

```
In [1]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
warnings.simplefilter('ignore')
```

```
In [4]: data = pd.read_csv('https://gist.githubusercontent.com/curran/a08a1080b88344b0c8a7,
data')
```

```
Out[4]:
```

	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
...	...	...	...	...	...
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 [5]: data.head()
```

```
Out[5]:
```

	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

```
In [6]: data.describe()
```

Out[6]:

	sepal_length	sepal_width	petal_length	petal_width
<b>count</b>	150.000000	150.000000	150.000000	150.000000
<b>mean</b>	5.843333	3.054000	3.758667	1.198667
<b>std</b>	0.828066	0.433594	1.764420	0.763161
<b>min</b>	4.300000	2.000000	1.000000	0.100000
<b>25%</b>	5.100000	2.800000	1.600000	0.300000
<b>50%</b>	5.800000	3.000000	4.350000	1.300000
<b>75%</b>	6.400000	3.300000	5.100000	1.800000
<b>max</b>	7.900000	4.400000	6.900000	2.500000

In [7]: `data.describe(include = 'object')`

Out[7]:

	species
<b>count</b>	150
<b>unique</b>	3
<b>top</b>	setosa
<b>freq</b>	50

In [8]: `data.isnull().sum()`

Out[8]:

```
sepal_length    0
sepal_width     0
petal_length    0
petal_width     0
species         0
dtype: int64
```

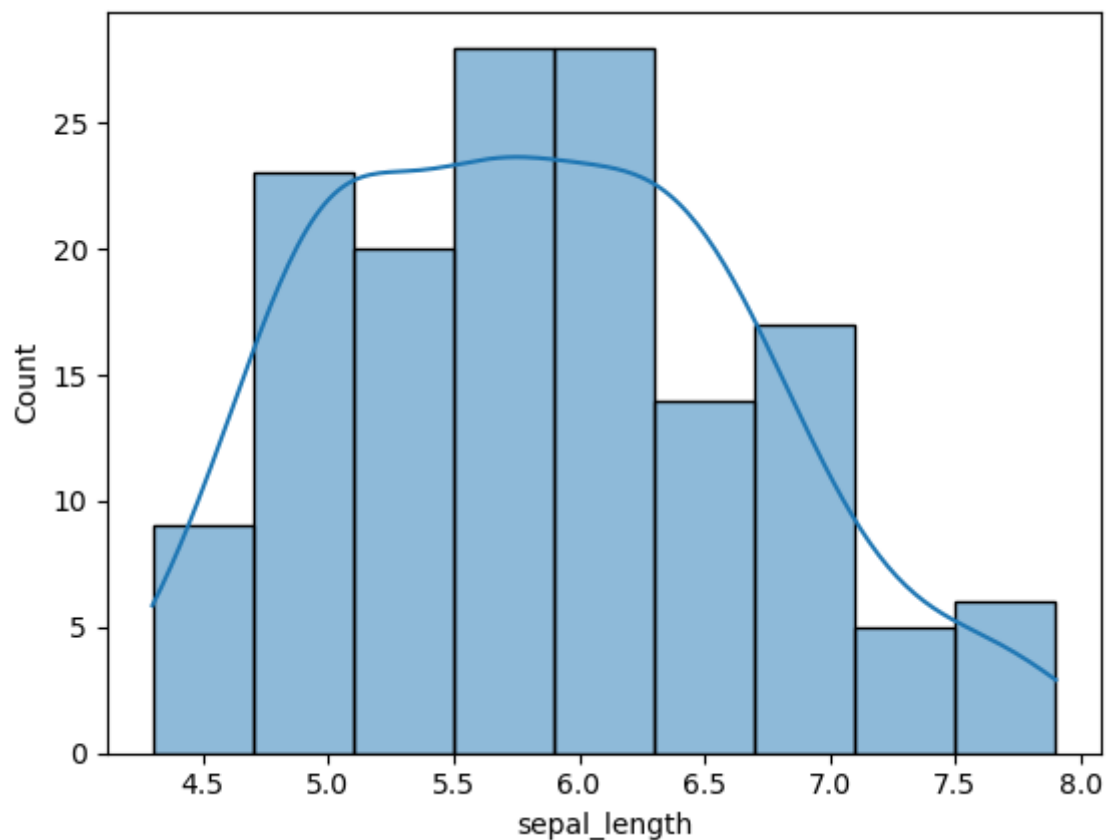
In [9]:

```
print("\n\nThe features in the dataset are as follows : ")
print("1. Sepal length : ", data['sepal_length'].dtype)
print("2. Sepal width : ", data['sepal_width'].dtype)
print("3. Petal length : ", data['petal_length'].dtype)
print("4. Petal width : ", data['petal_width'].dtype)
print("5. Species : ", data['species'].dtype)
```

```
The features in the dataset are as follows :
1. Sepal length : float64
2. Sepal width : float64
3. Petal length : float64
4. Petal width : float64
5. Species : object
```

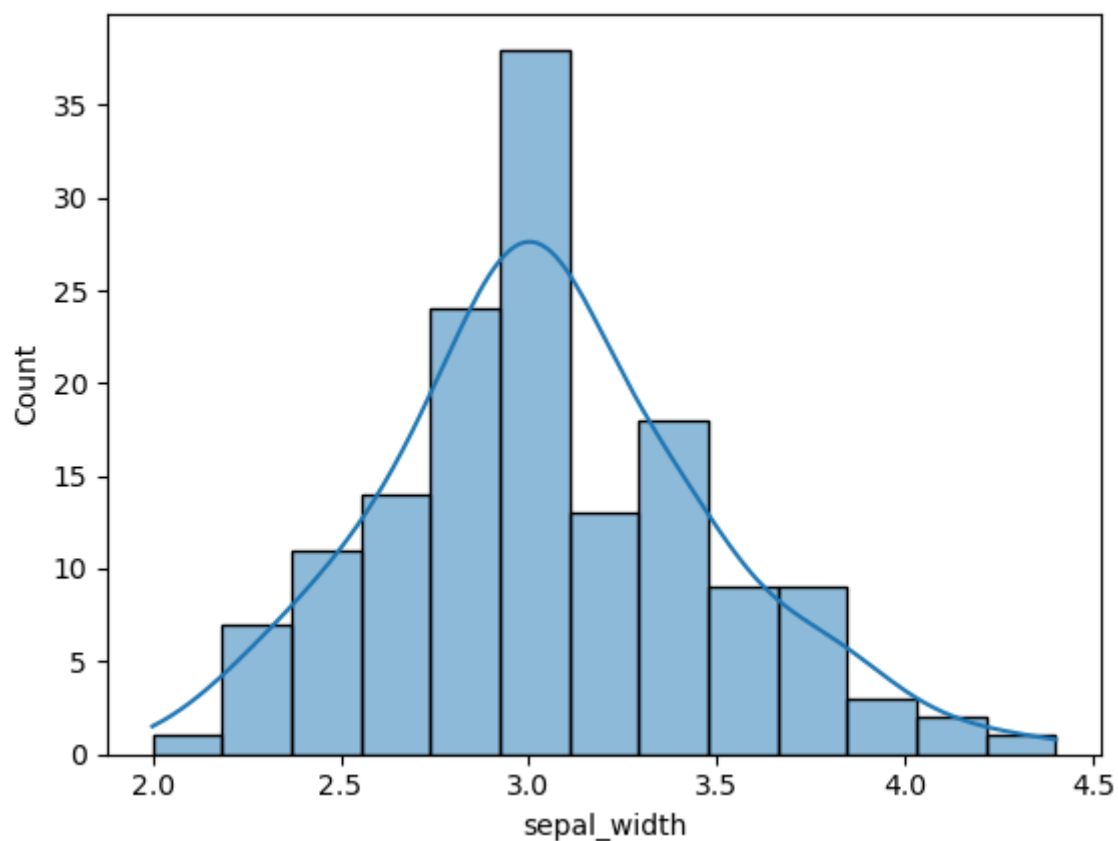
In [10]: `sns.histplot(x = data['sepal_length'], kde=True)`

Out[10]: `<AxesSubplot:xlabel='sepal_length', ylabel='Count'>`



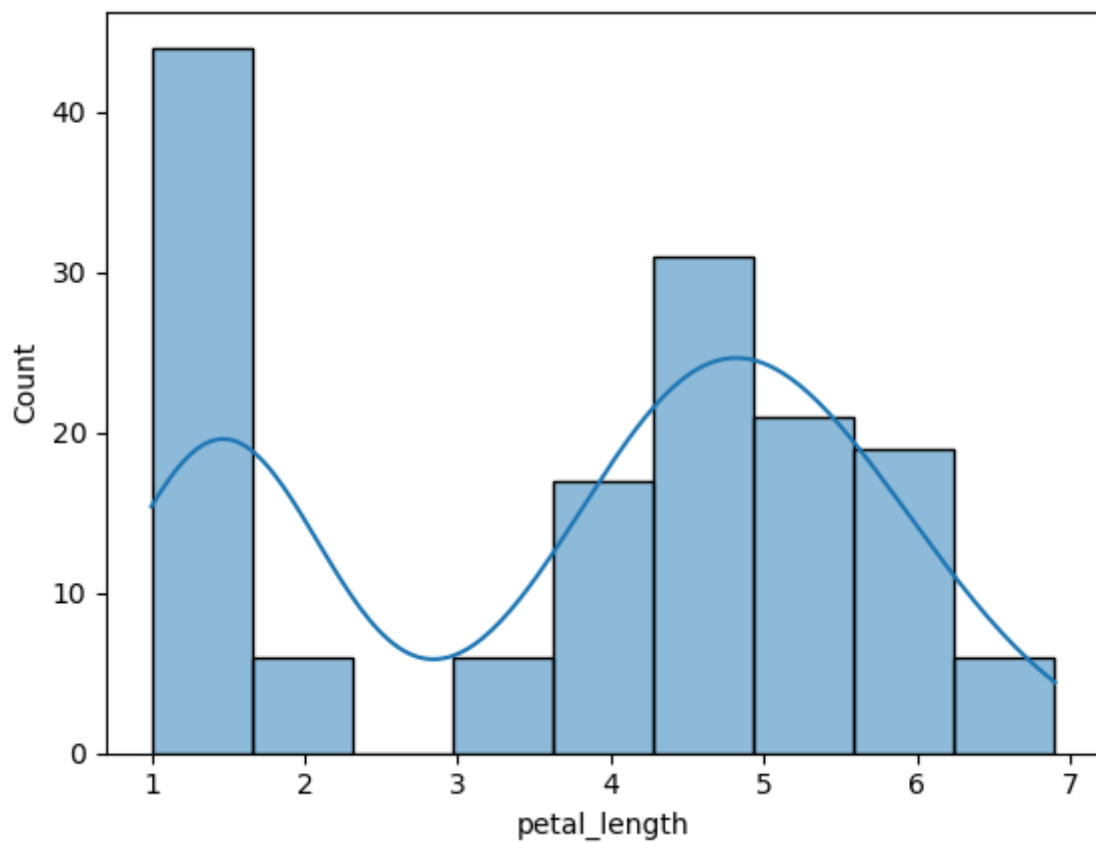
```
In [11]: sns.histplot(x = data['sepal_width'], kde=True)
```

```
Out[11]: <AxesSubplot:xlabel='sepal_width', ylabel='Count'>
```



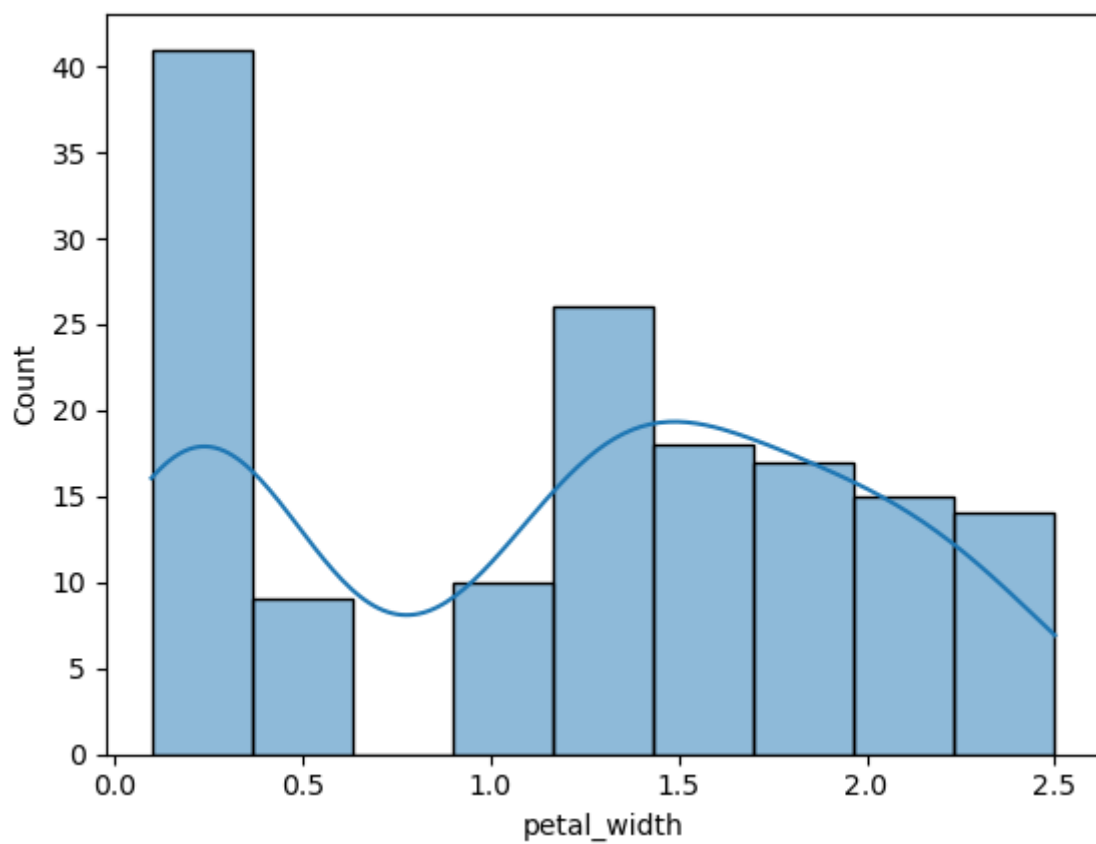
```
In [12]: sns.histplot(x = data['petal_length'], kde=True)
```

```
Out[12]: <AxesSubplot:xlabel='petal_length', ylabel='Count'>
```



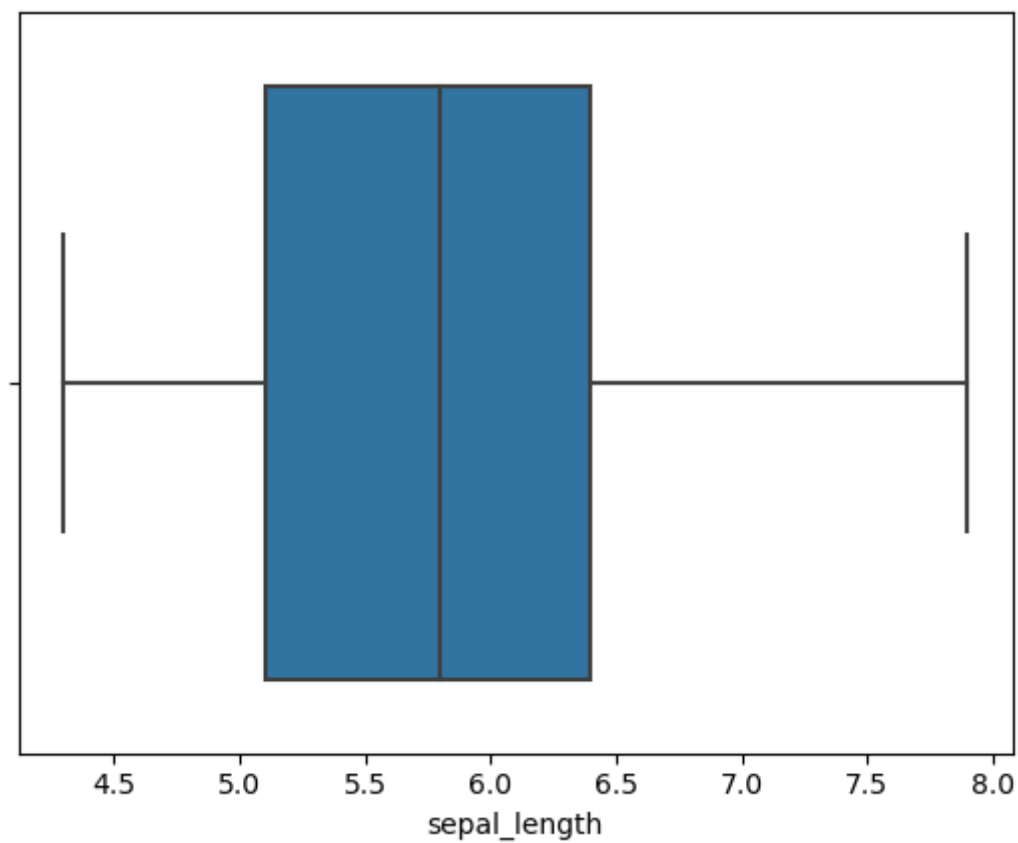
```
In [13]: sns.histplot(x = data['petal_width'], kde=True)
```

```
Out[13]: <AxesSubplot:xlabel='petal_width', ylabel='Count'>
```



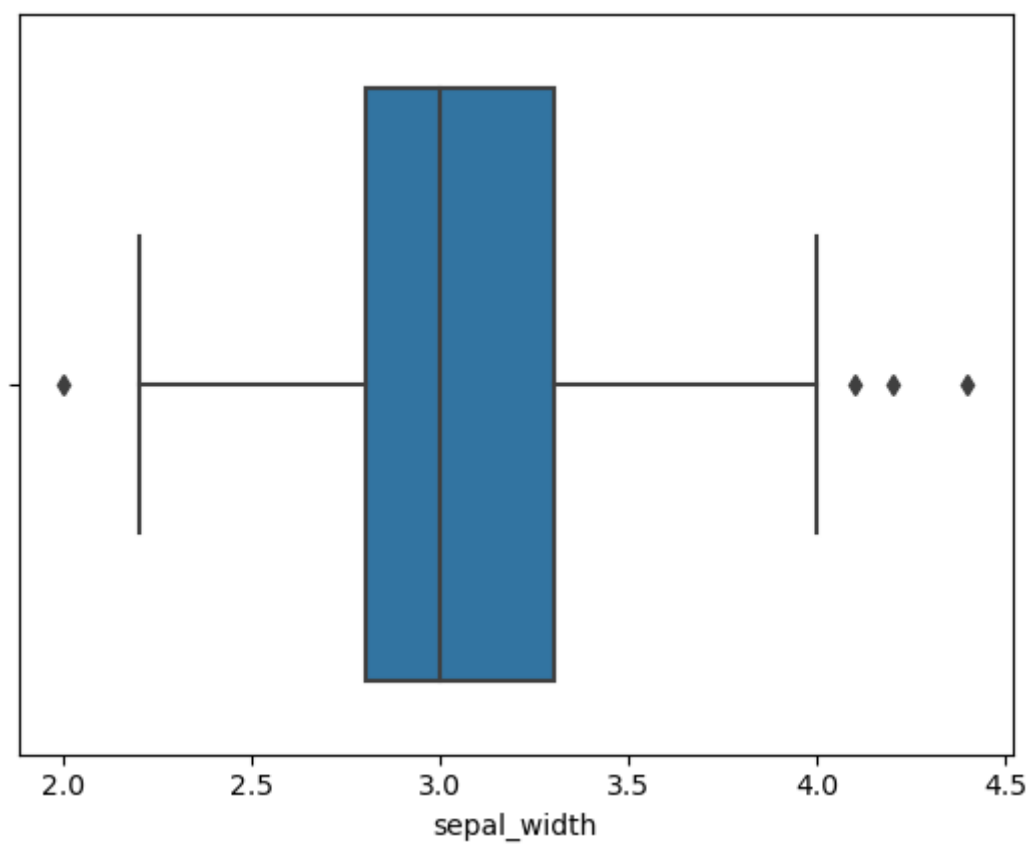
```
In [14]: sns.boxplot(data['sepal_length'])
```

```
Out[14]: <AxesSubplot:xlabel='sepal_length'>
```



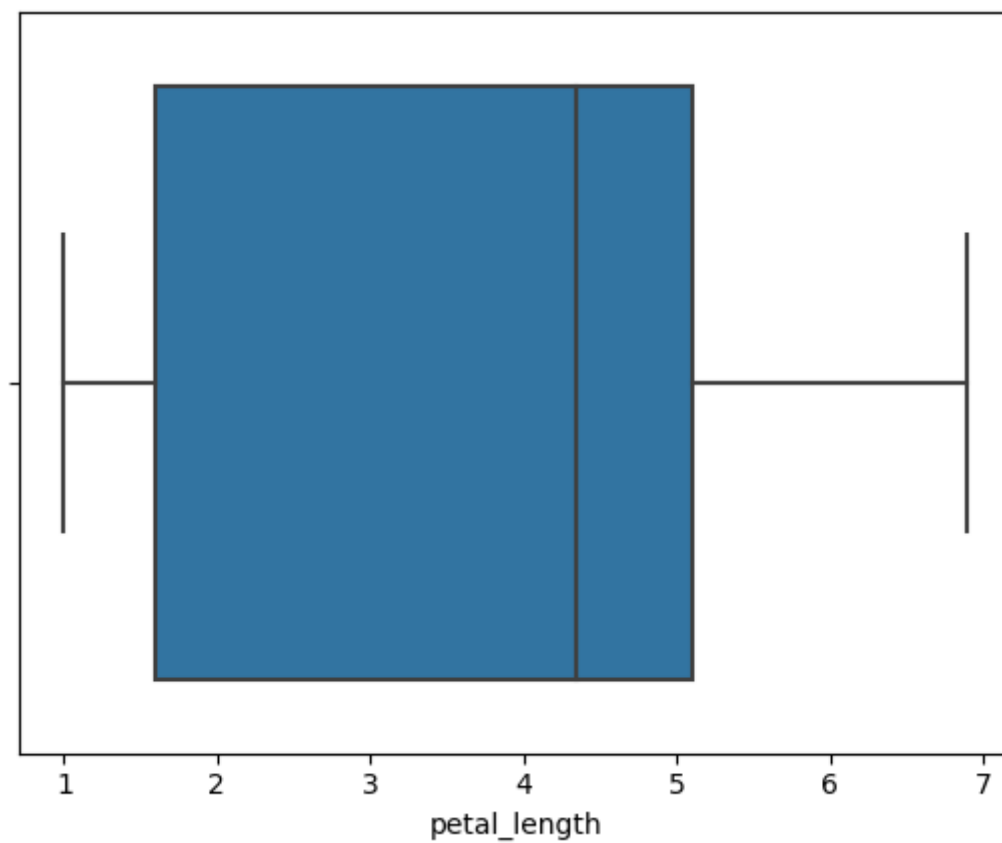
```
In [15]: sns.boxplot(data['sepal_width'])
```

```
Out[15]: <AxesSubplot:xlabel='sepal_width'>
```



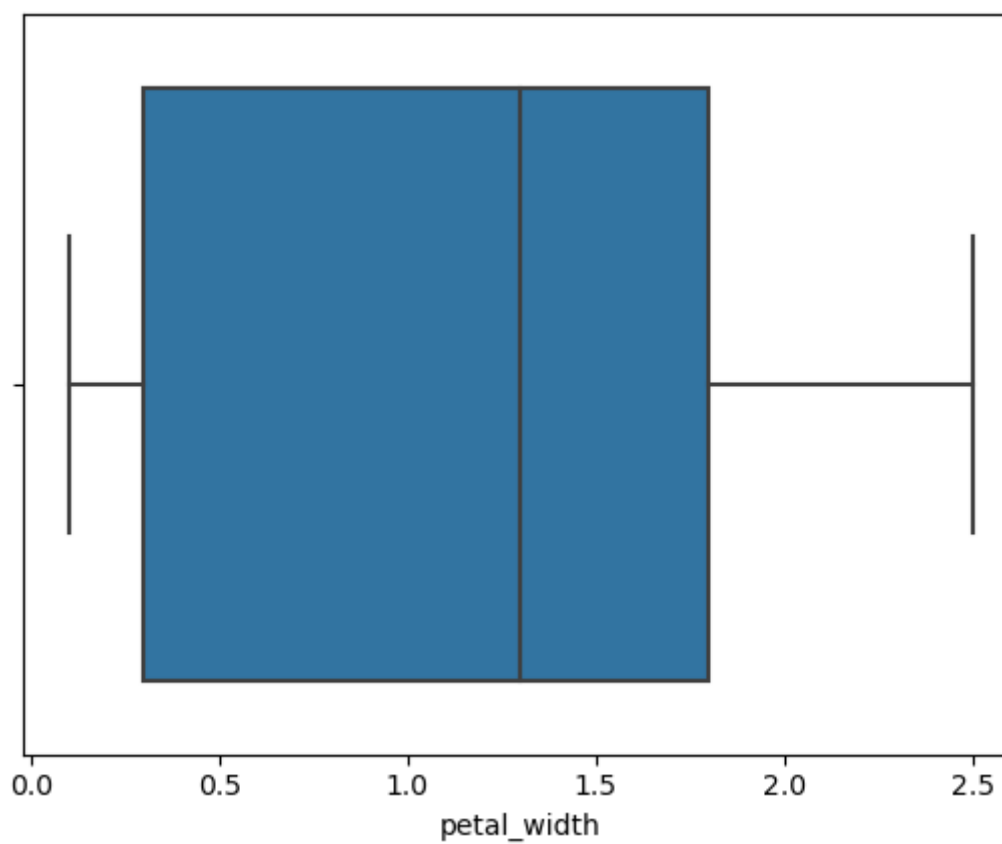
```
In [16]: sns.boxplot(data['petal_length'])
```

```
Out[16]: <AxesSubplot:xlabel='petal_length'>
```



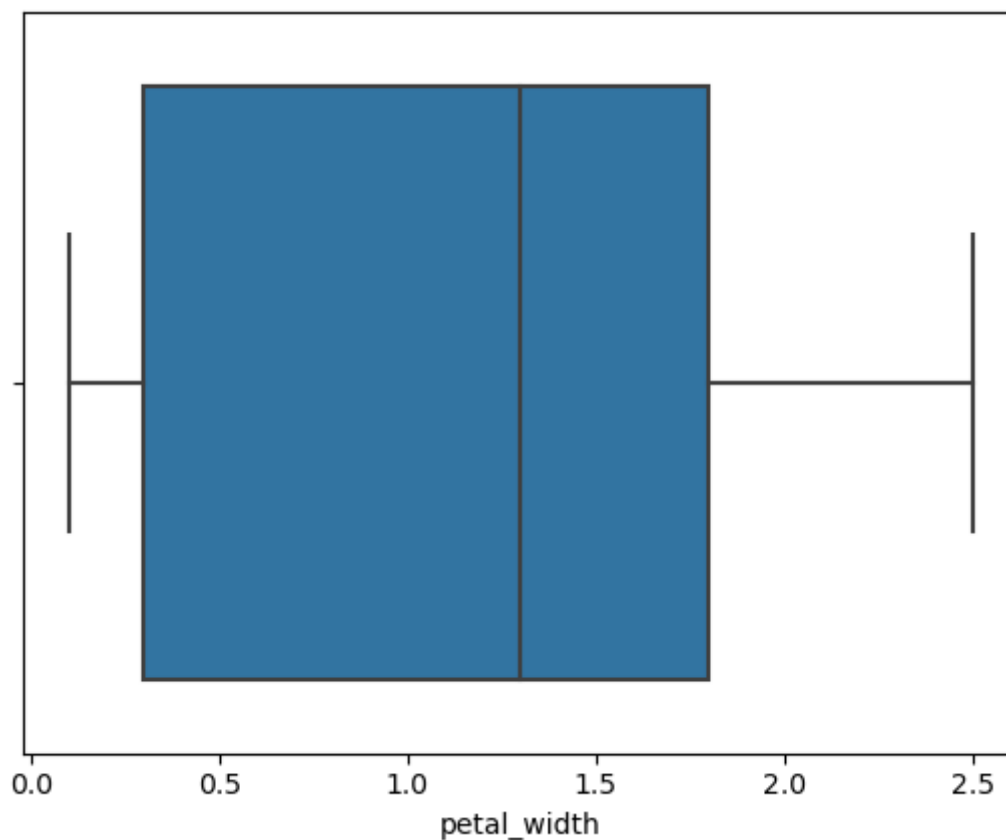
```
In [17]: sns.boxplot(data['petal_width'])
```

```
Out[17]: <AxesSubplot:xlabel='petal_width'>
```



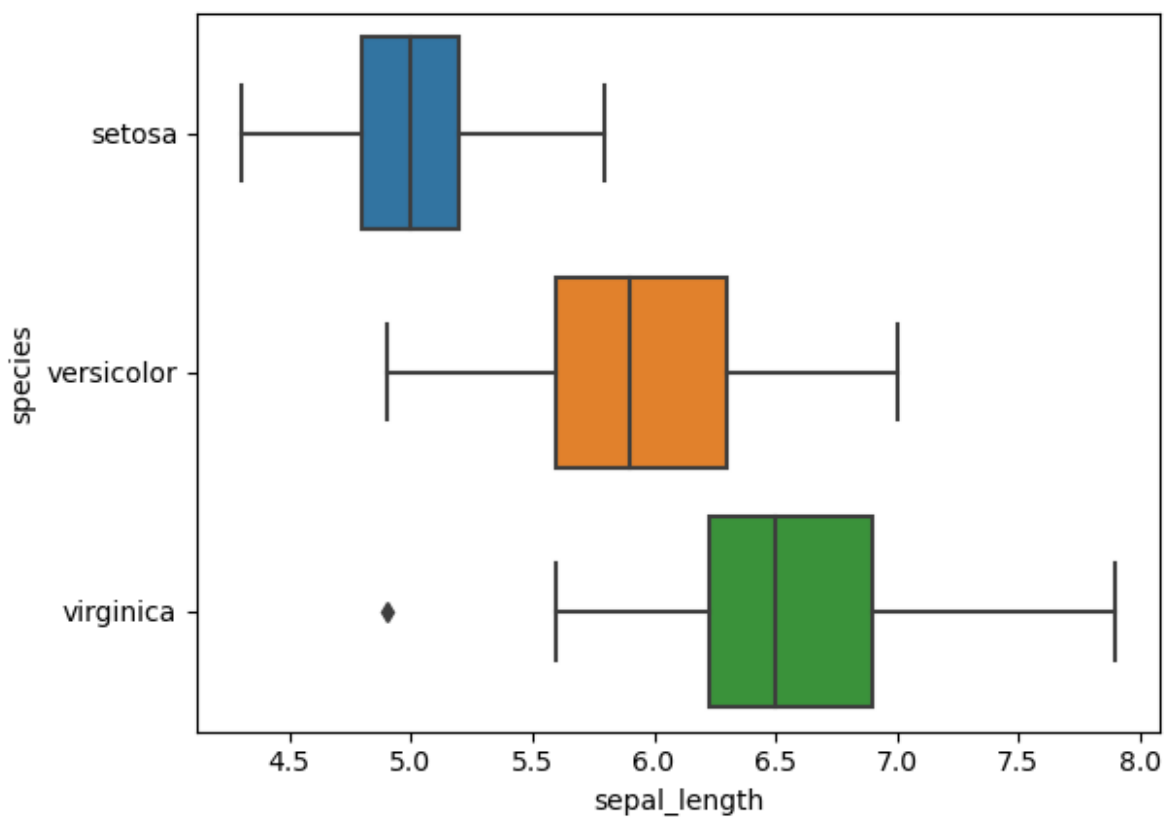
```
In [18]: sns.boxplot(data['petal_width'])
```

```
Out[18]: <AxesSubplot:xlabel='petal_width'>
```



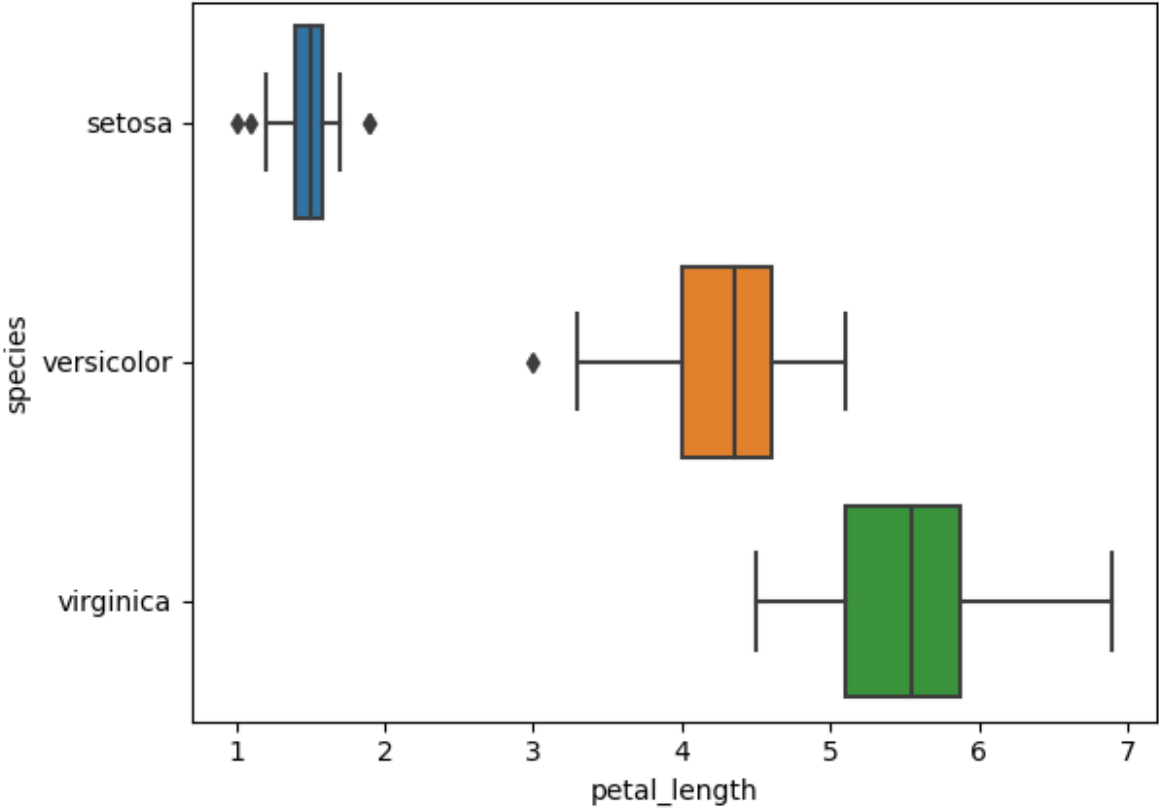
```
In [19]: sns.boxplot(x='sepal_length',y='species',data=data)
```

```
Out[19]: <AxesSubplot:xlabel='sepal_length', ylabel='species'>
```



```
In [20]: sns.boxplot(x='petal_length',y='species',data=data)
```

```
Out[20]: <AxesSubplot:xlabel='petal_length', ylabel='species'>
```



```
In [ ]:
```