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

 $Homework\ Project\ 2018/2019$

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1 THE CHOICE OF THE DATASET

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

The sourse for the data is the thematic web-site moviebodycounts.com. This dataset was processed and published on 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 lenth 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

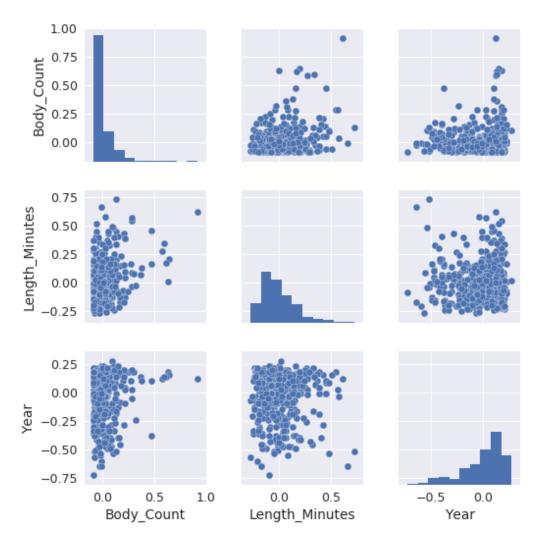
For this part of the task we choose three quantitative features: Body_Count, the number of on-screen deaths in the movie; Length_Minutes, the length in minutes; Year, the year of the release. These are quantitive features that, by our hypotheses, may be useful in cluster analysis of the dataset.

2.1 Preprocessing

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

```
In [11]: 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.

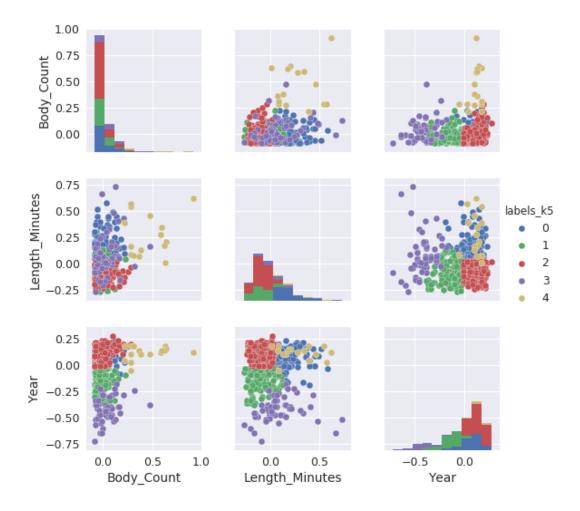


2.2 K-means application

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: 13.6126.

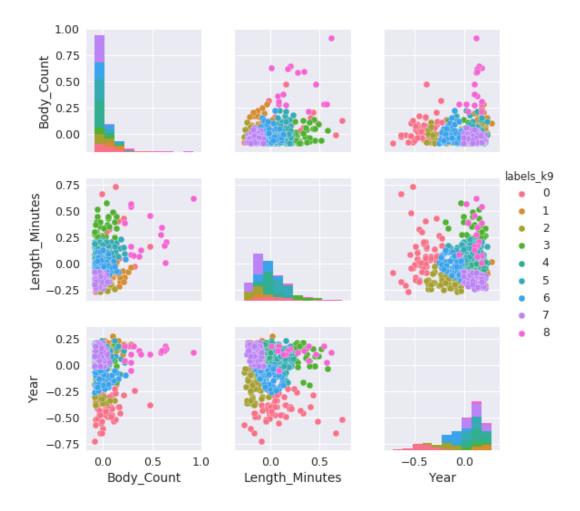
```
In [16]:
kmeans_k5 = KMeans(n_clusters=5, init='random', n_init=10, random_state=RANDOM_SEED)
kmeans_k5.fit(task_df)
task_df['labels_k5'] = pd.Series(kmeans_k5.predict(task_df))
print('Sum of squared distances from points to cluster centers, k=5:', kmeans_k5.inertia_)
sns.pairplot(task_df, hue='labels_k5', 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 (orange colored) is not large and contains movies with the highest number of deaths, they differ in length, and are relatively recent ones.

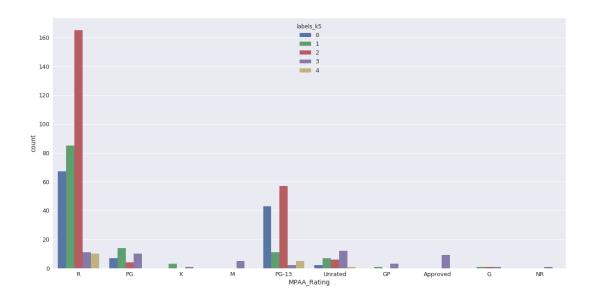
Now we apply K-means at k=9 and get a lot of smaller clusters:



Some clusters are obviously inherited from the pevious ones: new cluster 8 follows cluster 3 with the higest 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.

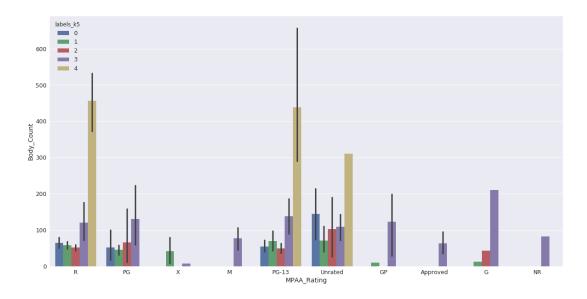
2.3 Interpretation

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



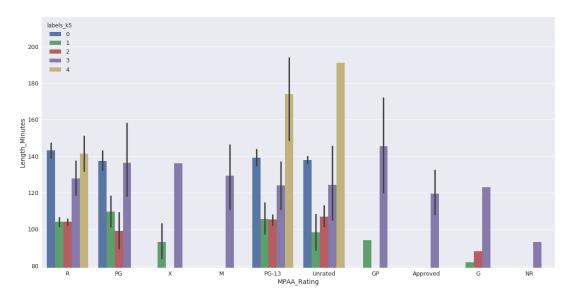
The plot shows the amount of movies of each rating in each cluster. For example we see that 165 R movies are in cluster 2. Clusters 0, 1, 2 aggregate the most part of the movies, mostly with R and PG-13 ratings. That may show that we have mostly adult films in the dataset. That is not a surprise due 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.



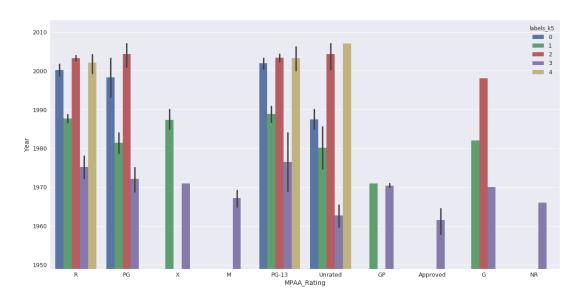
It's clear that cluster 4 contains the movies with the highest body count, as was supposed in the cluster interpretation. It contains the PG-13 movie with the highest body count in the dataset (836): "Lord of the Rings: Return of the King". The highest point of the black bars shows this movie.

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 avearage 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.



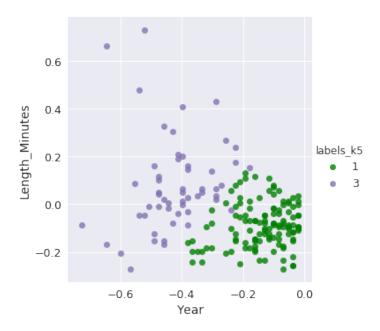
It can be seen that the cluster 3 contains mostly old movies, as was discovered before. Now we can see that these are mostly pre-1980 movies.

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.

2.4 Bootstrap

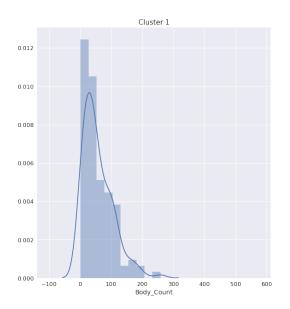
In this part of the paper we inspect two clusters: 1 and 3. As was mentioned, cluster 3 contains mostly old, pre-1980 movies and cluster 1 has movies from the 90-s.

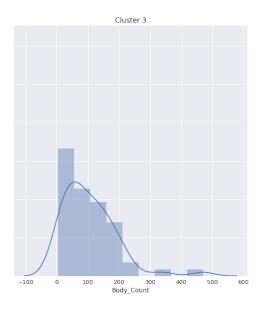
First, we consider length and release year, and then we focus on our main feature, the body count. From the scatter plot the difference between the clusters can be clearly seen.



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

```
In [48]:
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])
```



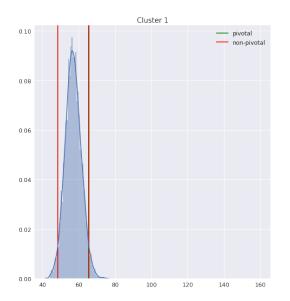


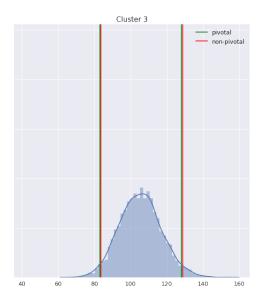
The parameters of the distributions are listed in the table. The distributions seem to be different but we cannot be sure as the samples are rather small.

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 it 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.

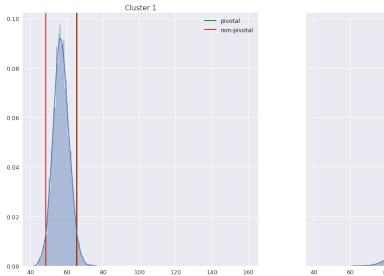
```
In [91]: def bootstrap sample(vec, size):
return np.random.choice(vec, size=(vec.shape[0], size), replace=True)
def bootstrap means(srs,
                            sample amount=5000):
  samples ix = bootstrap sample(srs.index, size=sample amount).T
  means = np.array([srs.loc[sample].mean() for 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):
```

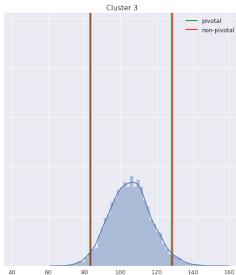
```
if not ax:
    ax = plt.gca()
for x in confidence_interval_pivotal(vec):
    line = ax.axvline(x=x, color='g')
line.set_label('pivotal')
for x in confidence_interval_non_pivotal(vec, 95):
    line = ax.axvline(x=x, color='r')
line.set_label('non-pivotal')
ax.legend(loc='best')
return sns.distplot(vec, 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:

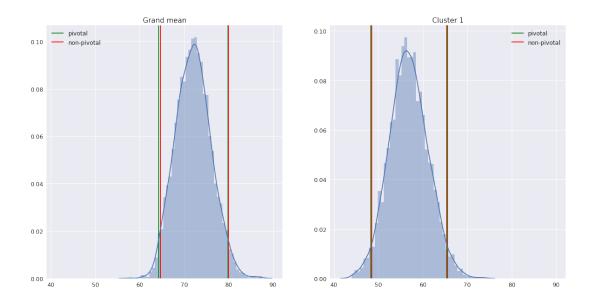
Parameter	Cluster 1	Grand mean
mean	56.844	72.157
pivotal	(48.317, 65.371)	(64.374, 79.340)
non-pivotal	(48.474, 65.590)	(64.65, 80.238)

Comparison between the grand mean and cluster 0:





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
- 4 PCA: Hidden Factor & Data visualization
- 5 2D regression
- 6 Applications
 - 1. MPAA Ratings interpretation. Sourse: 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