Iris Flower dataset

In [2]:
```
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np


'''downlaod iris.csv from https://raw.githubusercontent.com/uiuc-cse/data-fa14/gh-pages/data/iris.csv'''
#Load Iris.csv into a pandas dataFrame.
iris = pd.read_csv("iris.csv")
```

In [3]:
```
# (Q) how many data-points and features?
print (iris.shape)
```

```
(150, 5)
```

In [4]:
```
#(Q) What are the column names in our dataset?
print (iris.columns)
```

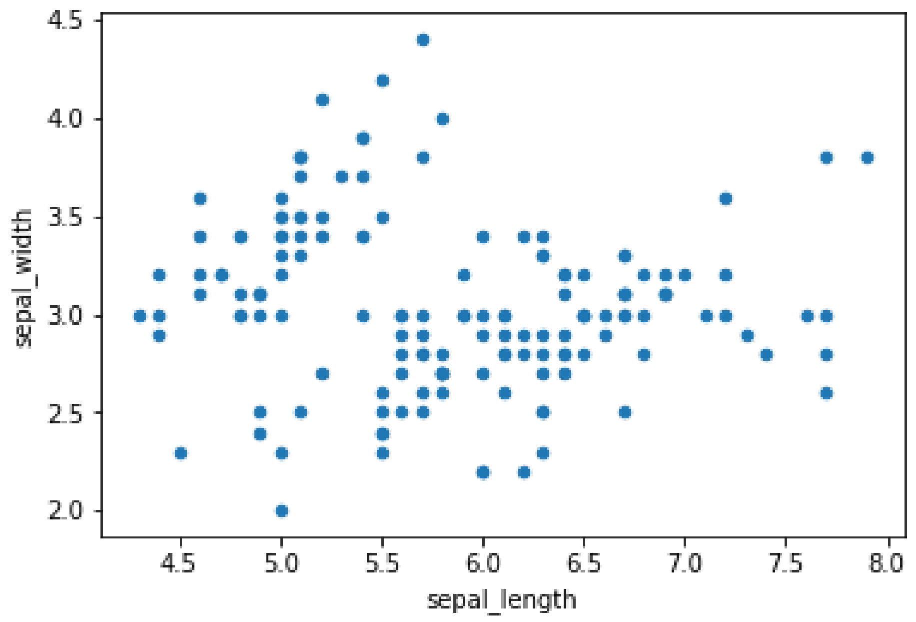
```
Index(['sepal_length', 'sepal_width', 'petal_length', 'petal_width',
       'species'],
      dtype='object')
```

In [5]:
```
#(Q) How many data points for each class are present?
#(or) How many flowers for each species are present?

iris["species"].value_counts()
# balanced-dataset vs imbalanced datasets
#Iris is a balanced dataset as the number of data points for every class is 50.
```

Out[5]:
```
virginica     50
setosa        50
versicolor    50
Name: species, dtype: int64
```

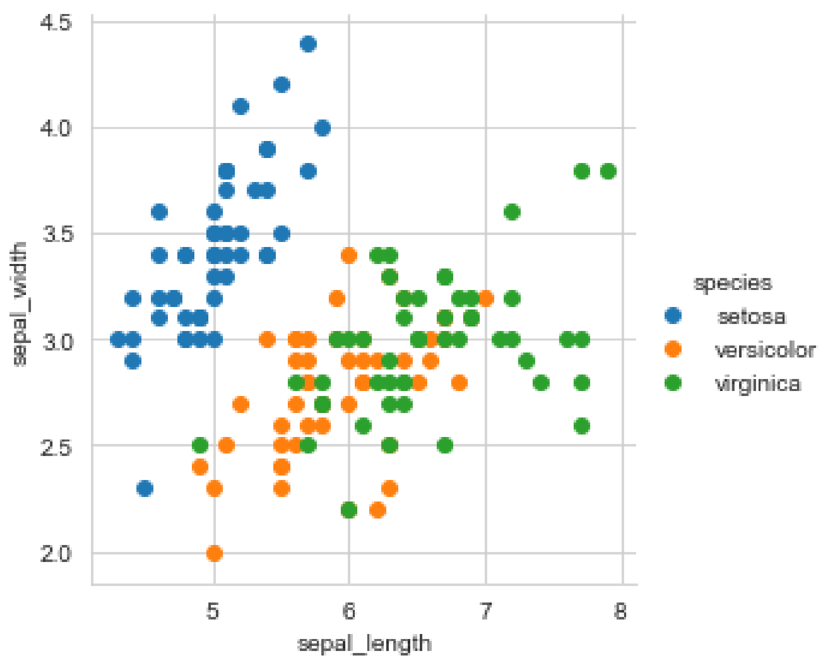
2-D Scatter Plot

In [6]:
```
#2-D scatter plot:
#ALWAYS understand the axis: labels and scale.

iris.plot(kind='scatter', x='sepal_length', y='sepal_width') ;
plt.show()

#cannot make much sense out it.
#What if we color the points by thier class-label/flower-type.
```



In [8]:

```python
# 2-D Scatter plot with color-coding for each flower type/class.
# Here 'sns' corresponds to seaborn.
sns.set_style("whitegrid");
sns.FacetGrid(iris, hue="species", height=4) \
   .map(plt.scatter, "sepal_length", "sepal_width") \
   .add_legend();
plt.show();

# Notice that the blue points can be easily seperated
# from red and green by drawing a line.
# But red and green data points cannot be easily seperated.
# Can we draw multiple 2-D scatter plots for each combination of features?
# How many cobinations exist? 4C2 = 6.
```



Observation(s):

1. Using sepal_length and sepal_width features, we can distinguish Setosa flowers from others.
2. Seperating Versicolor from Viginica is much harder as they have considerable overlap.

Pair-plot

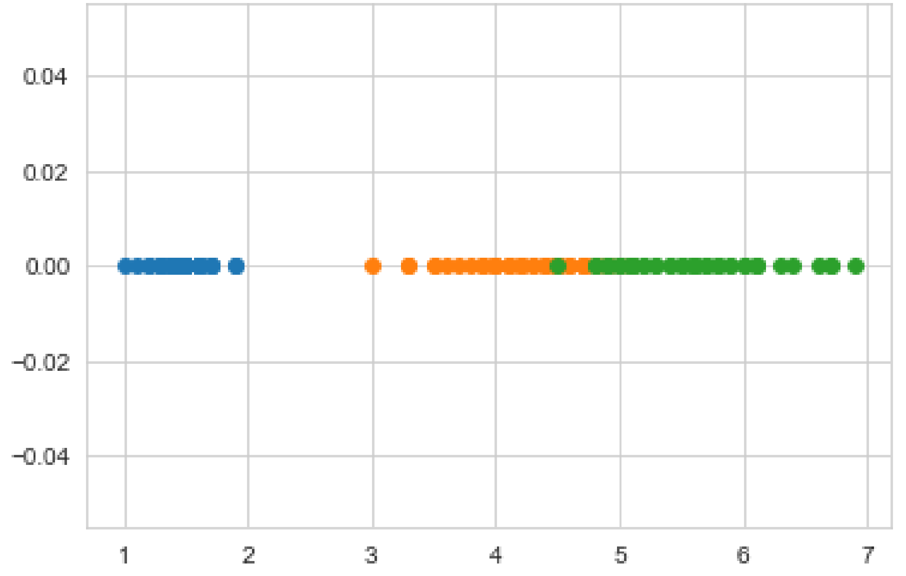
In [9]:
```python
# pairwise scatter plot: Pair-Plot
# Dis-advantages:
##Can be used when number of features are high.
##Cannot visualize higher dimensional patterns in 3-D and 4-D.
#Only possible to view 2D patterns.
plt.close();
sns.set_style("whitegrid");
sns.pairplot(iris, hue="species", height=3);
plt.show()
# NOTE: the diagnol elements are PDFs for each feature. PDFs are expalined below.
```

Observations

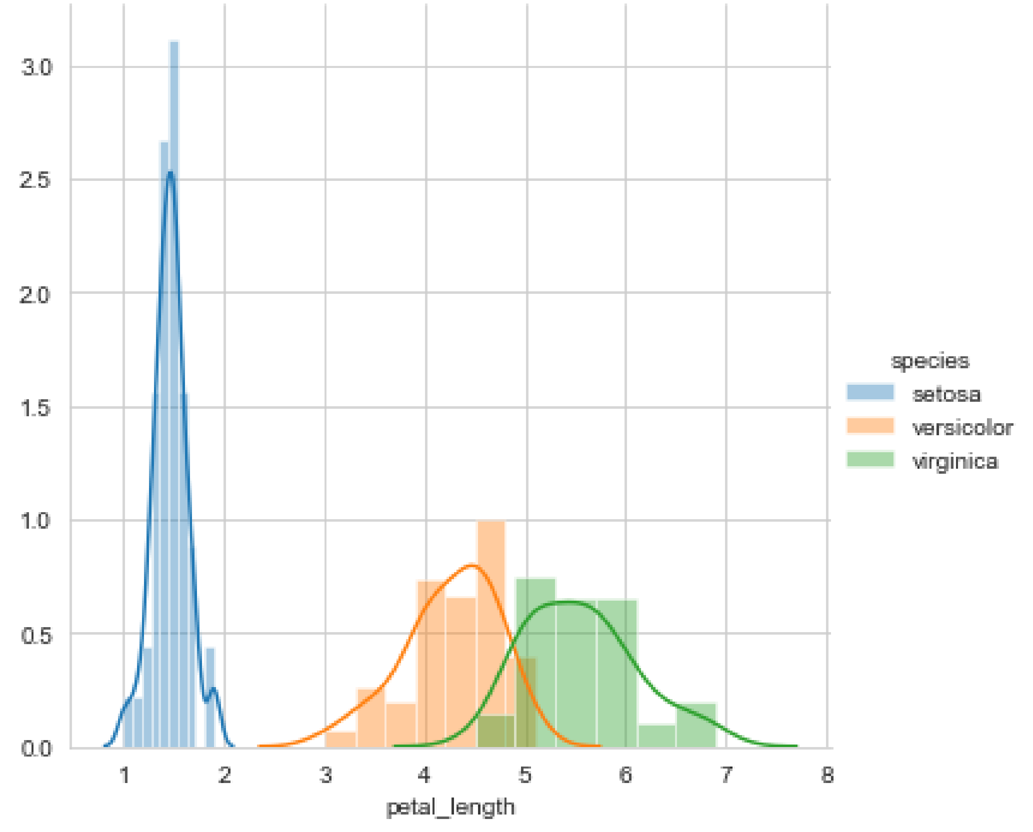
1. petal_length and petal_width are the most useful features to identify various flower types.
2. While Setosa can be easily identified (linearly seperable), Virnica and Versicolor have some overlap (almost linearly seperable).
3. We can find "lines" and "if-else" conditions to build a simple model to classify the flower types.

Histogram, PDF, CDF

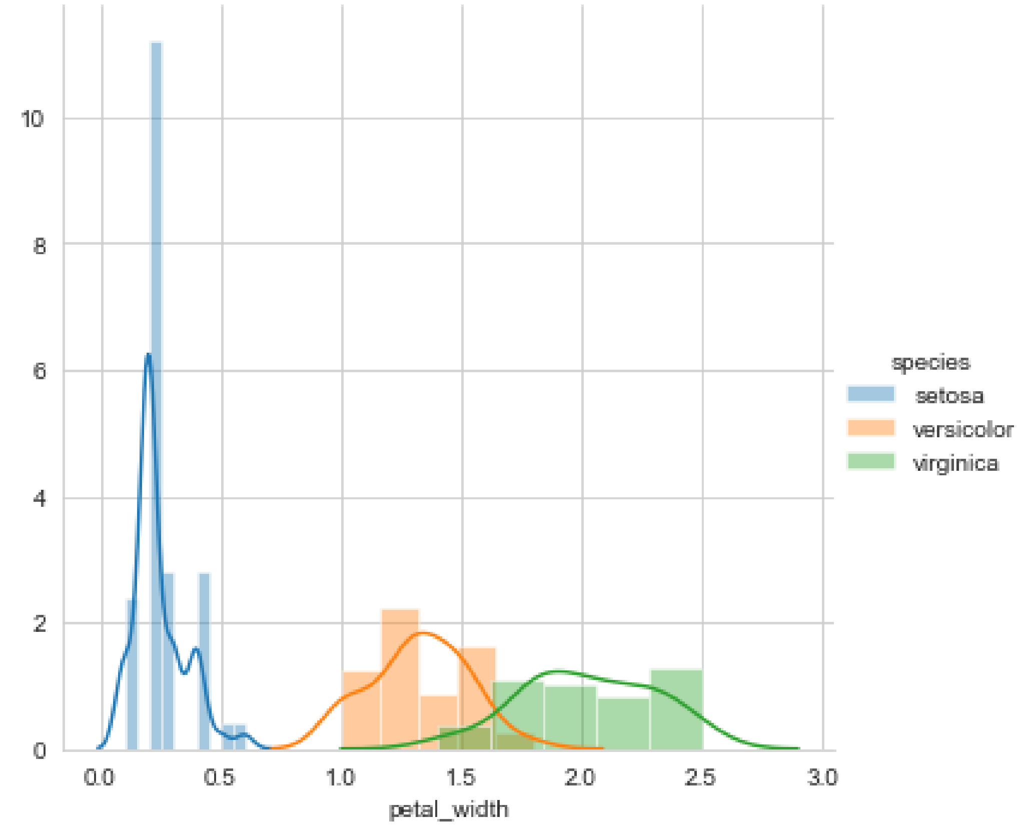
In [10]:
```
# What about 1-D scatter plot using just one feature?
#1-D scatter plot of petal-length
import numpy as np
iris_setosa = iris.loc[iris["species"] == "setosa"];
iris_virginica = iris.loc[iris["species"] == "virginica"];
iris_versicolor = iris.loc[iris["species"] == "versicolor"];
#print(iris_setosa["petal_length"])
plt.plot(iris_setosa["petal_length"], np.zeros_like(iris_setosa['petal_length']), 'o')
plt.plot(iris_versicolor["petal_length"], np.zeros_like(iris_versicolor['petal_length']), 'o')
plt.plot(iris_virginica["petal_length"], np.zeros_like(iris_virginica['petal_length']), 'o')

plt.show()
```



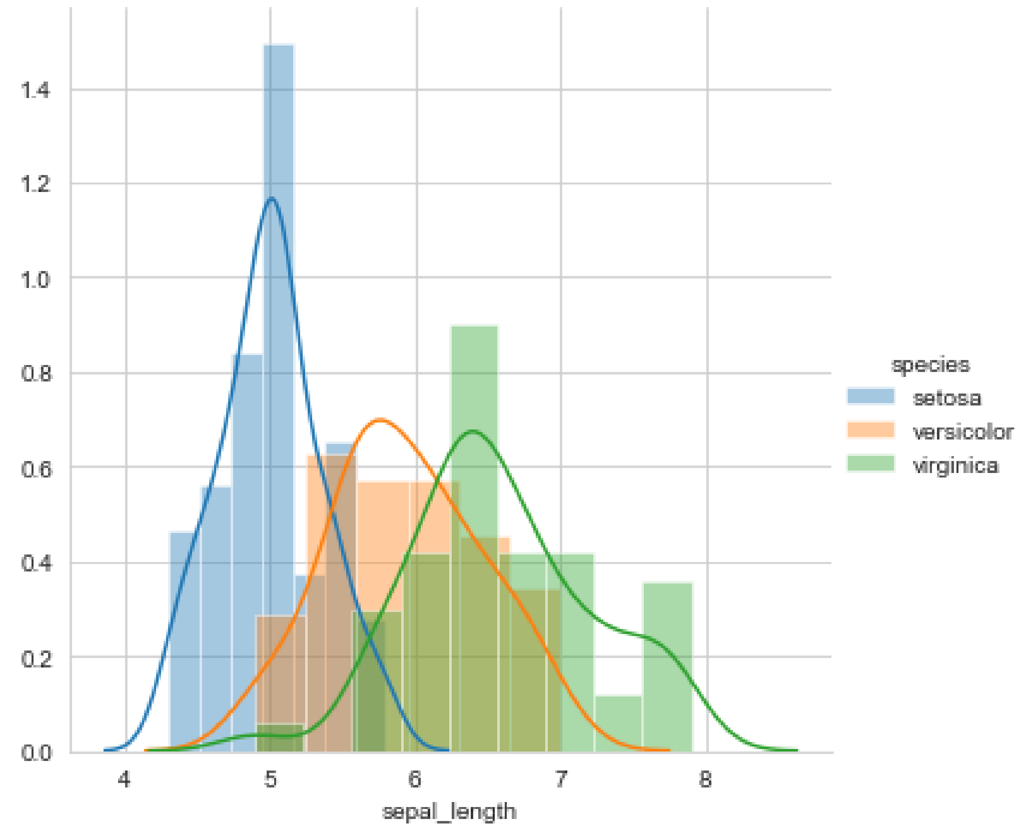
In [11]:
```
sns.FacetGrid(iris, hue="species", height=5) \
   .map(sns.distplot, "petal_length") \
   .add_legend();
plt.show();
```



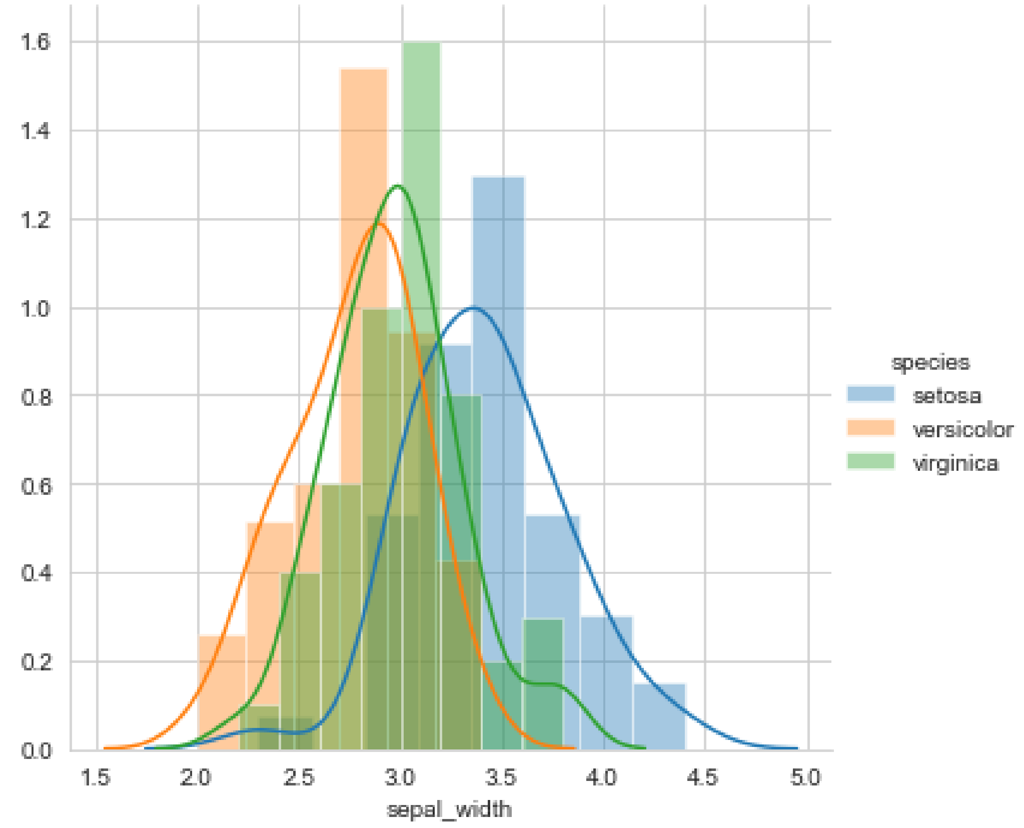
In [12]:
```
sns.FacetGrid(iris, hue="species", height=5) \
   .map(sns.distplot, "petal_width") \
   .add_legend();
plt.show();
```



In [13]:
```
sns.FacetGrid(iris, hue="species", height=5) \
   .map(sns.distplot, "sepal_length") \
   .add_legend();
plt.show();
```



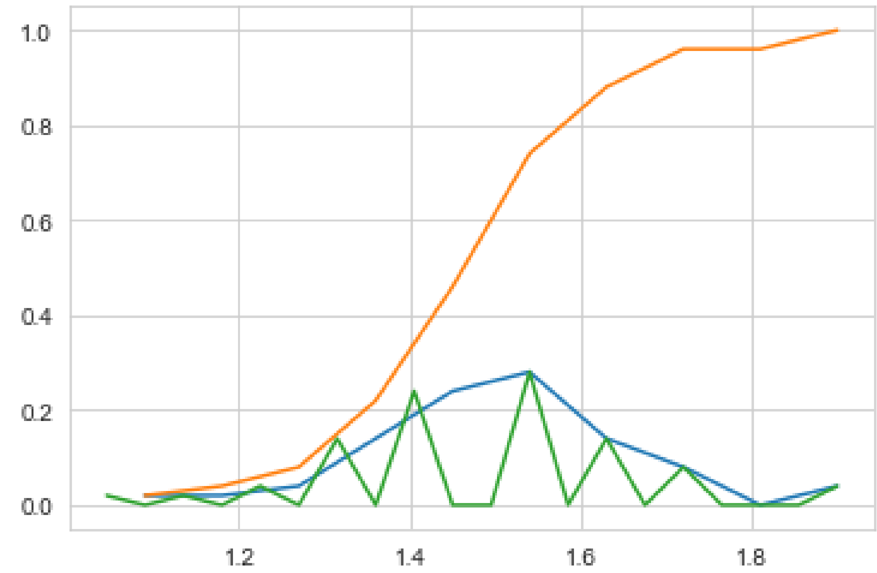
In [14]:
```
sns.FacetGrid(iris, hue="species", height=5) \
   .map(sns.distplot, "sepal_width") \
   .add_legend();
plt.show();
```



In [15]:
```
# How to compute PDFs using counts/frequencies of data points in each window.
# How window width effects the PDF plot.


# Interpreting a PDF:

## for each value of petal_length, what does the value on y-axis mean?
# Notice that we can write a simple if..else condition as if(petal_length) < 2.5 then flower type is setosa.
# Using just one feature, we can build a simple "model" suing if..else... statements.

# Can we say what percentage of versicolor points have a petal_length of less than 5?
```

In [16]:
```
# We can visually see what percentage of versicolor flowers have a
# petal_length of less than 5?


#Plot CDF of petal_length

counts, bin_edges = np.histogram(iris_setosa['petal_length'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges);
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf);
plt.plot(bin_edges[1:], cdf)


counts, bin_edges = np.histogram(iris_setosa['petal_length'], bins=20,
                                 density = True)
pdf = counts/(sum(counts))
plt.plot(bin_edges[1:],pdf);

plt.show();
```

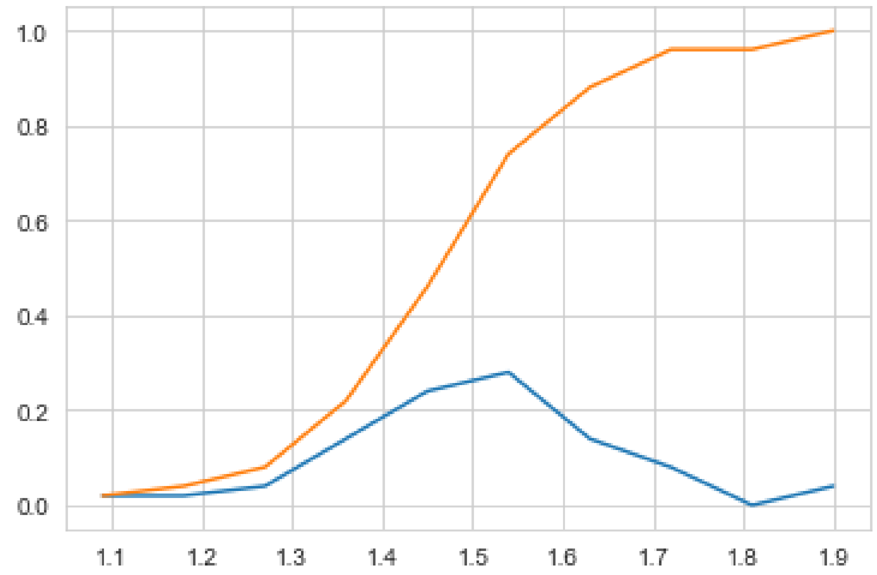
```
[0.02 0.02 0.04 0.14 0.24 0.28 0.14 0.08 0.   0.04]
[1.   1.09 1.18 1.27 1.36 1.45 1.54 1.63 1.72 1.81 1.9 ]
```



In [17]:

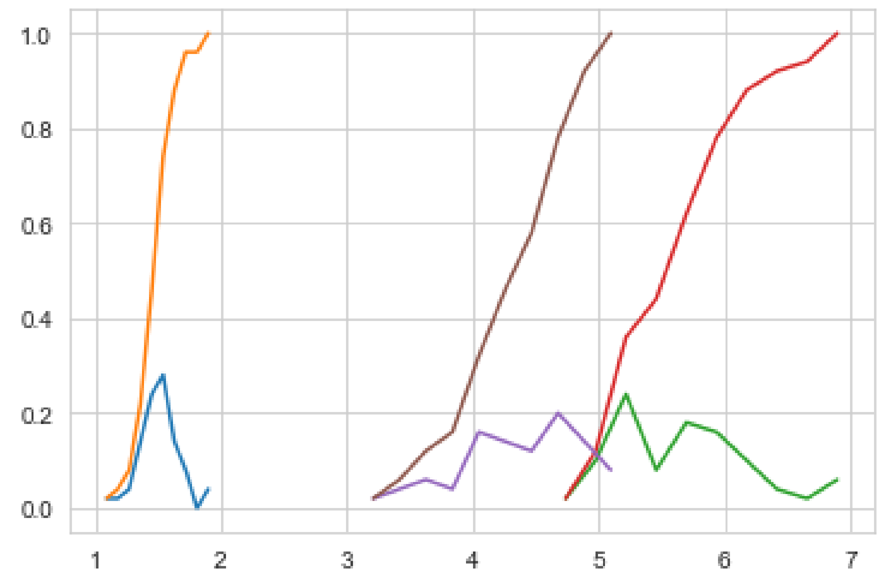
```python
# We can visually see what percentage of versicolor flowers have a
# petal_length of less than 1.6?


#Plot CDF of petal_length

counts, bin_edges = np.histogram(iris_setosa['petal_length'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)

#compute CDF
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)



plt.show();
```

```
[0.02 0.02 0.04 0.14 0.24 0.28 0.14 0.08 0.   0.04]
[1.   1.09 1.18 1.27 1.36 1.45 1.54 1.63 1.72 1.81 1.9 ]
```



In [18]:
```
# Plots of CDF of petal_length for various types of flowers.

# Misclassification error if you use petal_length only.

counts, bin_edges = np.histogram(iris_setosa['petal_length'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


# virginica
counts, bin_edges = np.histogram(iris_virginica['petal_length'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


#versicolor
counts, bin_edges = np.histogram(iris_versicolor['petal_length'], bins=10,
                                 density = True)
pdf = counts/(sum(counts))
print(pdf);
print(bin_edges)
cdf = np.cumsum(pdf)
plt.plot(bin_edges[1:],pdf)
plt.plot(bin_edges[1:], cdf)


plt.show();
```

```
[0.02 0.02 0.04 0.14 0.24 0.28 0.14 0.08 0.   0.04]
[1.   1.09 1.18 1.27 1.36 1.45 1.54 1.63 1.72 1.81 1.9 ]
[0.02 0.1  0.24 0.08 0.18 0.16 0.1  0.04 0.02 0.06]
[4.5  4.74 4.98 5.22 5.46 5.7  5.94 6.18 6.42 6.66 6.9 ]
[0.02 0.04 0.06 0.04 0.16 0.14 0.12 0.2  0.14 0.08]
[3.   3.21 3.42 3.63 3.84 4.05 4.26 4.47 4.68 4.89 5.1 ]
```



Mean, Variance and Std-dev

In [19]:
```
#Mean, Variance, Std-deviation,
print("Means:")
print(np.mean(iris_setosa["petal_length"]))
#Mean with an outlier.
print(np.mean(np.append(iris_setosa["petal_length"],50)));
print(np.mean(iris_virginica["petal_length"]))
print(np.mean(iris_versicolor["petal_length"]))

print("\nStd-dev:");
print(np.std(iris_setosa["petal_length"]))
print(np.std(iris_virginica["petal_length"]))
print(np.std(iris_versicolor["petal_length"]))
```

```
Means:
1.464
2.4156862745098038
5.552
4.26

Std-dev:
0.17176728442867115
0.5463478745268441
0.4651881339845204
```

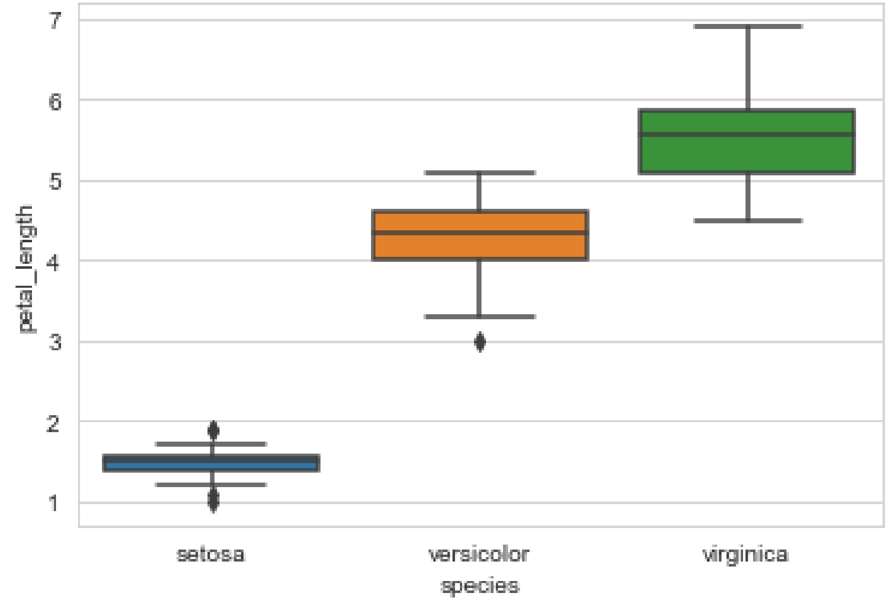
Median, Percentile, Quantile, IQR, MAD

In [20]:
```
#Median, Quantiles, Percentiles, IQR.
print("\nMedians:")
print(np.median(iris_setosa["petal_length"]))
#Median with an outlier
print(np.median(np.append(iris_setosa["petal_length"],50)));
print(np.median(iris_virginica["petal_length"]))
print(np.median(iris_versicolor["petal_length"]))


print("\nQuantiles:")
print(np.percentile(iris_setosa["petal_length"],np.arange(0, 100, 25)))
print(np.percentile(iris_virginica["petal_length"],np.arange(0, 100, 25)))
print(np.percentile(iris_versicolor["petal_length"], np.arange(0, 100, 25)))

print("\n90th Percentiles:")
print(np.percentile(iris_setosa["petal_length"],90))
print(np.percentile(iris_virginica["petal_length"],90))
print(np.percentile(iris_versicolor["petal_length"], 90))

from statsmodels import robust
print ("\nMedian Absolute Deviation")
print(robust.mad(iris_setosa["petal_length"]))
print(robust.mad(iris_virginica["petal_length"]))
print(robust.mad(iris_versicolor["petal_length"]))
```

```
Medians:
1.5
1.5
5.55
4.35

Quantiles:
[1.    1.4   1.5   1.575]
[4.5   5.1   5.55  5.875]
[3.   4.   4.35 4.6 ]

90th Percentiles:
1.7
6.3100000000000005
4.8

Median Absolute Deviation
0.14826022185056031
0.6671709983275211
0.5189107764769602
```

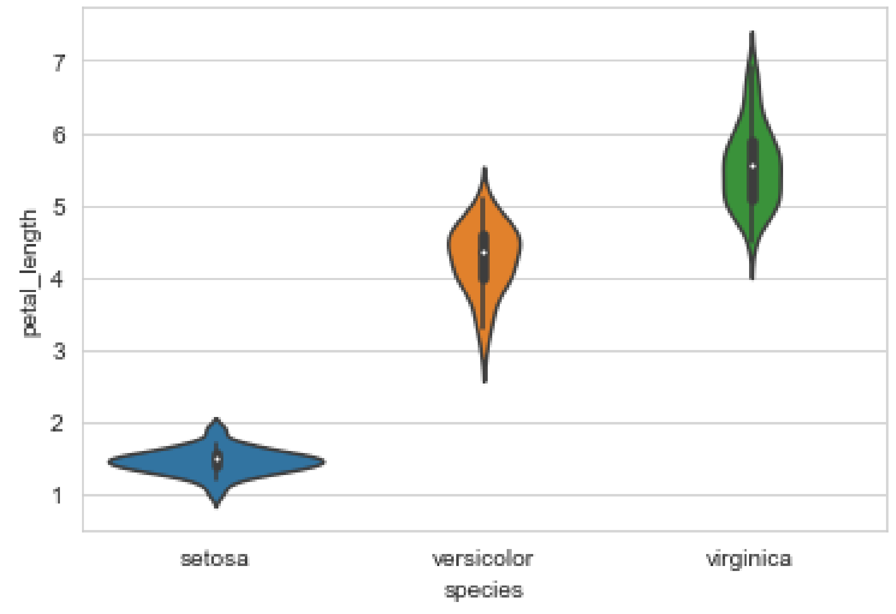
Box plot and Whiskers

In [21]:
```
sns.boxplot(x='species',y='petal_length', data=iris)
plt.show()
```



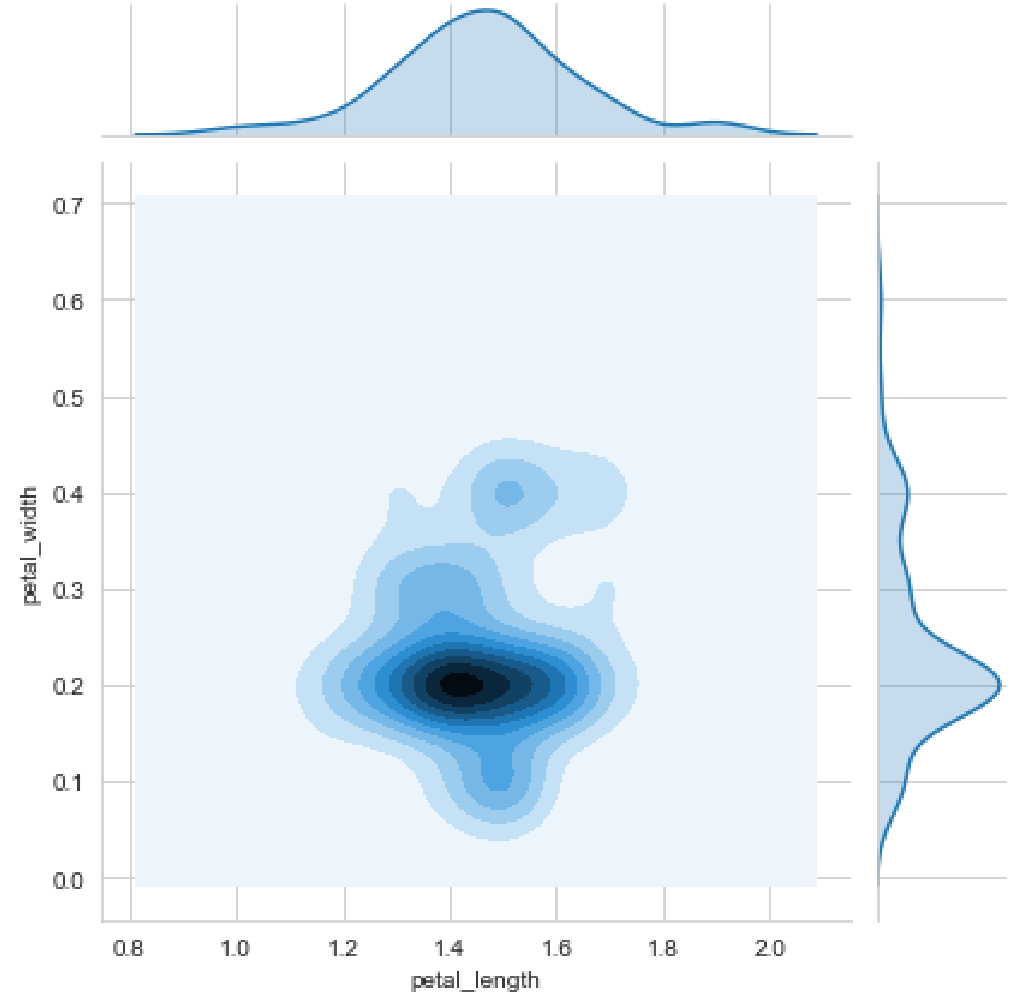
Violin plots

In [22]:
```
sns.violinplot(x="species", y="petal_length", data=iris, size=8)
plt.show()
```



Multivariate probability density, contour plot.

In [23]:
```
#2D Density plot, contors-plot
sns.jointplot(x="petal_length", y="petal_width", data=iris_setosa, kind="kde");
plt.show();
```



In [25]:
```
iris_virginica_SW = iris_virginica.iloc[:,1]
iris_versicolor_SW = iris_versicolor.iloc[:,1]
```

In [26]:
```
from scipy import stats
stats.ks_2samp(iris_virginica_SW, iris_versicolor_SW)
```

Out[26]:
```
Ks_2sampResult(statistic=0.26, pvalue=0.06779471096995852)
```

In [27]:
```
x = stats.norm.rvs(loc=0.2, size=10)
stats.kstest(x,'norm')
```

Out[27]:
```
KstestResult(statistic=0.24891960150941622, pvalue=0.495575609780464)
```

In [28]:
```
x = stats.norm.rvs(loc=0.2, size=100)
stats.kstest(x,'norm')
```

Out[28]: KstestResult(statistic=0.14332186743894548, pvalue=0.029573824992372134)

In [29]:
```
x = stats.norm.rvs(loc=0.2, size=1000)
stats.kstest(x,'norm')
```

Out[29]: KstestResult(statistic=0.1025760241341469, pvalue=1.2960861619016006e-09)