HomeAsignment

December 5, 2016

HA #1 Report on choosing dataset

Dataset history

The dataset comes from a 1994 study about the population biology of blacklip abalone (Haliotis rubra) from the North Coast and Islands of Bass Strait. It was published to the UCI Machine Learning Repository in 1995 by Sam Waugh from the Department of Computer Science at the University of Tasmania (Australia). The original dataset was modified by removing objects with missing values and scaling continuous values by dividing by 200.

Relevant information paragraph

The general problem of the dataset is the age (and thus count of rings) prediction of the abalone using its phisical measurements. In order to get the age of abalone the scientist should cut the shell through the cone at first, stain it and then count up its rings using microscope. Thereby it is time-consuming and definitely dull task. In that case the problem is sufficiently substantial. So, the principal reason I choose this dataset is its striking canonicity. Saying that I mean there are both nominal and real valued features, the amount of features and objects is good enought and, in addition, there is absence of missing data. Thus, the abalone dataset is highly prepared and comfortable for educational purpose. So, I hope I will be enjoy working on that though my Core Data Analysis course. It is clear. It is pleasant to calculate. So I suppose it is like Dostoevsky in Russian literature or Van Gogh art, it is a kind of Computer Science genre classics. That is why I choose the ablone dataset.

Explanation of the data (Attributes)

There are 8 features. Next I will descrbe them all with its accepted values. Sex is the nominal feature with the value from the set {M, F, I(infant)}. All next features were scaled by dividing by 200. Length feature is the longest shell measurement which takes values from the interval (0.075, 0.815). Diameter is a continuous feature which is perpendicular to length. Its values are from 0.055 to 0.650. Height is the vertical shell measurement with meat in particular. Whole weight (whole_w in table) is an abalon's full weight with the value from 0.002 to 2.826. Cognitively to note that the black abalone has sufficiently large mass. Sometimes it reaches up to 565 grams and more. Shucked weight is the meat mass measurement (without the shell, which is logical). Shucked_w's values are between 0.001 and 1.488 (which is 0.2 and 297.6 grams, respectively, in original dataset). The Viscera weight comes after the bleeding, so it is a gut weight taking values from 0.001 to 0.760 (grams dividing by 200). Next measurement is a shell mass after being dried, which is important to note, because of the fact that similar abalones can collect significantly different amount of water. And the target variable is a rings count what refers to the age by adding 1.5 year for each ring.

There are 4177 instances with 8 features

The dataset is located in "abalone.csv" file. Each string means 1 object with features separating by "," symbol.

Statistics additionals

The following table shows some statistic information like mean and standart diviation.

```
       Length    Diam      Height    Whole     Shucked  Viscera  Shell    Rings
Mean   0.524     0.408    0.140    0.829    0.359    0.181    0.239    9.934
SD   0.120   0.099    0.042    0.490    0.222    0.110    0.139    3.224
```

Finally, a few words about the **technologies** I use.

Core language is python v3.4. Pandas is the python's module for visualization and simple data processing. I use numpy for comfortable matrix operations and matplotlib for a graphical representation of data. In the end, sklearn python module is a powerful set of the most common machine learning tackle including the regression.

Next, I will try to comment on the nontrivial areas to clarify the situation.

HA #2 Gaussian, 95% confidence interval, bootstrap for the distribution of the mean

```
In [2]: import warnings
        warnings.filterwarnings('ignore')
        import sys
        import itertools
        import pandas as pd
        import numpy as np
        import math
        import matplotlib.pyplot as plt
        from random import randint
        %matplotlib inline
        from sklearn.model_selection import KFold
        from sklearn.metrics import accuracy_score, precision_score, recall_score,
```

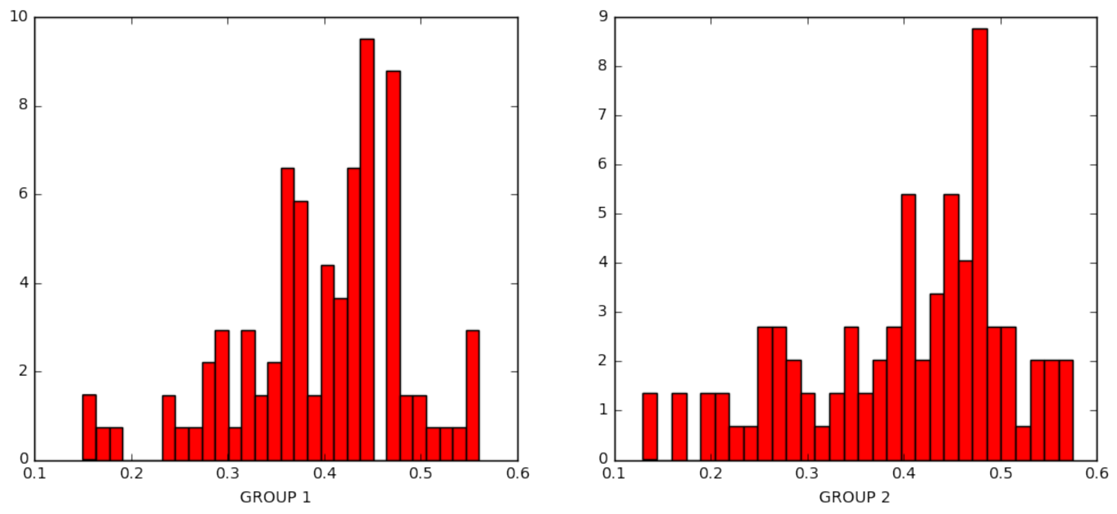
```
In [5]: pass_data = pd.read_csv('abalone.csv', header=None)
        pass_data.columns = ['Sex', 'Length', 'Diameter', 'Height', 'Whole_w', 'Shu
        pass_data.head(10) #there is data sample
```

```
Out[5]:   Sex  Length  Diameter  Height  Whole_w  Shucked_w  Viscera_w  Shell_w  Ri
        0   M   0.455     0.365   0.095   0.5140     0.2245     0.1010    0.150
        1   M   0.350     0.265   0.090   0.2255     0.0995     0.0485    0.070
        2   F   0.530     0.420   0.135   0.6770     0.2565     0.1415    0.210
        3   M   0.440     0.365   0.125   0.5160     0.2155     0.1140    0.155
        4   I   0.330     0.255   0.080   0.2050     0.0895     0.0395    0.055
        5   I   0.425     0.300   0.095   0.3515     0.1410     0.0775    0.120
        6   F   0.530     0.415   0.150   0.7775     0.2370     0.1415    0.330
        7   F   0.545     0.425   0.125   0.7680     0.2940     0.1495    0.260
        8   M   0.475     0.370   0.125   0.5095     0.2165     0.1125    0.165
        9   F   0.550     0.440   0.150   0.8945     0.3145     0.1510    0.320
```

i form two groups of abalones consist of 100 elements each and analyse its "diameter" feature as x

```
In [4]: ab_diams1 = np.array(list(pass_data["Diameter"][:100]), dtype=float)
        ab_diams2 = np.array(list(pass_data["Diameter"][100:200]), dtype=float)
        print("mean of the first group", ab_diams1.mean(), "|", "mean of the secon
mean of the first group 0.3948 | mean of the second group 0.4009
```

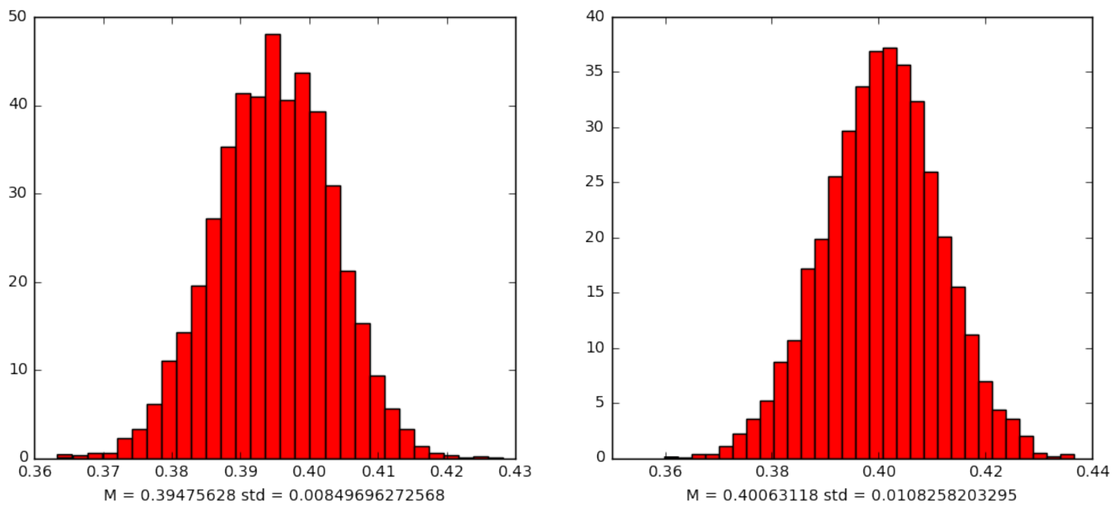
```
In [5]: plt.figure(figsize=(12, 5))
        plt.subplot(121)
        plt.xlabel("GROUP 1")
        bins1 = plt.hist(ab_diams1, 30, normed=1, facecolor='red', alpha=1)

        plt.subplot(122)
        plt.xlabel("GROUP 2")
        bins1 = plt.hist(ab_diams2, 30, normed=1, facecolor='red', alpha=1)
```



the question (it arose from the comparison of the means): whether snails in the second group have more wide shells in average than in the second or not? It is not clear from the graphs. Let's check it using bootstrap (i form 2 groups of vectors(5000 each) of abalones shell diameters with the length of 100 randomly from the first and second groups and then analyse the density func of difference with means in diam5000_1 and diam5000_2). We can do it thanks to central limit theorem (there are groups of 5000 independent mean values which limit to Gaussian function)

```
In [6]: diam5000_1 = np.array([[ab_diams1[randint(0, 99)] for i in range(100)] for
        diam5000_2 = np.array([[ab_diams2[randint(0, 99)] for i in range(100)] for
        means5000_1 = np.array([diam5000_1[i].mean() for i in range(5000)])
        means5000_2 = np.array([diam5000_2[i].mean() for i in range(5000)])
        mean5000_1 = means5000_1.mean()
        mean5000_2 = means5000_2.mean()
        std5000_1 = means5000_1.std()
        std5000_2 = means5000_2.std()
```

```
In [7]: plt.figure(figsize=(12, 5))
        plt.subplot(121)
        plt.xlabel("M = " + str(mean5000_1) + " std = " + str(std5000_1))
        bins1 = plt.hist(means5000_1, 30, normed=1, facecolor='red', alpha=1)

        plt.subplot(122)
        plt.xlabel("M = " + str(mean5000_2) + " std = " + str(std5000_2))
        bins2 = plt.hist(means5000_2, 30, normed=1, facecolor='red', alpha=1)
```



```
In [8]: print("abalones group 1 95% confidence interval ", (mean5000_1 - 1.96 * std
        print("abalones group 2 95% confidence interval ", (mean5000_2 - 1.96 * std

abalones group 1 95% confidence interval  (0.3781022330576666, 0.41141032694233332)
abalones group 2 95% confidence interval  (0.37941257215409091, 0.4218497878459091
```

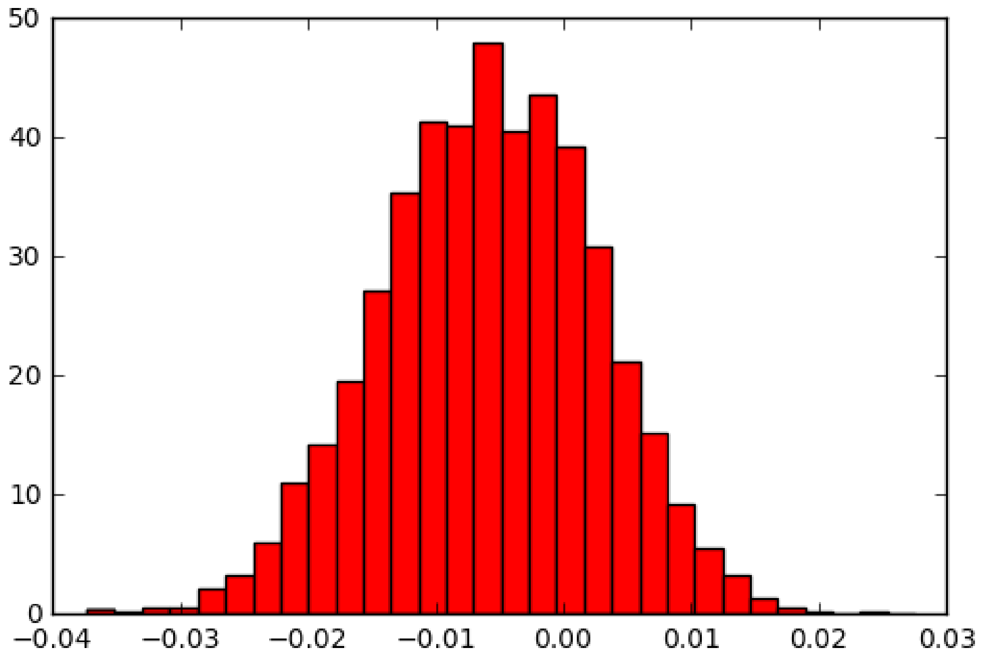
thus they INTERSECT. This time we can say nothing to answer the question.

```
In [9]: mean5000_diff = means5000_1 - mean5000_2
        mean_diff = mean5000_1 - mean5000_2
        int_ends = 1.96 * math.sqrt((math.pow(std5000_1, 2) / 5000) + (math.pow(std
        # print("MEAN", mean5000_diff.mean(), "| STD", mean5000_diff.std())
        print("95% confidence interval of the difference of the means:", (mean_dif
                                                                          mean_dif

95% confidence interval of the difference of the means: (-0.0062563673245446304, -0
```

so, there is no 0 point in interval and we can say that abalones of 2 groups are not equal (i mean the difference is not 0) in shell diameter feature with the confidence level of 95%. In addition, we can say that group 2 has greater shells in average because the difference confidens interval shifted to the negative side (left with respect to zero point) according to bootstrap method. This bias can also be shown by following histogram.

0.1 WERY WRONG CONCLUSION

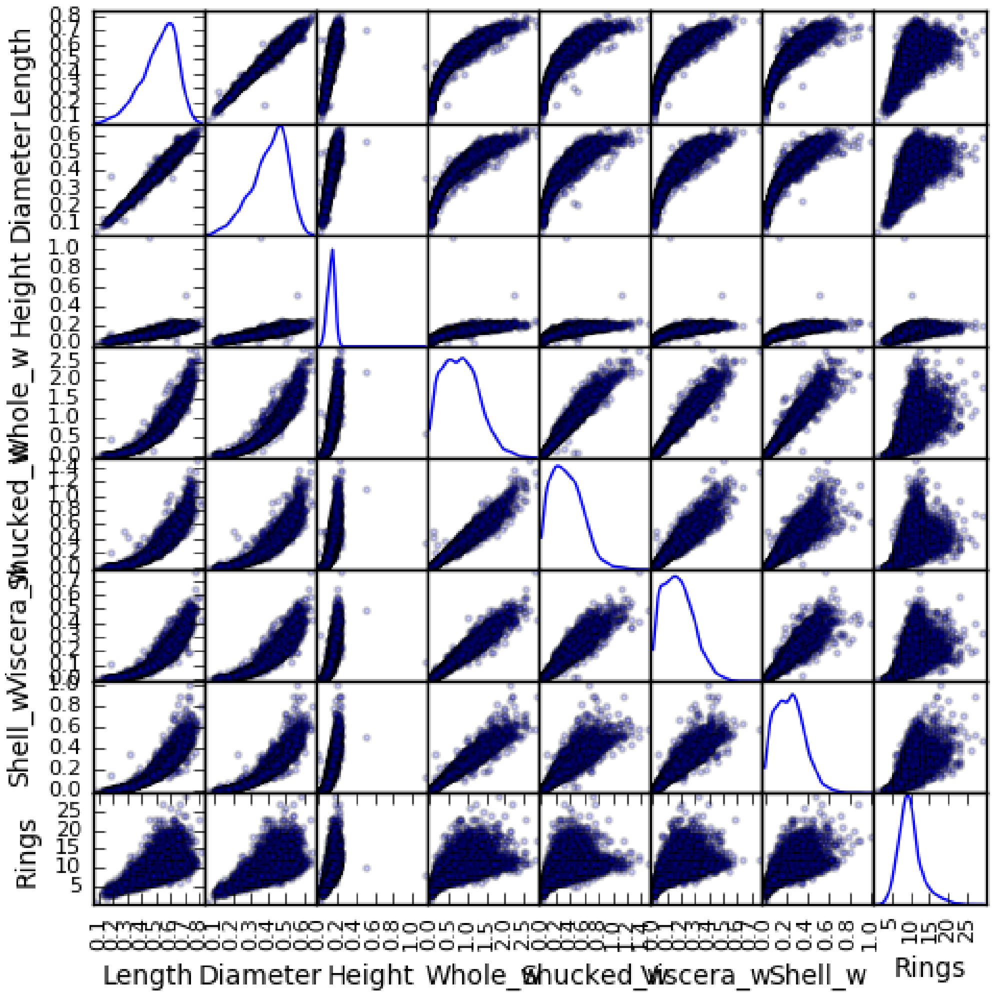
```
In [10]: bins = plt.hist(mean5000_diff, 30, normed=1, facecolor='red', alpha=1)
```



HA #3 Scatterplot, linear regression, correlation and determinacy coefficients

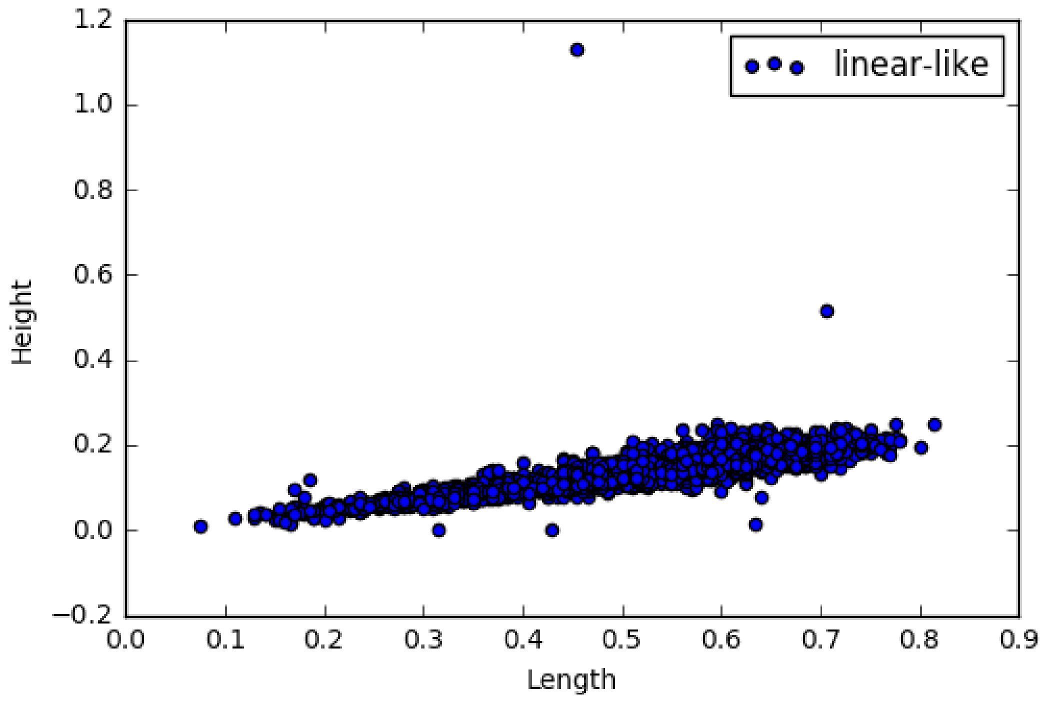
```
In [10]: from pandas.tools.plotting import scatter_matrix
```

```
In [8]: sc = scatter_matrix(pass_data, alpha=0.2, figsize=(6, 6), diagonal='kde')
```

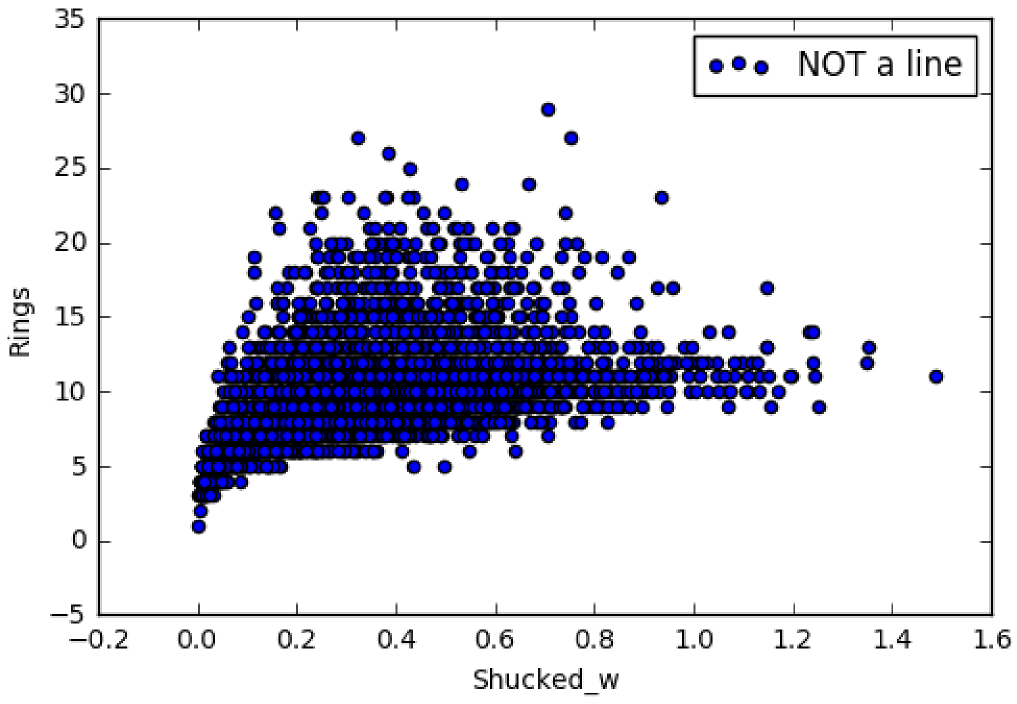


So, there are a lot of dependencies which look linear-like. In the following graph i've shown a Length-Height scatter plot which looks like a line most of all for me. What about non-linear, for instance, there is Whole_weight-Diameter plot, which looks like porabola. Also there are a lot of complex dependencies, like Shucked_weight-Rings. I have no idea what is it exactly, but i suppose it is not linear-like dependency (which is clear thanks to the fact that Rings count is the target variable of this data-set)

```
In [9]: s = pass_data.plot.scatter(x="Length", y="Height", label="linear-like")
```



```
In [4]: sc = pass_data.plot.scatter(x="Shucked_w", y="Rings", label="NOT a line")
```



Let's build a simple linear regression estimating a and b coefficient of a model. x-asix means lenght, y-axis means height.

$$y_i = ax_i + b + \varepsilon_i$$

Using the following formula.

$$\hat{b} = \bar{y} - \hat{a}\bar{x}$$

$$\hat{a} = \frac{\sum_i^n (x_i - \bar{x})(y_i - \bar{y})}{\sum_i^n (x_i - \bar{x})^2}$$

```
In [15]: X = np.array(list(pass_data["Length"]), dtype=float)
         Y = np.array(list(pass_data["Height"]), dtype=float)
         X_mean = np.mean(X)
         Y_mean = np.mean(Y)

         est_a = np.sum((X - X_mean) * (Y - Y_mean)) / np.sum((X - X_mean) ** 2)
         est_b = Y_mean - est_a * X_mean
         print("slope, a = ", est_a, "intersept, b = ", est_b)
```

```
slope, a =  0.288227930552 intersept, b =  -0.0115127591617
```

Accordingly to slope we can say, that, when the length of an abalone increases by 1 mm we predict that the height will increase by approximately ~0.288 mm.

```
In [16]: #make prediction
         Y_pred = est_a * X  + est_b
         #r coef
         Correlation = np.corrcoef(Y, Y_pred)[0][1]
         #R^2 calc
         Determinacy_coef = Correlation ** 2 # Unfortunately, the specific func fo

         print("r correlation coef =", Correlation, "| R^2 determinacy coef =", Det
```

```
r correlation coef = 0.827553609319 | R^2 determinacy coef = 0.684844976297
```

The sign of r means the sign of slope a. so if lenght of abalone grows the height grows too. The value of r ~0.827 is located near the 1. It indicates how closely spaced points to a straight line. 0.827 means very good (but not excellent) linear correlation. R^2 ~0.68 is a proportion of the variance of dispersion Y which is tacken into account by regressin of Y over X. 0.68 is ok for reasonable linear model (it should be at least 0.5)

NOT COMPULSORY Estimate the 95% confidence intervals of the slope, intercept, and correlation coefficient by using a 5000 strong bootstrap resampling technique

```
In [24]: slope_set = []
         intersept_set = []
         correlation_set = []
         abalone_set_size = pass_data.shape[0]
```

```
        for i in range(5000):
            FOO = np.array(pass_data[["Length", "Height"]].sample(n=abalone_set_si
            X = FOO[:, 0] #lenght
            Y = FOO[:, 1] #height
            X_mean = np.mean(X)
            Y_mean = np.mean(Y)
            est_a = np.sum((X - X_mean) * (Y - Y_mean)) / np.sum((X - X_mean) ** 2
            est_b = Y_mean - est_a * X_mean
            Y_pred = est_a * X  + est_b
            Correlation = np.corrcoef(Y, Y_pred)[0][1]
            #fill sets with estimations
            slope_set.append(est_a)
            intersept_set.append(est_b)
            correlation_set.append(Correlation)
```

To make things easier i will be using a non-pivotal method building intervals

```
In [19]: slope_set.sort()
         print("95% confidence interval for slope using bootstrap:", slope_set[125]
         #cut off 5% of values (2.5% from each side)
         intersept_set.sort()
         print("95% confidence interval for intersept using bootstrap:", intersept_
         correlation_set.sort()
         print("95% confidence interval for correlation using bootstrap:", correlat

95% confidence interval for slope using bootstrap: 0.283191585762 0.293251537416
95% confidence interval for intersept using bootstrap: -0.0140880689942 -0.00863279
95% confidence interval for correlation using bootstrap: 0.722545435808 0.90325820
```

Well, this intervals cover estimated sclope, intersept and correlation score with the 95% probability. In addition, we can see that this intervals cover an estimations that we found at previous task. The resulting estimates are close to the centers of the intervals.

HA #4 Cross-validation for testing prediction methods and fitting regression by using nature-inspired approaches

```
In [133]: # i will build a linear regression y = a * X + b like in the previous tas
          X = np.array(list(pass_data["Length"]), dtype=float)
          y = np.array(list(pass_data["Height"]), dtype=float)
          y[y == 0] = 0.00001

In [161]: #put every item randomly into one of 10 buckets
          indices_in_buckets = [[] for i in range(10)]
          for i in range(X.shape[0]):
              indices_in_buckets[np.random.randint(0, 10)].append(i)

          MSE_over_each_fold = []
          all_idx = set([i for i in range(X.shape[0])])
          for indices in indices_in_buckets:
```

```
        X_train, X_test = X[list(all_idx - set(indices))], X[indices]
        y_train, y_test = y[list(all_idx - set(indices))], y[indices]
        #build a regression over X_train and test on X_test
        X_tr_mean = np.mean(X_train)
        y_tr_mean = np.mean(y_train)
        est_a = np.sum((X_train - X_tr_mean) * (y_train - y_tr_mean)) / np.su
        est_b = y_tr_mean - est_a * X_tr_mean
        y_pred = est_a * X_test + est_b
        MSE_over_each_fold.append(((y_test - y_pred) ** 2).mean())
```

```
In [162]: MSE_over_each_fold
```

```
Out[162]: [0.000616174864292801,
           0.00026493464275016259,
           0.00026205201298679787,
           0.00023442159709623144,
           0.00025130582879782091,
           0.00025700944394991458,
           0.00032155498159154372,
           0.00031960571032660893,
           0.0026604600546613695,
           0.00027274003124381656]
```

```
In [163]: np.array(MSE_over_each_fold).mean()
```

```
Out[163]: 0.0005460259167697067
```

Thus, thanks to 10-fold cross-validation we can say how well the algorithm works for data at which it was not trained. In some parts it works better, in others it works worse, but it's pretty nice in average. Cross-validation gives us an idea about the quality of the algorithm on the new data.

Nature Inspired algorithm

```
In [155]: # here i wrote a simple class which is doing a nature inspired alorithm t

          def compute_relative_average_error(a, b, X, y):
              y_pred = a * X + b
              error = np.absolute(y_pred - y) / y
          #     error = (y_pred - y) ** 2
              return error.mean()


          class NatureInspired():
              def __init__(self, X, y, max_iter=100):
                  self.X = np.array(X)
                  self.y = np.array(y)
                  self.max_iter = max_iter
          #         compute boundary constants
                  def get_boundaries():
```

```
            a = []
            b = []
            for i, j in itertools.combinations(list(range(self.X.shape[0]
                if (self.X[i] - self.X[j]) != 0:
                    a.append((self.y[i] - self.y[j]) / (self.X[i] - self.
                    b.append((self.X[i] * self.y[j] - self.X[j] * self.y

#               print(a)
            a = sorted(a)[(len(a) // 5):(len(a) // 5) * 4]
            b = sorted(b)[(len(b) // 5):(len(b) // 5) * 4]
            a = np.array(a)
            b = np.array(b)

            return a.min(), a.max(), b.min(), b.max()

        self.am, self.Am, self.bm, self.Bm = get_boundaries()
#           print(self.am, self.Am, self.bm,  self.Bm)

        self.p = 100
        self.f = np.hstack((np.random.uniform(low=self.am, high=self.Am,
        self.elite = 0
        self.f_next = np.copy(self.f)


    def get_elite(self):
        rel_errors_means = np.array([compute_relative_average_error(a, b,
        print("min mean rel err:", rel_errors_means.min())
        return self.f[rel_errors_means.argmin()]


    def normalize_population(self):
        for idx, unit in enumerate(self.f_next):
            if unit[0] < self.am:
                self.f_next[idx, 0] = self.am
            elif unit[0] > self.Am:
                self.f_next[idx, 0] = self.Am
            if unit[1] < self.bm:
                self.f_next[idx, 1] = self.bm
            elif unit[1] > self.am:
                self.f_next[idx, 1] = self.Bm


    def do_mutation(self):
        self.f_next = self.f + (np.random.normal(size=(self.p, 2)) * (np.


    def run(self):
        self.elite = self.get_elite()
```

```
                for i in range(self.max_iter):
                    self.do_mutation()
                    self.normalize_population()
                    new_elite = self.get_elite()
                    self.elite = new_elite if compute_relative_average_error(new_
                    self.f = 0.7 * self.f_next + 0.3 * np.repeat([self.elite], se
```

```
In [156]: NI = NatureInspired(X=X, y=y)
          NI.run()
```

```
min mean rel err: 1.32092493424
min mean rel err: 1.31950159028
min mean rel err: 1.32085962743
min mean rel err: 1.32258826422
min mean rel err: 1.32611968459
min mean rel err: 1.27242436215
min mean rel err: 1.28963200875
min mean rel err: 1.29151780928
min mean rel err: 1.28325252977
min mean rel err: 1.28487633703
min mean rel err: 1.28088087467
min mean rel err: 1.27974725498
min mean rel err: 1.2781514729
min mean rel err: 1.28019968952
min mean rel err: 1.28133387898
min mean rel err: 1.27732662076
min mean rel err: 1.27856284553
min mean rel err: 1.28003140065
min mean rel err: 1.2765909655
min mean rel err: 1.27451729675
min mean rel err: 1.27131614901
min mean rel err: 1.27204797403
min mean rel err: 1.27443199279
min mean rel err: 1.27445094198
min mean rel err: 1.27524565376
min mean rel err: 1.275227704
min mean rel err: 1.2739351123
min mean rel err: 1.27332155211
min mean rel err: 1.27154537574
min mean rel err: 1.27043758861
min mean rel err: 1.27004553088
min mean rel err: 1.27020497628
min mean rel err: 1.26905537984
min mean rel err: 1.26800446413
min mean rel err: 1.26983374827
min mean rel err: 1.26669480787
min mean rel err: 1.26602918183
min mean rel err: 1.26705475808
min mean rel err: 1.26654762427
min mean rel err: 1.26699402993
min mean rel err: 1.26905981752
min mean rel err: 1.26630446266
min mean rel err: 1.26901781209
min mean rel err: 1.26681968496
min mean rel err: 1.26615941015
min mean rel err: 1.26603439121
min mean rel err: 1.26770565071
min mean rel err: 1.26540241672
min mean rel err: 1.26773671285
min mean rel err: 1.26244482625
min mean rel err: 1.2640968375
min mean rel err: 1.2623851241
min mean rel err: 1.26473746035
min mean rel err: 1.26426134701
min mean rel err: 1.2620763239
min mean rel err: 1.26265178943
min mean rel err: 1.25920569866
min mean rel err: 1.2631538538
min mean rel err: 1.26289856847
min mean rel err: 1.26109239404
min mean rel err: 1.26207678206
min mean rel err: 1.26034394165
min mean rel err: 1.26007339957
min mean rel err: 1.25949417913
min mean rel err: 1.25967876979
min mean rel err: 1.2526446858
min mean rel err: 1.2580699934
min mean rel err: 1.25792502331
min mean rel err: 1.25580109826
min mean rel err: 1.25448768899
min mean rel err: 1.25589668804
min mean rel err: 1.25556029195
min mean rel err: 1.25504703801
min mean rel err: 1.25187638451
min mean rel err: 1.25245478225
min mean rel err: 1.25309264241
min mean rel err: 1.25328629109
min mean rel err: 1.25234110324
min mean rel err: 1.25251954345
min mean rel err: 1.25383449638
min mean rel err: 1.25087046953
min mean rel err: 1.25197460793
min mean rel err: 1.24865642955
min mean rel err: 1.24914900505
min mean rel err: 1.24996313328
min mean rel err: 1.24981719686
min mean rel err: 1.2455553094
min mean rel err: 1.24619330903
min mean rel err: 1.24689150569
min mean rel err: 1.24748646674
min mean rel err: 1.24604062474
min mean rel err: 1.24471267826
min mean rel err: 1.243436702
min mean rel err: 1.24419075056
min mean rel err: 1.24365338011
min mean rel err: 1.23894476864
min mean rel err: 1.24060360018
min mean rel err: 1.236636457
min mean rel err: 1.2386494357
min mean rel err: 1.23884194742
min mean rel err: 1.23641897997
```

Well, we can see that the average relative error decreases (in general) from generation to generation. This algorithm can also minimize MSE and reachs a result such as CV-score in previous task of this home assignment (i mean 0.00055). For this porpose we need just change one error to another in function compute_relative_average_error, which is simple. Next, i print an elite a and b from last generation (i built 100 of them).

```
In [157]: NI.elite
```

```
Out[157]: array([ 0.16718049, -0.0526545 ])
```

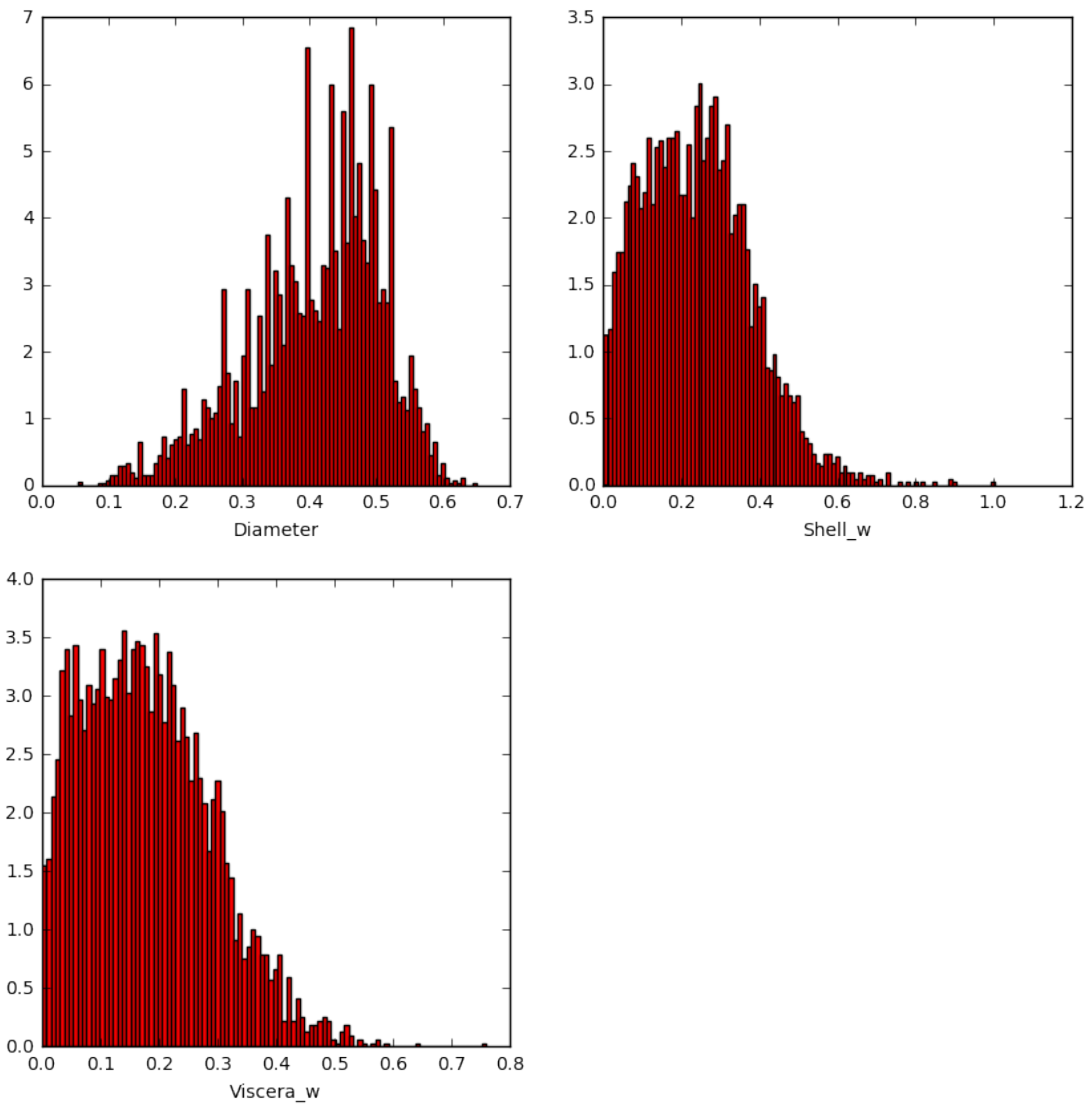
As a result we have a prediction rule y = 0.16718049 * X - 0.0526545, according to 100-th generation using NI approach.

HA #5 Contingency table, Quetelet index, Pearson chi-squared coefficient, visualization of association patterns

```
In [165]: pass_data.head(1)
```

```
Out[165]:    Sex  Length  Diameter  Height  Whole_w  Shucked_w  Viscera_w  Shell_w
          0   M   0.455     0.365   0.095    0.514     0.2245      0.101     0.15
```

```
In [16]: #compute hists to generate nominal features from quantitative
         plt.figure(figsize=(10, 10))
         plt.subplot(221)
         plt.xlabel("Diameter")
         bins1 = plt.hist(pass_data['Diameter'], 100, normed=1, facecolor='red', al

         # plt.figure(figsize=(10, 10))
         plt.subplot(222)
         plt.xlabel("Shell_w")
         bins1 = plt.hist(pass_data['Shell_w'], 100, normed=1, facecolor='red', alp
         # plt.figure(figsize=(10, 10))
         plt.subplot(223)
         plt.xlabel("Viscera_w")
         bins1 = plt.hist(pass_data['Viscera_w'], 100, normed=1, facecolor='red', a
```



```
In [22]: # I develope 3 nominal features by following thresholds
         Diam = [0, 0.3, 0.445, 0.53, 0.7]
         Shel_w = [0, 0.14, 0.22, 0.32, 1.2]
         vincera_w = [0, 0.066, 0.28, 0.8]

In [23]: Vincera_w_and_diam_category = pd.DataFrame(columns=['D1', 'D2', 'D3', 'D4'
         Vincera_w_and_shell_w_category = pd.DataFrame(columns=['S1', 'S2', 'S3', '
In [24]: for i in range(3):
             for j in range(4):
                 Vincera_w_and_diam_category.ix[i, j] = pass_data[(pass_data['Diame
                 Vincera_w_and_shell_w_category.ix[i, j] = pass_data[(pass_data['Sh
```

```
In [25]: Vincera_w_and_diam_category['Total'] = Vincera_w_and_diam_category.sum(axi
         Vincera_w_and_diam_category.ix[3,:] = Vincera_w_and_diam_category.sum(axis
         Vincera_w_and_shell_w_category['Total'] = Vincera_w_and_shell_w_category.s
         Vincera_w_and_shell_w_category.ix[3,:] = Vincera_w_and_shell_w_category.su
```

```
In [26]: Vincera_w_and_diam_category
```

```
Out[26]:           D1      D2      D3     D4    Total
         V1     596.0   124.0     0.0    0.0    720.0
         V2      25.0  1630.0   987.0   37.0   2679.0
         V3       0.0    13.0   465.0  300.0    778.0
         Total  621.0  1767.0  1452.0  337.0   4177.0
```

```
In [27]: Vincera_w_and_shell_w_category
```

```
Out[27]:            S1     S2      S3      S4   Total
         V1      714.0    5.0     0.0     1.0   720.0
         V2      424.0  807.0  1013.0   435.0  2679.0
         V3        0.0    3.0    83.0   692.0   778.0
         Total  1138.0  815.0  1096.0  1128.0  4177.0
```

```
In [28]: concontingency_t_diam = Vincera_w_and_diam_category.copy()
         concontingency_t_shell_w = Vincera_w_and_shell_w_category.copy()
         for i in range(3):
             concontingency_t_diam.ix[i,:-1] /= concontingency_t_diam.ix[3,:-1]
             concontingency_t_shell_w.ix[i,:-1] /= concontingency_t_shell_w.ix[3,:-

         concontingency_t_diam = concontingency_t_diam.round(3)
         concontingency_t_shell_w = concontingency_t_shell_w.round(3)
```

```
In [29]: # next i presented 2 conditional frequency tables
         concontingency_t_diam
```

```
Out[29]:            D1        D2       D3      D4   Total
         V1       0.96     0.070     0.00    0.00   720.0
         V2       0.04     0.922     0.68    0.11  2679.0
         V3       0.00     0.007     0.32    0.89   778.0
         Total  621.00  1767.000  1452.00  337.00  4177.0
```

There we can see, especially V1 given D1, V2 given D2 and V3 given D4, so, the almost conceptual rules are: D1 -> V1, D2 -> V2, D4 -> V3

```
In [30]: # conditional frequency
         concontingency_t_shell_w
```

```
Out[30]:              S1        S2         S3         S4    Total
         V1        0.627     0.006      0.000      0.001    720.0
         V2        0.373     0.990      0.924      0.386   2679.0
         V3        0.000     0.004      0.076      0.613    778.0
         Total  1138.000   815.000   1096.000   1128.000   4177.0
```

There we can see, especially V1 given S1, V2 given S2 and V3 given S4, so, the almost conceptual rules are: S2 -> V2, S4 -> V3, S1 -> V1

```
In [31]: # i calculate q(Vk|Sk) & q(Vk|Dl) using formula on slide 24
         Quetelet_relative_idx_t_diam = Vincera_w_and_diam_category.copy()
         Quetelet_relative_idx_t_shell_w = Vincera_w_and_shell_w_category.copy()

         Quetelet_relative_idx_t_diam = Quetelet_relative_idx_t_diam.drop(['Total']
         Quetelet_relative_idx_t_shell_w = Quetelet_relative_idx_t_shell_w.drop(['T

         Quetelet_relative_idx_t_diam['P(Vk)'] = Quetelet_relative_idx_t_diam.sum(a
         Quetelet_relative_idx_t_shell_w['P(Vk)'] = Quetelet_relative_idx_t_shell_w

         Quetelet_relative_idx_t_diam.ix[3,:] = Quetelet_relative_idx_t_diam.sum(ax
         Quetelet_relative_idx_t_shell_w.ix[3,:] = Quetelet_relative_idx_t_shell_w.

         for i in range(3):
             Quetelet_relative_idx_t_diam.ix[i,:-1] /= Quetelet_relative_idx_t_diam
             Quetelet_relative_idx_t_shell_w.ix[i,:-1] /= Quetelet_relative_idx_t_s


         # Quetelet calculations
         for j in range(4):
             Quetelet_relative_idx_t_diam.ix[:-1,j] -= Quetelet_relative_idx_t_diam
             Quetelet_relative_idx_t_diam.ix[:-1,j] /= Quetelet_relative_idx_t_diam
             Quetelet_relative_idx_t_shell_w.ix[:-1,j] -= Quetelet_relative_idx_t_s
             Quetelet_relative_idx_t_shell_w.ix[:-1,j] /= Quetelet_relative_idx_t_s

         Quetelet_relative_idx_t_diam = Quetelet_relative_idx_t_diam.round(3)
         Quetelet_relative_idx_t_shell_w = Quetelet_relative_idx_t_shell_w.round(3)
         Quetelet_relative_idx_t_diam.ix[:-1,:-1]
```

```
Out[31]:        D1      D2      D3      D4
         V1  4.568  -0.593  -1.000  -1.000
         V2 -0.937   0.438   0.060  -0.829
         V3 -1.000  -0.961   0.719   3.779
```

We intrested in the highest positive and negative values in this table. According to Quetelet index table we can say that on average the knowledge of D1 “adds” 456.8% to frequency of V1, the knowledge of D4 “adds” 377.9% to frequency of V3, similarly. On the other side, the knowledge of D4, for instance, reduces the frequency of V1 by 100%. We can interpret it similarly in other cases.

```
In [32]: Quetelet_relative_idx_t_shell_w.ix[:-1,:-1]

Out[32]:        S1     S2     S3     S4
         V1  2.640 -0.964 -1.000 -0.995
         V2 -0.419  0.544  0.441 -0.399
         V3 -1.000 -0.980 -0.593  2.294
```

According to this table we can say that the knowledge of S1 increases the frequency of V1 by 264% and, e.g. the knowledge of S2 reduces the frequency of V1 by 96.4% and so on.

Also i computed a summary Quetelet index which is the inner product of two tables that of co-occurrence relative frequency and Quetelet. For Viscera_w-Diam the result is Q = 1.155, it means that on average knowledge of Dl "adds" 115.5% to frequency of Vk. For Viscera_w-Shell_w the result is Q = 0.945, it means that on average knowledge of Sl "adds" 94.5% to frequency of Vk.

```
In [270]: # Comp chi-square-summary_quetelet_index over both tables
          # tables like on slide 37

          # Observed (relative) frequencies = first table
          first_table_diam = Vincera_w_and_diam_category.copy()
          first_table_shell = Vincera_w_and_shell_w_category.copy()
          first_table_diam /= pass_data.shape[0]
          first_table_shell /= pass_data.shape[0]
          first_table_diam = first_table_diam.round(3)
          first_table_shell = first_table_shell.round(3)

          # Frequencies expected under independence = second table
          second_table_diam = first_table_diam.copy()
          second_table_shell = first_table_shell.copy()
          for i in range(4):
              for j in range(4):
                  second_table_diam.ix[i, j] = second_table_diam.ix[i,4] * second_t
                  second_table_shell.ix[i, j] = second_table_shell.ix[i,4] * seconc

          second_table_diam = second_table_diam.round(3)
          second_table_shell = second_table_shell.round(3)

In [271]: first_table_diam

Out[271]:          D1     D2     D3     D4  Total
          V1    0.143  0.030  0.000  0.000  0.172
          V2    0.006  0.390  0.236  0.009  0.641
          V3    0.000  0.003  0.111  0.072  0.186
          Total 0.149  0.423  0.348  0.081  1.000

In [272]: first_table_shell

Out[272]:          S1     S2     S3     S4  Total
          V1    0.172  0.000  0.000  0.000  0.172
          V2    0.497  0.133  0.009  0.002  0.641
          V3    0.009  0.110  0.042  0.021  0.183
          Total 0.679  0.243  0.051  0.023  0.996
```

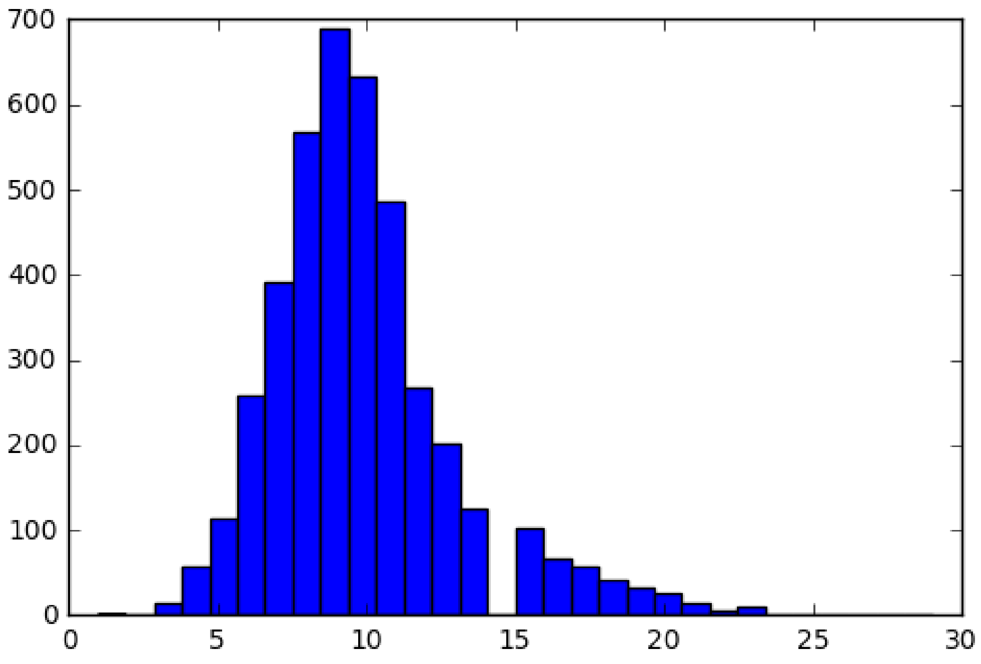
```
In [273]: second_table_diam

Out[273]:          D1     D2     D3     D4  Total
          V1     0.026  0.073  0.060  0.014  0.172
          V2     0.096  0.271  0.223  0.052  0.641
          V3     0.028  0.079  0.065  0.015  0.186
          Total  0.149  0.423  0.348  0.081  1.000

In [274]: second_table_shell

Out[274]:          S1     S2     S3     S4  Total
          V1     0.117  0.042  0.009  0.004  0.172
          V2     0.435  0.156  0.033  0.015  0.641
          V3     0.124  0.044  0.009  0.004  0.183
          Total  0.676  0.242  0.051  0.023  0.996

In [278]: # MAke r(k,l) tables
          r_k_l_diam_table = pd.DataFrame(columns=['D1', 'D2', 'D3', 'D4'], index=[
          r_k_l_shell_table = pd.DataFrame(columns=['S1', 'S2', 'S3', 'S4'], index=

          for i in range(3):
              for j in range(4):
                  r_k_l_diam_table.ix[i, j] = (first_table_diam.ix[i,j] - second_ta
                  r_k_l_shell_table.ix[i, j] = (first_table_shell.ix[i,j] - second_

In [279]: r_k_l_diam_table

Out[279]:          D1         D2         D3         D4
          V1   0.725603   -0.15915 -0.244949 -0.118322
          V2  -0.290474   0.228593  0.027529 -0.188567
          V3  -0.167332  -0.270396  0.180427  0.465403

In [280]: r_k_l_shell_table

Out[280]:           S1          S2          S3          S4
          V1    0.160794   -0.204939 -0.0948683 -0.0632456
          V2   0.0940042  -0.0582325  -0.132116  -0.106145
          V3   -0.326578    0.314643   0.347851   0.268794

In [285]: # X^2 calc
          print("X^2 viscera and diam:", (r_k_l_diam_table ** 2).sum().sum())
          print("X^2 viscera and shell:", (r_k_l_shell_table ** 2).sum().sum())

X^2 viscera and diam: 1.149041689715217
X^2 viscera and shell: 0.5207069460325856
```

1 NEEED TO COMMENT ON BY SLIDE 54# sd

HA #6 Tabular regression and correlation ratio

HI there! Now we build a tabular regression using Rings count as a target feature over Diameter and Shell_w

```
In [177]: h = plt.hist(pass_data['Rings'], bins=30)
```



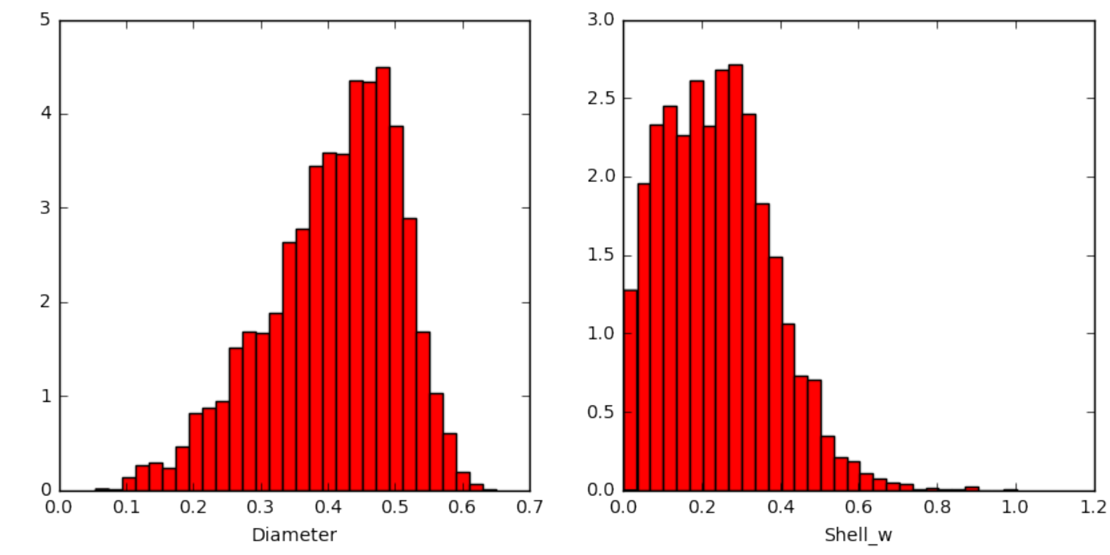
```
In [329]: rings_threshold = [0, 8, 12, 30]

In [330]: tab_regr_rings_diam = pd.DataFrame(columns=['num', 'diam mean', 'diam std
          tab_regr_rings_shell_w = pd.DataFrame(columns=['num', 'shell w mean', 'sh

          for i in range(4): #num
              this_group_data = pass_data[(pass_data['Rings'] > rings_threshold[i])

              tab_regr_rings_diam.ix[i, 'num'] = this_group_data.shape[0]
              tab_regr_rings_shell_w.ix[i, 'num'] = this_group_data.shape[0]

              tab_regr_rings_diam.ix[i, 'diam mean'] = this_group_data['Diameter'].
              tab_regr_rings_shell_w.ix[i, 'shell w mean'] = this_group_data['Shell

              tab_regr_rings_diam.ix[i, 'diam std'] = this_group_data['Diameter'].s
              tab_regr_rings_shell_w.ix[i, 'shell w std'] = this_group_data['Shell_
```

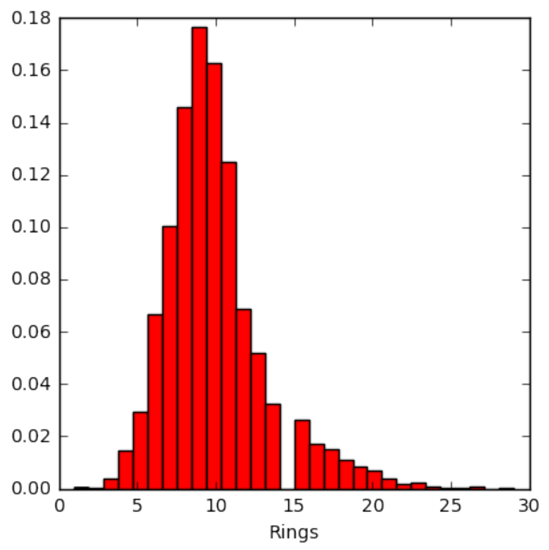
```
In [331]: tab_regr_rings_diam

Out[331]:         num diam mean   diam std
          young  1407  0.321276  0.0902919
          mat    2077   0.44799  0.0718845
          old     693  0.463506  0.0647218
          Total  4177  0.407881  0.0992399

In [332]: tab_regr_rings_shell_w

Out[332]:         num shell w mean shell w std
          young  1407     0.121394   0.0809648
          mat    2077     0.281119    0.113665
          old     693     0.350519    0.137686
          Total  4177     0.238831    0.139203

In [342]: # let's figure out the correlation ratio over two tabular regressions usi
          eta_diam = 1 - ((tab_regr_rings_diam.ix[:-1,0] / tab_regr_rings_diam.ix[-
          eta_shell = 1 - ((tab_regr_rings_shell_w.ix[:-1,0] / tab_regr_rings_shell

          print("Correlation ratio Rings/Diameter %.2f" % (eta_diam * 100), '%')
          print("Correlation ratio Rings/Shell_w %.2f" % (eta_shell * 100), '%')

Correlation ratio Rings/Diameter 38.97 %
Correlation ratio Rings/Shell_w 39.22 %
```

The second table shows the greater correlation. It means that relations are stronger between Rings and Shell_w than between Rings and Diameter.

HA #7 Prediction one binary feature by another one, metrics of accuracy

```
In [15]: #compute hists in order to binarize features (Diameter, Shell_w, Rings) i
         plt.figure(figsize=(10, 10))
         plt.subplot(221)
         plt.xlabel("Diameter")
         bins1 = plt.hist(pass_data['Diameter'], 30, normed=1, facecolor='red', alp

         plt.subplot(222)
         plt.xlabel("Shell_w")
         bins1 = plt.hist(pass_data['Shell_w'], 30, normed=1, facecolor='red', alph

         plt.subplot(223)
         plt.xlabel("Rings")
         bins1 = plt.hist(pass_data['Rings'], 30, normed=1, facecolor='red', alpha=
```





```
In [188]: X = pass_data[['Diameter', 'Shell_w', 'Rings']]

In [189]: X.head(1)

Out[189]:    Diameter  Shell_w  Rings
          0     0.365     0.15     15

In [190]: def binarize_diameter(x):
              return 0 if x < 0.46 else 1


          def binarize_shell_w(x):
              return 0 if x < 0.3 else 1
          def binarize_rings(x):
              return 0 if x < 10 else 1
```

```
In [191]: X['Diameter'] = X['Diameter'].apply(binarize_diameter)
          X['Shell_w'] = X['Shell_w'].apply(binarize_shell_w)
          X['Rings'] = X['Rings'].apply(binarize_rings)
          X.head(5)
```

```
Out[191]:    Diameter  Shell_w  Rings
          0         0        0      1
          1         0        0      0
          2         0        0      0
          3         0        0      1
          4         0        0      0
```

```
In [202]: # in this task I  use a constant prediction rule y_pred = X to predict ta
          # next, i build a prediction matrices(or confusion, which is equal) and c
          # including F1-measure and comment on the result

          # using the constant prediction rule
          # [[TP, FP],
          #  [FN, TN]]
          print("prediction table Rings-Diameter\n", confusion_matrix(X['Rings'], X
          print("prediction table Rings-Shell_w\n", confusion_matrix(X['Rings'], X[
          print("accuracy for diam:", accuracy_score(X['Rings'], X['Diameter']))
          print("accuracy for shell_w:", accuracy_score(X['Rings'], X['Shell_w']))
          precision_diam = precision_score(X['Rings'], X['Diameter'])
          precision_shell = precision_score(X['Rings'], X['Shell_w'])
          print("precision for diam:", precision_diam)
          print("precision for shell_w:", precision_shell)
          recall_diam = recall_score(X['Rings'], X['Diameter'])
          recall_shell = recall_score(X['Rings'], X['Shell_w'])
          print("recall for diam:", recall_diam)
          print("recall for shell_w:", recall_shell)
          print("F1 score for diam:", 2 * precision_diam * recall_diam / (precision
          print("F1 score for shell_w:", 2 * precision_shell * recall_shell / (prec
          # [[TP, FP],
          #  [FN, TN]]
```

```
prediction table Rings-Diameter
 [[1757  339]
 [ 918 1163]]
prediction table Rings-Shell_w
 [[1881  215]
 [ 954 1127]]
accuracy for diam: 0.699066315537
accuracy for shell_w: 0.720134067513
```

```
precision for diam: 0.774300932091
precision for shell_w: 0.839791356185
recall for diam: 0.558865929841
recall for shell_w: 0.541566554541
F1 score for diam: 0.649176667597
F1 score for shell_w: 0.658486707566
```

Thus, we can see that target feature predicted more accurately by binarized shell_w than by binarized diameter according to F1 score and accuracy. According to the precision score we can see the same situation. It means that by Shell_w we classified as 1-class the most part in truly 1-class targets than by Diameter. Next, according to recall, we found the opposite result. In that case we we classified the most part of 1-class targets by Diameter than by shell_w. So, using the constant prediction rule, we have good results in accuracy and precision in both ways to predict a target, but not so good in recall.

HA #8 K-means clustering

```
In [4]: # In this cell i wrote a simple class which is doing a version of K-means c
        #c_k - centers array
        #s_k - indices of items in original dataset which are covered by k-th class
        class KMeansClustering():

            def __init__(self, c_k, K):
                self.c_k = c_k #np.array
                self.s_k = [[] for i in range(K)] #indices in each class
                self.max_iter = 100


            def update_sets(self, X):
                def get_class(x):
                    distances = np.array([((c_k_i - x) ** 2).sum() for c_k_i in sel
                    return distances.argmin()

                self.s_k = [[] for i in range(len(self.s_k))]
                for idx, item in enumerate(X):
                    self.s_k[get_class(item)].append(idx)


                def update_centers(X):
                    c_k_dump = np.copy(self.c_k)
                    for i in range(self.c_k.shape[0]):
                        self.c_k[i] = X[self.s_k[i]].mean(axis=0)
                    self.c_k = self.c_k.round(4)

                    return c_k_dump

                return update_centers(X)
```

```
    def run(self, X): #required X matrix
        iterations = 0
        while np.count_nonzero(self.update_sets(X) != self.c_k):
            iterations += 1
            if iterations == self.max_iter:
                break
        return iterations
```

```
In [21]: # first of all i apply k = 3,4 and 7 with random generated (from uniform[(
         # to 4 quantitative features ['Length', 'Diameter', 'Whole_w', 'Shell_w']
         K = 3
         KMC = KMeansClustering(c_k=np.random.uniform(size=(K, pass_data[['Length',
         print(KMC.run(np.array(pass_data[['Length', 'Diameter', 'Whole_w', 'Shell_
         KMC.c_k

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Out[21]: array([[ 0.4033,  0.3077,  0.3488,  0.1057],
               [ 0.6657,  0.5252,  1.5683,  0.4383],
               [ 0.5717,  0.4477,  0.937 ,  0.2715]])

In [32]: K = 4
         KMC = KMeansClustering(c_k=np.random.uniform(size=(K, pass_data[['Length',
         print(KMC.run(np.array(pass_data[['Length', 'Diameter', 'Whole_w', 'Shell_
         KMC.c_k

21


Out[32]: array([[ 0.6861,  0.5414,  1.7413,  0.4834],
               [ 0.3652,  0.2768,  0.2564,  0.0786],
               [ 0.5198,  0.404 ,  0.6899,  0.2044],
               [ 0.6096,  0.4791,  1.1485,  0.3276]])

In [146]: K = 7
          KMC = KMeansClustering(c_k=np.random.uniform(size=(K, pass_data[['Length'
          print(KMC.run(np.array(pass_data[['Length', 'Diameter', 'Whole_w', 'Shell
          KMC.c_k

100


Out[146]: array([[    nan,     nan,     nan,     nan],
                [ 0.524 ,  0.4079,  0.8287,  0.2388],
                [    nan,     nan,     nan,     nan],
                [     nan,      nan,      nan,      nan],
                [     nan,      nan,      nan,      nan],
                [     nan,      nan,      nan,      nan],
                [     nan,      nan,      nan,      nan]])
```

Unfortunately, no one of more than 20 attemts converges with K=7 and randomly initialized centers using my K-means clustering realization. In following cells i choose centers manually.

```
In [147]: c_k = np.array([[0, 0, 0, 0],
                          [1, 1, 1, 1],
                          [0.5, 0.5, 0.5, 0.5]])
          K = 3
          KMC = KMeansClustering(c_k=c_k, K=K)
          print(KMC.run(np.array(pass_data[['Length', 'Diameter', 'Whole_w', 'Shel
          KMC.c_k

28


Out[147]: array([[ 0.4033,  0.3077,  0.3488,  0.1057],
                 [ 0.6657,  0.5252,  1.5683,  0.4383],
                 [ 0.5717,  0.4477,  0.937 ,  0.2715]])

In [148]: c_k = np.array([[0, 0, 0, 0],
                          [1, 1, 1, 1],
                          [0.5, 0.5, 0.5, 0.5],
                          [1.2,1.2,1.5,1.2]])
          K = 4
          KMC = KMeansClustering(c_k=c_k, K=K)
          print(KMC.run(np.array(pass_data[['Length', 'Diameter', 'Whole_w', 'Shel
          KMC.c_k

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Out[148]: array([[ 0.3654,  0.2769,  0.2568,  0.0787],
                 [ 0.6097,  0.4792,  1.1492,  0.3277],
                 [ 0.5201,  0.4042,  0.6909,  0.2048],
                 [ 0.6861,  0.5414,  1.7413,  0.4834]])

In [156]: c_k = np.array([[0, 0, 0, 0],
                          [1, 1, 1, 1],
                          [0.5, 0.5, 0.5, 0.5],
                          [1.2,1.2,1.5,1.2],
                          [0.5, 0.1, 2, 0.5],
                          [0.01, 0.2, 0.4, 0.6],
                          [0.2, 0.2, 0.2, 0.2]])
          K = 7
          KMC = KMeansClustering(c_k=c_k, K=K)
```

```
KMC.max_iter = 10
print(KMC.run(np.array(pass_data[['Length', 'Diameter', 'Whole_w', 'Shell
KMC.c_k
```

```
10
```

```
Out[156]: array([[    nan,     nan,     nan,     nan],
                 [ 0.524 ,  0.4079,  0.8287,  0.2388],
                 [    nan,     nan,     nan,     nan],
                 [    nan,     nan,     nan,     nan],
                 [    nan,     nan,     nan,     nan],
                 [    nan,     nan,     nan,     nan],
                 [    nan,     nan,     nan,     nan]])
```

Thus, in case of my dataset, i think, that there is no reason to initialize centers by hands because i can't figure out centers which would probably lead to a convergence of 7-means clustering, while for k=3 and k=4 random and manual initializations work the same. Therefore, random initialization from uniform distribution seems to me as a better choice.

What about K-constant...

```
In [30]: for i in range(3): #K=3, random init
             print(i, "-ckass;", 'k-size', pass_data.ix[KMC.s_k[i],:].shape[0], ';r
```

```
0 -ckass; k-size 1634 ;r mean over class 7.935128518971848 ;r std over class 2.415
1 -ckass; k-size 806 ;r mean over class 12.048387096774194 ;r std over class 3.105
2 -ckass; k-size 1737 ;r mean over class 10.832469775474957 ;r std over class 2.89
```

It is a nice result! We found 3 clasters with a small, mid and large number of rings like in HW6 where i set up a boundaries as rings_threshold = [0, 8, 12, 30].

```
In [33]: for i in range(4): #K=4, random init
             print(i, "-ckass;", 'k-size', pass_data.ix[KMC.s_k[i],:].shape[0], ';r
```

```
0 -ckass; k-size 460 ;r mean over class 12.41304347826087 ;r std over class 3.1621
1 -ckass; k-size 1118 ;r mean over class 7.283542039355993 ;r std over class 2.152
2 -ckass; k-size 1332 ;r mean over class 10.038288288288289 ;r std over class 2.70
3 -ckass; k-size 1267 ;r mean over class 11.262036306235201 ;r std over class 2.94
```

So, it's great again! Have a look, now we found an additional cluster which is located between threshold of 10 and 12. In conclusion, both 3-k and 4-k clustering give a good result, but i prefer the last way because the bigger, the better. Likewise, i have already had an idea to add this cluster (with 11 as mean) in HW 6. This is why i choose 4-k means clustering with random initializated centers.