0.005839	-0.045047	0.000198
2	0.323970	-0.031849	-0.046057	0.016789	-0.009430	0.164824
3	0.154522	0.495704	-0.018100	0.053622	0.097453	0.016320
4	-0.301522	0.061712	0.042083	-0.040495	0.094484	0.007149

```
[55]: print(X_reduced.shape) # Principal Components  
pd.DataFrame(X_reduced).loc[:4,:5]
```

```
(494, 17)
```

```
[55]:
```

	0	1	2	3	4	5
0	1.329772	0.758568	2.091228	0.017536	0.202127	0.458976
1	1.419002	-0.595590	-0.339652	0.319339	-0.155415	-0.096741
2	2.221437	1.216727	-3.464258	13.386820	8.751526	0.683249
3	3.332915	0.917429	-0.576504	-0.912837	0.175936	-0.065317
4	3.517164	0.778602	-1.502983	-0.131155	-0.392351	-1.131371

```
[56]: np.cumsum(np.round(pca.explained_variance_ratio_, decimals=4)*100)
```

```
[56]: array([ 44.67,  56.5 ,  62.99,  69.17,  74.78,  80.34,  85.14,  89.56,  
        92.84,  95.16,  96.83,  98.23,  99.49,  99.94,  99.99, 100. ,  
        100.01])
```

```
[57]: # 10-fold CV, with shuffle  
n = len(X_reduced)  
kf_10 = KFold(n_splits=10, shuffle=True, random_state=1)  
  
regr = LinearRegression()
```

```

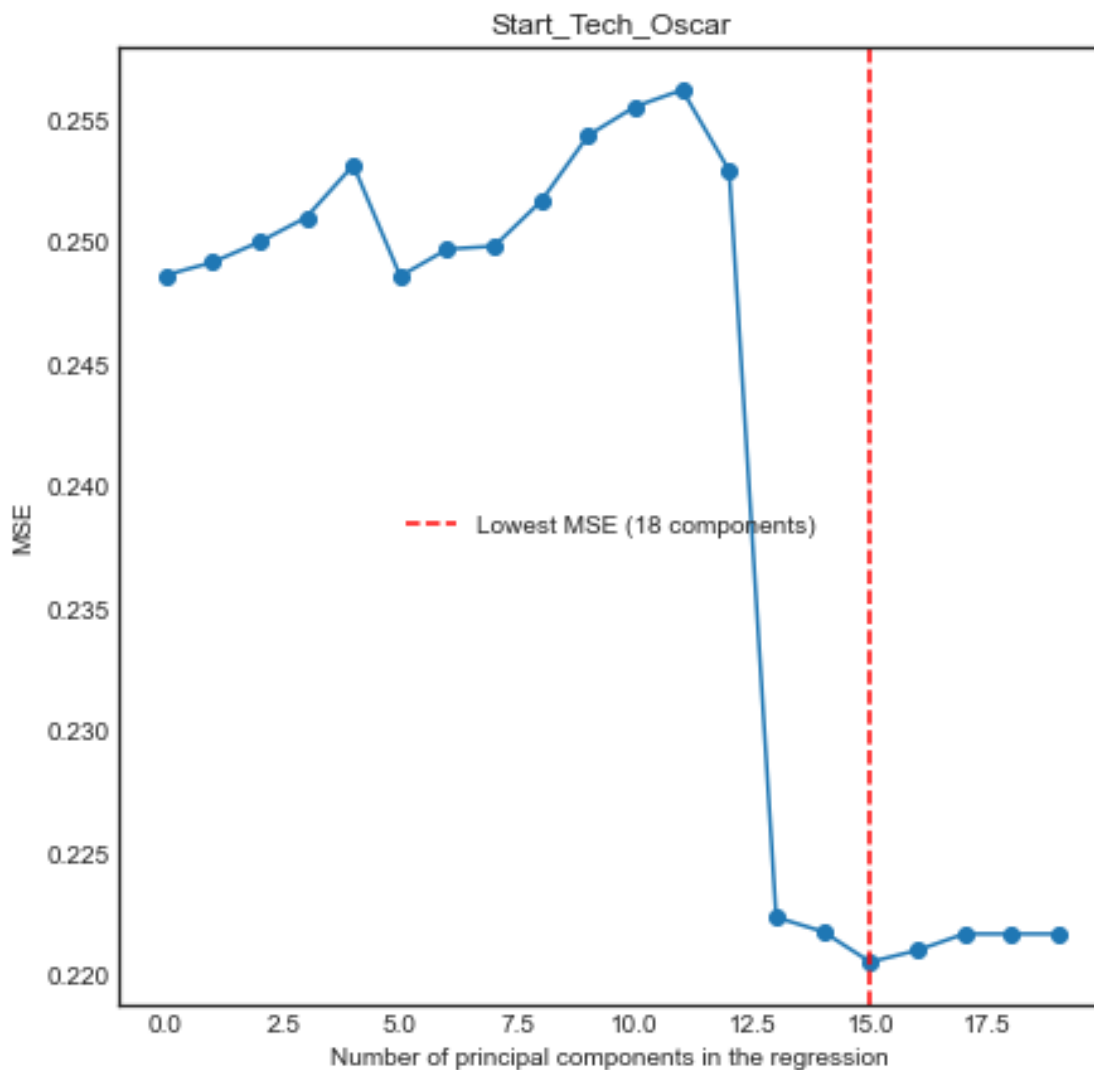
mse = []

# Calculate MSE with only the intercept (no principal components in regression)
score = -1*cross_val_score(regr, np.ones((n,1)), newY.ravel(), cv=kf_10,
    ↳scoring='neg_mean_squared_error').mean()
mse.append(score)

# Calculate MSE using CV for the 19 principle components, adding one component
    ↳at the time.
for i in np.arange(1, 20):
    score = -1*cross_val_score(regr, X_reduced[:,i], newY.ravel(), cv=kf_10,
    ↳scoring='neg_mean_squared_error').mean()
    mse.append(score)
plt.figure(figsize=(7, 7))
plt.plot(mse, '-o')
plt.xlabel('Number of principal components in the regression')
plt.ylabel('MSE')
plt.title('Start_Tech_Oscar')
plt.xlim(xmin=-1);
plt.axvline(15, linestyle="--", color="r", label="Lowest MSE (18 components)")
plt.legend(loc='center')

```

[57]: <matplotlib.legend.Legend at 0x21bb4d60b50>



```
[58]: regr_test = LinearRegression()
      regr_test.fit(X_reduced, newY)
      regr_test.coef_
```

```
[58]: array([ 1.87228106e-03,  8.11239933e-03,  1.78914460e-02,  2.13907617e-03,
            6.81624346e-02, -1.81636205e-02,  3.02496952e-02, -4.01603354e-04,
           -3.69052854e-03, -3.09438240e-02, -2.08973018e-02,  1.22460914e-01,
            3.62964344e-01,  1.42292123e-01, -4.60900244e-01,  3.61470596e-01,
           -7.17305902e-01])
```

After running CV shuffle for PCA, we found out that 15 components results in the lowest MSE; however, 15 components is high considering we have 18 variables. We will run different types of PCA to determine the optimal number of components.

```

[59]: pca2 = PCA()
X_reduced_train = pca2.fit_transform(scale(X_train))
n = len(X_reduced_train)

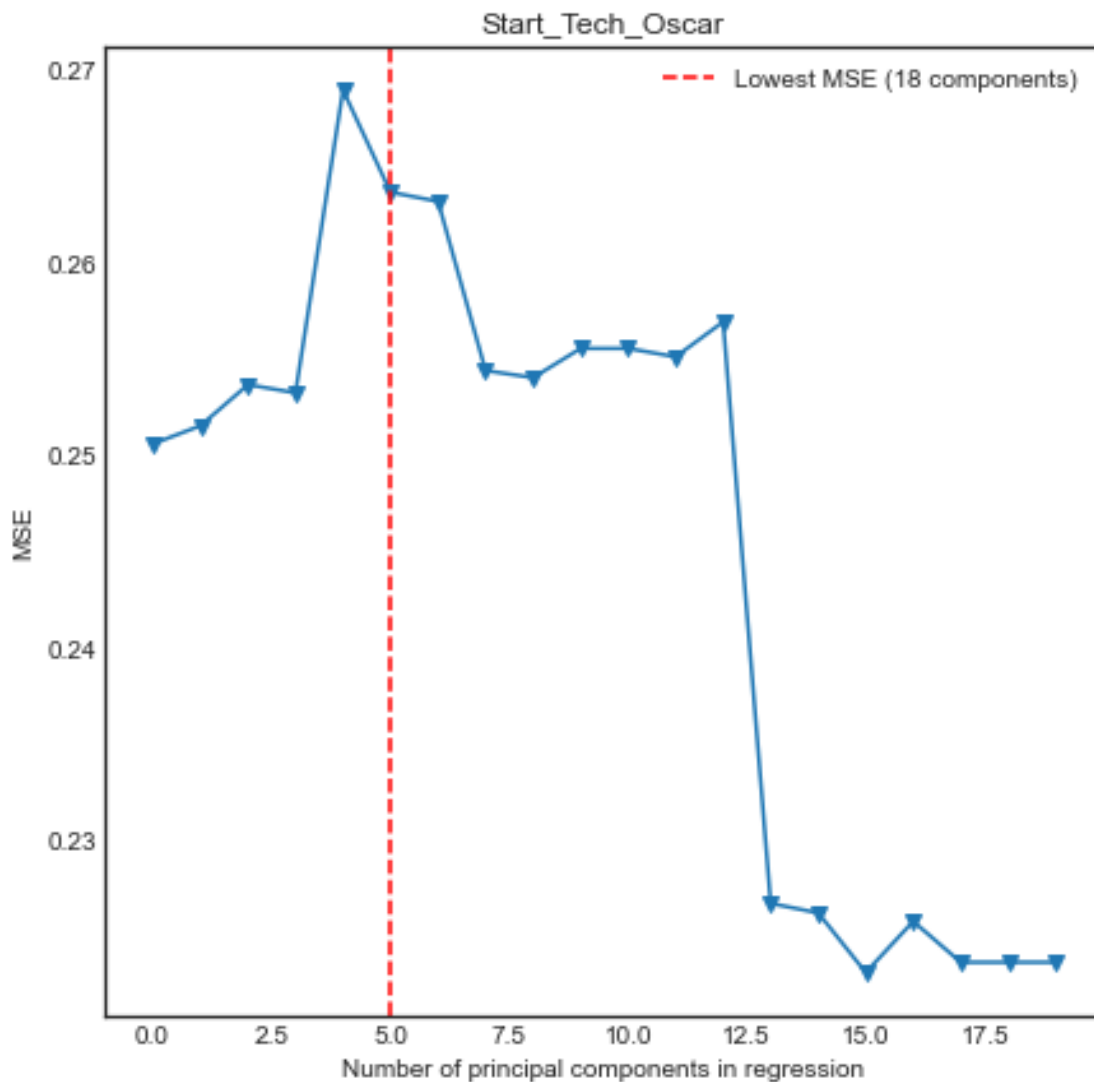
# 10-fold CV, with shuffle
kf_10 = KFold(n_splits=10, shuffle=True, random_state=1)

mse = []

# Calculate MSE with only the intercept (no principal components in regression)
score = -1*cross_val_score(regr, np.ones((n,1)), y_train, cv=kf_10,
    ↳scoring='neg_mean_squared_error').mean()
mse.append(score)

# Calculate MSE using CV for the 19 PCs, adding one component at the time.
for i in np.arange(1, 20):
    score = -1*cross_val_score(regr, X_reduced_train[:, :i], y_train, cv=kf_10,
    ↳scoring='neg_mean_squared_error').mean()
    mse.append(score)
plt.figure(figsize=(7, 7))
plt.plot(np.array(mse), '-v')
plt.xlabel('Number of principal components in regression')
plt.ylabel('MSE')
plt.title('Start_Tech_Oscar')
plt.axvline(5, linestyle="--", color="r", label="Lowest MSE (18 components)")
plt.legend(loc='best')
plt.xlim(xmin=-1);

```



```
[60]: X_reduced_test = pca2.transform(scale(X_test))[:, :7]
```

```
# Train regression model on training data
regr = LinearRegression()
regr.fit(X_reduced_train[:, :7], y_train)
```

```
# Prediction with test data
pred = regr.predict(X_reduced_test)
mean_squared_error(y_test, pred)
```

```
[60]: 0.24363911782518424
```

After running a PCA using training data, our model still indicates that 15 components will result in the minimal MSE despite being a large number of components.



```
[61]: n = len(X_train)

# 10-fold CV, with shuffle
kf_10 = KFold(n_splits=10, shuffle=True, random_state=0)

mse = []

for i in np.arange(1, 20):
    pls = PLSRegression(n_components=i)
    score = cross_val_score(pls, scale(X_train), y_train, cv=kf_10,
        ↳scoring='neg_mean_squared_error').mean()
    mse.append(-score)

plt.plot(np.arange(1, 20), np.array(mse), '-v')
plt.xlabel('Number of principal components in regression')
plt.ylabel('MSE')
plt.title('Start_Tech_Oscar')
plt.xlim(xmin=-1);
```

C:\Users\Zachary DeBar\anaconda3\lib\site-packages\sklearn\cross\_decomposition\\_pls.py:206: FutureWarning: As of version 0.24, n\_components(18) should be in [1, n\_features].n\_components=17 will be used instead. In version 1.1 (renaming of 0.26), an error will be raised.

warnings.warn(

C:\Users\Zachary DeBar\anaconda3\lib\site-packages\sklearn\cross\_decomposition\\_pls.py:206: FutureWarning: As of version 0.24, n\_components(18) should be in [1, n\_features].n\_components=17 will be used instead. In version 1.1 (renaming of 0.26), an error will be raised.

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C:\Users\Zachary DeBar\anaconda3\lib\site-packages\sklearn\cross\_decomposition\\_pls.py:206: FutureWarning: As of version 0.24, n\_components(18) should be in [1, n\_features].n\_components=17 will be used instead. In version 1.1 (renaming of 0.26), an error will be raised.

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C:\Users\Zachary DeBar\anaconda3\lib\site-packages\sklearn\cross\_decomposition\\_pls.py:206: FutureWarning: As of version 0.24, n\_components(18) should be in [1, n\_features].n\_components=17 will be used instead. In version 1.1 (renaming of 0.26), an error will be raised.

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C:\Users\Zachary DeBar\anaconda3\lib\site-packages\sklearn\cross\_decomposition\\_pls.py:206: FutureWarning: As of version 0.24, n\_components(18) should be in [1, n\_features].n\_components=17 will be used instead. In version 1.1 (renaming of 0.26), an error will be raised.

```

warnings.warn(
C:\Users\Zachary DeBar\anaconda3\lib\site-
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warnings.warn(
C:\Users\Zachary DeBar\anaconda3\lib\site-
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0.24, n_components(19) should be in [1, n_features].n_components=17 will be used
instead. In version 1.1 (renaming of 0.26), an error will be raised.
warnings.warn(
C:\Users\Zachary DeBar\anaconda3\lib\site-
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C:\Users\Zachary DeBar\anaconda3\lib\site-
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instead. In version 1.1 (renaming of 0.26), an error will be raised.

```

0.24, `n_components(19)` should be in `[1, n_features]`. `n_components=17` will be used instead. In version 1.1 (renaming of 0.26), an error will be raised.

```
warnings.warn(
```

C:\Users\Zachary DeBar\anaconda3\lib\site-

packages\sklearn\cross\_decomposition\\_pls.py:206: FutureWarning: As of version 0.24, `n_components(19)` should be in `[1, n_features]`. `n_components=17` will be used instead. In version 1.1 (renaming of 0.26), an error will be raised.

```
warnings.warn(
```

C:\Users\Zachary DeBar\anaconda3\lib\site-

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```
warnings.warn(
```

C:\Users\Zachary DeBar\anaconda3\lib\site-

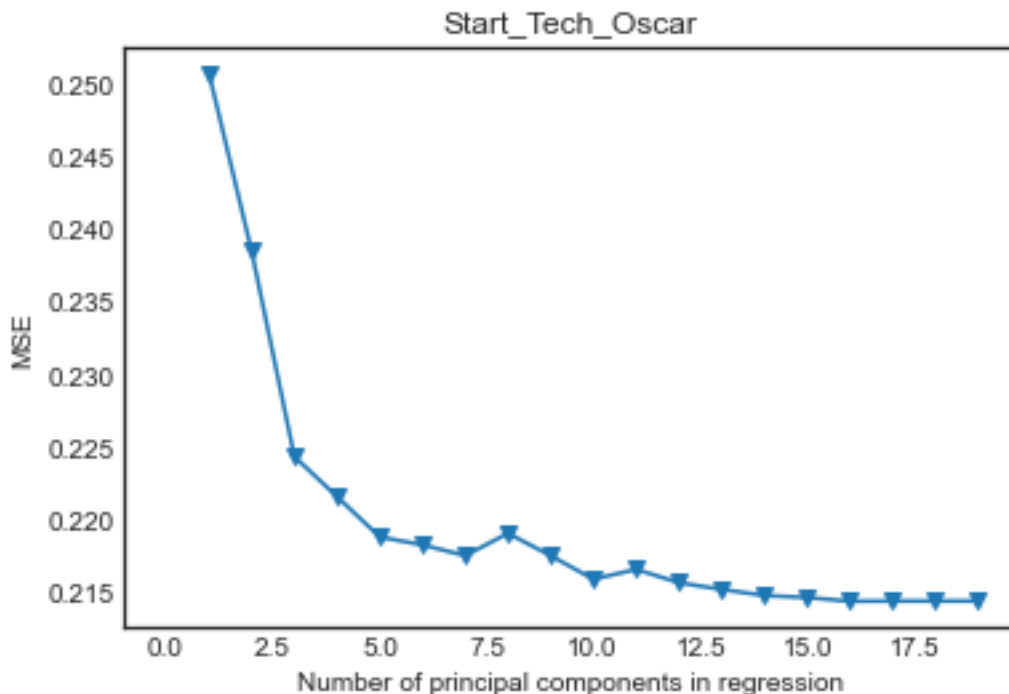
packages\sklearn\cross\_decomposition\\_pls.py:206: FutureWarning: As of version 0.24, `n_components(19)` should be in `[1, n_features]`. `n_components=17` will be used instead. In version 1.1 (renaming of 0.26), an error will be raised.

```
warnings.warn(
```

C:\Users\Zachary DeBar\anaconda3\lib\site-

packages\sklearn\cross\_decomposition\\_pls.py:206: FutureWarning: As of version 0.24, `n_components(19)` should be in `[1, n_features]`. `n_components=17` will be used instead. In version 1.1 (renaming of 0.26), an error will be raised.

```
warnings.warn(
```



```
[62]: pls = PLSRegression(n_components=2)
      pls.fit(scale(X_train), y_train)

      mean_squared_error(y_test, pls.predict(scale(X_test)))
```

```
[62]: 0.2340087208422181
```

After running a PLS, MSE is still lower as the number of components increases; however, unlike the previous PCA results which required 13+ components to significantly lower MSE, 5-7 components yielded an MSE fairly close to the minimum possible MSE. This implies that we can use fewer components without greatly sacrificing our model's performance.

### 0.2.1 Regularization Conclusion

The Lasso regression yielded the lowest MSE of 0.225 from the models we've created, and it was able to successfully shrink 7 coefficients to exactly 0.