3. Plotting for Exploratory data analysis (EDA)

(3.1) Basic Terminology

- What is EDA?
- Data-point/vector/Observation
- Data-set.
- Feature/Variable/Input-variable/Dependent-varibale
- Label/Indepdendent-variable/Output-varible/Class/Class-label/Response label
- Vector: 2-D, 3-D, 4-D,.... n-D

Q. What is a 1-D vector: Scalar

Iris Flower dataset

Toy Dataset: Iris Dataset: [https://en.wikipedia.org/wiki/Iris_flower_data_set] (https://en.wikipedia.org/wiki/Iris_flower_data_set%5D)

- A simple dataset to learn the basics.
- 3 flowers of Iris species. [see images on wikipedia link above]
- 1936 by Ronald Fisher.
- Petal and Sepal: http://terpconnect.umd.edu/~petersd/666/html/iris_with_labels.jpg (http://terpconnect.umd.edu/~petersd/666/html/iris_with_labels.jpg)
- Objective: Classify a new flower as belonging to one of the 3 classes given the 4 features.
- Importance of domain knowledge.
- Why use petal and sepal dimensions as features?
- Why do we not use 'color' as a feature?

In [1]:

```
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-
#Load Iris.csv into a pandas dataFrame.
iris = pd.read_csv("iris.csv")
```

In [2]:

```
# (Q) how many data-points and features?
print (iris.shape)
```

```
(150, 5)
```

In [3]:
```
#(Q) What are the column names in our dataset?
print (iris.columns)
```

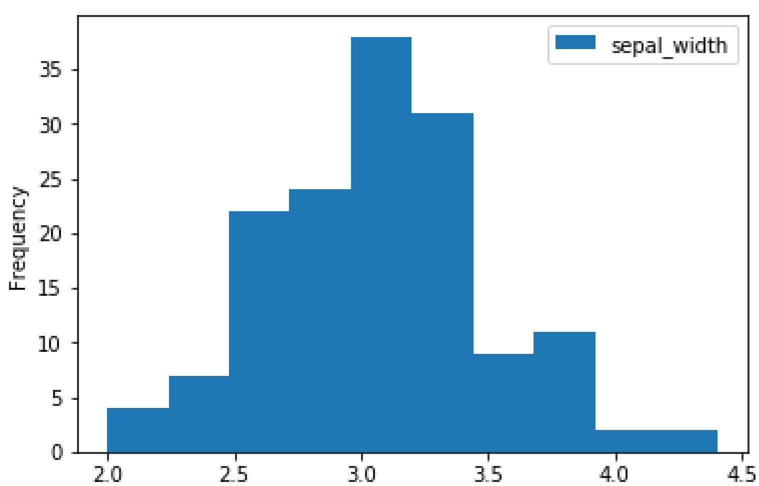
```
Index(['sepal_length', 'sepal_width', 'petal_length', 'petal_width',
       'species'],
      dtype='object')
```

In [4]:
```
#(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.
```

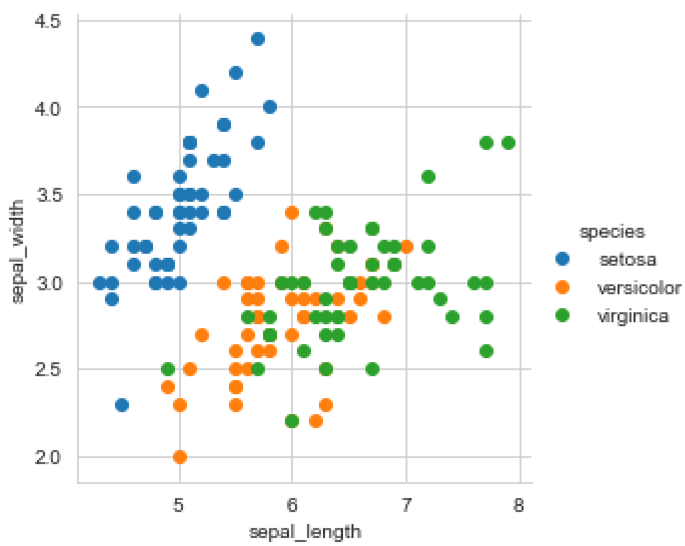
Out[4]:
```
versicolor    50
virginica     50
setosa        50
Name: species, dtype: int64
```

(3.2) 2-D Scatter Plot

In [5]:
```
#2-D scatter plot:
#ALWAYS understand the axis: labels and scale.

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

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



In [6]:
```
# 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.

3D Scatter plot

[https://plot.ly/pandas/3d-scatter-plots/ (https://plot.ly/pandas/3d-scatter-plots/)](https://plot.ly/pandas/3d-scatter-plots/)

Needs a lot to mouse interaction to interpret data.

What about 4-D, 5-D or n-D scatter plot?

(3.3) Pair-plot

In [7]:
```
# 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", size=3);
plt.show()
# NOTE: the diagnol elements are PDFs for each feature. PDFs are expalined below.
```

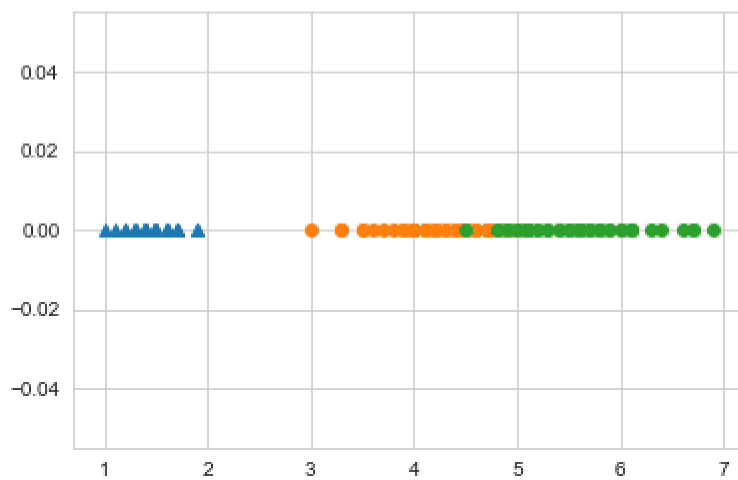
```
C:\Users\Admin\Anaconda3\lib\site-packages\seaborn\axisgrid.py:2065: UserWarni
ng: The `size` parameter has been renamed to `height`; pleaes update your cod
e.
  warnings.warn(msg, UserWarning)
C:\Users\Admin\Anaconda3\lib\site-packages\scipy\stats\stats.py:1713: FutureWa
rning: Using a non-tuple sequence for multidimensional indexing is deprecated;
use `arr[tuple(seq)]` instead of `arr[seq]`. In the future this will be interp
reted 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
```

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.

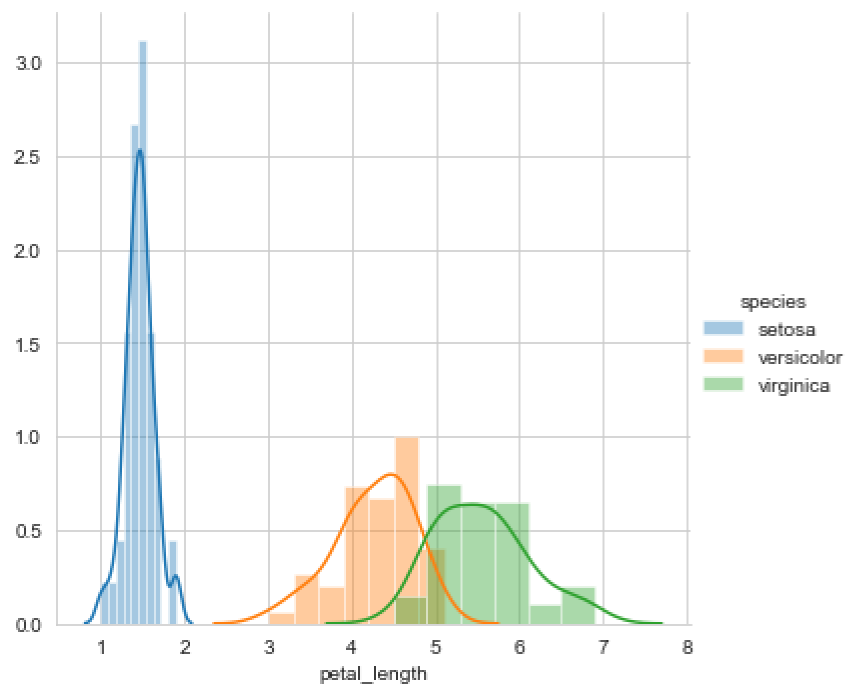
(3.4) Histogram, PDF, CDF

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[iris["species"] == "setosa"];
iris_virginica = iris[iris["species"] == "virginica"];
iris_versicolor = iris[iris["species"] == "versicolor"];
#print(iris_setosa["petal_length"])
plt.plot(iris_setosa["petal_length"], np.zeros_like(iris_setosa['petal_length']),
plt.plot(iris_versicolor["petal_length"], np.zeros_like(iris_versicolor['petal_len
plt.plot(iris_virginica["petal_length"], np.zeros_like(iris_virginica['petal_lengt

plt.show()
#Disadvantages of 1-D scatter plot: Very hard to make sense as points
#are overlapping a lot.
#Are there better ways of visualizing 1-D scatter plots?
```



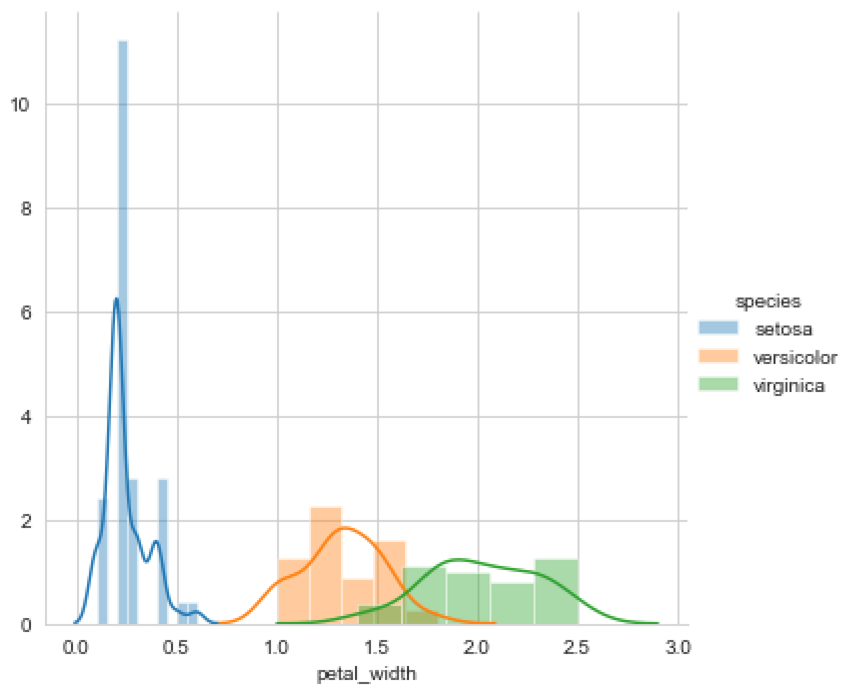
In [16]:
```
sns.FacetGrid(iris, hue="species", size=5) \
   .map(sns.distplot, "petal_length") \
   .add_legend();
plt.show();
```

```
C:\Users\Admin\Anaconda3\lib\site-packages\seaborn\axisgrid.py:230: UserWarnin
g: The `size` paramter has been renamed to `height`; please update your code.
  warnings.warn(msg, UserWarning)
C:\Users\Admin\Anaconda3\lib\site-packages\scipy\stats\stats.py:1713: FutureWa
rning: Using a non-tuple sequence for multidimensional indexing is deprecated;
use `arr[tuple(seq)]` instead of `arr[seq]`. In the future this will be interp
reted 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
```



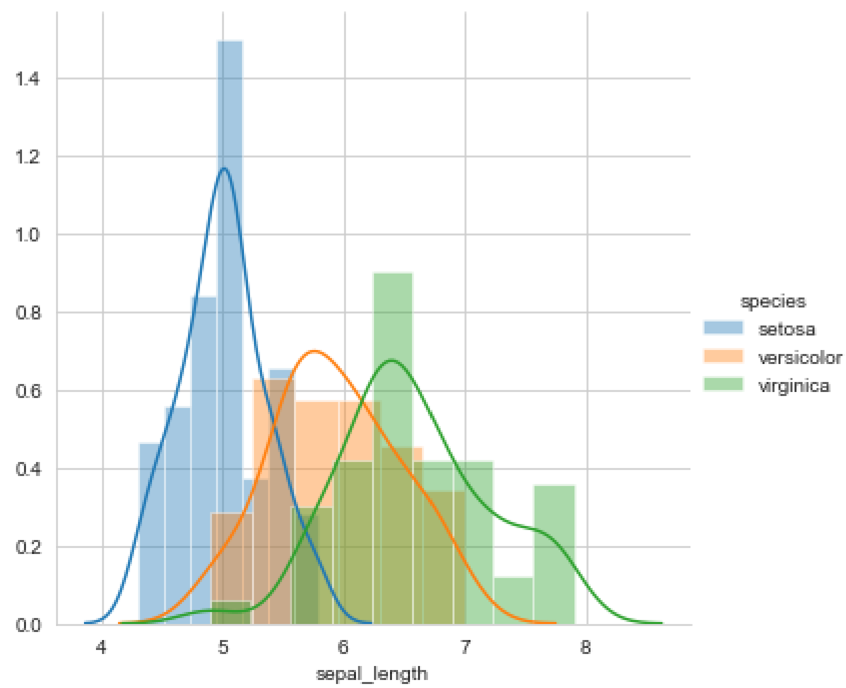
In [17]:
```
sns.FacetGrid(iris, hue="species", size=5) \
   .map(sns.distplot, "petal_width") \
   .add_legend();
plt.show();
```

```
C:\Users\Admin\Anaconda3\lib\site-packages\seaborn\axisgrid.py:230: UserWarnin
g: The `size` paramter has been renamed to `height`; please update your code.
  warnings.warn(msg, UserWarning)
C:\Users\Admin\Anaconda3\lib\site-packages\scipy\stats\stats.py:1713: FutureWa
rning: Using a non-tuple sequence for multidimensional indexing is deprecated;
use `arr[tuple(seq)]` instead of `arr[seq]`. In the future this will be interp
reted 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
```



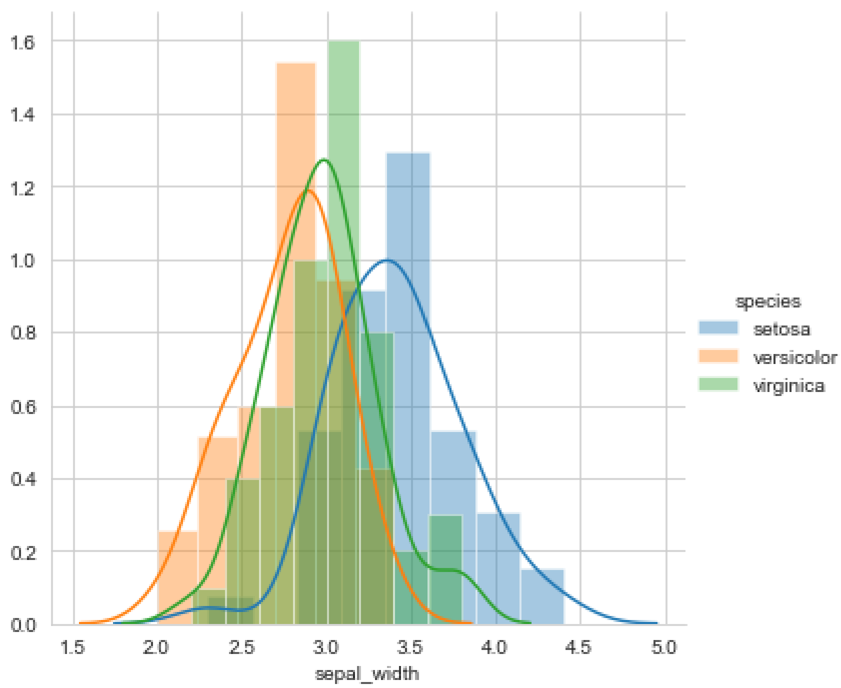
In [18]:
```
sns.FacetGrid(iris, hue="species", size=5) \
   .map(sns.distplot, "sepal_length") \
   .add_legend();
plt.show();
```

```
C:\Users\Admin\Anaconda3\lib\site-packages\seaborn\axisgrid.py:230: UserWarnin
g: The `size` paramter has been renamed to `height`; please update your code.
  warnings.warn(msg, UserWarning)
C:\Users\Admin\Anaconda3\lib\site-packages\scipy\stats\stats.py:1713: FutureWa
rning: Using a non-tuple sequence for multidimensional indexing is deprecated;
use `arr[tuple(seq)]` instead of `arr[seq]`. In the future this will be interp
reted 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
```



In [19]:
```
sns.FacetGrid(iris, hue="species", size=5) \
   .map(sns.distplot, "sepal_width") \
   .add_legend();
plt.show();
```

```
C:\Users\Admin\Anaconda3\lib\site-packages\seaborn\axisgrid.py:230: UserWarnin
g: The `size` paramter has been renamed to `height`; please update your code.
  warnings.warn(msg, UserWarning)
C:\Users\Admin\Anaconda3\lib\site-packages\scipy\stats\stats.py:1713: FutureWa
rning: Using a non-tuple sequence for multidimensional indexing is deprecated;
use `arr[tuple(seq)]` instead of `arr[seq]`. In the future this will be interp
reted 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
```

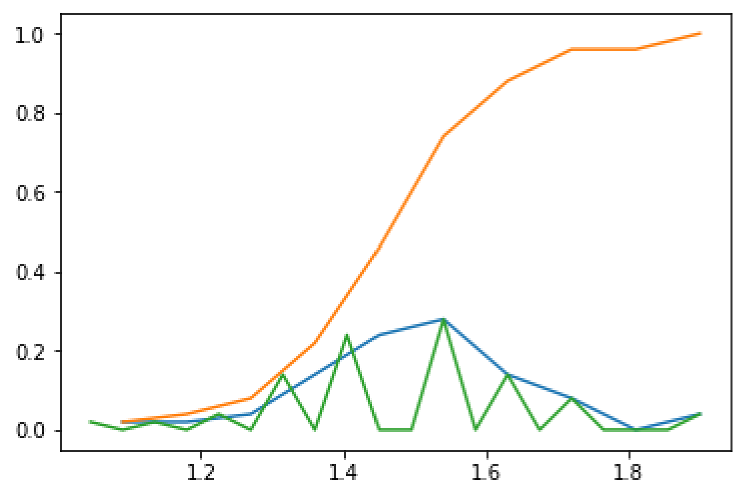


In [20]:
```
# Histograms and Probability Density Functions (PDF) using KDE
# How to compute PDFs using counts/frequencies of data points in each window.
# How window width effects the PDF plot.


# Interpreting a PDF:
## why is it called a density plot?
## Why is it called a probability plot?
## 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 t
# Using just one feature, we can build a simple "model" suing if..else... statemen

# Disadv of PDF: Can we say what percentage of versicolor points have a petal_leng

# Do some of these plots look like a bell-curve you studied in under-grad?
# Gaussian/Normal distribution.
# What is "normal" about normal distribution?
# e.g: Hieghts of male students in a class.
# One of the most frequent distributions in nature.
```

In [18]:

```
# Need for Cumulative Distribution Function (CDF)
# We can visually see what percentage of versicolor flowers have a
# petal_length of less than 5?
# How to construct a CDF?
# How to read a CDF?

#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();
```

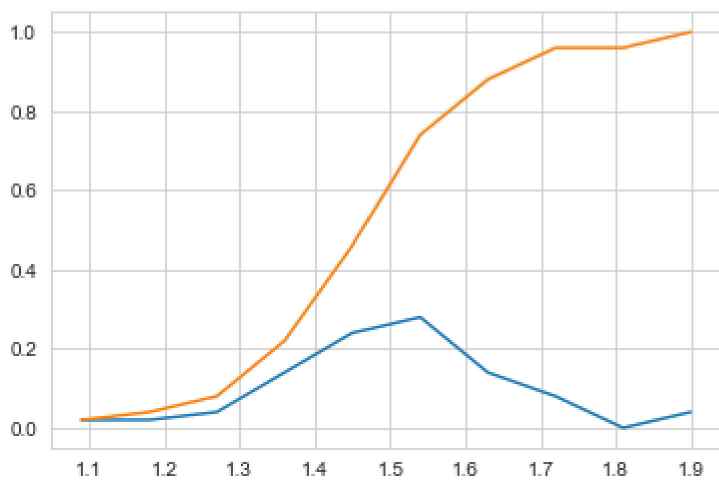
```
[0.02 0.02 0.04 0.14 0.24 0.28 0.14 0.08 0.   0.04]
[1.   1.09 1.18 1.27 1.36 1.45 1.54 1.63 1.72 1.81 1.9 ]
```



In [22]:

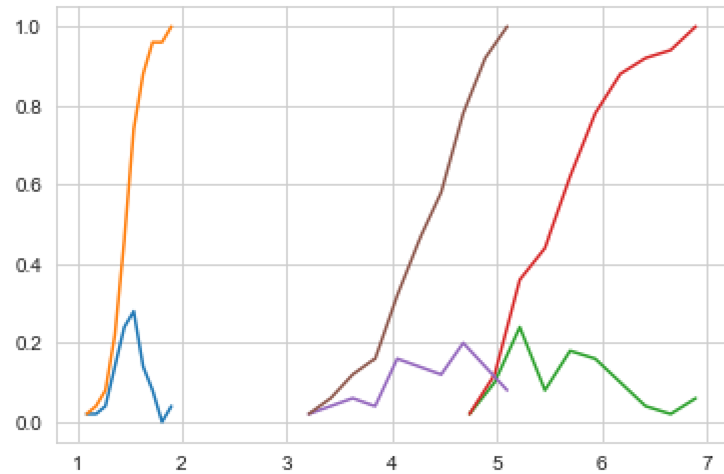
```
# Need for Cumulative Distribution Function (CDF)
# We can visually see what percentage of versicolor flowers have a
# petal_length of less than 1.6?
# How to construct a CDF?
# How to read a CDF?

#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 [23]:
```
# 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 ]
```



(3.5) Mean, Variance and Std-dev

In [24]:
```
#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
```

(3.6) Median, Percentile, Quantile, IQR, MAD

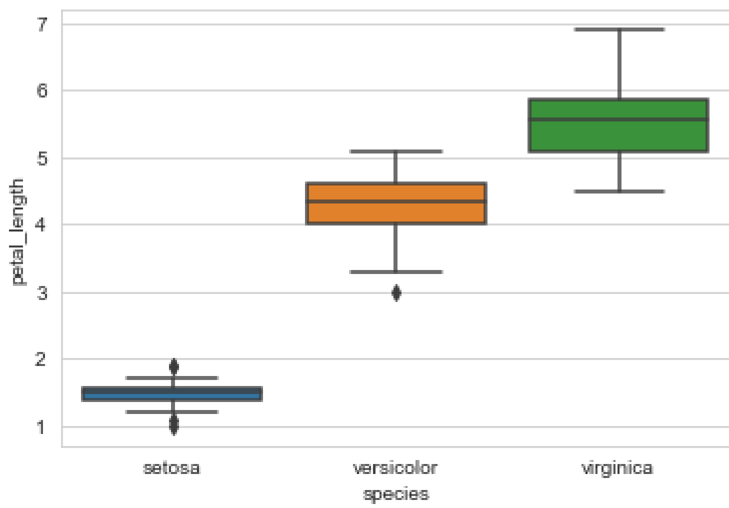
In [25]:
```
#Median, Quantiles, Percentiles, IQR.
print("\nMedians:")
print(np.median(iris_setosa["petal_length"]))
#Median with an outlier
print(np.median(np.append(iris_setosa["petal_length"],50)));
print(np.median(iris_virginica["petal_length"]))
print(np.median(iris_versicolor["petal_length"]))


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
```

(3.7) Box plot and Whiskers

In [26]:

```
#Box-plot with whiskers: another method of visualizing the  1-D scatter plot more
# The Concept of median, percentile, quantile.
# How to draw the box in the box-plot?
# How to draw whiskers: [no standard way] Could use min and max or use other compl
# IQR like idea.

#NOTE: IN the plot below, a technique call inter-quartile range is used in plottin
#Whiskers in the plot below donot correposnd to the min and max values.

#Box-plot can be visualized as a PDF on the side-ways.

sns.boxplot(x='species',y='petal_length', data=iris)
plt.show()
```



(3.8) Violin plots

In [29]:
```
# A violin plot combines the benefits of the previous two plots
#and simplifies them

# Denser regions of the data are fatter, and sparser ones thinner
#in a violin plot

sns.violinplot(x="species", y="petal_length", data=iris, size=8)
plt.show()
```

```
C:\Users\Admin\Anaconda3\lib\site-packages\scipy\stats\stats.py:1713: FutureWa
rning: Using a non-tuple sequence for multidimensional indexing is deprecated;
use `arr[tuple(seq)]` instead of `arr[seq]`. In the future this will be interp
reted 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
```