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Practical 10:Download the iris flower dataset or any other dataset intoa dataframe. Scan the dataset and given the interference as

1. List down the feature and types
2. Create histogram for each feature in the dataset
3. Create a boxplot for each seature in the dataset
4. Compare distributions and identify

Import seaborn library

In [ ]:

```
import seaborn as sns
```

Load the Iris dataset using seaborn

In [ ]:

```
df = sns.load_dataset('iris')
```

Display the dataframe

In [ ]:

```
df
```

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
...	...	...	...	...	...
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

Display the column names of the dataframe

In [ ]:

```
df.columns
```

Out [4]:

```
Index(['sepal_length', 'sepal_width', 'petal_length', 'petal_width',
       'species'],
      dtype='object')
```

Display information about the dataframe, including data types and missing values

In [ ]:

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
 #   Column        Non-Null Count  Dtype  
---  ------        --------------  -----  
 0   sepal_length  150 non-null    float64
 1   sepal_width   150 non-null    float64
 2   petal_length  150 non-null    float64
 3   petal_width   150 non-null    float64
 4   species       150 non-null    object 
dtypes: float64(4), object(1)
memory usage: 6.0+ KB
```

Display the data types of columns in the dataframe

In [ ]:

```
df.dtypes
```

Out [6]:

```
sepal_length    float64
sepal_width     float64
petal_length    float64
petal_width     float64
species          object
dtype: object
```

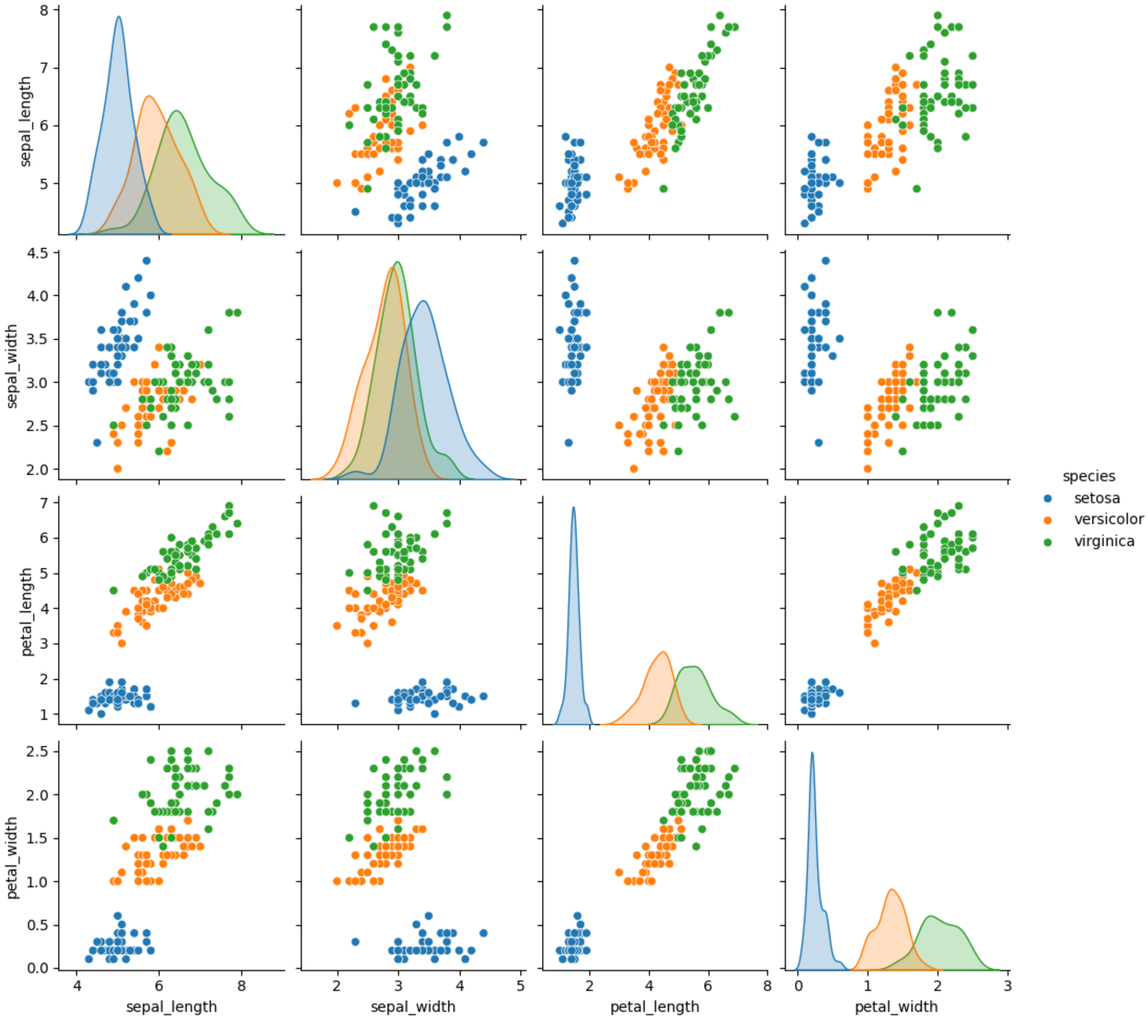
Create a pair plot to visualize pairwise relationships between different variables with hue based on species

In [ ]:

```
sns.pairplot(df,hue = 'species')
```

Out [7]:

```
<seaborn.axisgrid.PairGrid at 0x7a48a6ae37c0>
```



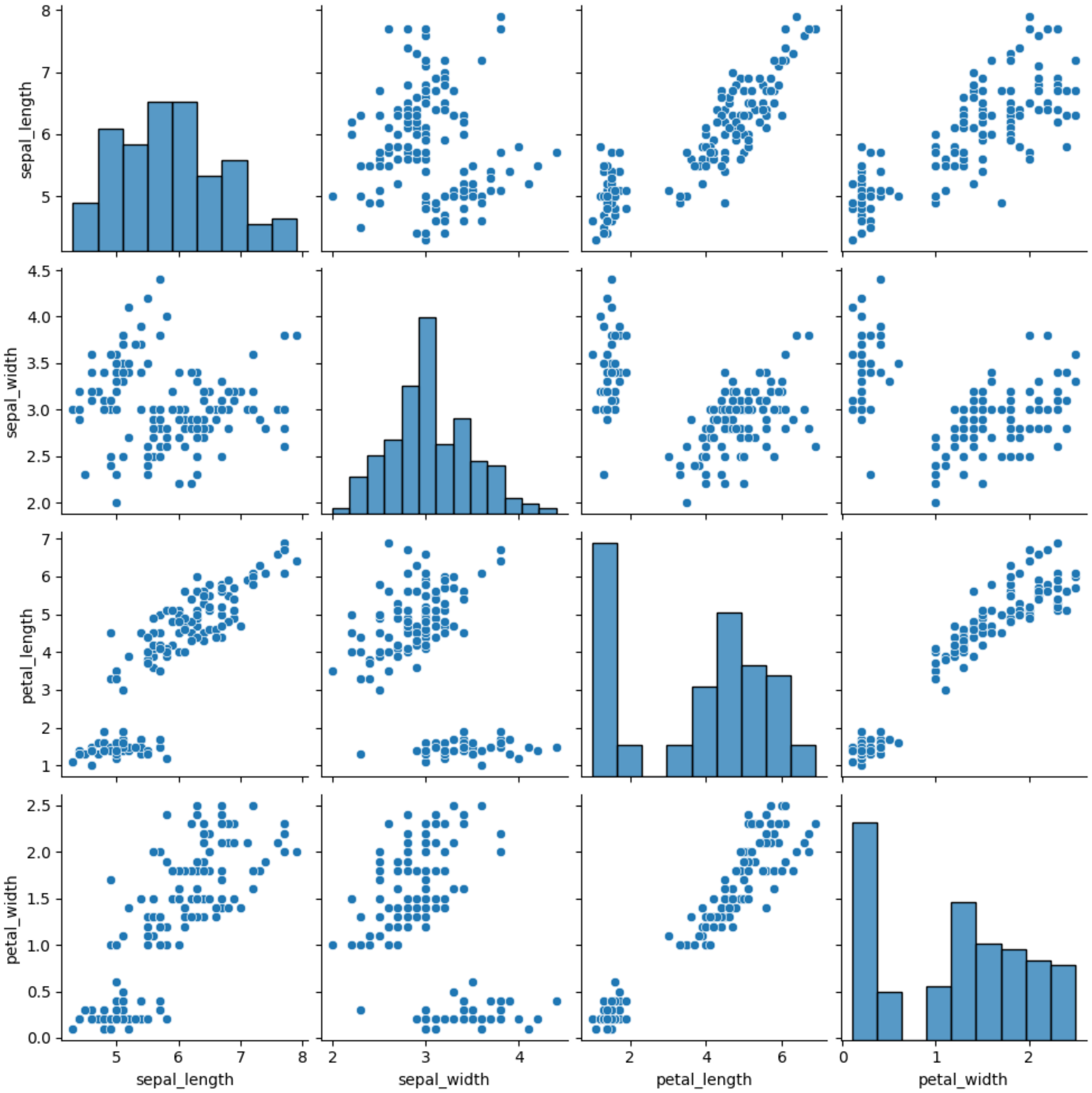
Create a pair plot to visualize pairwise relationships between different variables

In [ ]:

```
sns.pairplot(df)
```

Out [8]:

```
<seaborn.axisgrid.PairGrid at 0x7a48a106c700>
```



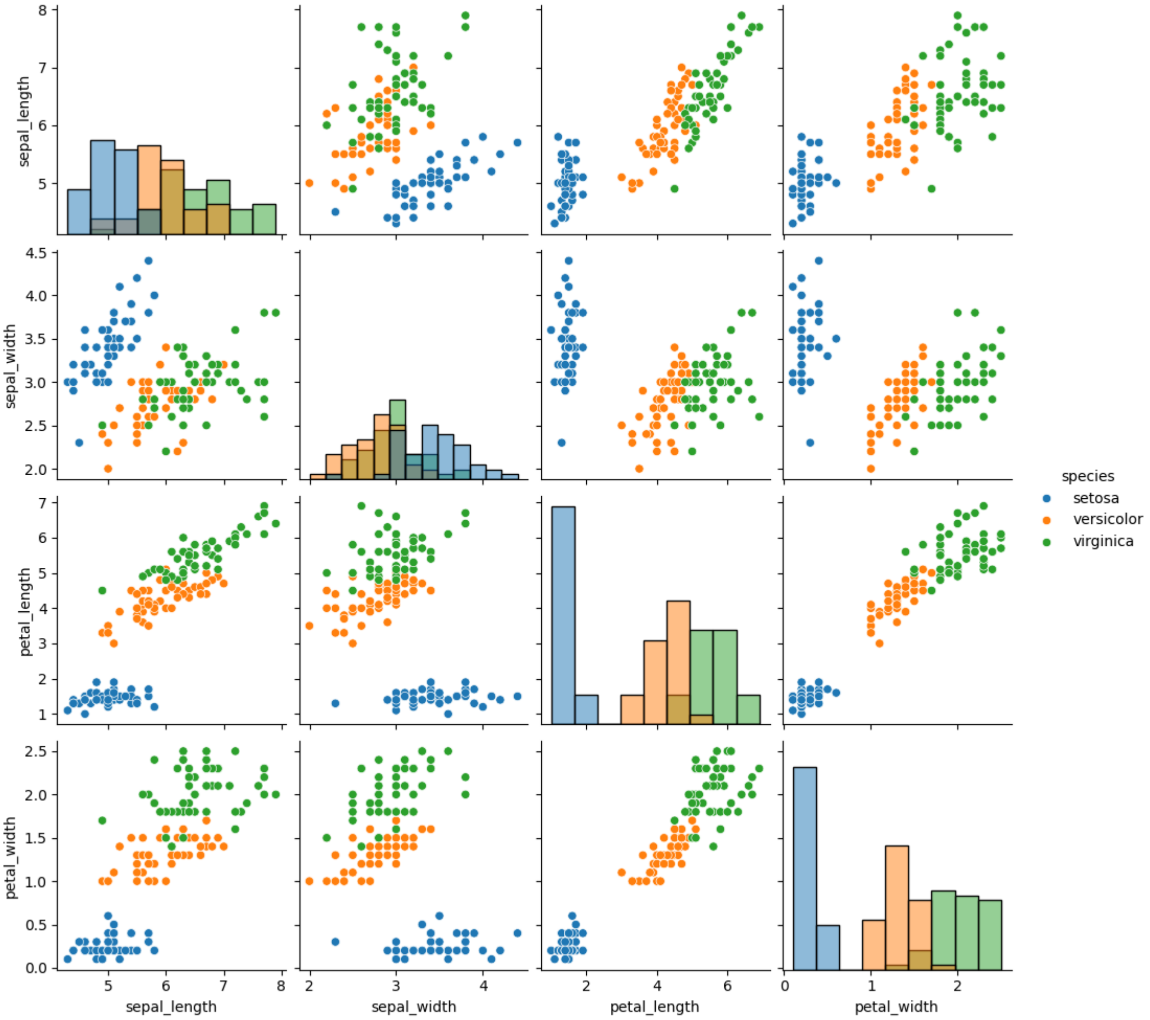
Create a pair plot to visualize pairwise relationships between different variables with hue based on species and histogram on the diagonal

In [ ]:

```
sns.pairplot(df,hue='species',diag_kind='hist')
```

Out [9]:

```
<seaborn.axisgrid.PairGrid at 0x7a48a1e3b400>
```



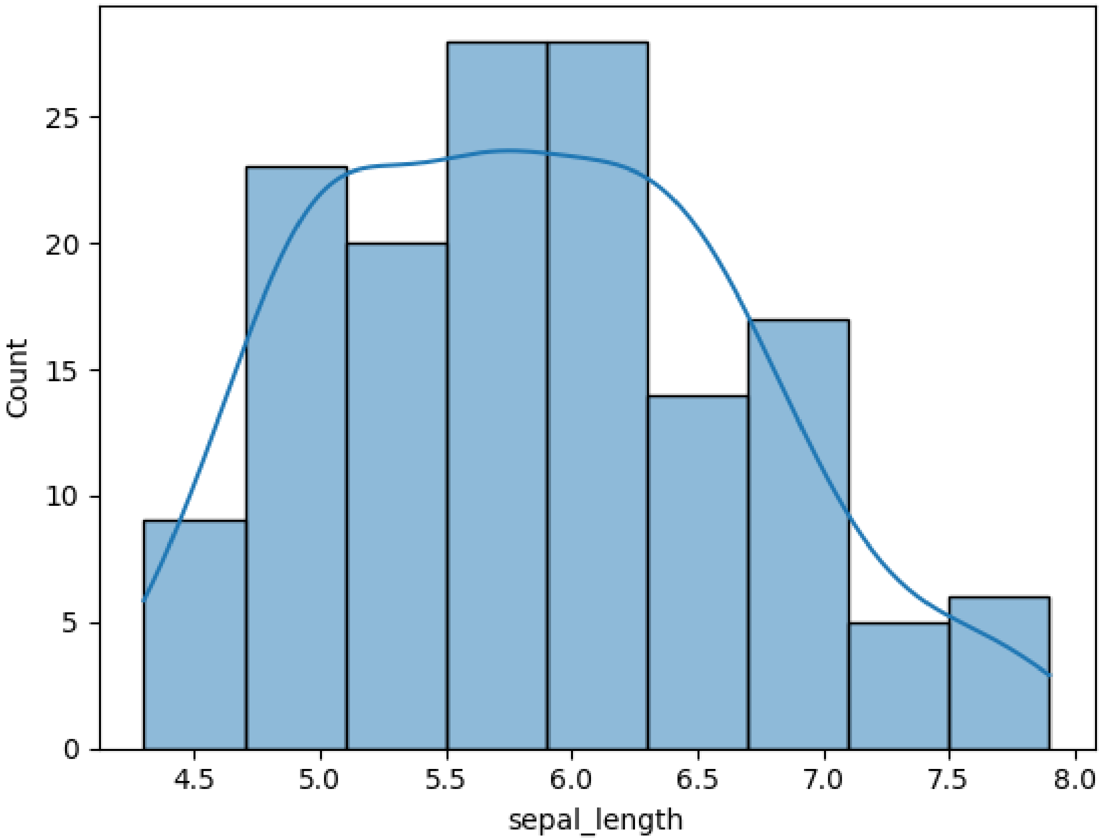
Create a histogram to visualize the distribution of sepal length with a kernel density estimate

In [ ]:

```
sns.histplot(df['sepal_length'],kde = True)
```

Out [10]:

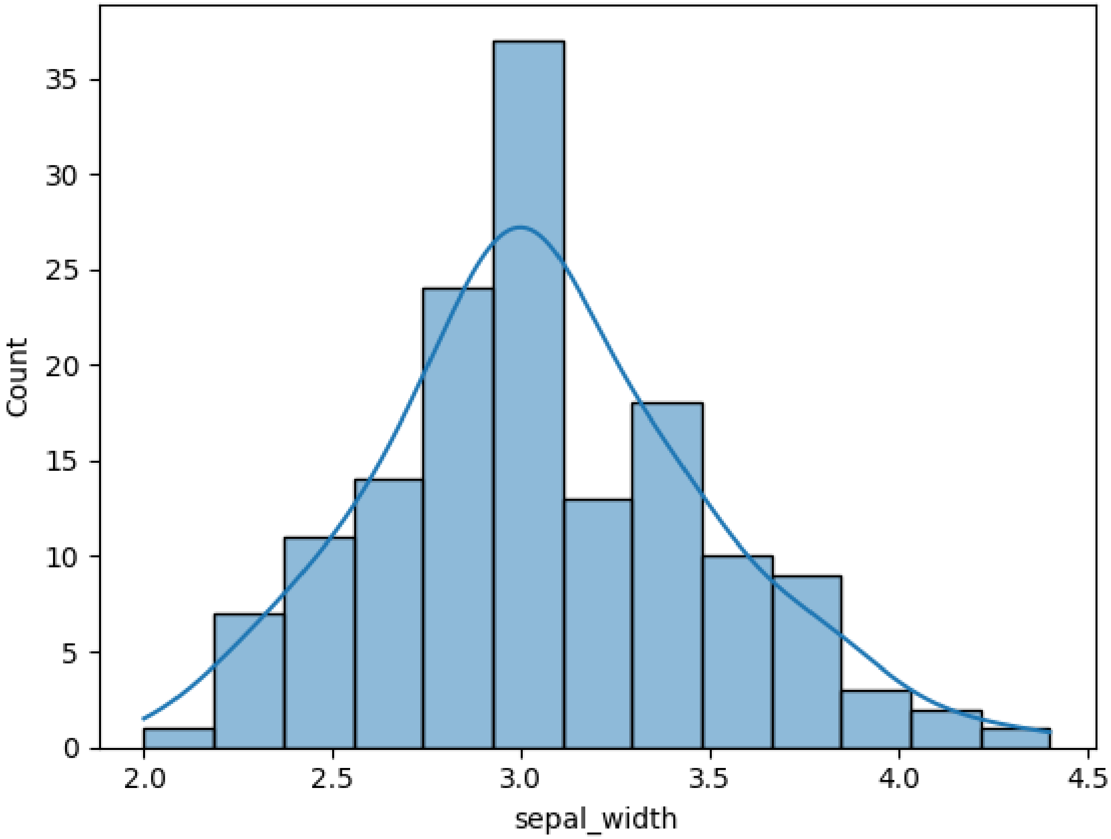
```
<Axes: xlabel='sepal_length', ylabel='Count'>
```



Create a histogram to visualize the distribution of sepal width with a kernel density estimate

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

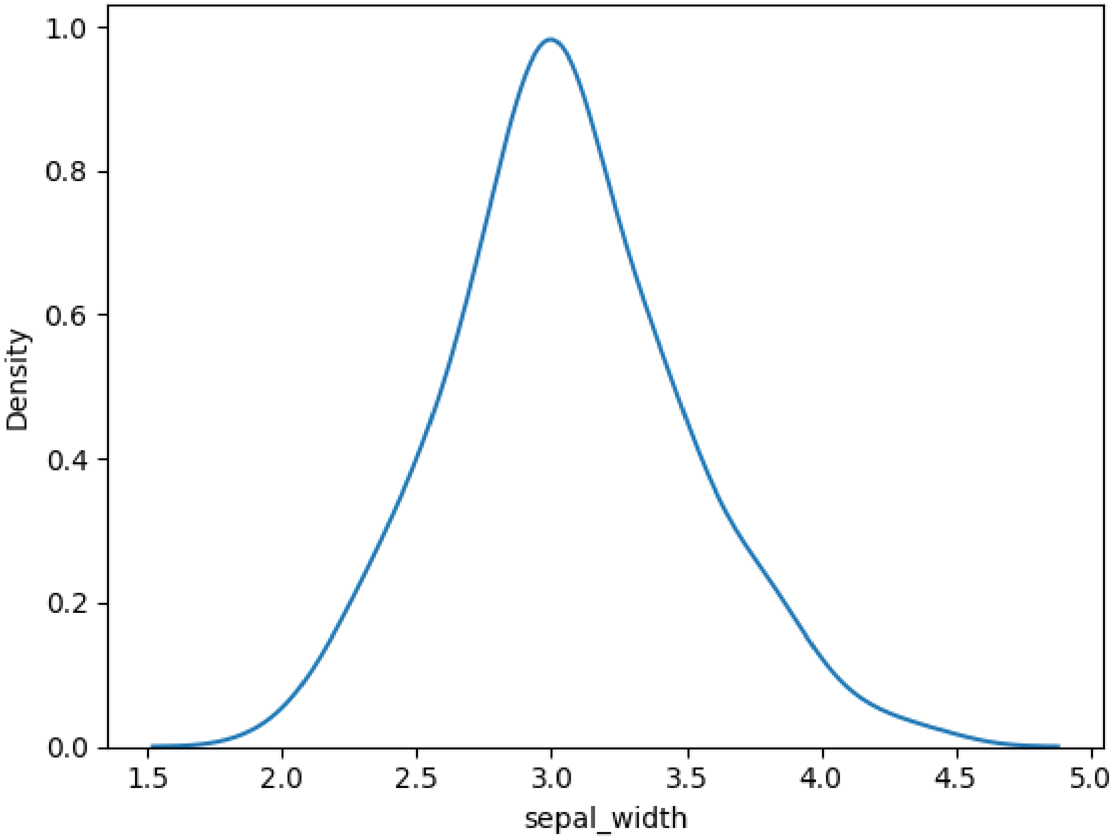
Out [11]:
```
<Axes: xlabel='sepal_width', ylabel='Count'>
```



Create a kernel density estimate plot to visualize the distribution of sepal width

```
In [ ]: sns.kdeplot(df['sepal_width'])
```

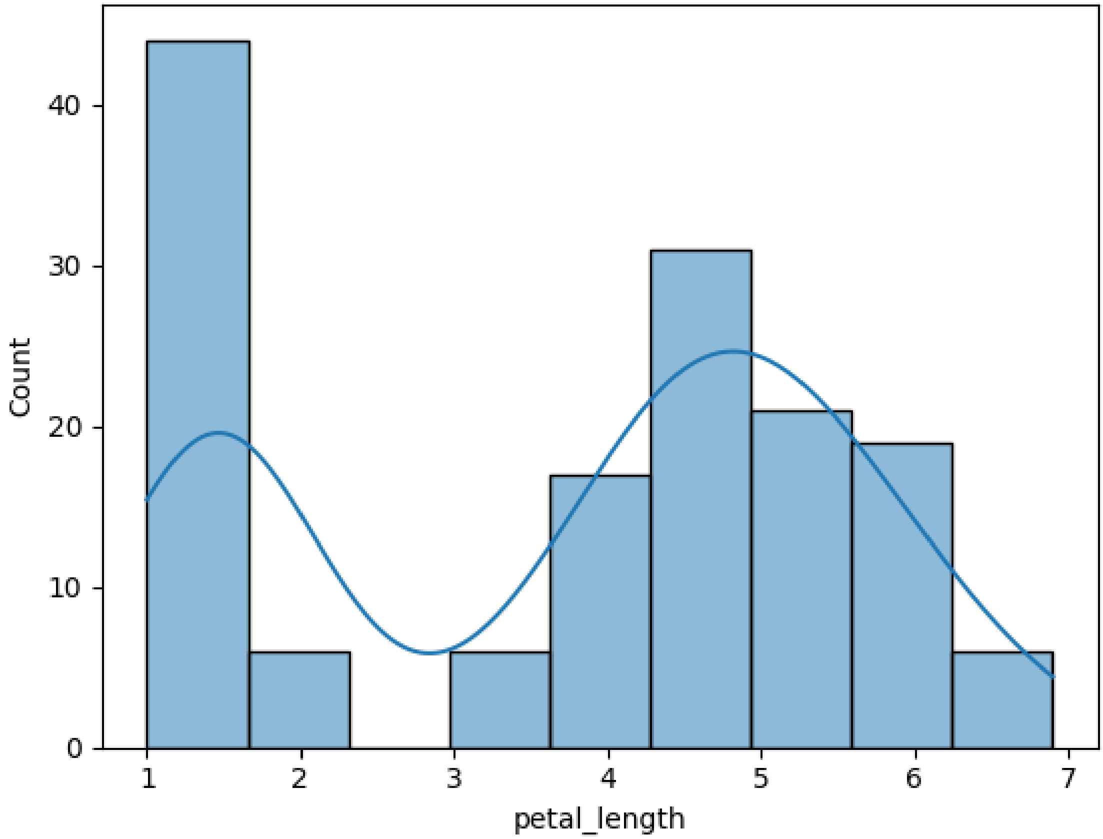
```
Out [12]: <Axes: xlabel='sepal_width', ylabel='Density'>
```



Create a histogram to visualize the distribution of petal length with a kernel density estimate

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

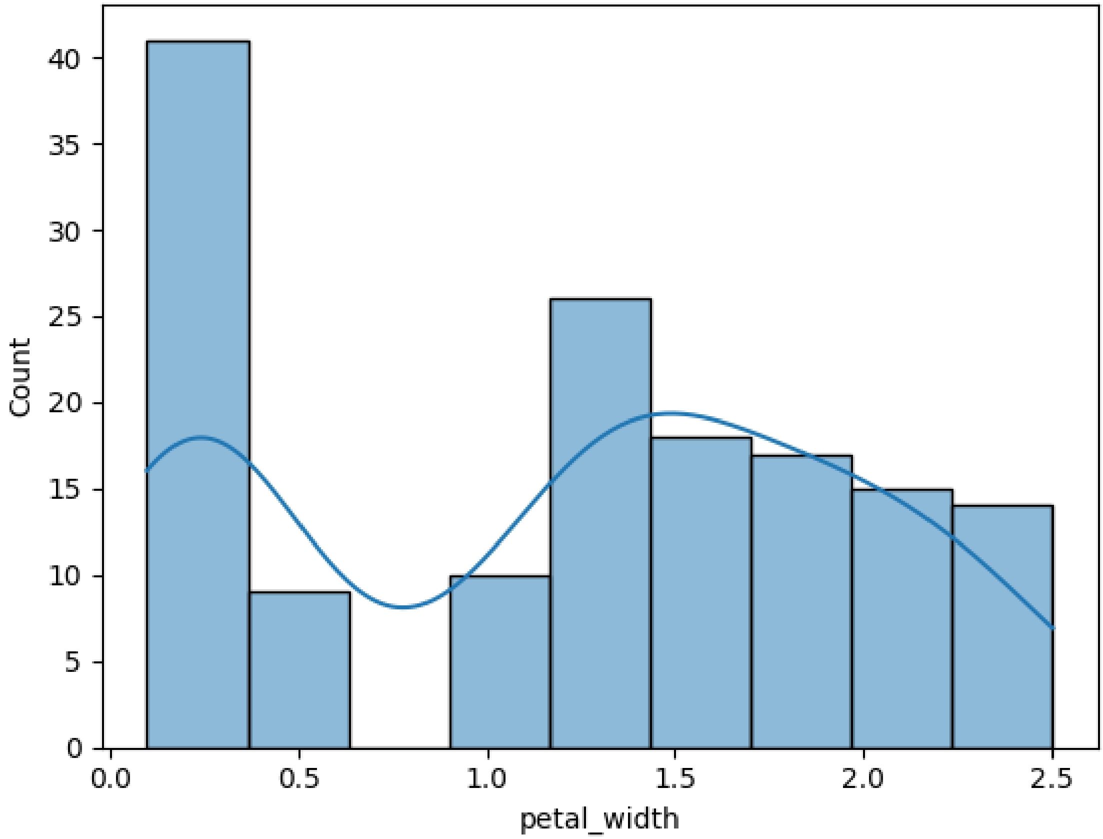
```
Out [13]: <Axes: xlabel='petal_length', ylabel='Count'>
```



Create a histogram to visualize the distribution of petal width with a kernel density estimate

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

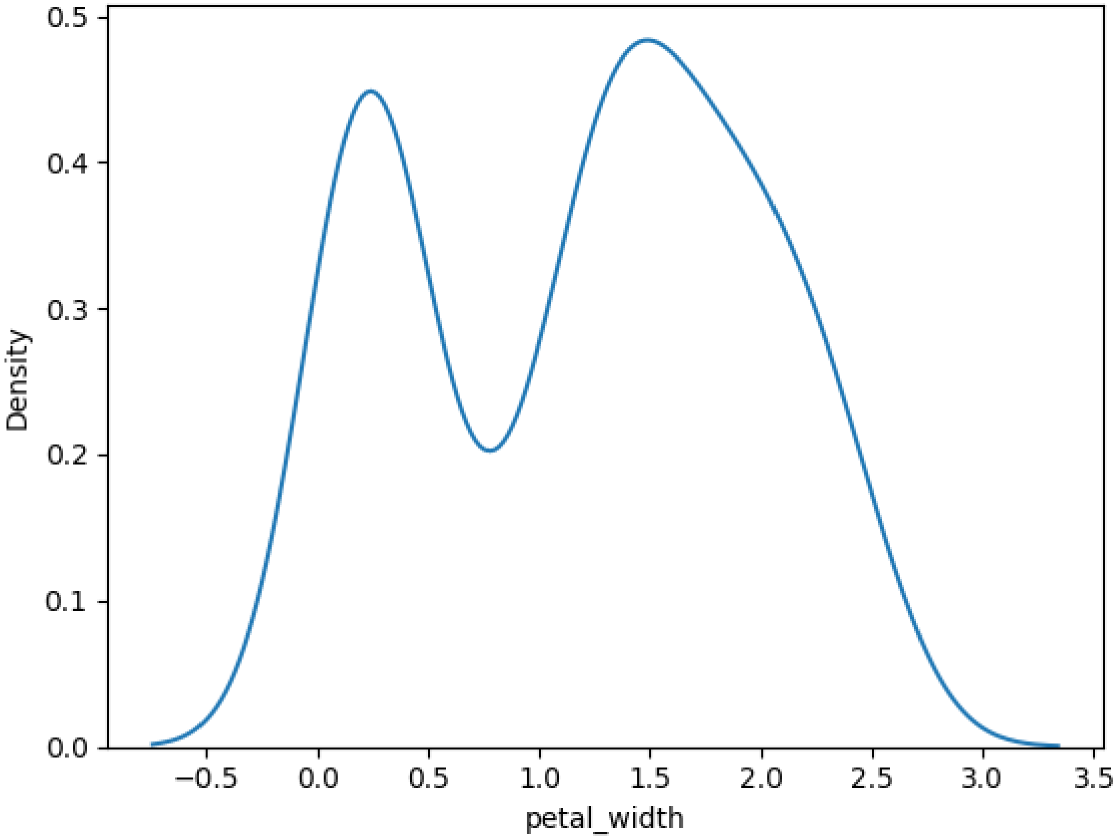
```
Out [14]: <Axes: xlabel='petal_width', ylabel='Count'>
```



Create a kernel density estimate plot to visualize the distribution of petal width

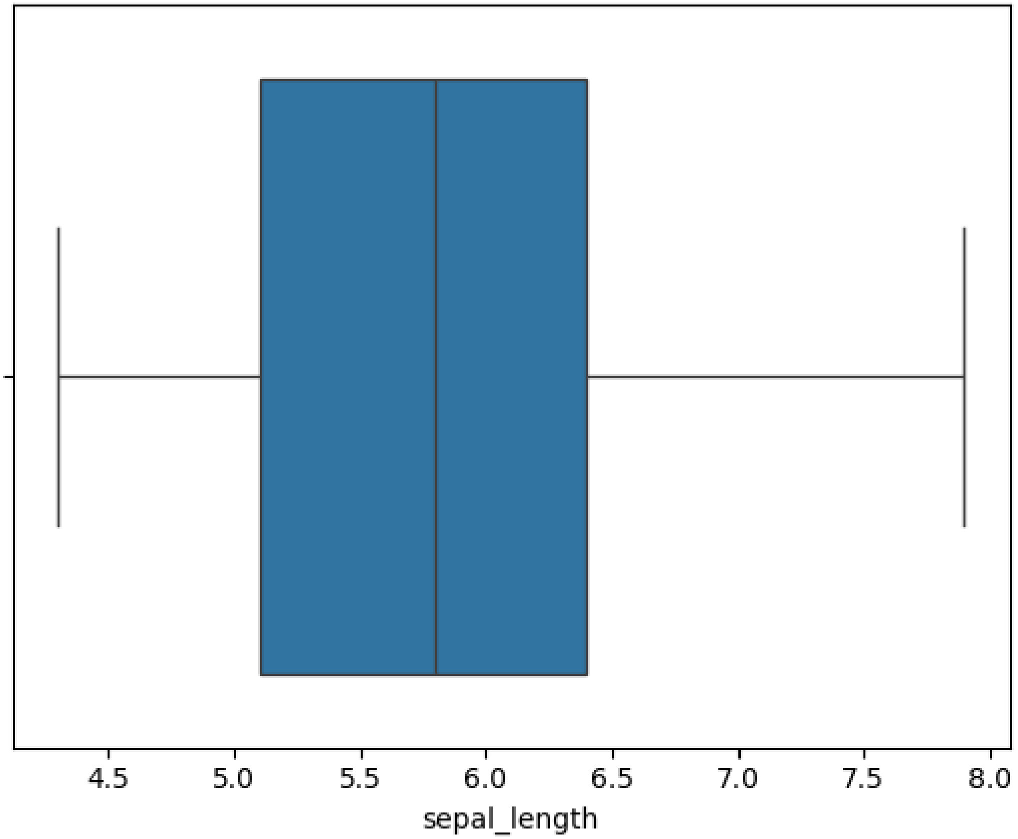
```
In [ ]: sns.kdeplot(df['petal_width'])
```

```
Out [15]: <Axes: xlabel='petal_width', ylabel='Density'>
```



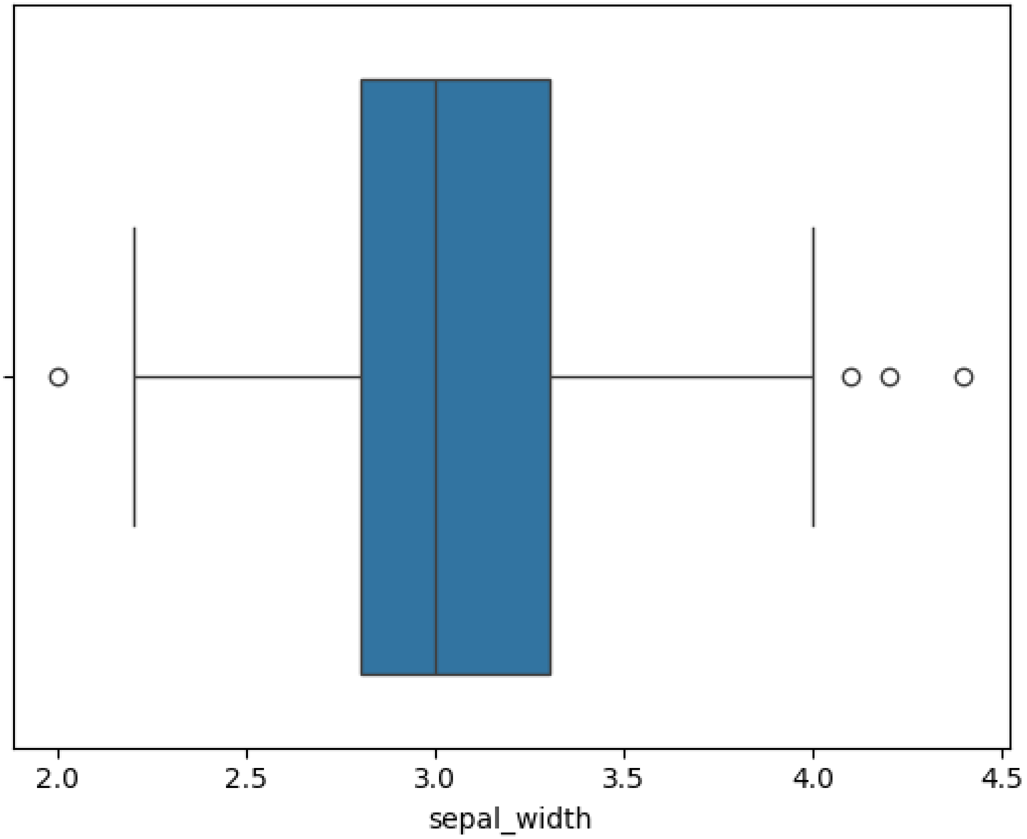
Create a box plot to visualize the distribution of sepal length

```
In [ ]: sns.boxplot(x=df['sepal_length']);
```



Create a box plot to visualize the distribution of sepal width

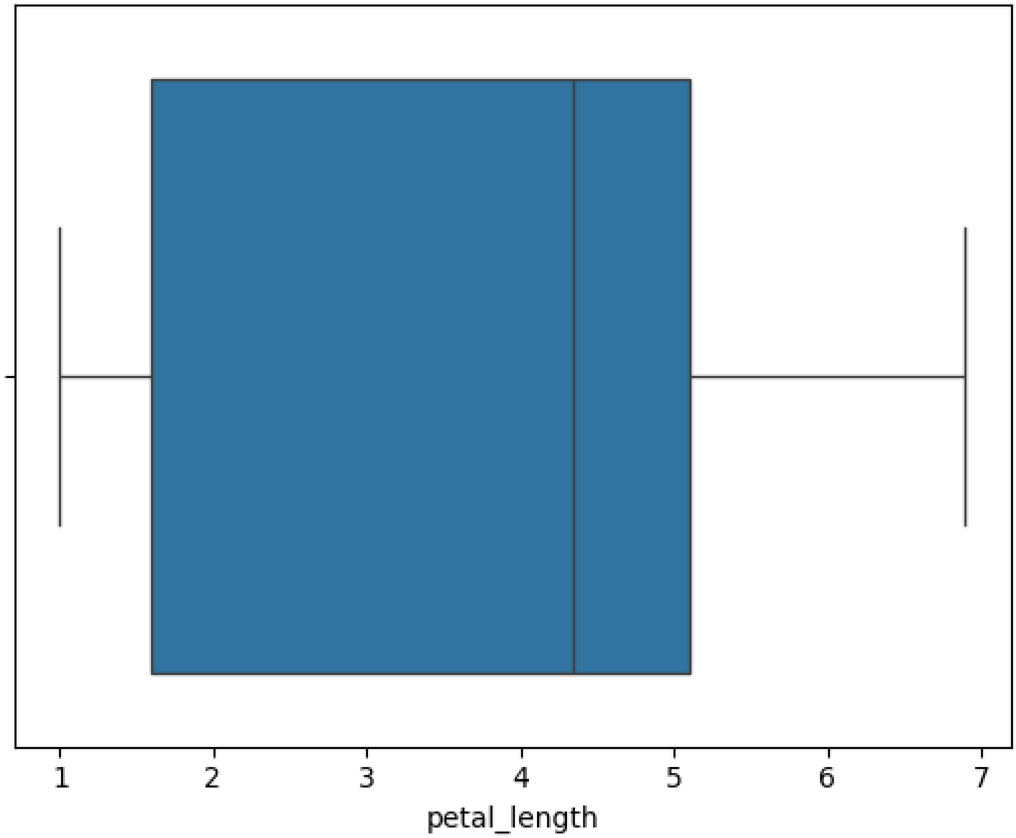
In [ ]:
```
sns.boxplot(x=df['sepal_width']);
```



Create a box plot to visualize the distribution of petal length

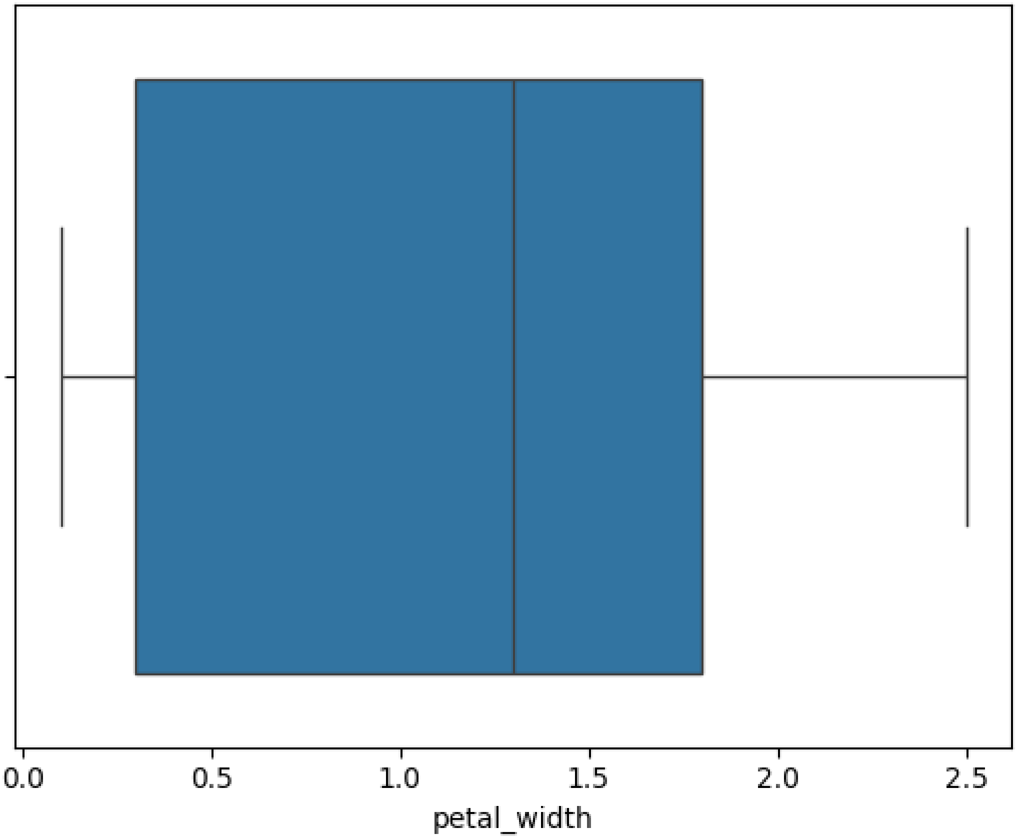
In [ ]:

```
sns.boxplot(x=df['petal_length']);
```



In [ ]:

```
sns.boxplot(x=df['petal_width']);
```


petal_width