AM 207, Pset 1

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In [1]:
```
# Up-front things
import matplotlib.pyplot as plt
import numpy as np
import csv
from mpl_toolkits.mplot3d import Axes3D
from matplotlib import cm
from matplotlib.ticker import LinearLocator, FormatStrFormatter
from scipy import stats
from scipy.stats import norm

font_val = 18
plt.rc('font', size=font_val)          # controls default text sizes
plt.rc('axes', titlesize=font_val)
plt.rc('axes', labelsize=font_val)    # fontsize of the x and y labels
plt.rc('legend', fontsize=(font_val-3))    # legend fontsize
plt.rc('font', family='Sans Serif')
```

Problem 1: Part A - Bayes Theorum

Your child has been randomly selected for Type I diabetes screening, using a highly accurate new test that boasts of a false positive rate of 1% and a false negative rate of 0%. The prevalence of of Type I diabetes in children is approximately 0.228%.

1.Should your child test positive, what is the probability that he/she has Type I diabetes?

Let H be the event that my child Has Type I diabetes and P be the event that the test is Positive. Now:

$$P(H \mid P) = \frac{P(P \mid H)\, P(H)}{P(P)}$$

which simplified becomes:

$$= \frac{1 - P(-P \mid H)\, P(H)}{P(P \mid H)P(H) + P(P \mid -H)P(-H))}$$

and evaluated:

$$= \frac{1\ * 0.00228}{1 * 0.00228 + 0.01 * (1 - 0.00228)} = 0.186$$

2.Should you be concerned enough to ask for further testing or treatment for your child? Suppose an independent test with the same false positive/false negative rate is available.

Given the Bayesian result above, I would be concerned enough to ask for further testing. An 18.6% chance of having the disease is not negligble.

Furthermore, the probability of having the disease given two positive tests is equivalent to repeating the above process but with the updated probability of having the disease being the value we determined above, namely 0.186

Thus:

$$P(H \mid P1P2) = \frac{P(P1P2 \mid H)\, P(H)}{P(P1P2)}$$

which simplified becomes:

$$= \frac{1\ * 0.186}{P(P1P2 \mid H)P(H) + P(P1P2 \mid -H)P(-H))}$$

and evaluated:

$$= \frac{1\ * 0.186}{1 * 0.186 + 0.01 * 0.01 * (1 - 0.186)} = 0.958$$

showing us it is extremely likely our child has Type I diabetes given two independent positive tests. If the second test reads negative, we know that the child does not have Type I diabetes, given that the false negative rate is zero.

Later, you read online that Type I diabetes is 6 times more prevalent in prematurely born children. **3.If this statistic is true, what is the probability that your child, who is prematurely born, has Type I diabetes?**

Repeating the process from number 1 but with new P(H)=6*0.00228:

$$P(H \mid P) = \frac{P(P \mid H)\, P(H)}{P(P)}$$

which simplified becomes:

$$= \frac{1 - P(-P \mid H)\, P(H)}{P(P \mid H)P(H) + P(P \mid -H)P(-H))}$$

and evaluated:

$$= \frac{1\ * 6 * 0.00228}{1 * 6 * 0.00228 + 0.01 * (1 - 6 * 0.00228)} = 0.581$$

4.Subjectively, given the new information, should you be concerned enough to ask for treatment for your child?

I would rather take another test, just in case. A 58% proability of having the disease is higher than before but the cost of treatment probably outweighs the cost of another diagnostic test, so I would rather do the latter before seaking treatment for my child.

Problem 1 - Part B: More Bayes Theorum

During shopping week, you're trying to decide between two classes based on the criteria that the class must have a lenient grading system.

Both classes have hard TFs who give assignments lower grades than the work merits. You know from rumors that in one class has 35% of the TF staff are harsh graders and in the other class 15% are harsh graders, but you don't know which class is which.

So, you decide to conduct an experiment: submit an assignment to be graded. Fortunately, both classes offer an optional Homework 0 that is graded as extra credit. Unfortunately, you only have time to complete the problem set for just one of these classes.

Suppose you randomly pick the Homework 0 from Class A to complete and suppose that you received a grade that you believe is lower than the quality of your work warrents.

Based on this evidence, what is the probability that Class A has the harsher grading system? Which class should you drop based on the results of your experiment (or do you not have sufficient evidence to decide)?

Let A be the event that class A is the harsher class and L be the event that I received a lower grade than deserved. -A is equivalent to event B, namely that B is the harsher class. Now:

$$P(A \mid L) = \frac{P(L \mid A)\, P(A)}{P(L)}$$

which simplified becomes:

$$= \frac{(0.35)\ *(0.5)}{P(L \mid A)P(A) + P(L \mid B)P(B))}$$

and evaluated:

$$= \frac{(0.35)\ *(0.5)}{0.35 * 0.5 + 0.15 * (0.5)} = 0.70$$

Based on the results of this experiment, I would drop Class A, since it is more likely to be the harsher graded class.

Problem 2: Part A - Computing MLE Parameter

What are the values for λ_0 and λ_1 that maximize the likelihood of the observed data? Support your answer with full and rigorous analytic derivations.

Using the MLE process we begin with:

$$L(x_1, x_2) = \prod_{i=0}^{3} (4)\lambda_1^2 (x_1^i)(x_2^i) e^{-\lambda_0((x_1^i)^2 + (x_2^i)^2)}$$

which when converted to log-likelihood becomes (dropping the superscript, i, because it is tedious to type out so many times):

$$\ln(L(x_1, x_2)) = 4\ln(4) + 8\ln(\lambda_1) + \sum_{i=0}^{3} (\ln(x_1) + \ln(x_2)) - \lambda_0 \sum_{i=0}^{3} (x_1^2 + x_2^2)$$

Now due to the PDF integrating to 1, we discover how to write λ_1 in terms of λ_0 in the following way:

$$1 = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} (4)\lambda_1^2 (x_1)(x_2) e^{-\lambda_0(x_1^2 + x_2^2)}\, dx_1\, dx_2$$

Through integration, we find:

$$\frac{1}{4\lambda_1^2} = \frac{1}{4\lambda_0^2}$$

or equivalently

$$\lambda_1 = \lambda_0$$

given that

$$\lambda_1, \lambda_0 > 0$$

We can now use this result in our log-likelihood estimation, replacing λ_1 with λ_0.

Taking a partial derivative of our log-likelihood equation with respect to λ_0, yields:

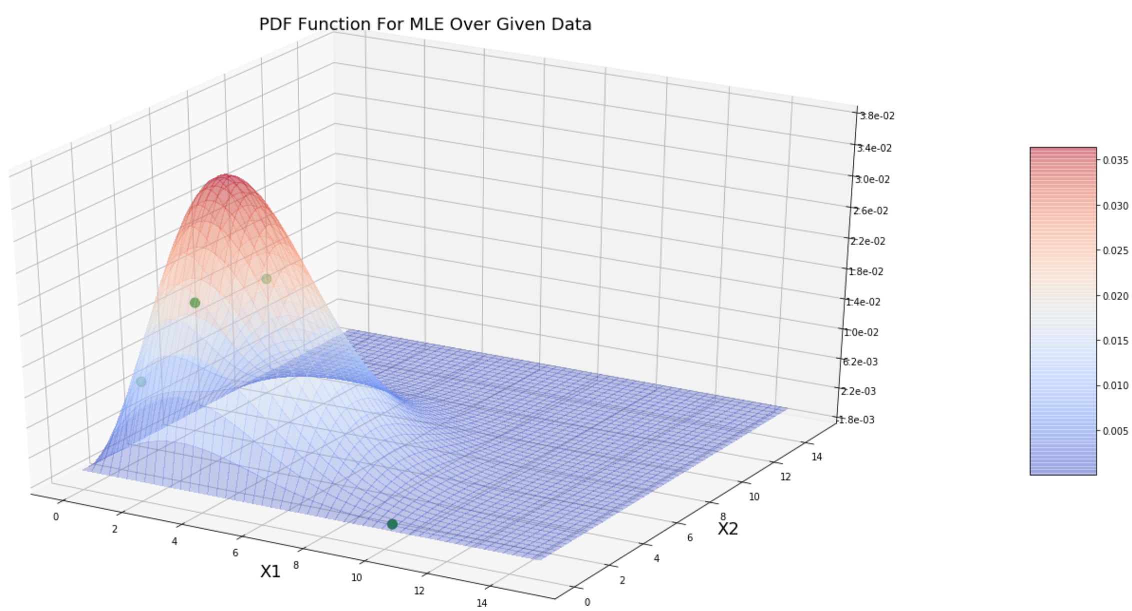
$$\frac{\partial \ell}{\partial \lambda_0} = \frac{8}{\lambda_0} - \sum_{i=0}^{3} x_1^2 + x_2^2 = 0$$

which simplified and used with our data yields:

$$\hat{\lambda}_1 = \hat{\lambda}_0 = \frac{8}{\sum_{i=0}^{3} (x_1^i)^2 + (x_1^i)^2} = \frac{8}{161} = 0.0497$$

Problem 2: Part B - Visualizing Data and Distribution

In [2]:
```python
# Problem 2, Part B:
# (2.B) Visualizing Data and Distribution
x=np.transpose(np.array([[0.5,2.5],[3.2,1.3],[2.72,5.84],[10.047,0.354]]))

# Function for PDF
lam=8/np.sum(np.square(x))

def PDF_func(x):
    return 4*lam**2*x[0]*x[1]*np.exp(-lam*(x[0]**2 + x[1]**2 ))

xspec = PDF_func(x)

# Mesh Grid Space
X1 = np.arange(0, 15, 0.05)
X2 = np.arange(0, 15, 0.05)
X1, X2 = np.meshgrid(X1, X2)
Z = PDF_func([X1,X2])

# Plot in 3D
fig = plt.figure(figsize=(20,10))
ax = fig.gca(projection='3d')

# Plot Surface
surf = ax.plot_surface(X1, X2, Z, cmap=cm.coolwarm,
                       linewidth=0, antialiased=False, alpha=.3, label='PDF')
# Add Points in Green:
ax.scatter(x[0,:], x[1,:], PDF_func(x), s=100, c='g', label='Given Data')

# Customize the z axis.
ax.zaxis.set_major_locator(LinearLocator(11))
ax.zaxis.set_major_formatter(FormatStrFormatter('%.01e'))

# Color bar which maps values to colors.
fig.colorbar(surf, shrink=0.5, aspect=5)

# Add titles and labels
ax.set_title('PDF Function For MLE Over Given Data')
ax.set_xlabel('X1')
ax.set_ylabel('X2')

plt.tight_layout()
plt.show()
```

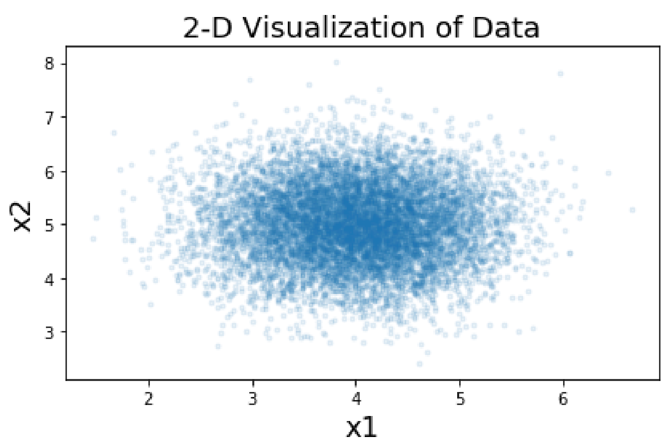


Problem 3: Part A - Visualization of Data and Distribution

(3.A.1) 2-D Visualization of the Distribution of Data

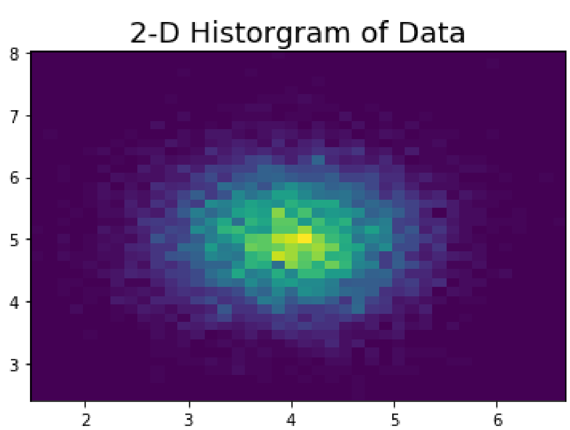
In [3]:
```
# Problem 3, Part A:
# Load in the data
data = np.genfromtxt(r'Homework_1_Data.txt', delimiter=',')
print('Data Shape:', np.shape(data))
print('Mean Along Each Dimension:', np.mean(data, axis=0))
print('Variance Along Each Dimension:', np.var(data, axis=0))

# (3.A.1) 2-D Visualization of the Distribution of Data
plt.scatter(data[:,0], data[:,1], marker='.', alpha=.1)
plt.title('2-D Visualization of Data')
plt.xlabel('x1')
plt.ylabel('x2')
plt.tight_layout()
plt.show()
```

```
Data Shape: (10000, 2)
Mean Along Each Dimension: [ 3.99276398  4.99814632]
Variance Along Each Dimension: [ 0.48564757  0.50525708]
```



(3.A.2) Visualize the PDF of the distribution of data

In [4]:
```
# (3.A.2) Visualize the PDF of the distribution of data
# 2-D Histogram
plt.hist2d(data[:,0], data[:,1], bins = 40, normed=True)
plt.title('2-D Historgram of Data')
plt.show()
```



Given the 2-dimensional histogram of the data, we observe that this data is most likely a 2-dimensional normal distribution, given that there is a concentration of points near the mean of each dimension of the data and there is some degree of symmetric about a minor and major axis of oval rings. The general form of this kind of normal distribution is:

$$f(x, y) = A \exp\left(-\left(\frac{(x-\bar{x})^2}{2\sigma_x^2} + \frac{(y-\bar{y})^2}{2\sigma_y^2}\right)\right)$$

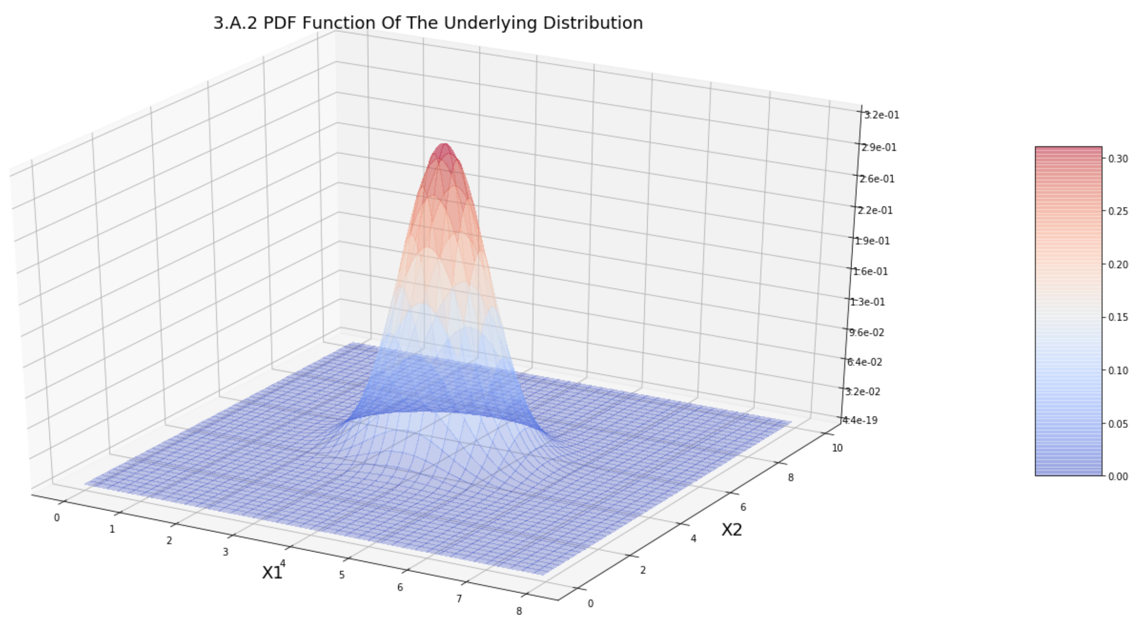
Citation: https://en.wikipedia.org/wiki/Gaussian_function#Two-dimensional_Gaussian_function (https://en.wikipedia.org/wiki/Gaussian_function#Two-dimensional_Gaussian_function)

We can visualize the coefficient, A, as the height of the peak at the mean value of the gaussian. To determine this value, we can apply the normalization condition for the volume under the Gaussian:

The volume under the Gaussian function is given by

$$V = 1 = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} f(x, y)\, dx\, dy = 2\pi A \sigma_x \sigma_y$$

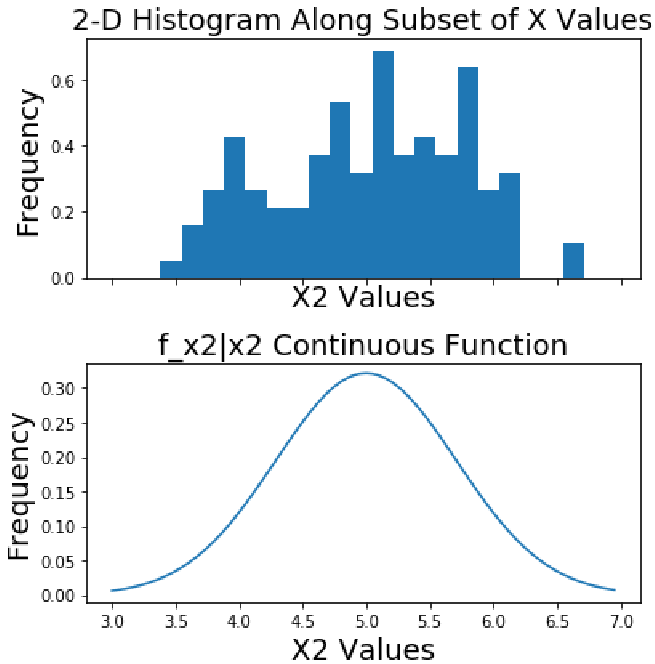
In [5]:
```
# Get the coefficient, A:
sigx = np.std(data, axis=0)[0]
sigy = np.std(data, axis=0)[1]

# Plot the 2-D Gaussian Function:
# Function for PDF
def PDF_func_2(x, mu, sig):
    A = 1/(2*np.pi*sigx*sigy)
    return A*np.exp(-(x[0]-mu[0])**2/(2*sig[0]**2) + -(x[1]-mu[1])**2/(2*sig[1]**2) )

# xspec = PDF_func_2(np.transpose(data), np.mean(data, axis=0), np.std(data, axis=0))

# Mesh Grid Space
X1_3 = np.arange(0, 8, 0.05)
X2_3 = np.arange(0, 10, 0.05)
X1_3, X2_3 = np.meshgrid(X1_3, X2_3)
Z_3 = PDF_func_2([X1_3,X2_3], np.mean(data, axis=0), np.std(data, axis=0))

# Plot in 3D
fig = plt.figure(figsize=(20,10))
ax = fig.gca(projection='3d')

# Plot Surface
surf = ax.plot_surface(X1_3, X2_3, Z_3, cmap=cm.coolwarm,
                       linewidth=0, antialiased=False, alpha=.3, label='PDF')

# Customize the z axis.
ax.zaxis.set_major_locator(LinearLocator(11))
ax.zaxis.set_major_formatter(FormatStrFormatter('%.01e'))

# Color bar which maps values to colors.
fig.colorbar(surf, shrink=0.5, aspect=5)

# Add titles and labels
ax.set_title('3.A.2 PDF Function Of The Underlying Distribution')
ax.set_xlabel('X1')
ax.set_ylabel('X2')

plt.tight_layout()
plt.show()
```

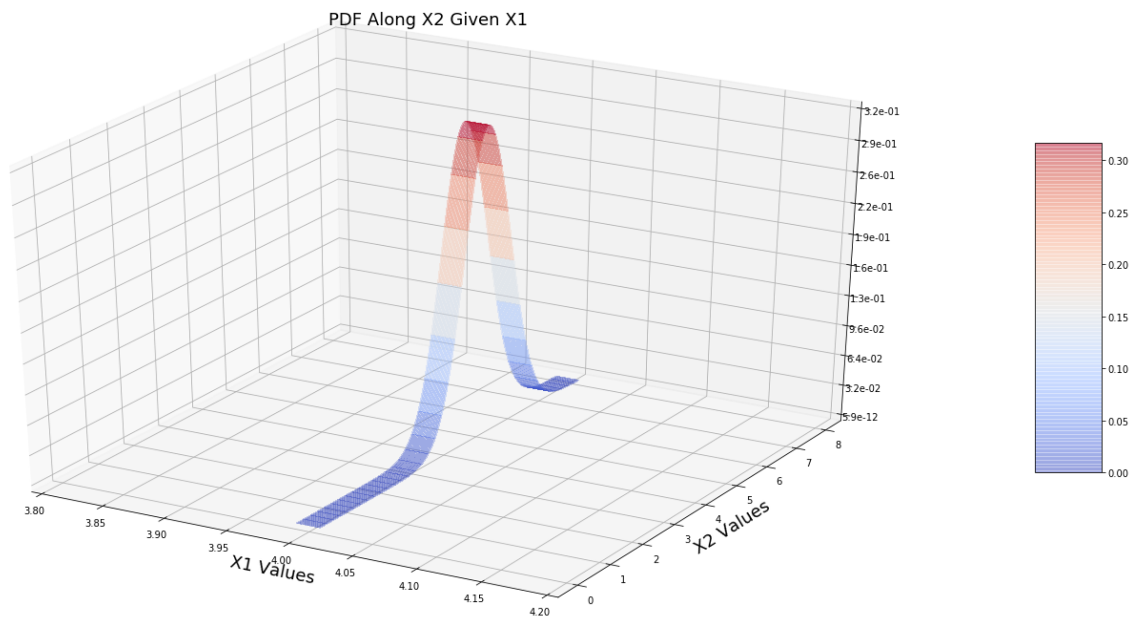


(3.A.3) Distribution defined by fx2|x1 for x1 contained in some range

To find the conditional distribution of x2 given x1, we can select data points where values of x1 are contained in a small sliver and compute the distribution of the remaining points along x2

In [6]:
```
# (3.A.3) Distribution defined by fx2|x1 for x1 contained in some range
# Get all points where x1 is in a certain range:
xr = [3.99, 4.01]
data_range_X = data[(data[:,0]>xr[0]) & (data[:,0]<xr[1]), :]

# Plot Histogram
fig, ax = plt.subplots(2,1,figsize=(6,6),sharex=True)
ax[0].hist(data_range_X[:,1], bins = 20, normed=True)
ax[0].set_title('2-D Histogram Along Subset of X Values')
ax[0].set_xlabel('X2 Values')
ax[0].set_ylabel('Frequency')
x2 = np.arange(3,7,.05)
ax[1].plot(x2, PDF_func_2([4.00, x2], np.mean(data, axis=0), np.std(data, axis=0)))
ax[1].set_xlabel('X2 Values')
ax[1].set_ylabel('Frequency')
ax[1].set_title('f_x2|x2 Continuous Function')
plt.tight_layout()
plt.show()

# Plot Disribution where X1 is at X==4
X2_3_2 = np.arange(0, 8, 0.05)
X1_3_2 = np.arange(3.99, 4.01, 0.001)
X1_3_2, X2_3_2 = np.meshgrid(X1_3_2, X2_3_2)
Z_3_2 = PDF_func_2([X1_3_2,X2_3_2], np.mean(data, axis=0), np.std(data, axis=0))

# Plot in 3D
fig = plt.figure(figsize=(20,10))
ax = fig.gca(projection='3d')

# Plot Surface
surf = ax.plot_surface(X1_3_2, X2_3_2, Z_3_2, cmap=cm.coolwarm,
                       linewidth=0, antialiased=False, alpha=.3, label='PDF')

# Customize the z axis.
ax.zaxis.set_major_locator(LinearLocator(11))
ax.zaxis.set_major_formatter(FormatStrFormatter('%.01e'))

# Color bar which maps values to colors.
fig.colorbar(surf, shrink=0.5, aspect=5)

ax.set_xlabel('X1 Values')
ax.set_ylabel('X2 Values')
ax.set_title('PDF Along X2 Given X1')
ax.set_xlim([3.8,4.2])
plt.tight_layout()
plt.show()
```

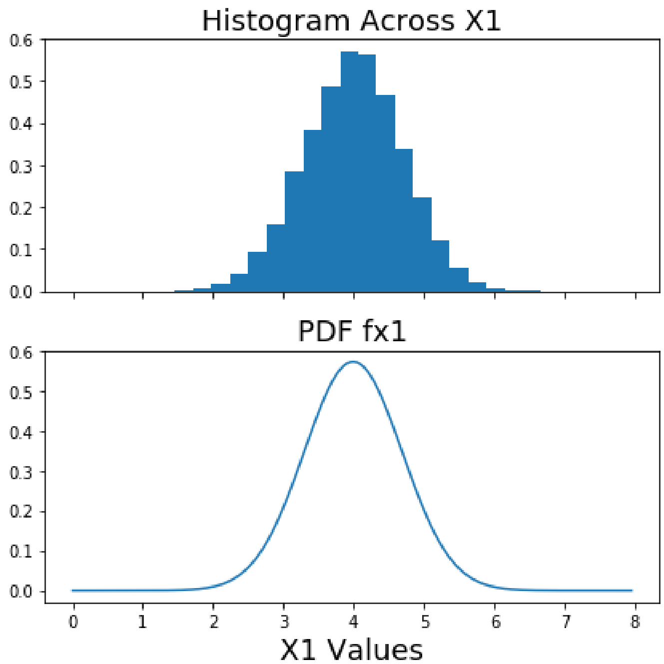




(3.A.4) Distribution defined by fx1

To find the distribution of x1, we can simply run the gaussian distribution along x1. Below we show the histogram and a normalized Gaussian function for fx1

In [7]:
```
# (3.A.4) Distribution Defined by fx1
x1 = np.arange(0,8,.05)
fig, ax = plt.subplots(2,1,figsize=(6,6),sharex=True)
ax[0].hist(data[:,0], bins=20, normed=True)
ax[0].set_title('Histogram Across X1')
ax[1].plot(x1, norm.pdf(x1,np.mean(data[:,0]), np.std(data[:,0])))
ax[1].set_title('PDF fx1')
ax[1].set_xlabel('X1 Values')

plt.tight_layout()
plt.show()
```



Problem 3: Part B - Bootstrapping

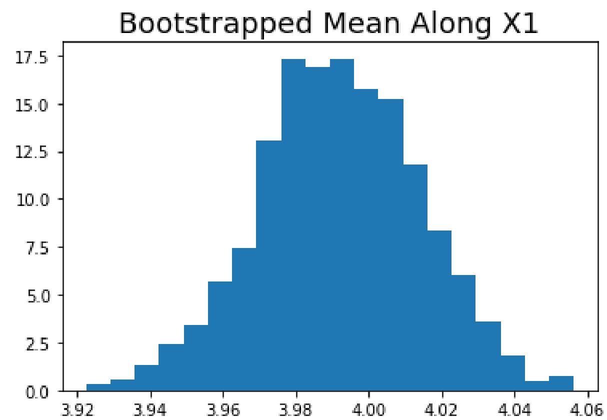
In this section, we will run a non-parametric bootstrap function to estimate certain parameters

In [8]:
```
# Bootstrapping Algorithm
def get_bootstrap_sample(data,nlen):
    randrow = np.random.choice(range(np.size(data,axis=0)), nlen, replace=True)
    if len(data.shape)==1:
        bootstrap_sample = data[randrow]
    else:
        bootstrap_sample = data[randrow,:]
    return(bootstrap_sample)

def perform_bootstrap(data,nlen,ntrials,func):
    if len(data.shape)==1:
        output = np.zeros(ntrials)
        for i in range(ntrials):
            sample = get_bootstrap_sample(data,nlen)
            output[i] = func(sample, axis=0)
    else:
        cols = np.size(data,1)
        output = np.zeros((ntrials, cols))
        for i in range(ntrials):
            sample = get_bootstrap_sample(data,nlen)
            output[i,:] = func(sample, axis=0)

    return(output)
```

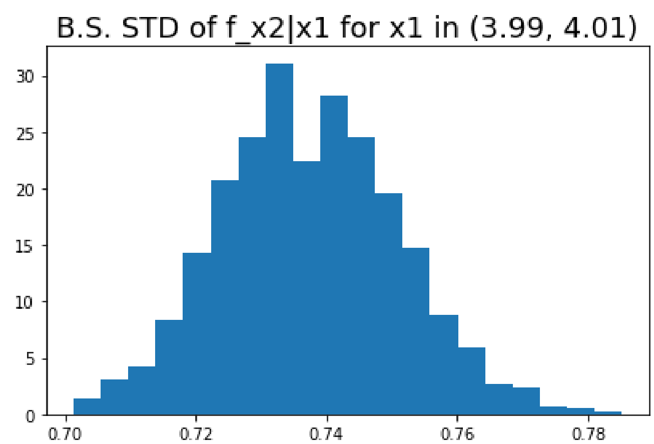
In [9]:
```
# Compute the Actual Parameters:
print('Data Shape:', np.shape(data))
print('Mean Along Each Dimension:', np.mean(data, axis=0))
print('Variance Along Each Dimension:', np.var(data, axis=0))

# Try the mean:
nsize = 1000
ntrials = 1000
mean_boot = perform_bootstrap(data, nsize, ntrials, np.mean)
std_boot = perform_bootstrap(data_range_X, nsize, ntrials, np.std)
```

```
Data Shape: (10000, 2)
Mean Along Each Dimension: [ 3.99276398  4.99814632]
Variance Along Each Dimension: [ 0.48564757  0.50525708]
```

In [10]:
```
#plot the distribution
b = 20
# Mean
fig, ax = plt.subplots()
ax.hist(mean_boot[:,0], bins=b, normed=True)
ax.set_title('Bootstrapped Mean Along X1')
plt.show()

print('Empirical Estimation of Mean X1: %.4f' % np.mean(mean_boot, axis=0)[0])
print('Mean of Original Data Set X1: %.4f' % np.mean(data, axis=0)[0])
print('Standard Error of the Mean X1: %.4f' % np.std(mean_boot, axis=0)[0])

# Standard Deviation
fig, ax = plt.subplots()
ax.hist(std_boot[:,1], bins=b, normed=True)
ax.set_title('B.S. STD of f_x2|x1 for x1 in (3.99, 4.01)')
plt.tight_layout()
plt.show()

print('Empirical Estimation of STD f_x2|x1: %.8f' % np.mean(std_boot[:,1]))
print('STD of f_x2_x1 from original: %.4f' % np.std(data_range_X))
print('Standard Error of STD Estimation: %.8f' % np.std(std_boot[:,1]))
```




```
Empirical Estimation of Mean X1: 3.9921
Mean of Original Data Set X1: 3.9928
Standard Error of the Mean X1: 0.0219
```




```
Empirical Estimation of STD f_x2|x1: 0.73742777
STD of f_x2_x1 from original: 0.7310
Standard Error of STD Estimation: 0.01363014
```

The above plots from the bootstrapping algorithm give us a sampling distribution of the mean and standard deviation along each component. From these plots, we can empirically estimate the mean by taking the mean of the sampling distribution. We can similarly estimate the standard deviation by taking the mean of the standard deviation sampling distribution.

3.B.3: Significant Digits of Standard Deviation Estimate

We can make an approximation to the standard error of a parameter by looking at the standard deviation around the sampling distribution. As a result, the first non-zero digit of the standard error gives us insight into the amount of significant digits in our empirical estimation. Since the error acts on the empirical estimation, all digits in the parameter estimate that are smaller than the first non-zero digit in the standard error are inconsequential. It makes sense to keep at least the first non-zero digit in the standard error value, and in some cases, it makes sense to keep at least the first two non-zero digits.

Empirical Estimation of STD of $f_{x2|x1}$: 0.73801035 $\pm$ 0.01302445 becomes 0.737 $\pm$ 0.013 when keeping the first two non-zero digits of the standard error calculation.

Problem 4: Missing Data

In [11]:
```
# (4) Missing Data
import pandas as pd
wine_data = pd.read_csv('wine_quality_missing.csv')
print('Original Shape (Rows x Columns):', wine_data.shape)
wine_data.head()
```

```
Original Shape (Rows x Columns): (178, 14)
```

Out[11]:

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue
0	14.23	1.71	2.43	15.6	127.0	2.80	3.06	0.28	2.29	5.64	1.04
1	13.20	1.78	2.14	NaN	100.0	2.65	2.76	0.26	1.28	4.38	1.05
2	13.16	2.36	2.67	18.6	101.0	2.80	3.24	0.30	2.81	5.68	1.03
3	14.37	1.95	2.50	NaN	113.0	3.85	3.49	0.24	2.18	7.80	0.86
4	13.24	2.59	2.87	21.0	118.0	2.80	2.69	0.39	NaN	4.32	1.04

In [12]:
```
wine_data = pd.read_csv('wine_quality_missing.csv')

# Show which columnas have at least one NaN entry at the beginning
NaNcols0 = wine_data.isnull().any(axis=0)
print('ORIGINAL:')
print('Columns that have at least one NaN entry:', np.sum(NaNcols0))

# (4.1) Drop Imputation
print('\nDROP IMPUTATION:')
wine_DropImp = wine_data[wine_data.notnull().all(axis=1)]
print('Shape With Drop Imputation (Rows x Columns):', wine_DropImp.shape)
NaNcols1 = wine_DropImp.isnull().any(axis=0)
print('Columns that have at least one NaN entry:', np.sum(NaNcols1))

# (4.2) Mean Imputation
print('\nMEAN IMPUTATION:')
wine_MeanImp = wine_data
for colname in wine_MeanImp.columns:
    NaNlocs = wine_MeanImp[colname].isnull()
    MEAN = np.mean(wine_MeanImp[colname])
    wine_MeanImp.loc[NaNlocs,colname] = MEAN

NaNcols2 = wine_MeanImp.isnull().any(axis=0)
print('Shape With Mean Imputation (Rows x Columns):', wine_MeanImp.shape)
print('Columns that have at least one NaN entry:', np.sum(NaNcols2), '\n')
wine_MeanImp.head()
```

```
ORIGINAL:
Columns that have at least one NaN entry: 13

DROP IMPUTATION:
Shape With Drop Imputation (Rows x Columns): (43, 14)
Columns that have at least one NaN entry: 0

MEAN IMPUTATION:
Shape With Mean Imputation (Rows x Columns): (178, 14)
Columns that have at least one NaN entry: 0
```

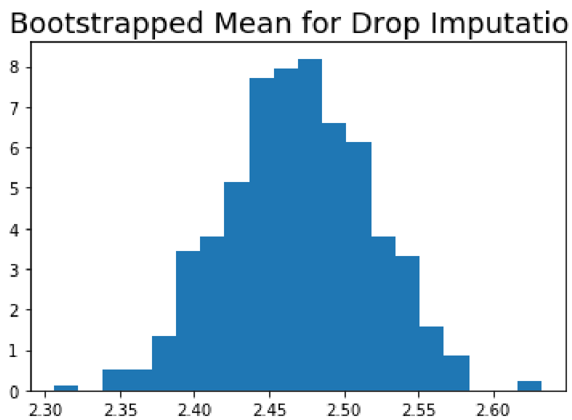
Out[12]:

	Alcohol	Malic acid	Ash	Alcalinity of ash	Magnesium	Total phenols	Flavanoids	Nonflavanoid phenols	Proanthocyanins	Color intensity	Hue
0	14.23	1.71	2.43	15.600000	127.0	2.80	3.06	0.28	2.290000	5.64	1.04
1	13.20	1.78	2.14	19.508861	100.0	2.65	2.76	0.26	1.280000	4.38	1.05
2	13.16	2.36	2.67	18.600000	101.0	2.80	3.24	0.30	2.810000	5.68	1.03
3	14.37	1.95	2.50	19.508861	113.0	3.85	3.49	0.24	2.180000	7.80	0.86
4	13.24	2.59	2.87	21.000000	118.0	2.80	2.69	0.39	1.596211	4.32	1.04

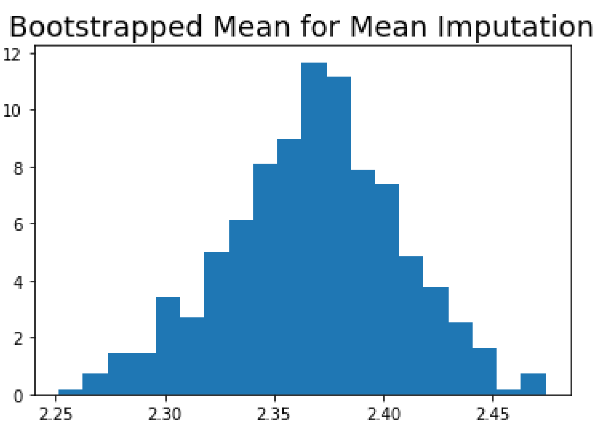
In [13]:
```
# (4.3) Empirical Estimation of PDF using bootstrap
nsize = 50
ntrials = 500

# Drop Imp
mean_boot_drop = perform_bootstrap(wine_DropImp['Ash'], nsize, ntrials, np.mean)
mean_boot_mean = perform_bootstrap(wine_MeanImp['Ash'], nsize, ntrials, np.mean)
```

```
/anaconda3/lib/python3.6/site-packages/pandas/core/series.py:696: FutureWarning:
Passing list-likes to .loc or [] with any missing label will raise
KeyError in the future, you can use .reindex() as an alternative.

See the documentation here:
http://pandas.pydata.org/pandas-docs/stable/indexing.html#deprecate-loc-reindex-listlike
  return self.loc[key]
```

In [14]:
```
b = 20
# Mean
fig, ax = plt.subplots()
ax.hist(mean_boot_drop, bins=b, normed=True)
ax.set_title('Bootstrapped Mean for Drop Imputation')
plt.show()

print('Drop Imputation - Estimation of Mean: %.4f' % np.mean(mean_boot_drop))
print('Mean of Original Drop Imp Set: %.4f' % wine_DropImp['Ash'].mean())
print('\nStandard Error of the Mean: %.4f' % np.std(mean_boot_drop))

# Mean
fig, ax = plt.subplots()
ax.hist(mean_boot_mean, bins=b, normed=True)
ax.set_title('Bootstrapped Mean for Mean Imputation')
plt.show()

print('Mean Imputation - Estimation of Mean: %.4f' % np.mean(mean_boot_mean))
print('Mean of Original Mean Imp Set: %.4f' % wine_MeanImp['Ash'].mean())
print('\nStandard Error of the Mean: %.4f' % np.std(mean_boot_mean))
```




```
Drop Imputation - Estimation of Mean: 2.4692
Mean of Original Drop Imp Set: 2.3698

Standard Error of the Mean: 0.0487
```




```
Mean Imputation - Estimation of Mean: 2.3676
Mean of Original Mean Imp Set: 2.3662

Standard Error of the Mean: 0.0392
```

(4.4) Comparing Standard Errors of the Mean for the two methods

By the definition of the drop imputation method, we remove all rows with missing values. This will leave us with less rows in total when compared to the mean imputation method where we replace missing values with the column mean. In particular, we see that the drop imputation methods leaves us with 43 rows, whereas the mean imputation method maintains the 178 rows of the original dataset.

We notice that the mean imputation methods demonstrates less standard error of the mean than does the drop imputation method. By performing the mean imputation method, we have increased the likelihood that we will pick out the mean value when doing a random sample of the original data. This is because we have increased the number of times the mean value occurs in the list of data. Therefore, your variance will shrink.