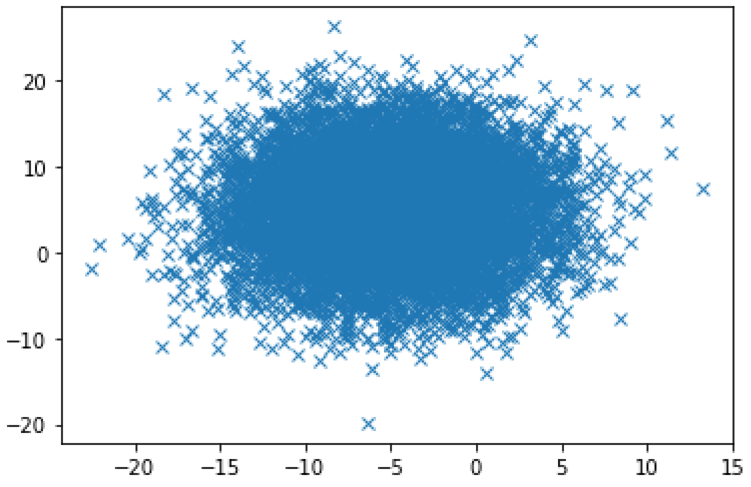
In [1]:
```
import pandas as pd
import matplotlib.pyplot as plt
import numpy as np
from scipy.stats import bernoulli
from scipy.stats import norm
%matplotlib inline

mnist = "./mnist_784.csv"
Names_files = "./Names/*"
PatientData = "./PatientData.csv"
```

In [2]:
```
#exercise 1
mean = [-5, 5]
cov = [[20, .8], [.8, 30]]
x,y = np.random.multivariate_normal(mean, cov, 10000).T
```

In [3]:
```
print(str(x.shape) + " , " + str(y.shape))
plt.plot(x, y, 'x') # nice it looks like the multivariate distribution seen in D
```

```
(10000,) , (10000,)
```

Out[3]:
```
[<matplotlib.lines.Line2D at 0x130a8b050>]
```



In [4]:
```
mean_x = np.sum(x)/len(x)
mean_y = np.sum(y)/len(y)
mean_vector = [mean_x, mean_y]
mean_vector # sweet that's basically what we want [-5, 5]
```

Out[4]:
```
[-5.039073740628995, 4.972532575433096]
```

In [5]:
```
var_x = x - mean_x
var_y = y - mean_y
var_matrix = np.array([var_x, var_y])
cov_matrix = np.dot(var_matrix, var_matrix.T.conj())/(len(x)-1)
cov_matrix
```

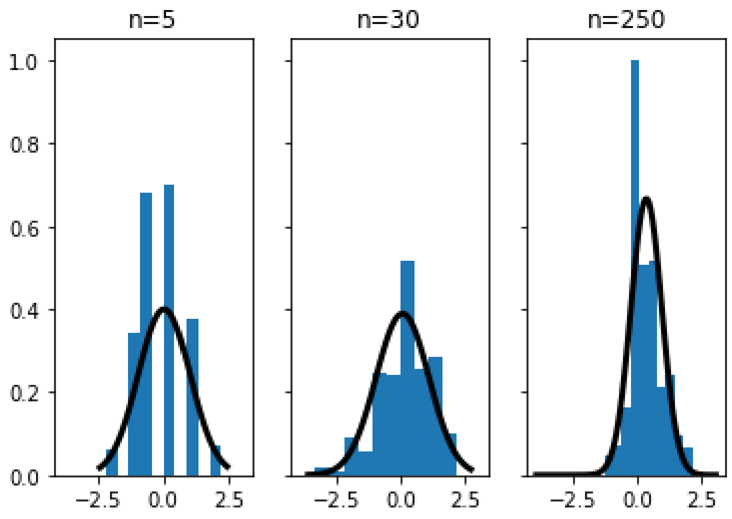
Out[5]:
```
array([[20.11548803,  0.67155382],
       [ 0.67155382, 30.87734551]])
```

In [6]:
```
np.cov(np.array([x,y])) # great this looks like the last thing
```

Out[6]:
```
array([[20.11548803,  0.67155382],
       [ 0.67155382, 30.87734551]])
```

In [7]:
```

#exercise 2
small_n = 5
medium_n = 30
big_n = 250
sample_size = 1000

# generate random bernoulli with 50% probability [-1,1]
#####
X_i = bernoulli.rvs(0.5, size=sample_size)
X_i = np.where(X_i==0, -1, X_i)
#####

Zn_small = [np.sum(X_i[i:(i+small_n)%sample_size])/np.sqrt(small_n) for i in ran
Zn_medium = [np.sum(X_i[i:(i+medium_n)%sample_size])/np.sqrt(medium_n) for i in
Zn_big = [np.sum(X_i[i:(i+big_n)%sample_size])/np.sqrt(big_n) for i in range(sam

fig, ax = plt.subplots(1,3, sharex=True, sharey=True)




# plot the density histogram of Zn w/ 5 samples
count_small, bins_small, y = ax[0].hist(Zn_small, density=True)
ax[0].set_title("n=5")
# plot normal curve
#######
mu, std = norm.fit(Zn_small)
xmin, xmax = plt.xlim()
x = np.linspace(xmin, xmax, 100)
p = norm.pdf(x, mu, std)
ax[0].plot(x, p, 'k', linewidth=3)
######

# plot the density histogram of Zn w/ 30 samples
count_medium, bins_medium, y = ax[1].hist(Zn_medium, density=True)
ax[1].set_title("n=30")
# plot normal curve
######
mu, std = norm.fit(Zn_medium)
xmin, xmax = plt.xlim()
x = np.linspace(xmin, xmax, 100)
p = norm.pdf(x, mu, std)
ax[1].plot(x, p, 'k', linewidth=3)
######

count_big, bins_big, y = ax[2].hist(Zn_big, density=True)
ax[2].set_title("n=250")
# plot the density histogram of Zn w/ 250 samples
######
mu, std = norm.fit(Zn_big)
xmin, xmax = plt.xlim()
x = np.linspace(xmin, xmax, 100)
p = norm.pdf(x, mu, std)
ax[2].plot(x, p, 'k', linewidth=3)
######
```

Out[7]:
```
[<matplotlib.lines.Line2D at 0x130c8e090>]
```



In [8]:
```
#exercise 3
patients = pd.read_csv(PatientData)
print(patients.shape)
#(451,280) -> 451 patients & 280 features

first_features = patients.iloc[:, 0:4]
display(first_features)
# breakdown:
# first column is index (provided by pandas)
# second column should be something important, could be age but the "13" in row
# third column is a discrete value, could be gender, seeing/not-seeing, hearing/
# fourth column looks too be height in centimeters.. no major outliers from the
# fifth column seems to be weight? Again, the "51" in row 4 looks suspicious,
# but if you compare row 4 to row 449, a 13 year old "boy" could compare to the
```

```
(451, 280)
```

	75	0	190	80
0	56	1	165	64
1	54	0	172	95
2	55	0	175	94
3	75	0	190	80
4	13	0	169	51
...	...	...	...	...
446	53	1	160	70
447	37	0	190	85
448	36	0	166	68
449	32	1	155	55
450	78	1	160	70

451 rows × 4 columns

In [9]:
```python
display(first_features.iloc[4, :])
display(first_features.iloc[449, :])
```

```
75       13
0         0
190     169
80       51
Name: 4, dtype: int64
75       32
0         1
190     155
80       55
Name: 449, dtype: int64
```

In [10]:
```python
# Are there missing values?
print(np.nan in patients) # False, so they aren't stored as NaNs
print('x' in patients) # False, not x's
display(patients.iloc[:,:15]) # there is a column of '?'
print('?' in patients) # True - assuming these are the missing values
patients.replace('?', np.nan, inplace=True)
patients = patients.astype(float)
patients.fillna(patients.mean(), inplace=True)
display(patients.iloc[:,:15])
```

```
False
False
```

	75	0	190	80	91	193	371	174	121	-16	13	64	-2	?	63
0	56	1	165	64	81	174	401	149	39	25	37	-17	31	?	53
1	54	0	172	95	138	163	386	185	102	96	34	70	66	23	75
2	55	0	175	94	100	202	380	179	143	28	11	-5	20	?	71
3	75	0	190	80	88	181	360	177	103	-16	13	61	3	?	?
4	13	0	169	51	100	167	321	174	91	107	66	52	88	?	84
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
446	53	1	160	70	80	199	382	154	117	-37	4	40	-27	?	63
447	37	0	190	85	100	137	361	201	73	86	66	52	79	?	73
448	36	0	166	68	108	176	365	194	116	-85	-19	-61	-70	84	84
449	32	1	155	55	93	106	386	218	63	54	29	-22	43	103	80
450	78	1	160	70	79	127	364	138	78	28	79	52	47	?	75

451 rows × 15 columns

```
True
```

	75	0	190	80	91	193	371	174	121	-16	13	64	-2	
0	56.0	1.0	165.0	64.0	81.0	174.0	401.0	149.0	39.0	25.0	37.0	-17.0	31.0	-13.592
1	54.0	0.0	172.0	95.0	138.0	163.0	386.0	185.0	102.0	96.0	34.0	70.0	66.0	23.000
2	55.0	0.0	175.0	94.0	100.0	202.0	380.0	179.0	143.0	28.0	11.0	-5.0	20.0	-13.592
3	75.0	0.0	190.0	80.0	88.0	181.0	360.0	177.0	103.0	-16.0	13.0	61.0	3.0	-13.592
4	13.0	0.0	169.0	51.0	100.0	167.0	321.0	174.0	91.0	107.0	66.0	52.0	88.0	-13.592

```
       75    0    190    80     91    193    371    174    121    -16    13    64    -2
...   ...  ...    ...   ...    ...    ...    ...    ...    ...    ...   ...   ...   ...
446  53.0  1.0  160.0  70.0   80.0  199.0  382.0  154.0  117.0  -37.0   4.0  40.0 -27.0   -13.592
447  37.0  0.0  190.0  85.0  100.0  137.0  361.0  201.0   73.0   86.0  66.0  52.0  79.0   -13.592
448  36.0  0.0  166.0  68.0  108.0  176.0  365.0  194.0  116.0  -85.0 -19.0 -61.0 -70.0    84.000
449  32.0  1.0  155.0  55.0   93.0  106.0  386.0  218.0   63.0   54.0  29.0 -22.0  43.0   103.000
450  78.0  1.0  160.0  70.0   79.0  127.0  364.0  138.0   78.0   28.0  79.0  52.0  47.0   -13.592

451 rows × 15 columns
```

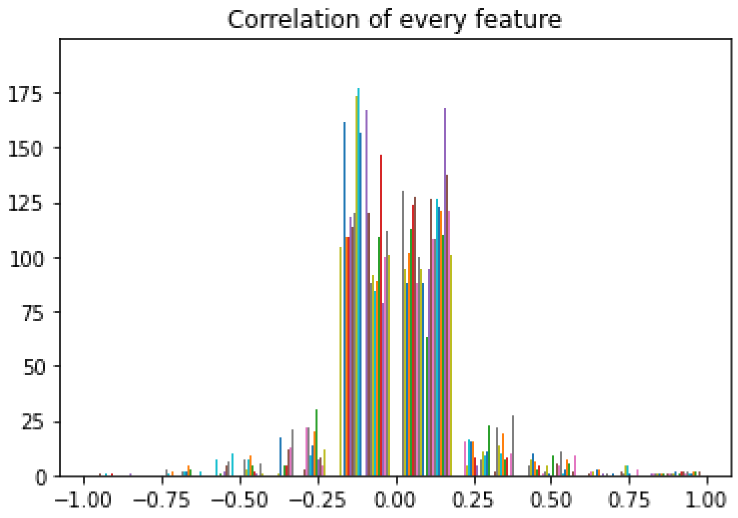
In [11]:

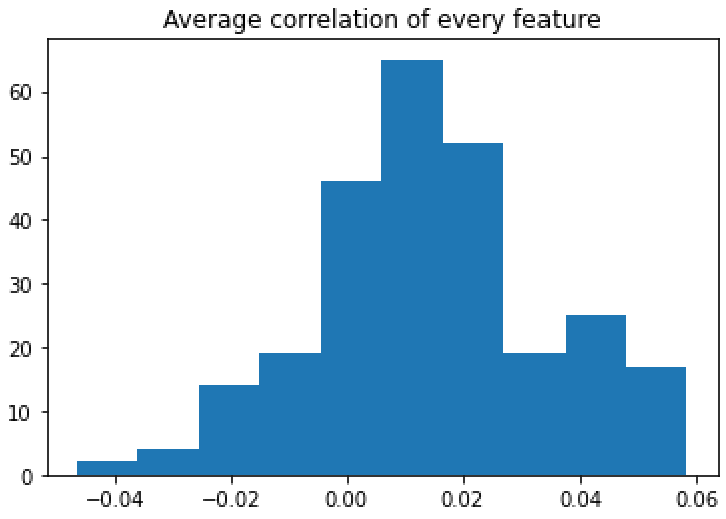
```python
# find the features highly related to patient's condition
# first get the correlation matrix
patients_correlation_matrix = patients.corr()
display(patients_correlation_matrix) # don't like how this is coming out
mean_patients_correlation_matrix = patients_correlation_matrix.mean()
display(mean_patients_correlation_matrix)
print("Max average correlation for column (features) in patients data: " + str(m
print("Min average correlation for column (features) in patients data: " + str(m

_ = plt.hist(patients_correlation_matrix)
plt.title("Correlation of every feature")
plt.show()

_ = plt.hist(mean_patients_correlation_matrix) # no column averages higher than
plt.title("Average correlation of every feature")
plt.show()

# so it seems the relationship between condition and patient features is not com
# that's expected but it's good to see
```

```
              75          0        190         80         91        193        371        174
   75   1.000000  -0.055041  -0.112350   0.380295  -0.004568   0.038057   0.195911   0.025302
    0  -0.055041   1.000000  -0.123334  -0.246827  -0.337234  -0.044792   0.072431  -0.184710
  190  -0.112350  -0.123334   1.000000  -0.076050  -0.006525   0.012415  -0.237587  -0.038591
   80   0.380295  -0.246827  -0.076050   1.000000   0.099938   0.118650   0.118545   0.149894
   91  -0.004568  -0.337234  -0.006525   0.099938   1.000000   0.021595   0.218655   0.397415
  ...        ...        ...        ...        ...        ...        ...        ...        ...
0.9.3  -0.042343   0.016981   0.066213  -0.048127  -0.066021   0.141499  -0.035300   0.048962
2.9.1  -0.277385   0.068776  -0.010166  -0.146893  -0.222871   0.059091  -0.039241  -0.185431
 23.3   0.016968   0.032459  -0.090840   0.061859   0.129723  -0.028268   0.256154   0.130142
 49.4  -0.204824   0.049385  -0.093933  -0.052486  -0.083224   0.019067   0.150904  -0.014721
    8  -0.096395  -0.176193   0.005325  -0.091773   0.323919  -0.101887   0.028097   0.097485

280 rows × 280 columns
```

```
75       -0.022651
0        -0.018982
190       0.017586
80        0.002338
91        0.055933
            ...
0.9.3     0.008868
2.9.1     0.023051
23.3      0.047668
49.4      0.051764
8         0.023707
Length: 280, dtype: float64
Max average correlation for column (features) in patients data: 0.05842101731584
5425
Min average correlation for column (features) in patients data: -0.0464566411358
2557
```

```
/usr/local/lib/python3.7/site-packages/matplotlib/axes/_axes.py:6628: RuntimeWar
ning: All-NaN slice encountered
  xmin = min(xmin, np.nanmin(xi))
/usr/local/lib/python3.7/site-packages/matplotlib/axes/_axes.py:6629: RuntimeWar
ning: All-NaN slice encountered
  xmax = max(xmax, np.nanmax(xi))
```





In [ ]:

```
# define strong featurees to be those over 0.75 or less than -0.75 => looks to b
strong_features = [i for i, corr in enumerate(patients_correlation_matrix.iloc[l
print(strong_features)
```

```
[279]
```

In [15]:
```
# Example 5: MNIST
import numpy as np
import pandas as pd
import sklearn.datasets as ds
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
```

In [16]:
```
mnist = ds.fetch_openml('mnist_784')
```

In [17]:
```
# There are 70000 different digits and 784 features for each.
# These features all correspond to an individual pixel in the image
mnist.data.shape
```

Out[17]:
```
(70000, 784)
```

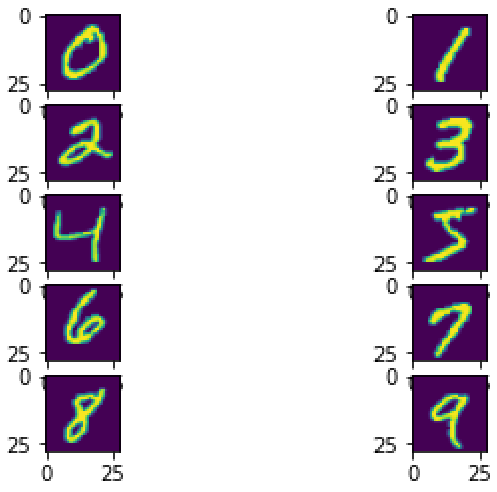
In [18]:
```
data = pd.DataFrame(data= np.c_[mnist['data'], mnist['target']],
                     columns= mnist['feature_names'] + ['target'])
```

In [19]:
```
# The dataset has all the values from 0 to 9 and they all occur at relatively si
data['target'].value_counts(sort=True)
```

Out[19]:
```
1    7877
7    7293
3    7141
2    6990
9    6958
0    6903
6    6876
8    6825
4    6824
5    6313
Name: target, dtype: int64
```

In [20]:
```
labels = mnist.target.tolist()
```

In [21]:
```
f, ax = plt.subplots(5,2)

for i in range(10):
  img = np.reshape(mnist.data[labels.index(str(i))], (28,28))
  ax[i//2,i%2].imshow(img)
```



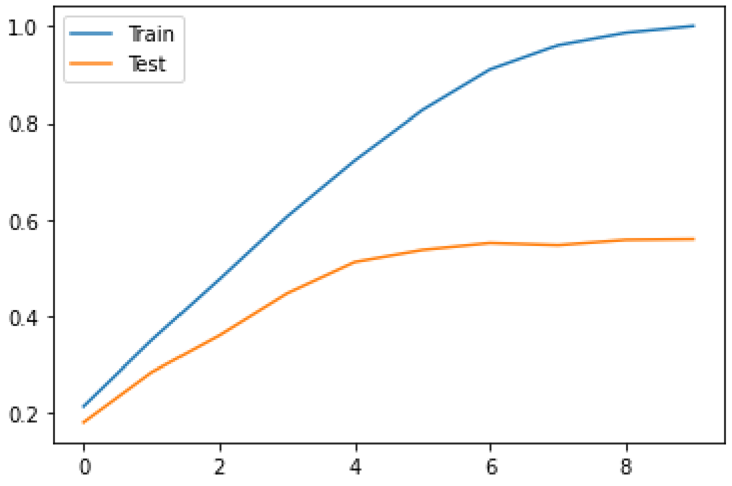
The train test split function in sklearn takes our dataset and splits it into two. The test and training sets. This allows our model to predict a model on our testing set and then tes this model on a set of data that is seperate from its testers.

The score in the DecisionTreeClassifier gives an average value to the accuracy of our predicitons.

In [22]:
```
X_train, X_test, Y_train, Y_test = train_test_split(mnist.data, mnist.target, tr
```

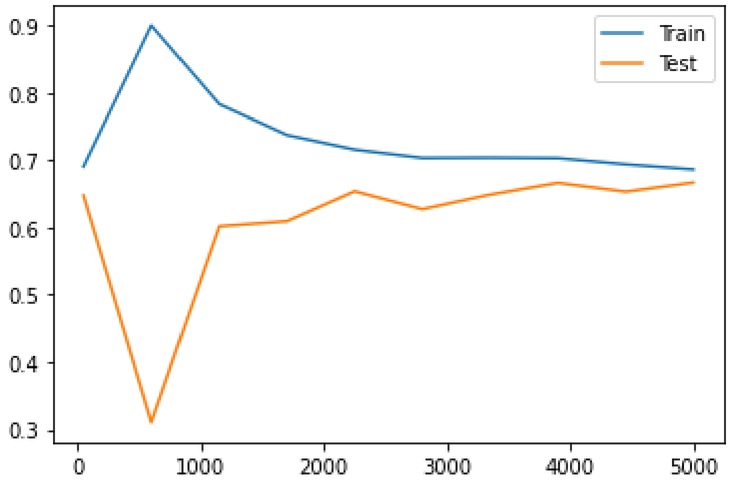
In [23]:
```
# We see that as our decision tree gets deeper and deeper, the training score go
# However, there are diminishing returns on the testing set as the model starts
x = np.linspace(0,9,10)
train_score = list()
test_score = list()

for i in range(1,11):
  tree = DecisionTreeClassifier(max_depth=i)
  tree.fit(X_train, Y_train)
  train_score.append(tree.score(X_train, Y_train))
  test_score.append(tree.score(X_test, Y_test))

plt.plot(x, train_score, label="Train")
plt.plot(x, test_score, label="Test")
plt.legend()
```

Out[23]:
```
<matplotlib.legend.Legend at 0x7fe6f95296a0>
```



In [24]:
```
# By changing the split, instead we see a score that starts to merge.
# This is due to the larger set of training data being less likely to overfit
x = np.linspace(50,5000,10)
train_score = list()
test_score = list()

tree = DecisionTreeClassifier(max_depth=5)

for i in range(10):
  X_train, X_test, Y_train, Y_test = train_test_split(mnist.data, mnist.target,
  tree.fit(X_train, Y_train)
  train_score.append(tree.score(X_train, Y_train))
  test_score.append(tree.score(X_test, Y_test))

plt.plot(x, train_score, label="Train")
plt.plot(x, test_score, label="Test")
plt.legend()
```

Out[24]:
```
<matplotlib.legend.Legend at 0x7fe6f9507e10>
```



In [61]:
```
# Exercise 4
import pandas as pd
import glob
import os
import sys
```

In [62]:
```
# Load data - takes a while to run
path = os.getcwd()
all_files = glob.glob(path + '/Names/*.txt')

li = []

for filename in all_files:
    df = pd.read_csv(filename, header=None)
    df.columns = ['Name','Gender','Frequency']
    df['Year'] = os.path.basename(filename)[3:7]
    li.append(df)

df = pd.concat(li, axis=0, ignore_index=True)
df
```

Out[62]:

	Name	Gender	Frequency	Year
0	Emily	F	25953	2000
1	Hannah	F	23075	2000
2	Madison	F	19967	2000
3	Ashley	F	17997	2000
4	Sarah	F	17689	2000
...	...	...	...	...
1858684	Winfrey	M	5	1935
1858685	Yancy	M	5	1935
1858686	Yazzie	M	5	1935
1858687	Zaragoza	M	5	1935
1858688	Zenas	M	5	1935

1858689 rows × 4 columns

In [63]:
```
# Exercise 4.1 Write a program that on input k and XXXX, returns the top k names

k = 6
year = 1883

df_result = df.loc[df['Year'] == str(year)]
df_result.sort_values(by=['Frequency'], ascending=[False]).head(k)
```

Out[63]:

	Name	Gender	Frequency	Year
1825295	John	M	8894	1883
1825296	William	M	8387	1883
1824241	Mary	F	8012	1883
1825297	James	M	5223	1883
1825298	Charles	M	4826	1883
1825299	George	M	4736	1883

In [64]:
```
# Exercise 4.2 Write a program that on input Name returns the frequency for men
name = 'Mary'

print('People with the name {}:'.format(name))
print('Male: '+ str(df[(df['Name'] == name) & (df['Gender'] == 'M')].Frequency.s
print('Female: '+ str(df[(df['Name'] == name) & (df['Gender'] == 'F')].Frequency
```

```
People with the name Mary:
Male: 15158
Female: 4118058
```

In [65]:
```
# Exercise 4.3 It could be that names are more diverse now than they were in 188
# the most popular for that year, though its frequency that year may have been d
# Modify the above to return the relative frequency.

name = 'Mary'

print('People with the name {}:'.format(name))

male_frequency = df[(df['Name'] == name) & (df['Gender'] == 'M')].Frequency.sum(
male_relative_frequency = male_frequency / df[df['Gender'] == 'M'].Frequency.sum
female_frequency = df[(df['Name'] == name) & (df['Gender'] == 'F')].Frequency.su
female_relative_frequency = female_frequency / df[df['Gender'] == 'F'].Frequency

print("Male: {}\t Relative Frequency: {}".format(male_frequency, male_relative_f
print("Female: {}\t Relative Frequency: {}".format(female_frequency, female_rela
```

```
People with the name Mary:
Male: 15158      Relative Frequency: 8.813286137579444e-05
Female: 4118058  Relative Frequency: 0.024387181356545513
```

In [135…
```
# Exercise 4.4 Find all the names that used to be more popular for one gender, b
pd.options.mode.chained_assignment = None  # default='warn'

starting_year = 1880
ending_year = 2015

starting_m_df = df[(df['Year'] == str(starting_year)) & (df["Gender"] == "M")]
starting_m_df["RelativeFrequency"] = starting_m_df['Frequency']/starting_m_df.Fr

starting_f_df = df[(df['Year'] == str(starting_year)) & (df["Gender"] == "F")]
starting_f_df["RelativeFrequency"] = starting_f_df['Frequency']/starting_f_df.Fr

ending_m_df = df[(df['Year'] == str(ending_year)) & (df["Gender"] == "M")]
ending_m_df["RelativeFrequency"] = ending_m_df['Frequency']/ending_m_df.Frequenc

ending_f_df = df[(df['Year'] == str(ending_year)) & (df["Gender"] == "F")]
ending_f_df["RelativeFrequency"] = ending_f_df['Frequency']/ending_f_df.Frequenc

li_f = []
li_m = []

m_name_list = ending_m_df.Name.tolist()
f_name_list = ending_f_df.Name.tolist()

# print(ending_f_df[ending_f_df["Name"] == "Emma"].RelativeFrequency.values[0])

for row in starting_m_df.itertuples():
    if row.Name in f_name_list:
        if row.RelativeFrequency < (ending_f_df[ending_f_df["Name"] == row.Name]
            li_m.append(row.Name)

for row in starting_f_df.itertuples():
    if row.Name in m_name_list:
        if row.RelativeFrequency < (ending_m_df[ending_m_df["Name"] == row.Name]
            li_f.append(row.Name)

print("The names that are used to be more popular on male:")
print(li_m)
print()
print("The names that are used to be more popular on female:")
print(li_f)
```

```
The names that are used to be more popular on male:
['Harley', 'Emery', 'Riley', 'Taylor', 'Morgan', 'Allie', 'Mary', 'Emerson', 'Jo
rdan', 'Madison', 'Aubrey', 'Elliott', 'Dallas', 'Addison', 'Frances', 'Alma',
'Parker', 'Logan', 'Anna', 'Bailey', 'Dana', 'Hunter', 'Sydney', 'Finley', 'Lind
sey', 'Emma', 'Noel', 'Palmer', 'Shirley', 'Avery', 'Carson', 'Elizabeth', 'Jun
e', 'Lacy', 'Addie', 'Ashley', 'Clara', 'Clare', 'Florence', 'Ida', 'Ivory', 'Qu
incy', 'Shelby', 'Elliot', 'Ivey', 'Lindsay', 'Rose', 'Tyler', 'Vivian', 'Alliso
n', 'Annie', 'Cora', 'Dora', 'Drew', 'Eliza', 'Elsie', 'Grace', 'Hallie', 'Hatti
e', 'Hope', 'Nellie', 'Reese', 'Ruby', 'Stacy', 'Cleo', 'Daisy', 'Denver', 'Edi
e', 'Edith', 'Flora', 'Hayden', 'Holly', 'Hudson', 'Ivy', 'Jewel', 'Justice', 'K
atherine', 'Kelly', 'Lillie', 'Mattie', 'Merida', 'Nora', 'Nova', 'Payton', 'Pre
sley', 'Reece']

The names that are used to be more popular on female:
['John', 'William', 'George', 'James', 'Clyde', 'Frank', 'Eddie', 'Charles', 'He
nry', 'Robert', 'Joseph', 'Ray', 'Thomas', 'Walter', 'Clarence', 'Theo', 'August
ine', 'Clifford', 'Harry', 'Leo', 'Arthur', 'Edgar', 'Glenn', 'Isa', 'Jesse', 'J
oe', 'Louis']
```

In [6]:

```
# Written Problem 2
V = np.array([[0,1],[1,0],[1,0]]) # matrix of basis vectors by column
P1 = [3, 1, 0]
P2 = [3, 2, 0]
P3 = [3, 3, 1]
point_mat = np.array([P1, P2, P3])
projection = np.matmul(np.matmul(np.matmul(V, np.linalg.inv(np.matmul(V.T, V))),
projection
```

Out[6]:

```
array([[3. , 1. , 0. ],
       [3. , 2.5, 0.5],
       [3. , 2.5, 0.5]])
```

In [ ]: