In [ ]:

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INGENIERÍA EN BIOTECNOLOGÍA
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GBI6 - BIOINFORMÁTICA
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In [ ]:

```python
# librerias
import numpy as np
import matplotlib.pyplot as plt
import matplotlib.mlab as mlab
import math
import seaborn as sns
import pandas as pd
```

In [ ]:

```python
data = pd.read_csv("iris.csv")
data
```

Out[2]:

	Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm	Species
0	1	5.1	3.5	1.4	0.2	Iris-setosa
1	2	4.9	3.0	1.4	0.2	Iris-setosa
2	3	4.7	3.2	1.3	0.2	Iris-setosa
3	4	4.6	3.1	1.5	0.2	Iris-setosa
4	5	5.0	3.6	1.4	0.2	Iris-setosa
...	...	...	...	...	...	...
145	146	6.7	3.0	5.2	2.3	Iris-virginica
146	147	6.3	2.5	5.0	1.9	Iris-virginica
147	148	6.5	3.0	5.2	2.0	Iris-virginica
148	149	6.2	3.4	5.4	2.3	Iris-virginica
149	150	5.9	3.0	5.1	1.8	Iris-virginica

150 rows × 6 columns

In [ ]:

In [ ]:

```
data.describe(percentiles = None, include=None, exclude=None)
```

In [ ]:

Out[4]:		Id	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm
	count	150.000000	150.000000	150.000000	150.000000	150.000000
	mean	75.500000	5.843333	3.054000	3.758667	1.198667
	std	43.445368	0.828066	0.433594	1.764420	0.763161
	min	1.000000	4.300000	2.000000	1.000000	0.100000
	25%	38.250000	5.100000	2.800000	1.600000	0.300000
	50%	75.500000	5.800000	3.000000	4.350000	1.300000
	75%	112.750000	6.400000	3.300000	5.100000	1.800000
	max	150.000000	7.900000	4.400000	6.900000	2.500000

In [ ]:

```python
import scipy.stats as stats
params = [(5.84,0.82,'blue'), (3.05, 0.43, 'red'), (3.75, 1.76, 'orange'), (1.19,0.7,'green

for mean, variance, color in params:
    x = np.linspace(mean - 3*math.sqrt(variance), mean + 3*math.sqrt(variance), 100)
    sigma = math.sqrt(variance)
    label = '$\mu = %.1f, \ \sigma^2=%.1f$' %(mean, variance)
    y_norm = stats.norm.pdf(x, mean, sigma)
    plt.plot(x, y_norm, label=label, c = color)
plt.xlim(-5,10)
plt.ylim(0,1)
plt.xlabel('X')
plt.ylabel('$ϕ_{μ,σ^2}(X)$')
plt.title('Distribución Normal')
plt.legend(title = "Parámetros")
plt.show()
```
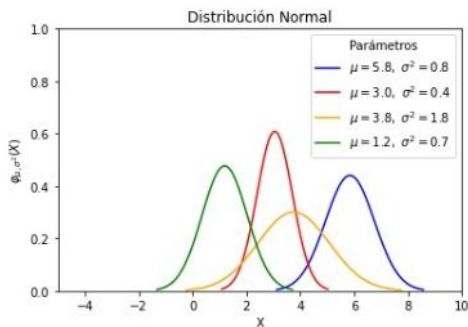
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