Conceptual and Theoretical Questions

Q1 - Law of Total Variance / Expectation

Begin with the definition of the expectation function:

$$E[X] = \sum_x x \cdot p(X = x)$$

From here, the conditional expectation is logical

$$E_X[X|Y] = \sum_x x \cdot p(X=x|Y=y)$$

So,

$$E_Y[E_X[X|Y]] = \sum_y p(Y=y) \left[\sum_x x \cdot p(X=x|Y=y)
ight]$$

Putting p(Y=y) together with p(X=x|Y=y) results in the joint distribution of X and Y: $\sum_{y}\sum_{x}x\cdot p(X=x,Y=y)$

Summing the joint distribution along y gives the marginal distribution of X:

$$\sum_x x \cdot p(X=x)$$

Which is the definition of E[X]

Because variance is defined in terms of the expectation function

$$\operatorname{var}[X] = E[X^2] - E[X]^2$$

Then, using the first equation,

$$E = E_Y[E_X[X^2|Y]] - E_Y[E_X[X|Y]]^2$$

 $=E_Y[E_X[X^2|Y]]-E_Y[E_X[X|Y]]^2$ Rewrite $E_X[X^2|Y]$ as $\mathrm{var}_X[X|Y]+E_X[X|Y]^2$:

$$= E_Y[var_X[X|Y] + E_Y[E_X[X|Y]^2] - E_Y[E_X[X|Y]]^2$$

Finally, combine the last two terms to form variance

$$= E_Y[\mathrm{var}_X[X|Y]] + \mathrm{var}_Y[E_X[X|Y]]$$

The expectation of a random vector is simply a vector with its elements as the corresponding expected values of each component.

It is known that the expectation of the sum of two random variables is equal to the sum of their individual expectations:

$$E[X+Y] = \sum_x \sum_y \left(x+y
ight) \cdot p(x,y)$$

Distribute:

$$egin{aligned} E[X+Y] &= \sum_x \sum_y x \cdot p(x,y) + \sum_x \sum_y y \cdot p(x,y) \ E[X+Y] &= \sum_x x \cdot p(x,y) + \sum_y y \cdot p(x,y) \ E[X+Y] &= E[X] + E[Y] \end{aligned}$$

The above logic applies to random vectors as well, just on an element by element basis.

Covariance is defined as cov(X, Y) = E[(X - E[X])(Y - E[Y])]

Generalize to vectors where a random vector is
$$\sum_i X$$
: $\mathrm{cov}(X,Y) = E[(\sum_i x_i - E[\sum_i x_i])(\sum_j y_j - E[\sum_j y_j])]$

Rewrite to bring the sum operators out:

$$egin{aligned} \operatorname{cov}(X,Y) &= \sum_{i,j} E[x_i y_j] - E[x_i] E[y_j] \ \operatorname{cov}(X,Y) &= \sum_{i,j} \operatorname{cov}(x_i,y_j) \end{aligned}$$

The posterior distribution can be estimated as a product of the likelihood and prior $p(\mu)$ distributions.

The likelihood function is defined as the conditional probability of observing the dataset X given the model parameters. So,

$$L(X|\mu) = \prod_{i=1}^N N(x_i|\mu,\Sigma)$$

Thus, the posterior distribution is

$$egin{aligned} p(\mu|X) &= N(\mu|\mu_0,\Sigma_0) \cdot \prod_{i=1}^N rac{1}{\sqrt{2\pi\Sigma^2}} \exp\left(-rac{(x_i-\mu)^2}{2\Sigma^2}
ight) \ p(\mu|X) &= N(\mu|\mu_0,\Sigma_0) \cdot (2\pi\Sigma^2)^{-N/2} \cdot \prod_{i=1}^N \exp\left(-rac{(x_i-\mu)^2}{2\Sigma^2}
ight) \ p(\mu|X) &= (2\pi\Sigma_0^2)^{-1/2} \exp\left(-rac{(\mu-\mu_0)^2}{2\Sigma_0^2}
ight) \left[-rac{N}{2} \ln{(2\pi\Sigma_0^2)} - \sum_{i=1}^N rac{(x_i-\mu)^2}{2\Sigma_0^2}
ight] \end{aligned}$$

The likelihood function $L(x|\mu,\lambda)$ is

$$\left(rac{\lambda}{2\pi}
ight)^{N/2}\prod_{i=1}^N\exp\left(-rac{\lambda(x_i-\mu)^2}{2}
ight)$$

Simplify, as in (2.152):

$$\left[\lambda^{rac{1}{2}}\exp\left(-rac{\lambda\mu^2}{2}
ight)
ight]^N\exp\left(\lambda\mu\sum_{i=1}^Nx_i-rac{\lambda}{2}\sum_{i=1}^Nx_i^2
ight)$$

As per (2.153), the prior can be expressed as:

$$\left[\lambda^{rac{1}{2}}\exp\left(-rac{\lambda\mu^2}{2}
ight)
ight]^{eta}\exp\left(c\lambda\mu-d\lambda
ight)$$

c,d, and β are constants. Multiplying the prior and likelihood gives:

$$\left[\lambda^{rac{1}{2}}\exp\left(-rac{\lambda\mu^2}{2}
ight)
ight]^{eta+N}\exp\left[\lambda\left((c+\sum x_i)\mu+(d+rac{1}{2}\sum x_i^2)
ight)
ight]$$

Since the posterior is in the same form as the prior, simply with new values given for c, d, and β , multiplying the prior and likelihood functions return a Gaussian and Gamma distribution.

Using the prior as a template, the posterior can be expressed with c_p , d_p , and β , using their prior values:

$$egin{aligned} eta_p &= eta + N \ c_p &= c + \sum x_i \ d_p &= d + \sum x_i^2 \end{aligned}$$

Q5 - Covariance of Independent RVs

Covariance is formally defined as

$$cov_{XY} = E[(X - \mu_X)(Y - \mu_Y)]$$

Where
$$E[X] = \mu_X$$
 and $E[Y] = \mu_Y$

If the definition above is expanded to

$$= E[XY - \mu_Y X - \mu_X Y + \mu_Y \mu_X]$$

Then it is possible to use the property of the expectation function, that $E[A_1+A_2]=E[A_1]+E[A_2]$, which results in

$$= E[XY] - E[\mu_Y X] - E[\mu_X Y] + E[\mu_Y \mu_X]$$

Factor out the constants, as E[aX] = aE[X]

$$= E[XY] - \mu_Y E[X] - \mu_X E[Y] + \mu_Y \mu_X = E[XY] - \mu_X \mu_Y - \mu_X \mu_Y + \mu_Y \mu_X = E[XY] - \mu_X \mu_Y$$

Finally, notice that because X and Y are independent, then E[XY]=E[X]E[Y] , resulting in $\mu_X\mu_Y-\mu_X\mu_Y=0$

Q6 - Kullback-Leibler Divergence

Kullback-Leiber Divergence is defined as:

$$KL(p||q) = -\int p(x) \ln q(x) dx + \int p(x) \ln p(x) dx$$

Or, combining the integrals:

$$KL(p||q) = -\int p(x) \ln rac{q(x)}{p(x)} dx$$

The Gaussian distribution is mathematically expressed as

$$N(\mu,\sigma^2) = rac{1}{\sqrt{2\pi}} \mathrm{exp}\left(-rac{(x-\mu)^2}{2\sigma^2}
ight)$$

And its natural logarithm (for ease of calculation later):

$$\ln N(\mu,\sigma) = rac{1}{2} \ln 2\pi - rac{(x-\mu)^2}{2\sigma^2}$$

Evaluating the KL Divergence:

$$\begin{split} &=-\int p(x)\left[\frac{1}{2}\ln 2\pi -\frac{(x-m)^2}{2s^2}\right]dx + \int p(x)\left[\frac{1}{2}\ln 2\pi -\frac{(x-\mu)^2}{2\sigma^2}\right]dx \\ &=-\int p(x)\left[-\frac{1}{2}\ln 2\pi -\frac{(x-m)^2}{2s^2}\right]dx - \frac{1}{2}\ln \left(2\pi\sigma^2\right) - \frac{1}{2} \\ &=\frac{1}{2}\ln \left(2\pi s^2\right) + \int p(x)\frac{(x-m)^2}{2s^2}dx - \frac{1}{2}\ln \left(2\pi\sigma^2\right) - \frac{1}{2} \\ &=\frac{1}{2}\ln \left(2\pi s^2\right) + \frac{1}{2s^2}\int p(x)(x^2-2mx+m^2)dx - \frac{1}{2}\ln \left(2\pi\sigma^2\right) - \frac{1}{2} \\ &=\frac{1}{2}\ln \left(2\pi s^2\right) + \frac{1}{2s^2}\left[\int x^2 \cdot p(x)dx - 2m\int x \cdot p(x)dx + m^2\int p(x)dx\right] - \frac{1}{2}\ln \left(2\pi\sigma^2\right) - \frac{1}{2} \end{split}$$

Use $E[g(x)] = \int g(x) p(x) dx$:

$$=rac{1}{2}{
m ln}\left(2\pi s^2
ight)+rac{1}{2s^2}igl[E[X^2]-2m\cdot E[X]+m^2igr]-rac{1}{2}{
m ln}\left(2\pi\sigma^2
ight)-rac{1}{2}$$

$$\begin{split} \mathsf{Use}\, E[X^2] &= \mathrm{var}[X] + E[X]^2 = \sigma^2 + \mu^2 \\ &= \frac{1}{2}\mathrm{ln}\,(2\pi s^2) + \frac{1}{2s^2}\big[\sigma^2 + \mu^2 - 2m\mu + m^2\big] - \frac{1}{2}\mathrm{ln}\,(2\pi\sigma^2) - \frac{1}{2} \\ &= \frac{1}{2}\mathrm{ln}\,(2\pi s^2) + \frac{1}{2s^2}\big[\sigma^2 + (\mu - m)^2\big] - \frac{1}{2}\mathrm{ln}\,(2\pi\sigma^2) - \frac{1}{2} \end{split}$$

Finally, simplify:

$$-\ln\left(rac{s}{\sigma}
ight)+rac{\sigma^2}{2s^2}+rac{(\mu-m)^2}{2s^2}-rac{1}{2}$$

Part a

The expectation of a continuous RV is $E[X] = \int x \cdot p(x) dx$

Apply to the given inverse gamma function:

$$egin{aligned} E[X] &= rac{eta^{lpha}}{\Gamma(lpha)} \int_{0}^{\infty} x^{-lpha} \exp{(-rac{eta}{x})} dx \ E[X] &= rac{eta^{lpha}}{\Gamma(lpha)} \cdot rac{\Gamma(lpha-1)}{eta^{lpha-1}} \ E[X] &= rac{eta}{\Gamma(lpha)} \cdot \Gamma(lpha-1) \ E[X] &= rac{eta}{lpha-1} \end{aligned}$$

Part b

Here, the likelihood function is $L(lpha,eta)=\prod_{i=1}^N p(x_i|lpha,eta)$:

Change the product to a summation by taking the log of the likelihood function:

$$egin{aligned} &\ln\left(L(lpha,eta)
ight) = \sum_{i=1}^N \lnrac{eta^lpha}{\Gamma(lpha)} + \ln x_i^{-lpha-1} - rac{eta}{x_i} \ &\ln\left(L(lpha,eta)
ight) = N \cdot \lnrac{eta^lpha}{\Gamma(lpha)} + \sum_{i=1}^N \ln x_i^{-lpha-1} - rac{eta}{x_i} \end{aligned}$$

Maximize eta with $rac{\partial L}{\partial eta} = 0$

$$egin{aligned} rac{\partial L}{\partial eta} &= rac{Nlpha}{eta} - \sum_{i=1}^N rac{1}{x_i} = 0 \ eta_{ML} &= rac{Nlpha}{\sum_{i=1}^N x_i^{-1}} \end{aligned}$$

Maximize lpha with $rac{\partial L}{\partial lpha} = 0$

$$egin{aligned} rac{\partial L}{\partial lpha} &= N \cdot \ln rac{eta^{lpha}}{\Gamma(lpha)} + \sum_{i=1}^{N} \ln x_i^{-lpha-1} - rac{eta}{x_i} \ 0 &= N rac{\partial}{\partial lpha} igg(\ln rac{eta^{lpha}}{\Gamma(lpha)} igg) + \sum_{i=1}^{N} rac{\partial}{\partial lpha} \ln x_i^{-lpha-1} \end{aligned}$$

Solve for α to find α_{ML}

Part c

A distribution belongs in the exponential distribution family if it follows the following form:

$$p(x|\theta) = h(x)g(\theta) \exp(\theta^{\mathrm{T}}u(x))$$

f(x) fits this condition, where $g(heta)=rac{eta^{lpha}}{\Gamma(lpha)}$ and $h(x)=x^{-lpha-1}$

Part d, e

Y becomes a gamma distribution with the given parameters, resulting in a PDF of:

$$p(x) = rac{eta^lpha}{\Gamma(lpha)} x^{lpha-1} \exp{(-eta x)}$$

Using the given parameters:

$$p(x) = ce^{-cx}$$

As this is still of the exponential distribution family, a proper prior would be the gamma distribution $\Gamma(c|a,b)$

Where a=1,b=2

The posterior becomes

$$p(c|x_i) = \Gamma(c|a=1,b=2)c^N \sum_i^N e^{-cx_i}$$

For N observations

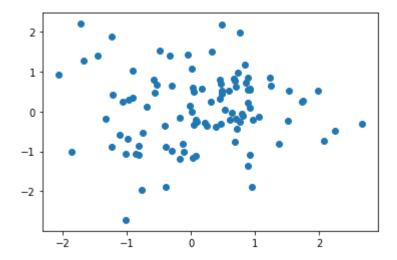
Application Questions

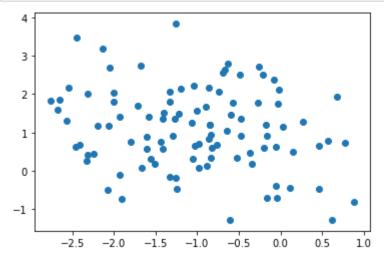
```
In []: # Using Python 3.8.1

# Imports
import numpy as np
import matplotlib.pyplot as plt
from scipy.optimize import minimize
from scipy import stats
from sklearn.metrics import RocCurveDisplay
from sklearn.mixture import GaussianMixture
from sklearn.cluster import KMeans
import random
import math
```

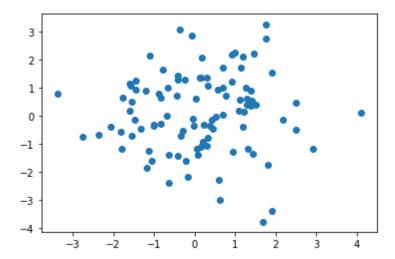
1. Sampling from a Distribution (15 pts)

Out[]: <matplotlib.collections.PathCollection at 0x1c1139029a0>

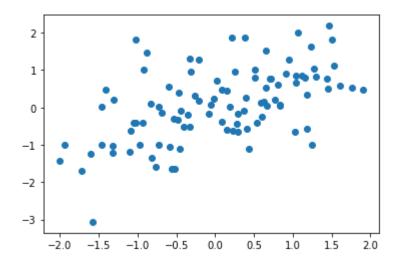




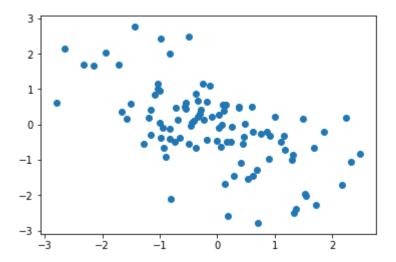
Out[]: '\nIt is evident that increasing the variance of x1 and x2 increases the spre ad across both axes. \n'



Out[]: '\nThe distribution of the samples now resembles a line with a positive slope
 \n'



Out[]: '\nThe distribution of the samples now resembles a line with a negative slope
 \n'



```
Covariance matrix:

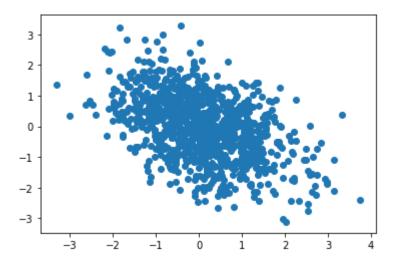
[[ 1.2127543 -0.72850594]

[-0.72850594 1.24061739]]

Average:

(-0.07355973165570365, -0.08993759472706986)
```

Out[]: <matplotlib.collections.PathCollection at 0x1c1139a54f0>



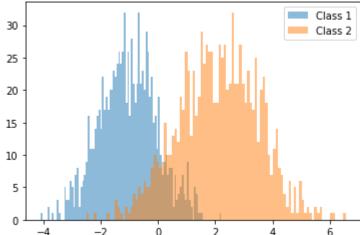
```
In [ ]: # Part i, j
        gaussian = lambda samples: np.random.multivariate normal(
                                         mean=[0,0],
                                         cov=[[1,-0.5],[-0.5,1]],
                                         size=samples)
        def gaussian_average(sampling_size):
            data = gaussian(sampling size)
            mean = (np.average([x[0] for x in data]),
                     np.average([y[1] for y in data]))
            print("Average for sampling size = {:<2}:".format(sampling_size),</pre>
                     mean)
        def gaussian_cov(sampling_size):
            data = gaussian(sampling size)
            cov = np.cov(data, rowvar=False)
            print("Cov(x1,x2), sample size = " + str(sampling_size) + ":{:<35}".format</pre>
         (cov[0][1]))
        gaussian_average(10)
        gaussian average(100)
        gaussian average(1000)
        gaussian cov(10)
        gaussian_cov(100)
        gaussian_cov(1000)
         _="""
        As the sampling size increases, the mean and the covariance both approach the
         parameters given to the model in g), and are more consistent as the distribut
        ion is sampled multiple times. With a sample size of 10, the covariance and me
        an are very volatile, jumping around as they are sampled multiple times. At a
         sampling size of 1000, these values vary much less. It is possible for an est
        imate with a smaller sampling size to be as accurate compared to that of one w
        ith a higher sampling size, but it will not be as likely or conssitent
        Average for sampling size = 10: (0.202329068815451, -0.5301533705299037)
        Average for sampling size = 100: (-0.02809361651484865, 0.12531132990124305)
        Average for sampling size = 1000: (0.05145237148377632, -0.0674404753671594)
        Cov(x1,x2), sample size = 10:-0.12617159471219894
        Cov(x1,x2), sample size = 100:-0.5427987874001927
        Cov(x1,x2), sample size = 1000:-0.5102361321055116
```

2. Bayes Classifier (15 pts)

```
In []: # Part a, b
        def class_init(samples_a, samples_b):
            class_1 = np.random.normal(loc=-1, scale=1, size=samples_a)
            class 2 = np.random.normal(loc=2, scale=np.sqrt(2), size=samples b)
            return class_1, class_2
```

```
In [ ]: # Part c
        class 1 b, class 2 b = class init(1000, 1000)
        def part_c_hist(class_1, class_2):
            plt.figure(10)
            plt.hist(x=class_1, bins=100, alpha=0.5, label="Class 1")
            plt.hist(x=class_2, bins=100, alpha=0.5, label="Class 2")
            plt.title("Distribution of samples from class 1 and 2")
            plt.legend()
        part_c_hist(class_1_b, class_2_b)
```



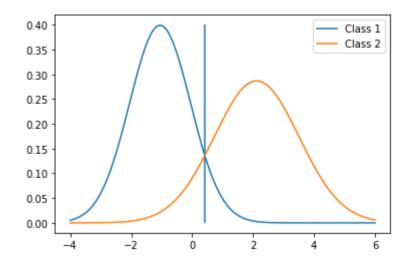


```
In [ ]: # Part d Using MLE to estimate distribution parameters
        def obj(params, data):
            mean, st dev = params
            # Logarithms make the likelihood function easier
            # to work with, as discussed in class. Although
            # MLE maximizes the likelihood function, minimizing
            # the negative likelihood function is also equivalent.
            neg_log_likelihood = -np.sum(stats.norm.logpdf(
                                             loc=mean,
                                             scale=st_dev))
            return neg_log_likelihood
        def calc mle(class 1, class 2):
            init_guess = np.array([0, 1])
            # MLE - Class 1
            mean_1, st_dev_1 = minimize(
                                 lambda params: obj(params, class 1),
                                 x0=init_guess, method="Powell").x
            print(f"Class 1 - Mean={mean_1}, var={st_dev_1**2}")
            # MLE - Class 2
            mean 2, st dev 2 = minimize(
                                 lambda params: obj(params, class 2),
                                 x0=init guess, method="Powell").x
            print(f"Class 2 - Mean={mean_2}, var={st_dev_2**2}")
            # The scipy docs advise to use Powell or Nelder-Mead
            # method for noisy data, which is indeed the case.
            return [(mean 1, st dev 1), (mean 2, st dev 2)]
        est_stats_b = calc_mle(class_1_b, class_2_b)
```

Class 1 - Mean=-1.0528562718551424, var=1.0007035501395347 Class 2 - Mean=2.1141778963763302, var=1.9351940597506507

```
In [ ]: | # Part e
        def plot_mle_pdf(est_stats):
            mean_1, st_dev_1 = est_stats[0]
            mean 2, st dev 2 = est stats[1]
            plt.figure(11)
            pdf_x = np.linspace(-4,6,num=1000)
            mle_pdf_1 = stats.norm.pdf(x=pdf_x, loc=mean_1, scale=st_dev_1)
            mle_pdf_2 = stats.norm.pdf(x=pdf_x, loc=mean_2, scale=st_dev_2)
            plt.plot(pdf_x, mle_pdf_1, label="Class 1")
            plt.plot(pdf_x, mle_pdf_2, label="Class 2")
            ints = np.argwhere(np.diff(np.sign(mle_pdf_1 - mle_pdf_2)))
            plt.vlines(pdf_x[ints], ymin=0, ymax=0.4)
            plt.legend()
            print(f"Decision boundary = {pdf_x[ints][0][0]}, classify as class 1 if be
        low this value and class 2 if above")
            return pdf_x[ints[0][0]]
        bound_b = plot_mle_pdf(est_stats_b)
        The decision boundary is simple: it indicates a change in which probability of
        the two distributions is higher.
```

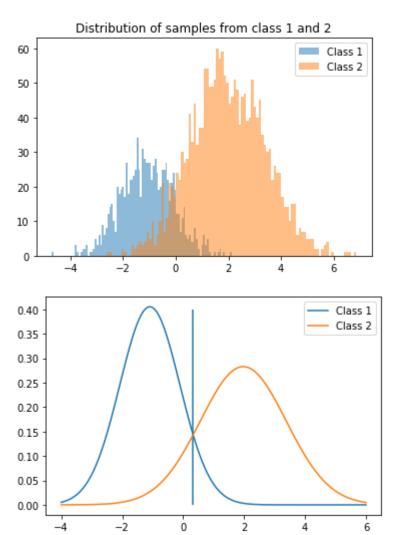
Decision boundary = 0.4144144144144146, classify as class 1 if below this value and class 2 if above



```
In [ ]: # Part g
     class_1_ub, class_2_ub = class_init(1000, 2000)
```

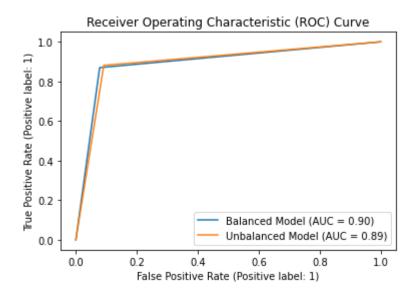
```
In [ ]: part_c_hist(class_1_ub, class_2_ub)
    est_stats_ub = calc_mle(class_1_ub, class_2_ub)
    bound_ub = plot_mle_pdf(est_stats_ub)
```

Class 1 - Mean=-1.0927148762043832, var=0.9694407673810834 Class 2 - Mean=1.9716067823721273, var=1.9904796077492188 Decision boundary = 0.32432432432432456, classify as class 1 if below this value and class 2 if above



```
In [ ]: | # Part h, i
        class 1 tests = np.random.normal(loc=-1, scale=1, size=2000)
        class 2 tests = np.random.normal(loc=2, scale=np.sqrt(2), size=2000)
        test set = np.concatenate((class 1 tests, class 2 tests))
        # Ground truth labels
        gt_labels = np.array([0] * 2000 + [1] * 2000)
        predict b = np.array([1 if i > bound b else 0 for i in test set])
        predict ub = [1 if i > bound ub else 0 for i in test set]
        error b = [1 if predict b[i] == gt labels[i] else 0 for i in range(len(test se
        t))]
        error_ub = [1 if predict_ub[i] == gt_labels[i] else 0 for i in range(len(test_
        set))]
        print("Balanced model error rate: ", 1 - np.average(error_b))
        print("Unbalanced model error rate: ", 1 - np.average(error_ub))
        fig_roc, ax = plt.subplots()
        plt.title("Receiver Operating Characteristic (ROC) Curve")
        plt.xlabel("False Positive Rate (FPR)")
        plt.ylabel("True Positive Rate (TPR)")
        RocCurveDisplay.from predictions(y true=gt labels, y pred=predict b, ax=ax, na
        me="Balanced Model")
        RocCurveDisplay.from_predictions(y_true=gt_labels, y_pred=predict_ub, ax=ax, n
        ame="Unbalanced Model")
```

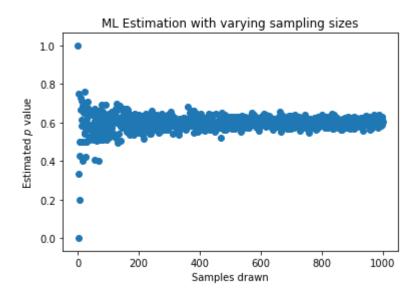
Out[]: <sklearn.metrics. plot.roc curve.RocCurveDisplay at 0x21cbc4665b0>



3. MLE, MAP, Bernoulli Distribution, and Beta Prior (15 pts)

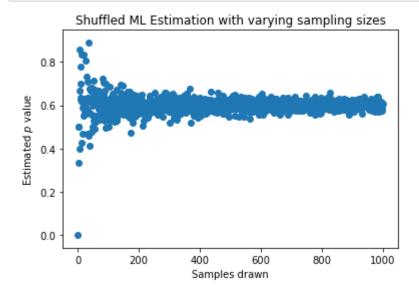
```
In [ ]: # Part a, b
        bernoulli = []
        def bernoulli_mle(samples):
            bernoulli = np.random.binomial(n=1, p=0.6, size=samples)
            b guess = 0.5
            def obj_bernoulli(p, data):
                 return -np.sum(stats.bernoulli.logpmf(data, p=p))
            p_est = minimize(lambda v:
                                 obj_bernoulli(p=v, data=bernoulli),
                                 x0=b guess, method="Nelder-Mead").x
            return p_est
        bern samples a = np.random.binomial(n=1, p=0.6, size=1000)
        sample_nums = np.arange(start=1, stop=1001, step=1)
        bernoulli_samples = np.array([bernoulli_mle(i) for i in sample_nums])
        plt.figure(300)
        plt.scatter(sample_nums, bernoulli_samples)
        plt.xlabel("Samples drawn")
        plt.ylabel("Estimated $p$ value")
        plt.title("ML Estimation with varying sampling sizes")
```

Out[]: Text(0.5, 1.0, 'ML Estimation with varying sampling sizes')



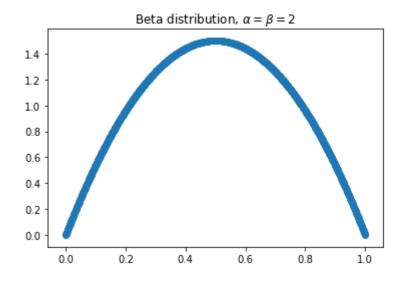
```
In []: # Part c
    random.shuffle(bernoulli)
    bernoulli_samples = np.array([bernoulli_mle(i) for i in sample_nums])
    plt.figure(301)
    plt.scatter(sample_nums, bernoulli_samples)
    plt.xlabel("Samples drawn")
    plt.ylabel("Estimated $p$ value")
    plt.title("Shuffled ML Estimation with varying sampling sizes")

_="""
    When the sampling size is very small, the estimated values for p vary greatly
    and nearly span the entire range of p. However, as the sampling size increase
    s, the estimated value for p quickly reduces in variability and stays close to
    its actual value, 0.6. There does not appear to be any noticeable difference b
    etween the results of parts b and c, with the only change in procedure being t
    he shuffling of the dataset, which is logical.
"""
```



```
In []: # Part d
    beta_x = np.linspace(0, 1.0, num=1000)
    beta = stats.beta.pdf(x=beta_x, a=2, b=2)
    plt.figure(302)
    plt.scatter(beta_x, beta)
    plt.title(r"Beta distribution, $\alpha=\beta=2$")
```

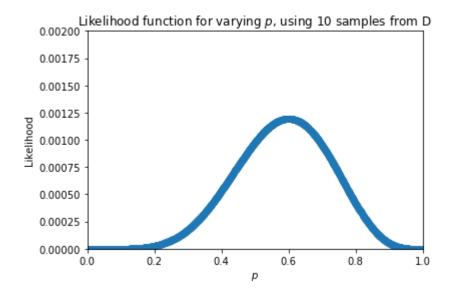
Out[]: Text(0.5, 1.0, 'Beta distribution, \$\\alpha=\\beta=2\$')



```
In [ ]: # Part e - plotting likelihood vs p for 10 samples
        p_binned = np.linspace(0, 1, num=1000)
        def likelihood gen(samples):
             part_e_samples = bern_samples_a[:samples]
             def bern_likelihood(p):
                 return math.prod(
                     [p^{**}x_i * (1 - p)^{**}(1-x_i)
                         for x_i in part_e_samples]
                 )
             likelihood = [bern_likelihood(p) for p in p_binned]
             print("Max probability", max(likelihood))
             return likelihood
        plt.figure(303)
        plt.scatter(p_binned, likelihood_gen(10))
        plt.axis([0,1,0,0.002])
        plt.title("Likelihood function for varying $p$, using 10 samples from D")
        plt.ylabel("Likelihood")
        plt.xlabel("$p$")
```

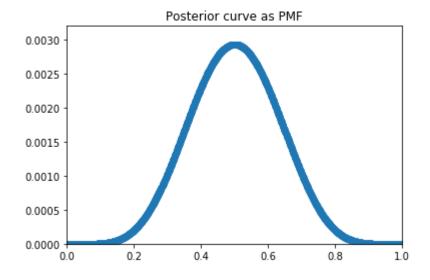
Max probability 0.001194389611605917

Out[]: Text(0.5, 0, '\$p\$')



```
In [ ]: # Part f - generating posterior curve
        plt.figure(304)
        plt.axis([0, 1, 0, .0032])
        plt.title("Posterior curve as PMF")
        posterior = np.multiply(beta, likelihood gen(10))
        print("sum before", np.sum(posterior))
        # Normalize the curve for part q, so that sum(posterior) = 1
        posterior = np.multiply(posterior, 2)
        # posterior = np.divide(posterior,
                                   np.sum(posterior))
                                 # np.trapz(posterior, beta x))
        print("sum", np.sum(posterior))
        print("max pt", max(posterior))
        plt.scatter(beta x, posterior)
        The addition of the prior distribution made the resulting curve thinner and ta
        ller compared to the likelihood function itself, which indicates a higher cert
        ainty of the model's estimation.
        # Part q - MAP estimation (mode of posterior)
        p mode = beta x[list(posterior).index(max(posterior))]
        print("MAP Estimation of p: ", p_mode)
        # Part h
        def expec(moment=1, d=posterior[posterior != 0]):
            return np.sum(
                         [(p_binned[i]**moment) * d[i] for i in range(len(d))])
        variance = lambda d: expec(moment=2, d=d) - expec(d=d)**2
        print("Variance of p: ", variance(posterior))
```

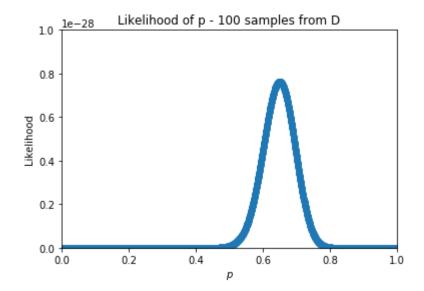
Max probability 0.0009765576074170125 sum before 0.499000999000999 sum 0.998001998001998 max pt 0.0029296698867100684 MAP Estimation of p: 0.4994994994995 Variance of p: 0.017131869129871163

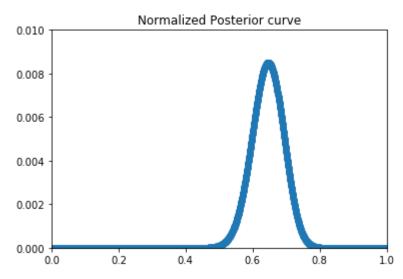


```
In [ ]: | # Part i
        plt.figure(305)
        plt.axis([0,1,0,1E-28])
        plt.scatter(p binned, likelihood gen(100))
        # print(likelihood_gen(100))
        plt.title("Likelihood of p - 100 samples from D")
        plt.xlabel("$p$")
        plt.ylabel("Likelihood")
        plt.figure(306)
        plt.axis([0, 1, 0, 0.01])
        plt.title("Normalized Posterior curve")
        posterior = np.multiply(beta, likelihood_gen(100))
        print(np.sum(posterior))
        posterior = np.divide(posterior,
                                 np.sum(posterior))
                                 # np.trapz(posterior, beta_x))
        plt.scatter(beta_x, posterior)
        p_mode = beta_x[list(posterior).index(max(posterior))]
        print("MAP Estimation of p: ", p_mode)
        print("Variance of p: ", variance(posterior))
```

Max probability 7.61619441740692e-29 Max probability 7.61619441740692e-29 1.2256420492255538e-26

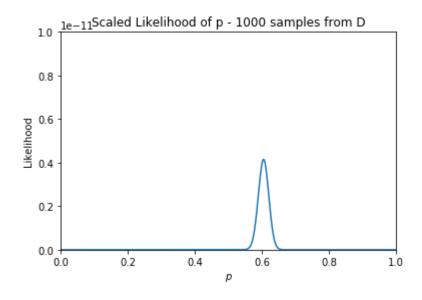
MAP Estimation of p: 0.6466466466466466 Variance of p: 0.0021828331924485522

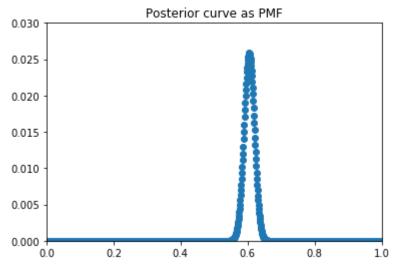




```
In [ ]: # Part j
        plt.figure(307)
        plt.axis([0, 1, 0, 1E-11])
        plt.plot(p binned, np.multiply(likelihood gen(1000), 1E280))
        plt.title("Scaled Likelihood of p - 1000 samples from D")
        plt.xlabel("$p$")
        plt.ylabel("Likelihood")
        plt.figure(308)
        plt.axis([0, 1, 0, 0.03])
        plt.title("Posterior curve as PMF")
        posterior = np.multiply(beta, likelihood_gen(1000))
        posterior = np.divide(posterior,
                                 np.sum(posterior))
                                 # np.trapz(posterior, beta_x))
        plt.scatter(beta_x, posterior)
        p_mode = beta_x[list(posterior).index(max(posterior))]
        print("MAP Estimation of p: ", p_mode)
        print("Variance of p: ", variance(posterior))
        As the number of samples from the distribution increased, the likelihood and p
        osterior curves became much thinner, indicating the model is more certain abou
        t the likelihood of what p is. Numerically this is shown by the variance decre
        asing by about a factor of 10 between each run. The MAP estimate of p also imp
        roves, with the estimated value using 1000 samples having a lower error compar
        ed to that of 100 samples compared to that of 10 samples.
```

Max probability 4.146793529948664e-292 Max probability 4.146793529948664e-292 MAP Estimation of p: 0.6046046046046046 Variance of p: 0.0002378733070729222

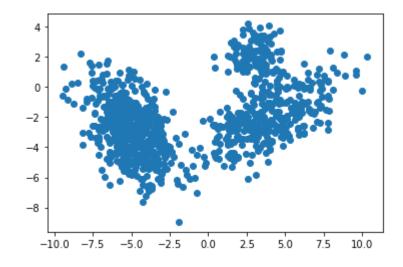




4. Gaussian Mixture Model (15 pts)

```
In [ ]: # Part a
        gm = GaussianMixture(n_components=3,covariance_type='full')
        weights = np.array([0.1, 0.6, 0.3])
        mu = np.array([[3,2], [-5,-3], [4,-2]])
        covariances = np.array([
            [[1,0],[0,1]],
            [[2,-1],[-1,3]],
            [[6,3],[3,3]]
        ])
        gm.weights_ = weights
        gm.means_ = mu
        gm.covariances_ = covariances
        data, labels_actual = gm.sample(1000)
        gm_x, gm_y = data.transpose()
        plt.figure(400)
        plt.scatter(gm_x, gm_y)
```

Out[]: <matplotlib.collections.PathCollection at 0x1c125a8a1c0>

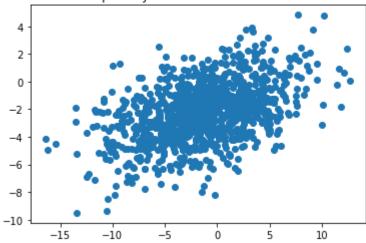


```
In [ ]: # Part b - calculated mean, covariance
    emp_cov = np.cov(m=data.transpose())
    emp_mean = (np.average(gm_x), np.average(gm_y))
    print("Empirical Covariance", emp_cov)
    print("Empriical mean", emp_mean)
```

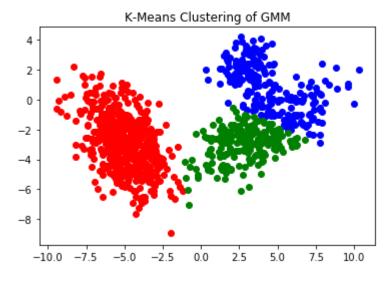
```
Empirical Covariance [[21.72112132  4.86851449]
  [ 4.86851449  4.90657213]]
Empriical mean (-1.3887208286203578, -2.2131131171768033)
```

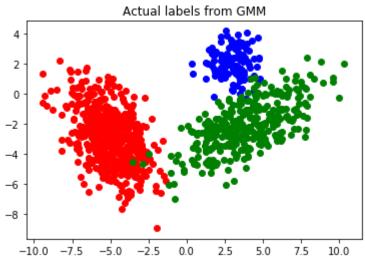
```
In [ ]: | # Part c, d
        emp_gauss = np.random.multivariate_normal(
                                mean=emp_mean,
                                 cov=emp cov,
                                 size=1000)
        plt.figure(401)
        plt.scatter(emp_gauss[:,0], emp_gauss[:,1])
        plt.title("MV Gaussian from empirically calculated mean and covariance from a
         GMM")
         ="""
        While the range of the mv gaussian does appear to match that of the GMM, the m
        ean of the GMM was sparsely populated with clusters nearby but not directly on
        the mean. The MV gaussian on the other hand is centered around its mean (by de
        finition). The GMM has three relatively distinct groupings of samples, while t
        he MV gaussian is one large group, as expected since it is only one gaussian d
        istribution.
```

MV Gaussian from empirically calculated mean and covariance from a GMM



```
In [ ]: # Part e - Using K-Means Clustering
        alg = KMeans(n clusters=3)
        pred_labels = alg.fit_predict(data)
        plt.figure(403)
        plt.title("K-Means Clustering of GMM")
        def color(label val):
            if label_val == 0:
                return "blue"
            if label val == 1:
                return "red"
            if label_val == 2:
                return "green"
        for i in range(0,3):
            gm_x_n = [gm_x[x_i] for x_i in range(len(gm_x)) if pred_labels[x_i] == i]
            gm_y_n = [gm_y[y_i] for y_i in range(len(gm_y)) if pred_labels[y_i] == i]
            plt.scatter(gm_x_n, gm_y_n, color=color(i))
        plt.figure(404)
        plt.title("Actual labels from GMM")
        for i in range(0,3):
            gm_x_n = [gm_x[x_i] for x_i in range(len(gm_x)) if labels_actual[x_i] == i
        ]
            gm_y_n = [gm_y[y_i] for y_i in range(len(gm_y)) if labels_actual[y_i] == i
        ]
            plt.scatter(gm_x_n, gm_y_n, color=color(i))
         ="""
        The K-Means clustering appears to work effectively with
        clusters amply spaced from each other, such as the leftmost
        group of points, but with the right two groups intersecting,
        it mistakes the right half of component 3 for component 1.
```





In []: