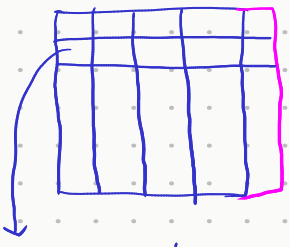
Plotting for Exploratory Data Analysis:-

→ Analyzing data using plotting tools, statistics, linear algebra etc.,

→ Column to be predicted = class label / dependant variable

Data already there = data points / vectors → n dimensional numerical array.

→ columns are called features / input variable / independent variable



1 row = 1 array/vector.

→ 1D vectors = Scalar.

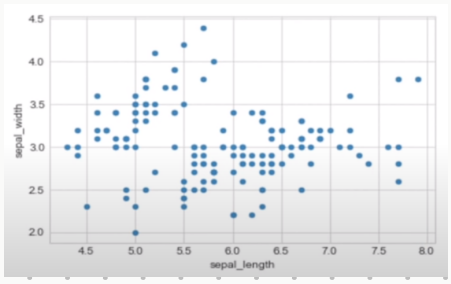
[a], [1], [3.1]

'a' 1 3.1

→ Balanced Dataset → Each class has equal number of datapoints.

→ When reading a plot, always read axis labels & values. It doesn't always start at 0.

→ iris.plot(kind=scatter, x="sepal length", y="petal_width");



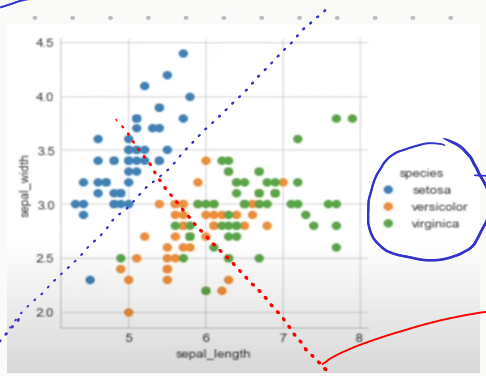
(sns.scatterplot() only plots one plot
sns.FacetGrid() can plot multiple plots.)

→ import seaborn as sns

sns.set_style("whitegrid") → white grid structure

sns.FacetGrid(iris, hue="species", size=4).map(plt.scatter, "sepal_length", "sepal_width").add_legend();

- iris: dataset
- hue="species": by which column should the dataset be colored
- size=4: size
- map(plt.scatter, ...): type of plot
- "sepal_length": x-Axis
- "sepal_width": y-Axis



→ legend.

→ can't separate as too many outliers.

→ line could separate setosa from versicolor & virginica (this is called linear separable)

Observations:- ① S_length & S_width can separate setosa flowers from others.

② Separating versicolor & virginica is harder.

QUICK SEABORN INTRODUCTION:-

→ Simpler way to plot attractive plots.

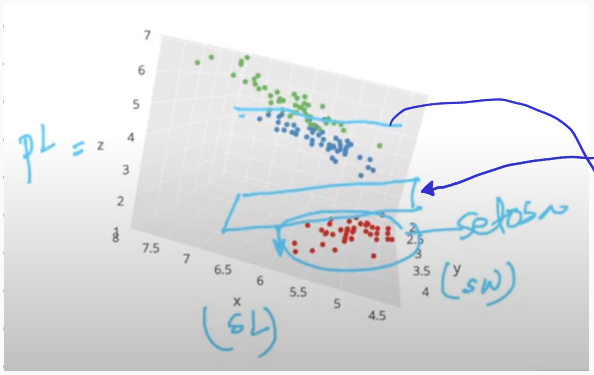
→ high level interface to matplotlib.

→ some features include:

- default aesthetic themes
- custom color palettes
- * Visualizing info from matrices & dataframes.
- * attractive statistical plots.
- * easily displaying distributions

→ Seaborn is a complement, not a substitute of matplotlib

3D Scatter Plot :-



when 3D plot is plotted, we use a plane to separate instead of a line.

Plotting petal length helps notice that plotting a line can seperate them which we were not able to do in a 2D plot.

Drawbacks :- → while being interactive is a pro, it can't be viewed on 2D surfaces like paper or in an ipynb.

→ Since we can't visualize 4D datasets, we use pair plots.

↓

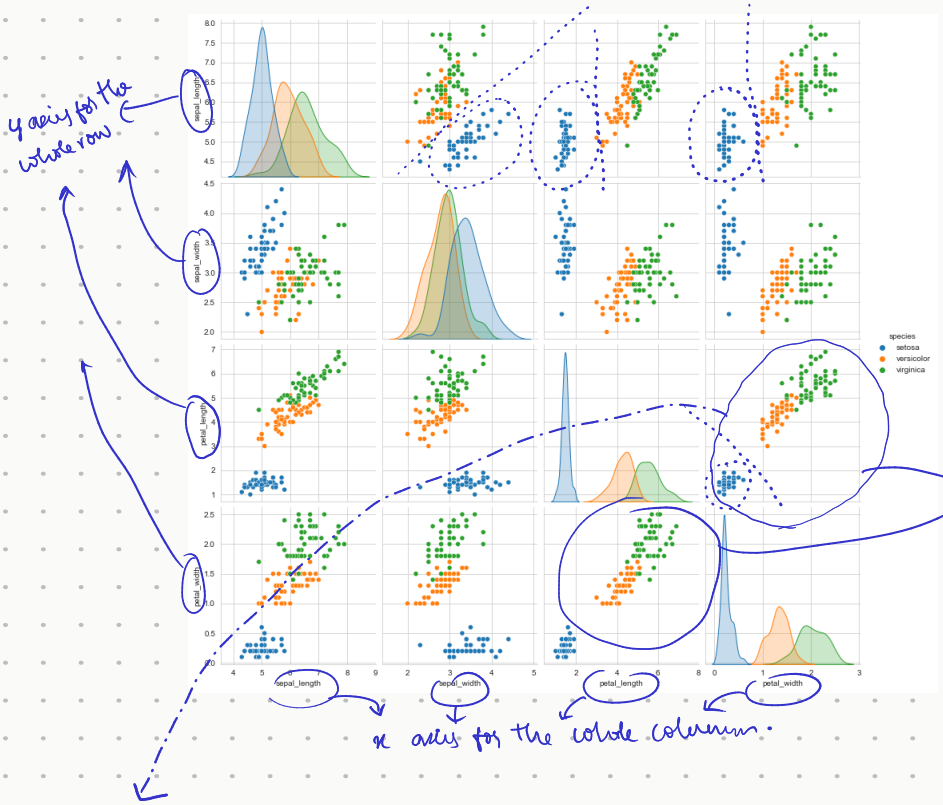
there are 4 variable $\Rightarrow {}^4C_2$ pairs are possible.

↓

6 → {(SL, SW), (SW, PL), (SL, PL), (PW, PL), (SL, PW), (SW, PW)}

Since we can't visualize 4D, we try & visualize these 6.

< sns.pairplot(iris, hue="species", size=3) >



y axis for the whole row

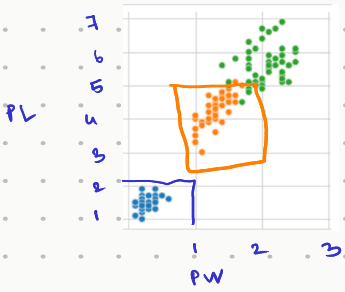
(The diagonal plots are PDFs of each feature)

mirrors. As both are b/w PL, PW.

Similarly there are 3 pairs in total.

So we focus only on 6 plots.

x axis for the whole column.



$\Rightarrow$ if PL ≤ 2 & PW ≤ 1 then flower type = setosa

if (PW ≤ 2 & PW ≥ 1) & (PL ≤ 5 & PL ≥ 2.5) then versicolor

→ There will be some error but that's OK.

Drawback of pairplots :-

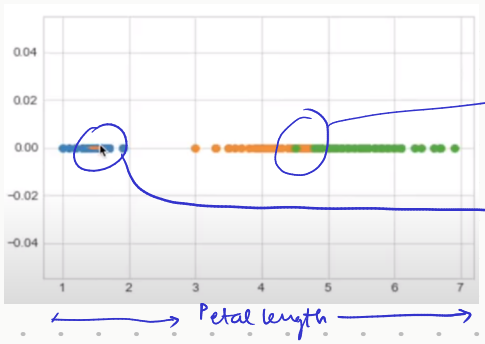
→ When dimensionality is 4, we get ${}^4C_2$ plots

If the dimensionality is n, we will get ${}^nC_2$ plots which is not that useful.

So we use techniques like PCA, t-SNE that will help with this.

In real world, we limit pairplots to only important features & not apply it on all features.

1D Scatter Plots :-



→ harder to read.

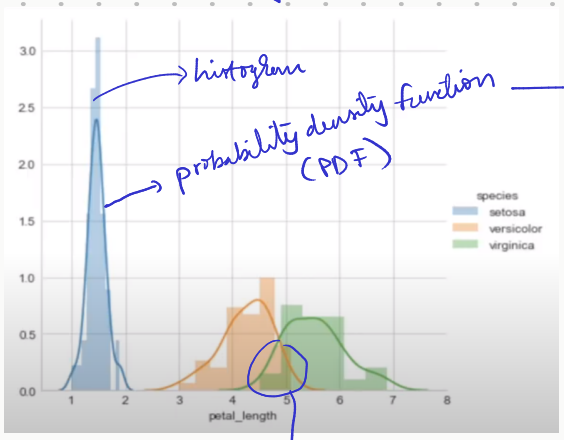
→ green overlaps orange.

→ Number of points here is not clear.

To overcom this, instead of using a scatterplot, we can use a histogram

```
sns.FacetGrid(iris, hue="species", size=5).
    map(sns.distplot, "petal_length").add_legend()
```

distplot aka histogram aka density plot



→ histogram

→ probability density function (PDF) → Smoothed histogram. Smoothed using kernel Density Estimation. (KDE)

→ y-axis: count.

if petal length < 2 then setosa.

if petal length > 2 & petal length < 4.7 then versicolor ≈

if petal length > 4.7 then virginica ≈

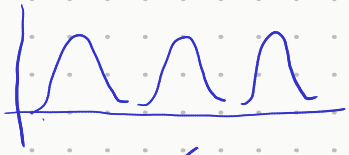
But there will be some

overlapping region

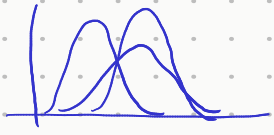
Univariate Analysis :-

→ Analysis of one variable (uni + variate)

→ The farther the distributions are, the better.

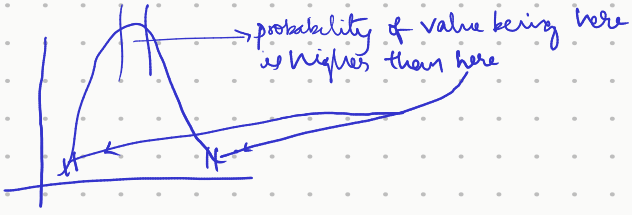


✓



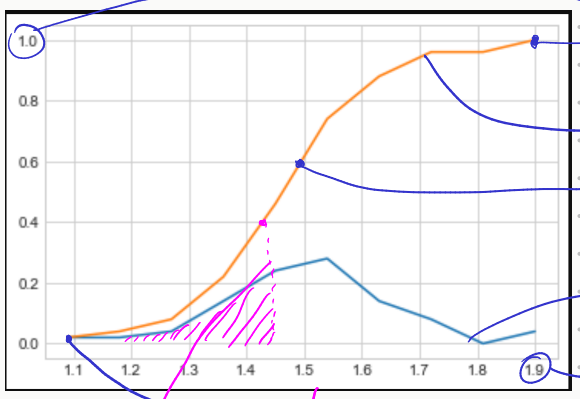
✗

PDF → probability of variable to be in the range of values. Ex:-



Cumulative Data Function :- (CDF)

→ What % of values are ≤ the value at that point.



100 % of the values are ≤ 1.9

CDF

60% of the values are ≤ 1.5

PDF

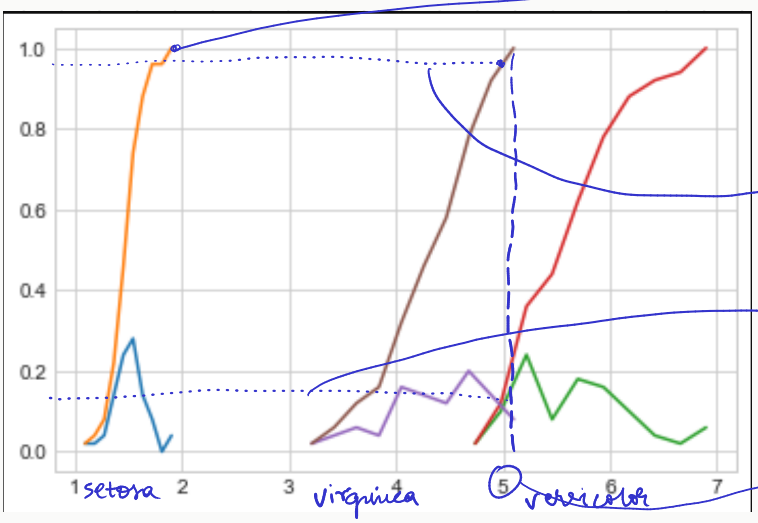
0 % of the values are ≤ 1.1

Differentiation of CDF = PDF

integration of PDF = CDF

The CDF value at this point = sum(values) till that point = cumulative sum.

→ Using CDF, we can make assumptions such as



100 % of setosa flowers petal length ≤ 2.

95% of virginica have petal length ≤ 5

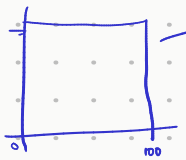
⇒ error % = 5 %

15% of versicolor have petal length ≤ 5

⇒ 85% are ≥ 5.

⇒ error % = 15 %

bin = number of bars in a region in a histogram.



→ 1 bin

→ np.histogram returns counts & bin_edges.

How to compute CDF ? :-

```
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)
```

→ number of bins

→ if false, it will just return the number of samples in each bin (aka normal hist). But if its true returns PDF

→ cumulative sum.

→ Another way to plot CDF :-

sns.kdeplot(data, cumulative = True)

→ But can't adjust bins in this.

Mean, Variance & Standard deviation :-

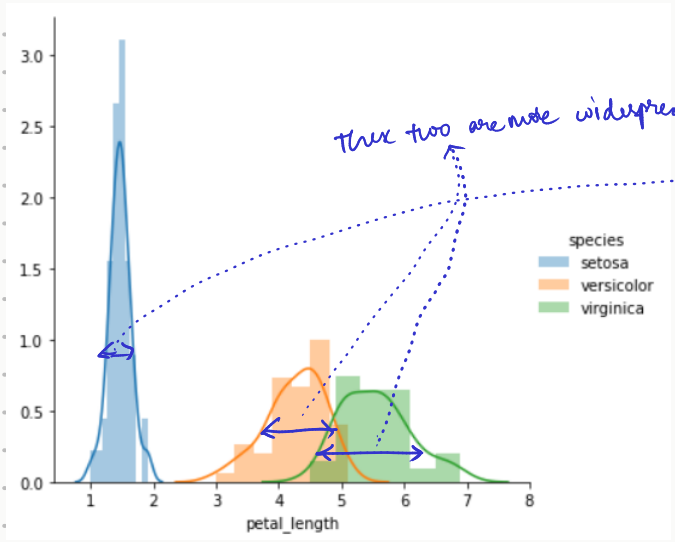
Mean = $\frac{1}{n} \wedge \sum_{i=1}^{n} (x_i)$

Gives an average value. But outliers affect this value. For ex; mean of setosa = 1.464.

Adding one extra value 50 will change the mean to 2.41.

How does mean help ?

Spread = how spreaded is the graph.



These two are more widespread than setosa.

We calculate standard deviation which gives us a range. Useful when we can't plot the data.

std_dev = $\sqrt{\text{variance}}$ → unit

variance = $\frac{1}{n} \sum_{i=1}^{n} (\mu_i - x_i)^2$ → unit²

Square because diff could be -ve.

μ_i → mean of dataset

Now we can use this to estimate type of iris

np.mean() → mean

np.std() → standard deviations.

μ of setosa = 1.4

std-dev of setosa = 0.171

Now if flower is in the range (1.4 − 0.171) to (1.4 + 0.171)

it could be a setosa.

Median :-

→ To overcome mean outlier problem, we use median.

→ Median = sort all elements & pick middle element.

if number of elements = even, mean of middle two elements = median.

→ Median is not corrupted as long as number of corrupted elements ≤ 50% of total elements.

np.median() to get median.

Percentile & Quantile :-

Let x be an array containing some values (100 values)

$x = [\ _0 \ldots\ldots\ldots\ldots\ _{100}]$

Let x_s be the sorted version of x.

x_s = [0, 1, 2 ... 50, 51 ... 99, 100] → indices.

The mean of elements at positions 50, 51 = median of x

↳ this is also known as the 50th percentile.

↳ 50% of the values are ≤ this value.

Similarly x[10] = 10th percentile.

↳ 10% of the values are ≤ this value.

→ 25th, 50th, 75th, 100th percentiles are called Quantiles.

How to get percentile?

np.percentile(dataset, 90) → will give 90th percentile

np.percentile(dataset, np.arange(0,100,25)) → will give 0th percentile, 25th percentile, 50th percentile & 75th percentile.

↳ takes care of sorting. We don't have to pass a sorted array.

→ 90th & 95th percentile in ecommerce helps make sense out of data.

ex:- In Amazon, 90th percentile of delivery dates tell us 90% of orders are delivered in ≤ that days & they can work on improving that by adding more trucks, personnel etc.,

→ Duplicate value shift percentile.

```
a1=[1,2,3,4,5]
a2=[1,2,2,2,2,2,2,2,2,3,4,5]
print(np.percentile(a1,90)) -- 4.6
print(np.percentile(a2,90)) -- 3.9
```

Median Absolute Deviation:-

→ Same notion as standard deviation.

$$\text{median}\left(|\underbrace{x_i - \text{median}}_{\text{deviation}}|\right)_{i=1}^{n}$$

absolute deviation

Aman Sharma

I have seen many students are confused about why we are using SD rather than MAD
Don't worry I have an example

e.g
1,2,3,4,5
if you calculate the standard deviation of this number it will be 1.4142

now calculate MAD it will come around 1

now add or append 50
1,2,3,4,5,50
the standard deviation will be 17.1884
and MAD will be 1.5

so this is the power of MAD>SD.Try to explain all this concept with an example.

How to calculate?

→ Not readily available in numpy.

```
from statsmodels import robust
robust.mad(dataset)
```

mean → median

standard deviations → Median Absolute Deviations → don't have problems with outliers.

IQR:- Inter Quartile Region = 75th percentile − 25th percentile.

↳ 50% of values lie in this range.

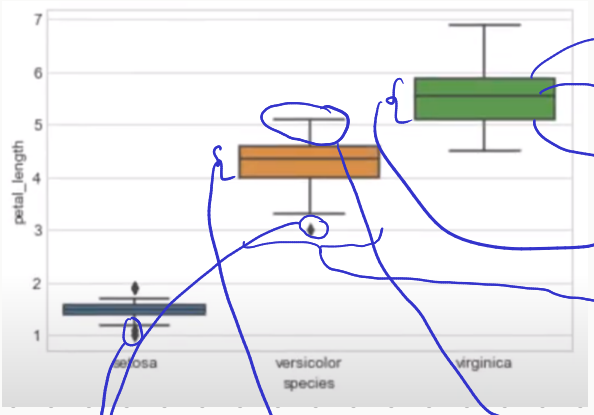
Boxplot & whiskers :-

→ histograms are not good at telling where the percentile lies.

→ We use boxplots for this.

→ ex:- for iris dataset :-

```
sns.boxplot(x="species", y="petal_length", data=iris)
```



→ 75th percentile

→ 50th percentile

→ 25th percentile.

→ how wide it is.

→ this width has no significance

→ Whiskers. There's no fixed way of coming up with them.

Seaborn calculates them as 1.5 * IQR

Whiskers are drawn in such a way that most of the points lie b/w them.

outliers. But not always.

IQR.

→ Box plot also tells us the skewness of the data. If box is cut in half, it means data isn't that skewed. Otherwise it is skewed. Sometimes it may also mean spread of data is high, like in the above graph.

Detecting outliers :-

if the point lies within $\left[(Q_1 - (1.5 * IQR)), (Q_3 + (1.5 * IQR))\right]$

it is not an outlier. Otherwise it is.

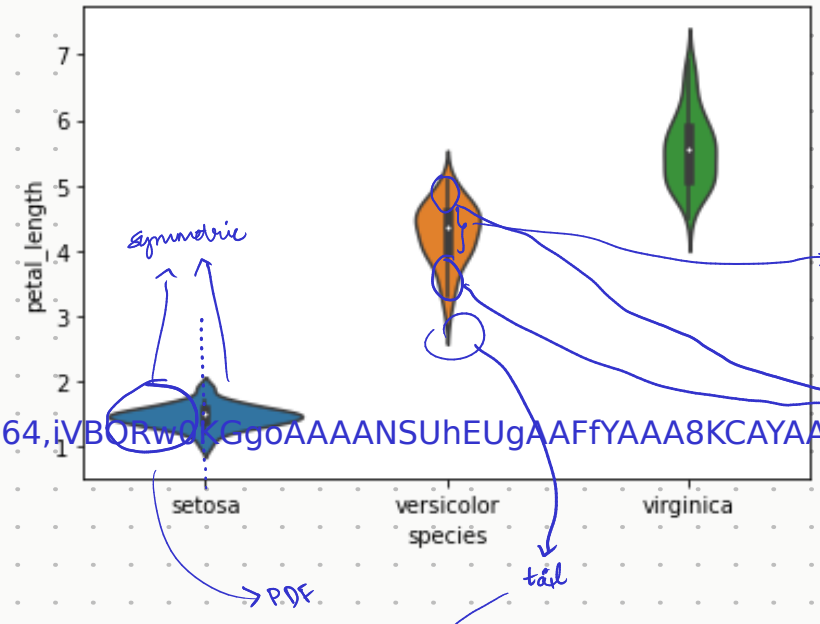
Whiskers are extended based on the following conditions:
The value/Extent of whiskers are decided based on minimum value of the following two conditions:
(1) + or - 1.5 * IQR
(2) Maximum / Minimum value present in the data set.
>The whiskers are extended-above up to
minimum value of (Max value present in data set AND Q3+1.5 IQR)
>The whiskers are extended-below up to
minimum value of (Min value present in data set AND Q1-1.5 IQR)
JUSTIFICATION:
** This rule is mentioned clearly in the Data Mining: Concepts and Techniques
Book by Jiawei Han Page No. 50
Book PDF Source: https://www.pdfdrive.com/data-mining-concepts-and-techniques-3rd-2011-e34881113.html

Violin Plots :-

→ Best of both histogram & box plots.

How to plot :-

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



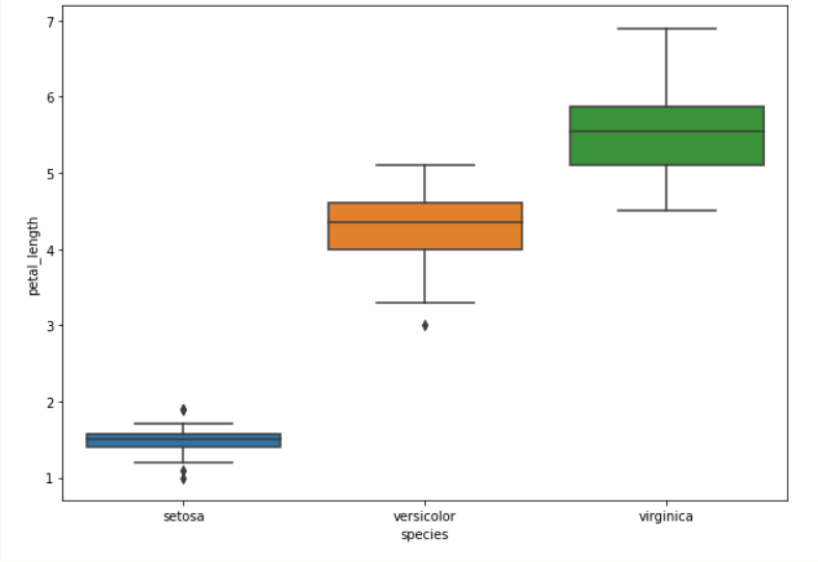
Violin plots have longer tail if there are outliers.

How to have plots of various sizes :-

size of plot

subplot 111

```
plt.figure(figsize=(10,7))
ax=plt.subplot(111)
sns.boxplot(x='species',y='petal_length', data=iris,ax=ax)
plt.show()
```



Multivariate probability Density & contour plot :-

→ Univariate → histogram, CDF, PDF

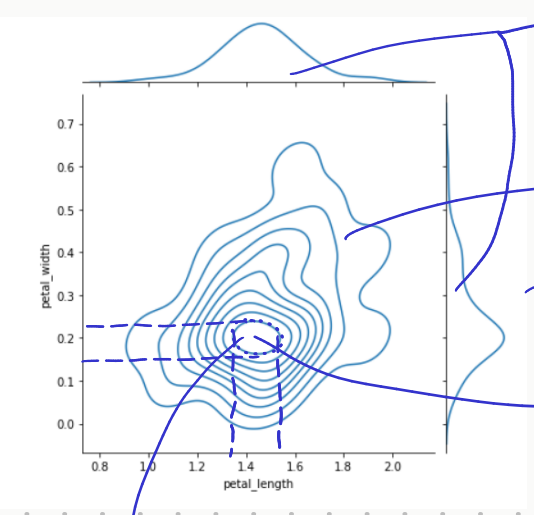
Bivariate → Scatter plot, pair plot.

→ For multivariate we use Scatter plot.

How to plot ?

```
sns.jointplot(x="petal length", y="petal width", data=iris_Setosa, kind="kde")
plt.show()
```

→ The third dimension for this contour plot = density.

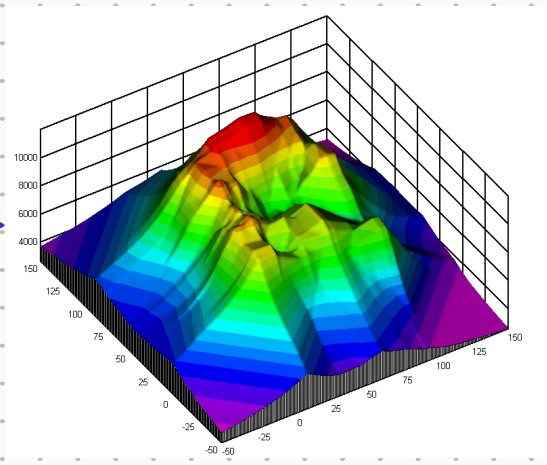


Normal PDFs

contour plot

3D perspective.
Like child projections.

top most point.



This area has the most density (most points)