

Javier Palomares Homework 1 a

Programming Questions

```
In [1]: import numpy as np
```

Question 1

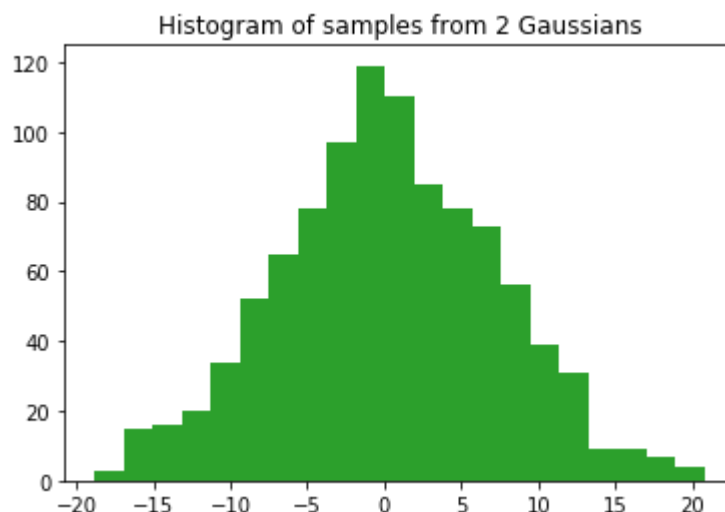
Create 1000 samples from a Gaussian distribution with mean -10 and standard deviation 5. Create another 1000 samples from another independent Gaussian with mean 10 and standard deviation 5.

```
In [2]: numSamples = 1000
mean1 = -10
stdDev1 = 5
samples1 = np.random.normal(mean1, stdDev1, numSamples)
mean2 = 10
stdDev2 = 5
samples2 = np.random.normal(mean2, stdDev2, numSamples)
```

Part a

Take the sum of 2 these Gaussians by adding the two sets of 1000 points, point by point, and plot the histogram of the resulting 1000 points. What do you observe?

```
In [14]: samplesSum = samples1 + samples2
import matplotlib.pyplot as plt
plt.hist(samplesSum, bins='auto')
plt.title('Histogram of samples from 2 Gaussians')
plt.show()
```



I observed a Gaussian distribution centered around 0. It also looks like the standard deviation is greater than 5.

Part b

Estimate the mean and the variance of the sum

I estimate the mean is 0, and the variance is around 7^2 . I estimated this visually from the histogram

```
In [105]: print('The mean is {}'.format(np.mean(samplesSum)))  
          print('The variance is {}'.format(np.var(samplesSum)))
```

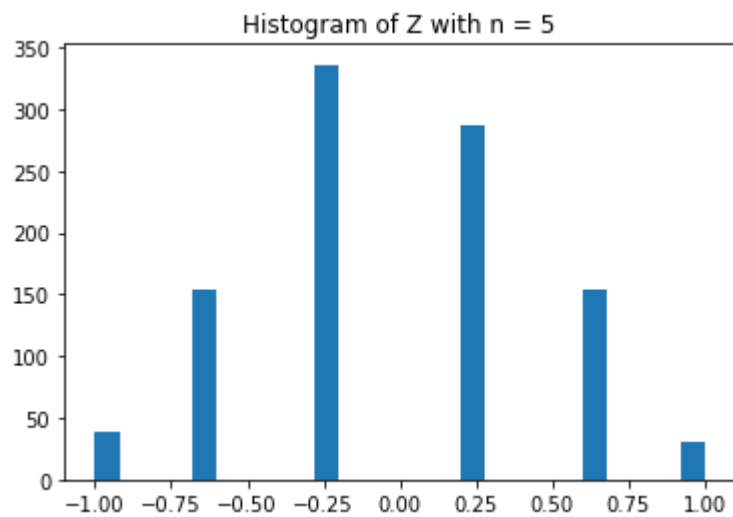
```
The mean is 0.2581822261091743  
The variance is 50.48010707953012
```

Question 2: Central Limit Theorem

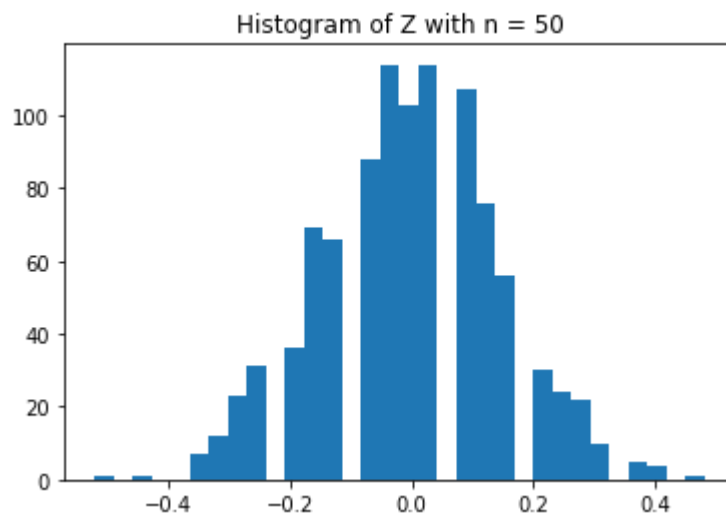
Let X_i be an iid Bernoulli random variable with value $\{-1, 1\}$. Look at the random variable $Z_n = \frac{1}{n} \sum_{i=1}^n X_i$. By taking 1000 draws from Z_n , plot its histogram. Check that for small n (say, 5-10) Z_n does not look that much like a Gaussian, but when n is bigger (already by the time $n = 30$ or 50) it looks much more like a Gaussian. Check also for much bigger n : $n = 250$, to see that at this point, one can really see the bell curve.

Small n

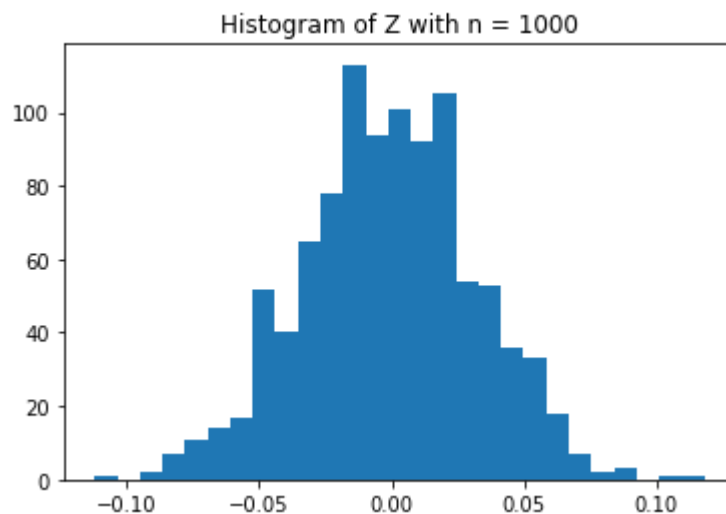
```
In [195]: def replaceInArray(arr,toReplace,replaceWith):  
          for i in range(len(arr)):  
              if(arr[i] == toReplace):  
                  arr[i] = replaceWith  
  
          numTrials = 1000  
          z = np.zeros(numTrials)  
          n = 5  
          p = .5  
          for i in range(numTrials):  
              x=np.random.binomial(size=n, n=1, p=p)  
              replaceInArray(x,0,-1)  
              z[i] = 1/n * np.sum(x)  
          plt.hist(z, bins='auto')  
          plt.title('Histogram of Z with n = 5')  
          plt.show()
```



```
In [196]: z = np.zeros(numTrials)
n = 50
p = .5
for i in range(numTrials):
    x=np.random.binomial(size=n, n=1, p=p)
    replaceInArray(x,0,-1)
    z[i] = 1/n * np.sum(x)
plt.hist(z, bins='auto')
plt.title('Histogram of Z with n = 50')
plt.show()
```



```
In [203]: z = np.zeros(numTrials)
n = 1000
p = .5
for i in range(numTrials):
    x=np.random.binomial(size=n, n=1, p=p)
    replaceInArray(x,0,-1)
    z[i] = 1/n * np.sum(x)
plt.hist(z, bins='auto')
plt.title('Histogram of Z with n = 1000')
plt.show()
```

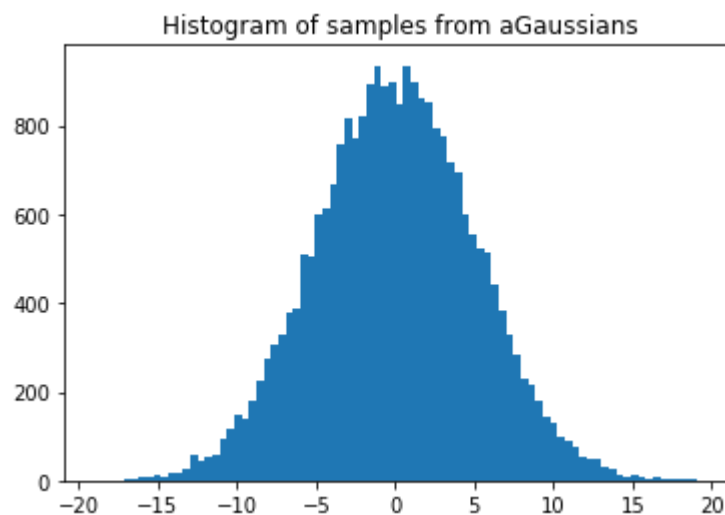


The histogram looks more like a Gaussian with $n=1000$

Question 3

Estimate the mean and standard deviation from 1 dimensional data: generate 25,000 samples from a Gaussian distribution with mean 0 and standard deviation 5. Then estimate the mean and standard deviation of this gaussian using elementary numpy commands, i.e., addition, multiplication, division (do not use a command that takes data and returns the mean or standard deviation).

```
In [106]: numSamples = 25000
mean = 0
stdDev = 5
samples = np.random.normal(mean, stdDev, numSamples)
plt.hist(samples, bins='auto')
plt.title('Histogram of samples from aGaussians')
plt.show()
```



Visually, I estimate the mean is 0, and the stdDev is around 5.

Computing the mean and standard deviation from elemental operations, I found:

```
In [107]: sum = 0
for i in range(numSamples):
    sum += samples[i]
mean = sum / numSamples

variance = 0
for i in range(numSamples):
    variance += (samples[i] - mean)**2
variance /= numSamples
```

```
In [108]: print("The mean is {}".format(mean))
          print("The standard deviation is {}".format(np.sqrt(variance)))
```

The mean is 0.016334245976241328

The standard deviation is 5.033722935531415

Question 4

Estimate the mean and covariance matrix for multi-dimensional data: generate 10,000 samples of 2 dimensional data from the Gaussian distribution. Then, estimate the mean and covariance matrix for this multi-dimensional data using elementary numpy commands, i.e., addition, multiplication, division (do not use a command that takes data and returns the mean or standard deviation).

```
In [111]: numSamples = 10000
          mean = [-5,5]
          covarianceMatrix = [[20, .8], [.8, 30]]
          samples = np.random.multivariate_normal(mean, covarianceMatrix, numSa
          mples)
          X = samples[:,0]
          Y = samples[:,1]

          #Covariance_x_y E [ (X - E[x])) (Y - E[Y]) ]
          meanX = 0
          meanY = 0
          for i in range(numSamples):
              meanX += X[i]
              meanY += Y[i]
          meanX /= numSamples
          meanY /= numSamples

          #Covariance_x_y E [ (X - E[x])) (Y - E[Y]) ]
          def covXY(X,Y,meanX,meanY):
              numSamples = len(X)
              cov = 0
              for j in range(numSamples):
                  cov += (X[j] - meanX)*(Y[j] - meanY)
              cov /= numSamples
              return cov

          cov = [[covXY(X,X,meanX,meanY), covXY(X,Y,meanX,meanY)],
                  [covXY(Y,X,meanY,meanX), covXY(Y,Y,meanY,meanY)]]
          print("The mean of X is {}".format(meanX))
          print("The mean of Y is {}".format(meanY))
          print("The covariance matrix is")
          print(np.matrix(cov))
```

The mean of X is -4.997486816532748

The mean of Y is 5.053318489738599

The covariance matrix is

```
[[ 20.18486288  0.8123284 ]
 [ 0.8123284  30.10707126]]
```

Question 5

Download from Canvas/Files the dataset PatientData.csv. Each row is a patient and the last column is the condition that the patient has. Do data exploration using Pandas and other visualization tools to understand what you can about the dataset.

```
In [277]: import pandas as pd
filepath='./PatientData.csv'
df = pd.read_csv(filepath,header=None)
df.info()
df.describe()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 452 entries, 0 to 451
Columns: 280 entries, 0 to 279
dtypes: float64(120), int64(155), object(5)
memory usage: 988.8+ KB
```

```
Out[277]:
```

	0	1	2	3	4	5	6	
count	452.000000	452.000000	452.000000	452.000000	452.000000	452.000000	452.000000	452
mean	46.471239	0.550885	166.188053	68.170354	88.920354	155.152655	367.207965	166.188053
std	16.466631	0.497955	37.170340	16.590803	15.364394	44.842283	33.385421	37.170340
min	0.000000	0.000000	105.000000	6.000000	55.000000	0.000000	232.000000	105.000000
25%	36.000000	0.000000	160.000000	59.000000	80.000000	142.000000	350.000000	142.000000
50%	47.000000	1.000000	164.000000	68.000000	86.000000	157.000000	367.000000	164.000000
75%	58.000000	1.000000	170.000000	79.000000	94.000000	175.000000	384.000000	170.000000
max	83.000000	1.000000	780.000000	176.000000	188.000000	524.000000	509.000000	780.000000

8 rows × 275 columns

For example:

(a) How many patients and how many features are there?

```
In [144]: numPatients= df.shape[0]
numFeatures = df.shape[1]
print("There are {} patients and {} feature".format(numPatients,numFeatures))
```

There are 452 patients and 280 feature

b) What is the meaning of the first 4 features? See if you can understand what they mean.

```
In [140]: feature1 = df.loc[:,0]
feature2 = df.loc[:,1]
feature3 = df.loc[:,2]
feature4 = df.loc[:,3]

# patient condition is the last column
patientCondition = df.loc[:,numFeatures-1]

print("feature1  type")
print(feature1.get_dtype_counts())

print("\nfeature2  type")
print(feature2.get_dtype_counts())

print("\nfeature3  type")
print(feature3.get_dtype_counts())

print("\nfeature4  type")
print(feature4.get_dtype_counts())
```

```
feature1  type
int64      1
dtype: int64
```

```
feature2  type
int64      1
dtype: int64
```

```
feature3  type
int64      1
dtype: int64
```

```
feature4  type
int64      1
dtype: int64
```

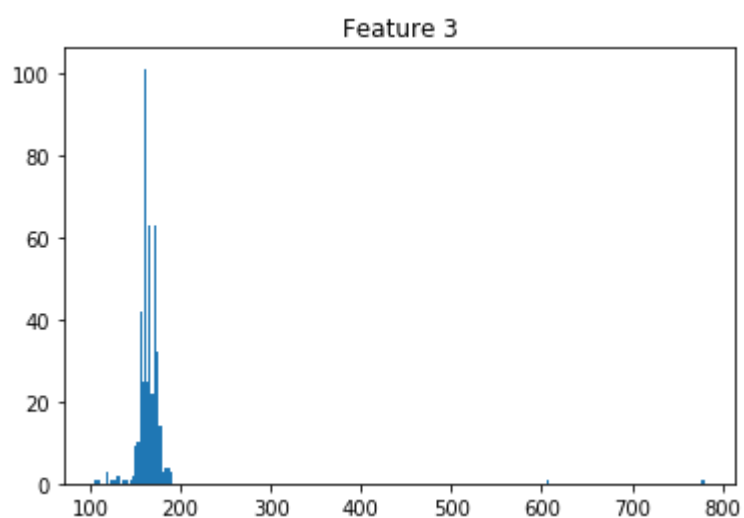
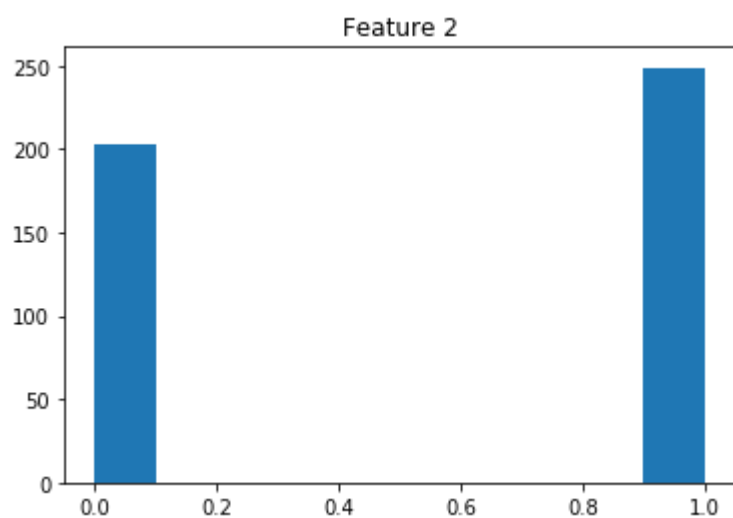
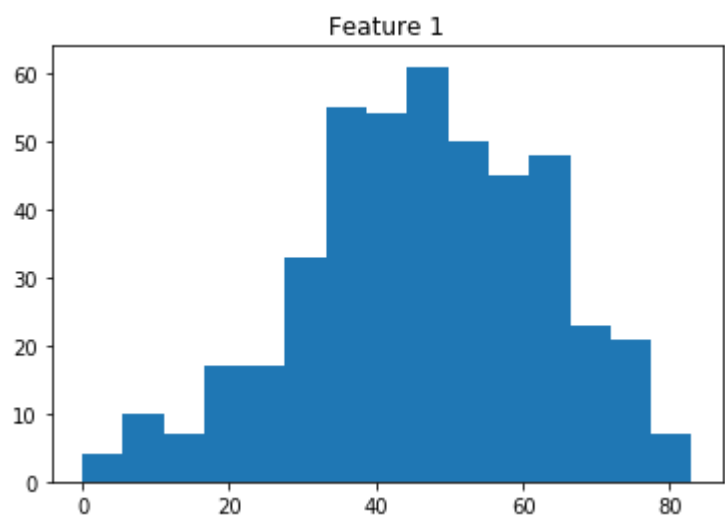

In [136]: `import matplotlib.pyplot as plt`

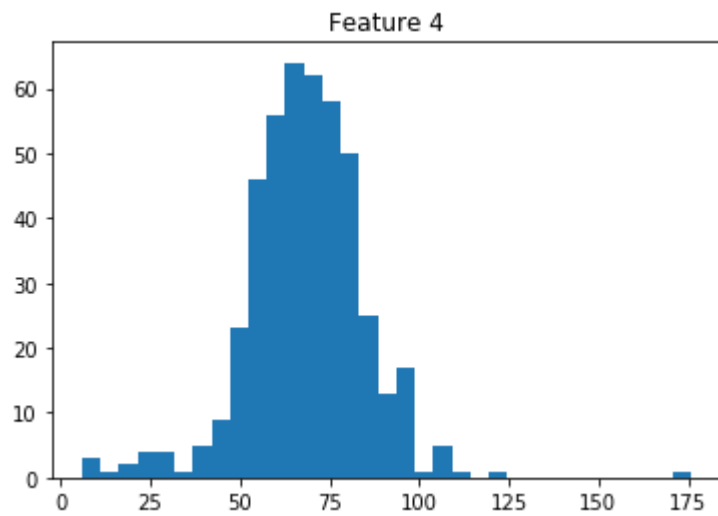
```
plt.hist(feature1, bins='auto')  
plt.title('Feature 1')  
plt.show()
```

```
plt.hist(feature2, bins='auto')  
plt.title('Feature 2')  
plt.show()
```

```
plt.hist(feature3, bins='auto')  
plt.title('Feature 3')  
plt.show()
```

```
plt.hist(feature4, bins='auto')  
plt.title('Feature 4')  
plt.show()
```





Looking at the range of values, it looks like

- first column is age in years,
- second column is a binary variable representing the gender
- third column is weight in pounds
- fourth column is height in inches

c) Are there missing values? Replace them with the average of the corresponding feature column

```

In [279]: nanMatrix = ~df.applymap(np.isreal)
# find all the columns that have missing values
nanCols = nanMatrix.all(0)
for col in range(len(nanCols)):
    if(nanCols[col]):
        # the column has missing values.
        # replace them with the mean
        values = df.iloc[:,col]
        s = 0
        n = 0
        # find the mean of the column
        for row in range(len(values)):
            if str.isnumeric(values.iloc[row]):
                s += float(values.iloc[row])
                n += 1
        mean = s/n
        for row in range(len(values)):
            # replace numeric strings with their numeric value
            if str.isnumeric(values.iloc[row]):
                df.iloc[row,col] = float(values.iloc[row])
            # replace nans with the mean value
            else:
                df.iloc[row,col] = mean
df.info()
df.describe()

```

```

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```

Out[279]:

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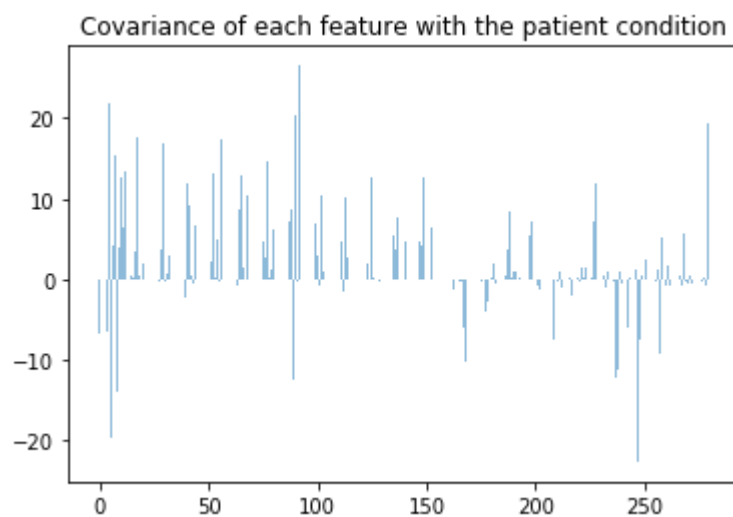
d) How could you test which features strongly influence the patient condition and which do not
 I will test for strong influence by computing the covariance of each feature with the patientCondition

```
In [293]: featureCovariance = np.zeros(numFeatures)
          for i in range(len(featureCovariance)):
              feature = df.iloc[:,i]
              featureCovariance[i] = np.cov(feature.astype('float'),patientCondition)[0][1]
```

List what you think are the three most important features.

```
In [297]: x = np.arange(len(featureCovariance))

          plt.bar(x, featureCovariance, align='center', alpha=0.5)
          plt.title('Covariance of each feature with the patient condition')
          plt.show()
```



```
In [302]: np.argsort(featureCovariance)[-3:]
```

```
Out[302]: array([90,  4, 92], dtype=int64)
```

The features with the highest covariance are in columns at position 90, 4, 92