

THE RUSSIAN GOVERNMENT  
FEDERAL STATE AUTONOMUS EDUCATIONAL INSTITUTION  
FOR HIGHER PROFESSIONAL EDUCATION  
NATIONAL RESEARCH UNIVERSITY  
“HIGHER SCHOOL OF ECONOMICS”

**The Analysis of On-screen Movie Kills**

Homework Project 2018/2019

**The team:**

Boris Tseitlin

Konstantin Romashchenko

Yulia Gurova

**MSc Program Data Science**

1<sup>st</sup> year

Faculty of Computer Science

Moscow 2018

# Table Of Contents

<b>1</b>	<b>THE CHOICE OF THE DATASET</b>	<b>3</b>
<b>2</b>	<b>K-means clustering</b>	<b>4</b>
2.1	Preprocessing . . . . .	4
2.2	K-means application . . . . .	5
2.3	Interpretation . . . . .	7
2.4	Bootstrap . . . . .	10
<b>3</b>	<b>Contingency Table Analysis</b>	<b>14</b>
3.1	Relative probabilities tables . . . . .	16
3.2	Quetelet index tables . . . . .	17
3.3	Chi-square & Quetelet index . . . . .	18
<b>4</b>	<b>PCA: Hidden Factor &amp; Data visualization</b>	<b>20</b>
4.1	Visualization . . . . .	22
4.2	Hidden factor analysis . . . . .	24
<b>5</b>	<b>2D regression</b>	<b>25</b>
<b>6</b>	<b>Conclusion</b>	<b>29</b>
<b>7</b>	<b>Applications</b>	<b>30</b>

# 1 THE CHOICE OF THE DATASET

The dataset that is used for the project contains information about on-screen deaths in movies. There are 545 movies (more than 100 objects) and 8 characteristics including names, so the dataset meets the requirements.

The source for the data is the thematic web-site [moviebodycounts.com](http://moviebodycounts.com). This dataset was processed and published on [figshare.com](http://figshare.com). It was gathered in accordance with the [rules](#), which are published on the web-site. We took several characteristics for the consideration: the release year of the film, MPAA rating (Motion Picture Association of America film rating system), genre or genres, the name of the director, the length of the film in minutes, IMDB rating based on user ratings. The main feature that we consider is the number of on-screen deaths in the movie.

The analysis of the data may reveal how the ratings depend on the number of deaths, how this number relates to the release year and so on. Moreover, genre and length of the film combined with on-screen violence may provide information on age ratings. This is a good set for the classification and clustering problems, as the films are grouped by genres and MPAA ratings. Movies in these groups are similar inside the groups, but dissimilar between them.

This analysis may be the first step to the automation of age rating systems. Moreover it may be helpful in the development of recommendation systems. And, as watching movies is the common interest of our team, the work with the dataset will inspire us to further conquest in Data Analysis.

## 2 K-means clustering

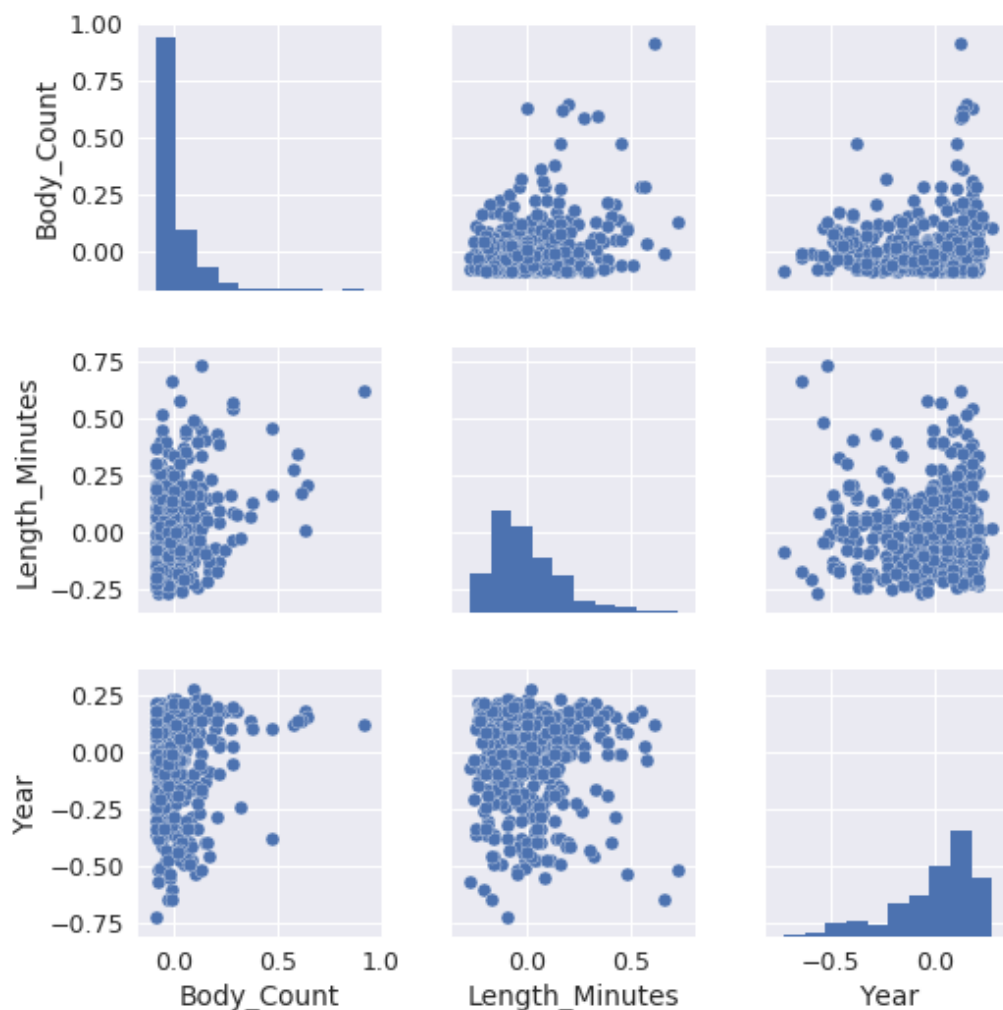
For this part of the task we choose three quantitative features: *Body\_Count*, the number of on-screen deaths in the movie; *Length\_Minutes*, the length in minutes; *Year*, the year of the release. These are quantitative features that, by our hypotheses, may be useful in cluster analysis of the dataset.

### 2.1 Preprocessing

First we standardize the dataset. We center by mean and normalize by range:

```
def normalize(vec):  
    return (vec - vec.mean())/(vec.max() - vec.min())
```

Before applying clustering methods, we visualize data on all possible pairplots. There are no obvious clusters in the two-dimensional visualization.



Clusters might follow a categorical feature already present in data. A categorical attribute with the least amount of variants we have is the MPAA rating. We color the plots with accordance to the ratings to see how they divide our data.

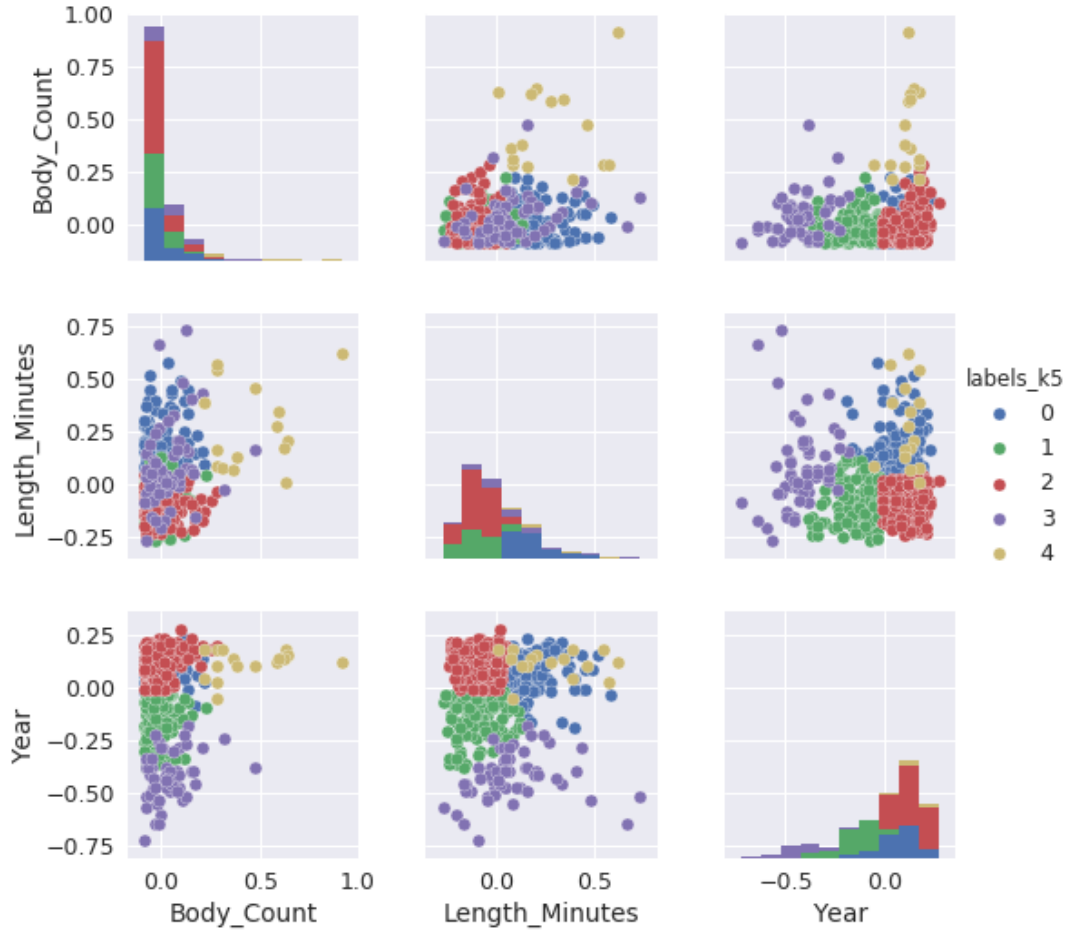


## 2.2 K-means application

The first method we apply to find the clusters is k-means at  $k=5$ . We take random initializations of 5 cluster centers and choose the best by k-means criteria from 10 initializations. The sum of squared distances from points to cluster centers, the K-means criterion: 13.613.

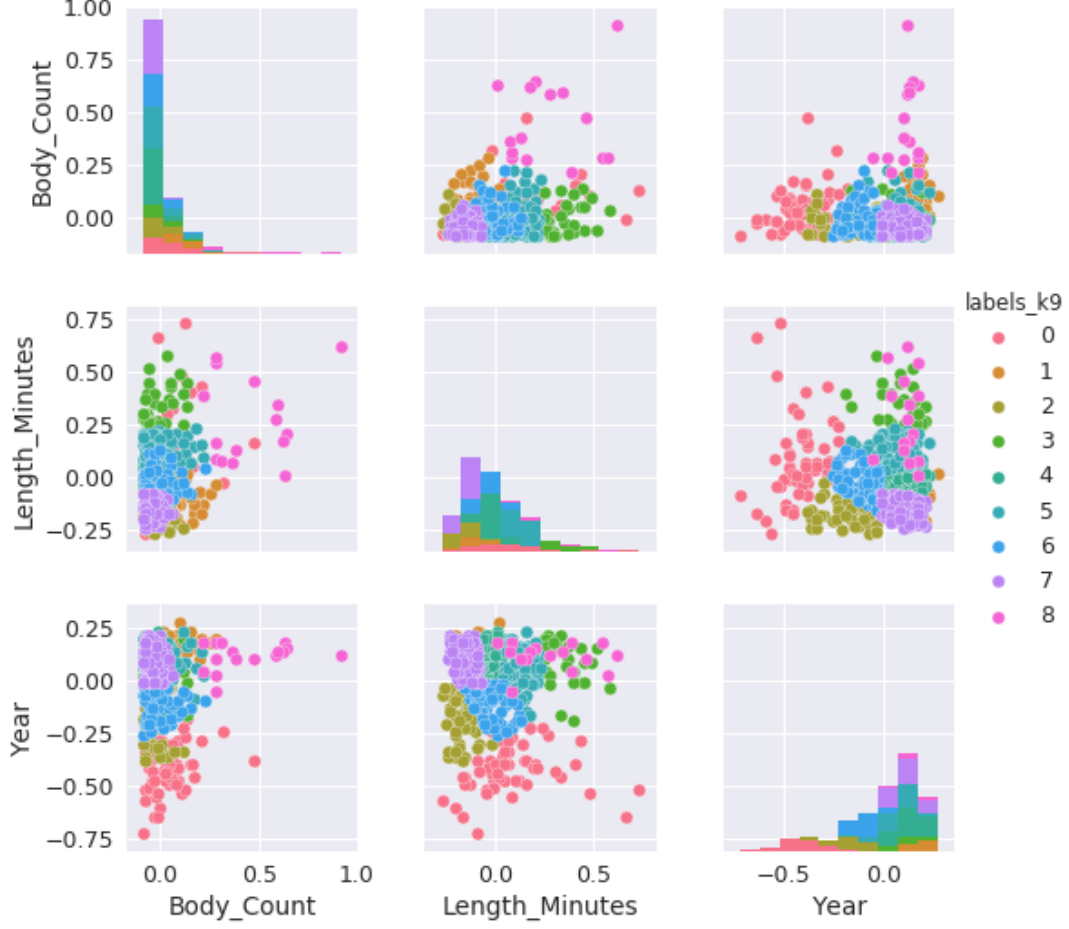
```
kmeans_k5 = KMeans(n_clusters=5, init='random', n_init=10, random_state=RANDOM_SEED)
kmeans_k5.fit(task_df)
task_df['labels_k5'] = pd.Series(kmeans_k5.predict(task_df))
print('Sum of squared distances from points to cluster centers, k=5:', kmeans_k5.inertia_)
sns.pairplot(task_df, hue='labels_k5', vars=quant_features)
```

We visualize the obtained clusters using pairplots. They don't match to MPAA\_Rating directly, but divide the data into reasonable descriptive categories.



We would specially distinguish cluster 3 (purple colored), the old films, mostly not long and with small amount of deaths. Cluster 4 (yellow colored) is not large and contains movies with the highest number of deaths, they differ in length, and are relatively recent ones.

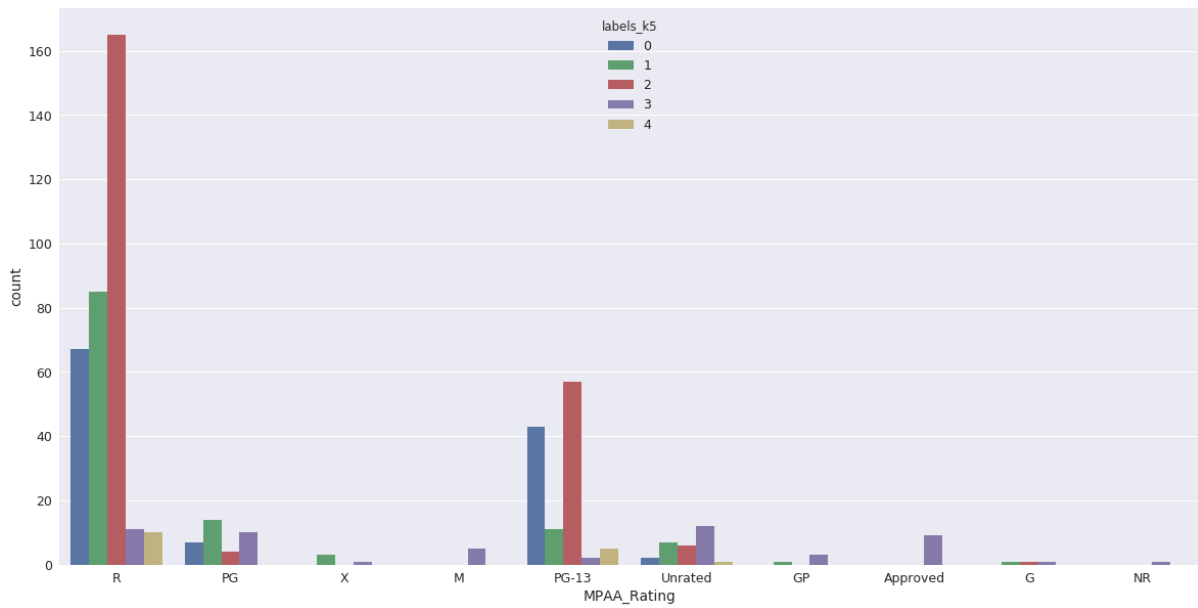
Now we apply K-means at  $k=9$  and get a lot of smaller clusters. Sum of squared distances from points to cluster centers,  $k=9$ : 10.079.



Some clusters are obviously inherited from the previous ones: new cluster 8 follows cluster 3 with the highest body count, the new cluster 0 follows the discussed cluster 3 (with old films) from the previous plot. Besides these two, there are many small clusters at the main body of the films, overlapping on most pairplots, without potent interpretation. We conclude that 9 clusters are too many for this dataset, and 5 clusters describe the data better: the cluster boundaries are clearer and clusters are reasonably interpretable.

## 2.3 Interpretation

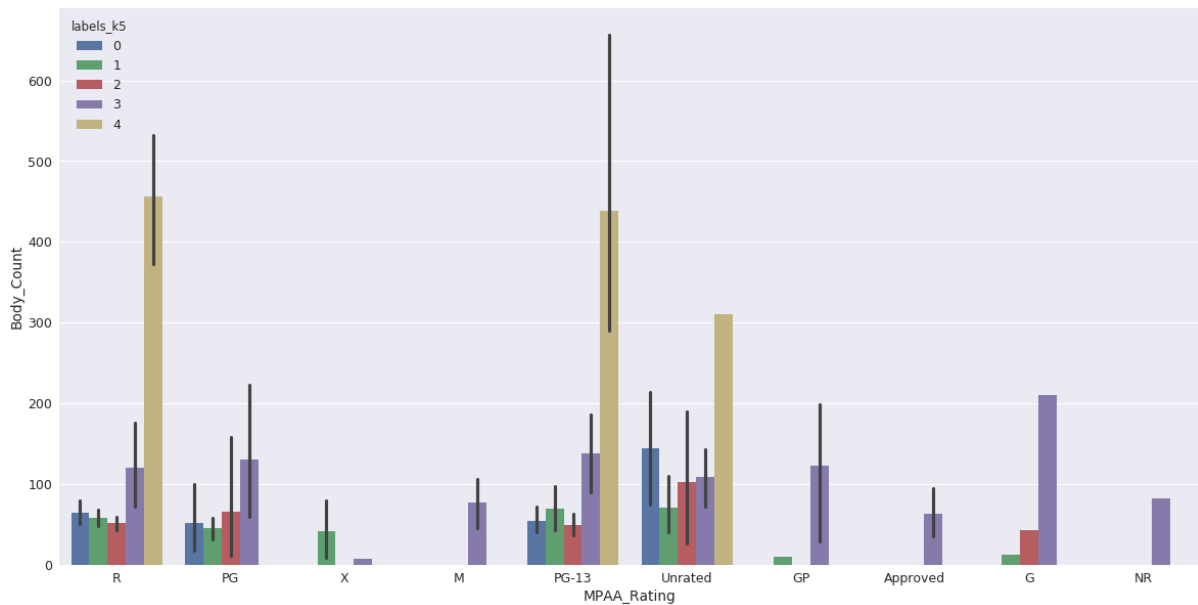
For the rest of this task we consider the partition with  $k=5$ . First we explore how movies are distributed among clusters, minding their MPAA ratings (the correspondence of the ratings is in Application 1).



The plot shows the amount of movies of each rating in each cluster. For example we see that 165 R movies are in cluster 2. Clusters 0, 1, 2 aggregate the most part of the movies, mostly with R and PG-13 ratings. That may show that we have mostly adult films in the dataset. That is not a surprise due to considered subject. The number of films at the clusters are: 2 - 233, 1 - 122, 0 - 119, 3 - 55, 4 - 16.

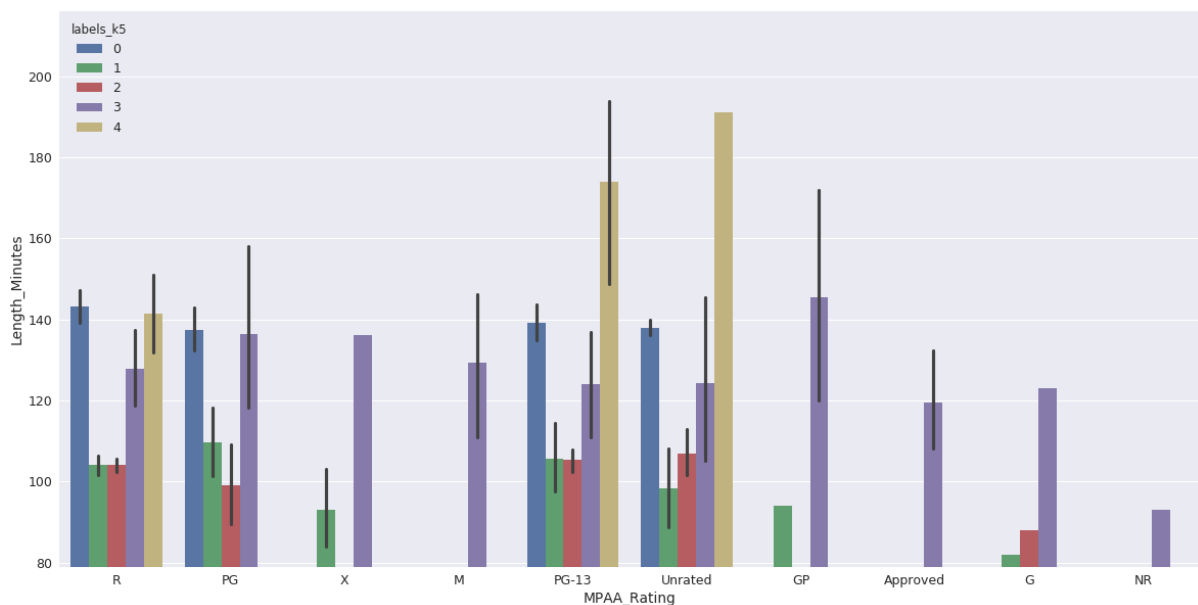
Next we compare the mean values of features between the clusters. The following barplot shows the mean body count per clusters, separated by ratings. The height of each bar shows the average body count of movies of a certain rating in a cluster. The vertical black bar represents the spread - the highest point shows the maximum, the lowest point shows the minimum.





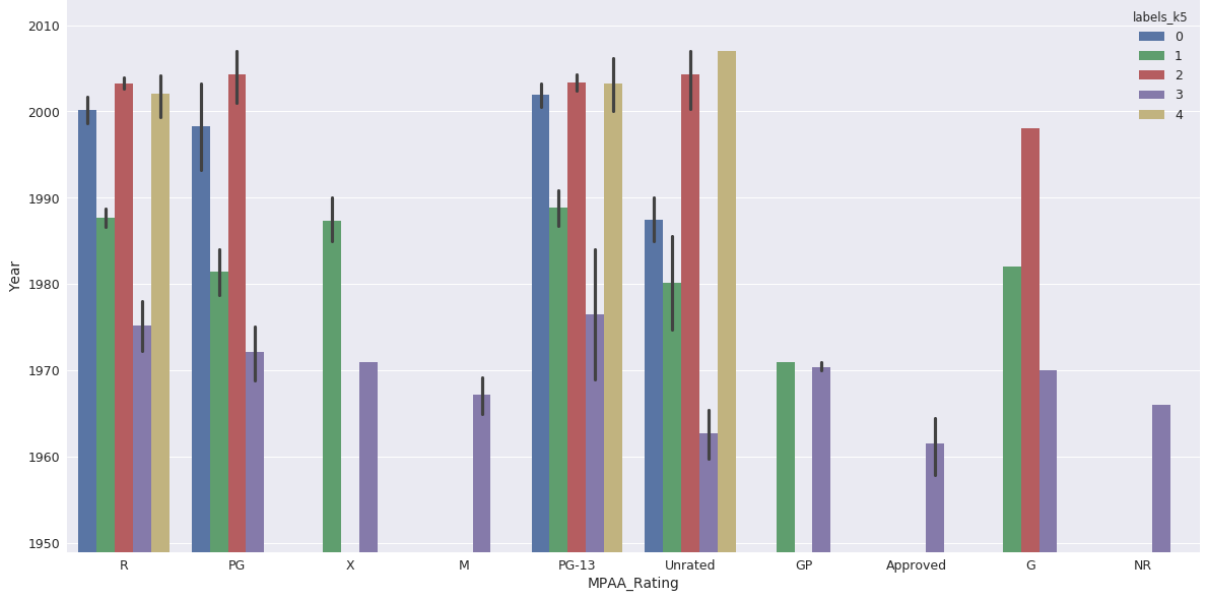
It's clear that cluster 4 contains the movies with the highest body count, as was supposed in the cluster interpretation. It contains the PG-13 movie with the highest body count in the dataset (836): "*Lord of the Rings: Return of the King*". The highest point of the black bars shows this movie.

Next we consider the average length of the movies by clusters:



This plot is not very informative. We can see that clusters 1 and 2 are on average the shortest ones. And the movies from the cluster 4, with highest body count, are long on average.

Next we consider the release years of movies by cluster and ratings.



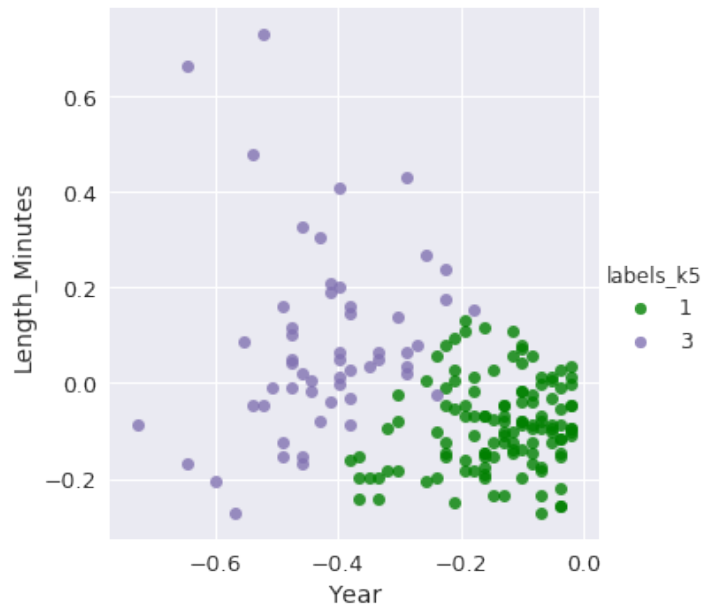
It can be seen that the cluster 3 contains mostly old movies, as was discovered before. Now we can see that these are mostly pre-1980 movies. Cluster 1 contains movies from about the 90-s. And it is interesting that the highest body count movies, captured by cluster 4, are mostly recent - post-2010.

Moreover, from this diagram it can be seen that for some ratings there are films only from one-two clusters, mostly from the third one, capturing old films. These ratings were used in previous years, but then were renamed or changed. As there are only several such movies in our dataset, we do not think it influence any results.

## 2.4 Bootstrap

In this part of the paper we inspect two clusters: 1 and 3. As was mentioned, cluster 3 contains mostly old, pre-1980 movies and cluster 1 has movies from the 90-s.

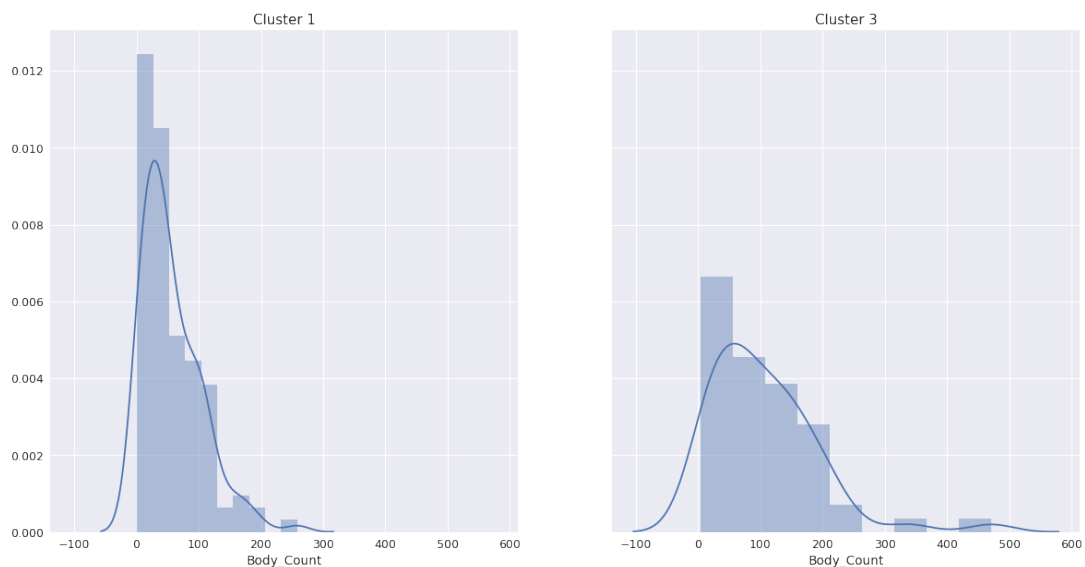
First, we consider length and release year, and then we focus on our main feature, the body count. From the scatter plot the difference between the clusters can be clearly seen.



We inspect the distribution of our primary feature, body count, in the two clusters.

```
print(cluster_0[target_feature].describe())
print(cluster_1[target_feature].describe())
fig = plt.figure(figsize=(20,10))
axes = fig.subplots(1, 2, sharex=True, sharey=True)

sns.distplot(cluster_0.Body_Count, ax=axes[0])
sns.distplot(cluster_1.Body_Count, ax=axes[1])
```

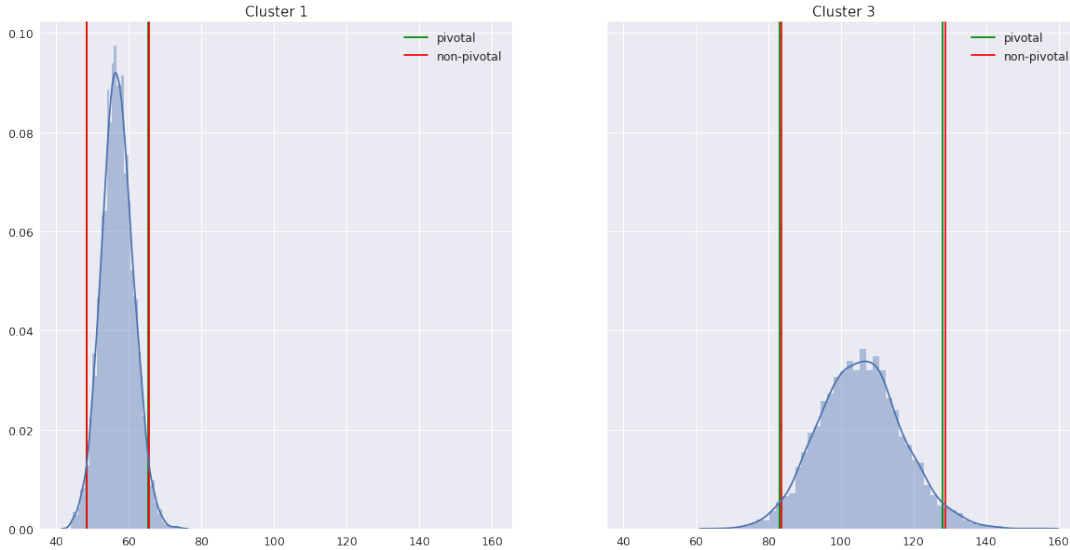


The parameters of the distributions are listed in the table. The distributions seem to be different but we cannot be sure as the samples are rather small.

Parameter	Cluster 1	Cluster 3
count	122.000000	55.000000
mean	56.795082	105.654545
std	47.931414	87.318323
min	1.000000	4.000000
25%	20.000000	44.500000
50%	42.500000	91.000000
75%	87.250000	147.000000
max	258.000000	471.000000

To compare the distribution between the clusters we apply bootstrap in both pivotal and non-pivotal versions with 5000 samples. We obtain that the distributions of Body\_Count really differ between these clusters. They not only have different means, as evident by confidence intervals, but also have different bell shapes.

We provide the following histogram plots for bootstrap sample means. Green lines show pivotal 95% confidence intervals, red lines show 95% non-pivotal confidence intervals. It is interesting that pivotal and non-pivotal confidence intervals are nearly identical. From that we conclude that the distribution of the feature is approximately Gaussian.



Parameter	Cluster 1	Cluster 3
mean	56.844	105.385
pivotal	(48.317, 65.371)	(82.949, 127.823)
non-pivotal	(48.474, 65.590)	(83.672, 128.711)

The code for bootstrap implementation and the confidence intervals is below. We use pivotal and non-pivotal bootstrap for the confidence intervals.

```
def bootstrap_sample(vec, size):
    return np.random.choice(vec, size=(vec.shape[0], size), replace=True)

def bootstrap_means(srs, sample_amount=5000):
    samples_ix = bootstrap_sample(srs.index, size=sample_amount).T
    means = np.array([srs.loc[sample].mean() for sample in samples_ix])
    return means

b_means_cluster_0 = bootstrap_means(cluster_0.Body_Count)
b_means_cluster_1 = bootstrap_means(cluster_1.Body_Count)

def confidence_interval_pivotal(vec):
    mean = vec.mean()
    std = vec.std()
    return [mean-1.96*std, mean+1.96*std]

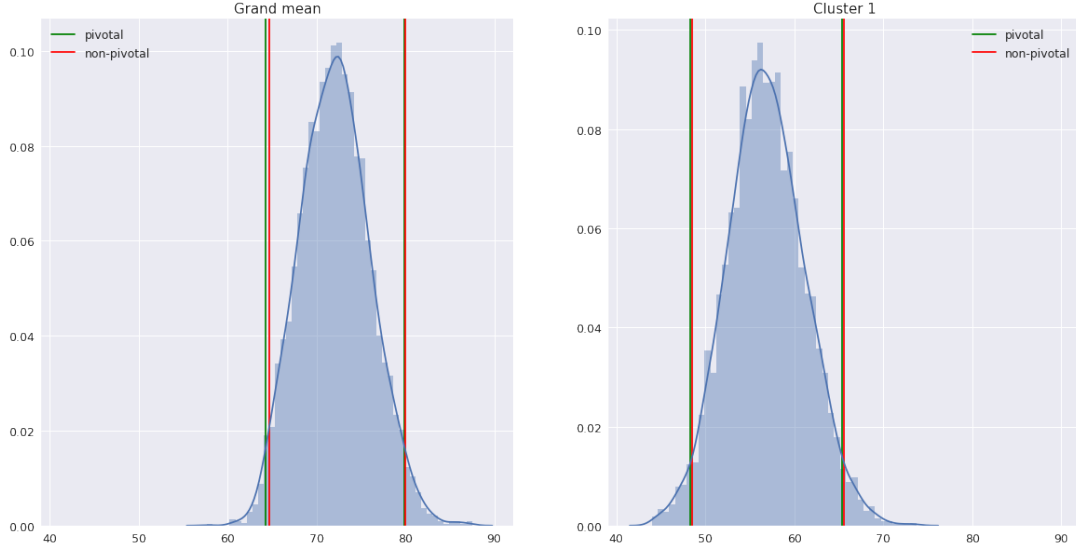
def confidence_interval_non_pivotal(vec, alpha):
    left = np.percentile(vec, (100-alpha)/2)
    right = np.percentile(vec, alpha+(100-alpha)/2)
    return [left, right]

def distplot_with_conf_intervals(vec, ax=None):
    if not ax:
        ax = plt.gca()
    for x in confidence_interval_pivotal(vec):
        line = ax.axvline(x=x, color='g')
        line.set_label('pivotal')
    for x in confidence_interval_non_pivotal(vec, 95):
        line = ax.axvline(x=x, color='r')
        line.set_label('non-pivotal')
    ax.legend(loc='best')
    return sns.distplot(vec, ax=ax, norm_hist=False)
```

Next we build the 95% confidence intervals for the grand mean of the feature by using bootstrap. Also we use bootstrap to compare cluster 0 to the grand mean. We obtain:

Parameter	Cluster 1	Grand mean
mean	56.844	72.157
pivotal	(48.317, 65.371)	(64.374, 79.34)
non-pivotal	(48.474, 65.590)	(64.65, 80.238)

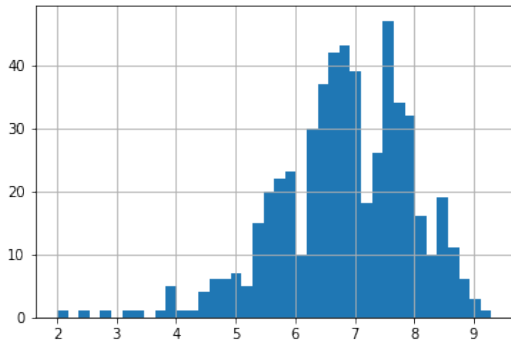
Comparison between the grand mean and cluster 1:



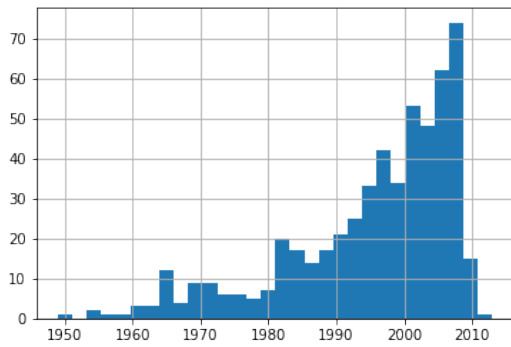
We pay attention here to the fact that the bell shape of cluster 1 body count resembles the grand mean bell shape closely.

### 3 Contingency Table Analysis

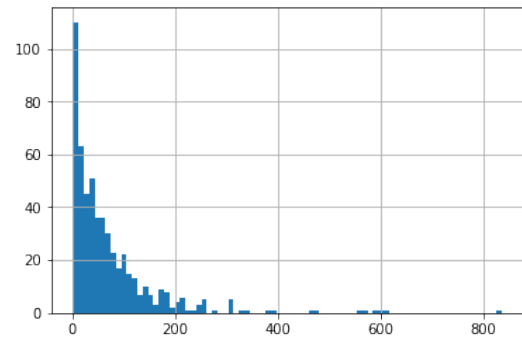
In this part of the paper we consider the contingency tables. We take three nominal features from the dataset, producing them by splitting the quantitative features. Consider the histograms for IMDB\_Rating, Year and Body\_count:



IMDB\_Rating



Year



Body\_count

To make the features we split all three attributes with reasonable visible thresholds, shown on the plots. We take 4 intervals for each attribute. For the IMDB rating we choose 6, 7 and 8 as thresholds, as they are caught by the histogram. It can be really well interpreted as very bad, bad, good and very good films. For the Year we choose 1980, 1990, 2000, 2005 as thresholds. In the previous part we had the cluster of old movies, which are filmed before 1980, and we can use it here to set the thresholds. For the Body count the thresholds were chosen to make the groups approximately equal. For the on-screen deaths we have chosen 20, 50, 120.

```
def categorize_func(split_points):
    def categorize(param):
        split_points.sort()
        if (param < split_points[0]):
            return '<' + str(split_points[0])
        for index in range(len(split_points) - 1):
            if param < split_points[index + 1]:
                return '' + str(split_points[index])
        return '' + str(split_points[-1])
    return categorize

bodies = df['Body_Count'].apply(categorize_func([10, 100, 200]))
imdb_rating = df['IMDB_Rating'].apply(categorize_func([5.0, 7.0, 8.0]))
year = df['Year'].apply(categorize_func([1990, 2000, 2005]))
```

Next we build the contingency tables for the determined features:

```
contingency_table_imdb_bodies = pd.crosstab(bodies, imdb_rating, margins=True, \
                                             margins_name='Total')
contingency_table_year_bodies = pd.crosstab(bodies, year, margins=True, margins_name='Total')
```

IMDB_Rating Body_Count	<6.0	≥6.0	≥7.0	≥8.0	Total
<20	28	65	47	22	162
≥120	14	20	44	14	92
≥20	28	40	39	23	130
≥50	39	49	52	21	161
Total	109	174	182	80	545

Year	<1980	≥1980	≥1990	≥2000	≥2005	Total
Body_Count						
<20	12	14	39	44	53	162
≥120	20	10	13	24	25	92
≥20	10	23	48	19	30	130
≥50	23	25	39	30	44	161
Total	65	72	139	117	152	545

The first table shows the joint distribution of the IMDB rating and the number of deaths. The second shows the joint distribution between the Year and the number of deaths.

### 3.1 Relative probabilities tables

To see the relative probabilities we build the relative frequency tables over the same features:

```
def make_relative(probabilites_df):
    res = probabilites_df.copy()
    res.drop(index='Total', columns='Total', inplace=True)
    for col in res:
        for row in res[col].index:
            res[col][row] /= probabilites_df['Total'][row]
    return res

def normalize(contingency_df):
    res = contingency_df.copy()
    res = res.astype('float')
    for col in res:
        for row in res[col].index:
            res[col][row] /= contingency_df['Total']['Total']
    return res

make_relative(normalize(contingency_table_imdb_bodies)) * 100
```

The table for the rating and the number of deaths:



IMDB_Rating	<6.0	≥6.0	≥7.0	≥8.0
Body_Count				
<20	17.283951	40.123457	29.012346	13.580247
≥20	21.538462	30.769231	30.000000	17.692308
≥50	24.223602	30.434783	32.298137	13.043478
≥120	15.217391	21.739130	47.826087	15.217391

We conclude that a film with more than 200 body count probably will be well appreciated: it has probability nearly 48% to have 7 and 22% to have 6, while the film with <20 deaths will most probably have 6 (40%) and less probably 7 (29%).

The table for the year and the number of deaths:

Year	<1980	≥1980	≥1990	≥2000	≥2005
Body_Count					
<20	7.407407	8.641975	24.074074	27.160494	32.716049
≥20	7.692308	17.692308	36.923077	14.615385	23.076923
≥50	14.285714	15.527950	24.223602	18.633540	27.329193
≥120	21.739130	10.869565	14.130435	26.086957	27.173913

We see that if a movie has high amount of deaths it is most probably a new one or a very old one. And, as we have much more new films in the dataset, the probability for each cathegory of deaths increases with year (except one cell).

## 3.2 Quetelet index tables

Now we build Quetelet index tables:

```
def make_quetelet(probabilites_df):
    res = probabilites_df.copy()
    res.drop(index='Total', columns='Total', inplace=True)
    for col in res:
        for row in res[col].index:
            res[col][row]=(probabilites_df[col][row]/probabilites_df['Total'][row] - \
                            probabilites_df[col]['Total']) / probabilites_df[col]['Total']
    return res
make_quetelet(normalize(contingency_table_imdb_bodies)) * 100
make_quetelet(normalize(contingency_table_year_bodies)) * 100
```

IMDB_Rating	<6.0	≥6.0	≥7.0	≥8.0
Body_Count				
<20	-13.580247	25.674046	-13.122371	-7.484568
≥120	-23.913043	-31.909045	43.215480	3.668478
≥20	7.692308	-3.625111	-10.164835	20.528846
≥50	21.118012	-4.672664	-3.283052	-11.141304

The table shows the relative probability compared to the average. We can conclude that films that have 120 or more bodies are more appreciated: they have odds to have rating more than 8.0  $\approx 4\%$  more than average and chance that film will have rating less than 6.0 is  $\approx 23\%$  less than average.

Year	<1980	≥1980	≥1990	≥2000	≥2005
Body_Count					
<20	-37.891738	-34.585048	-5.608846	26.516830	17.304256
≥120	82.274247	-17.723430	-44.596497	21.516165	-2.567220
≥20	-35.502959	33.920940	44.770338	-31.919790	-17.257085
≥50	19.780220	17.537957	-5.022566	-13.202739	-2.010461

This is a quetelet table for year and the number of deaths. We conclude that the films with the highest amount of deaths have probability  $\approx 82\%$  more than average to be released before 1980. At the same time films with less than 20 deaths are most probably released after 2000.

### 3.3 Chi-square & Quetelet index

We apply Pearson's chi-squared test to measure correlation between two variables. The value is the same as Summary Quetelet index. It shows the average relative increase in the prediction of the number of the number of deaths in the movie, when the year or the IMDB rating becomes known.

First, we find expected number of films in each category under assumption of independence of features. Also we find number of degrees of freedom. Let's consider the Year and the Body\_Count:

```
obs_values_year_bodies = trunc_total(contingency_table_year_bodies)
exp_values_year_bodies = expected_values(contingency_table_year_bodies)
degrees_of_freedom_year_bodies = reduce(mul, map(lambda x: x - 1, \
                                                obs_values_year_bodies.shape), 1)
ddof_year_bodies = obs_values_year_bodies.size - degrees_of_freedom_year_bodies - 1
```

The tables for observed frequencies and expected under the independence condition:

Year	<1980	≥1980	≥1990	≥2000	≥2005
Body_Count					
<20	12	14	39	44	53
≥120	20	10	13	24	25
≥20	10	23	48	19	30
≥50	23	25	39	30	44

Year	<1980	≥1980	≥1990	≥2000	≥2005
Body_Count					
<20	19.321101	21.401835	41.317431	34.777982	45.181651
≥120	10.972477	12.154128	23.464220	19.750459	25.658716
≥20	15.504587	17.174312	33.155963	27.908257	36.256881
≥50	19.201835	21.269725	41.062385	34.563303	44.902752

The obtained degrees of freedom amount for  $\chi^2$  test is 12. Now we apply the  $\chi^2$  test for the hypothesis of independence between year and number of bodies:

```
scipy.stats.chisquare(trunc_total(contingency_table_year_bodies), \
    expected_values(contingency_table_year_bodies), ddof=ddof_year_bodies, axis=None)
```

We can see that critical pvalue is less than  $10^{-4}$ . So we reject the hypothesis of independence between year and number of deaths with level of confidence 99.99%.

Now consider the same tables for the other feature, IMDB rating, with number of bodies. Observed frequencies and expected under the independence condition:

IMDB_Rating	<6.0	≥6.0	≥7.0	≥8.0
Body_Count				
<20	28	65	47	22
≥120	14	20	44	14
≥20	28	40	39	23
≥50	39	49	52	21

MDB_Rating	<6.0	≥6.0	≥7.0	≥8.0
Body_Count				
<20	32.4	51.721101	54.099083	23.779817
≥120	18.4	29.372477	30.722936	13.504587
≥20	26.0	41.504587	43.412844	19.082569
≥50	32.2	51.401835	53.765138	23.633028

The number of degrees of freedom is 9, and it is expectedly less than in previous case as we have less categories for rating.

The  $\chi^2$  test results for the hypothesis of independence between the IMDB rating and number of bodies:

Power\_divergenceResult(statistic=18.231013449960972, pvalue=0.03258602359739147)

The critical pvalue here is about 3%. So we can reject the hypothesis of independence with level of confidence 95%, but we cannot reject the hypothesis with level of confidence 97% or higher.

Now we compute chi-square summary quetelet index tables for both features:

IMDB_Rating	<6.0	Total	≥6.0	≥7.0
Body_Count				
<20	-3.802469	5.071541	16.688130	-6.167515
Total	3.239576	18.231013	6.566671	7.175824
≥120	-3.347826	9.798763	-6.381809	19.014811
≥20	2.153846	1.461151	-1.450044	-3.964286
≥50	8.236025	1.899559	-2.289605	-1.707187

Year	<1980	Total	≥1980	≥1990	≥2000	≥2005
Body_Count						
<20	-4.547009	9.262296	-4.841907	-2.187450	11.667405	9.171256
Total	12.906996	39.298444	5.572056	11.545967	6.805703	2.467722
≥120	16.454849	13.407037	-1.772343	-5.797545	5.163880	-0.641805
≥20	-3.550296	14.499397	7.801816	21.489762	-6.064760	-5.177126
≥50	4.549451	2.129715	4.384489	-1.958801	-3.960822	-0.884603

The quetelet index is the sum of the values in the table. We compute it to make sure that it is equal to  $\chi^2$  statistics, which we obtained previously, and the result is supported.

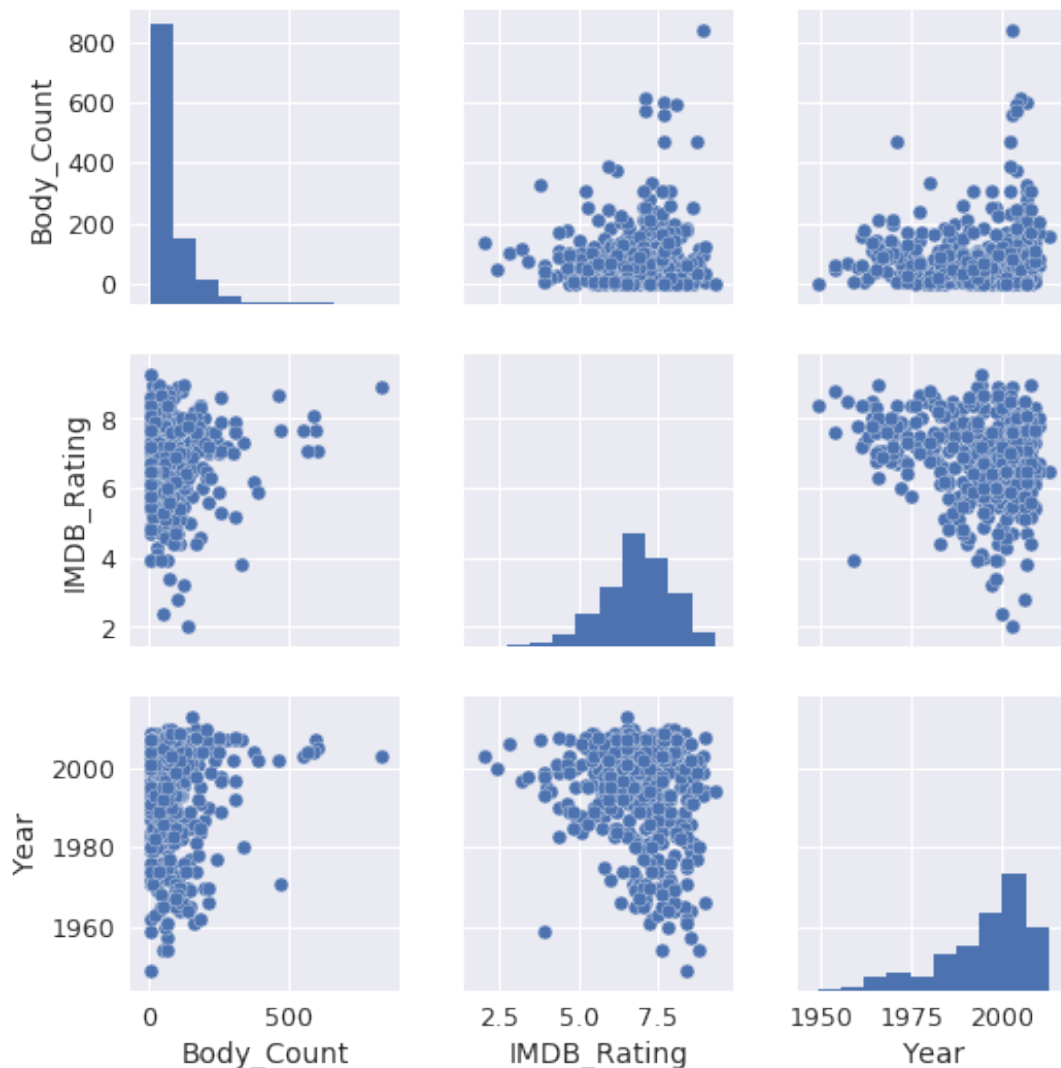
## 4 PCA: Hidden Factor & Data visualization

In this part of the paper we apply principal component analysis. We choose three features to take into consideration. First one is the Body\_Count, as the main feature of interest. The second one is Year, as we know from the previous analysis that they are well connected. The third one is IMDB rating.

First we center and normalize the features. There are two ways of normalization, by standard deviation and by range:

```
def normalize_range(vec):
    return (vec - vec.mean())/(vec.max() - vec.min())
def normalize_std(vec):
    return (vec - vec.mean())/(vec.std())
```

Recall the plots of joint and self distributions of the features:



First we apply PCA and inspect the data scatter explained by each PC. We apply PCA to data centered and normalized by range, as proper PCA application requires data to be on the same scale.

```
pc_range = PCA()
pc_range.fit(task_df_normalized_range)
scatter = data_scatter(task_df_normalized_range)
contibs = pd.Series([pc_contrib(s) for s in pc_range.singular_values_])
contibs_rel = pd.Series([pc_contrib_rel(s, scatter) for s in pc_range.singular_values_])
print('Data scatter', scatter)
print('Contributions', contibs, contibs_rel)

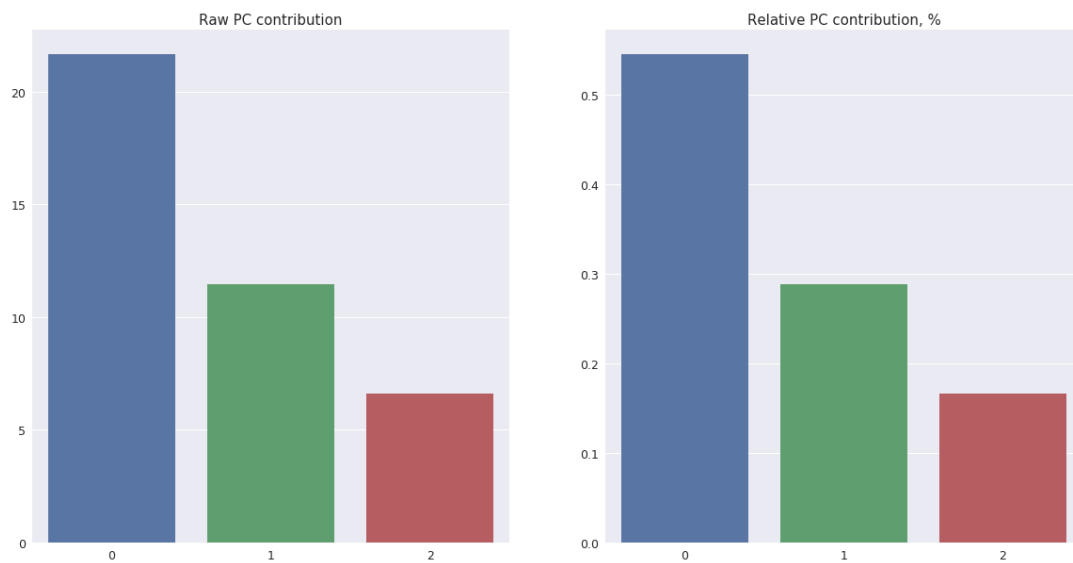
fig = plt.figure(figsize=(20,10))
axes = fig.subplots(1, 2, sharex=True)
axes[0].set_title('Raw PC contribution')
```

```
sns.barplot(contibs.index, contibs.values, ax=axes[0])
axes[1].set_title('Relative PC contribution, %')
sns.barplot(contibs_rel.index, contibs_rel.values, ax=axes[1])
```

The contributions of the components to the explanation of data scatter in distribution are:

# of Component	Raw contribution	Relative contribution
0	21.672266	0.545363
1	11.44299	0.287985
2	6.622589	0.166651

So, the first PC explains 55% of data scatter, the second one explains 29%, the third one 17%. The diagram illustrates the numbers from the table.

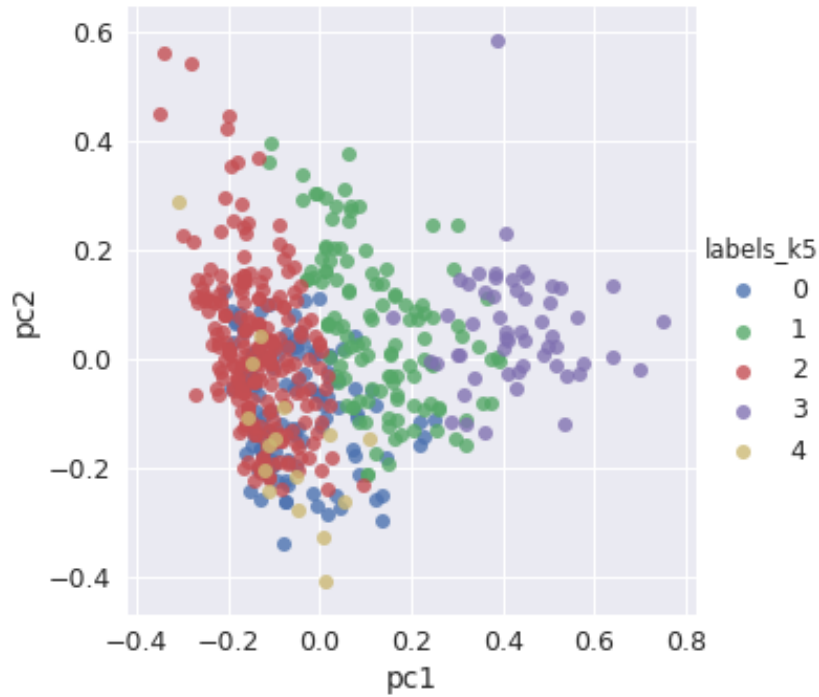


## 4.1 Visualization

We will use K-means ( $k = 5$ ) cluster labels from part 2 to see how PCA helps visualize them.

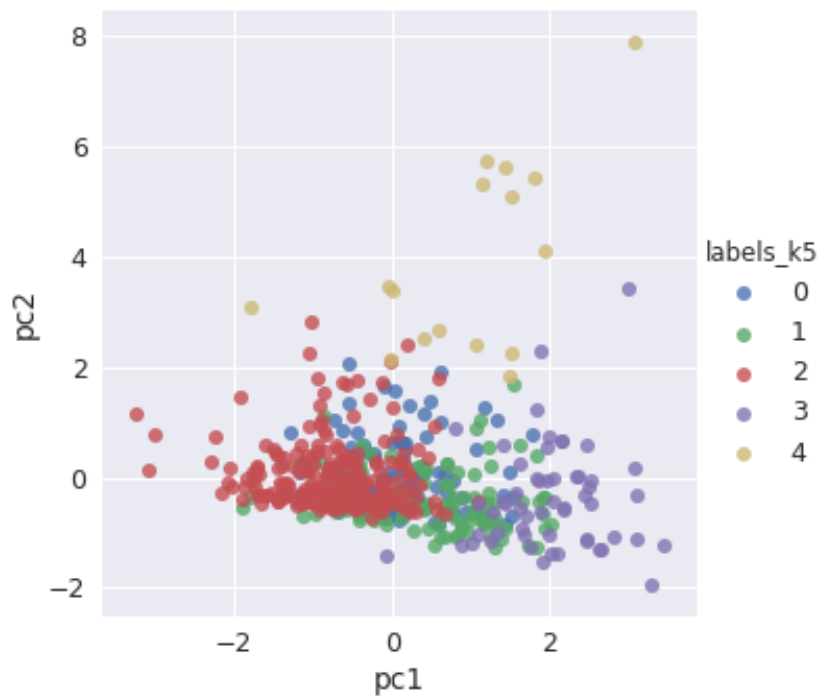
We apply PCA to data with clusters centered by mean and normalized by range and plot the first two principal components.

```
pc_range = PCA(n_components = 2)
pca_result = pc_range.fit_transform(task_df_normalized_range)
pca_result = pd.DataFrame(pca_result, columns=['pc1', 'pc2'])
pca_result['labels_k5'] = labels_k5
fig = plt.figure(figsize=(20,10))
sns.lmplot(x='pc1', y='pc2', fit_reg=False, hue='labels_k5', data=pca_result)
```



Evidently the clusters are easily separatable, except for 0 and 4, which tend to overlap with other clusters.

Next we apply PCA to data normalized by standard deviation. The code is similar, the resulting plot is as follows:



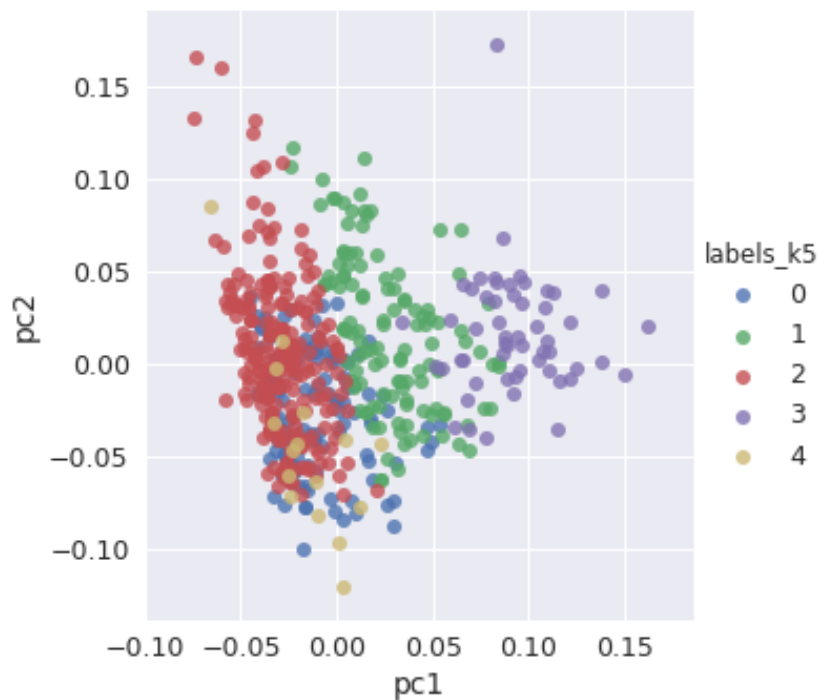
This one is much less descriptive, clusters overlap alot.  
Next, we implement and apply conventional PCA.

```
def conv_pca(X):
    X = X - X.mean(axis=0)

    covariance_matrix = (X.T.dot(X))/X.shape[0]

    eigvals, eigvectors = np.linalg.eig(covariance_matrix)
    order = np.argsort(eigvals)
    ind1, ind2 = order[-2:][::-1] # top 2 max eigvalues indices
    eigvectors = -eigvectors.T
    pc1 = X.dot(eigvectors[ind1]) / np.sqrt(X.shape[0]*abs(eigvals[ind1]))
    pc2 = X.dot(eigvectors[ind2]) / np.sqrt(X.shape[0]*abs(eigvals[ind2]))
    return pc1, pc2
```

Firstly we apply conventional PCA to data normalized by range:



The results are nearly identical to those of model-based PCA. That is expected. When using conventional PCA it's important to center our data (while model-based PCA can be applied to non-centered data). Here the data is centered, so we get same results.

## 4.2 Hidden factor analysis

In this part we try to uncover the hidden factor behind selected features and determine which of them contribute the most. In this function we implement applying PCA, extracting the first singular triplet and rescaling it:



```

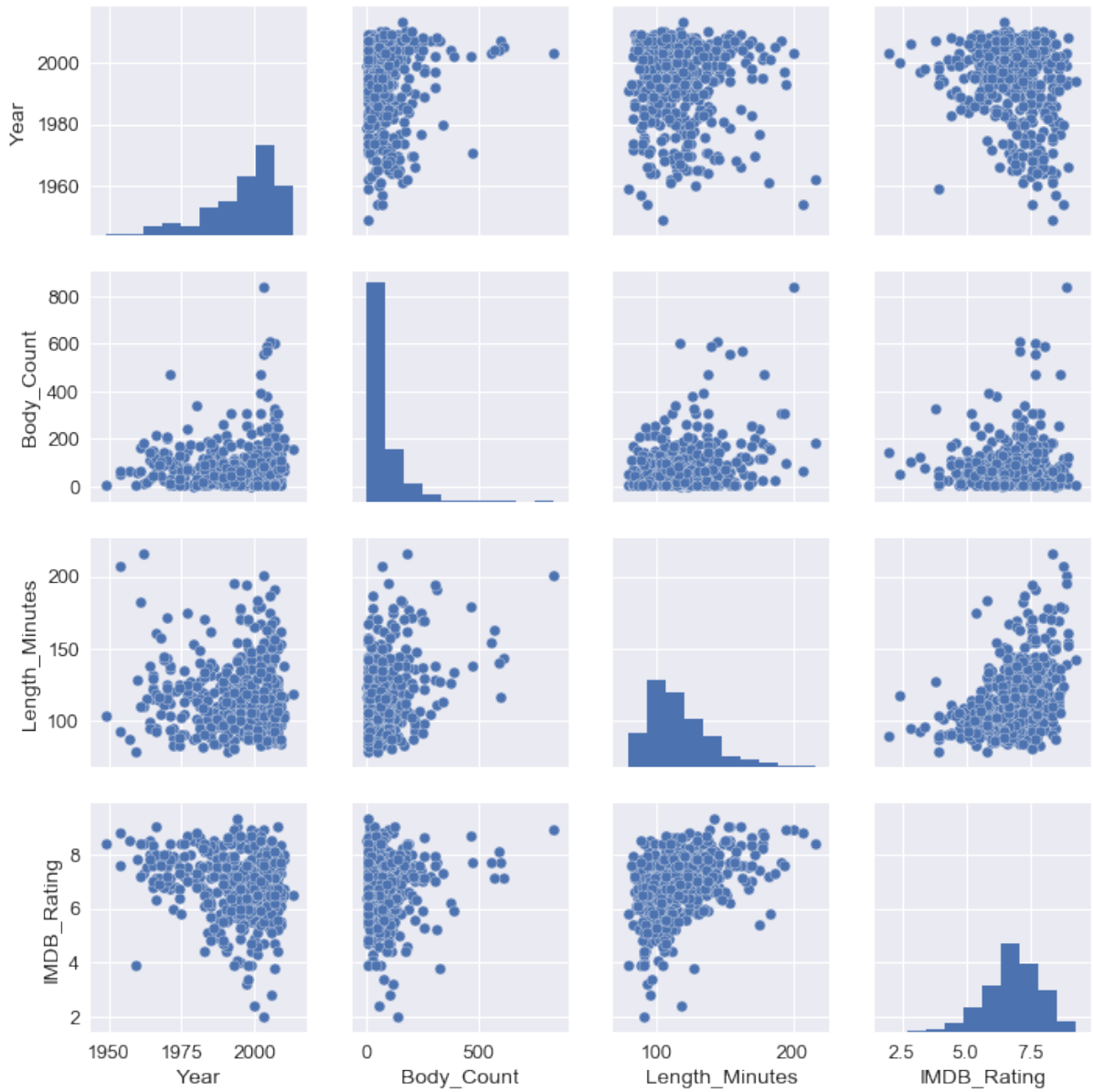
def get_feature_weights(X):
    u, s, vh = np.linalg.svd(X)
    z = abs(u[:, 0])
    sigma = max(s)
    c = abs(vh[:, 0])
    alpha = 1/c.sum()
    feature_weights = c*alpha
    contrib = sigma**2 / data_scatter(X)
    return feature_weights, contrib
weights, contrib = get_feature_weights(task_df)
print(list(task_df.columns))
print(contrib*100, weights.round(3)*100)
['Body_Count', 'IMDB_Rating', 'Year']
99.78585508347525 [ 3.5 96.4  0.1]

```

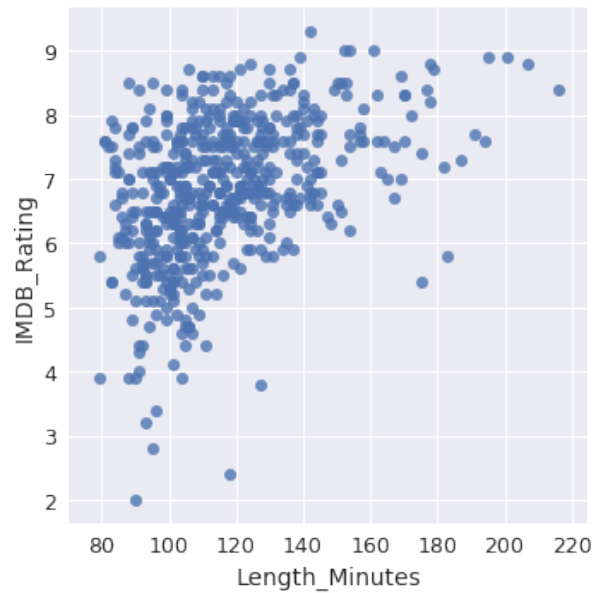
So, on the 0-100 rank we obtain that the first principal component explains 99.8% of data scatter. The most contributing feature is IMDB\_Rating, which determines 96.4% of the PC.

## 5 2D regression

In this part of the paper we examine the 2D regressions. First, we choose two variables to take into consideration. All the scatter-plots are presented on the picture.



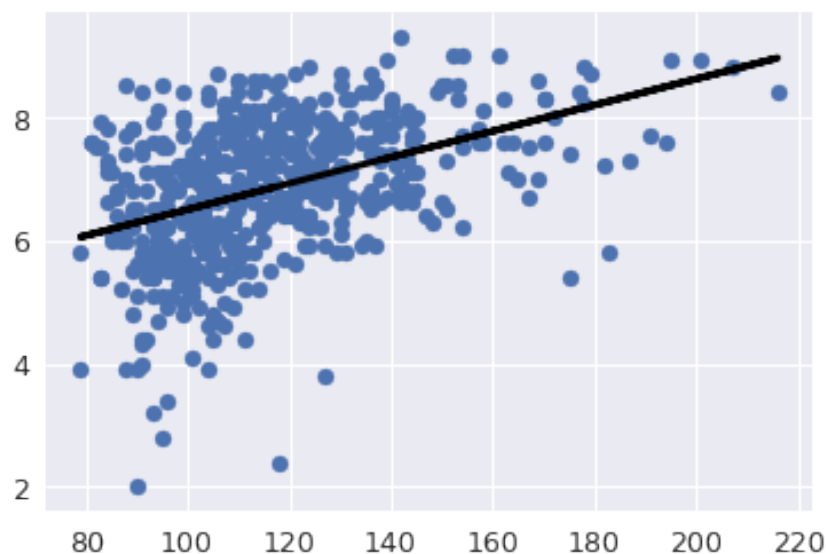
None of these are "linear-like" plots. We choose Length\_Minutes and IMDB\_Rating as the best options. First, we explore separately their scatter-plot.



Based on the visualization, we expect positive correlation here. We build a regression of Length\_Minutes to IMDB\_Rating.

```
training_x = df['Length_Minutes'].values.reshape(-1, 1)
training_y = df['IMDB_Rating'].values
classifier = LinearRegression().fit(training_x, training_y)
predicted_y = classifier.predict(training_x)
plt.scatter(training_x, training_y)
plt.plot(training_x, predicted_y, color='black', linewidth=3)
classifier.coef_
```

The visualization of the regression line:



The slope of the regression is 0.0211439. That means that every additional minute of a film gives increase in 0.0211439 to its rating. It doesn't seem

much, but these 0.02 may raise the film on tens of places in the search or in the top-movies rating, as there are >5 mln movies on IMDB rated at ten-point scale.

This correlation may follow the suggested hypothesis: the production of the long movie usually requires a bigger budget, which will be approved if the film is supposed to be good. So, long films are generally among the good ones.

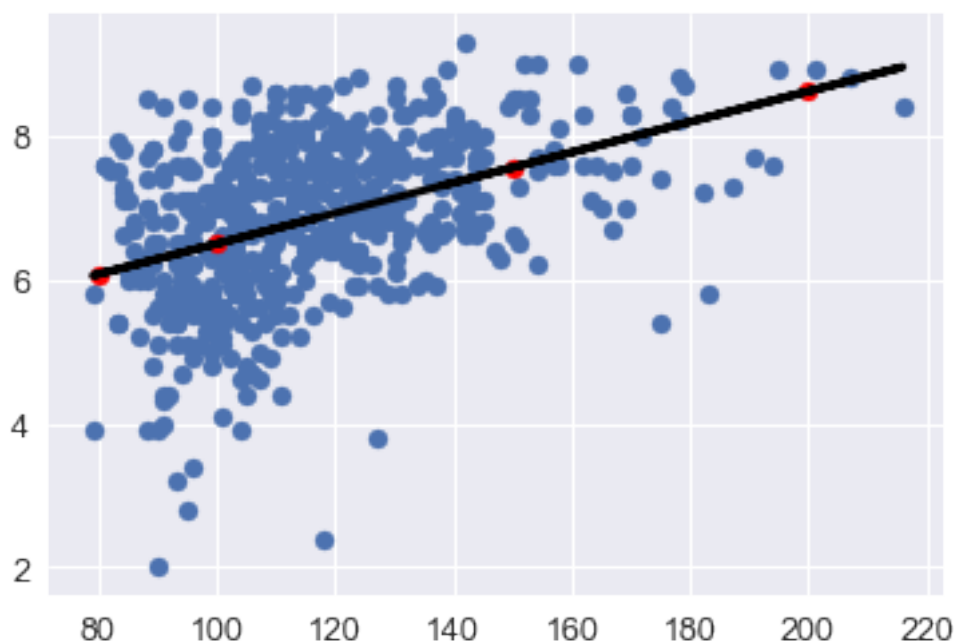
The determinacy coefficient and mean absolute error:

```
classifier.score(training_x, training_y)
Out[14]: 0.18600394479373705
mean_absolute_error(training_y, predicted_y)
Out[15]: 0.7823580398705626
```

The determinacy coefficient is 0.186, which is very low value. At the same time mean absolute error is very high: at 0.782. It shows that the regression model works really bad on these features.

Nevertheless, we try to predict values of rating by the length of movie. We take four values for the length of the movie: [80, 100, 150, 200] minutes. The predicted ratings are: [6.0716766 , 6.49455604, 7.55175466, 8.60895327].

```
lengths_to_predict = np.array([60, 90, 150])
predicted_ratings = classifier.predict(lengths_to_predict.reshape(-1, 1))
```



## 6 Conclusion

In this project we explore the data on movies. The first section contains the description of the dataset and some hypothesis. In the next section we apply the clustering methods to analyze the data. The third section contains the contingency table analysis,  $\chi^2$  and Quetelet index. In the next one we study the hidden factors by principal component analysis. Then, we use 2D regression to find few more patterns.

The main feature of the consideration was the number of on-screen deaths in the movies. There are several things of great interest among the patterns and correlations that we found. The old films, which were filmed before 1980 stay aside from the others as they are mostly long and highly-rated. Modern films, of course, have a higher amount of deaths. And the films with a lot of violence are rated with stronger restrictions by MPAA.

PC analysis revealed the high ability of IMDB rating to describe the other numerical features, as it is the main contributor to the first component. That shows that the ratings really reflect some important properties and summarize them.

## 7 Applications

### 1. MPAA Ratings interpretation. Source: [MPAA](#)

- **G General audiences.** All ages admitted. Nothing that would offend parents for viewing by children.
- **PG Parental Guidance Suggested.** Some material may not be suitable for children. Parents urged to give "parental guidance". May contain some material parents might not like for their young children.
- **M:** Suggested for Mature Audiences parental discretion advised (before 1984). The same as modern PG.
- **GP** All Ages Admitted Parental Guidance Suggested (before 1972). Renamed to PG.
- **PG-13 Parents Strongly Cautioned.** Some material may be inappropriate for children under 13. Parents are urged to be cautious. Some material may be inappropriate for pre-teenagers.
- **R Restricted.** Under 17 requires accompanying parent or adult guardian. Contains some adult material. Parents are urged to learn more about the film before taking their young children with them.
- **NC-17 Adults Only.** No One 17 and Under Admitted. Clearly adult. Children are not admitted.
- **X.** No one under 17 admitted (before 1984). Was renamed to NC-17