2-2-3-pca-dimensionality-reduction

March 22, 2024

#PCA

[ ]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.datasets import load_breast_cancer
```

[ ]:
```
breast=load_breast_cancer()
breast_data=breast.data
print(breast_data)
print(breast_data.shape)
```

```
[[1.799e+01 1.038e+01 1.228e+02 … 2.654e-01 4.601e-01 1.189e-01]
 [2.057e+01 1.777e+01 1.329e+02 … 1.860e-01 2.750e-01 8.902e-02]
 [1.969e+01 2.125e+01 1.300e+02 … 2.430e-01 3.613e-01 8.758e-02]
 …
 [1.660e+01 2.808e+01 1.083e+02 … 1.418e-01 2.218e-01 7.820e-02]
 [2.060e+01 2.933e+01 1.401e+02 … 2.650e-01 4.087e-01 1.240e-01]
 [7.760e+00 2.454e+01 4.792e+01 … 0.000e+00 2.871e-01 7.039e-02]]
(569, 30)
```

[ ]:
```
breast_labels=breast.target
print(breast_labels)
print(breast_labels.shape)
```

```
[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 1 0 0 0 0 0 0 0 0 0 1 0 1 1 1 1 1 0 0 1 0 0 1 1 1 1 0 1 0 0 1 1 1 1 0 1 0 0
 1 0 1 0 0 1 1 1 0 0 1 0 0 0 1 1 1 0 1 1 0 0 1 1 1 0 0 1 1 1 1 0 1 1 0 1 1
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 0 1 0 0 1 1 1 1 1 0 1 1 1 1 1 0 1 1 1 0 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1
 1 0 1 1 1 1 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 0 1 1 1 1 1 0 1 1
 0 1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1 0 1
 1 1 1 1 1 1 0 1 0 1 1 0 1 1 1 1 1 1 0 0 1 0 1 0 1 1 1 1 1 1 0 1 1 0 1 0 1 0 0
```

```
 1 1 1 0 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 1 1 1 1 1 1 1 0 0 0 0 0 0 1]
(569,)
```

[ ]:
```
labels=np.reshape(breast_labels,(569,1))
final_breast_data=np.concatenate([breast_data,labels],axis=1)
print(final_breast_data.shape)
```

```
(569, 31)
```

[ ]:
```
breast_dataset=pd.DataFrame(final_breast_data)
print(breast_dataset.head())
```

```
      0      1       2       3        4        5       6        7       8   \
0  17.99  10.38  122.80  1001.0  0.11840  0.27760  0.3001  0.14710  0.2419
1  20.57  17.77  132.90  1326.0  0.08474  0.07864  0.0869  0.07017  0.1812
2  19.69  21.25  130.00  1203.0  0.10960  0.15990  0.1974  0.12790  0.2069
3  11.42  20.38   77.58   386.1  0.14250  0.28390  0.2414  0.10520  0.2597
4  20.29  14.34  135.10  1297.0  0.10030  0.13280  0.1980  0.10430  0.1809

        9   …     21      22      23      24      25      26      27  \
0  0.07871  …  17.33  184.60  2019.0  0.1622  0.6656  0.7119  0.2654
1  0.05667  …  23.41  158.80  1956.0  0.1238  0.1866  0.2416  0.1860
2  0.05999  …  25.53  152.50  1709.0  0.1444  0.4245  0.4504  0.2430
3  0.09744  …  26.50   98.87   567.7  0.2098  0.8663  0.6869  0.2575
4  0.05883  …  16.67  152.20  1575.0  0.1374  0.2050  0.4000  0.1625

       28       29   30
0  0.4601  0.11890  0.0
1  0.2750  0.08902  0.0
2  0.3613  0.08758  0.0
3  0.6638  0.17300  0.0
4  0.2364  0.07678  0.0

[5 rows x 31 columns]
```

[ ]:
```
features=breast.feature_names
print(features)
```

```
['mean radius' 'mean texture' 'mean perimeter' 'mean area'
 'mean smoothness' 'mean compactness' 'mean concavity'
 'mean concave points' 'mean symmetry' 'mean fractal dimension'
 'radius error' 'texture error' 'perimeter error' 'area error'
 'smoothness error' 'compactness error' 'concavity error'
 'concave points error' 'symmetry error' 'fractal dimension error'
 'worst radius' 'worst texture' 'worst perimeter' 'worst area'
 'worst smoothness' 'worst compactness' 'worst concavity'
 'worst concave points' 'worst symmetry' 'worst fractal dimension']
```

[ ]:
```
features_labels=np.append(features,'label')
```

[ ]:
```
breast_dataset.columns=features_labels
breast_dataset.head()
```

[ ]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	\
0	17.99	10.38	122.80	1001.0	0.11840	
1	20.57	17.77	132.90	1326.0	0.08474	
2	19.69	21.25	130.00	1203.0	0.10960	
3	11.42	20.38	77.58	386.1	0.14250	
4	20.29	14.34	135.10	1297.0	0.10030	

	mean compactness	mean concavity	mean concave points	mean symmetry	\
0	0.27760	0.3001	0.14710	0.2419	
1	0.07864	0.0869	0.07017	0.1812	
2	0.15990	0.1974	0.12790	0.2069	
3	0.28390	0.2414	0.10520	0.2597	
4	0.13280	0.1980	0.10430	0.1809	

	mean fractal dimension	…	worst texture	worst perimeter	worst area	\
0	0.07871	…	17.33	184.60	2019.0	
1	0.05667	…	23.41	158.80	1956.0	
2	0.05999	…	25.53	152.50	1709.0	
3	0.09744	…	26.50	98.87	567.7	
4	0.05883	…	16.67	152.20	1575.0	

	worst smoothness	worst compactness	worst concavity	worst concave points	\
0	0.1622	0.6656	0.7119	0.2654	
1	0.1238	0.1866	0.2416	0.1860	
2	0.1444	0.4245	0.4504	0.2430	
3	0.2098	0.8663	0.6869	0.2575	
4	0.1374	0.2050	0.4000	0.1625	

	worst symmetry	worst fractal dimension	label
0	0.4601	0.11890	0.0
1	0.2750	0.08902	0.0
2	0.3613	0.08758	0.0
3	0.6638	0.17300	0.0
4	0.2364	0.07678	0.0

[5 rows x 31 columns]

[ ]:
```
breast_dataset['label'].replace(0,'Benign',inplace=True)
breast_dataset['label'].replace(1,'Malignant',inplace=True)
breast_dataset.tail()
```

[ ]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	\
564	21.56	22.39	142.00	1479.0	0.11100	
565	20.13	28.25	131.20	1261.0	0.09780	
566	16.60	28.08	108.30	858.1	0.08455	
567	20.60	29.33	140.10	1265.0	0.11780	
568	7.76	24.54	47.92	181.0	0.05263	

	mean compactness	mean concavity	mean concave points	mean symmetry	\
564	0.11590	0.24390	0.13890	0.1726	
565	0.10340	0.14400	0.09791	0.1752	
566	0.10230	0.09251	0.05302	0.1590	
567	0.27700	0.35140	0.15200	0.2397	
568	0.04362	0.00000	0.00000	0.1587	

	mean fractal dimension	…	worst texture	worst perimeter	worst area	\
564	0.05623	…	26.40	166.10	2027.0	
565	0.05533	…	38.25	155.00	1731.0	
566	0.05648	…	34.12	126.70	1124.0	
567	0.07016	…	39.42	184.60	1821.0	
568	0.05884	…	30.37	59.16	268.6	

	worst smoothness	worst compactness	worst concavity	\
564	0.14100	0.21130	0.4107	
565	0.11660	0.19220	0.3215	
566	0.11390	0.30940	0.3403	
567	0.16500	0.86810	0.9387	
568	0.08996	0.06444	0.0000	

	worst concave points	worst symmetry	worst fractal dimension	label
564	0.2216	0.2060	0.07115	Benign
565	0.1628	0.2572	0.06637	Benign
566	0.1418	0.2218	0.07820	Benign
567	0.2650	0.4087	0.12400	Benign
568	0.0000	0.2871	0.07039	Malignant

[5 rows x 31 columns]

[ ]:
```
from sklearn.preprocessing import StandardScaler
x=breast_dataset.loc[:,features].values
x=StandardScaler().fit_transform(x)
print(x.shape)
```

(569, 30)

[ ]:
```
np.mean(x),np.std(x)
```

[ ]: (-6.118909323768877e-16, 1.0)

[ ]:
```
feat_cols=['feature'+str(i) for i in range(x.shape[1])]
```

[ ]:
```
normalised_breast=pd.DataFrame(x,columns=feat_cols)
print(normalised_breast)
```

```
     feature0  feature1  feature2  feature3  feature4  feature5  feature6  \
0    1.097064 -2.073335  1.269934  0.984375  1.568466  3.283515  2.652874
1    1.829821 -0.353632  1.685955  1.908708 -0.826962 -0.487072 -0.023846
2    1.579888  0.456187  1.566503  1.558884  0.942210  1.052926  1.363478
3   -0.768909  0.253732 -0.592687 -0.764464  3.283553  3.402909  1.915897
4    1.750297 -1.151816  1.776573  1.826229  0.280372  0.539340  1.371011
..        …         …         …         …         …         …         …
564  2.110995  0.721473  2.060786  2.343856  1.041842  0.219060  1.947285
565  1.704854  2.085134  1.615931  1.723842  0.102458 -0.017833  0.693043
566  0.702284  2.045574  0.672676  0.577953 -0.840484 -0.038680  0.046588
567  1.838341  2.336457  1.982524  1.735218  1.525767  3.272144  3.296944
568 -1.808401  1.221792 -1.814389 -1.347789 -3.112085 -1.150752 -1.114873

     feature7  feature8  feature9  …  feature20  feature21  feature22  \
0    2.532475  2.217515  2.255747  …   1.886690  -1.359293   2.303601
1    0.548144  0.001392 -0.868652  …   1.805927  -0.369203   1.535126
2    2.037231  0.939685 -0.398008  …   1.511870  -0.023974   1.347475
3    1.451707  2.867383  4.910919  …  -0.281464   0.133984  -0.249939
4    1.428493 -0.009560 -0.562450  …   1.298575  -1.466770   1.338539
..        …         …         …  …         …          …         …
564  2.320965 -0.312589 -0.931027  …   1.901185   0.117700   1.752563
565  1.263669 -0.217664 -1.058611  …   1.536720   2.047399   1.421940
566  0.105777 -0.809117 -0.895587  …   0.561361   1.374854   0.579001
567  2.658866  2.137194  1.043695  …   1.961239   2.237926   2.303601
568 -1.261820 -0.820070 -0.561032  …  -1.410893   0.764190  -1.432735

     feature23  feature24  feature25  feature26  feature27  feature28  \
0     2.001237   1.307686   2.616665   2.109526   2.296076   2.750622
1     1.890489  -0.375612  -0.430444  -0.146749   1.087084  -0.243890
2     1.456285   0.527407   1.082932   0.854974   1.955000   1.152255
3    -0.550021   3.394275   3.893397   1.989588   2.175786   6.046041
4     1.220724   0.220556  -0.313395   0.613179   0.729259  -0.868353
..         …         …         …         …         …         …
564   2.015301   0.378365  -0.273318   0.664512   1.629151  -1.360158
565   1.494959  -0.691230  -0.394820   0.236573   0.733827  -0.531855
566   0.427906  -0.809587   0.350735   0.326767   0.414069  -1.104549
567   1.653171   1.430427   3.904848   3.197605   2.289985   1.919083
568  -1.075813  -1.859019  -1.207552  -1.305831  -1.745063  -0.048138

     feature29
0     1.937015
1     0.281190
```

```
2     0.201391
3     4.935010
4    -0.397100
..         …
564  -0.709091
565  -0.973978
566  -0.318409
567   2.219635
568  -0.751207

[569 rows x 30 columns]
```

[ ]:
```
normalised_breast.tail()
```

[ ]:
```
     feature0  feature1  feature2  feature3  feature4  feature5  feature6  \
564  2.110995  0.721473  2.060786  2.343856  1.041842  0.219060  1.947285
565  1.704854  2.085134  1.615931  1.723842  0.102458 -0.017833  0.693043
566  0.702284  2.045574  0.672676  0.577953 -0.840484 -0.038680  0.046588
567  1.838341  2.336457  1.982524  1.735218  1.525767  3.272144  3.296944
568 -1.808401  1.221792 -1.814389 -1.347789 -3.112085 -1.150752 -1.114873

     feature7  feature8  feature9  …  feature20  feature21  feature22  \
564  2.320965 -0.312589 -0.931027  …   1.901185   0.117700   1.752563
565  1.263669 -0.217664 -1.058611  …   1.536720   2.047399   1.421940
566  0.105777 -0.809117 -0.895587  …   0.561361   1.374854   0.579001
567  2.658866  2.137194  1.043695  …   1.961239   2.237926   2.303601
568 -1.261820 -0.820070 -0.561032  …  -1.410893   0.764190  -1.432735

     feature23  feature24  feature25  feature26  feature27  feature28  \
564   2.015301   0.378365  -0.273318   0.664512   1.629151  -1.360158
565   1.494959  -0.691230  -0.394820   0.236573   0.733827  -0.531855
566   0.427906  -0.809587   0.350735   0.326767   0.414069  -1.104549
567   1.653171   1.430427   3.904848   3.197605   2.289985   1.919083
568  -1.075813  -1.859019  -1.207552  -1.305831  -1.745063  -0.048138

     feature29
564  -0.709091
565  -0.973978
566  -0.318409
567   2.219635
568  -0.751207

[5 rows x 30 columns]
```

[ ]:
```
from sklearn.decomposition import PCA
pca_breast=PCA(n_components=2)
principalComponent_breast=pca_breast.fit_transform(x)
```

[ ]:
```
principal_breast_Df=pd.
  ↪DataFrame(data=principalComponent_breast,columns=['principal component␣
  ↪1','principal component 2'])
principal_breast_Df.tail()
```

[ ]:

	principal component 1	principal component 2
564	6.439315	-3.576817
565	3.793382	-3.584048
566	1.256179	-1.902297
567	10.374794	1.672010
568	-5.475243	-0.670637

[ ]:
```
print('Explained variation per principal component:{}'.format(pca_breast.
  ↪explained_variance_ratio_))
```

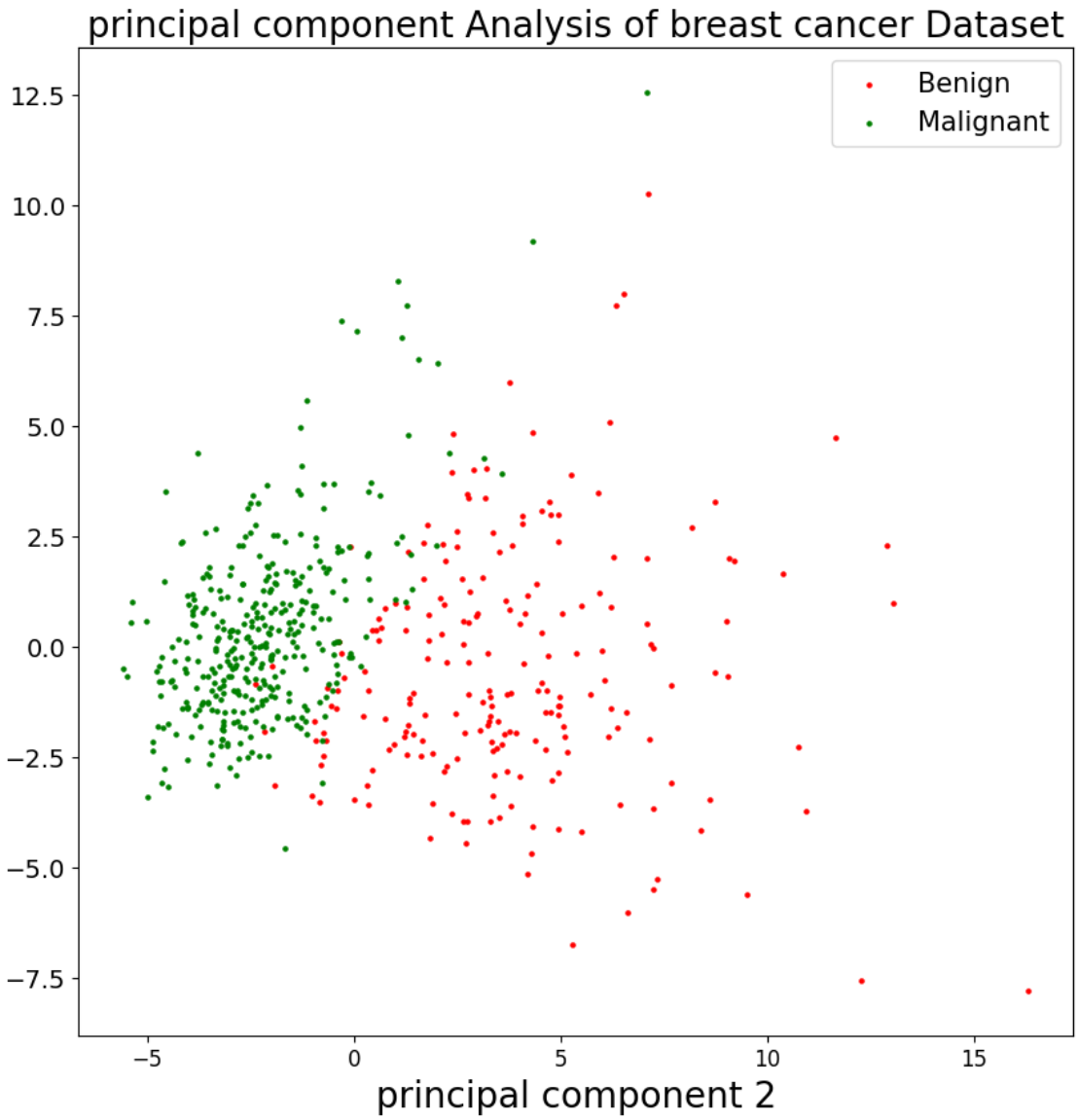
```
Explained variation per principal component:[0.44272026 0.18971182]
```

[ ]:
```
import matplotlib.pyplot as plt
plt.figure()
plt.figure(figsize=(10,10))
plt.xticks(fontsize=12)
plt.yticks(fontsize=14)
plt.xlabel('principal component 1',fontsize=20)
plt.xlabel('principal component 2',fontsize=20)
plt.title("principal component Analysis of breast cancer Dataset",fontsize=20)
targets=['Benign','Malignant']
colors=['r','g']
for target,color in zip(targets,colors):
  indicesToKeep=breast_dataset['label']==target
  plt.scatter(principal_breast_Df.loc[indicesToKeep,'principal component 1'],
              principal_breast_Df.loc[indicesToKeep,'principal component␣
  ↪2'],c=color,s=5)
plt.legend(targets,prop={'size':15})
```

[ ]:
```
<matplotlib.legend.Legend at 0x789e09558d90>
```

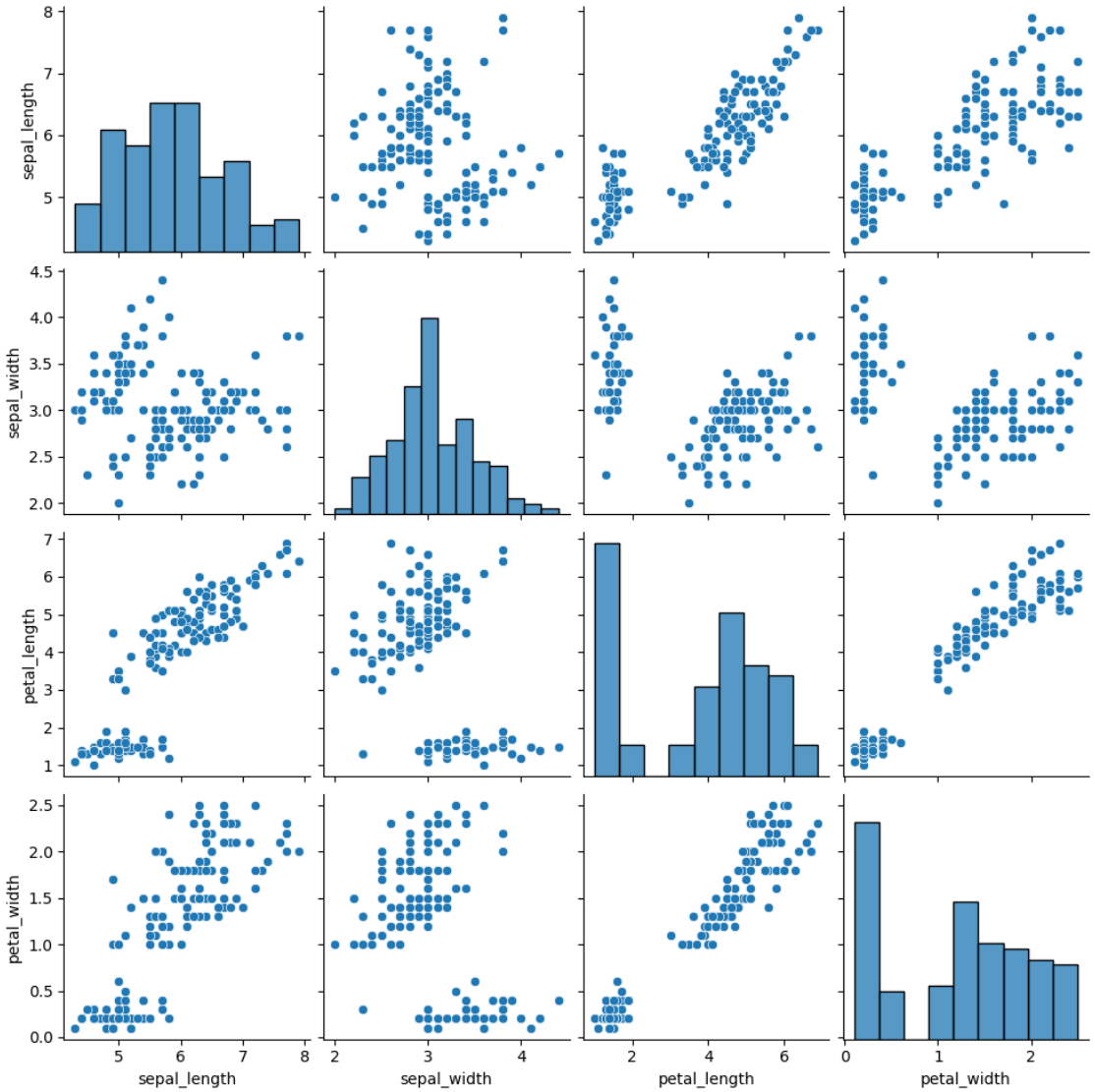


```
<Figure size 640x480 with 0 Axes>
```

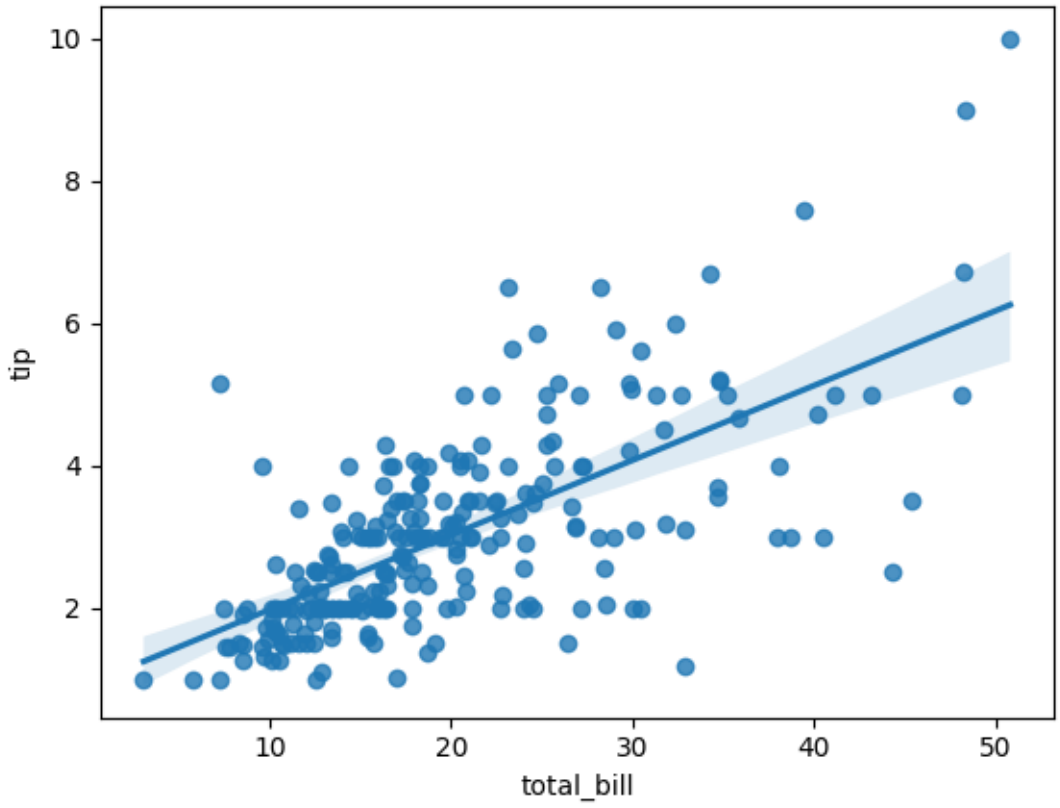


#2.3Correlation_Regression

[ ]:
```
import seaborn as sns
import matplotlib.pyplot as plt
df=sns.load_dataset('iris')
sns.pairplot(df,kind='scatter')
plt.show()
```



[ ]:
```
import seaborn as sb
from matplotlib import pyplot as plt
df=sb.load_dataset('tips')
sb.regplot(x='total_bill',y='tip',data=df)
plt.show()
```




```
[ ]: import matplotlib.pyplot as plt
     from scipy import stats
```

```
[ ]: x=[5,7,8,7,2,17,2,9,4,11,12,6]
     y=[99,86,87,111,6,103,87,94,78,77,85,86]
```

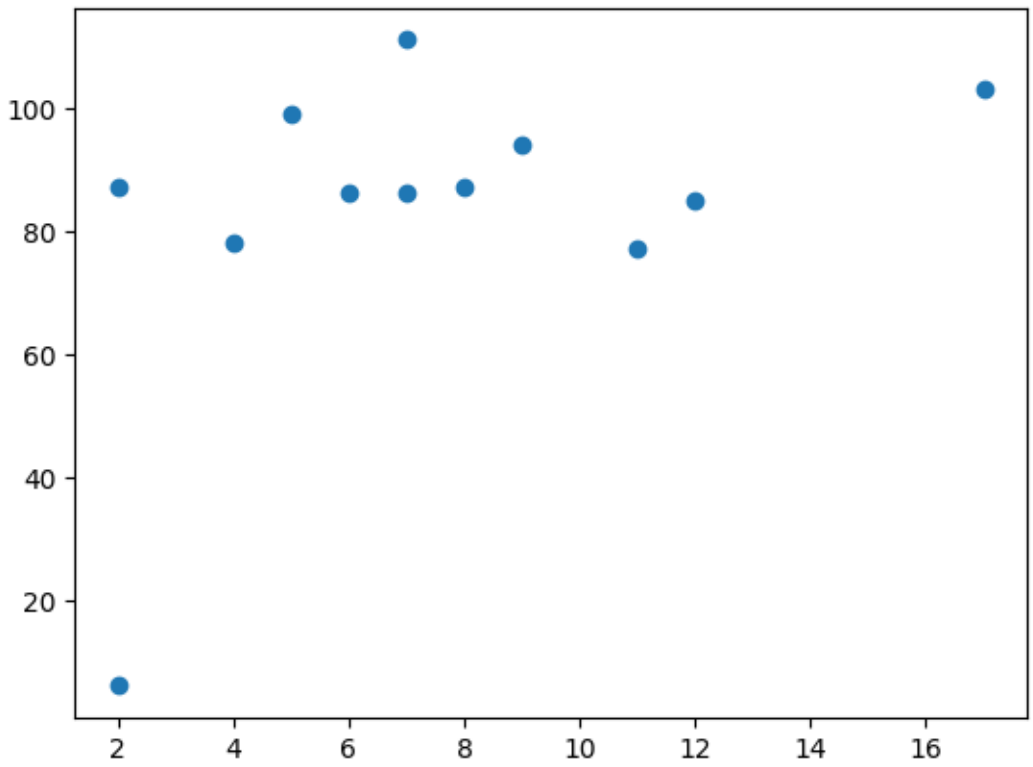
```
[ ]: slope,intercept,r,p,std_err=stats.linregress(x,y)
```

```
[ ]: def myfunc(x):
       return slope*x+intercept
```

```
[ ]: mymodel=list(map(myfunc,x))
```

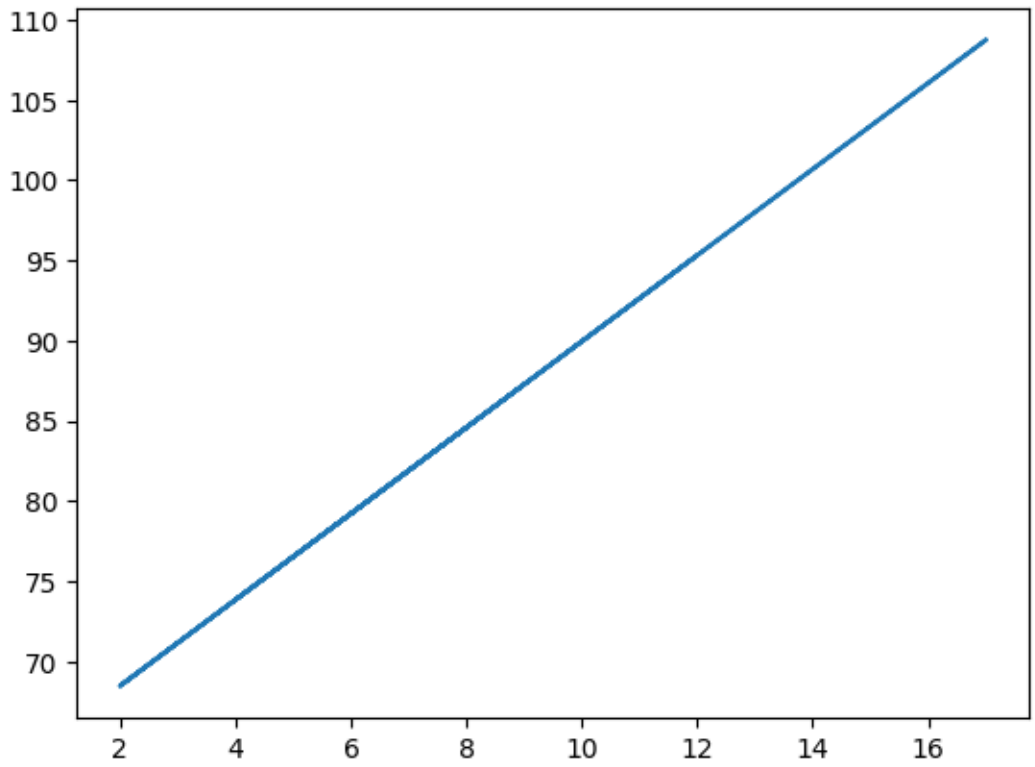
```
[ ]: plt.scatter(x,y)
```

```
[ ]: <matplotlib.collections.PathCollection at 0x789e03ca4b50>
```



[ ]:
```
plt.plot(x,mymodel)
```

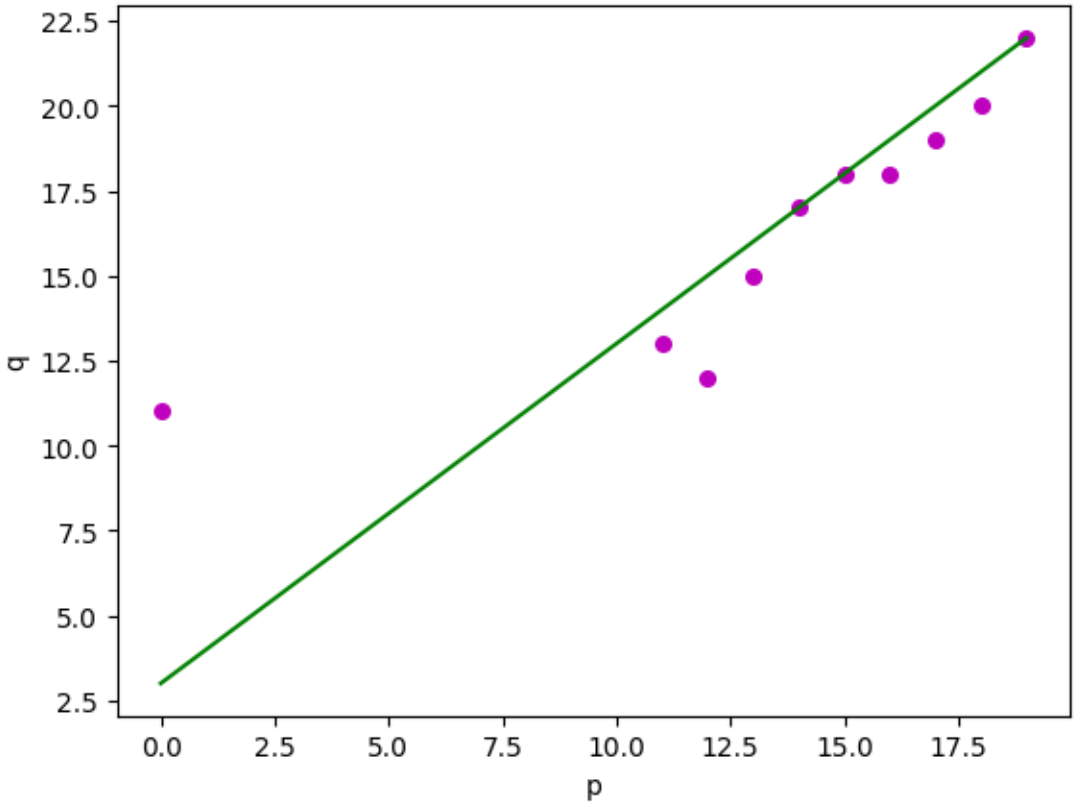
[ ]:
```
[<matplotlib.lines.Line2D at 0x789e039f8340>]
```



[ ]:
```
import numpy as nmp
import matplotlib.pyplot as mtplt
def estimate_coeff(p,q):
  n1=nmp.size(p)
  m_p=nmp.mean(p)
  m_q=nmp.mean(q)

  SS_pq=nmp.sum(q*p)-n1*m_q*m_p
  SS_pp=nmp.sum(p*q)-n1*m_q*m_p

  b_1=SS_pq/SS_pp
  b_0=m_q-b_1*m_p

  return(b_0,b_1)

def plot_regression_line(p,q,b):
  mtplt.scatter(p,q,color='m',marker='o',s=30)

  q_pred=b[0]+b[1]*p

  mtplt.plot(p,q_pred,color='g')
  mtplt.xlabel('p')
```

```
  mtplt.ylabel('q')
  mtplt.show()

def main():
  p=nmp.array([0,11,12,13,14,15,16,17,18,19])
  q=nmp.array([11,13,12,15,17,18,18,19,20,22])
  b=estimate_coeff(p,q)
  print('estimateed coefficients are:\nb_0={}\\nb_1={}'.format(b[0],b[1]))
  plot_regression_line(p,q,b)
if __name__=='__main__':
    main()
```

```
estimateed coefficients are:
b_0=3.0\nb_1=1.0
```



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