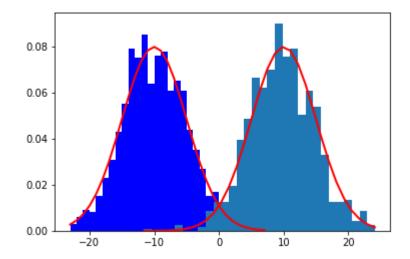
EE460J Lab 1

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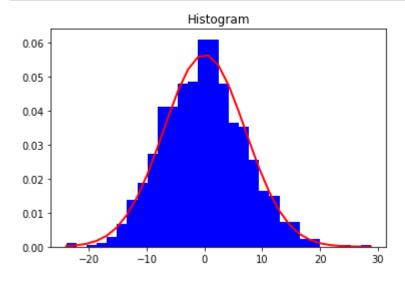
```
In [1]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
```

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]:
        #generate random samples
        n = 1000
        mean 1 = -10
        std 1 = 5
        samples_1 = np.random.normal(mean_1, std_1, n)
        mean 2 = 10
        std 2 = 5
        samples_2 = np.random.normal(mean_2, std_2, n)
        #plot values
        count_1, bins_1, ignored_1 = plt.hist(samples_1, bins=30, density=True, color=
        "blue")
        plt.plot(bins 1, 1/(std 1 * np.sqrt(2 * np.pi)) *
                     np.exp( - (bins_1 - mean_1)**2 / (2 * std_1**2) ),
                     linewidth=2, color='r')
        count_2, bins_2, ignored_2 = plt.hist(samples_2, bins=30, density=True)
        plt.plot(bins_2, 1/(std_2 * np.sqrt(2 * np.pi)) *
                     np.exp( - (bins 2 - mean 2)**2 / (2 * std 2**2) ),
                    linewidth=2, color='r')
        plt.show()
```



(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?



I realized that the sum of these samples, which were taken from normal distributions, resulted in what looks like samples from a new normal distribution.

(b) Estimate the mean and the variance of the sum.

Because both these samples were taken from normal distributions, the new mean μ is the sum of the previous means ($\mu = \mu_1 + \mu_2 \approx 0$), and the new variance σ^2 is the sum of the previous variances ($\sigma^2 = \sigma_1^2 + \sigma_2^2 \approx 50$), meaning that the new standard deviation $\sigma \approx 7.07$

```
In [4]: print("Validating findings:")
    print("μ = ", samples.mean())
    print("σ^2 = ", samples.var())
    print("σ = ", np.sqrt(samples.var()))

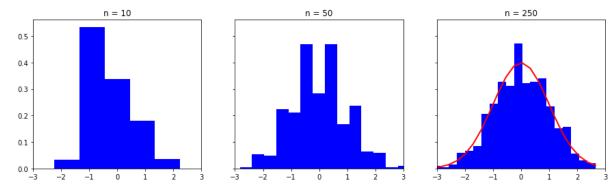
Validating findings:
    μ = -0.07091284499160103
    σ^2 = 50.1021026126512
    σ = 7.078283874828079
```

2. Central Limit Theorem - Let X_i be an i.i.d. Bernoulli random variable with value $\{-1,1\}$. Look at the random variable Z_n . By taking 1000 draws from Zn, plot its histogram. Check that for small n (say, 5-10) Zn 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.

```
In [5]: # function for generating samples from Z_n
def Z_n(samples, n):
    bernoulli = [-1,1] #values for bernoulli rv
    result = []
    for i in range(samples):
        sample = 0 #generate sample of Z_n
        for j in range(n):
            sample += np.random.choice(bernoulli) #sum of bernoulli rvs
        sample /= np.sqrt(n) #normalize
        result.append(sample)

    return result
```

```
In [6]:
        samples = 1000
        fig, ax = plt.subplots(1,3, sharex=True, sharey=True) # three plots
        fig.set figwidth(15)
        n = 5 #num. of bernoulli rvs
        result = Z n(samples, n)
        count, bins, ignored = ax[0].hist(result, bins=5, density=True, color="blue")
        ax[0].title.set text("n = 10")
        ax[0].set xlim(-3,3)
        n = 50
        result = Z_n(samples, n)
        count, bins, ignored = ax[1].hist(result, bins=15, density=True, color="blue")
        ax[1].title.set_text("n = 50")
        n = 250
        result = Z n(samples, n)
        count, bins, ignored = ax[2].hist(result, bins=20, density=True, color="blue")
        ax[2].plot(bins, 1/(1 * np.sqrt(2 * np.pi)) *
                     np.exp( - (bins - 0)**2 / (2 * 1**2) ),
                     linewidth=2, color='r')
        ax[2].title.set_text("n = 250")
        plt.show()
```



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 [7]: #generate random samples
n = 25000
mean = 0
std = 5
samples = np.random.normal(mean, std, n)
```

Lab 1 Code 9/9/2019

```
In [8]: mean measured = 0 #compute mean for samples
        for s in samples:
            mean measured += s / n
        var measured = 0 #compute variance: squared differences from mean
        for s in samples:
            var measured += (s - mean measured)**2 / n
        std measured = np.sqrt(var measured) #compute standard deviation
In [9]: | print(mean measured)
        print(std_measured)
        -0.03248411366746434
        5.009505066748479
```

4. Estimate the mean and covariance matrix for multi-dimensional data: generate 10,000 samples of 2 dimensional data from the Gaussian distribution

```
In [10]: n = 10000
         mean = [-5, 5]
         covariance = [[20, .8], [.8, 30]]
         samples = np.random.multivariate normal(mean, covariance, n).T
         mean measured = [0, 0]
In [11]:
         for s in samples[0]:
             mean_measured[0] += s / n # compute mean for X
         for s in samples[1]:
             mean_measured[1] += s / n # compute mean for y
In [12]: covariance_measured = [[0,0],[0,0]]
         for s in samples[0]:
             covariance measured[0][0] += (s - mean measured[0])**2 / n # compute vari
         ance for X
         for s in samples[1]:
             covariance_measured[1][1] += (s - mean_measured[1])**2 / n # compute vari
         ance for y
         for i in range(n):
             covariance_measured[0][1] += (samples[0][i] - mean_measured[0])*(samples[1
         [i] - mean_measured[0]) / n # compute covariance
             covariance_measured[1][0] = covariance_measured[0][1]
In [13]: | print(np.array(covariance measured))
```

```
[[19.97417036 0.75320876]
[ 0.75320876 29.57771188]]
```

5. 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 [14]: # make sure to add header=None, otherwise the first row is treated as a header
patients = pd.read_csv("PatientData.csv", header=None)
print(patients.shape) # 452 patients, 279 features
display(patients)

(452, 280)

	0	1	2	3	4	5	6	7	8	9	 270	271	272	273	274	275	276
0	75	0	190	80	91	193	371	174	121	-16	 0.0	9.0	-0.9	0.0	0	0.9	2.9
1	56	1	165	64	81	174	401	149	39	25	 0.0	8.5	0.0	0.0	0	0.2	2.1
2	54	0	172	95	138	163	386	185	102	96	 0.0	9.5	-2.4	0.0	0	0.3	3.4
3	55	0	175	94	100	202	380	179	143	28	 0.0	12.2	-2.2	0.0	0	0.4	2.6
4	75	0	190	80	88	181	360	177	103	-16	 0.0	13.1	-3.6	0.0	0	-0.1	3.9
447	53	1	160	70	80	199	382	154	117	-37	 0.0	4.3	-5.0	0.0	0	0.7	0.6
448	37	0	190	85	100	137	361	201	73	86	 0.0	15.6	-1.6	0.0	0	0.4	2.4
449	36	0	166	68	108	176	365	194	116	-85	 0.0	16.3	-28.6	0.0	0	1.5	1.0
450	32	1	155	55	93	106	386	218	63	54	 -0.4	12.0	-0.7	0.0	0	0.5	2.4
451	78	1	160	70	79	127	364	138	78	28	 0.0	10.4	-1.8	0.0	0	0.5	1.6

452 rows × 280 columns

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

452 patients, 279 features

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

First feature could be age of patient. Second could be male or female. Third could be height in centimeters. Fourth could be mass in kilograms.

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

There are missing values.

```
In [15]: print("Missing values: ",'?' in patients.values)
    patients.replace('?', np.nan, inplace=True) # replace question marks in dataf
    rame with NaNs
    patients = patients.astype(float)
    patients.fillna(patients.mean(), inplace=True) # replace NaNs with the averag
    e of column
```

Missing values: True

(d) How could you test which features strongly influence the patient condition and which do not?

The features are strongly correlated or inversely correlated with the patient's condition have the strongest influence. The features that have little to no correlation do not have a strong influence.

	0	1	2	3	4	5	6	7	8	9	 270	271	272	27:
0	1.00	-0.06	-0.11	0.38	-0.00	0.04	0.20	0.03	0.10	-0.27	 0.16	-0.16	0.08	0.0
1	-0.06	1.00	-0.12	-0.25	-0.34	-0.05	0.07	-0.18	-0.08	0.07	 0.23	-0.04	0.09	0.0
2	-0.11	-0.12	1.00	-0.07	-0.01	0.01	-0.24	-0.04	0.03	0.06	 -0.02	-0.07	-0.09	-0.0
3	0.38	-0.25	-0.07	1.00	0.10	0.12	0.12	0.15	0.12	-0.17	 0.05	-0.03	0.05	0.0
4	-0.00	-0.34	-0.01	0.10	1.00	0.02	0.22	0.40	0.05	-0.15	 -0.20	0.09	-0.23	-0.0
275	-0.04	0.01	0.07	-0.05	-0.07	0.14	-0.03	0.05	0.25	0.08	 -0.09	-0.01	-0.09	-0.0
276	-0.27	0.07	-0.01	-0.14	-0.22	0.06	-0.04	-0.18	0.02	0.06	 0.12	0.09	-0.07	-0.0
277	0.02	0.03	-0.09	0.06	0.13	-0.03	0.26	0.13	-0.02	0.30	 0.00	0.67	0.56	-0.0
278	-0.20	0.05	-0.09	-0.05	-0.08	0.02	0.15	-0.01	0.00	0.26	 80.0	0.56	0.34	-0.0
279	-0.09	-0.18	0.01	-0.09	0.32	-0.10	0.03	0.10	-0.12	0.02	 -0.16	0.04	-0.07	-0.04

280 rows × 280 columns

```
In [18]: strongly_corr_features
```

Out[18]: [279]

In []:

Lab 1 Written Questions

$$|x| = 0 \quad |x| = 1$$

$$|x| = 0 \quad |x| = 0$$

$$|x|$$

Page 2 P(Heads) = 3 Since N=100 > 30, we approximate using Central Limit Theorem. $\mu = (100)(\frac{2}{3}) = \frac{200}{3}$ $\frac{2}{5} = (100)(\frac{2}{3})(\frac{1}{3}) = \frac{200}{9}$ P(Heads = 50) = P(Jaco) = 50 - 3 = \$\overline{\pi}(-3,536)\pi.00020|