Seaborn

In [1]: ```python
import seaborn as sns
```

In [2]: ```python
ap=sns.load_dataset("iris")
```

In [3]: ap

Out[3]:

	sepal_length	sepal_width	petal_length	petal_width	species
0	5.1	3.5	1.4	0.2	setosa
1	4.9	3.0	1.4	0.2	setosa
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa
4	5.0	3.6	1.4	0.2	setosa
5	5.4	3.9	1.7	0.4	setosa
6	4.6	3.4	1.4	0.3	setosa
7	5.0	3.4	1.5	0.2	setosa
8	4.4	2.9	1.4	0.2	setosa
9	4.9	3.1	1.5	0.1	setosa
10	5.4	3.7	1.5	0.2	setosa
11	4.8	3.4	1.6	0.2	setosa
12	4.8	3.0	1.4	0.1	setosa
13	4.3	3.0	1.1	0.1	setosa
14	5.8	4.0	1.2	0.2	setosa
15	5.7	4.4	1.5	0.4	setosa
16	5.4	3.9	1.3	0.4	setosa
17	5.1	3.5	1.4	0.3	setosa
18	5.7	3.8	1.7	0.3	setosa
19	5.1	3.8	1.5	0.3	setosa
20	5.4	3.4	1.7	0.2	setosa
21	5.1	3.7	1.5	0.4	setosa
22	4.6	3.6	1.0	0.2	setosa
23	5.1	3.3	1.7	0.5	setosa
24	4.8	3.4	1.9	0.2	setosa
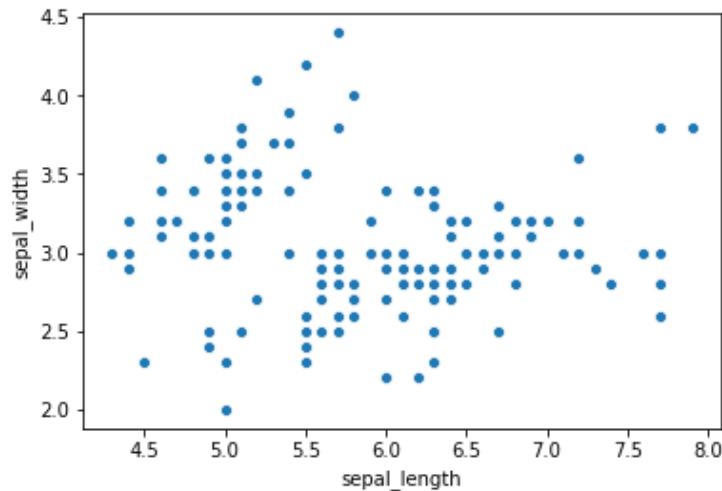
	sepal_length	sepal_width	petal_length	petal_width	species
25	5.0	3.0	1.6	0.2	setosa
26	5.0	3.4	1.6	0.4	setosa
27	5.2	3.5	1.5	0.2	setosa
28	5.2	3.4	1.4	0.2	setosa
29	4.7	3.2	1.6	0.2	setosa
...	...	...	...	...	...
120	6.9	3.2	5.7	2.3	virginica
121	5.6	2.8	4.9	2.0	virginica
122	7.7	2.8	6.7	2.0	virginica
123	6.3	2.7	4.9	1.8	virginica
124	6.7	3.3	5.7	2.1	virginica
125	7.2	3.2	6.0	1.8	virginica
126	6.2	2.8	4.8	1.8	virginica
127	6.1	3.0	4.9	1.8	virginica
128	6.4	2.8	5.6	2.1	virginica
129	7.2	3.0	5.8	1.6	virginica
130	7.4	2.8	6.1	1.9	virginica
131	7.9	3.8	6.4	2.0	virginica
132	6.4	2.8	5.6	2.2	virginica
133	6.3	2.8	5.1	1.5	virginica
134	6.1	2.6	5.6	1.4	virginica
135	7.7	3.0	6.1	2.3	virginica
136	6.3	3.4	5.6	2.4	virginica
137	6.4	3.1	5.5	1.8	virginica
138	6.0	3.0	4.8	1.8	virginica
139	6.9	3.1	5.4	2.1	virginica
140	6.7	3.1	5.6	2.4	virginica
141	6.9	3.1	5.1	2.3	virginica

	sepal_length	sepal_width	petal_length	petal_width	species
142	5.8	2.7	5.1	1.9	virginica
143	6.8	3.2	5.9	2.3	virginica
144	6.7	3.3	5.7	2.5	virginica
145	6.7	3.0	5.2	2.3	virginica
146	6.3	2.5	5.0	1.9	virginica
147	6.5	3.0	5.2	2.0	virginica
148	6.2	3.4	5.4	2.3	virginica
149	5.9	3.0	5.1	1.8	virginica

150 rows × 5 columns
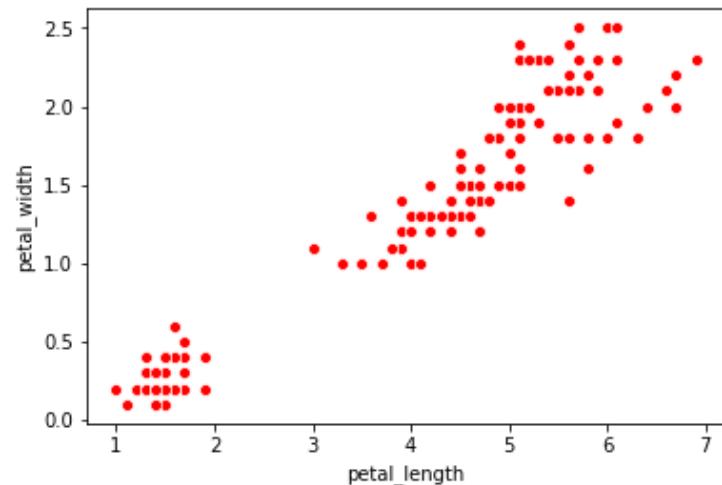
```
In [6]: sns.scatterplot(x="sepal_length",y="sepal_width",data=ap)
```

Out[6]: <matplotlib.axes._subplots.AxesSubplot at 0x20b81443588>

In [34]: `sns.scatterplot(x="petal_length",y="petal_width",data=ap,color="red")`

Out[34]: `<matplotlib.axes._subplots.AxesSubplot at 0x20b8558a358>`
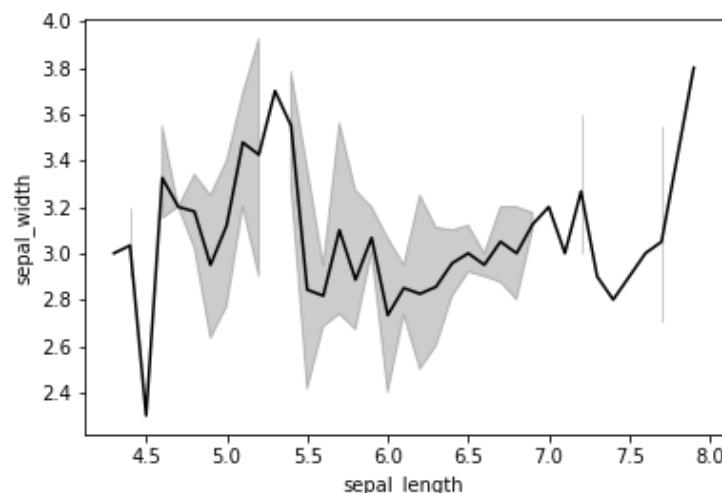
In [35]: `sns.lineplot(x="sepal_length",y="sepal_width",data=ap,color="black")`

```
C:\Users\anikp\Anaconda3\lib\site-packages\scipy\stats\stats.py:1713: FutureWarning: Using a non-tuple sequence for multidimen
sional indexing is deprecated; use `arr[tuple(seq)]` instead of `arr[seq]`. In the future this will be interpreted as an array
index, `arr[np.array(seq)]`, which will result either in an error or a different result.
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```
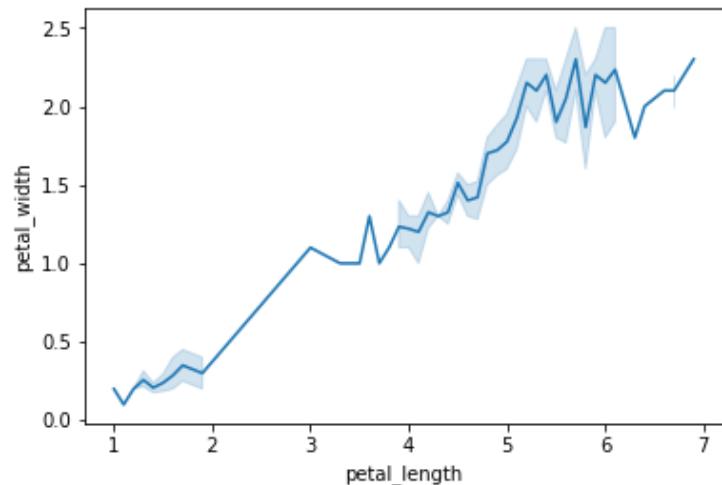
Out[35]: `<matplotlib.axes._subplots.AxesSubplot at 0x20b858a7a58>`
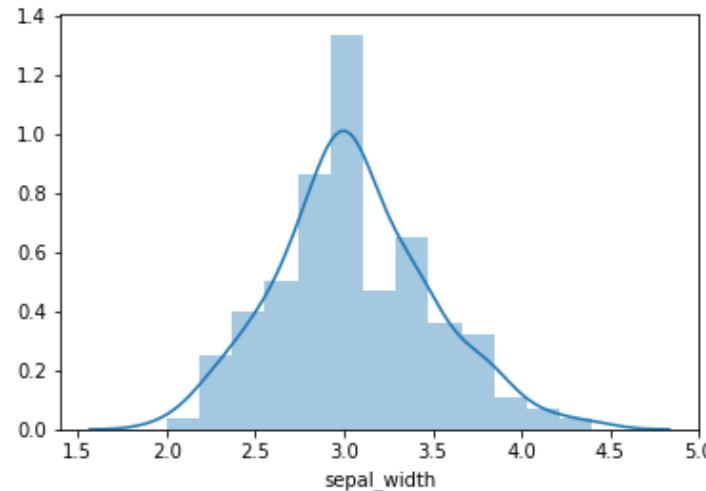
In [18]: `sns.lineplot(x="petal_length",y="petal_width",data=ap)`

Out[18]: `<matplotlib.axes._subplots.AxesSubplot at 0x20b82f06c18>`
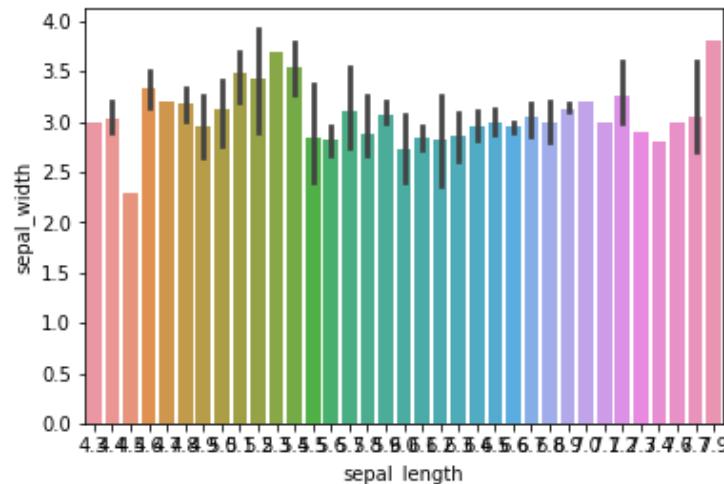
In [14]: `sns.distplot(ap["sepal_width"])`

Out[14]: `<matplotlib.axes._subplots.AxesSubplot at 0x20b82ad25c0>`
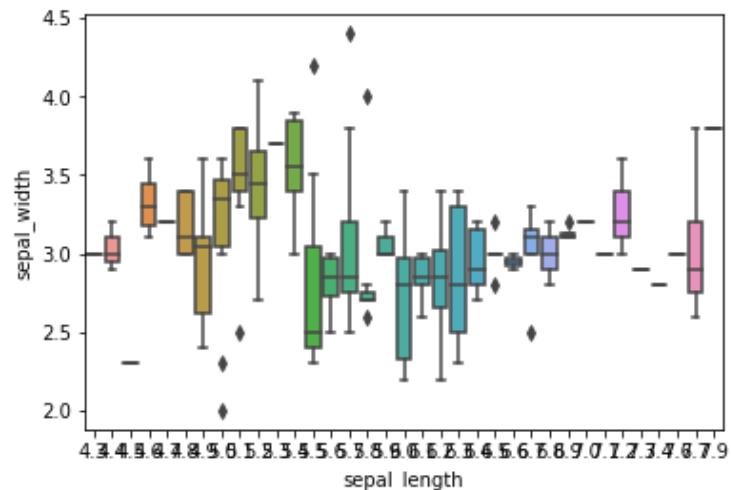
In [15]: `sns.barplot(x="sepal_length",y="sepal_width",data=ap)`

Out[15]: `<matplotlib.axes._subplots.AxesSubplot at 0x20b82b18d68>`
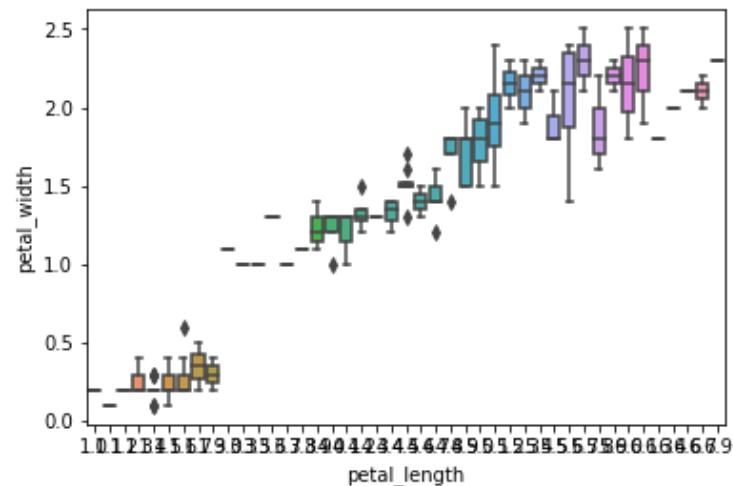
In [16]: `sns.boxplot(x="sepal_length",y="sepal_width",data=ap)`

Out[16]: `<matplotlib.axes._subplots.AxesSubplot at 0x20b82c38cf8>`

In [19]:
```python
sns.boxplot(x="petal_length",y="petal_width",data=ap)
```

Out[19]: `<matplotlib.axes._subplots.AxesSubplot at 0x20b8301f5c0>`
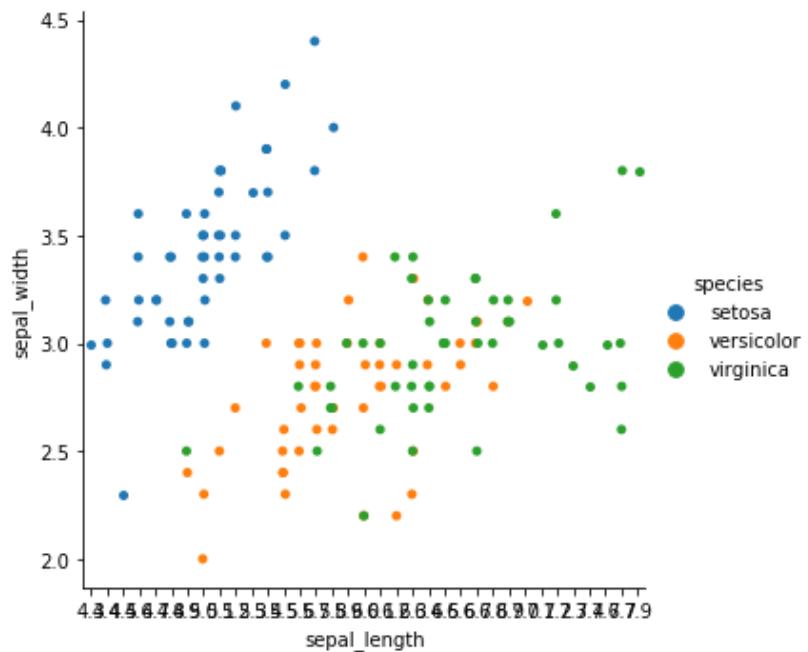
In [22]: `ap.describe()`

Out[22]:

|	sepal_length	sepal_width	petal_length	petal_width
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.057333	3.758000	1.199333
std	0.828066	0.435866	1.765298	0.762238
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000
75%	6.400000	3.300000	5.100000	1.800000
max	7.900000	4.400000	6.900000	2.500000
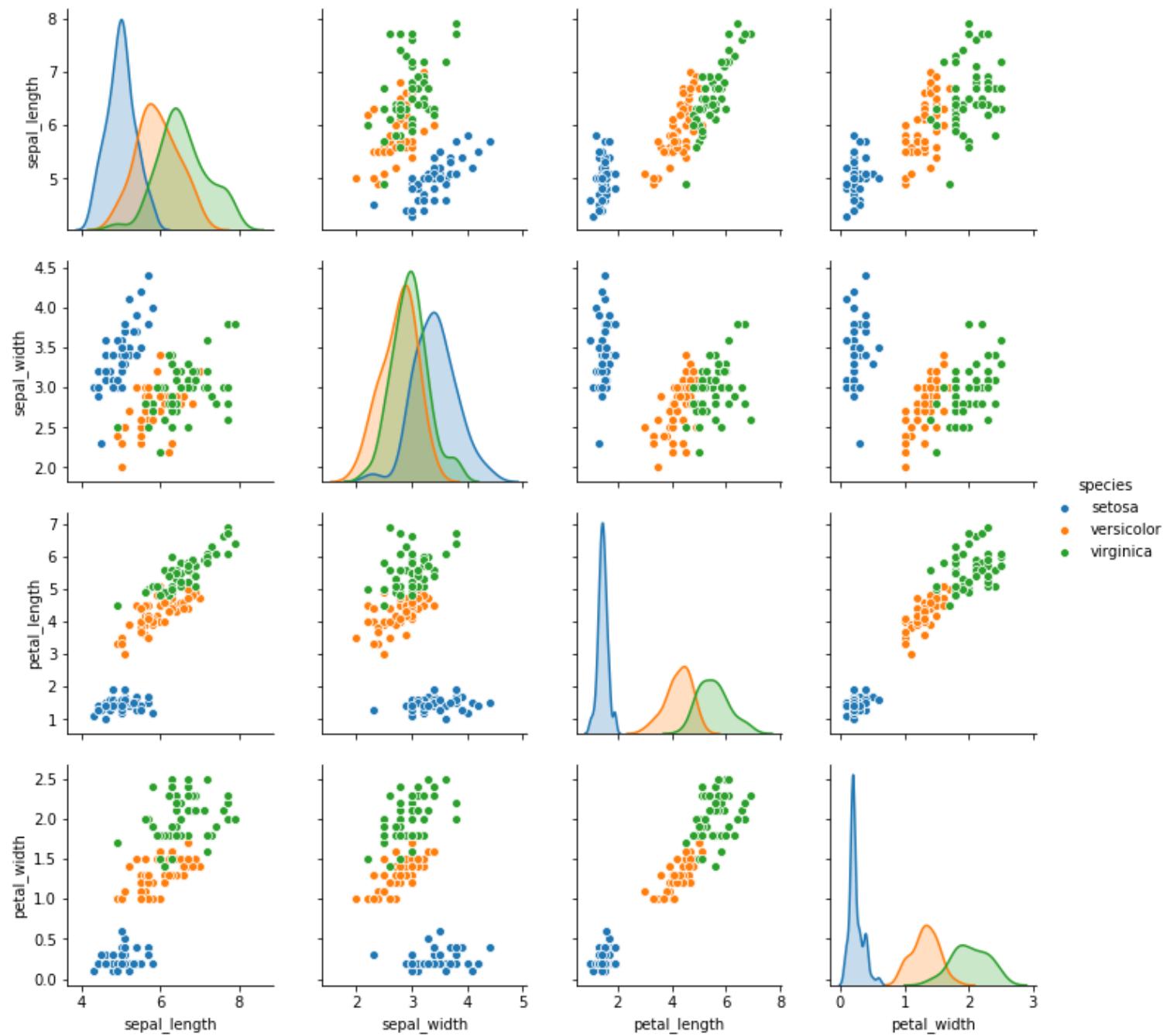
In [30]:
```python
sns.catplot(x="sepal_length",y="sepal_width",hue="species",data=ap)
```

Out[30]: `<seaborn.axisgrid.FacetGrid at 0x20b84f39668>`

In [27]: `sns.pairplot(ap,hue="species")`

Out[27]: `<seaborn.axisgrid.PairGrid at 0x20b83112e48>`
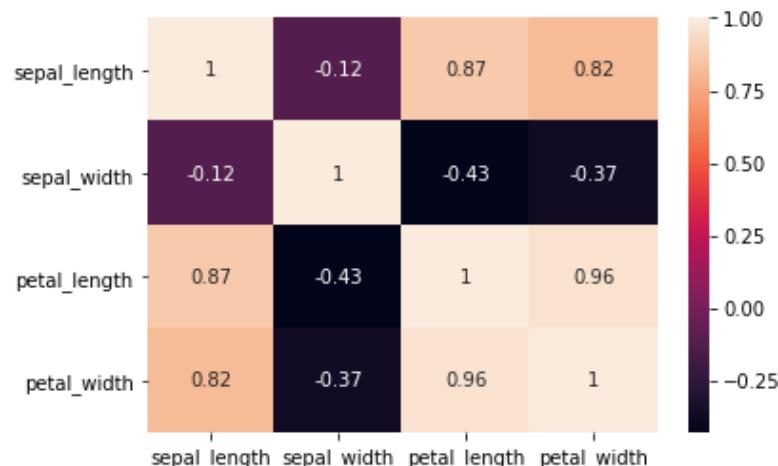
In [28]: `ap.corr()`

Out[28]:

	sepal_length	sepal_width	petal_length	petal_width
sepal_length	1.000000	-0.117570	0.871754	0.817941
sepal_width	-0.117570	1.000000	-0.428440	-0.366126
petal_length	0.871754	-0.428440	1.000000	0.962865
petal_width	0.817941	-0.366126	0.962865	1.000000

In [32]: `sns.heatmap(ap.corr(),annot=True)`

Out[32]: `<matplotlib.axes._subplots.AxesSubplot at 0x20b854f7e10>`

In [ ]:

In [33]: `ap.to_csv("iris.csv")`