Homework: Principal Components Analysis

Computational Linear Algebra for Large Scale Problems

Politecnico di Torino

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Introduction.

The following report focuses on the analysis of a motorcycle dataset extracted from bikez.com on April 30th 2022, consisting in a preprocessed and cleansed version of the dataset.

```
In [1]: import random
    import numpy as np
    import pandas as pd
    import seaborn as sns

from matplotlib import pyplot as plt
    import matplotlib.patheffects as pe
%matplotlib inline

from sklearn.preprocessing import StandardScaler, MinMaxScaler
    from sklearn.decomposition import PCA
    from sklearn.cluster import KMeans
    from sklearn.metrics import silhouette_score
In [2]: input_file = 'cla4lsp22_bikez_curated.csv' # csv file storing the database to be used
```

Preparation (Setting the Random State)

Initialization of the random state to be used in random processes to perform random but reproducible experiments and analysis on the dataset.

```
In [3]: def set_randomState(id1, id2):
    rs = min(id1, id2) # compute the lower ID student number
    return rs

In [4]: # Initialization of the random state

    bergadano_id = 304415
    cadau_id = 304861
    rs = set randomState(bergadano id, cadau id)
```

Exercise 1 (Loading and Preparing the Data)

Loading the dataset from a csv input file into a PandasDataFrame and selection of some rows.

Dataset visualization

In [6]: # Print some rows and columns of the dataframe to visualize the structure of the dataset
display(workdf)

	Brand	Model	Year	Category	Rating	Displacement (ccm)	Power (hp)	Torque (Nm)	Engine cylinder	Engine stroke	 Dry weight (kg)
1	acabion	gtbo 55	2007	Sport	2.6	1300.0	541.0	420.0	In-line four	four- stroke	 360.0
4	acabion	gtbo 70	2007	Prototype / concept model	3.1	1300.0	689.0	490.0	In-line four	four- stroke	 300.0
6	access	ams 3.20 supercross	2016	ATV	NaN	280.0	18.8	NaN	Single cylinder	four- stroke	 225.0
7	access	ams 4.30 supermoto efi	2016	ATV	NaN	359.3	29.5	NaN	Single cylinder	four- stroke	 236.0
8	access	ams 4.38 sm gear shift	2016	ATV	NaN	449.0	37.6	NaN	Single cylinder	four- stroke	 236.0
38459	zündapp	roller super	1968	Scooter	NaN	49.0	NaN	NaN	Single cylinder	two- stroke	 83.5
38462	zündapp	z 2 g	1923	Sport	NaN	211.0	2.8	NaN	Single cylinder	two- stroke	 73.0
38466	zündapp	z 22	1923	Sport	NaN	211.0	2.3	NaN	Single cylinder	two- stroke	 58.0
38468	zündapp	z 249	1923	Sport	NaN	249.0	2.8	NaN	Single cylinder	two- stroke	 76.0
38471	zündapp	z 300	1929	Sport	NaN	298.0	26.0	NaN	Single cylinder	two- stroke	 105.0

13673 rows × 27 columns

```
In [7]: # Set some variables with column names
labels_name = {'Brand', 'Model', 'Year', 'Category', 'Rating'}
```

```
In [8]: # Exctract from the DataFrame labels and features
labels = workdf.loc[:, list(labels_name)]
features = workdf.loc[:, list(features_name)]
```

	Year	Model	Category	Brand	Rating
1	2007	gtbo 55	Sport	acabion	2.6
4	2007	gtbo 70	Prototype / concept model	acabion	3.1
6	2016	ams 3.20 supercross	ATV	access	NaN
7	2016	ams 4.30 supermoto efi	ATV	access	NaN
8	2016	ams 4.38 sm gear shift	ATV	access	NaN
38459	1968	roller super	Scooter	zündapp	NaN
38462	1923	z 2 g	Sport	zündapp	NaN
38466	1923	z 22	Sport	zündapp	NaN
38468	1923	z 249	Sport	zündapp	NaN
38471	1929	z 300	Sport	zündapp	NaN

13673 rows × 5 columns

_	Bore (mm) suspe		Rear suspension	Front brakes	Rear tire	Fuel capacity (Its)	Torque (Nm)	Power (hp)	Rear brakes	Seat height (mm)	Fr suspens
	1	81.0	not given/unknown	not given/unknown	other	NaN	420.0	541.0	not given/unknown	NaN	given/unknc
	4	81.0	not given/unknown	not given/unknown	other	NaN	490.0	689.0	not given/unknown	NaN	given/unkno
	6	NaN	not given/unknown	single disc	other	14.0	NaN	18.8	single disc	NaN	given/unknc
	7	NaN	not given/unknown	single disc	other	14.0	NaN	29.5	single disc	NaN	given/unkno

8	NaN	not given/unknown	single disc	other	14.0	NaN	37.6	single disc	NaN	of
•••										
38459	39.0	not given/unknown	expanding brake (drum brake)	other	NaN	NaN	NaN	expanding brake (drum brake)	NaN	given/unkno
38462	62.0	other	not given/unknown	other	6.0	NaN	2.8	not given/unknown	NaN	01
38466	62.0	other	not given/unknown	other	6.0	NaN	2.3	not given/unknown	NaN	01
38468	68.0	other	expanding brake (drum brake)	other	6.1	NaN	2.8	expanding brake (drum brake)	NaN	ot
38471	68.0	not given/unknown	expanding brake (drum brake)	other	NaN	NaN	26.0	expanding brake (drum brake)	NaN	given/unkno

13673 rows × 22 columns

display(workdf)

As can be noticed, the dataset is composed by several columns, which can be divided into *Features* and *Labels* and into *Categorical* and *Numerical* ones.

```
In [11]:
         # Select the columns to drop at random among three possible sets of two columns
         first_set_of_features = ["Front brakes", "Rear brakes"]
         second set of features = ["Front tire", "Rear tire"]
         third set of features = ["Front suspension", "Rear suspension"]
         features to drop = [first set of features,
                             second set of features,
                             third_set_of_features]
         # Set the numpy random seed as the random state rs
         random.seed(rs)
         columns to drop = features to drop[random.randint(0, 2)]
         # Drop the columns from the dataframe
         print(f"The columns: {columns to drop} were randomly dropped.")
         workdf = workdf.drop(columns to drop, axis=1)
         categorical features name = categorical features name - set(columns to drop)
         features name = features name - set(columns to drop)
        The columns: ['Front brakes', 'Rear brakes'] were randomly dropped.
         # Print some rows and columns of the labels dataframe to visualize the structure
In [12]:
                                                                         # of the dataset
```

Displacement Power Torque Engine Engine Cooling **Brand** Model Year Category Rating (ccm) (hp) (Nm) cylinder stroke systen In-line fouracabion qtbo 55 2007 Sport 2.6 1300.0 541.0 420.0 Liquic four stroke acabion qtbo 70 2007 Prototype 3.1 1300.0 689.0 490.0 In-line four-Liquic four / concept stroke

				model							
6	access	ams 3.20 supercross	2016	ATV	NaN	280.0	18.8	NaN	Single cylinder	four- stroke	 Ai
7	' access	ams 4.30 supermoto efi	2016	ATV	NaN	359.3	29.5	NaN	Single cylinder	four- stroke	 Ai
8	access	ams 4.38 sm gear shift	2016	ATV	NaN	449.0	37.6	NaN	Single cylinder	four- stroke	 Ai
•••							•••				 ••
38459	zündapp	roller super	1968	Scooter	NaN	49.0	NaN	NaN	Single cylinder	two- stroke	 Ai
38462	zündapp	z 2 g	1923	Sport	NaN	211.0	2.8	NaN	Single cylinder	two- stroke	 Ai
38466	z ündapp	z 22	1923	Sport	NaN	211.0	2.3	NaN	Single cylinder	two- stroke	 Ai
38468	z ündapp	z 249	1923	Sport	NaN	249.0	2.8	NaN	Single cylinder	two- stroke	 Ai
38471	zündapp	z 300	1929	Sport	NaN	298.0	26.0	NaN	Single cylinder	two- stroke	 Ai

13673 rows × 25 columns

Missing data evaluation

In this subsection, the issue of missing values in the original dataset is faced.

Evaluating the effect of dropping rows with at least one missing value

```
In [13]: print("Dropping null values evaluation.")
    print(f"\tNumber of rows in the DataFrame \
        before dropping null values: {len(workdf)}")
    workdf_droppedNullValues = \
        workdf.loc[:, list(features_name)].dropna()
    print(f"\tNumber of rows in the DataFrame \
        after dropping null values: {len(workdf_droppedNullValues)}")
    print(f"Percentage of dropped rows: \
        {(len(workdf)-len(workdf_droppedNullValues)) / len(workdf) * 100:.2f}%")
```

```
Dropping null values evaluation.

Number of rows in the DataFrame before dropping null values: 13673

Number of rows in the DataFrame after dropping null values: 2042

Percentage of dropped rows: 85.07%
```

Before removing all rows with at least one missing value, the dataframe which one is being worked with contains, meaning it contains 13673 rows. After the removal of all the rows with at least one missing value, the length is 2042.

85.07% entries have been dropped.

All these entries removal would result in a significant loss of information.

Evaluating missing data by column

```
In [14]: print("Percentage of missing values by column.")
         percs = (workdf.loc[:, list(features name)].isnull().mean() * 100).\
         sort values(ascending=False)
         for c, p in percs.items():
             print(f"\t{c}: {p:.2f}%")
         Percentage of missing values by column.
                 Torque (Nm): 56.55%
                 Dry weight (kg): 41.91%
                 Seat height (mm): 36.99%
                 Wheelbase (mm): 33.01%
                 Power (hp): 32.58%
                Bore (mm): 24.63%
                 Stroke (mm): 24.63%
                 Fuel capacity (lts): 18.89%
                Displacement (ccm): 2.48%
                Transmission type: 0.00%
                Engine cylinder: 0.00%
                Gearbox: 0.00%
                 Fuel control: 0.00%
                 Front suspension: 0.00%
                Fuel system: 0.00%
                Rear tire: 0.00%
                Engine stroke: 0.00%
                 Front tire: 0.00%
                 Cooling system: 0.00%
                 Rear suspension: 0.00%
```

A considerable number of columns have a high percentage of missing values along the rows.

The removal of all the rows with at least one column missing a value would result in an important loss of information concerning (potential) numerical features such as *Torque*, *Dry weight* or *Seat height*

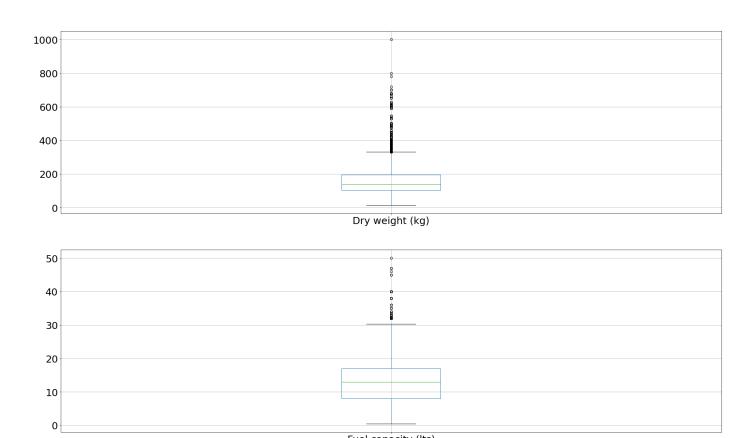
Evaluating missing data by rows

```
print ("Rows with missing value in 0, 1 or more columns")
In [15]:
         null counts = workdf.isnull().sum(axis=1).value counts().sort index(ascending=False)
         for c, r in null counts.items():
             print(f"\t{r} rows with: {c} null values")
        print("Percentage of rows with missing values in 0, 1 or more columns")
        null counts = workdf.isnull().sum(axis=1).value counts().sort values(ascending=False)
         for c, r in null counts.items():
            print(f"\t{r/len(workdf)*100}% rows with: {c} null values")
        Rows with missing value in 0, 1 or more columns
                9 rows with: 10 null values
                223 rows with: 9 null values
                273 rows with: 8 null values
                 384 rows with: 7 null values
                761 rows with: 6 null values
                1356 rows with: 5 null values
                3261 rows with: 4 null values
                1906 rows with: 3 null values
                2167 rows with: 2 null values
                2107 rows with: 1 null values
                1226 rows with: 0 null values
        Percentage of rows with missing values in 0, 1 or more columns
                23.849923206319023% rows with: 4 null values
                15.848753016894609% rows with: 2 null values
                15.409931982739705% rows with: 1 null values
                13.93988151832078% rows with: 3 null values
                 9.917355371900827% rows with: 5 null values
```

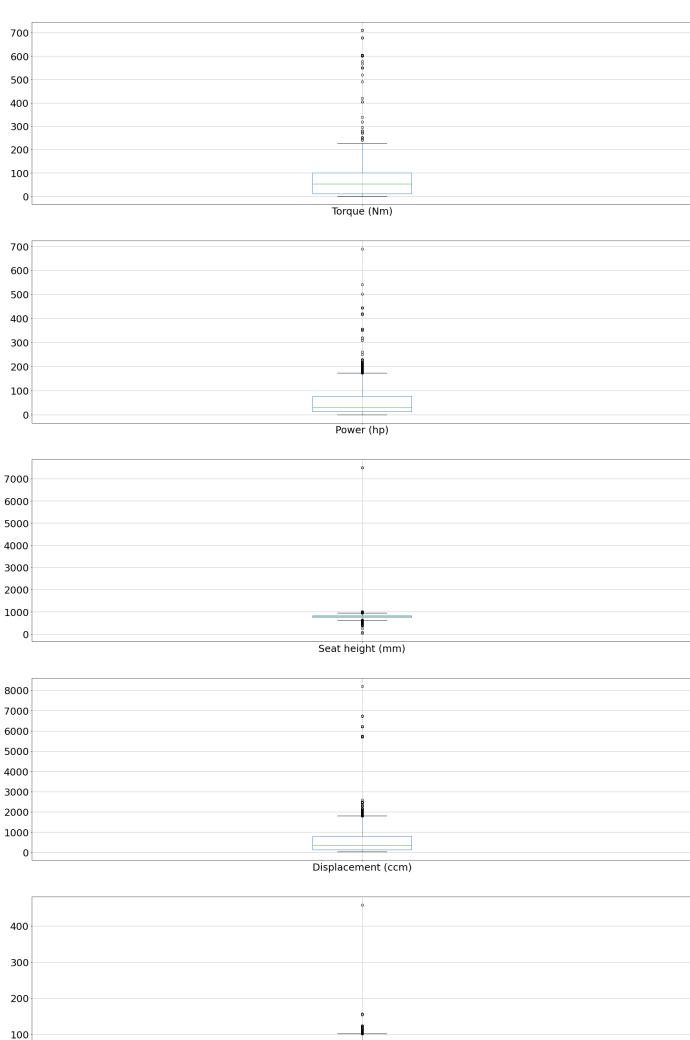
```
8.9665764645652% rows with: 0 null values
5.565713449864697% rows with: 6 null values
2.8084546185913846% rows with: 7 null values
1.9966357054048125% rows with: 8 null values
1.6309515102757257% rows with: 9 null values
0.06582315512323558% rows with: 10 null values
```

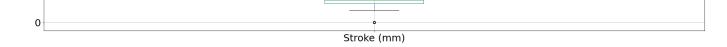
Evaluating the distribution of the features

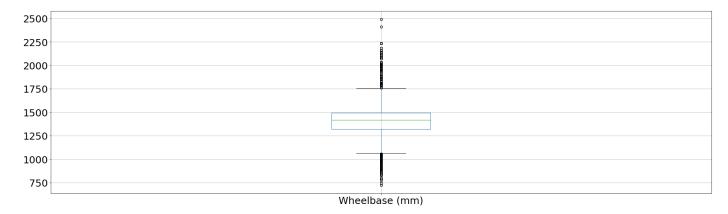
Box plot of different numerical features

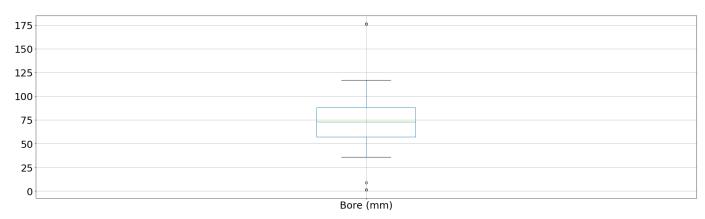


ruel capacity (its)









```
from statistics import mode
In [17]:
         for column in numerical features.columns:
            feature values = numerical features[column]
            mean = feature values.mean()
             variance = feature values.var()
             std deviation = feature values.std()
             median = feature values.median()
             mode value = mode(feature values)
             print(f"Column: {column}")
            print(f"\tMean: {mean}")
            print(f"\tVariance: {variance} (Standard deviation: {std_deviation})")
             print(f"\tMode: {mode value}")
            print(f"\tMedian: {median}")
             print()
        Column: Dry weight (kg)
                Mean: 161.24265927977854
```

Variance: 7213.2708660164 (Standard deviation: 84.93097706971467)
Mode: 110.0
Median: 140.0

Column: Fuel capacity (lts)
Mean: 13.073586113615882
Variance: 36.32543157004767 (Standard deviation: 6.027058284938654)
Mode: 17.0
Median: 13.0

Column: Torque (Nm)
Mean: 63.11679851876782

Variance: 4056.5032598498274 (Standard deviation: 63.69068424699037) Mode: 60.0

Median: 54.1

```
Column: Power (hp)
       Mean: 50.48904317639402
       Variance: 2675.684503999229 (Standard deviation: 51.72701909059934)
       Mode: 27.0
       Median: 29.4
Column: Seat height (mm)
       Mean: 791.5507835171213
       Variance: 18036.922861877483 (Standard deviation: 134.30161153864643)
       Mode: 790.0
       Median: 790.0
Column: Displacement (ccm)
       Mean: 543.4662966851658
       Variance: 289775.67639495526 (Standard deviation: 538.3081611818227)
       Mode: 125.0
       Median: 354.0
Column: Stroke (mm)
       Mean: 64.59754488112526
       Variance: 340.0976230478999 (Standard deviation: 18.441735901153663)
       Mode: 57.8
       Median: 61.2
Column: Wheelbase (mm)
       Mean: 1417.216593886463
       Variance: 29135.558279040324 (Standard deviation: 170.69141243495622)
       Mode: 1400.0
       Median: 1420.0
Column: Bore (mm)
       Mean: 72.45569141193648
       Variance: 354.5505268535157 (Standard deviation: 18.829512124681184)
       Mode: 54.0
       Median: 73.0
```

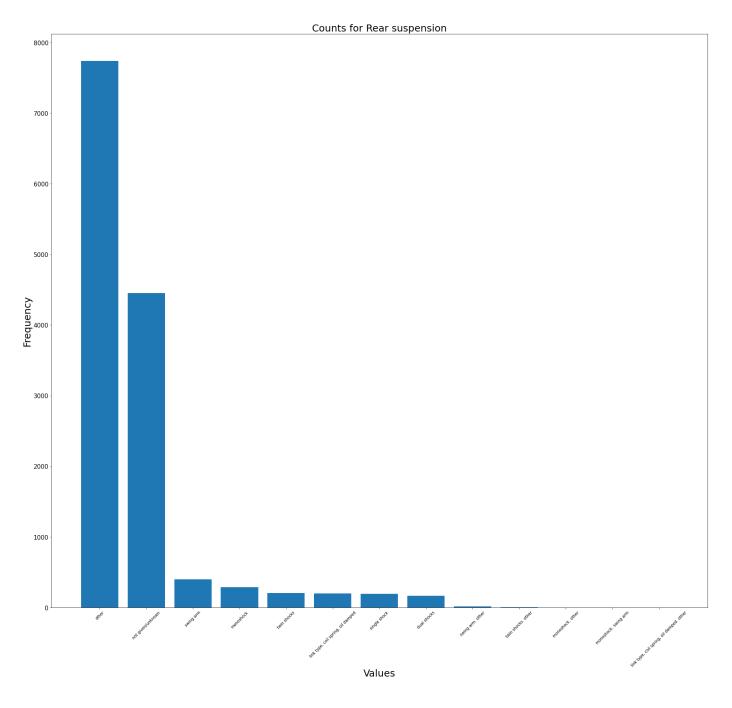
As can be observed from the sampling distribution represented by the box plots and the statistical measures reported above, many numerical features exhibit very high variances, significantly deviating from the mean. Additionally, there are a considerable number of outliers present.

This suggests that replacing missing values with measures such as the mean, median, or mode, as well as sampling from a Gaussian distribution, would lead to data distortion and not provide an accurate estimation of the missing values.

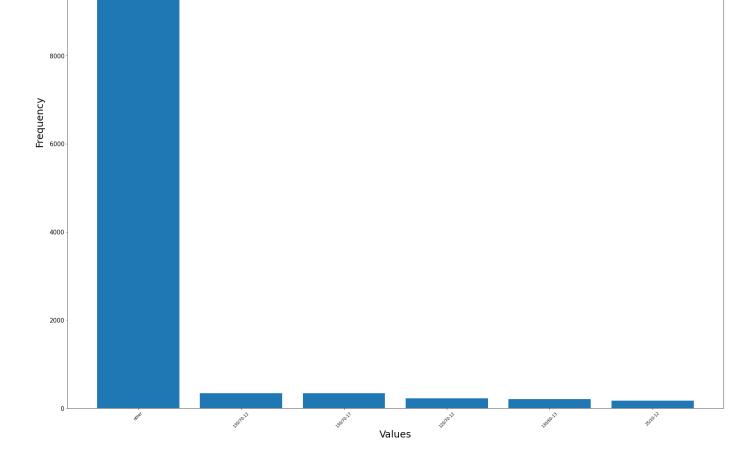
```
In [18]: | categorical features = workdf.loc[:, list(features name)].select dtypes\
         (exclude=[np.number])
         # considering only features whose values are categorical
         counts = {}
         for column in categorical features.columns: # Calculate the counts for each column
            counts[column] = categorical features[column].value counts(dropna=True)
         th = 15
         plt.figure(figsize=(30, 350))
         plt.suptitle('Frequency of values for each categorical feature ', fontsize = 40)
         plot counter = 1
         for column, count in counts.items():
             if len(count)>th:
                count top th = count.head(th)
                sum remaining = count.iloc[th:].sum()
                count top th['Remaining'] = sum remaining
                 plt.subplot(len(categorical features.columns),1,plot counter)
```

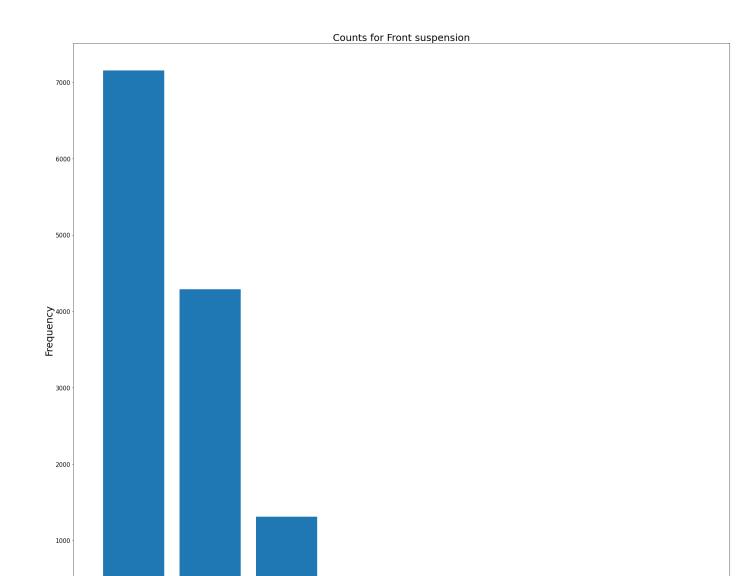
```
plot counter+=1
    plt.bar(count top th.index, count top th.values)
   plt.xlabel('Values', fontsize = 25)
   plt.xticks(rotation=45)
   plt.yticks(fontsize = 15)
   plt.ylabel('Frequency', fontsize = 25)
   plt.title(f"Counts for {column}", fontsize = 25)
else:
   plt.subplot(len(categorical features.columns),1,plot counter)
   plot counter+=1
   plt.bar(count.index, count.values)
   plt.xlabel('Values', fontsize = 25)
   plt.xticks(rotation=45)
   plt.yticks(fontsize = 15)
   plt.ylabel('Frequency', fontsize = 25)
   plt.title(f"Counts for {column}", fontsize = 25)
```

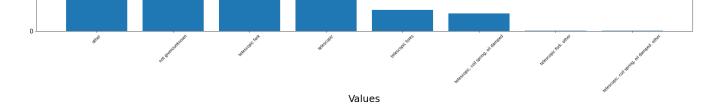
Frequency of values for each categorical feature

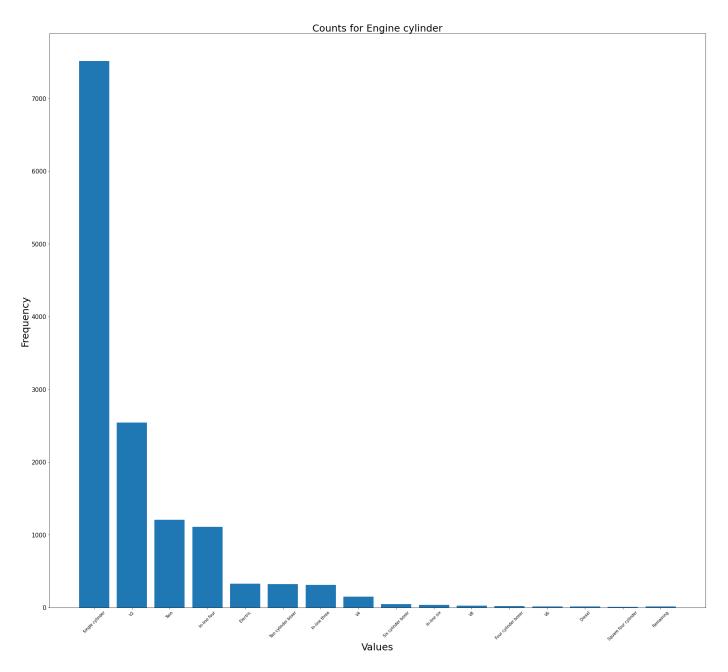


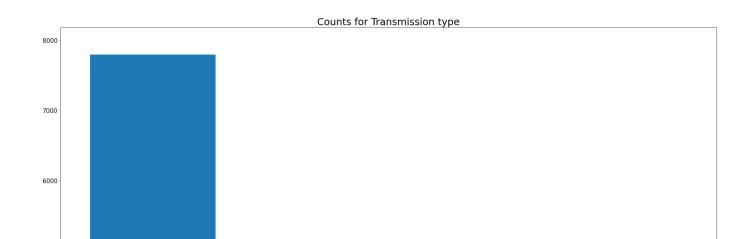


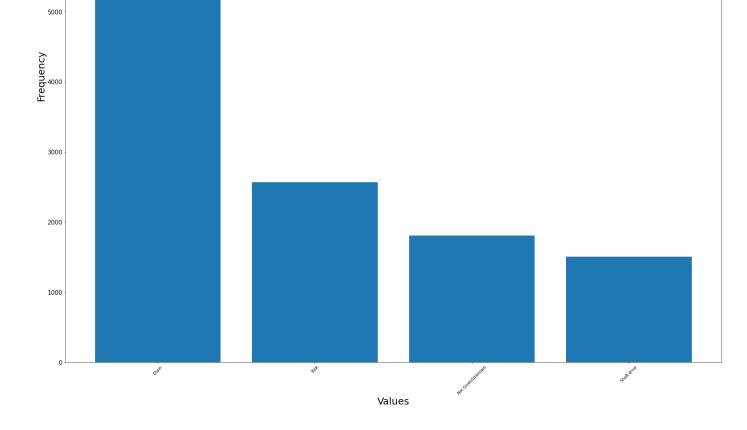


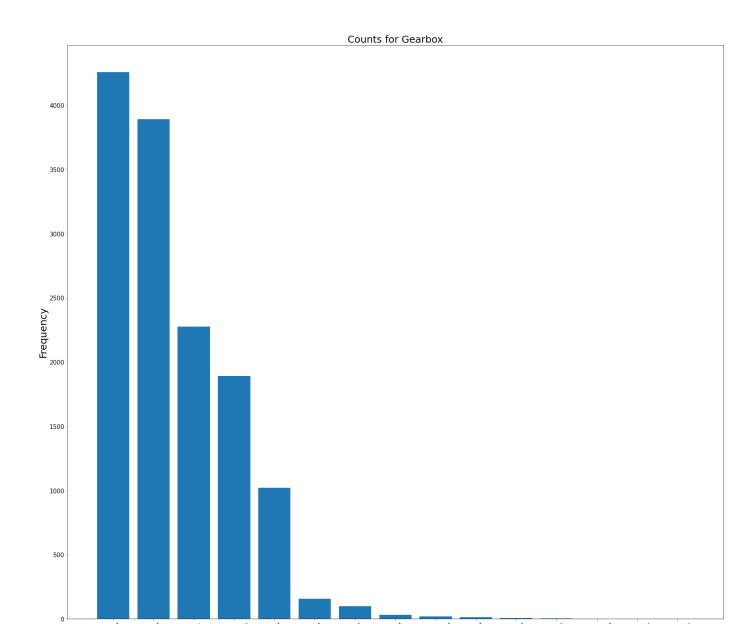




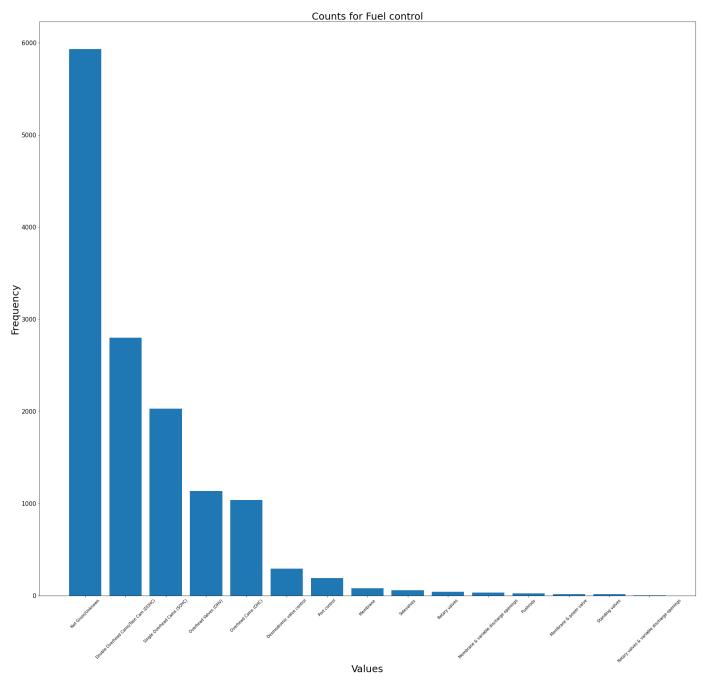


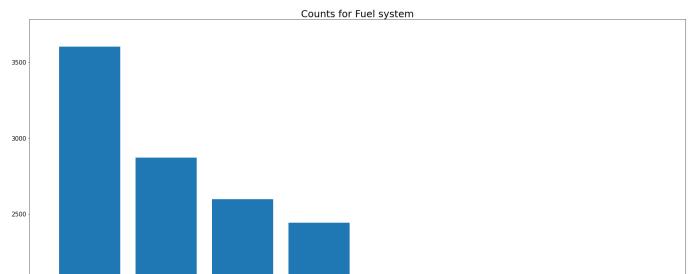


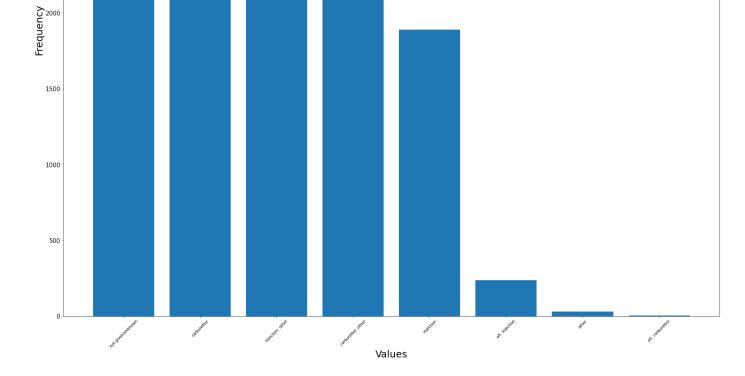


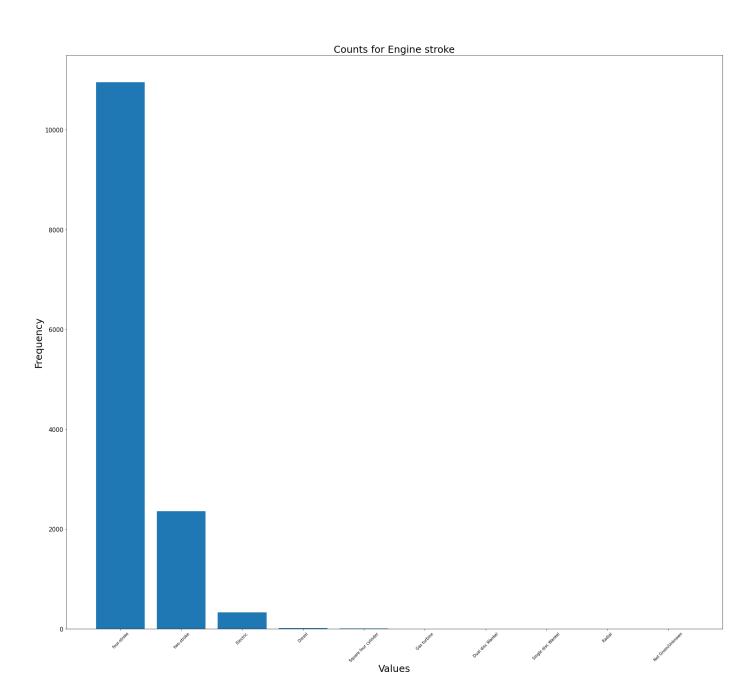


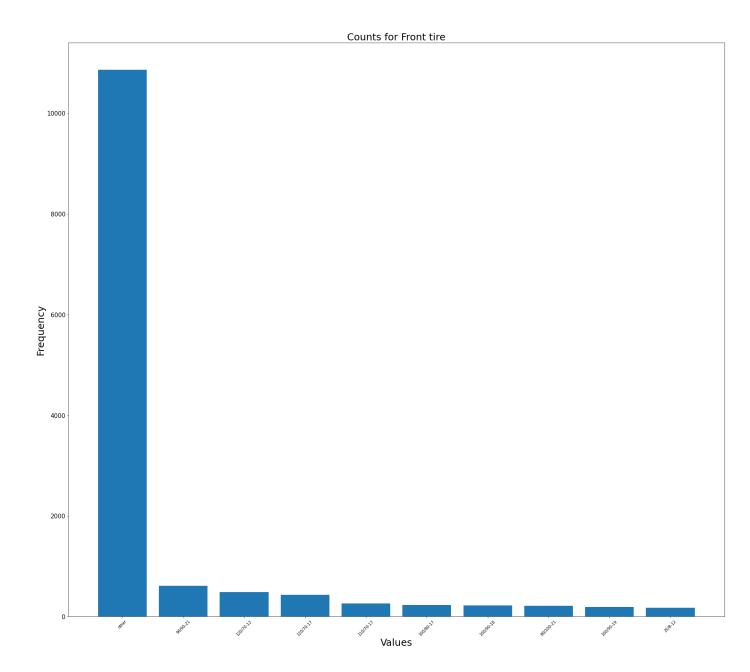


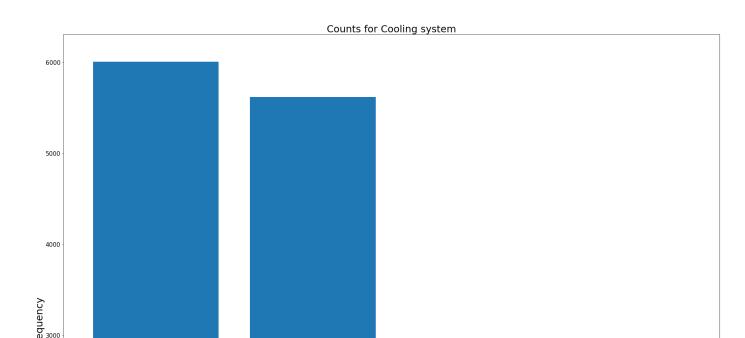


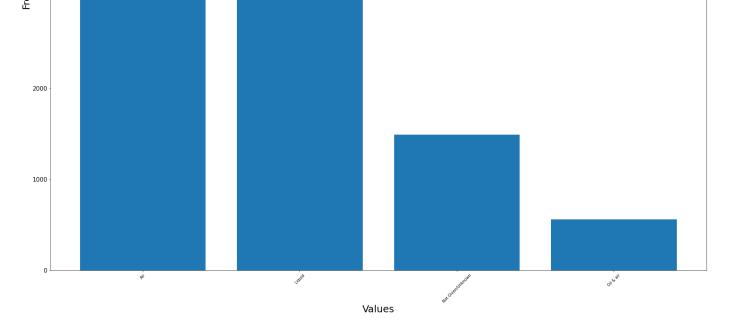












In the case of the categorical features, the frequency analysis of each unique value reveals a lack of homogeneity in the graphs. Some features exhibit a single value that is significantly more frequent than others, while others show three or four values with notably higher frequencies than the average. Additionally, several features display numerous values with similarly low frequencies.

All of this suggests the absence of a unified strategy.

Based on the information provided, the following strategy was employed to replace the missing data.

For each feature, a probability distribution was created based on the sampling distribution of the available values. The missing values were then sampled from this distribution. The more frequent a particular value was present in the data, the more likely it was to be sampled.

This approach was designed to preserve information (all available values were retained) and to account for the heterogeneity in the distribution of values within each feature.

```
def fill missing values with sampling (df, column name):
In [19]:
            column = df[column name]
             # Calculate probability distribution from available data
             available data column = column.dropna() # Remove missing values
             probability distribution = available data column.value counts(normalize=True)
             # Generate random samples from the probability distribution
             num missing values = column.isnull().sum()
             fill samples = np.random.choice(probability distribution.index,\
                                            size=num missing values,\
                                             p=probability distribution.values)
             # Replace missing values with generated samples
             column filled = column.copy()
             column filled[column filled.isnull()] = fill samples
             return column filled
         workdf filledNullValues = workdf.copy()
         for column in numerical features.columns: # fill missing values: only numerical
                                                    # features have missing values
             if numerical features[column].isnull().any():
                 workdf filledNullValues[column] = \
                 fill missing values with sampling (numerical features, column)
```

```
In [20]: # Evaluation after missing value replacement.

print("Percentage of missing values by column.")
percs = (workdf_filledNullValues.isnull().mean() * 100).sort_values(ascending=False)
for c, p in percs.items():
    print(f"\t{c}: {p:.2f}%")
```

Percentage of missing values by column.

Rating: 46.52% Model: 0.07% Brand: 0.00%

Fuel control: 0.00% Front suspension: 0.00%

Rear tire: 0.00%
Front tire: 0.00%
Fuel system: 0.00%
Seat height (mm): 0.00%
Wheelbase (mm): 0.00%
Dry weight (kg): 0.00%
Transmission type: 0.00%
Cooling system: 0.00%
Stroke (mm): 0.00%

Fuel capacity (lts): 0.00%

Bore (mm): 0.00%
Gearbox: 0.00%
Engine stroke: 0.00%
Engine cylinder: 0.00%
Torque (Nm): 0.00%
Power (hp): 0.00%

Displacement (ccm): 0.00%

Category: 0.00% Year: 0.00%

Rear suspension: 0.00%

In [21]: display(workdf_filledNullValues)

	Brand	Model	Year	Category	Rating	Displacement (ccm)	Power (hp)	Torque (Nm)	Engine cylinder	Engine stroke	•••	Cooling systen
1	acabion	gtbo 55	2007	Sport	2.6	1300.0	541.0	420.0	In-line four	four- stroke		Liquic
4	acabion	gtbo 70	2007	Prototype / concept model	3.1	1300.0	689.0	490.0	In-line four	four- stroke		Liquic
6	access	ams 3.20 supercross	2016	ATV	NaN	280.0	18.8	41.3	Single cylinder	four- stroke		Ai
7	access	ams 4.30 supermoto efi	2016	ATV	NaN	359.3	29.5	106.0	Single cylinder	four- stroke		Ai
8	access	ams 4.38 sm gear shift	2016	ATV	NaN	449.0	37.6	133.0	Single cylinder	four- stroke		Ai
•••												
38459	zündapp	roller super	1968	Scooter	NaN	49.0	95.0	100.0	Single cylinder	two- stroke		Ai
38462	zündapp	z 2 g	1923	Sport	NaN	211.0	2.8	54.0	Single cylinder	two- stroke		Ai
38466	zündapp	z 22	1923	Sport	NaN	211.0	2.3	49.0	Single cylinder	two- stroke	•••	Ai

38468	zündapp	z 249	1923	Sport	NaN	249.0	2.8	80.0	Single cylinder	two- stroke	 Ai
38471	zündapp	z 300	1929	Sport	NaN	298.0	26.0	38.5	Single cylinder	two- stroke	 Ai

13673 rows × 25 columns

Exercise 2: Encoding of categorical data

Since PCA requires fully numerical features, the categorical features in the current database need to be encoded to serve this purpose. Specifically, one-hot encoding has been chosen as the encoding method.

Each unique value related to a specific feature is encoded as 1 (indicating its presence) or 0 (indicating its absence) in the one-hot encoding process.

Particular attention is also given to the subset of columns that have multiple values separated by a delimiter (for details, refer to the code snippet below). Each individual value is extracted and placed in a specific separate column.

As a result of this process, the number of features is significantly higher compared to the original number, but any implicit order among the categories is created.

```
In [22]:
```

```
# visualize categorical features with original encoding
display(workdf_filledNullValues.loc[:, list(categorical_features_name)])
```

	Engine cylinder	Front suspension	Rear suspension	Transmission type	Gearbox	Fuel control	Rear tire	Fuel system
1	In-line four	not given/unknown	not given/unknown	Not Given/Unknown	6-speed	Not Given/Unknown	other	other
4	In-line four	not given/unknown	not given/unknown	Not Given/Unknown	6-speed	Not Given/Unknown	other	other
6	Single cylinder	not given/unknown	not given/unknown	Chain	Automatic	Overhead Valves (OHV)	other	carburettor
7	Single cylinder	not given/unknown	not given/unknown	Chain	Automatic	Overhead Cams (OHC)	other	efi. injection
8	Single cylinder	other	not given/unknown	Chain	5-speed	Overhead Cams (OHC)	other	carburettor
•••								
38459	Single cylinder	not given/unknown	not given/unknown	Not Given/Unknown	Not Given/Unknown	Not Given/Unknown	other	carburettor. other
38462	Single cylinder	other	other	Belt	2-speed	Not Given/Unknown	other	carburettor
38466	Single cylinder	other	other	Belt	Not Given/Unknown	Not Given/Unknown	other	carburettor
38468	Single cylinder	other	other	Belt	3-speed	Not Given/Unknown	other	carburettor
38471	Single cylinder	not given/unknown	not given/unknown	Chain	Not Given/Unknown	Overhead Valves (OHV)	other	carburettor

```
In [23]: Xworkdf = workdf filledNullValues.loc[:, list(features name)] # features selected
         separator = '. ' # Values containing the string '. ' have to be split, since it is used
                          # to separate a list of characteristics in a unique string
         for column in categorical features name:
            split columns df = Xworkdf[column].str.split(separator, expand=True) # a dataframe
                                                   # with one column for each split is obtained
             for col in split columns df.columns: # for each column 'col' of the
                                                  # dataframe split columns df
                pref = f"{column} {col}"
                one hot encoding df = pd.get dummies(split columns df[col], prefix=pref)
                                                 # a dataframe whose categorical values are
                                                 # encoded with 'one hot encoding' is created
                Xworkdf = pd.concat([Xworkdf, one hot encoding df], axis=1) # append
                                                    # the new dataframe to Xworkdf
            Xworkdf = Xworkdf.drop(column, axis=1) # delete original column since it
                                                     # is redudant in the new dataframe
         Xfeatures name = set(Xworkdf.columns)
         Xcategorical features name = set(Xworkdf.columns) - numerical features name
```

In [24]: # visualize categorical features with one hot encoding
display(Xworkdf.loc[:, list(Xcategorical_features_name)])

	Front tire_0_25/8- 12	Front tire_0_110/70- 17	Rear tire_0_130/60- 13	Fuel control_4_discharg	Fuel control_2_	Rear tire_0_120/70- 12	Front tire_0_90/90- 21	G
1	0	0	0	0	0	0	0	
4	0	0	0	0	0	0	0	
6	0	0	0	0	0	0	0	
7	0	0	0	0	0	0	0	
8	0	0	0	0	0	0	0	
•••								
38459	0	0	0	0	0	0	0	
38462	0	0	0	0	0	0	0	
38466	0	0	0	0	0	0	0	
38468	0	0	0	0	0	0	0	
38471	0	0	0	0	0	0	0	

13673 rows × 176 columns

Exercise 3: Preprocessing and PCA

Before applying PCA, it is necessary to apply data preprocessing techniques.

The following tecniques have been considered.

- StandardScaler: it standardizes features by removing the mean and scaling to unit variance
- MinMaxScaler; it scales and translates each feature to a specific range, such as between zero and one, based on the training set.

Yworkdf Yworkdf std Yworkdf mm

Variance of multiple dataframes.

		Xworkat	xworkat_sta	xworkat_mm
feature type	feature name			
numerical features	Dry weight (kg)	7069.491917	1.000073	0.007288
	Fuel capacity (lts)	35.850689	1.000073	0.014631
	Torque (Nm)	4135.065512	1.000073	0.008238
	Power (hp)	2678.183682	1.000073	0.005647
	Seat height (mm)	17548.138589	1.000073	0.000315
categorical features	Cooling system_0_No	0.097048	1.000073	0.097048
	Cooling system_0_Oi	0.039215	1.000073	0.039215
	Cooling system_1_	0.039215	1.000073	0.039215
	Cooling system_1_Given/Unknown	0.097048	1.000073	0.097048
	Cooling system_2_air	0.039215	1.000073	0.039215

185 rows × 3 columns

Variances of features in original dataset and variances of the scaled datasets have been compared.

Variance measures the spread of values in a set of values around the mean.

It is very important to apply data scaling techniques as PCA tecnique is based on the following concept: higher variance indicates a more informative feature.

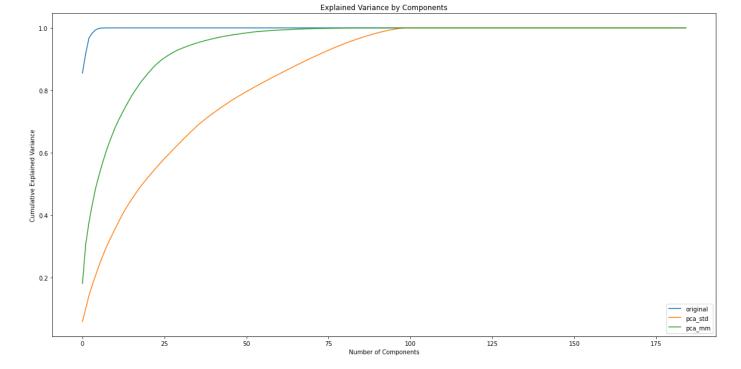
The analysis of variances for individual features reveals a significant change before and after both scaling processes. This change is particularly pronounced in the case of categorical features.

PCA application

Principal Component Analysis (PCA) is applied to three different versions of the preprocessed dataset: original, scaled via StandardScaler and scaled via MinMaxScaler. In this phase, we apply Principal Component Analysis on the preprocessed dataset:

- original dataset
- dataset whose features are scaled via StandardScaler
 - dataset whose features are scaled via MinMaxScaler

```
pca instances = {
In [27]:
            'original': PCA(),
            'pca std': PCA(),
             'pca mm': PCA()
         dataFrames = {
             'original': Xworkdf,
             'pca std': Xworkdf std,
             'pca mm': Xworkdf mm
         for k in pca instances.keys():
             pca_instances[k].fit(dataFrames[k])
         # Plotting cumulative explained variance
         plt.figure(figsize=(20, 10))
         for k in pca instances.keys():
            plt.plot(np.cumsum(pca instances[k].explained variance ratio ), label=k)
         plt.xlabel('Number of Components')
         plt.ylabel('Cumulative Explained Variance')
         plt.title('Explained Variance by Components')
        plt.legend()
         plt.show()
```



The **cumulative explained variance** for each dataset is plotted and then evaluated. It shows the proportion of the total variance encapsulated within the first N components.

If a given percentage α of the variance is contained within the first N components, it implies that it is possible to reduce available data to N dimensions whilst retaining α of its variance.

As can be seen from the plot, the original dataset requires a significant lower number of principal components to retain an given percentage of variance of data. This is happens since PCA is sensitive to the variances of the feature scales. The fact the original dataset is not scaled reflects in features with high variances dominating the principal components therefore leading to a less balanced representation of the original features.

Exercise 4: Dimensionality Reduction and Interpretation of the PCs

PCA is used to make the dataset less dimensional while still attempting to retain the majority of the original variance (or an acceptable percentage).

The minimum number of principal components required to explain at least 35% of the total variance for the scaled dataset described above is computed.

```
explained, expressed as a percentage.
Returns:
- int: The minimum number of principal components required to explain
       the specified threshold proportion of the total variance.
      Returns -1 if an error occurs.
Example usage:
>>> explained variances = [0.3, 0.2, 0.15, 0.1, 0.1, 0.05, 0.04, 0.03, 0.02, 0.01]
>>> threshold = 80
>>> min components = min PCs(explained variances, threshold)
>>> print(min components)
.....
threshold /= 100 # Convert threshold from percentage to ratio
cumulative explained variance ratio = 0
for i, val in enumerate (explained variance ratio):
    cumulative explained variance ratio += val # Calculate cumulative explained
                                                # variance ratio up to i
    if cumulative explained variance ratio >= threshold: # Check if cumulative
        # explained variance ratio is greater than or equal to the threshold
        return i + 1  # Return the number of components needed to explain the
                      # threshold proportion of the total variance
return -1 # Return -1 if an error occurs
```

```
In [30]: max_comp = 5
min_number_components = {}
for k in keys_to_be_considered:
    min_number_components[k] = min_PCs(pca_instances[k].explained_variance_ratio_, 35)
    # Number of components needed to explain at least 35% of the total variance.

m = {}
for k in keys_to_be_considered:
    m[k] = min(min_number_components[k], max_comp) # limit the number of components
    # to a maximum fixed value

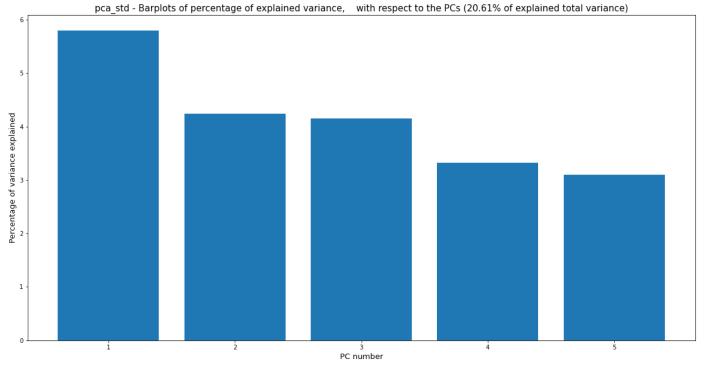
for k in keys_to_be_considered:
    print(f"{k}.")
    print(f"{k}.")
    print(f"\tm = {m[k]} (min between {max_comp} and\
    {min_number_components[k]}, number of components needed\
    to explain at least 35% of the total variance.)")
```

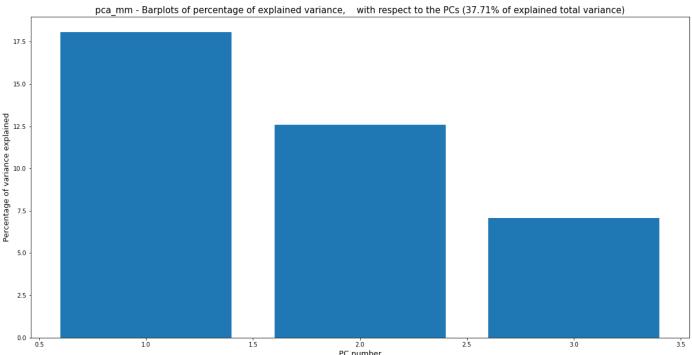
- Standardized data: 11 components are needed to explain at least 35% of the total variance, but only the first 5 are selected.
- Min/Max scaled data: 3 Components are needed to explain at least 35% of the total variance

The fact that fewer components are required to explain the same percentage of the overall variance implies that the MinMax scaled data is less difficult or simpler to deal with than the standardized data.

The barplots of percentage of explained variance, with respect to the PCs considered above have been plot.

```
In [31]: for k in keys_to_be_considered:
```





The top features that contribute the most to each of the first few main components for the two datasets are listed in the excerpt that follows. The features are sorted according to the absolute values of the weights they get in the PCs, with the top features receiving the greatest weights. This ranking gives information

about the original factors that are responsible for the separation in the data that is shown in the PCs: components that carry the heaviest weights are thought to affect the PC the most.

```
In [32]: top_features_number = 5 # number of features with the highest absolute weight in a PC
         for k in keys_to_be_considered: # for each dataframe
             top features df = pd.DataFrame()
             i = 0 # 1st PC
            while i < (m[k]): # for each PC among the first m Pcs</pre>
                 p = pca instances[k].components [i] # weights in the PC
                 feat names = dataFrames[k].columns # corresponding feature (i.e., name)
                 top features = sorted([(w, n) for w, n in zip(p, feat names)], \
                                       key=lambda tup: -abs(tup[0]))[:top features number]
                                         # top features with the highest absolute weights
                 # store information in a DataFrame for visualization purposes
                 for count, f in enumerate(top features):
                    level1 = [f"PC{i+1}"]
                    level2 = [count+1]
                    multi index = pd.MultiIndex.from arrays([level1, level2], \
                                                             names=['PC', 'rank'])
                     top features df = pd.concat([top features df, \
                                                  pd.DataFrame({"Name": [f[1]], \
                                                                 "Weight": [f[0]]}, multi index)])
                 i+=1 # next PC
             extern level columns = pd.MultiIndex.from tuples([('Feature', 'Name'),\
                                                                ('Feature', 'Weight')])
             top features df.columns = extern level columns
             print("Number of features with the highest absolute weight in a PC" + " - " + k)
             display(top features df)
```

Number of features with the highest absolute weight in a PC - pca std

Name

Fe	at	:u	re

Weight

			3
PC	rank		
PC1	1	Fuel control_1_Overhea	0.207733
	2	Fuel control_3_Ca	0.205900
	3	Fuel control_4_(DOHC)	0.205900
	4	Fuel control_0_Doubl	0.205900
	5	Fuel control_2_Cams/Twi	0.205900
PC2	1	Rear suspension_0_no	0.268512
	2	Rear suspension_1_given/unknown	0.268512
	3	Front suspension_1_given/unknown	0.267222
	4	Front suspension_0_no	0.267222
	5	Rear suspension_0_other	-0.220356
PC3	1	Rear suspension_1_type	0.277248
	2	Rear suspension_2_coi	0.277248
	3	Rear suspension_3_spring	0.277248
	4	Rear suspension_4_oi	0.277248

	5	Rear suspension_5_damped	0.277248
PC4	1	Engine stroke_0_Squar	0.377061
	2	Engine stroke_1_fou	0.377061
	3	Engine stroke_2_cylinder	0.377061
	4	Engine cylinder_2_cylinder	0.377061
	5	Engine cylinder_0_Squar	0.377061
PC5	1	Engine cylinder_2_Wankel	0.394210
	2	Engine stroke_1_dis	0.394210
	3	Engine stroke_2_Wankel	0.394210
	4	Engine cylinder_1_dis	0.394210
	5	Engine stroke_0_Dua	0.346415

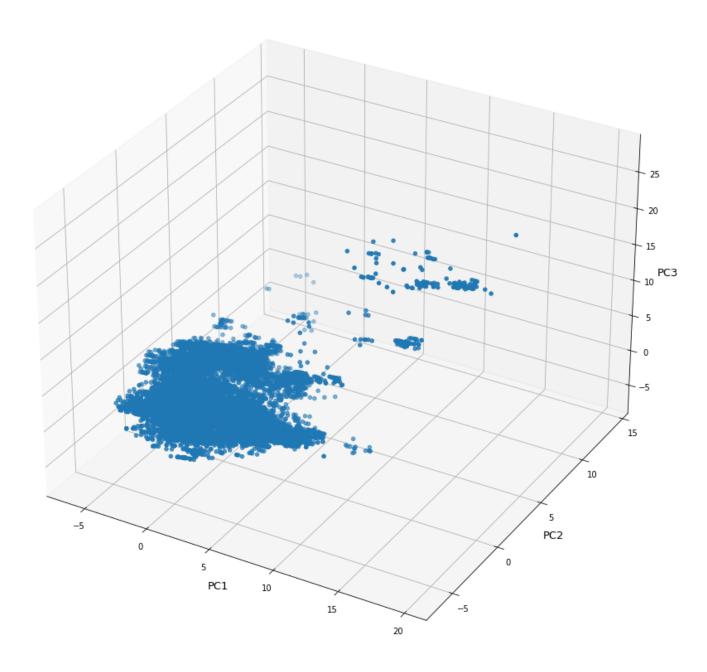
Number of features with the highest absolute weight in a PC - pca_mm

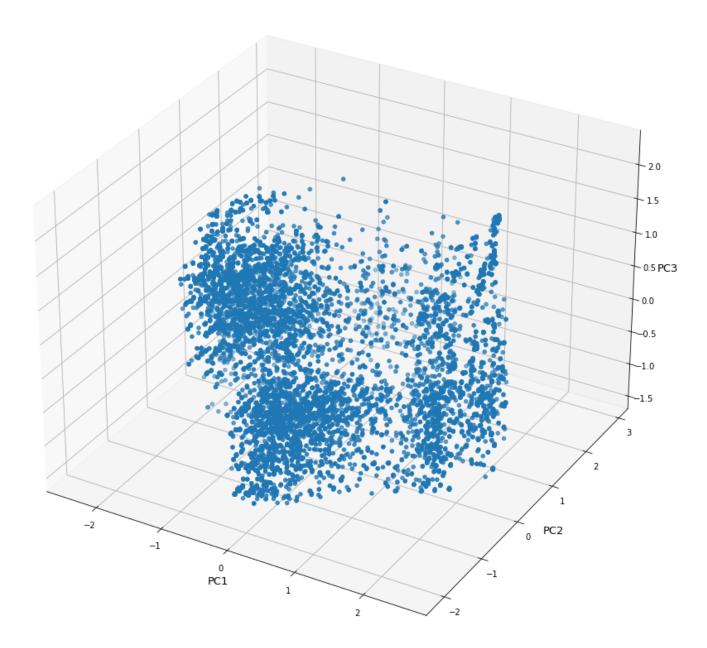
			Feature
		Name	Weight
PC	rank		
PC1	1	Rear suspension_0_no	0.270294
	2	Rear suspension_1_given/unknown	0.270294
	3	Front suspension_0_no	0.264314
	4	Front suspension_1_given/unknown	0.264314
	5	Rear suspension_0_other	-0.257855
PC2	1	Engine cylinder_1_cylinder	-0.294279
	2	Engine cylinder_0_Singl	-0.294196
	3	Fuel system_0_carburettor	-0.246047
	4	Front suspension_1_given/unknown	0.215935
	5	Front suspension_0_no	0.215935
PC3	1	Fuel control_0_No	-0.316091
	2	Fuel control_1_Given/Unknown	-0.316091
	3	Fuel control_2_Cam	0.258153
	4	Fuel control_3_(SOHC)	0.258153
	5	Fuel control_0_Singl	0.258153

The PCA scores, which reflect data projected onto the PCs (i.e., on m PCs as computed above), are then computed for the dataset. These results are used to create a scatter plot in 2D or 3D with point marked according to the original dataset's classifications. This visualization makes it easier to comprehend how the data are distributed in the space with fewer dimensions.

```
# score graph with respect to the first 1 PCs
if m[k] == 2:
   1 = 2
   plt.figure(figsize=(20, 18))
   plt.scatter(scores[:, 0], scores[:, 1])
   plt.xlabel("PC1", fontsize=13) # PC1 on axis x
   plt.ylabel("PC2", fontsize=13) # PC2 on axis y
   plt.title(f'{k} - Score graph with respect to the first {1} PCs', fontsize=15)
else:
   1 = 3
   fig = plt.figure(figsize=(20, 15))
   ax = fig.add subplot(111, projection='3d')
   ax.scatter(scores[:, 0], scores[:, 1], scores[:, 2])
   ax.set xlabel("PC1", fontsize=13) # PC1 on axis x
   ax.set_ylabel("PC2", fontsize=13) # PC2 on axis y
   ax.set zlabel("PC3", fontsize=13) # PC3 on axis z
   plt.title(f'{k} - Score graph with respect to the first {1} PCs', fontsize=15)
```

pca_std - Score graph with respect to the first 3 PCs

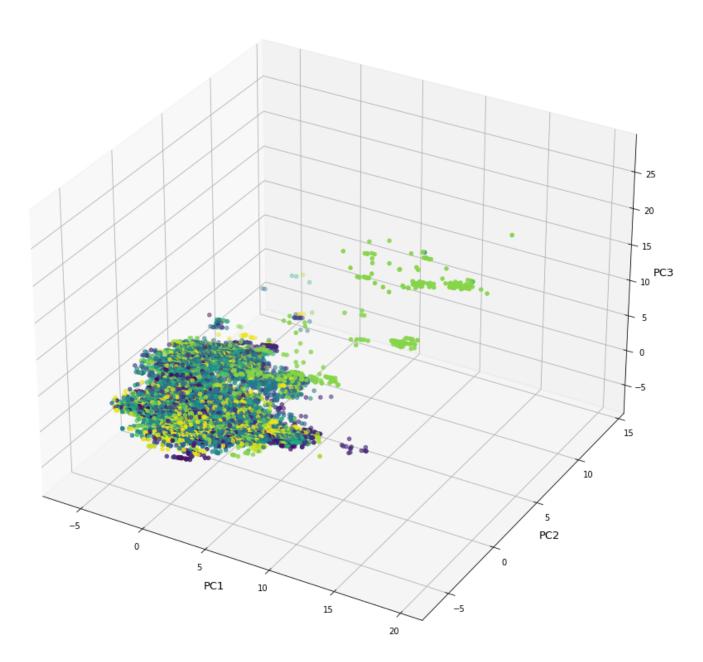


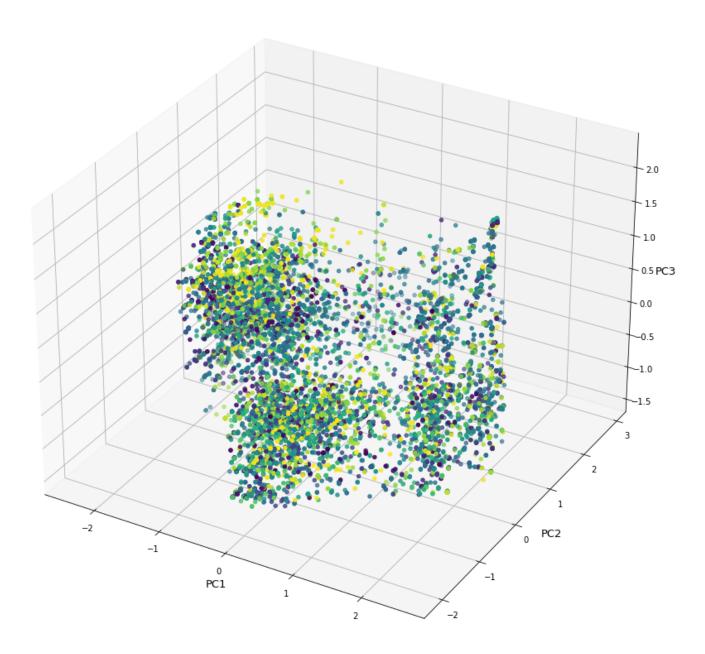


```
In [34]: label = pd.factorize(workdf['Brand'])[0] # encode 'Brand' column with numbers to color
                                                   # points according to brand
         for k in keys to be considered:
             df transformed = pca instances[k].transform(dataFrames[k]) # apply PCA
                                                                         # transformation
             scores = df transformed[:, :m[k]] # compute scores for the first m PCs
             # score graph with respect to the first 1 PCs - points coloured according to
             # their brand
             if m[k] == 2:
                1 = 2
                plt.figure(figsize=(20, 18))
                 plt.scatter(scores[:, 0], scores[:, 1], c = label)
                plt.xlabel("PC1", fontsize=13) # PC1 on axis x
                plt.ylabel("PC2", fontsize=13) # PC2 on axis y
                 plt.title(f'\{k\} - Score graph with respect to the first {1} PCs\
                 - points coloured according to their brand', fontsize=15)
             else:
                 1 = 3
```

```
fig = plt.figure(figsize=(20, 15))
ax = fig.add_subplot(111, projection='3d')
ax.scatter(scores[:, 0], scores[:, 1], scores[:, 2], c = label)
ax.set_xlabel("PC1", fontsize=13) # PC1 on axis x
ax.set_ylabel("PC2", fontsize=13) # PC2 on axis y
ax.set_zlabel("PC3", fontsize=13) # PC3 on axis z
plt.title(f'{k} - Score graph with respect to the first {1} PCs\
- points coloured according to their brand', fontsize=15)
```

pca_std - Score graph with respect to the first 3 PCs - points coloured according to their brand

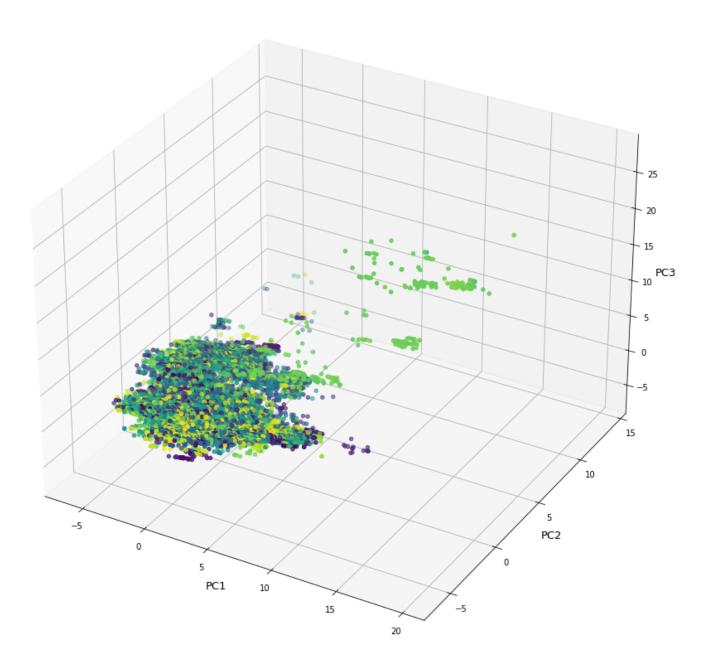


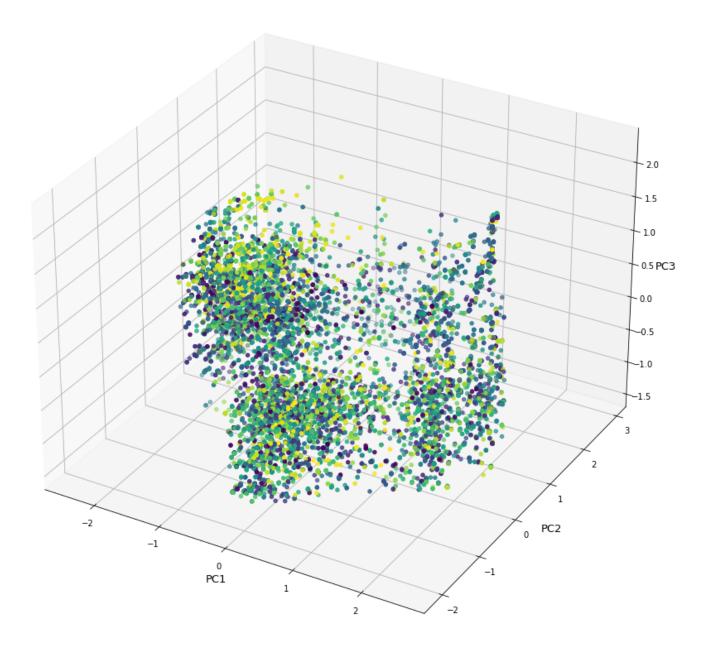


```
In [35]: label = pd.factorize(workdf['Model'])[0] # encode 'Model' column with numbers to color
                                                   # points according to model
         for k in keys to be considered:
             df_transformed = pca_instances[k].transform(dataFrames[k]) # apply PCA
                                                                         # transformation
             scores = df transformed[:, :m[k]] # compute scores for the first m PCs
             # score graph with respect to the first 1 PCs - points coloured according to their
             # model
            if m[k] == 2:
                1 = 2
                plt.figure(figsize=(20, 18))
                plt.scatter(scores[:, 0], scores[:, 1], c = label)
                plt.xlabel("PC1", fontsize=13) # PC1 on axis x
                plt.ylabel("PC2", fontsize=13) # PC2 on axis y
                plt.title(f'\{k\} - Score graph with respect to the first {1} PCs -\
                points coloured according to their model', fontsize=15)
             else:
                1 = 3
```

```
fig = plt.figure(figsize=(20, 15))
ax = fig.add_subplot(111, projection='3d')
ax.scatter(scores[:, 0], scores[:, 1], scores[:, 2], c = label)
ax.set_xlabel("PC1", fontsize=13) # PC1 on axis x
ax.set_ylabel("PC2", fontsize=13) # PC2 on axis y
ax.set_zlabel("PC3", fontsize=13) # PC3 on axis z
plt.title(f'{k} - Score graph with respect to the first {1} PCs\
- points coloured according to their model', fontsize=15)
```

pca_std - Score graph with respect to the first 3 PCs - points coloured according to their model





The purpose of the graphs plotted above is to show the points in the space defined by the PCs considered.

The points are also marked according to their 'Brand' or 'Model'. This is done to search for patterns of categories in the PCs space.

```
In [36]: for k in keys_to_be_considered:
    if m[k] == 2:
        l = 2
    else:
        l = 3

    explained_variance_ratio = pca_instances[k].explained_variance_ratio_[:1]
    print(f"{k} - Explained variance ratio of the first l = {l}",\
        explained_variance_ratio)
    explained_variance_ratio_mean_cum = np.cumsum(explained_variance_ratio)\
    .mean()
    print(f"{k} - Mean_cumulative_explained_variance",\
        explained_variance_ratio_mean_cum)
```

 $pca_std - Explained variance ratio of the first 1 = 3 [0.05796135 0.0424229 0.04156129]$

```
pca_std - Mean cumulative explained variance 0.10009704469842351 pca_mm - Explained variance ratio of the first l = 3 [0.18062356 0.1257731 0.07067388] pca_mm - Mean cumulative explained variance 0.2880302452020029
```

The percentage of overall variation that each PC accounts for is shown by the explained variance ratio for the first 3 PCs. The representation related to the Min/Max scaled dataset is much more effective.

Exercise 5: k-Means

The k-Means clustering algorithm is run with the aim to find out interesting clusters within the data.

The algorithm is run on the PCs space.

```
In [37]: # Version 1. Full PC Space
In [38]: kmeans = {}
         silhouette scores = {}
         k best = {}
         for key in keys to be considered:
             df_transformed = pca_instances[key].transform(dataFrames[key]) # apply PCA
                                                                             # transformation
             df transformed = pd.DataFrame(df transformed, \
                                           columns=[f'PC{i+1}' for i in\
                                                    np.arange(df transformed.shape[1])])\
                                                                      # corresponding dataFrame
             k values = np.arange(3, 11) # values for k to be considered in the k-MEANS
                                         # algorithm
             silhouette scores[key] = []
             for k in k values:
                 kmeans[key] = KMeans(n clusters=k, random state=rs, n init=10).\
                 fit(df transformed) # Fit the k-Means model
                 silhouette scores[key].append(silhouette score(df transformed,\
                                                               kmeans[key].labels ))
                                     # silhouette score computation
             k best[key] = k values[np.argmax(silhouette scores[key])] # optimal number
                             # of clusters such that it maximises the silhouette score
             print(f''\{key\} - k opt = \{k best[key]\}'')
             # Run the algorithm with the optimal number of clusters
             kmeans[key] = KMeans(n_clusters=k_best[key], random state=rs, n init=10)
             kmeans[key].fit(df transformed)
        pca std - k opt = 10
        pca mm - k opt = 7
In [39]: # Version 2. PC Space of dimension m as in ex 4.
In [40]: kmeans = {}
         silhouette scores = {}
         k best = {}
         for key in keys to be considered:
            df transformed = pca instances[key].transform(dataFrames[key])[:, :m[key]]
                                                                 # apply PCA transformation
             df transformed = pd.DataFrame(df transformed, columns=[f'PC{i+1}' for i in\
                                                                    np.arange(m[key])])
                                                                  # corresponding dataFrame
             k values = np.arange(3, 11) # values for k to be considered in the k-MEANS
                                         # algorithm
```

```
pca_std - k opt = 6
pca_mm - k opt = 6
```

Silhouette coefficient is used to evaluate the optimal number of cluster numbers (i.e., the number of clusters maximing such measure is considered).

The silhouette score is a metric used to evaluate the quality of clusters in clustering analysis. It measures how well each sample in a cluster is assigned to its own cluster compared to other clusters. The silhouette score can range from -1 to 1, with higher values indicating better cluster assignments (i.e., a score close to 1 indicates that the sample is well-matched to its own cluster and poorly matched to neighboring clusters.)

Exercise 6: Clusters and Centroid Interpretation and Visualization

The k-Means algorithm with the optimal number of clusters is run.

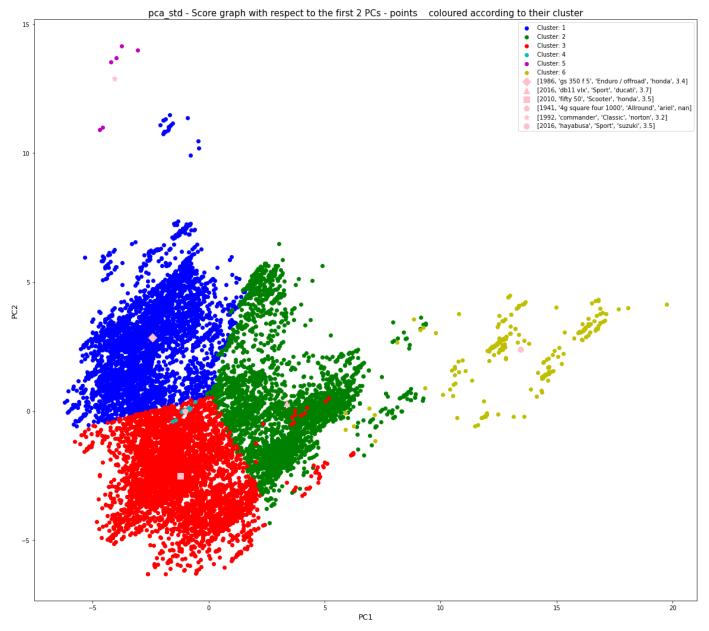
```
In [41]: primary_colors = ['b', 'g', 'r', 'c', 'm', 'y', 'k', 'w']
         additional colors = ['orange', 'purple', 'brown', 'pink']
         color dictionary = {
            0: primary colors[0],
            1: primary colors[1],
            2: primary colors[2],
            3: primary colors[3],
            4: primary colors[4],
            5: primary colors[5],
            6: primary colors[6],
            7: primary colors[7],
            8: additional colors[0],
            9: additional colors[1],
            10: additional colors[2],
            11: additional colors[3]
         marker dictionary = {
            0: 'D', # Rombo
            1: '^',  # Triangolo
            2: 's',  # Quadrato
            3: 'p', # Pentagono
            4: '*', # Stella
            5: 'h', # Esagono
            6: 'H', # Esagono con spigoli più pronunciati
             7: '+', # Più
             8: 'x', # Croce
```

```
11: ',', # Pixel
In [42]: def name the centroid(centroid, points, labels):
             Assigns a name to the centroid based on the surrounding points and their labels.
            Arguments:
             - centroid: array, the coordinates of the centroid
             - points: array, the surrounding points represented as an ND array
             - labels: list of arrays, the labels corresponding to the surrounding points
            Returns:
             - selected labels: list, the selected labels for the centroid
            Description:
             - Each point contributes to the voting process in an inversely proportional manner
                 to its distance from the centroid.
             - Note: If a point has a distance of zero, it contributes 10 times the maximum
                 contribution to avoid infinite weight.
             11 11 11
             selected labels = []
             distances = np.linalg.norm(points - centroid, axis=1) # Calculating Euclidean
                                                   # distances between points and centroid
            weights = np.array([1/n if n!=0 else -1 for n in distances])
             weights = np.where(weights != -1, weights, np.max(weights) * 10)
             for l in labels: # for each label feature
                 # 1: array with label of each point
                 votes = {}
                unique val = set(1)
                 for u in unique val:
                     indexes = [index for index, element in enumerate(1) if element == u]
                     votes[u] = np.sum(weights[indexes])
                 selected label = max(votes, key=lambda k: votes[k])
                 selected labels.append(selected label)
             return selected labels
In [43]: for key in keys to be considered:
             df transformed = pca instances[key].transform(dataFrames[key]) # apply PCA
                                                                        # transformation
             clusters = np.arange(0,k best[key])
             # score graphs with respect to the first 1 PCs, with points coloured according
             #to their cluster
            1 = 2
            plt.figure(figsize=(20, 18))
             for cluster in clusters:
                 plt.scatter(df transformed[kmeans[key].labels == cluster, 0],\
                             df transformed[kmeans[key].labels == cluster, 1],\
                             c = color dictionary[cluster], \
                             label=f"Cluster: {cluster+1}")
            plt.xlabel("PC1", fontsize=13) # PC1 on axis x
            plt.ylabel("PC2", fontsize=13) # PC2 on axis y
            plt.title(f'{key} - Score graph with respect to the first {1} PCs - points\
```

coloured according to their cluster', fontsize=15)

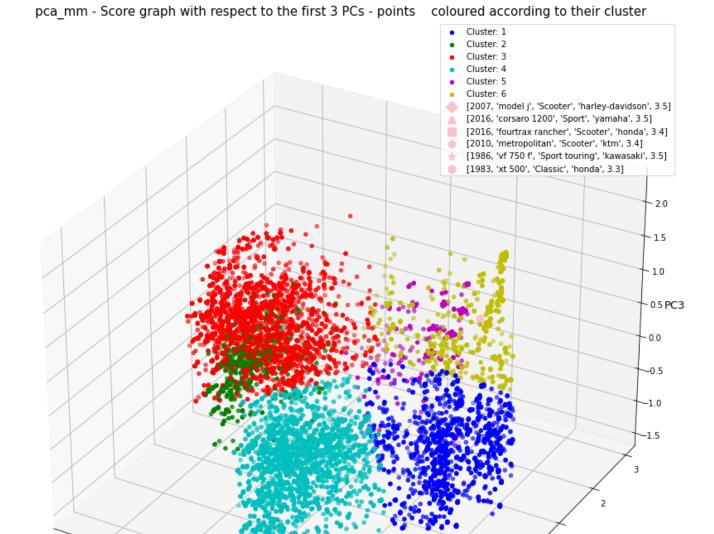
9: 'o', # Cerchio 10: '.', # Punto

```
for cluster in clusters:
    # Assign a name to the centroid based on the labels of the points
    # belonging to the cluster.
    mask = kmeans[key].labels == cluster
    indices = np.where(mask)[0]
    corresponding labels = workdf.iloc[indices]
    labels = []
    for label in labels name:
        labels.append(corresponding labels[label].tolist())
    assigned labels = name the centroid(kmeans[key].\
                                        cluster centers [cluster, :1],\
                                        df transformed[kmeans[key] \
                                                       .labels == cluster, :1],\
                                        labels)
    name = list(assigned labels)
    #plt.text(kmeans[key].cluster centers [cluster, 0], \
    #kmeans[key].cluster centers [cluster, 1], " "+str(name),\
    #ha='left', path effects=[pe.withStroke(linewidth=5, foreground='white')])
    plt.scatter(kmeans[key].cluster centers [cluster, 0], \
                kmeans[key].cluster centers [cluster, 1], \
                s=100, c = color dictionary[len(color dictionary)-1], \
                marker=marker dictionary[cluster], label = name)
                                                             # centroid plotted
plt.legend()
fig = plt.figure(figsize=(20, 15))
ax = fig.add subplot(111, projection='3d')
for cluster in clusters:
    ax.scatter(df transformed[kmeans[key].labels == cluster, 0],\
               df transformed[kmeans[key].labels == cluster, 1],\
               df transformed[kmeans[key].labels == cluster, 2],\
               c = color dictionary[cluster], \
               label=f"Cluster: {cluster+1}")
ax.set xlabel("PC1", fontsize=13) # PC1 on axis x
ax.set ylabel("PC2", fontsize=13) # PC2 on axis y
ax.set_zlabel("PC3", fontsize=13) # PC3 on axis z
plt.title(f'{key} - Score graph with respect to the first {1} PCs - points\
coloured according to their cluster', fontsize=15)
for cluster in clusters:
    # Assign a name to the centroid based on the labels of the points
    # belonging to the cluster.
    mask = kmeans[key].labels == cluster
    indices = np.where(mask)[0]
   corresponding labels = workdf.iloc[indices]
    labels = []
    for label in labels name:
        labels.append(corresponding labels[label].tolist())
    assigned labels = name the centroid(kmeans[key].\
                                        cluster centers [cluster, :1],\
                                        df transformed[kmeans[key].\
                                                       labels_ == cluster, :1],\
                                        labels)
    name = list(assigned labels)
    #ax.text(kmeans[key].cluster centers [cluster, 0], \
    #kmeans[key].cluster centers [cluster, 1], kmeans[key].cluster centers\
    # [cluster, 2], " "+str(name), ha='left', path_effects=[pe.withStroke\
    #(linewidth=5, foreground='white')])
    ax.scatter(kmeans[key].cluster centers [cluster, 0], \
```



15

20



The clusters are plotted in a 2D scatter plot and in a 3D one. Points belonging to the same cluster are drawn in the same color. The centroids of the clusters are also shown. They can be interpreted as the 'average' object in each cluster.

2

PC2

-2

-1

PC1

To each centroid a name that describes the average motorcycle in the cluster represented by it has been given. To choose such name, the following criterion has been considered. The name to the centroid is assigned based on the surrounding points and their labels. In particular, all labels of all points of the cluster whose centroid has to be named have been taken into account. The name of the centroid is chosen as a list of features: each point contributes to the assignment of a specific label in an inversely proportional manner to its distance from the centroid. The closer a point is to the centroid, the higher its contribution is. (Note that if a point has a distance of zero, it contributes 10 times the maximum contribution to avoid infinite weight.)

Exercise 7: Clusters and Centroids Evaluation

(optional)

Internal and external evaluation of the clusters obtained from the k-Means algorithm applied to the principal components of the 2 datasets.

Internal evaluation

The internal evaluation is done in terms of the silhouette score of the clusters.

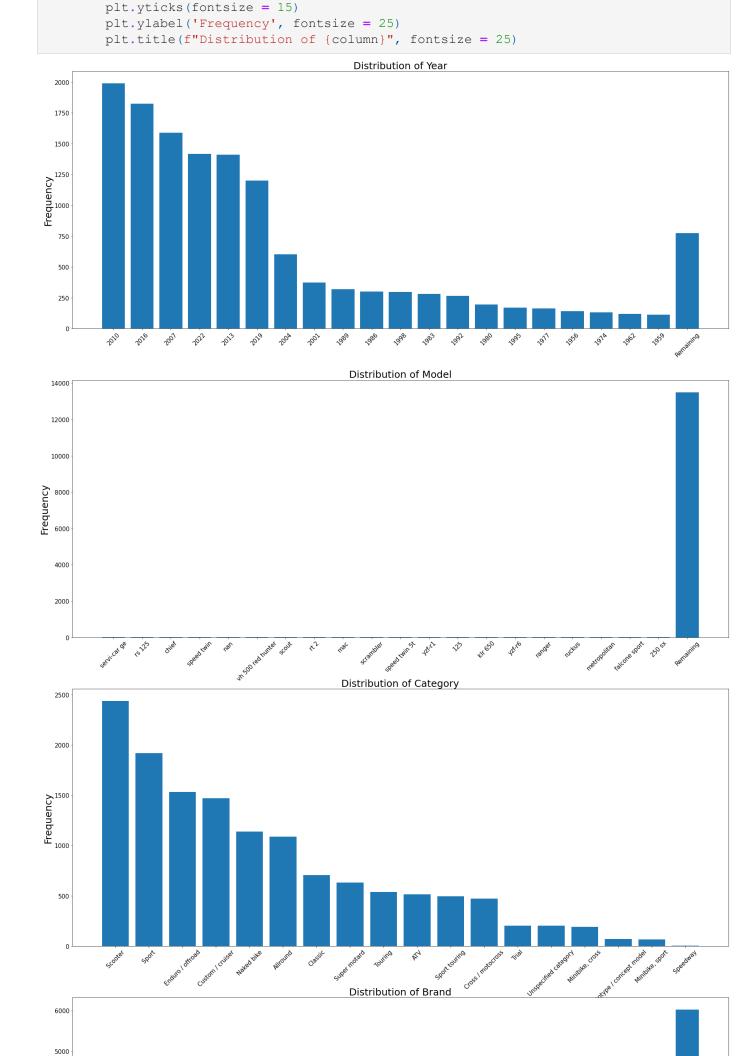
External evaluation

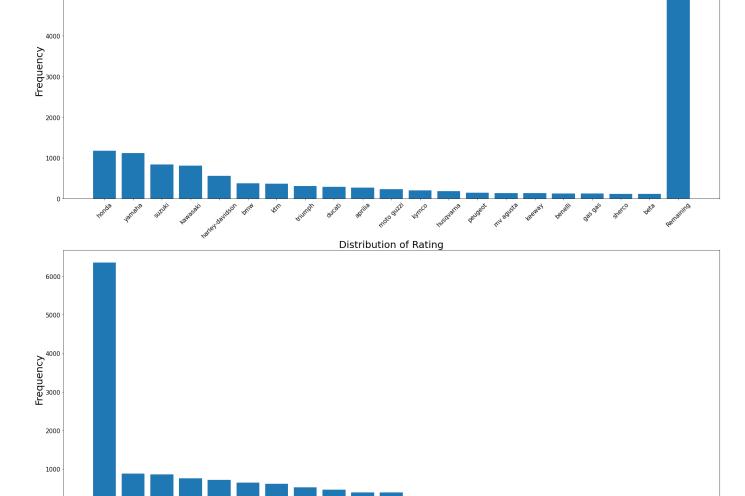
The external evaluation is done by looking at the distribution of the values of the available labels inside clusters.

Labels distribution in the dataset (clusters independent)

Before the external evaluation, it is important to evaluate how the labels are distributed into the dataset, independently of the clusters.

```
In [45]: counts = {}
         for label in labels name: # Calculate the counts for each label column
             counts[label] = workdf[label].astype(str).value counts(dropna=False)
         th = 20
         plt.figure(figsize=(30, 70))
         #plt.suptitle('Frequency of values for each label', fontsize = 40)
         plot counter = 1
         for column, count in counts.items():
            if len(count)>th:
                 count top th = count.head(th)
                 sum remaining = count.iloc[th:].sum()
                count top th['Remaining'] = sum remaining
                 plt.subplot(len(labels name),1,plot counter)
                 plot counter+=1
                 plt.bar(count top th.index, count top th.values)
                 #plt.xlabel('Values', fontsize = 25)
                 plt.xticks(rotation=45, fontsize = 15)
                 plt.yticks(fontsize = 15)
                plt.ylabel('Frequency', fontsize = 25)
                plt.title(f"Distribution of {column}", fontsize = 25)
             else:
                 plt.subplot(len(labels name),1,plot counter)
                 plot counter+=1
                 plt.bar(count.index, count.values)
                 #plt.xlabel('Values', fontsize = 25)
                 plt.xticks(rotation=45, fontsize = 15)
```





	Year	Frequency
0	2010	1988
1	2016	1823
2	2007	1588
3	2022	1417
4	2013	1412
5	2019	1200
6	2004	601
7	2001	373
8	1989	320
9	1986	300
10	1998	298
11	1983	281
12	1992	266
13	1980	194

35

ran

3.0

3.6

33 31

3,2

3.0

14	1995	169
15	1977	164
16	1956	142
17	1974	133
18	1962	118
19	1959	113
20	1965	107
21	1971	94
22	1953	91
23	1968	91
24	1950	52
25	1938	52
26	1932	34
27	1929	33
28	1935	31
29	1926	30
30	1941	29
31	1923	25
32	1947	24
33	1944	14
34	1917	14
35	1920	14
36	1914	11
37	1911	8
38	1908	6
39	1902	4
40	1899	3
41	1896	3
42	1905	3

	Model	Frequency
0	servi-car ge	13
1	rs 125	12
2	chief	12
3	speed twin	10
4	nan	10
•••		
10053	nsr 125	1

10054	nsc110 vision	1
10055	ns 400 r	1
10056	nr 750	1
10057	z 300	1

10058 rows × 2 columns

	Category	Frequency
0	Scooter	2437
1	Sport	1917
2	Enduro / offroad	1533
3	Custom / cruiser	1468
4	Naked bike	1139
5	Allround	1088
6	Classic	706
7	Super motard	631
8	Touring	538
9	ATV	514
10	Sport touring	495
11	Cross / motocross	473
12	Trial	202
13	Unspecified category	201
14	Minibike, cross	192
15	Prototype / concept model	70
16	Minibike, sport	64
17	Speedway	5

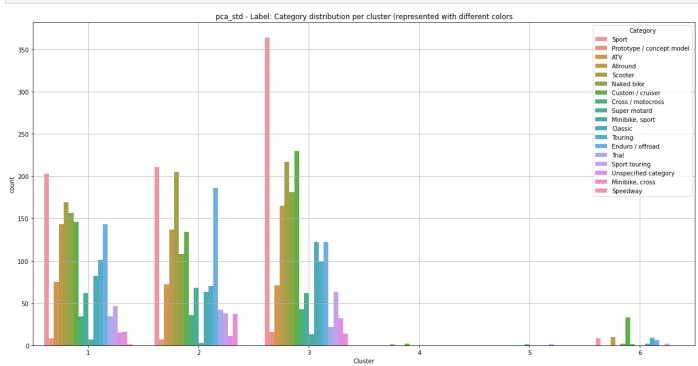
	Brand	Frequency
0	honda	1179
1	yamaha	1118
2	suzuki	839
3	kawasaki	809
4	harley-davidson	562
•••		
478	mbs	1
479	midual	1
480	swaygo	1
481	mission	1
482	livewire	1

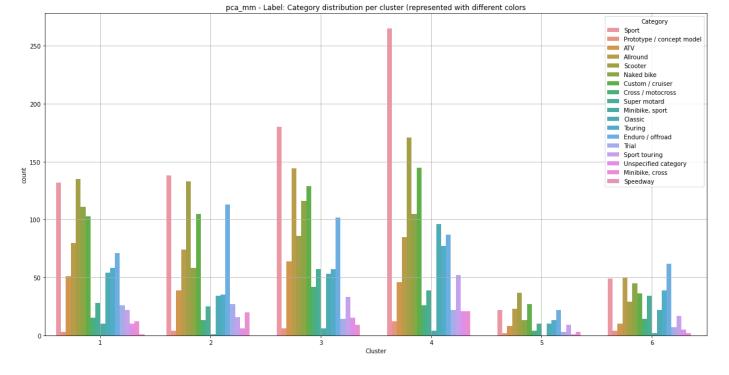
	Rating	Frequency
0	nan	6361
1	3.5	877
2	3.4	855
3	3.6	759
4	3.3	717
5	3.7	645
6	3.2	618
7	3.8	528
8	3.1	464
9	3.9	396
10	3.0	390
11	2.9	264
12	4.0	189
13	2.8	183
14	2.7	121
15	4.1	78
16	2.6	74
17	2.5	48
18	2.4	28
19	2.3	21
20	2.2	14
21	4.2	10
22	2.1	9
23	2.0	9
24	1.9	5
25	1.7	3
26	4.3	3
27	1.8	2
28	1.5	1
29	4.4	1

As can be seen from the plots and the tables showing the distribution of each label:

- **Rating** label is not well-balanced, and, most importantly, it is not avalaible for more than 6000 entries. It cannot be useful to make an external evaluation of clusters;
- Brand is not well-balanced, there are hundreds of different values and many different values among the
 entries. The most frequent values are very frequent, but there are also many very rare values, making

- difficult to interpret them and to use them for external evaluation of clusters;
- **Model** is not well-balanced, there are thousands of different values, making difficult to interpret them and to use them for external evaluation of clusters;
- **Year** is not well-balanced, since recent years are much more frequent than others. They can not be used for clusters evaluation;
- Category is reasonably well-balanced. It is possible to try using it for clusters external evaluation.





As can be seen from the plots above, **Category** label is not so meaningful in performing external evaluation of clusters.

In the standard-scaled data, the values are spread across the first 3 clusters. The only interesting label values are the *sport* value which is predominant in cluster 3 and *custom/cruiser* value which is much more frequent in cluster 5 than all other values. In addition, most of 'Category information' is in the first 3 clusters.

In the min/max-scaled data, the values are spread across all the clusters. The only interesting label values is the *sport* value which is much more frequent in cluster 2 than all other values.

This can also be noticed by the representation of the data in the PCs space, where different categories do not involve the occurrence of interesting patterns of categories in the PCs space.