Exercise 1: 3/7 points.
Exercise 2: 7/9 points.
Exercise 3: 6.75/9 points.
Total marks: 16.75/25 points.

Exercise sheet 3

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ex1))

1/1P

1)) You want to predict whether a patient will develop lung cancer, and you are given the years of smoking as well as their age as a feature.Considering the equation of the logistic regression,what are X and Y in this case?

The independent (predictor) variable X is the years of smoking and age The dependent variable Y is lung cancer

---

2)) What are the outputs of the logistic model and the logistic function? What are their ranges? 1/2P

logistic function;

$$p(x) = \frac{1}{1 + \exp -(\beta_0 + \beta 1 x)}$$

logistic regression model, log likelihhod will be;

l(x) = $\sum_{k=1}^{K} y_k \log_b p(x_k) + \sum_{k=1}^{K} (1 - y_k) \log_b (1 - p(x_k))$

logistic function models probabilities p(X) using a function that gives outputs between 0 and 1 that is 0<p(x)<1.

Same range is for logistic regression model as between 0 and 1 that is 0<l(x)<1

missing: log odds as outputs of logistic model

---

3)) 0/2P

We want to assess the statisticalsignificance of the predictor mean radius. Let us say we have two different models to estimate the target variable: Model 1 has all nine predictor variables. Model 2 has eight predictor variables, all but the 'mean radius'. What is our null hypothesis here? Which statistical test would you apply to compare the fit of the two models? Which result of the statistical test would let you conclude whether the predictor variable 'mean radius' is statistically significant or not?

-we want to determine wether there is a significant difference in the two models one with the

Insert

predictor mean radius and the other without. -Null Hypothesis:all regression coefficients are zero (differences in group mean) . -The ANOVA-F-test -The p-value is used to conclude.A low p-value <0.05 means we reject the null hypothesis.in other words, a predictor that has a low p-value is likely to be a meaningful addition to your model because changes in the predictor's value are related to changes in the response variable.

---

4)) Which assumptions have to be fufilled to apply logistic regression? are they fufilled in this example? 1/2P

-Fitting of logistic regression models is done in an iterative process(Newton-Raphson method)-Non-convergence may occur due to violation of model assumptions:Linear class separation possible with not too large class overlap. No colinearities among regressor variables

---

ex2))

In [ ]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import statsmodels as sm
```

1. Data correlation

_a. Load the raw Diabetes CSV file onto your notebook, which its data has not been standardized (file: diabetes*raw.csv). Create separate dataframes for the target variable (“Y”) and the input variables (all columns except “Y”). Examine the correlation properties between the input variables by plotting a correlation heatmap using the Pandas corr() function and the Seaborn heatmap() function. (1P)*

In [ ]:
```
diabetes = pd.read_csv('diabetes_raw.csv')
diabetes.head()
```

Out[ ]:

	AGE	SEX	BMI	BP	S1	S2	S3	S4	S5	S6	Y
0	59	2	32.1	101.0	157	93.2	38.0	4.0	4.8598	87	151
1	48	1	21.6	87.0	183	103.2	70.0	3.0	3.8918	69	75
2	72	2	30.5	93.0	156	93.6	41.0	4.0	4.6728	85	141
3	24	1	25.3	84.0	198	131.4	40.0	5.0	4.8903	89	206
4	50	1	23.0	101.0	192	125.4	52.0	4.0	4.2905	80	135

In [ ]:
```
diabetes_target = pd.DataFrame(diabetes, columns=['Y'])
diabetes_target.head()
```

Out[ ]:

	Y
0	151
1	75
2	141
3	206
4	135

In [ ]:

```
diabetes_input = pd.DataFrame(diabetes, columns=['AGE','SEX','BMI','BP','S1
diabetes_input.head()
```

Out[ ]:

	AGE	SEX	BMI	BP	S1	S2	S3	S4	S5	S6
0	59	2	32.1	101.0	157	93.2	38.0	4.0	4.8598	87
1	48	1	21.6	87.0	183	103.2	70.0	3.0	3.8918	69
2	72	2	30.5	93.0	156	93.6	41.0	4.0	4.6728	85
3	24	1	25.3	84.0	198	131.4	40.0	5.0	4.8903	89
4	50	1	23.0	101.0	192	125.4	52.0	4.0	4.2905	80

In [ ]:

```
diabetes_input.corr()
```

Out[ ]:

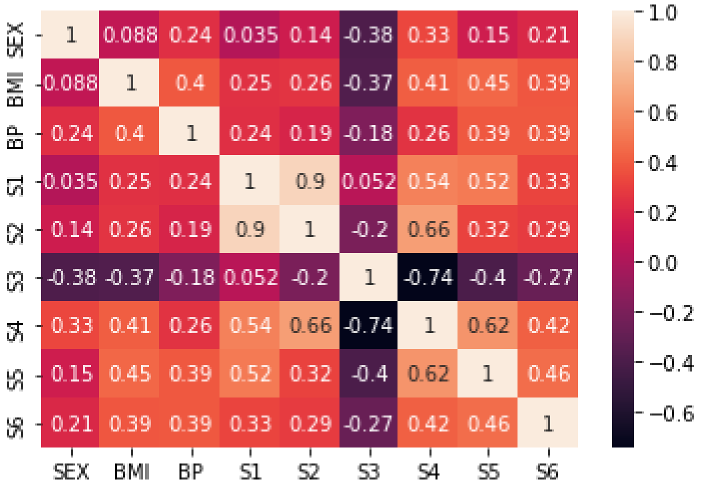
	AGE	SEX	BMI	BP	S1	S2	S3	S4	
AGE	1.000000	0.173737	0.185085	0.335428	0.260061	0.219243	-0.075181	0.203841	0.2
SEX	0.173737	1.000000	0.088161	0.241010	0.035277	0.142637	-0.379090	0.332115	0.1
BMI	0.185085	0.088161	1.000000	0.395411	0.249777	0.261170	-0.366811	0.413807	0.4
BP	0.335428	0.241010	0.395411	1.000000	0.242464	0.185548	-0.178762	0.257650	0.3
S1	0.260061	0.035277	0.249777	0.242464	1.000000	0.896663	0.051519	0.542207	0.5
S2	0.219243	0.142637	0.261170	0.185548	0.896663	1.000000	-0.196455	0.659817	0.3
S3	-0.075181	-0.379090	-0.366811	-0.178762	0.051519	-0.196455	1.000000	-0.738493	-0.3
S4	0.203841	0.332115	0.413807	0.257650	0.542207	0.659817	-0.738493	1.000000	0.6
S5	0.270774	0.149916	0.446157	0.393480	0.515503	0.318357	-0.398577	0.617859	1.0
S6	0.301731	0.208133	0.388680	0.390430	0.325717	0.290600	-0.273697	0.417212	0.4

In [ ]:

```
sns.heatmap(diabetes_input.iloc[:,1:].corr(), xticklabels=diabetes_input.il
```

Out[ ]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fa3d6f47400>
```



Well done. 1/1 point.

b. Observe the variable “S3” (high-density lipoproteins) at the correlation plot. Which variable has the strongest positive correlation with it, and which variable has the strongest negative correlation with it? (1P)

The variable with the strongest positive correlation with S3 is S1, and with the strongest negative correlation is S4.

As the question asks for the strongest positive correlation, the answer is S3 has strong positive correlation with itself. Nevertheless, your thought process is in the right direction. And correct answer for strongest negative correlation. 0.5/1 point.

---

2. Data standardization

a. Read this article to learn more about when and why we need to standardize variables in a regression model: https://statisticsbyjim.com/regression/standardize-variables-regression/. (1P) 1/1 point.

b. Scale the range of the Diabetes dataset using the Sklearn StandardScaler() function. Perform two linear regression analysis using the Statsmodels OLS function: one for the standardized, and one for the non-standardized datasets. Which differences do you observe at the outcome summary? Explain the reasons behind these differences. (2P)

In [ ]:
```
from sklearn import preprocessing
import statsmodels.api as sm
```

In [ ]:
```
X = diabetes[['AGE','SEX','BMI','BP','S1','S2','S3','S4','S5','S6']]
Y = diabetes[['Y']]
model = sm.OLS(Y,X).fit()
print(model.summary())
```

```
                            OLS Regression Results
===========================================================================
============
Dep. Variable:                      Y   R-squared (uncentered):
0.896
Model:                            OLS   Adj. R-squared (uncentered):
0.894
Method:                 Least Squares   F-statistic:
372.3
Date:                Tue, 03 May 2022   Prob (F-statistic):
2.76e-205
Time:                        22:49:35   Log-Likelihood:
-2398.3
No. Observations:                 442   AIC:
4817.
Df Residuals:                     432   BIC:
4857.
Df Model:                          10
Covariance Type:            nonrobust
===========================================================================
===
                 coef    std err          t      P>|t|      [0.025      0.9
75]
---------------------------------------------------------------------------
---
AGE            0.0223      0.223      0.100      0.920      -0.415       0.
460
SEX          -26.0728      5.956     -4.378      0.000     -37.779     -14.
366
BMI            5.3537      0.735      7.288      0.000       3.910       6.
798
BP             1.0178      0.230      4.418      0.000       0.565       1.
471
S1             1.2636      0.330      3.824      0.000       0.614       1.
913
S2            -1.2849      0.347     -3.705      0.000      -1.967      -0.
603
S3            -3.0683      0.372     -8.250      0.000      -3.799      -2.
337
S4            -5.5080      5.588     -0.986      0.325     -16.492       5.
476
S5             5.5034      9.429      0.584      0.560     -13.030      24.
036
S6             0.1234      0.279      0.443      0.658      -0.425       0.
671
===========================================================================
===
Omnibus:                        2.175   Durbin-Watson:                   1.
990
Prob(Omnibus):                  0.337   Jarque-Bera (JB):                2.
000
Skew:                           0.081   Prob(JB):                        0.
368
Kurtosis:                       2.713   Cond. No.                     1.02e
+03
===========================================================================
===

Notes:
[1] R² is computed without centering (uncentered) since the model does not
contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is corr
ectly specified.
[3] The condition number is large, 1.02e+03. This might indicate that there
```

```
are
strong multicollinearity or other numerical problems.
```

In [ ]:
```
scaler = preprocessing.StandardScaler()

# standardization of dependent variables
diabetes_scaled = scaler.fit_transform(diabetes_input)
diabetes_target_scaled = scaler.fit_transform(diabetes_target)

new_model = sm.OLS(diabetes_target_scaled,diabetes_scaled).fit()
print(new_model.summary())
```

```
                                 OLS Regression Results
==========================================================================================
Dep. Variable:                      y   R-squared (uncentered):
0.518
Model:                            OLS   Adj. R-squared (uncentered):
0.507
Method:                 Least Squares   F-statistic:
46.38
Date:                Tue, 03 May 2022   Prob (F-statistic):
2.68e-62
Time:                        22:49:35   Log-Likelihood:
-466.00
No. Observations:                 442   AIC:
952.0
Df Residuals:                     432   BIC:
992.9
Df Model:                          10
Covariance Type:            nonrobust
==========================================================================================
===
                 coef    std err          t      P>|t|      [0.025      0.9
75]
----------------------------------------------------------------------------
---
x1            -0.0062      0.037     -0.168      0.867      -0.079       0.
066
x2            -0.1481      0.038     -3.922      0.000      -0.222      -0.
074
x3             0.3211      0.041      7.822      0.000       0.240       0.
402
x4             0.2004      0.040      4.964      0.000       0.121       0.
280
x5            -0.4893      0.257     -1.903      0.058      -0.995       0.
016
x6             0.2945      0.209      1.408      0.160      -0.117       0.
706
x7             0.0624      0.131      0.476      0.634      -0.195       0.
320
x8             0.1094      0.100      1.098      0.273      -0.086       0.
305
x9             0.4640      0.106      4.375      0.000       0.256       0.
673
x10            0.0418      0.041      1.026      0.305      -0.038       0.
122
==========================================================================================
===
Omnibus:                        1.506   Durbin-Watson:                    2.
029
Prob(Omnibus):                  0.471   Jarque-Bera (JB):                 1.
404
Skew:                           0.017   Prob(JB):                         0.
496
Kurtosis:                       2.726   Cond. No.                          2
1.7
==========================================================================================
===

Notes:
[1] R² is computed without centering (uncentered) since the model does not
contain a constant.
[2] Standard Errors assume that the covariance matrix of the errors is corr
ectly specified.
```

```
                    non-standardized:
standardized

Adj. R-squared:         0.896
0.518

F statistic prob:       2.76e-205
2.68e-62
```

The most significant difference we observe is in the standard errors and the coefficients. In the standarized data, the standard error has decreased significantly in SEX, S4 and S5, as well as all the coefficients. Overall, we see a more homogeneous data. Almost every values have less p values after standardized

One of the reasons of this is that the standarization is transforming the units of the regression coefficients so that standardization makes the variables be in the same scale.

Well done for the programming part. Condition number and reducing multi-collinearity should be the focus of explanation here, thereby deducting 1 point for less on-point explanation. Please refer to the solution sheet for detailed solutions. 1/2 points.

---

3. Data transformation

a. One of the important assumptions of linear regression is that the model residuals are normally distributed. There are some data transformation techniques to fix the issue of non-normality of model residuals, such as the Box-Cox transformation. Explain how this technique works. State one of the benefits of transforming non-normal variables into a normal shape. (2P)

The Box-Cox transformation transforms our data so that it closely resembles a normal distribution. That way, if your data isn't normal, applying a Box-Cox means that you are able to run a broader number of tests.

Box-Cox Transformation converts non-normal data to normal data by raising the distribution to a power of lambda (λ). The algorithm can automatically decide the lambda (λ) parameter that best transforms the distribution into normal distribution. The lambda (λ) parameter has a range of -5 < λ < 5.

The main benefit is the fact of achieving real and truthful conclusions when performing tests on the data. The errors after modeling should be normal to draw a valid conclusion by hypothesis testing.

Good explanation. For more precise explanation of the second part, please refer to the solution sheet. 2/2 points.

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4. Confounding variables

a. The presence of confounding variables affects the variables being studied, which causes the result to not reflect the actual relationship between the variables. Read this article to learn more about confounding variables: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4017459/. (1P) 1/1 point.

b. Briefly describe how would you use linear regression to adjust for the confounding effects of age and gender in the Diabetes dataset. (1P)

Regression analysis describes how the changes in each independent variable are related to changes in the dependent variable. When you perform regression analysis, you need to isolate the role of each variable.

To accomplish this goal, you must minimize the effect of confounding variables. Regression analysis does this by estimating the effect that changing one independent variable has on the dependent variable while holding all the other independent variables constant.

Age and gender are frequent confounders, so an adjustment is needed in order to avoid these confounding effects.

Adjustment for age or gender involves a computational procedure to mimic a situation in which the men and women in the data set were of the same age or gender. This computation eliminates the influence of age/gender on the treatment effect.

Therefore, a multivariable regression analysis allows the study of multiple independent variables at the same time, with adjustment of their regression coefficients for possible confounding effects between variables.

Good explanation, but does not precisely answer the "how". Please refer to the solution sheet. 0.5/1 point.

---

ex3))

In [ ]:

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

In [ ]:

```
dataset = pd.read_csv("mlr_vma.csv",sep=';')
dataset.head()
```

Out[ ]:

	Unnamed: 0	0	1	2	3	4	5	6	
0	0	-47.917424	1.356240	0.744463	-0.645120	-0.454320	0.361636	-1.196207	0.8
1	1	146.564877	0.110923	0.264041	-0.291694	0.507493	-0.600639	-1.424748	-0.5
2	2	-21.967189	-0.501757	-0.383730	0.513267	0.578153	-0.529760	-0.518270	-0.8
3	3	32.408397	0.931280	-0.670939	0.975545	-0.713919	0.331263	0.611676	1.0
4	4	73.846658	-0.719844	1.716209	-1.763040	-0.688602	0.343618	-0.301104	-1.4

---

1))

There are three assumptions of linear regression

1- Model residuals are normally distributed

2- p < n (fewer regressors/variable/feature than data points/observation)

3- no collinearities

0/1P

Well, that is right, but the key question was to understand the failure scenario.

---

2))

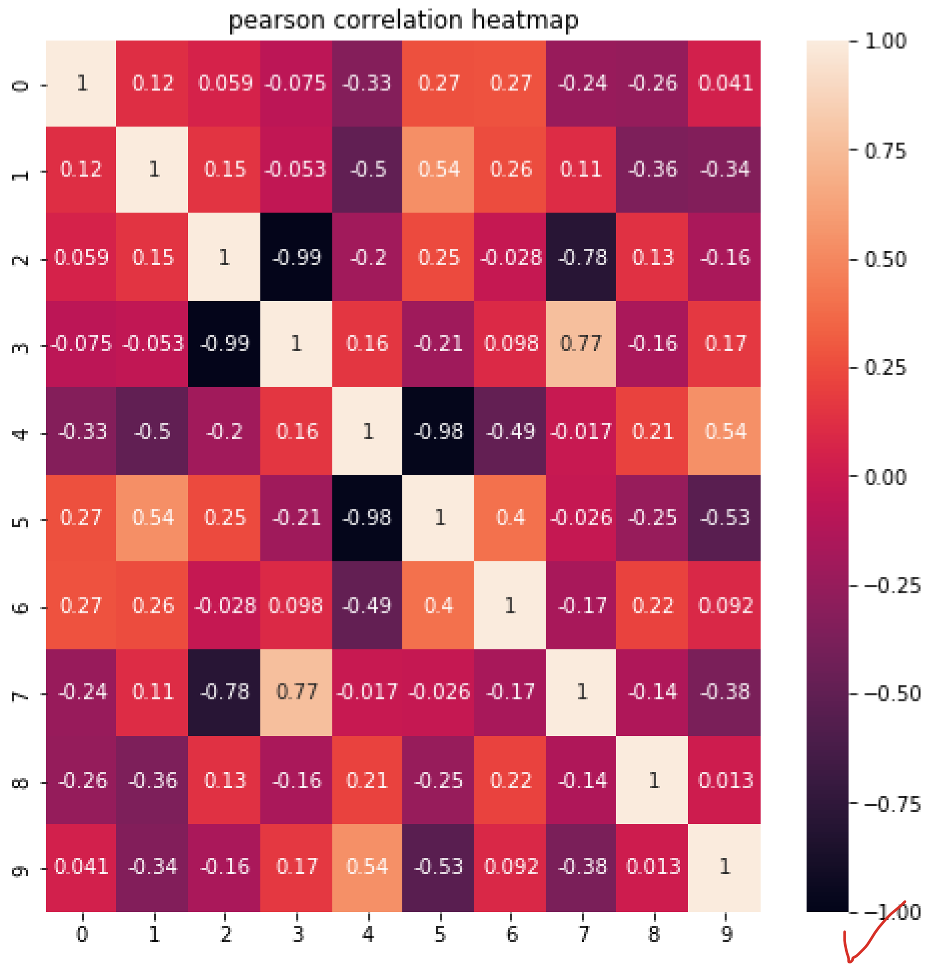
---

a)

In [ ]:
```
df = pd.DataFrame(dataset.iloc[:, 1:])
R1 = np.corrcoef(df, rowvar=False)
print(R1)
```

```
[[ 1.          0.12497988  0.05908911 -0.07497015 -0.32934373  0.26737311
   0.27464886 -0.2414412  -0.2576009   0.04065293]
 [ 0.12497988  1.          0.15025429 -0.05293082 -0.49916974  0.53704704
   0.25569712  0.11354459 -0.36369279 -0.33602962]
 [ 0.05908911  0.15025429  1.         -0.99024272 -0.19537037  0.24703481
  -0.02821149 -0.78376515  0.13370814 -0.15894425]
 [-0.07497015 -0.05293082 -0.99024272  1.          0.1608018  -0.2107795
   0.09833535  0.76700661 -0.15910737  0.16973281]
 [-0.32934373 -0.49916974 -0.19537037  0.1608018   1.         -0.98408529
  -0.49015468 -0.01742893  0.21221458  0.54270776]
 [ 0.26737311  0.53704704  0.24703481 -0.2107795  -0.98408529  1.
   0.40281321 -0.02598373 -0.24641039 -0.53187612]
 [ 0.27464886  0.25569712 -0.02821149  0.09833535 -0.49015468  0.40281321
   1.         -0.16696175  0.21788207  0.09197533]
 [-0.2414412   0.11354459 -0.78376515  0.76700661 -0.01742893 -0.02598373
  -0.16696175  1.         -0.13744055 -0.3758909 ]
 [-0.2576009  -0.36369279  0.13370814 -0.15910737  0.21221458 -0.24641039
   0.21788207 -0.13744055  1.          0.0130826 ]
 [ 0.04065293 -0.33602962 -0.15894425  0.16973281  0.54270776 -0.53187612
   0.09197533 -0.3758909   0.0130826   1.        ]]
```

In [ ]:
```
plt.figure(figsize=(8, 8))
spearman_heatmap = sns.heatmap(df.corr(method = 'pearson'), vmin=-1, vmax=1
spearman_heatmap.set_title('pearson correlation heatmap');
```



1/1

b)

In [ ]:
```
from scipy.stats import shapiro

df = pd.DataFrame(dataset.iloc[:, 1:])

test_df = np.random.normal(loc=20, scale=5, size=(10, 10))
stat, p = shapiro(test_df)
print(p)
```

0.47318804264068604

0-

~~p > 0.05 so it is normally distributed~~

resdiuals need to be normal distributed, not the data

1-

p = n (regressors/variable/feature = data points/observation)

but should be p < n -> this assumption is violated

2-

there is colinearities between 2 and 3 (-0.99)

but should be no collinearities -> this assumption is violated

1/1

c)

In [ ]:
```
df
```

Out[ ]:

	0	1	2	3	4	5	6	7	
0	-47.917424	1.356240	0.744463	-0.645120	-0.454320	0.361636	-1.196207	0.812526	-0.18
1	146.564877	0.110923	0.264041	-0.291694	0.507493	-0.600639	-1.424748	-0.544383	-0.22
2	-21.967189	-0.501757	-0.383730	0.513267	0.578153	-0.529760	-0.518270	-0.808494	0.35
3	32.408397	0.931280	-0.670939	0.975545	-0.713919	0.331263	0.611676	1.031000	-0.38
4	73.846658	-0.719844	1.716209	-1.763040	-0.688602	0.343618	-0.301104	-1.478522	0.17
5	-60.170661	-1.220844	-0.243689	0.196861	1.215729	-1.328186	-1.057711	0.822545	1.85
6	36.139561	0.821903	2.303411	-1.987569	-0.294327	0.091761	1.564644	-2.619745	1.53
7	-46.341769	-0.562288	1.565791	-1.412304	0.970874	-0.908024	-1.913280	-1.724918	-0.46
8	9.707755	-1.463515	0.140692	-0.234587	-0.186718	0.005113	-0.327662	-0.392108	0.96
9	49.671415	-0.234137	-0.434048	0.542560	0.187014	-0.469474	1.523030	-0.234153	-0.13

In [ ]:
```
df = df.drop(['3', '5'], axis=1)
```

columns 2 and 3 are colinear, columns 4 and 5 are colinears,

so discarded col 3 and 5 not to be colinear

In [ ]:
```
df.shape
```

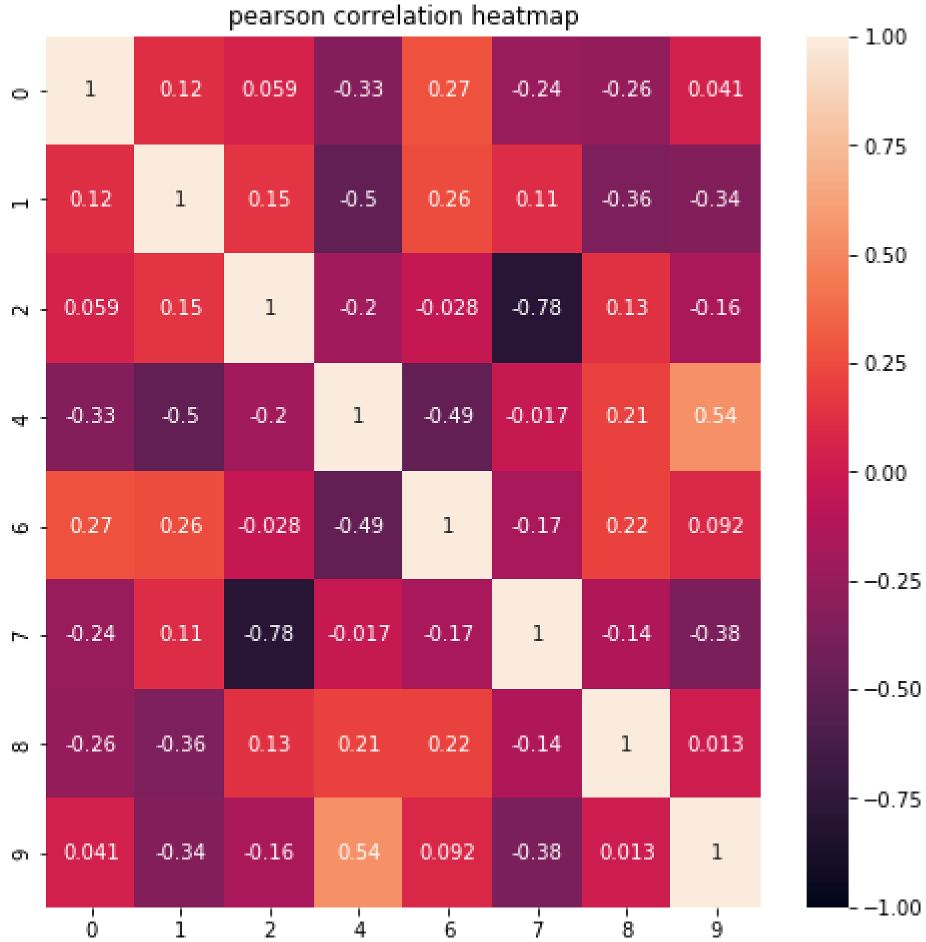
Out[ ]:
```
(10, 8)
```

n: 10 observations > p: 8 features

so p < n holds

In [ ]:
```
plt.figure(figsize=(8, 8))
spearman_heatmap = sns.heatmap(df.corr(method = 'pearson'), vmin=-1, vmax=1
spearman_heatmap.set_title('pearson correlation heatmap');
```

1/1



---

3))

In [ ]:
```
dataset2 = pd.read_csv("y_mlr_vma.csv",sep=';')
df2 = pd.DataFrame(dataset2.iloc[:, 1:])
df2.head()
```

Out[ ]:

	y
0	-37.395291
1	57.080023
2	15.940968
3	-2.437328
4	32.772880

you forgot to standardize the data 0.5 / 1

In [ ]:
```
x = sm.add_constant(df)

result = sm.OLS(df2, x).fit()
```

d)

In [ ]:
```
print(result.summary())
```

```
                            OLS Regression Results
===========================================================================
===
Dep. Variable:                      y   R-squared:                       1.
000
Model:                            OLS   Adj. R-squared:                  1.
000
Method:                 Least Squares   F-statistic:                 3.070e
+04
Date:                Tue, 03 May 2022   Prob (F-statistic):            0.00
441
Time:                        22:49:39   Log-Likelihood:                 14.
388
No. Observations:                  10   AIC:                            -1
0.78
Df Residuals:                       1   BIC:                            -8.
053
Df Model:                           8
Covariance Type:            nonrobust
===========================================================================
===
                 coef    std err          t      P>|t|      [0.025      0.9
75]
---------------------------------------------------------------------------
---
const          0.0399      0.078      0.514      0.698      -0.946       1.
026
0              0.4180      0.001    356.763      0.002       0.403       0.
433
1              0.0803      0.096      0.838      0.556      -1.137       1.
298
2             -0.2476      0.207     -1.194      0.444      -2.881       2.
386
4              0.2338      0.171      1.367      0.402      -1.939       2.
407
6              0.1546      0.093      1.669      0.344      -1.022       1.
332
7             -0.1101      0.192     -0.573      0.669      -2.549       2.
329
8             21.6424      0.107    201.684      0.003      20.279      23.
006
9             11.6124      0.186     62.599      0.010       9.255      13.
969
===========================================================================
===
Omnibus:                        0.491   Durbin-Watson:                   1.
167
Prob(Omnibus):                  0.782   Jarque-Bera (JB):                0.
251
Skew:                           0.329   Prob(JB):                        0.
882
Kurtosis:                       2.590   Cond. No.                         3
52.
===========================================================================
===

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is corr
ectly specified.
```

```
/home/cuneyt/.local/lib/python3.8/site-packages/scipy/stats/stats.py:1541:
UserWarning: kurtosistest only valid for n>=20 ... continuing anyway, n=10
  warnings.warn("kurtosistest only valid for n>=20 ... continuing "
```

as it can be seen in the model summary, R-square and Adjusted R square values are 1.0, some of the p > 0.05 which are normally distributed, some of p < 0.05 which are correlated

1/1

wrong conclusion

not true in general. what is the meaning of a p-value?

e)

model performed well because R-squared is 1.0 which means our model explains 100.0% of the change in our 'y' variable accurately. F statistics probability is 0.00441% meaning that accuracy of the null hypothesis has this rate of chance.

alpha error

f)

missed feature 9 because you missed standardization

0.5/1

values 0 and 8 have p < 0.05 having significants when we apply 2c by discarding values of 3 and 5. If we do not discard colinearitis and apply n > p values, then all result.summary() gives us nothing because assumptions do not hold, so applying 2c is important to get summary results correctly

yes, but you could have dropped other columns to get the same solution. you missed that.

g)

to select informative features, we need to look at coefficients that how change in that variable affects the independent variable. Also their p values are less than 0.05 or close to 0.05

no. if the coefficient is high, but it is highly insignificant, you could make a high error

what counts here is the p-value

(after applying 2c, discarding column 3 and 5)

value: 0, coeff: 0.4180, P>|t|1: 0.002

value: 8, coeff: 21.6424, P>|t|1: 0.003

value: 9, coeff:11.6124, P>|t|1: 0.010

0.75 / 1

so these 3 columns (0, 8 and 9) are most informative ones, rest can be considered as noise.

In [ ]: