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HOMEWORK REPORT

Subject: *Basic Methods of Data Analysis*

Student	*M. Kirdin*
Student	*V. Kropotin*
Student	*V. Pendishchuk*
Professor	*B. Mirkin*

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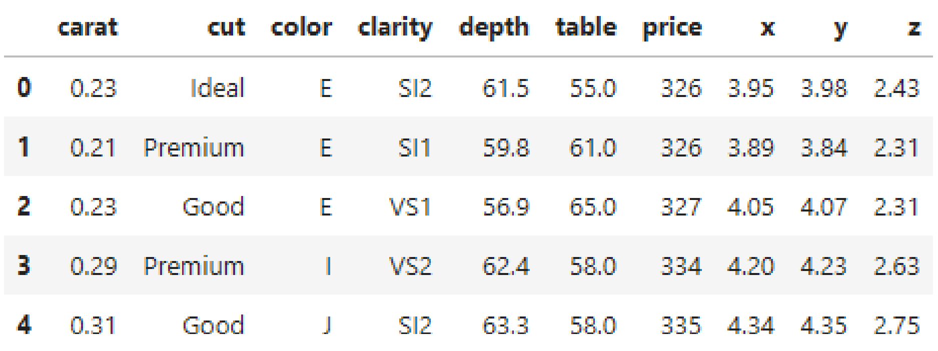
1 DATA

1.1 Description

We chose the Diamonds Price Dataset since it has a variety of easily interpretable features (see fig. 1) as well as an abundance of data. It has 50,000 entities and 10 features, which are:

- **Carat.** Weight of a diamond, carats (quantitative).
- **Cut.** Cutting quality (categorical).
- **Color.** Color from J (worst) to D (best) (categorical).
- **Clarity.** Clarity from left to right is worst to best: I1, SI2, SI1, VS2, VS1, VVS2, VVS1, IF (categorical).
- **x.** Length, mm (quantitative).
- **y.** Width, mm (quantitative).
- **z.** Depth, mm (quantitative).
- **depth.** Percentage depth z/(mean(x,y)), % (quantitative).
- **table.** Width of the widest point at the top of the diamond, mm (quantitative).
- **price.** Diamond's price (quantitative).



	carat	cut	color	clarity	depth	table	price	x	y	z
0	0.23	Ideal	E	SI2	61.5	55.0	326	3.95	3.98	2.43
1	0.21	Premium	E	SI1	59.8	61.0	326	3.89	3.84	2.31
2	0.23	Good	E	VS1	56.9	65.0	327	4.05	4.07	2.31
3	0.29	Premium	I	VS2	62.4	58.0	334	4.20	4.23	2.63
4	0.31	Good	J	SI2	63.3	58.0	335	4.34	4.35	2.75

Figure 1. Sample data from the Diamonds Price Dataset

1.2 Preprocessing

In this work we considered a sample of 2,000 entities from this dataset, since it contains enough data to derive nontrivial relations in data while not being demanding in terms of computational power. Since all categorical features imply some sort of order in their values, it was decided to use ordinal encoding by assigning different integer values to different classes in ascending order from worst to best. Furthermore, in most calculations standard scaling was used to center and normalize the data.

2 CORRELATION COEFFICIENT

2.1 Pairwise distributions

To understand which pair of features is the best for constructing a linear regression on, we have to take into account their distributions. As shown on fig. 2, there are several features of interest: "x", "y", "z", "carat" and "price". Features "x", "y" and "z", with the exception of some outliers, are distributed in a linear pattern and their distributions wrt "carat" look like polynomial functions. This is an expected behavior, since "carat" is roughly the product of "x", "y", "z", which are linearly distributed with each other, and diamond density.

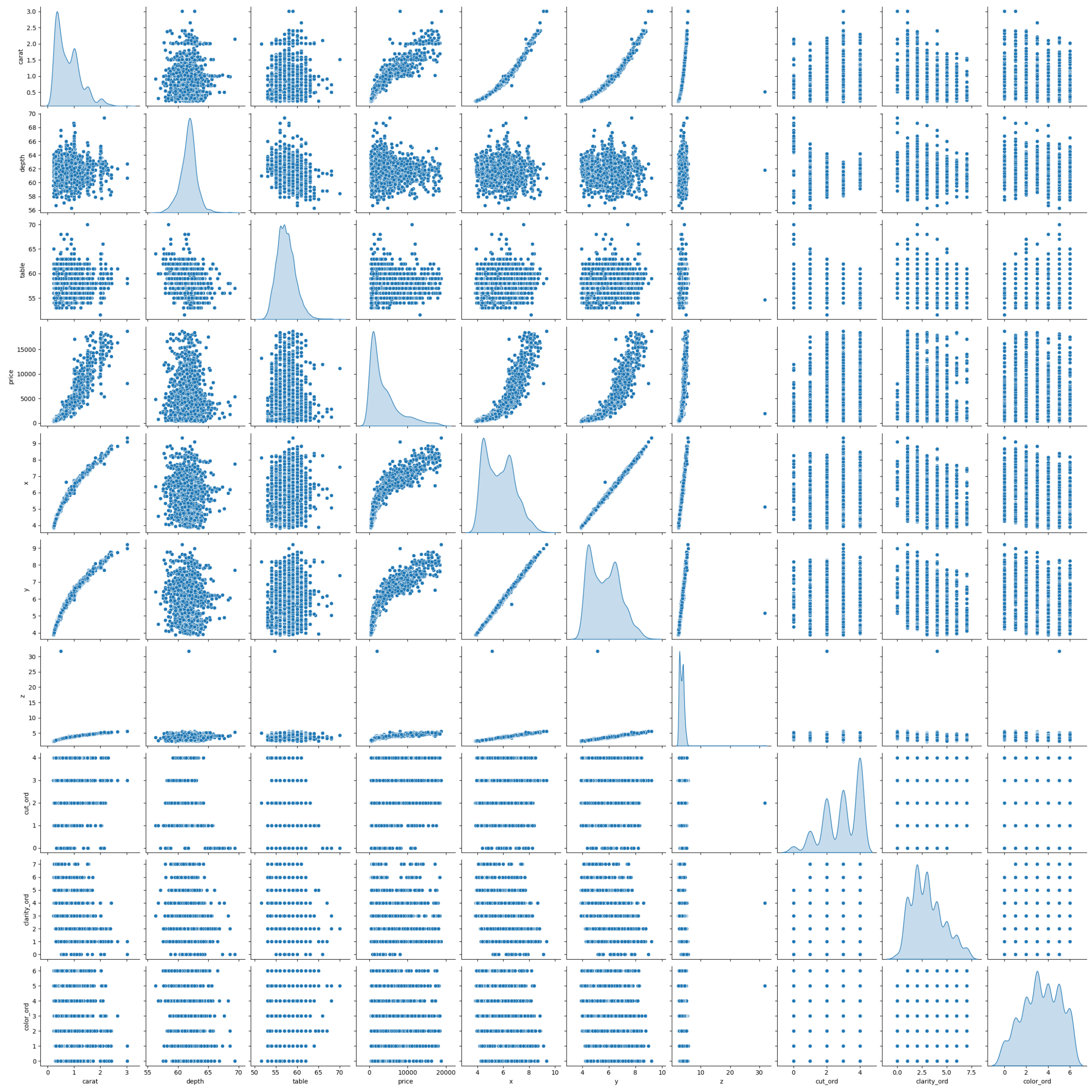


Figure 2. Pairwise scatter plots of all the features in data

2.2 Linear regression

In this task we will consider the pair "carat" and "price", because their distribution is not as trivial as those of diamonds' physical dimensions wrt each other or their mass (fig. 3).

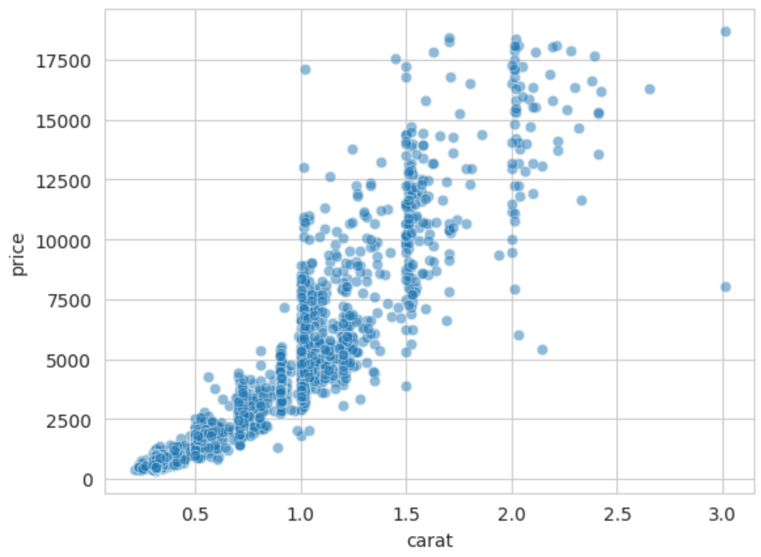


Figure 3. Distribution "carat" and "price" wrt each other

First, a regular linear regression of "price" over "carat" was constructed. As shown on fig. 4, this line has a positive slope, hence the diamond's price tends to positively correlate with its mass, which is to be expected. Next, the correlation and R^2 coefficient, also known as *the coefficient of determination*, were computed:

$$\rho = 0.9240,\ R^2 = 0.8537.$$

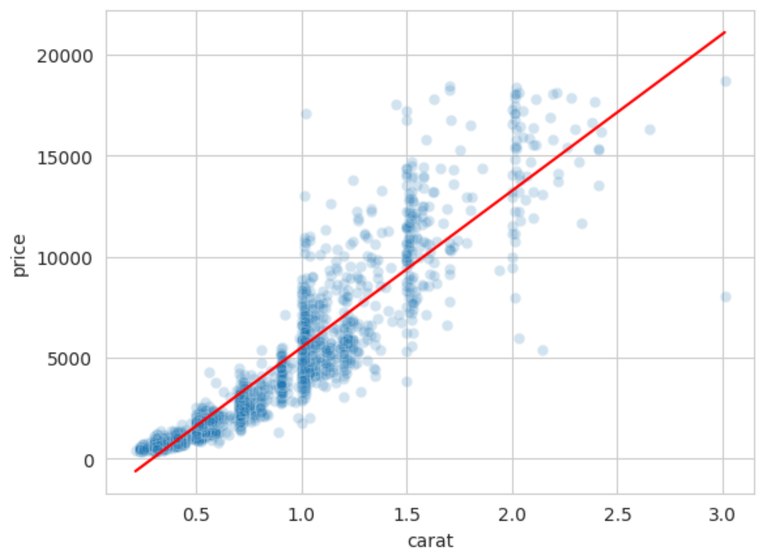


Figure 4. Linear regression of "price" over "carat"

Since R^2 coefficient is the proportion of variance of the target feature taken into account by linear regression, in our case 85.37% of "price" variance is taken into account.

After that, a set

$$x = \begin{pmatrix} 0.3000 & 863 \\ 0.3100 & 788 \\ 0.4000 & 662 \\ 2.0100 & 17078 \end{pmatrix}$$

of four random pairs of "carat" and "price" values was chosen to compare the predicted and true "price" values. To do this, the percentile deviations were found:

$$\Delta y_{\text{true}} = (89.9245\%,\ 79.1276\%,\ -30.2385\%,\ 21.8683\%)^T,$$
$$\Delta y_{\text{pred}} = (892.5046\%,\ 379.1018\%,\ -23.2178\%,\ 27.9890\%)^T,$$

where Δy_{true} is relative deviation of predicted from true values and Δy_{pred} is the other way round. From this we can conclude that the regression line tends to underestimate the price of diamonds with lower mass.

Finally, mean absolute percentile error(MAPE) relative to both true and predicted over the whole data was considered in order to measure the mean deviation of the data from the predictor line and vice versa:

$$\text{MAPE}_{\text{true}} = 39.2063\%,\ \text{MAPE}_{\text{pred}} = 121.4897\%.$$

These values indicate that, similarly to the previous case, regression on this pair features tends to underestimate the "price" feature. There is also another interpretation: $\text{MAPE}_{\text{true}}$ is data analysis(DA) view on MAPE, while $\text{MAPE}_{\text{pred}}$ is machine learning(ML) view on MAPE; hence, while in terms of DA the line we constructed is good, while the opposite is true in terms of ML.

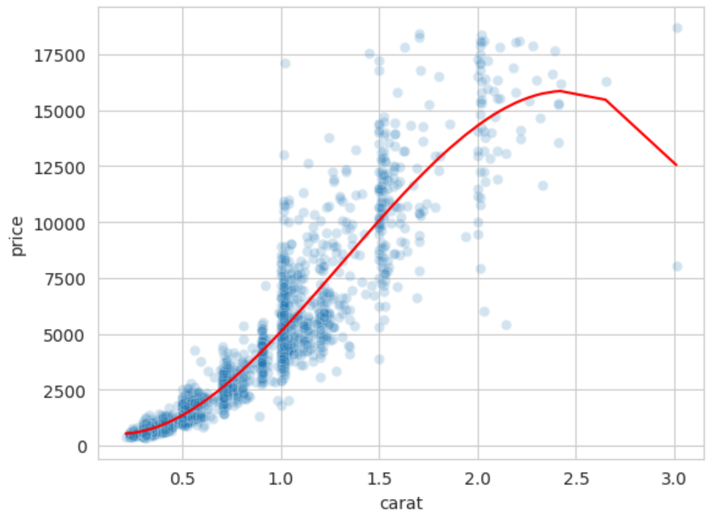


Figure 5. Polynomial regression of "price" over "carat"

We also tried polynomial regression with a third degree polynomial, as seen on fig. 5. This resulting in following MAPE values:

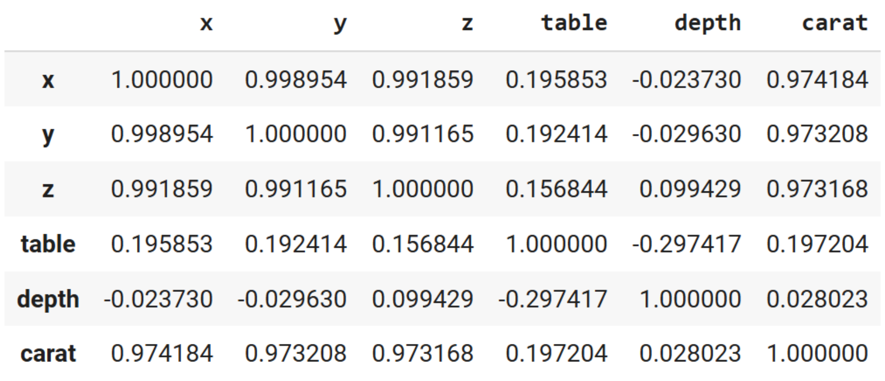
$$\text{MAPE}_{\text{true}} = 39.2063\%,\ \text{MAPE}_{\text{pred}} = 37.0984\%.$$

This indicates that the polynomial curve uses more data and does not underestimate the price.

3 PCA/SVD

For principal component analysis (PCA), the following subset of features was considered: x, y, z, depth, table, carat. These features were chosen for the following reasons:

- These features are all continuous, and that makes them easier to interpret as coordinates in a linear space, as opposed to categorical features.
- These features all relate to the same aspect - the size of a diamond: x, y, z and table describe the dimensions of a diamond, depth is a ratio calculated from the main dimensions, and carat is a diamond's weight.
- All features, except depth, correlate to some extent with each other (fig. 6).



	x	y	z	table	depth	carat
x	1.000000	0.998954	0.991859	0.195853	-0.023730	0.974184
y	0.998954	1.000000	0.991165	0.192414	-0.029630	0.973208
z	0.991859	0.991165	1.000000	0.156844	0.099429	0.973168
table	0.195853	0.192414	0.156844	1.000000	-0.297417	0.197204
depth	-0.023730	-0.029630	0.099429	-0.297417	1.000000	0.028023
carat	0.974184	0.973208	0.973168	0.197204	0.028023	1.000000

Figure 6. Correlation matrix for the features chosen for PCA

The data was standardized using three different techniques covered in class, resulting in three different datasets:

- z-scoring:
$$y_{iv} = \frac{x_{iv} - mean_v}{std_v}$$
- range normalization:
$$y_{iv} = \frac{x_{iv} - mean_v}{max_v - min_v}$$
- ranking normalization:
$$y_{iv} = \frac{x_{iv} - min_v}{max_v - min_v}$$

After standardization, singular value decomposition (SVD) was computed for the three standardized datasets and the original subset of the dataset, with the latter added for the sake of comparison. From the obtained decomposition results, data scatter and principal component contributions were computed.

Table 1. SVD results for the non-standardized data

Data scatter: 2875588.8702								
Singular value σ_v	Natural contribution	Contribution %	Singular vector components (loadings)					
			x	y	z	table	depth	carat
1694.9	2872698.57	100.	-0.067	-0.067	-0.041	-0.679	-0.727	-0.009
41.3	1706.5	0.	0.213	0.212	0.103	0.667	-0.669	0.087
34.3	1177.21	0.	0.588	0.583	0.372	-0.307	0.155	0.242
2.2	4.99	0.	-0.203	-0.273	0.153	0.016	0.009	0.928
1.	1.09	0.	-0.119	-0.326	0.898	0.017	-0.022	-0.270
0.7	0.5	0.	-0.741	0.656	0.142	0.003	-0.003	0.008

Table 2. SVD results for the z-scoring standardized data

Data scatter: 2394.								
Singular value σ_v	Natural contribution	Contribution %	Singular vector components (loadings)					
			x	y	z	table	depth	carat
39.9	1594.93	66.62	0.498	0.498	0.496	0.123	-0.000	0.493
22.6	512.65	21.41	0.012	0.010	0.103	-0.668	0.736	0.040
16.5	271.48	11.34	0.078	0.087	-0.003	-0.733	-0.669	0.020

Table 2. (continued)

Singular value σ_v	Natural contribution	Contribution %	Singular vector components (loadings)					
			x	y	z	table	depth	carat
3.8	14.4	0.6	0.280	0.293	0.282	0.022	0.019	-0.869
0.6	0.4	0.02	0.730	-0.683	-0.039	-0.004	0.000	-0.008
0.4	0.14	0.01	-0.367	-0.439	0.814	-0.001	-0.103	-0.004

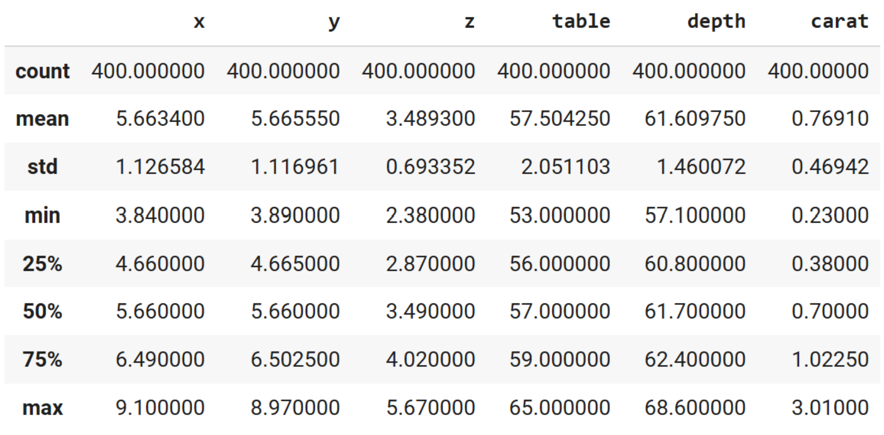
Table 3. SVD results for the range standardized data

Data scatter: 84.7789								
Singular value σ_v	Natural contribution	Contribution %	Singular vector components (loadings)					
			x	y	z	table	depth	carat
8.2	66.5	78.43	0.524	0.537	0.513	0.093	0.001	0.407
3.5	12.38	14.6	0.018	0.020	0.103	-0.906	0.410	0.025
2.3	5.43	6.4	0.084	0.101	-0.100	-0.413	-0.896	-0.017
0.7	0.45	0.53	0.226	0.248	0.229	0.024	0.030	-0.913
0.1	0.02	0.02	0.730	-0.683	-0.020	-0.005	-0.004	-0.011
0.1	0.01	0.01	-0.367	-0.415	0.815	-0.001	-0.171	-0.005

Table 4. SVD results for the ranking standardized data

Data scatter: 3600976.1901								
Singular value σ_v	Natural contribution	Contribution %	Singular vector components (loadings)					
			x	y	z	table	depth	carat
1794.6	3220431.16	89.43	-0.446	-0.452	-0.436	-0.409	-0.408	-0.270
505.8	255844.96	7.1	-0.288	-0.306	-0.268	0.558	0.586	-0.310
343.3	117845.97	3.27	-0.021	-0.025	0.091	-0.718	0.689	-0.023
77.4	5992.18	0.17	0.296	0.322	0.048	-0.061	-0.079	-0.893
25.9	672.25	0.02	0.342	0.335	-0.853	-0.046	0.093	0.183
13.8	189.67	0.01	0.716	-0.697	0.010	-0.005	-0.010	-0.012

From the table 1 one can see the enormous scatter of non-standardized data. This is likely due to the different features scales (fig. 7) - while the diamond size dimensions x, y, z and the weight in carats are in single digits, table and depth have average values of 57.5 and 61.6 respectively. When squared, table and depth contribute greatly to the data scatter, exceeding the contributions of other features many times over. This affects the results of PCA, as can be seen from the 100% contribution of the first principal component in Table 1. Therefore, the use of standardization is essential in order to properly apply PCA to the given data.



	x	y	z	table	depth	carat
count	400.000000	400.000000	400.000000	400.000000	400.000000	400.00000
mean	5.663400	5.665550	3.489300	57.504250	61.609750	0.76910
std	1.126584	1.116961	0.693352	2.051103	1.460072	0.46942
min	3.840000	3.890000	2.380000	53.000000	57.100000	0.23000
25%	4.660000	4.665000	2.870000	56.000000	60.800000	0.38000
50%	5.660000	5.660000	3.490000	57.000000	61.700000	0.70000
75%	6.490000	6.502500	4.020000	59.000000	62.400000	1.02250
max	9.100000	8.970000	5.670000	65.000000	68.600000	3.01000

Figure 7. Descriptive statistics for the features chosen for PCA

The data scatter for ranking standardized data is also worth mentioning, as it is even greater than that of non-standardized data. This may be explained by the fact that most of the features chosen for PCA follow normal distribution, and thus, when ranking normalization is applied, most of the values in the dataset become large values close to 50. In general, SVD for ranking normalization has shown to produce results similar to those for non-standardized data, which suggests a high degree of information loss due to how features are distributed.

As an example, let us describe the results in the table 2. Here one can see that the summary contribution of the first two principal components to the data scatter equals $66.62 + 21.41 = 88.03\%$, with the first principal component contributing the most. From the loading components it can be seen the first principal component is positively correlated with x, y, z, table and carat and negatively correlated with depth. While the first component's correlations with table and depth is positive and negative respectively, the second component's correlations with the same features is inverted. From singular vector values, the first component is generally greater when diamond's dimensions and weight are higher. Thus, intuitively, the first component corresponds to how "large" a diamond is.

After data preprocessing, the first two principal components obtained via SVD were visualized for two normalization methods - z-scoring and range normalization (fig. 10). Additionally, two groups of diamonds were considered to help facilitate the understanding of these visualizations. These groups are:

1. Diamonds with large weight in carats (carat > 2.1).
2. Diamonds with low depth ratios (depth < 58.5).

The thresholds that define the groups were determined from the distribution graphs of corresponding features (fig. 8, 9).

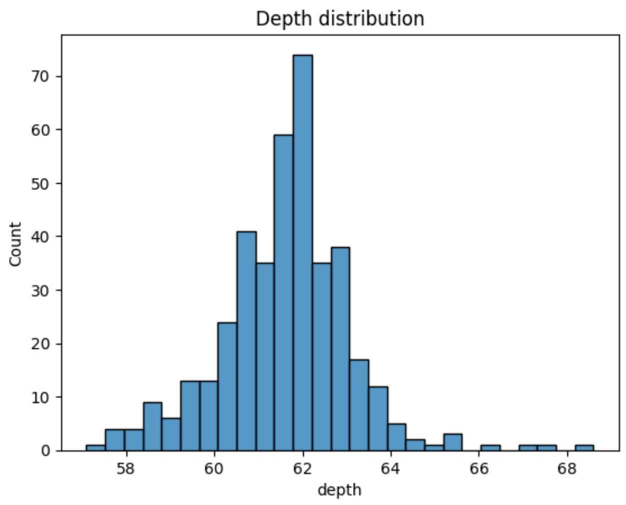


Figure 8. Depth feature distribution

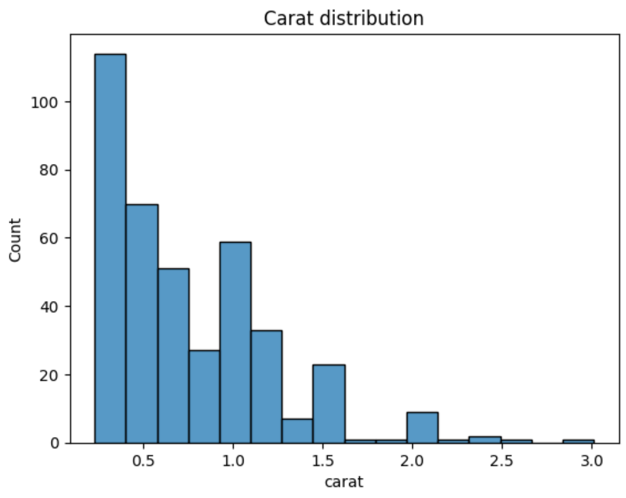


Figure 9. Carat feature distribution

Overall, the visualizations for both normalization techniques share many similarities in the overall distribution of instances. The most noticeable difference is that the visualizations are flipped vertically - the signs of the second principal component coordinates on these two visualizations are opposites. This is merely the result of us flipping the signs in accordance to the largest loading values to make the visualizations prettier. Another notable difference is that instances on the left are a bit more scattered along the second principal component axis. This can be attributed to greater data scatter contribution of the second principal component for z-standardized data (21.41% vs. 14.6% for z-scoring and range normalization respectively).

Due to the fact that most features (x, y, z, depth, table) follow normal distribution, and carat seems to follow the Pareto distribution (the Matthew principle), z-scoring seems to be more suitable for the given data.

As for the groups, it seems that larger weight in carat coincides with larger values of the first principal component, while smaller depth ratios coincide with lesser second principal component values. This follows from the observation that both groups seem to denote the outliers in the respective axes.

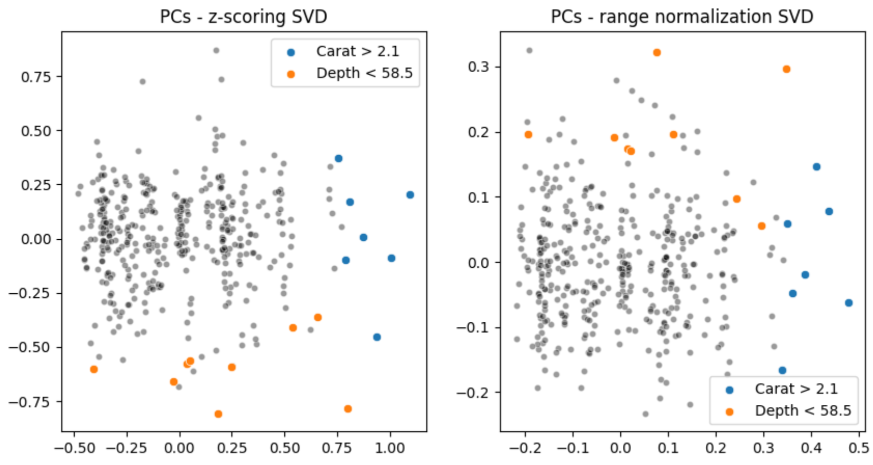


Figure 10. Visualizations of the first two principal components for z-scoring and range normalization

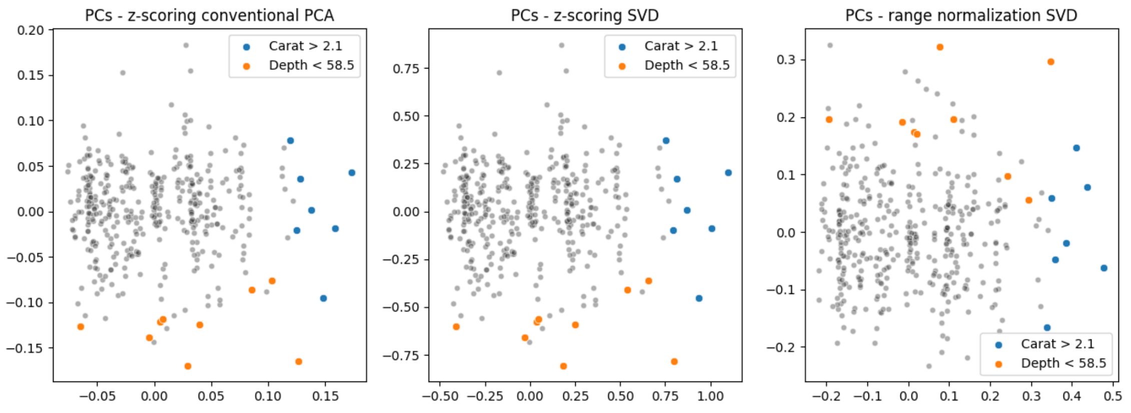


Figure 11. Visualizations of the first two principal components computed with SVD and conventional PCA

Comparing the visualizations obtained for the SVD-based PCA approach with the visualization obtained for the conventional PCA approach on z-standardized data on fig. 11, one can see that the visualizations corresponding to z-standardized data are virtually the same, with the only difference being different scales. Thereafter, the visualizations of the two groups are also in the same positions.

Looking at the hidden factor ranking in table 5, it is easy to see that the score is naturally correlated with diamond's dimensions and weight. Intuitively it follows that the hidden factor describes how large a diamond is.

Table 5. Top 10 instances by their hidden score

x	**y**	**z**	**carat**	**table**	**depth**	**score**
9.10	8.97	5.67	3.01	58.0	62.7	100.000000
8.82	8.75	5.45	2.65	61.0	62.0	98.484294
8.85	8.76	5.17	2.41	61.0	58.7	89.666102
8.60	8.56	5.24	2.33	58.0	61.1	86.891979
8.33	8.28	5.21	2.22	58.0	62.7	86.601659
7.89	7.81	5.04	2.00	60.0	64.2	86.520889
7.97	7.86	5.03	2.04	60.0	63.6	86.141693
8.22	8.30	5.08	2.11	60.0	61.5	86.105723
8.22	8.16	5.10	2.08	59.0	62.3	85.170271
8.39	8.31	4.82	2.04	64.0	57.7	84.878480

4 CLUSTER ANALYSIS AND CLUSTER INTERPRETATION

To understand the general pricing patterns a following subset of features was explored via K-Means algorithm:

- ”depth”;
- ”table”;
- ”carat”;
- ”price”.

These features denote the physical parameters of a diamond and were scaled to have normal distribution before the clustering algorithm was applied to them.

Then, using the build-in K-Means algorithm with 4 and 7 clusters were applied to the data. It was initialized to start with twelve sets of random centers for each number of clusters used. Algorithm’s performance was measured with inertia metric:

$$L = \sum_{k=1}^{K} \sum_{i \in S_k} \sum_{v \in V} (y_{iv} - c_{kv})^2 ,$$

where K is the number of clusters;

S_k is the number of objects in k-th cluster;

V is the set of features;

y_{iv} is value of feature v of the i-th object from cluster k;

c_{kv} is value of feature v of the center of cluster k.

After the evaluation, for each number of clusters the best-performing cluster set was chosen for further analysis. On those the absolute and relative deviations from grand mean for each feature were calculated:

$$d_{abs} = (c_{kv} - c_v),\ d_{rel} = \frac{c_{kv} - c_v}{c_v} \cdot 100\%.$$

For each cluster in each table deviations in a feature of more than 30% were marked with green(positive deviations) and red(negative deviation) backgrounds.

Table 6. Best set for K-Means with 4 clusters

	depth	**table**	**carat**	**price**
grand mean	61.7409	57.3868	0.7865	3858.1980
cluster 1 (234 instances)				
center	61.4547	58.0838	1.6865	12463.5812
grand mean devation	-0.2861	0.6970	0.9000	8605.3832
rel. grand mean deviation	-0.46%	1.21%	114.44%	223.04%

Table 6. (continued)

	depth	table	carat	price
grand mean	61.7409	57.3868	0.7865	3858.1980
cluster 2 (854 instances)				
center	62.0034	56.1681	0.4438	1276.4660
grand mean devation	0.2625	-1.2187	-0.3427	-2581.7320
rel. grand mean deviation	0.43%	-2.12%	-43.57%	-66.92%
cluster 3 (512 instances)				
center	62.5969	57.3387	1.0456	5258.8340
grand mean devation	0.8560	-0.0481	0.2592	1400.6360
rel. grand mean deviation	1.39%	-0.08%	32.95%	36.30%
cluster 4 (400 instances)				
center	60.2520	59.6425	0.6599	2543.2325
grand mean devation	-1.4889	2.2557	-0.1266	-1314.9655
rel. grand mean deviation	-2.41%	3.93%	-16.10%	-34.08%

According to the table 6, those four clusters correspond to extremely valuable, extremely cheap, moderately valuable and moderately cheap diamonds respectively. Interestingly, "depth" and "table" do not deviate that much from their respective grand means and do not correlate with neither "price" nor "carat".

Similar conclusion can be made for the case with 7 clusters. As shown on the table 7, they correspond to various "price" and "mass" ranges with clusters in similar range being divided based on their "depth" and "table" deviations.

Table 7. Best set for K-Means with 7 clusters

	depth	table	carat	price
grand mean	61.7409	57.3868	0.7865	3858.1980
cluster 1 (193 instances)				
center	61.5523	58.2466	1.7496	13071.0829
grand mean devation	-0.1885	0.8598	0.9631	9212.8849
rel. grand mean deviation	-0.31%	1.50%	122.46%	238.79%
cluster 2 (290 instances)				
center	60.5655	57.3117	0.4779	1450.8103
grand mean devation	-1.1753	-0.0751	-0.3085	-2407.3877
rel. grand mean deviation	-1.90%	-0.13%	-39.23%	-62.40%

Table 7. (continued)

	depth	**table**	**carat**	**price**
grand mean	61.7409	57.3868	0.7865	3858.1980
cluster 3 (350 instances)				
center	62.3123	58.0829	0.4388	1231.0829
grand mean devation	0.5714	0.6961	-0.3476	-2627.1151
rel. grand mean deviation	0.93%	1.21%	-44.20%	-68.09%
cluster 4 (192 instances)				
center	59.7719	60.8776	0.8353	3704.7188
grand mean devation	-1.9690	3.4908	0.0488	-153.4792
rel. grand mean deviation	-3.19%	6.08%	6.21%	-3.98%
cluster 5 (184 instances)				
center	63.7891	58.3761	1.0024	4422.3478
grand mean devation	2.0483	0.9893	0.2159	564.1498
rel. grand mean deviation	3.32%	1.72%	27.45%	14.62%
cluster 6 (431 instances)				
center	62.1624	55.0935	0.4575	1338.5963
grand mean devation	0.4216	-2.2933	-0.3290	-2519.6017
rel. grand mean deviation	0.68%	-4.00%	-41.83%	-65.31%
cluster 7 (360 instances)				
center	61.7317	56.6878	1.1141	6222.5278
grand mean devation	-0.0092	-0.6990	0.3277	2364.3298
rel. grand mean deviation	-0.01%	-1.22%	41.66%	61.28%

Overall, "depth" and "table" seem to have no correlation to both the diamond's price and its mass. Increasing the number of classes seems to subdivide the price ranges into smaller pieces determined by their "table" and "depth".

5 CONTINGENCY TABLE

5.1 Feature selection

Let's select the price feature and make it binarized according to the following criteria: $0 - 1000$, $1000 - 2500$, $2500 - 5000$, $5000 - 10000$, $10000+$. For the second feature, we will choose the clustering into 4 classes obtained in the previous paragraph, and we will work with these two categorical features.

5.2 Contingency table

To calculate the Contingency table, let's calculate how many elements fell into each pair from the Cartesian product of the binarized cluster price (the results are presented in Table 8).

Table 8. Contingency table

bin-price/cluster	**cluster 1**	**cluster 2**	**cluster 3**	**cluster 4**
$0 - 1000$	465	119	1	0
$1000 - 2500$	302	131	25	0
$2500 - 5000$	79	98	233	0
$5000 - 10000$	2	58	247	45
$10000+$	0	1	7	187

Now let's calculate the conditional probabilities, to do this, calculate the sum of the matrix from Table 8 by columns and rows, respectively, and divide the matrices into the calculated total statistics, taking into account the dimensions. The results are presented in Tables 9 and 10, respectively.

Values where the probability is greater than 70% are marked in green, and probabilities greater than 50% but less than 70% are blue. In Table 9, the probability of 80.6% (marked in green) shows that belonging to cluster 4 entails the probability of 80.6% that the price is more than 10,000. It also follows from belonging to cluster 1 that the price will be in the range from 0 to 1000 with a probability of 54.83% (marked in blue). In Table 10, belonging to the price categories of $0 - 1000$ and $1000 - 2500$ entails a high probability of belonging to 1 cluster (79.49% and 65.94%), for average prices ($2500 - 5000$ and $5000 - 10000$) there is a high probability of 3 clusters of 56.83% and 70.17% respectively. And with almost a single probability (95.9%), if an element has a price of more than 10,000, then it belongs to the 4th cluster.

Thus, we can conclude that clusters are very strongly related to the price, and the higher the cluster number, the higher the prices and vice versa.

Next, we calculate the Quetelet indices, the results are presented in Table 11 (colors indicate statistically significant results, green is greater than 0.3, red is less than -0.3). It can be concluded that low price values are associated with cluster 1 (as we noted above), and negatively affect clusters 3,4. And medium and high prices give a positive boost to clusters 3 and 4, respectively.

5.3 Average Quetelet index and Pearson's chi-squared

We calculate Q and φ using formulas, the implementation of which can be found in the Appendix A, $Q = sum(sum(pq)) = 1.3181$, $\varphi = sum(sum([(pab - pi).*(pab - pi)]./pi)) = 1.3181$. We get that phi-squared value is equal to the average Quetelet index.

5.4 Confidence level

$\chi^2 = 2000 \cdot 1.3181 = 2636.2685$. This is a high value which provides for rejection of the hypothesis of independence at both 95% and 99% confidence levels. Since we have 5 and 4 unique values for the features, we get $(5-1)(4-1) = 12$ degrees of freedom, and the critical chi squared values for 95% and 99% are 21.0 and 26.2, respectively. To reject the independence hypothesis in either case, one needs the number of objects greater than $\dfrac{21.0}{\varphi} = 15.93$ and greater than $\dfrac{26.2}{\varphi} = 19.87$, that are 16 and 20, respectively.

Table 9. column-conditional probabilities

bin-price/cluster	**cluster 1**	**cluster 2**	**cluster 3**	**cluster 4**
0 – 1000	0.5483	0.2924	0.0019	0.
1000 – 2500	0.3561	0.3219	0.0487	0.
2500 – 5000	0.0932	0.2408	0.4542	0.
5000 – 10000	0.0024	0.1425	0.4815	0.194
10000+	0.	0.0025	0.0136	0.806

Table 10. row-conditional probabilities

bin-price/cluster	**cluster 1**	**cluster 2**	**cluster 3**	**cluster 4**
0 – 1000	0.7949	0.2034	0.0017	0.
1000 – 2500	0.6594	0.286	0.0546	0.
2500 – 5000	0.1927	0.239	0.5683	0.
5000 – 10000	0.0057	0.1648	0.7017	0.1278
10000+	0.	0.0051	0.0359	0.959

Table 11. Quetelet indices

bin-price/cluster	**cluster 1**	**cluster 2**	**cluster 3**	**cluster 4**
$0 - 1000$	0.8747	-0.0004	-0.9933	-1.
$1000 - 2500$	0.5552	0.4055	-0.7872	-1.
$2500 - 5000$	-0.5456	0.1746	1.2156	-1.
$5000 - 10000$	-0.9866	-0.1903	1.7357	0.1021
$10000+$	-1.	-0.9748	-0.86	7.267

6 BOOTSTRAPPING

Table 12. Characteristics of clusters 3 and 4, grand mean

	Mean	**Standard deviation**
grand mean	57.3868	2.1540
cluste 3	57.3263	1.7518
cluste 4	58.1060	2.0878

Table 13. Bootstrapping results for table, 95% confidence intervals

	left bound	**right bound**
grand mean (pivotal)	57.2925	57.4814
grand mean (non-pivotal)	57.2997	57.4843
grand mean - mean in cluster 3 (pivotal)	-0.117	0.237
grand mean - mean in cluster 3 (non-pivotal)	-0.114	0.236
mean in cluster 3 - mean in cluster 4 (pivotal)	-1.089	-0.471
mean in cluster 3 - mean in cluster 4 (non-pivotal)	-1.095	-0.458

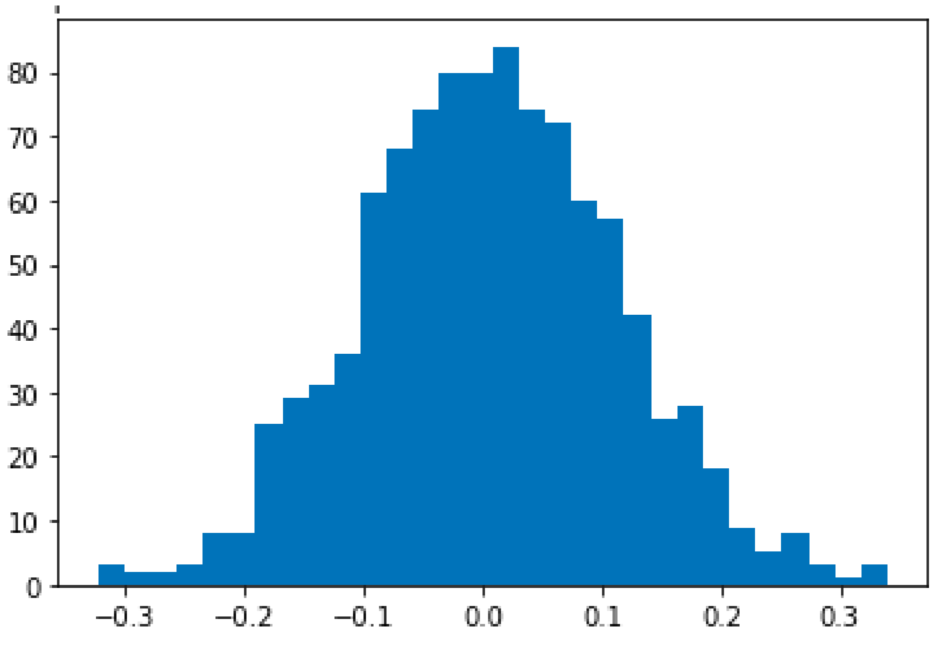


Figure 12. Bootstrap of ground mean of "table"

6.1 Confidence interval for grand mean of table

We chose the "table" feature and clusters 3 and 4, because for this feature, the average in the two selected clusters is very close to the overall average for the entire dataset. In Table 13, the first two lines show the results of calculating the 95% confidence interval for the "table" feature across the entire sample (the whole sample distribution presented in fig. 12 with 4000 iterations in bootstrap). As you can see, since the number of observations in the sample is large (2000), the results of pivotal and non-pivotal methods give very close estimates on the boundaries of the confidence interval.

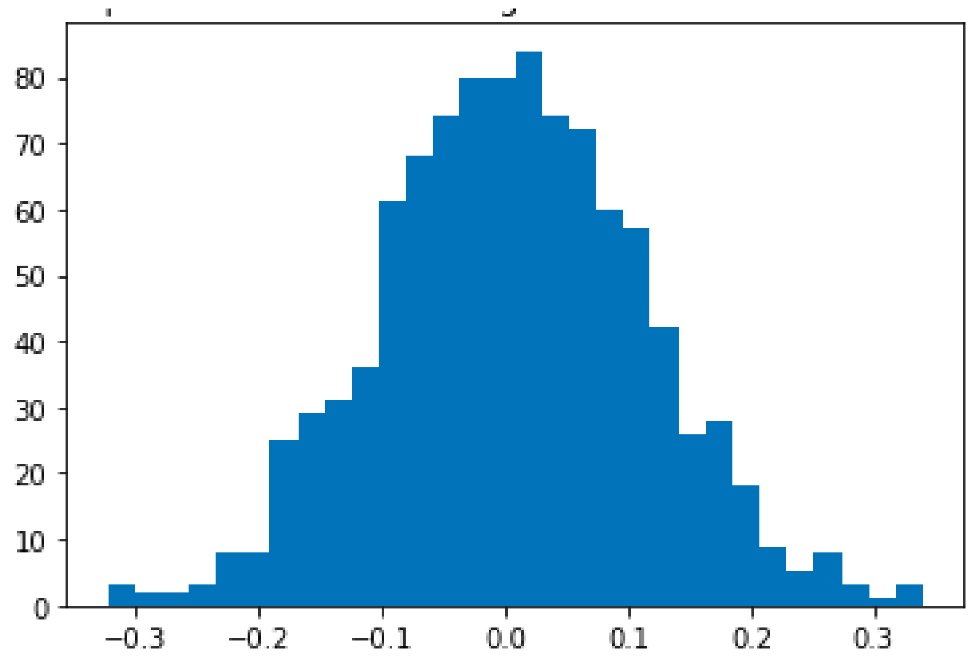


Figure 13. Bootstrap of difference between grand mean and mean in cluster 3 of "table" feature

6.2 Comparison of means in two selected clusters

As you can see from Table 12, the average in cluster 3 is slightly less than the average in cluster 4, as well as the standard deviation. From the last two rows of Table 13, we can conclude that the average in cluster 3 is statistically significantly less than the average in cluster 4 for the significance level of 5%, since the 95% confidence interval does not include 0 (this is done for both pivotal and non-pivotal approaches). A bootstrapped sample for the difference in averages between cluster 3 and cluster 4 is presented in fig. 13 with 4000 iterations in bootstrap). The distribution is quite symmetrical, but the part of the distribution near the value of -0.1 has a density higher than the symmetrical part near to 0.1, which creates a slight bias on average in the negative direction (the average in cluster 3 is less than the average in cluster 4).

6.3 Testing hypothesis that mean in cluster 3 coincide with grand mean

Let's choose cluster 3, since the average value of the "table" feature within this cluster is closest to the average of the entire sample. To test the hypothesis of the equality of the two averages using bootstrap at the 5% significance level, we need to look at the confidence interval for the difference built using bootstrap. As can be seen from Table 13 (lines 3 and 4), for both approaches, pivotal and non-pivotal, the confidence interval contains 0, which means that the null hypothesis of equality of averages does not deviate at the 5% significance level. In fig. 14 you can see the distribution of bootstrap difference between mean in cluster 3 and mean in cluster 4.

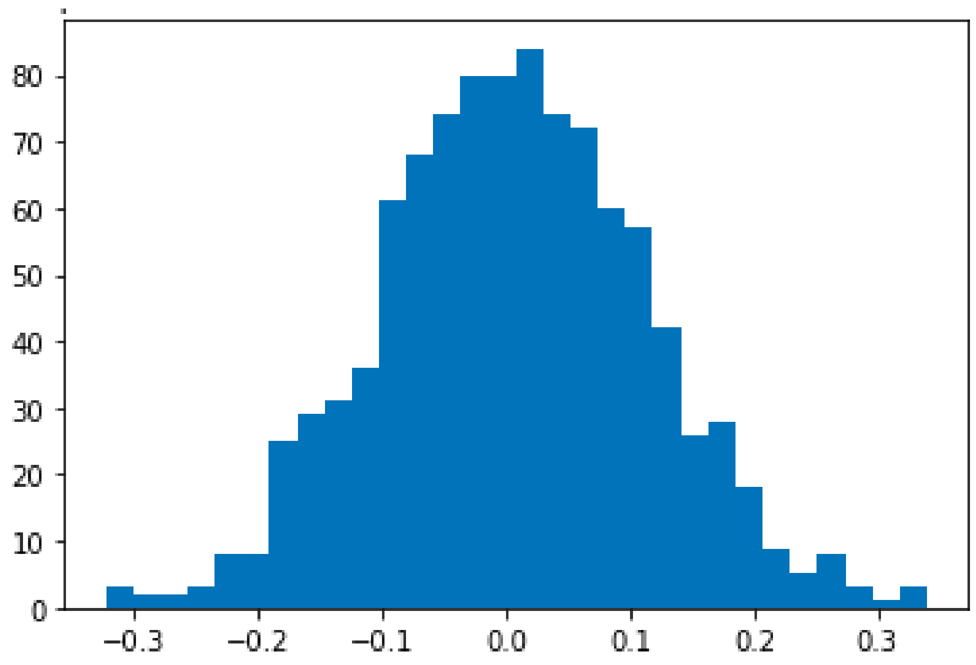


Figure 14. Bootstrap of difference between mean in cluster 3 and mean in cluster 4

APPENDIX A

Listing A.1 Data preprocessing, correlation matrix, K-Means.

```
import matplotlib.pyplot as plt
import pandas as pd
import numpy as np
import seaborn as sns

np.random.seed(42)

from platform import system

source = ("data\\" if system() == "Windows" else "data/") + "
   diamonds.csv"

N = 2000

df = pd.read_csv(source).sample(n=N, random_state=42)

print(df.shape)
df.head(8)

df["cut_ord"] = df["cut"].map(
    {"Fair": 0.0, "Good": 1.0, "Very Good": 2.0, "Premium": 3.0,
       "Ideal": 4.0}
)
df["clarity_ord"] = df["clarity"].map(
    {
        "I1": 0.0,
        "SI2": 1.0,
        "SI1": 2.0,
        "VS2": 3.0,
        "VS1": 4.0,
        "VVS2": 5.0,
        "VVS1": 6.0,
        "IF": 7.0,
    }
)
```

```
df["color_ord"] = df["color"].map(
    {
        "J": 0.0,
        "I": 1.0,
        "H": 2.0,
        "G": 3.0,
        "F": 4.0,
        "E": 5.0,
        "D": 6.0,
    }
)
df.head()

df = df.drop(["cut", "clarity", "color"], axis=1)
# df = pd.get_dummies(df, columns=["color"])


# # Assignment 1. Correlation coefficient
#
# With the data preprocessed, we have 1 categorical feature and 9
    numerical features. In this task a linear regression should be
    made with a pair of features and several metrics calculated on
    its prediction results.

df.head()

df.corr()


# Let's see the pairvise scatterplots of all the features in our
   data.

pplot = sns.pairplot(df, diag_kind="kde")
pplot.savefig("media/pairplot.png")
plt.show()

with sns.axes_style("whitegrid"):
    sns.scatterplot(df, x="carat", y="price", alpha=0.5)
plt.show()
```

```
from sklearn.linear_model import LinearRegression


x = df["carat"].to_numpy().reshape(-1, 1)
y = df["price"].to_numpy().reshape(-1, 1)

reg = LinearRegression().fit(x, y)
y_pred = reg.predict(x).reshape(-1, 1)

with sns.axes_style("whitegrid"):
    sns.scatterplot(df, x="carat", y="price", alpha=0.2)
    sns.lineplot(df, x="carat", y=y_pred.flatten(), color="r")
plt.show()

corr = df.corr()["carat"]["price"]
corr

ss_res = ((y - y_pred) ** 2).sum()
ss_tot = ((y - np.mean(y)) ** 2).sum()

determinacy = 1.0 - ss_res / ss_tot
determinacy


# Let's check whether the calculated coefficient of determination
    is correct. Since we are using least-squares linear regression
   , it should be equal to the correlation coefficient squared.

np.abs(determinacy - corr**2) < 1e-9


# Linear regression coefficients

a = corr * np.std(y) / np.std(x)
b = np.mean(y) - a * np.mean(x)


# Let's check the relative deviations of predicted values from
   true values and vise-versa for a set of 4 randomly selected
   instances.
```

```
idx = np.random.randint(0, y.shape[0] - 1, size=4)

x_cut = x[idx]
y_cut = y[idx]

dy_cut = y_cut - (a * x_cut + b)

dev_from_true = 100 * dy_cut / y_cut
dev_from_pred = 100 * dy_cut / (a * x_cut + b)

x_cut

y_cut

dev_from_true

dev_from_pred


# Now, let's do the same for each instance in the dataset

dy = y - (a * x + b)

tot_dev_from_true = np.abs(100 * dy / y).mean()
tot_dev_from_pred = np.abs(100 * dy / (a * x + b)).mean()

print(
    f"MAPE(relative to true values): {tot_dev_from_true:0.4f}%\
       nMAPE(relative to predicted values): {tot_dev_from_pred:0.4
       f}%"
)


# Now let's try polynomial regression.

x_stacked = np.hstack([np.ones_like(x), x, x**2, x**3])

reg = LinearRegression().fit(x_stacked, y)
```

```
with sns.axes_style("whitegrid"):
    sns.scatterplot(df, x="carat", y="price", alpha=0.2)
    sns.lineplot(df, x="carat", y=reg.predict(x_stacked).flatten
        (), color="r")
plt.show()

y_stacked = reg.predict(x_stacked).reshape(-1, 1)
dy_stacked = y - y_stacked



tot_dev_from_true_stacked = np.abs(100 * dy / y).mean()
tot_dev_from_pred_stacked = np.abs(100 * dy / y_stacked).mean()

print(
    f"MAPE(relative to true values): {tot_dev_from_true_stacked
       :0.4f}%\nMAPE(relative to predicted values): {
       tot_dev_from_pred_stacked:0.4f}%"
)

x = df["x"].to_numpy().reshape(-1, 1)
y = df["carat"].to_numpy().reshape(-1, 1)

x_stacked = np.hstack([np.ones_like(x), x, x**2, x**3])

reg = LinearRegression().fit(x_stacked, y)

with sns.axes_style("whitegrid"):
    sns.scatterplot(df, x="x", y="carat", alpha=0.2)
    sns.lineplot(df, x="x", y=reg.predict(x_stacked).flatten(),
       color="r")
plt.show()



# # Assignment 3. K-means clustering
#
# For the K-means clustering we will use the following features:
    'depth', 'table', 'carat' and 'price'. First, we standardize
   our features:

from sklearn.preprocessing import StandardScaler
```

```
frame = df[["depth", "table", "carat", "price"]]

frame_std = pd.DataFrame(
    StandardScaler().fit(frame).transform(frame),
    columns=["depth", "table", "carat", "price"],
)
frame.head()

frame_std.head()

from sklearn.cluster import KMeans

state = np.random.RandomState(seed=42)

grand_mean = frame.to_numpy().mean(axis=0)
print(f"Grand mean: {grand_mean}")

for n in [4, 7]:
    intertiae = []
    kmeans = []
    for i in range(12):
        kmeans += [KMeans(n_clusters=n, random_state=state,
           n_init=1).fit(frame_std)]
        intertiae += [kmeans[i].inertia_]

    best_idx = np.argmin(np.array(intertiae[1:]))
    clusters = kmeans[best_idx + 1]

    print(
        f"\n\nn_clusters: {n}\nall intertia values:\n\n{intertiae
           }\n\nbest k-means inertia(run #{best_idx+1}): {clusters
           .inertia_:0.4f}\n"
    )

    table_vals = pd.DataFrame(
        [[1, 2, 3, 4]], columns=["depth", "table", "carat", "
           price"]
    )
    for j in range(clusters.n_clusters):
        cluster = frame[clusters.labels_ == j]
        cluster_center = cluster.to_numpy().mean(axis=0)
        new_row = pd.DataFrame(
            [
                cluster_center,
                cluster_center - grand_mean,
                (cluster_center - grand_mean) / grand_mean,
            ],
            columns=["depth", "table", "carat", "price"],
            index=[j * 3 + k for k in range(3)],
        )
        table_vals = pd.concat([table_vals, new_row])
        print(
            f"cluster #{j+1}.\n# of elements: {cluster.shape[0]}\
               ncenter: {cluster_center}\ngrand mean deviation:{
               cluster_center - grand_mean}\nrelative grand mean
               deviation: {(cluster_center - grand_mean)/
               grand_mean}\n"
        )
    table_vals.to_csv(f"{n}_clusters.csv")
```

Listing A.2 PCA/SVD.

```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt

SEED = 42
np.random.seed(SEED)

np.set_printoptions(suppress=True)

# !curl -L -o diamonds-price-dataset.zip https://www.kaggle.
   com/api/v1/datasets/download/amirhosseinmirzaie/diamonds-
   price-dataset
# !unzip diamonds-price-dataset.zip

"""# Dataset & feature selection"""

N = 400
df = pd.read_csv('diamonds.csv').sample(n=N, random_state=
   SEED)

print("Shape:", df.shape)
df.head()

"""Features chosen: `x`, `y`, `z`, `table`, `depth` and `
   carat`. All of these features describe the size of a
   diamond."""

data = df[['x', 'y', 'z', 'table', 'depth', 'carat']]

data.head()

data.describe()

data.corr()

"""# Data standardization"""

means = data.mean(axis=0)
```

```
means

stds = data.std(axis=0)
stds

ranges = data.max(axis=0) - data.min(axis=0)
ranges

# Z-score normalization
data_zs = (data - means) / stds

# Range normalization
data_rd = (data - means) / ranges

# Ranking normalization
data_rn = 100.0 * (data - data.min(axis=0)) / ranges

# Performing singular value decomposition
uzs, szs, vzs = np.linalg.svd(data_zs)
urd, srd, vrd = np.linalg.svd(data_rd)
urn, srn, vrn = np.linalg.svd(data_rn)
uns, snss, vns = np.linalg.svd(data)

print("Singular values for z-score normalization:", szs.round
   (1))
print("Singular values for range normalization:", srd.round
   (1))
print("Singular values for ranking normalization:", srn.round
   (1))
print("Singular values for no standardization:", snss.round
   (1))

contrib_zs = np.square(szs)
contrib_rd = np.square(srd)
contrib_rn = np.square(srn)
contrib_ns = np.square(snss)

print("PC natural contributions (z-score normalization):",
   contrib_zs.round(2))
print("PC natural contributions (range normalization):",
   contrib_rd.round(2))
print("PC natural contributions (ranking normalization):",
   contrib_rn.round(2))
print("PC natural contributions (no standardization):",
   contrib_ns.round(2))

ds_zs = np.square(data_zs).to_numpy().sum()
ds_rd = np.square(data_rd).to_numpy().sum()
ds_rn = np.square(data_rn).to_numpy().sum()
ds_ns = np.square(data).to_numpy().sum()

print("Data scatter by definition (z-score normalization):
   %.4f" % ds_zs)
print("Data scatter by definition (range normalization): %.4f
   " % ds_rd)
print("Data scatter by definition (ranking normalization):
   %.4f" % ds_rn)
print("Data scatter by definition (no standardization): %.4f"
    % ds_ns)

ds_contib_zs = contrib_zs.sum()
ds_contib_rd = contrib_rd.sum()
ds_contib_rn = contrib_rn.sum()
ds_contib_ns = contrib_ns.sum()

print("Data scatter from contributions (z-score normalization
   ): %.4f" % ds_contib_zs)
print("Data scatter from contributions (range normalization):
    %.4f" % ds_contib_rd)
print("Data scatter from contributions (ranking normalization
   ): %.4f" % ds_contib_rn)
print("Data scatter from contributions (no standardization):
   %.4f" % ds_contib_ns)

"""From the results one can see that the calculated data
   scatter is the same for all versions of standardization,
   which is consistent with the theory."""

contrib_zs_percent = 100.0 * contrib_zs / ds_zs
contrib_rd_percent = 100.0 * contrib_rd / ds_rd
```

```
contrib_rn_percent = 100.0 * contrib_rn / ds_rn
contrib_ns_percent = 100.0 * contrib_ns / ds_ns

print("PC percentage contributions (z-score normalization):",
    contrib_zs_percent.round(2))
print("PC percentage contributions (range normalization):",
   contrib_rd_percent.round(2))
print("PC percentage contributions (ranking normalization):",
    contrib_rn_percent.round(2))
print("PC percentage contributions (no standardization):",
   contrib_ns_percent.round(2))

for i in range(6):
x_arrstr = np.char.mod('%.3f', vrn[i].round(3))
#combine to a string
print(" & ".join(x_arrstr))

vzs

"""Here we see that the contrast between principle component
   contributions is  starker for range normalization - 78% PC1
    contribution for r-standardization vs. 67% PC1
   contribution for z-standardization.

Ranking normalization brings PC1 contribution even further up
    to 89%, closer to the non-standardizaed contribution
   distribution.

# Principal components visualization

For the purpose of visualizing two first principal components
    and the differences between them, let us use two features
   to define two separate groups of dataset instances: `depth`
    and `carat`.

The first group are diamonds with small depth ratios (< 58.5,
    as shown below). The second group are diamonds of large
   weight (> 2.1 carats, as shown below).

## Defining instance groups
```

```
"""

sns.histplot(data['depth']).set_title('Depth distribution')

# Diamonds with small depth ratios
depth_group = df[df['depth'] < 58.5]
depth_group.shape

sns.histplot(data['carat']).set_title('Carat distribution')

# Diamonds with large weight
carat_group = df[df['carat'] > 2.1]
carat_group.shape

depth_group.index.intersection(carat_group.index)

"""As one can see, the two groups do not overlap."""

carat_group_indices = df.index.get_indexer(carat_group.index.
   tolist())
depth_group_indices = df.index.get_indexer(depth_group.index.
   tolist())

"""## Calculating principal components

### Z-score normalized data PCs
"""

pcs1_zs = vzs[0]
pcs1_zs

"""Larger loading components are positive, thus the sign for
   factors remains unchanged."""

pc1_zs = uzs[:, 0] * np.sqrt(szs[0])

pcs2_zs = vzs[1]
pcs2_zs

"""Larger loading components are negative, thus the sign for
```

```
   factors is changed to negative."""

pc2_zs = uzs[:, 1] * np.sqrt(szs[1])

"""### Range normalized data PCs"""

pcs1_rd = vrd[0]
pcs1_rd

"""Larger loading components are positive, thus the sign for
   factors remains unchanged."""

pc1_rd = urd[:, 0] * np.sqrt(srd[0])

pcs2_rd = vrd[1]
pcs2_rd

"""Larger loading components are negative, thus the sign for
   factors is changed to negative."""

pc2_rd = -urd[:, 1] * np.sqrt(srd[1])

"""## Visualization"""

fig, axs = plt.subplots(1, 2, figsize=(10,5))

axs[0].set_title('PCs - z-scoring SVD')
sns.scatterplot(x=pc1_zs, y=pc2_zs, s=80, color="black",
   marker=".", alpha=0.4, ax=axs[0])
sns.scatterplot(x=pc1_zs[carat_group_indices], y=pc2_zs[
   carat_group_indices], label='Carat > 2.1', ax=axs[0])
sns.scatterplot(x=pc1_zs[depth_group_indices], y=pc2_zs[
   depth_group_indices], label='Depth < 58.5', ax=axs[0])

axs[1].set_title('PCs - range normalization SVD')
sns.scatterplot(x=pc1_rd, y=pc2_rd, s=80, color="black",
   marker=".", alpha=0.4, ax=axs[1])
sns.scatterplot(x=pc1_rd[carat_group_indices], y=pc2_rd[
   carat_group_indices], label='Carat > 2.1', ax=axs[1])
sns.scatterplot(x=pc1_rd[depth_group_indices], y=pc2_rd[
   depth_group_indices], label='Depth < 58.5', ax=axs[1])

"""On the resulting plots one can see that overall the
   visualization for both normalization techniques share many
   similarities in the overall distribution of instances.

As for the groups, it seems that larger weight in carat
   coincides with larger values of PC1, while smaller depth
   ratios coincide with lesser PC2 values. This follows from
   the observation that both groups seem to denote the
   outliers in the respective axes.

# Conventional PCA
"""

# The covariance matrix
cov = (data_zs.T @ data_zs) / (data_zs.shape[0] - 1)
cov

# Performing spectral decomposition
la, c = np.linalg.eig(cov)

print('Eigenvalues:', la)

print('Eigenvectors:', c)

"""The eigenvalues and the corresponding eigen vectors are
   already correctly ordered. Let us now compute the first two
    principal components."""

c1 = c[:, 0]

print('Eigenvector 1:', c1)

c2 = c[:, 1]

print('Eigenvector 2:', c2)

"""Largest components in both eigenvectors are positive, thus
    we don't need to invert the signs on the corresponding
   factors."""

z1 = (data_zs @ c1) / np.sqrt(la[0] * (data_zs.shape[0] - 1))
z2 = (data_zs @ c2) / np.sqrt(la[1] * (data_zs.shape[0] - 1))

z1 = z1.to_numpy()
z2 = z2.to_numpy()

fig, axs = plt.subplots(1, 3, figsize=(15,5))

axs[0].set_title('PCs - z-scoring conventional PCA')
sns.scatterplot(x=z1, y=z2, s=80, color=".2", marker=".", ax=
   axs[0], alpha=0.4)
sns.scatterplot(x=z1[carat_group_indices], y=z2[
   carat_group_indices], ax=axs[0], label='Carat > 2.1')
sns.scatterplot(x=z1[depth_group_indices], y=z2[
   depth_group_indices], ax=axs[0], label='Depth < 58.5')

axs[1].set_title('PCs - z-scoring SVD')
sns.scatterplot(x=pc1_zs, y=pc2_zs, s=80, color=".2", marker=
   ".", ax=axs[1], alpha=0.4)
sns.scatterplot(x=pc1_zs[carat_group_indices], y=pc2_zs[
   carat_group_indices], ax=axs[1], label='Carat > 2.1')
sns.scatterplot(x=pc1_zs[depth_group_indices], y=pc2_zs[
   depth_group_indices], ax=axs[1], label='Depth < 58.5')

axs[2].set_title('PCs - range normalization SVD')
sns.scatterplot(x=pc1_rd, y=pc2_rd, s=80, color=".2", marker=
   ".", ax=axs[2], alpha=0.4)
sns.scatterplot(x=pc1_rd[carat_group_indices], y=pc2_rd[
   carat_group_indices], ax=axs[2], label='Carat > 2.1')
sns.scatterplot(x=pc1_rd[depth_group_indices], y=pc2_rd[
   depth_group_indices], ax=axs[2], label='Depth < 58.5')

"""The resulting figures are very similar, the differences in
    coordinates are mostly caused from the use of different
   normalization techniques.

# Hidden ranking factor
"""
```

```
pcs1_rn = vrn[0]
pcs1_rn

"""Larger loading components are negative, thus the sign for
   factors is changed to negative."""

pcs1_rn = -vrn[0]
pcs1_rn

pc1_rn = -urn[:, 0]

# Percentage scaling
pc1_rn_m = 100 * pc1_rn / np.max(pc1_rn)

sns.histplot(pc1_rn_m).set_title("Hidden factors, scaled to
   0-100")

"""Now, let's take the best instances in terms of their
   hidden factor:"""

sub_df = df.loc[data.index.tolist()][['x', 'y', 'z', 'carat',
    'table', 'depth']]

sub_df['score'] = pc1_rn_m

sub_df.sort_values('score', ascending=False)[:20]

"""Looking at the table, it is easy to see that the score is
   naturally correlated with diamond's dimensions and weight.
   Intuitively it follows that the hidden factor describes how
    large a diamond is."""
```

Listing A.3 Contingency table and bootstrap.

```
import numpy as np
import matplotlib.pyplot as plt
from tqdm import tqdm
from scipy.stats import norm
import pandas as pd
from tqdm import tqdm
from sklearn.cluster import KMeans

## clustering

from platform import system

source = ("data\\" if system() == "Windows" else "./") + "
   diamonds.csv"

N = 2000

df = pd.read_csv(source).sample(n=N, random_state=42)

print(df.shape)
print(df.head(8))

from sklearn.preprocessing import StandardScaler

frame = df[["depth", "table", "carat", "price"]]

frame_std = pd.DataFrame(
StandardScaler().fit(frame).transform(frame),
columns=["depth", "table", "carat", "price"],
)
print(frame.head())


state = np.random.RandomState(seed=42)

grand_mean = frame.to_numpy().mean(axis=0)
print(f"Grand mean: {grand_mean}")

for n in [4]:
```

```
intertiae = []
kmeans = []
for i in tqdm(range(12)):
kmeans += [KMeans(n_clusters=n, random_state=state, n_init=1)
   .fit(frame_std)]
intertiae += [kmeans[i].inertia_]

best_idx = np.argmin(np.array(intertiae[1:]))
clusters = kmeans[best_idx + 1]

print(
f"\n\nn_clusters: {n}\nall intertia values:\n\n{intertiae}\n\
   nbest k-means inertia(run #{best_idx+1}): {clusters.
   inertia_:0.4f}\n"
)

table_vals = pd.DataFrame(
[[1, 2, 3, 4]], columns=["depth", "table", "carat", "price"]
)

for j in range(clusters.n_clusters):
cluster = frame[clusters.labels_ == j]
cluster_center = cluster.to_numpy().mean(axis=0)
new_row = pd.DataFrame(
[
cluster_center,
cluster_center - grand_mean,
(cluster_center - grand_mean) / grand_mean,
],
columns=["depth", "table", "carat", "price"],
index=[j * 3 + k for k in range(3)],
)
table_vals = pd.concat([table_vals, new_row])
print(
f"cluster #{j+1}.\n# of elements: {cluster.shape[0]}\ncenter:
    {cluster_center}\ngrand mean deviation:{cluster_center -
   grand_mean}\nrelative grand mean deviation: {(
   cluster_center - grand_mean)/grand_mean}\n"
)
```

```
p = plt.hist(df['price'])

def binarization(x):
if x<1000:
return 0
elif x<2500:
return 1
elif x<5000:
return 2
elif x<10000:
return 3
else:
return 4

# binarization of price
feature1 = np.array(df['price'].apply(binarization))

# 4-means clustering
feature2 = clusters.labels_


def get_contingency_table(feature1,feature2):
unique1 = np.unique(feature1)
unique2 = np.unique(feature2)
mat = np.zeros((len(unique1),len(unique2)))
for i in range(len(unique1)):
for j in range(len(unique2)):
mat[i,j] = np.sum((feature1==unique1[i])*(feature2==unique2[j
   ]))
return mat

tab = get_contingency_table(feature1,feature2)
print(tab)

t1 = np.sum(tab,axis=0)
print(t1)

t2 = np.sum(tab,axis=1)
print(t2)
```

```
# column-conditional probabilities
np.set_printoptions(precision=4)
tc = tab/t1.reshape(1,4)
print(tc)

# row-conditional probabilities
np.set_printoptions(precision=4)
tr = tab/t2.reshape(5,1)
print(tr)

pab=tab/2000
print(pab)

# marginal row
p1=np.sum(pab,axis=0)
print(p1)

# marginal column
p2=np.sum(pab,axis=1)
print(p2)

# independence matrix
pi=(p2.reshape(5,1))@(p1.reshape(1,4))
print(pi)

# Quetelet indices
np.set_printoptions(precision=4,suppress=True)
q=pab/pi-1
print(q)

# Quetelet-Pearson decomposition
pq=pab*q
print(pq)

# sum Quetelet indices
Q=np.sum(np.sum(pq))
print(Q)

# Pearson phi-squared value
phi=np.sum(np.sum([(pab-pi)*(pab-pi)]/pi))
```

```
print(phi)

# The phi-squared value is equal to the average Quetelet
   index indeed

X2=2000*phi
print(X2)

# number of degrees of freedom
print((4-1)*(5-1))



# At 12 degrees of freedom, the critical chi-squared values
   are 21.0 and 26.2, at the confidence level 95% and 99%,
   respectively
# To reject the independence hypothesis in either case, one
   needs the number of objects greater than 21.0 /phi=15.93
   and greater than 26.2/phi=19.87, that are 16 and 20,
   respectively.

## Taks 5

def bootstrap(x, num_samples):
mean_arr = []
for i in range(num_samples):
mean_arr.append(np.mean(np.random.choice(x, len(x))))
return mean_arr

def bootstrap_difference(x, y, num_samples):
mean_arr = []
for i in range(num_samples):
mean_arr.append(np.mean(np.random.choice(x, len(x)))-np.mean(
   np.random.choice(y, len(y))))
return mean_arr

def bootstrap_confidence_interval(x, num_samples, alpha=0.05,
    pivotal=True):
mean_arr = bootstrap(x, num_samples)
if pivotal:
mean = np.mean(mean_arr)
```

```
std = np.std(mean_arr)
return mean + (-norm.isf(alpha/2))*std, mean + (-norm.isf(1-
   alpha/2))*std

else:
return np.quantile(mean_arr, alpha/2), np.quantile(mean_arr,
   1-alpha/2)

def bootstrap_confidence_interval_diff(x, y, num_samples,
   alpha=0.05, pivotal=True):
mean_arr = bootstrap_difference(x,y, num_samples)
if pivotal:
mean = np.mean(mean_arr)
std = np.std(mean_arr)
return mean + (-norm.isf(alpha/2))*std, mean + (-norm.isf(1-
   alpha/2))*std

else:
return np.quantile(mean_arr, alpha/2), np.quantile(mean_arr,
   1-alpha/2)

def test_hypothesis_by_boostrap(x, y, num_samples, alpha
   =0.05, pivotal=True):
left_bound, right_bound = bootstrap_confidence_interval_diff(
   x, y, num_samples, alpha=alpha, pivotal=pivotal)
if left_bound<0 and right_bound>0:
return True
else:
return False

def plot_hist(x, title):
p = plt.hist(mean_arr,bins=30)
plt.title(title)
plt.show()


# 1. Plot a graph and 95% interval using the
   bootstrap_confidence_interval function
# 2. Select 2 clusters, build a bootstrap and a bootstrap of
   the difference in each (here you can also add confidence
   intervals to compare them qualitatively + write confidence
   intervals for each cluster)
# 3. Test the hypothesis using the function


## we choose the table feature and 3.4 clusters, since the
   difference between groud mean is very small

sample_groud = np.array(frame['table'])

print(np.mean(sample_groud))

print(np.std(sample_groud))

# I_95 pivotal of ground mean
print(bootstrap_confidence_interval(sample_groud, 4000, alpha
   =0.05, pivotal=True))

# I_95 non-pivotal of ground mean
print(bootstrap_confidence_interval(sample_groud, 4000, alpha
   =0.05, pivotal=False))

bootstrap_ground = bootstrap(sample_groud, 4000)

lb,rb = bootstrap_confidence_interval(sample_groud, 4000,
   alpha=0.05, pivotal=True)
print(f"I_95 of ground mean (pivotal): ({lb:.3f}, {rb:.3f})")
lb,rb = bootstrap_confidence_interval(sample_groud, 4000,
   alpha=0.05, pivotal=False)
print(f"I_95 of ground mean (non-pivotal): ({lb:.3f}, {rb:.3f
   })")
plot_hist(bootstrap_ground, 'bootstrap of ground mean')


sample_cluster_3 = np.array(frame[clusters.labels_ == 2]['
   table'])
bootstrap_ground_3_mean = bootstrap_difference(sample_groud,
   sample_cluster_3, 4000)

print(np.mean(sample_cluster_3))
print(np.std(sample_cluster_3))

lb,rb = bootstrap_confidence_interval_diff(sample_groud,
   sample_cluster_3, 4000, alpha=0.05, pivotal=True)
print(f"I_95 of difference between ground mean and mean in
   cluster 3 (pivotal): ({lb:.3f}, {rb:.3f})")
lb,rb = bootstrap_confidence_interval_diff(sample_groud,
   sample_cluster_3, 4000, alpha=0.05, pivotal=False)
print(f"I_95 of difference between ground mean and mean in
   cluster 3 (non-pivotal): ({lb:.3f}, {rb:.3f})")
plot_hist(bootstrap_ground_3_mean, 'bootstrap of difference
   between grand mean and mean in cluster 3')


sample_cluster_4 = np.array(frame[clusters.labels_ == 3]['
   table'])
bootstrap_3_4_mean = bootstrap_difference(sample_cluster_3,
   sample_cluster_4, 4000)

print(np.mean(sample_cluster_4))

print(np.std(sample_cluster_4))

lb,rb = bootstrap_confidence_interval_diff(sample_cluster_3,
   sample_cluster_4, 4000, alpha=0.05, pivotal=True)
print(f"I_95 of difference between mean in cluster 3 and mean
    in cluster 4 (pivotal): ({lb:.3f}, {rb:.3f})")
lb,rb = bootstrap_confidence_interval_diff(sample_cluster_3,
   sample_cluster_4, 4000, alpha=0.05, pivotal=False)
print(f"I_95 of difference between mean in cluster 3 and mean
    in cluster 4 (non-pivotal): ({lb:.3f}, {rb:.3f})")
plot_hist(bootstrap_3_4_mean, 'bootstrap of difference
   between mean in cluster 3 and mean in cluster 4')

## testing hypothesis

test_pivotal = test_hypothesis_by_boostrap(sample_groud,
   sample_cluster_3, 4000, alpha=0.05, pivotal=True)
test_non_pivotal = test_hypothesis_by_boostrap(sample_groud,
   sample_cluster_3, 4000, alpha=0.05, pivotal=False)

if test_pivotal:
print("Hypothesis is that ground mean equal to mean in
   cluster 3 is not rejected (pivotal)")
else:
print("Hypothesis is that ground mean equal to mean in
   cluster 3 not rejected (pivotal)")
print()
if test_non_pivotal:
print("Hypothesis is that ground mean equal to mean in
   cluster 3 is not rejected (non-pivotal)")
else:
print("Hypothesis is that ground mean equal to mean in
   cluster 3 not rejected (non-pivotal)")
```