In [43]:
```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
```

In [44]:
```
from sklearn import metrics
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split
```

Loading the data

In [45]:
```
iris = pd.read_csv("iris.csv")
```

In [46]:
```
print(iris.shape)
```

```
(150, 5)
```

In [47]:
```
iris.head()
```

Out[47]:

	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

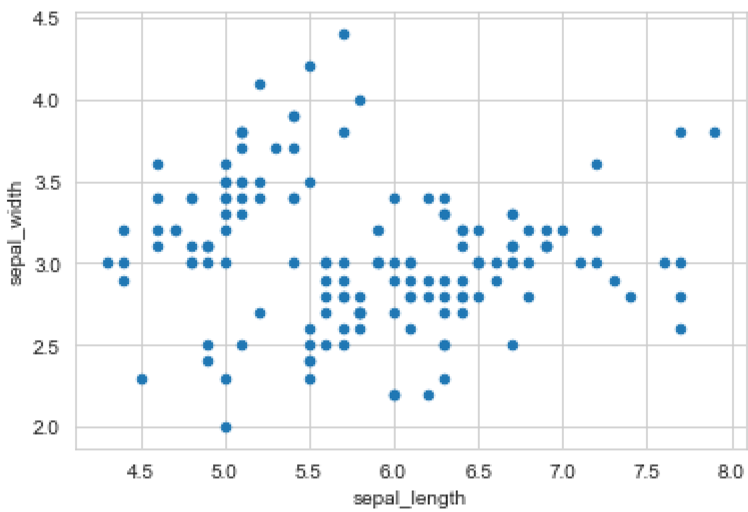
In [48]:
```
iris["species"].value_counts()
```

Out[48]:
```
versicolor    50
setosa        50
virginica     50
Name: species, dtype: int64
```

This clearly indicates that the dataset iris is clealy a balanced dataset. And each of the species contains the same number of datapoints

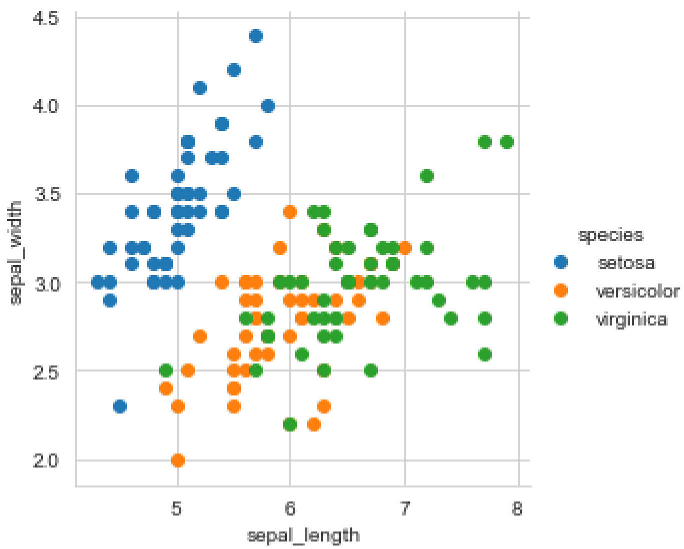
2DD Scatter plot

In [49]:
```
iris.plot(kind='scatter', x='sepal_length', y='sepal_width') ;
plt.show()
```



this does not make sence out of it let us visualize more i.e use colour for each class so that we can define the things better

In [50]:
```
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.

Observation

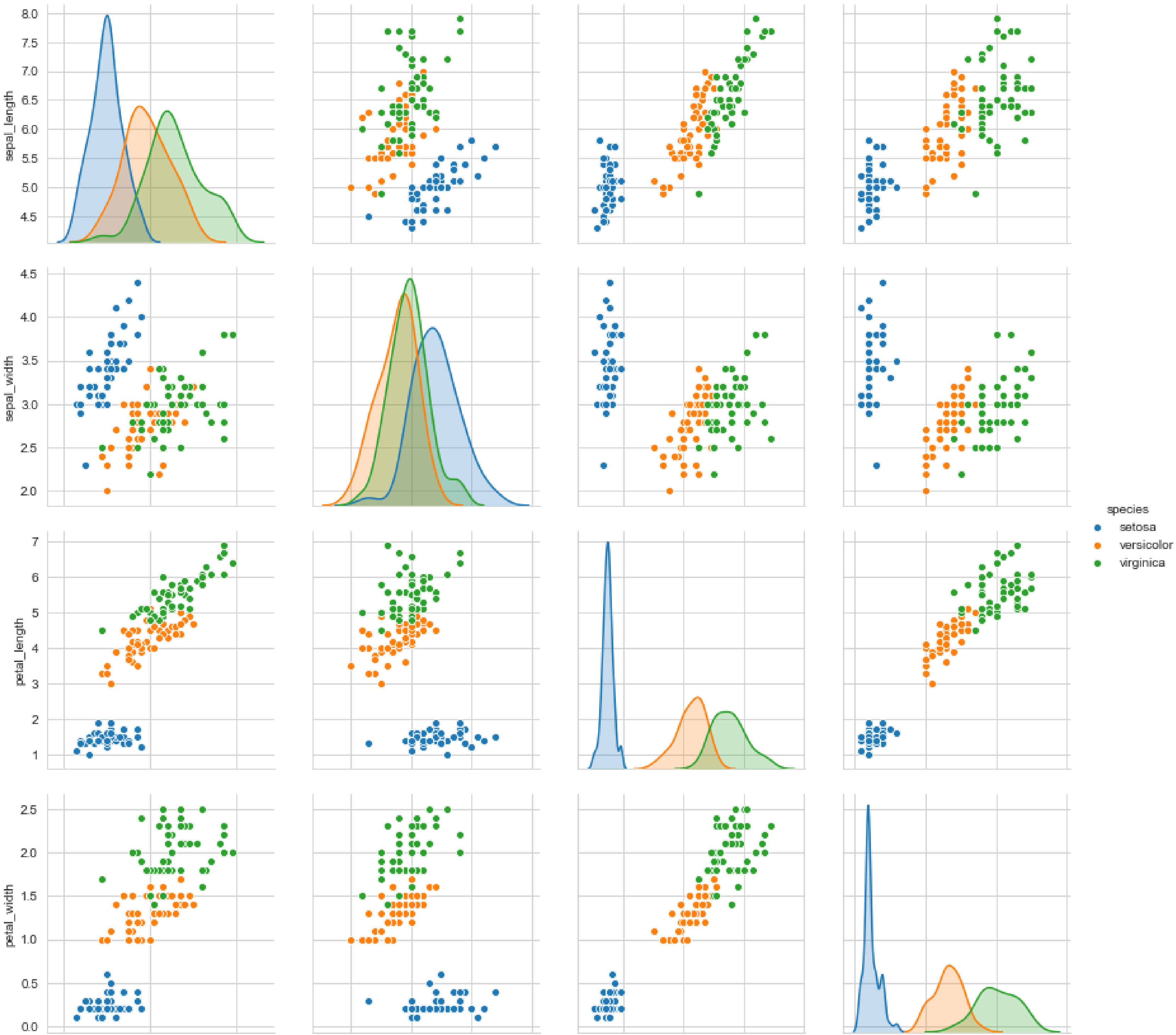
1: Using sepal_length and sepal_width features, we can distinguish Setosa flowers from others.

2: Seperating Versicolor from Viginica is much harder as they have considerable overlap.

3D Scatter plot

Pair plot

In [51]:
```
plt.close();
sns.set_style("whitegrid");
sns.pairplot(iris, hue="species", height=3);
plt.show()
```


sepal_length
sepal_width
petal_length
petal_width
species
setosa
versicolor
virginica

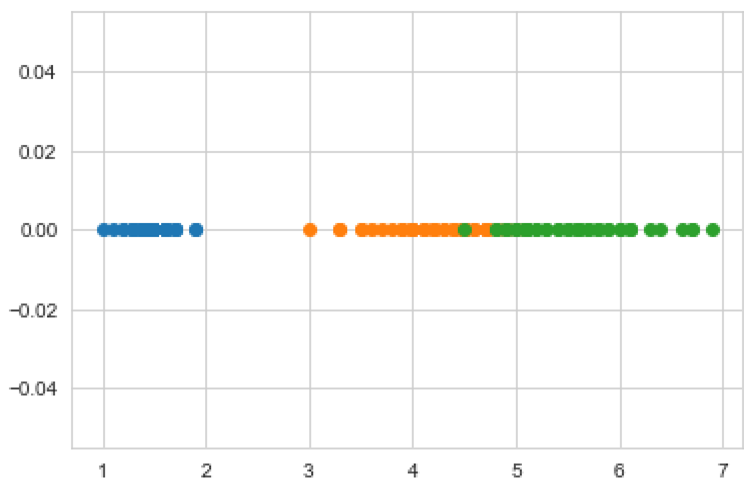
Observations

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 [52]:

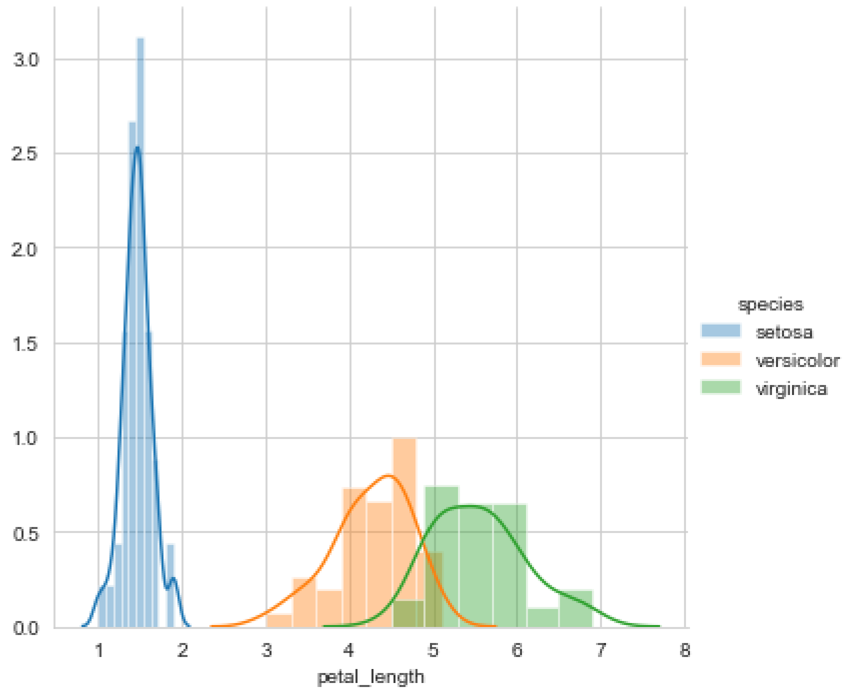
```
iris_setosa = iris.loc[iris["species"] == "setosa"];
iris_virginica = iris.loc[iris["species"] == "virginica"];
iris_versicolor = iris.loc[iris["species"] == "versicolor"];
#print(iris_setosa["petal_length"])
plt.plot(iris_setosa["petal_length"], np.zeros_like(iris_setosa['petal_length']), 'o')
plt.plot(iris_versicolor["petal_length"],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

plt.show()
```



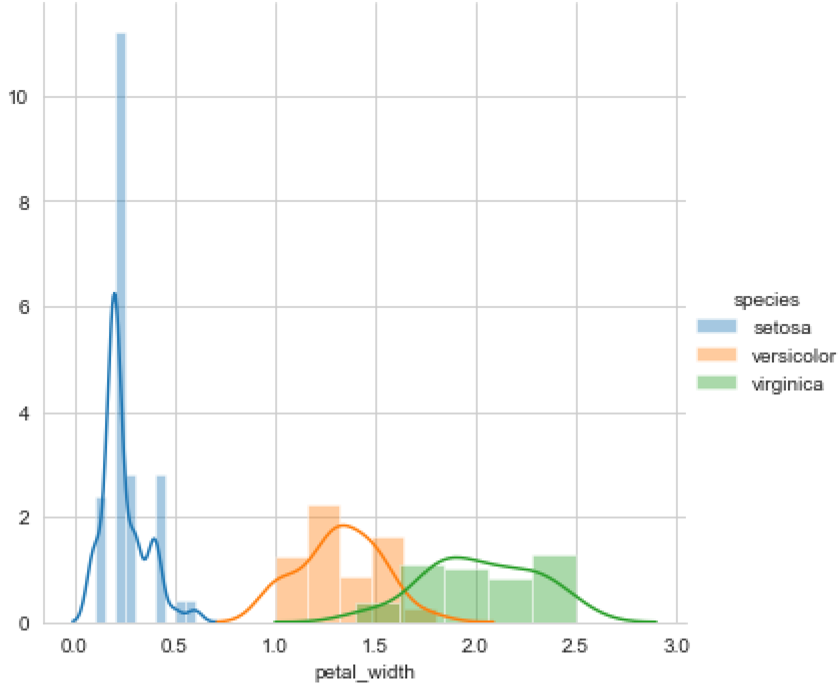
Here the points are overlapping a lot.

In [53]:
```
sns.FacetGrid(iris, hue="species", size=5) \
   .map(sns.distplot, "petal_length") \
   .add_legend();
plt.show();
```

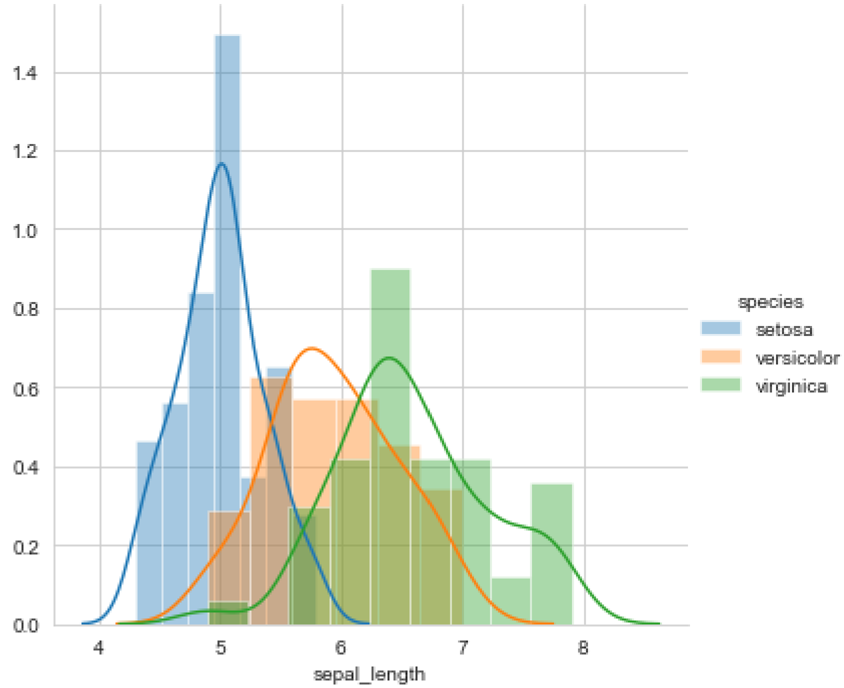
```
C:\Users\SUNNY\Anaconda3\lib\site-packages\seaborn\axisgrid.py:230: UserWarning: The `size` paramter has been
renamed to `height`; please update your code.
  warnings.warn(msg, UserWarning)
```



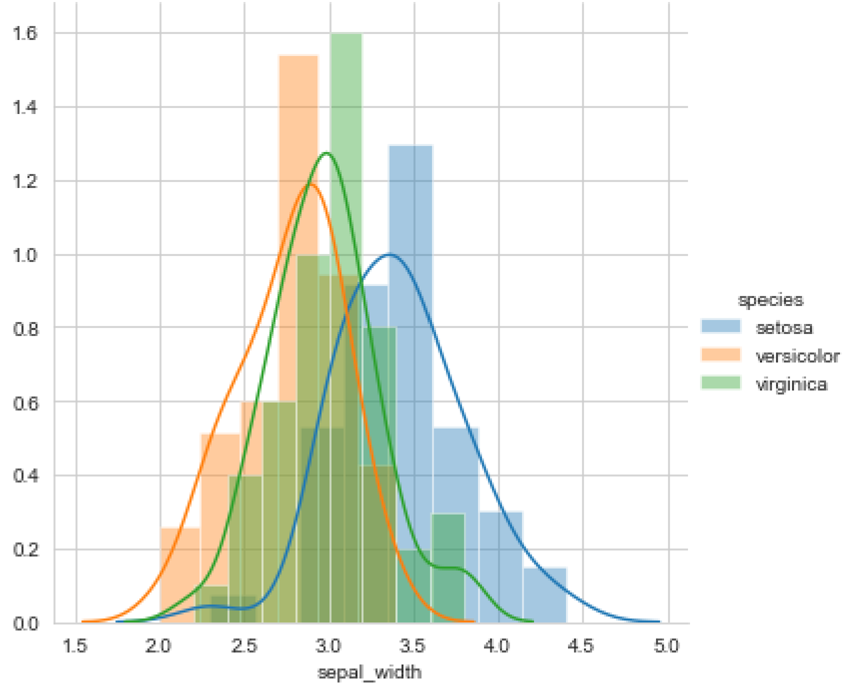
In [54]:
```
sns.FacetGrid(iris, hue="species", size=5) \
   .map(sns.distplot, "petal_width") \
   .add_legend();
plt.show();
```



In [55]:
```
sns.FacetGrid(iris, hue="species", size=5) \
   .map(sns.distplot, "sepal_length") \
   .add_legend();
plt.show();
```

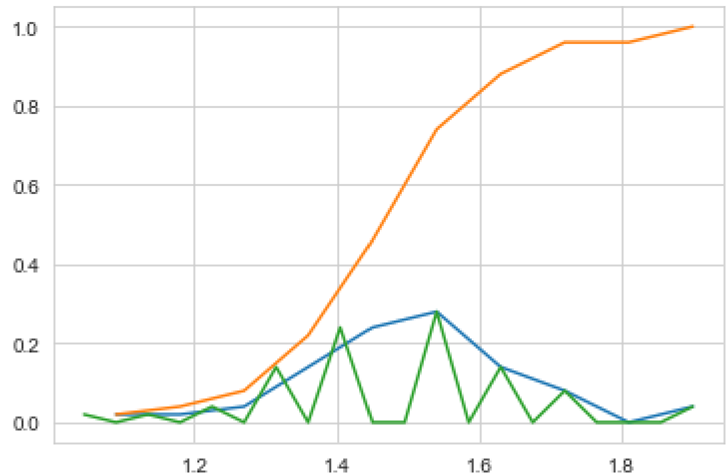


In [56]:
```
sns.FacetGrid(iris, hue="species", size=5) \
   .map(sns.distplot, "sepal_width") \
   .add_legend();
plt.show();
```



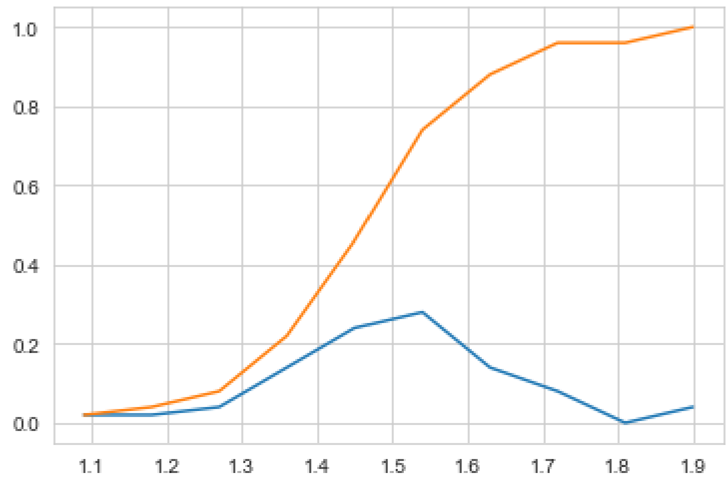
In [57]:
```
# Need for Cumulative Distribution Function (CDF)
# We can visually see what percentage of versicolor flowers have a

#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 ]
```



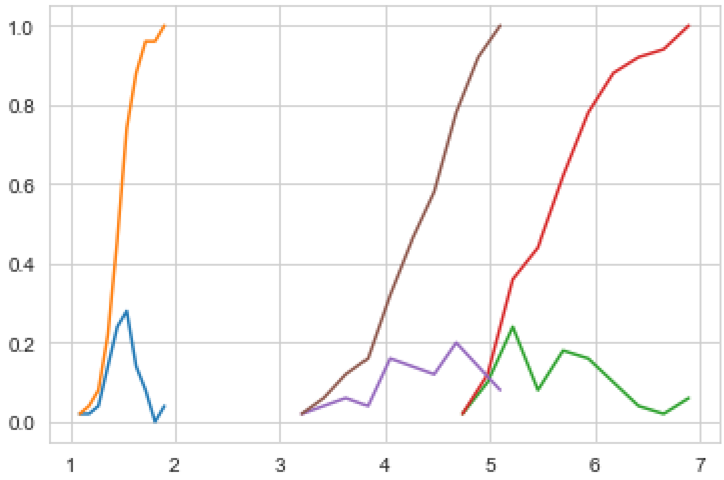
In [58]:
```
# Need for Cumulative Distribution Function (CDF)
# We can visually see what percentage of versicolor flowers have a

#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 [59]:
```
# 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 [60]:
```
#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
```

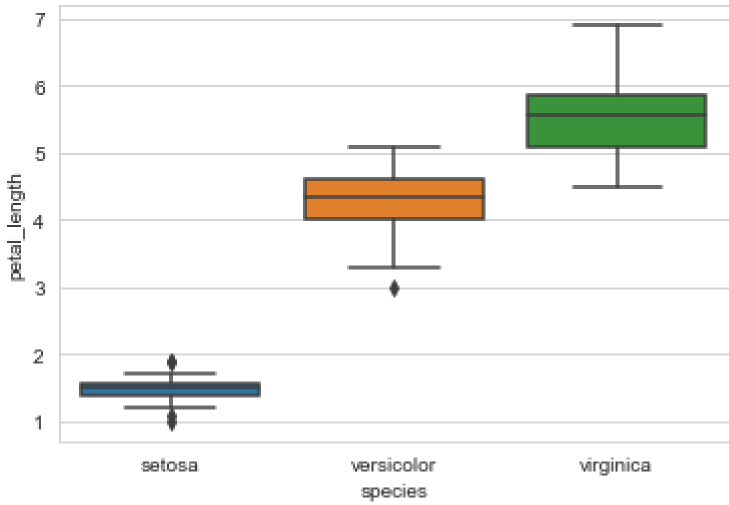
Median, Percentile, Quantile, IQR, MAD

In [61]:
```
#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
```

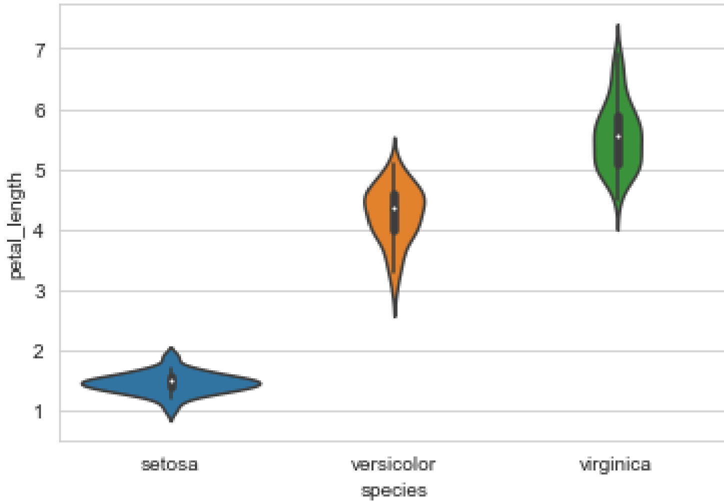
Box plot and Whiskers

In [62]:
```
#Box-plot with whiskers: another method of visualizing the  1-D scatter plot more intuitivey.
# The Concept of median, percentile, quantile.


# IN the plot below, a technique call inter-quartile range is used in plotting the whiskers.
#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()
```

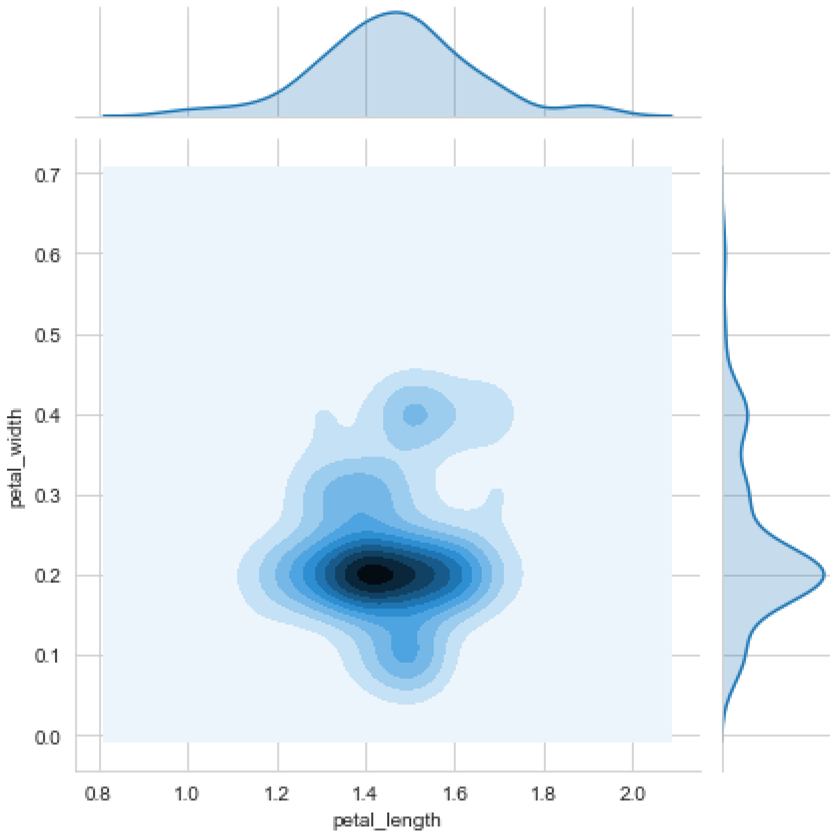


violin plots

In [63]:
```
# 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()
```



In [64]:
```
#2D Density plot, contors-plot
sns.jointplot(x="petal_length", y="petal_width", data=iris_setosa, kind="kde");
plt.show();
```



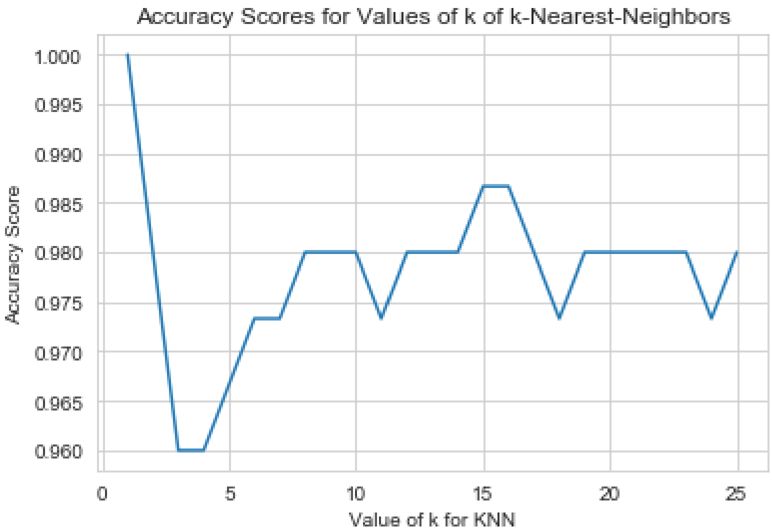
Modeling with scikit learn

In [76]:
```
X = iris.drop([ 'species'], axis=1)
y = iris['species']
print(X.head())
print("_"*100)

print(X.shape)
print("_"*100)
print(y.head())
print("_"*100)
print(y.shape)
```

```
   sepal_length  sepal_width  petal_length  petal_width
0           5.1          3.5           1.4          0.2
1           4.9          3.0           1.4          0.2
2           4.7          3.2           1.3          0.2
3           4.6          3.1           1.5          0.2
4           5.0          3.6           1.4          0.2
____________________________________________________________________________________________________
(150, 4)
____________________________________________________________________________________________________
0    setosa
1    setosa
2    setosa
3    setosa
4    setosa
Name: species, dtype: object
____________________________________________________________________________________________________
(150,)
```

Initialization the knn model

In [66]:
```
k_range = list(range(1,26))
scores = []
for k in k_range:
    knn = KNeighborsClassifier(n_neighbors=k)
    knn.fit(X, y)
    y_pred = knn.predict(X)
    scores.append(metrics.accuracy_score(y, y_pred))

plt.plot(k_range, scores)
plt.xlabel('Value of k for KNN')
plt.ylabel('Accuracy Score')
plt.title('Accuracy Scores for Values of k of k-Nearest-Neighbors')
plt.show()
```



Initialization Logistic Regression

In [67]:
```
logreg = LogisticRegression()
logreg.fit(X, y)
y_pred = logreg.predict(X)
print(metrics.accuracy_score(y, y_pred))
```

```
0.96

C:\Users\SUNNY\Anaconda3\lib\site-packages\sklearn\linear_model\logistic.py:432: FutureWarning: Default solve
r will be changed to 'lbfgs' in 0.22. Specify a solver to silence this warning.
  FutureWarning)
C:\Users\SUNNY\Anaconda3\lib\site-packages\sklearn\linear_model\logistic.py:469: FutureWarning: Default multi
_class will be changed to 'auto' in 0.22. Specify the multi_class option to silence this warning.
  "this warning.", FutureWarning)
```

By splitting the dataset pseudo-randomly into a two separate sets, we can train using one set and test using another.

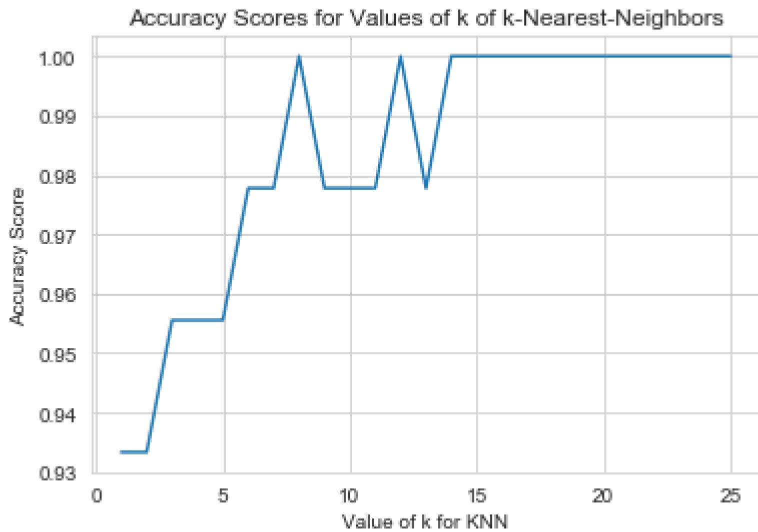
This ensures that we won't use the same observations in both sets. More flexible and faster than creating a model using all of the dataset for training.

Spiting the data into train and test data

In [68]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=5)
print(X_train.shape)
print(y_train.shape)
print(X_test.shape)
print(y_test.shape)
```

```
(105, 4)
(105,)
(45, 4)
(45,)
```

In [77]:
```
##
#initialization the KNN MODEL

k_range = list(range(1,26))
scores = []
for k in k_range:
    knn = KNeighborsClassifier(n_neighbors=k)
    knn.fit(X_train, y_train)
    y_pred = knn.predict(X_test)
    scores.append(metrics.accuracy_score(y_test, y_pred))

plt.plot(k_range, scores)
plt.xlabel('Value of k for KNN')
plt.ylabel('Accuracy Score')
plt.title('Accuracy Scores for Values of k of k-Nearest-Neighbors')
plt.show()
```



In [70]:
```
##  initialization Logistic regression


logreg = LogisticRegression()
logreg.fit(X_train, y_train)
y_pred = logreg.predict(X_test)
print(metrics.accuracy_score(y_test, y_pred))
```

```
0.9333333333333333

C:\Users\SUNNY\Anaconda3\lib\site-packages\sklearn\linear_model\logistic.py:432: FutureWarning: Default solve
r will be changed to 'lbfgs' in 0.22. Specify a solver to silence this warning.
  FutureWarning)
C:\Users\SUNNY\Anaconda3\lib\site-packages\sklearn\linear_model\logistic.py:469: FutureWarning: Default multi
_class will be changed to 'auto' in 0.22. Specify the multi_class option to silence this warning.
  "this warning.", FutureWarning)
```

In [ ]:

In [ ]:

In [ ]:

In [ ]: