In [63]:
```
from IPython.core.display import HTML
def css_styling():
    styles = open("styles/custom.css", "r").read()
    return HTML(styles)
css_styling()
```

Out[63]:

Computational Statistics for Data Analysis

"Statistics is the discipline of using data samples to support claims about populations."

In this notebook, we will get familiar with Descriptive statistics that comprise concepts, terms, measures and tools that help to describe, show and summarize the data in a meaningful way. When analysing data, such as the price of flats renting per year, it is possible to use both descriptive and inferential statistics in order to analyse the results and draw some conclusions. We will discuss basic concepts, terms and procedures, like mean, median, variance, correlation, etc., to explore, describe and summarize the given set of data.

Statistics is based on 2 main concepts:

- A **population** is a collection of objects, items ("units") about which information is sought.
- A **sample** is a part of the population that is observed.

1 Descriptive Statistics.

- 1.1 Getting data
- 1.2 Data preparation
- 1.3 Improving data as a pandas DataFrame
- 1.4 Data cleaning

"Are the men more likely to become high income professionals i.e. to receive income bigger than 50K?"

Some people believe it is true, but **without data analysis** to support it, this claim is a case of **anecdotal evidence**:

- There are a **small number of samples** (personal experience, friends, etc.).
- There is a **selection bias**: most *believers* are interested in this claim because their first babies were late.
- There is a **confirmation bias**: believers might be more likely to contribute data that confirm it.
- Sources are **innaccurate**: personal stories are subject to memory deformations.

1.1 Getting Data

Let us consider a public database, called "Adult" dataset hosted on the UCI's Machine Learning Repository (https://archive.ics.uci.edu/ml/datasets/Adult (https://archive.ics.uci.edu/ml/datasets/Adult)), that contains approximately 32.000 observations about different financial parameters of US population.

1.2 Data preparation

One of the reasons we are using a general-purpose language such as Python rather than a stats language like R is that for many projects the *hard* part is preparing the data, not doing the analysis.

The most common steps are:

1. **Getting the data**. Data can be directly read from a file or it might be necessary to scrap the web.
2. **Parsing the data**. Of course, this depends on what format it is in: plain text, fixed columns, CSV, XML, HTML, etc.
3. **Cleaning the data**. Survey responses and other data files are almost always incomplete. Sometimes there are multiple codes for things like, *not asked*, *did not know*, and *declined to answer*. And there are almost always errors. A simple strategy is to remove or ignore incomplete records.
4. **Building data structures**. Once you read the data, you usually want to store it in a data structure that lends itself to the analysis you want to do.

If the data fits into memory, building a data structure is usually the way to go. If not, you could build a database, which is an out-of-memory data structure. Most databases provide a mapping from keys to values, so they are like dictionaries.

Let us read the dataset:

In [1]:
```
file = open('files/adult.data', 'r')
```

In [2]:
```
def chr_int(a):
    if a.isdigit():
        return int(a)
    else:
        return 0

data=[]
for line in file:
     data1=line.split(', ')
     if len(data1)==15:
        data.append([chr_int(data1[0]),data1[1],chr_int(data1[2]),data1[3],chr_int(data1[
            data1[7],data1[8],data1[9],chr_int(data1[10]),chr_int(data1[11]),chr_int(data
            data1[14]])
```

In [3]:
```
print data[1:2]
```

```
[[50, 'Self-emp-not-inc', 83311, 'Bachelors', 13, 'Married-civ-spouse', 'Exec-manageria
l', 'Husband', 'White', 'Male', 0, 0, 13, 'United-States', '<=50K\n']]
```

1.3 Importing data as a pandas DataFrame

In [4]:
```
%matplotlib inline
import pandas as pd

df = pd.DataFrame(data) #  Two-dimensional size-mutable, potentially heterogeneous tabula

df.columns = ['age', 'type_employer', 'fnlwgt', 'education',
              "education_num","marital", "occupation", "relationship", "race","sex",
              "capital_gain", "capital_loss", "hr_per_week","country","income"]
df.head()
```

Out[4]:

	age	type_employer	fnlwgt	education	education_num	marital	occupation	relationship	race	sex
0	39	State-gov	77516	Bachelors	13	Never-married	Adm-clerical	Not-in-family	White	Male
1	50	Self-emp-not-inc	83311	Bachelors	13	Married-civ-spouse	Exec-managerial	Husband	White	Male
2	38	Private	215646	HS-grad	9	Divorced	Handlers-cleaners	Not-in-family	White	Male
3	53	Private	234721	11th	7	Married-civ-spouse	Handlers-cleaners	Husband	Black	Male
4	28	Private	338409	Bachelors	13	Married-civ-spouse	Prof-specialty	Wife	Black	Female

In [5]:
```
df.tail()
```

Out[5]:

	age	type_employer	fnlwgt	education	education_num	marital	occupation	relationship	race	
32556	27	Private	257302	Assoc-acdm	12	Married-civ-spouse	Tech-support	Wife	White	F
32557	40	Private	154374	HS-grad	9	Married-civ-spouse	Machine-op-inspct	Husband	White	
32558	58	Private	151910	HS-grad	9	Widowed	Adm-clerical	Unmarried	White	F
32559	22	Private	201490	HS-grad	9	Never-married	Adm-clerical	Own-child	White	
32560	52	Self-emp-inc	287927	HS-grad	9	Married-civ-spouse	Exec-managerial	Wife	White	F

In [6]:
```
df.shape
```

Out[6]: (32561, 15)

Let's count the number of items per country:

In [7]:
```
counts = df.groupby('country').size()

print counts
# also: df.outcome.value_counts()
```

```
country
?                              583
Cambodia                        19
Canada                         121
China                           75
Columbia                        59
Cuba                            95
Dominican-Republic              70
Ecuador                         28
El-Salvador                    106
England                         90
France                          29
Germany                        137
Greece                          29
Guatemala                       64
Haiti                           44
Holand-Netherlands               1
Honduras                        13
Hong                            20
Hungary                         13
India                          100
Iran                            43
Ireland                         24
Italy                           73
Jamaica                         81
Japan                           62
Laos                            18
Mexico                         643
Nicaragua                       34
Outlying-US(Guam-USVI-etc)      14
Peru                            31
Philippines                    198
Poland                          60
Portugal                        37
Puerto-Rico                    114
Scotland                        12
South                           80
Taiwan                          51
Thailand                        18
Trinadad&Tobago                 19
United-States                29170
Vietnam                         67
Yugoslavia                      16
dtype: int64
```

In [8]:
```
counts = df.groupby('age').size() # grouping by age
print counts
```

```
age
17    395
18    550
19    712
20    753
21    720
22    765
23    877
24    798
25    841
26    785
27    835
28    867
29    813
30    861
31    888
32    828
33    875
34    886
35    876
36    898
37    858
38    827
39    816
40    794
41    808
42    780
43    770
44    724
45    734
46    737
     ...
60    312
61    300
62    258
63    230
64    208
65    178
66    150
67    151
68    120
69    108
70     89
71     72
72     67
73     64
74     51
75     45
76     46
77     29
78     23
79     22
80     22
81     20
82     12
83      6
84     10
85      3
86      1
87      1
88      3
90     43
Length: 73, dtype: int64
```

In [9]:
```
ml = df[(df.sex == 'Male')] # grouping by sex
ml.shape
```

Out[9]: (21790, 15)

In [10]:
```
ml1 = df[(df.sex == 'Male')&(df.income=='>50K\n')]
ml1.shape
```

Out[10]: (6662, 15)

Let's separate male from female according to the income.

In [11]:
```
fm =df[(df.sex == 'Female')]
fm.shape
```

Out[11]: (10771, 15)

In [76]:
```
df1=df[(df.income=='>50K\n')]

print 'The rate of people with high income is: ', int(len(df1)/float(len(df))*100), '%.'
print 'The rate of men with high income is: ', int(len(ml1)/float(len(ml))*100), '%.'
print 'The rate of women with high income is: ', int(len(fm1)/float(len(fm))*100), '%.'
```

```
The rate of people with high income is:  24 %.
The rate of men with high income is:  30 %.
The rate of women with high income is:  10 %.
```

In [12]:
```
fm1 =df[(df.sex == 'Female')&(df.income=='>50K\n')]
fm1.shape
```

Out[12]: (1179, 15)

1.4 Data Cleaning

The most common steps are:

- **Sample the data**. If the amount of raw data is huge, processing all of them may require an extensive amount of processing power which may not be practical. In this case, it is quite common to sample the input data to reduce the size of data that need to be processed.
- **Impute missing data**. It is quite common that some of the input records are incomplete in the sense that certain fields are missing or have input error. In a typical tabular data format, we need to validate each record contains the same number of fields and each field contains the data type we expect. In case the record has some fields missing, we have the following choices:
- (a) Discard the whole record if it is incomplete;
- (b) Infer the missing value based on the data from other records. A common approach is to fill the missing data with the average, or the median.

- **Normalize numeric value**. Normalize data is about transforming numeric data into a uniform range.

- **Reduce dimensionality**. High dimensionality can be a problem for some machine learning methods. There are two ways to reduce the number of input features. One is about *removing irrelevant* input variables, another one is about *removing redundant* input variables.
- **Add derived features**. In some cases, we may need to compute additional attributes from existing attributes (f.e. converting a geo-location to a zip code, or converting the age to an age group).
- **Discretize numeric value into categories**. Discretize data is about cutting a continuous value into ranges and assigning the numeric with the corresponding bucket of the range it falls on. For numeric attribute, a common way to generalize it is to discretize it into ranges, which can be either constant width (variable height/frequency) or variable width (constant height).

- **Binarize categorical attributes**. Certain machine learning models only take binary input (or numeric input). In this case, we need to convert categorical attribute into multiple binary attributes, while each binary attribute corresponds to a particular value of the category.

- **Select, combine, aggregate data**. Designing the form of training data is the most important part of the whole predictive modeling exercise because the accuracy largely depends on whether the input features are structured in an appropriate form that provide strong signals to the learning algorithm. Rather than using the raw data as it is, it is quite common that multiple pieces of raw data need to be combined together, or aggregating multiple raw data records along some dimensions.

2 Exploratory Data Analysis.

2.1 Summarizing the data:

2.1.1 Sample Mean

If you have a sample of n values, x_i, the **sample mean** is the sum of the values divided by the number of values:

$$\mu = \frac{1}{n}\sum_i x_i$$

The **mean** is the most basic and important summary statistic. It describes the central tendency of a sample.

There is a small difference!

In [13]:
```
print 'The average age of men is: ', ml['age'].mean(), '.'
print 'The average age of women is: ', fm['age'].mean(), '.'
```

```
The average age of men is:  39.4335474989 .
The average age of women is:  36.8582304336 .
```

This difference in sample means can be considered a first evidence of our hypothesis!

Comment: *Later, we will work with both concepts: the population mean and the sample mean. Do not confuse them! Remember, the first one is the mean of samples taken from the population and the second one is the mean of the whole population.*

In [14]:
```
print 'The average age of high-income men is: ', ml1['age'].mean(), '.'
print 'The average age of high-income women is: ', fm1['age'].mean(), '.'
```

```
The average age of high-income men is:  44.6257880516 .
The average age of high-income women is:  42.1255301103 .
```

2.1.2 Sample Variance

Usually, mean is not a sufficient descriptor of the data, we can do a little better with two numbers: mean and **variance**:

$$\sigma^2 = \frac{1}{n}\sum_i (x_i - \mu)^2$$

Variance σ^2 describes the *spread* of data. The term $(x_i - \mu)$ is called the *deviation from the mean*, so variance is the mean squared deviation.

The square root of variance, σ, is called the **standard deviation.** We define standard deviation because variance is hard to interpret (in the case the units are grams, the variance is in grams squared). Let's get the basic statistics for our example data:

In [15]:
```
ml_mu = ml['age'].mean()
fm_mu = fm['age'].mean()
ml_var = ml['age'].var()
fm_var = fm['age'].var()
ml_std = ml['age'].std()
fm_std = fm['age'].std()
print 'Statistics of age for men: mu:', ml_mu, 'var:', ml_var, 'std:', ml_std
print 'Statistics of age for women: mu:', fm_mu, 'var:', fm_var, 'std:', fm_std
```

```
Statistics of age for men: mu: 39.4335474989 var: 178.773751745 std: 13.3706301925
Statistics of age for women: mu: 36.8582304336 var: 196.383706395 std: 14.0136970994
```

In [16]:
```
ml_mu_hr = ml['hr_per_week'].mean()
fm_mu_hr = fm['hr_per_week'].mean()
ml_var_hr = ml['hr_per_week'].var()
fm_var_hr = fm['hr_per_week'].var()
ml_std_hr = ml['hr_per_week'].std()
fm_std_hr = fm['hr_per_week'].std()
print 'Statistics of hours per week for men: mu:', ml_mu_hr, 'var:', ml_var_hr, 'std:', m
print 'Statistics  of hours per week for women: mu:', fm_mu_hr, 'var:', fm_var_hr, 'std:'
```

```
Statistics of hours per week for men: mu: 42.4280862781 var: 146.888467171 std: 12.1197
552439
Statistics  of hours per week for women: mu: 36.410361155 var: 139.506797 std: 11.81129
95475
```

2.1.3 Sample Median

The statistical median is an order statistic that gives the *middle* value of a sample. It is a value more robust to ouliers.

In [17]:
```
ml_median= ml['age'].median()
fm_median= fm['age'].median()
print "Median age per men and women: ", ml_median, fm_median

ml_median_age= ml1['age'].median()
fm_median_age= fm1['age'].median()
print "Median age per men and women with high-income: ", ml_median_age, fm_median_age
```

```
Median age per men and women:  38.0 35.0
Median age per men and women with high-income:  44.0 41.0
```

In [18]:
```
ml_median_hr= ml['hr_per_week'].median()
fm_median_hr= fm['hr_per_week'].median()
print "Median hours per week per men and women: ", ml_median_hr, fm_median_hr
```

```
Median hours per week per men and women:  40.0 40.0
```

2.1.4 Summarizing the data: Quantiles & Percentiles

Order the sample $\{x_i\}$, then find x_p so that it divides the data into two parts where:

- a fraction p of the data values are less than or equal to x_p and
- the remaining fraction $(1-p)$ are greater than x_p.

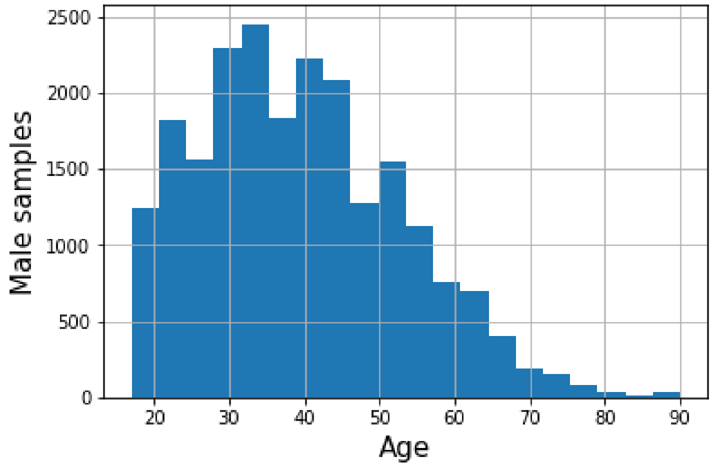
That value x_p is the pth-quantile, or 100×pth percentile.

5-number summary: $x_{min}, Q_1, Q_2, Q_3, x_{max}$, where Q_1 is the 25×pth percentile, Q_2 is the 50×pth percentile and Q_3 is the 75×pth percentile.

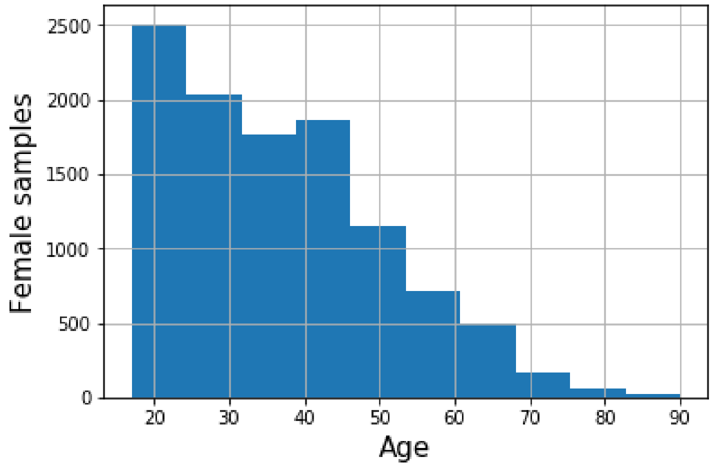
2.2 Histogram

The most common representation of a distribution is a **histogram**, which is a graph that shows the frequency of each value. Let us visualize the histogram for the age of the male and female populations in our example:

In [19]:
```
import matplotlib.pyplot as plt
ml_age=ml['age']
ml_age.hist(normed=0, histtype='stepfilled', bins=20)

plt.xlabel('Age',fontsize=15)
plt.ylabel('Male samples',fontsize=15)
plt.show()
```

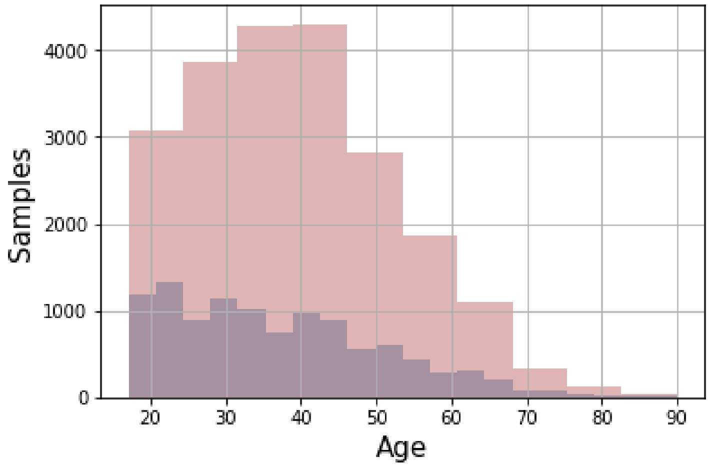


In [20]:
```
fm_age=fm['age']

fm_age.hist(normed=0, histtype='stepfilled', bins=10)
plt.xlabel('Age',fontsize=15)
plt.ylabel('Female samples',fontsize=15)
plt.show()
```

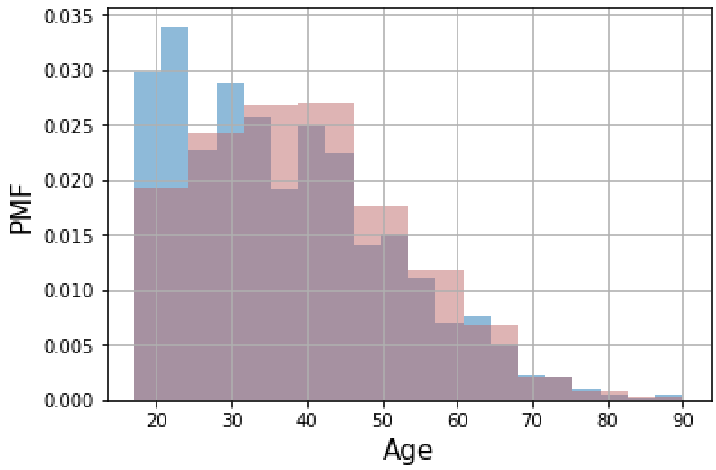


Let's compare both populations:

In [21]:
```
import seaborn as sns
fm_age.hist(normed=0, histtype='stepfilled', alpha=.5, bins=20)   # default number of bir
ml_age.hist(normed=0, histtype='stepfilled', alpha=.5, color=sns.desaturate("indianred",
plt.xlabel('Age',fontsize=15)
plt.ylabel('Samples',fontsize=15)
plt.show()
```



In [22]:
```
fm_age.hist(normed=1, histtype='stepfilled', alpha=.5, bins=20)   # default number of bir
ml_age.hist(normed=1, histtype='stepfilled', alpha=.5, color=sns.desaturate("indianred",
plt.xlabel('Age',fontsize=15)
plt.ylabel('PMF',fontsize=15)
plt.show()
```



In [23]:
```
import scipy.stats as stats
```

2.3 Data Distributions

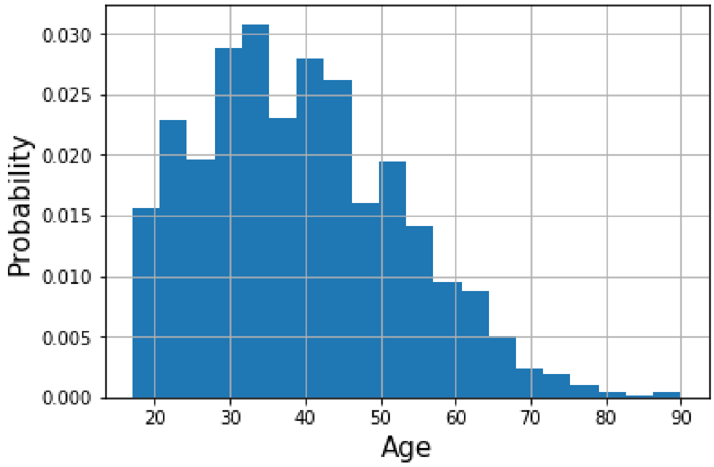
Summarizing can be dangerous: very different data can be described by the same statistics. It must be validated by inspecting the data.

We can look at the **data distribution**, which describes how often (frequency) each value appears.

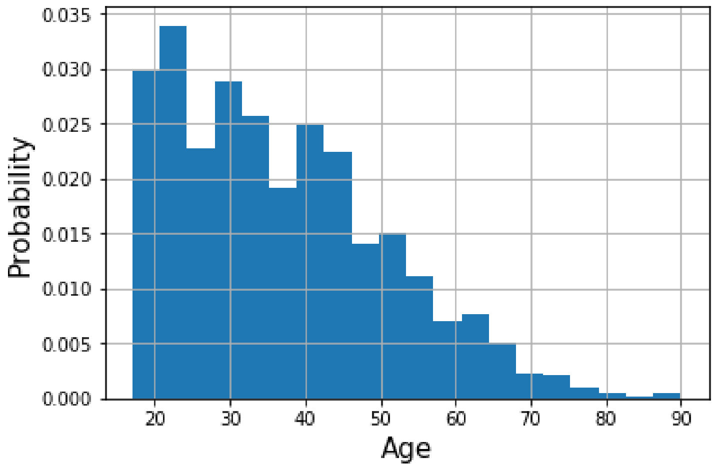
We can normalize the frequencies of the histogram by dividing/normalizing by n, the number of samples. The normalized histogram is called **Probability Mass Function (PMF)**.

Let's visualize and compare the MPF of male and female age in our example:

In [24]:
```
ml_age.hist(normed=1, histtype='stepfilled', bins=20)
plt.xlabel('Age',fontsize=15)
plt.ylabel('Probability',fontsize=15)
plt.show()
```

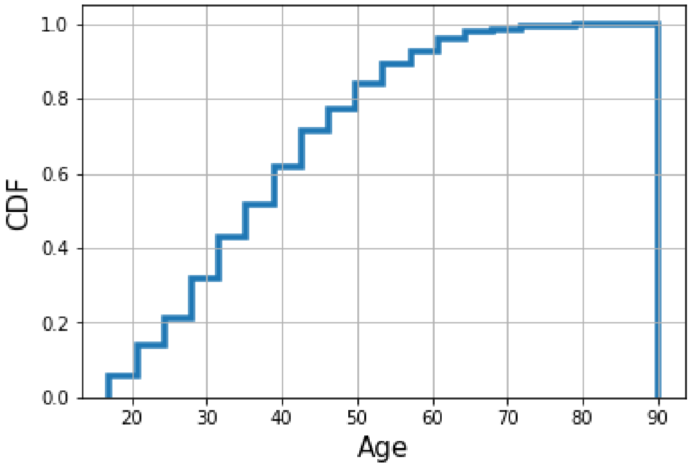


In [25]:
```
fm_age.hist(normed=1, histtype='stepfilled', bins=20)
plt.xlabel('Age',fontsize=15)
plt.ylabel('Probability',fontsize=15)
plt.show()
```

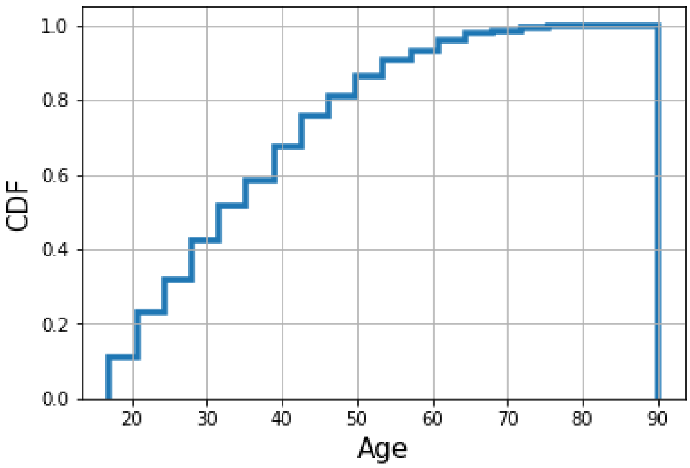


The **cumulative distribution function (CDF)**, or just distribution function, describes the probability that a real-valued random variable X with a given probability distribution will be found to have a value less than or equal to x. For our example, the CDFs will be:

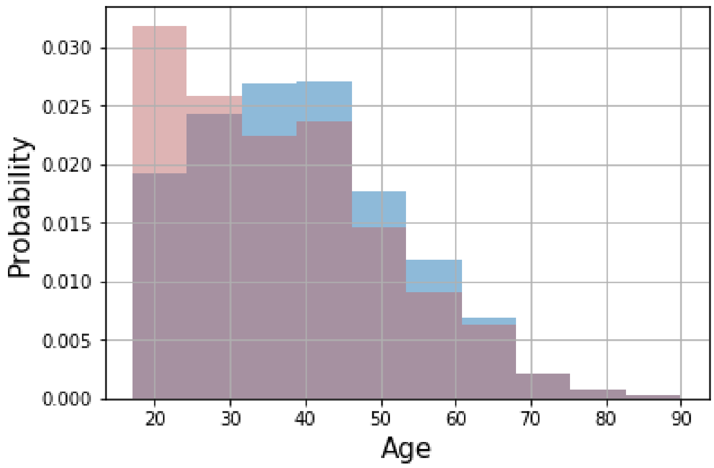
In [26]:
```
ml_age.hist(normed=1, histtype='step', cumulative=True, linewidth=3.5, bins=20)
plt.xlabel('Age',fontsize=15)
plt.ylabel('CDF',fontsize=15)
plt.show()
```



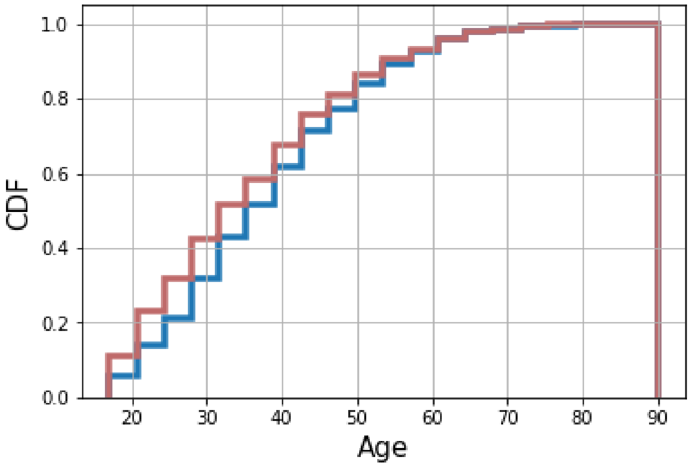
In [27]:
```
fm_age.hist(normed=1, histtype='step', cumulative=True, linewidth=3.5, bins=20)
plt.xlabel('Age',fontsize=15)
plt.ylabel('CDF',fontsize=15)
plt.show()
```



In [28]:
```
ml_age.hist(bins=10, normed=1, histtype='stepfilled', alpha=.5)   # default number of bir
fm_age.hist(bins=10, normed=1, histtype='stepfilled', alpha=.5, color=sns.desaturate("inc
plt.xlabel('Age',fontsize=15)
plt.ylabel('Probability',fontsize=15)
plt.show()
```



In [29]:
```
ml_age.hist(normed=1, histtype='step', cumulative=True,  linewidth=3.5, bins=20)
fm_age.hist(normed=1, histtype='step', cumulative=True,  linewidth=3.5, bins=20, color=sr
plt.xlabel('Age',fontsize=15)
plt.ylabel('CDF',fontsize=15)
plt.show()
```



In [30]:
```
print "The mean sample difference is ", ml_age.mean() - fm_age.mean()
```

```
The mean sample difference is  2.57531706528
```

2.4 Outliers

Ouliers are data samples with a value that is far from the central tendency.

We can find outliers by:

- Computing samples that are *far* from the median.
- Computing samples whose value *exceeds the mean* by 2 or 3 standard deviations.

This expression will return a series of boolean values that you can then index the series by:

In [31]:
```
df['age'].median()
```

Out[31]: 37.0

Let's see how many outliers we can detect in our example:

In [32]:
```
len(df[(df.income == '>50K\n') & (df['age'] < df['age'].median() - 15)])
```

Out[32]: 5

In [33]:
```
len(df[(df.income == '>50K\n') & (df['age'] > df['age'].median() + 35)])
```

Out[33]: 69

If we think that outliers correspond to errors, an option is to trim the data by discarding the highest and lowest values.

In [34]:
```
df2 = df.drop(df.index[(df.income=='>50K\n') & (df['age']>df['age'].median() + 35) & (df[
df2.shape
```

Out[34]: (32492, 15)

In [35]:
```
ml1_age=ml1['age']
fm1_age=fm1['age']

ml2_age = ml1_age.drop(ml1_age.index[(ml1_age > df['age'].median() + 35) & (ml1_age > df[
fm2_age = fm1_age.drop(fm1_age.index[(fm1_age > df['age'].median() + 35) & (fm1_age > df[
```

In [36]:
```
mu2ml = ml2_age.mean()
std2ml = ml2_age.std()
md2ml = ml2_age.median()
# Computing the mean, std, median, min and max for the high-income male population
print "Men statistics: Mean:", mu2ml, "Std:", std2ml, "Median:", md2ml, "Min:", ml2_age.m
```

```
Men statistics: Mean: 44.3179821239 Std: 10.0197498572 Median: 44.0 Min: 19 Max: 72
```

In [37]:
```
mu3ml = fm2_age.mean()
std3ml = fm2_age.std()
md3ml = fm2_age.median()
# Computing the mean, std, median, min and max for the high-income female population
print "Women statistics: Mean:", mu2ml, "Std:", std2ml, "Median:", md2ml, "Min:", fm2_age
```

```
Women statistics: Mean: 44.3179821239 Std: 10.0197498572 Median: 44.0 Min: 19 Max: 72
```

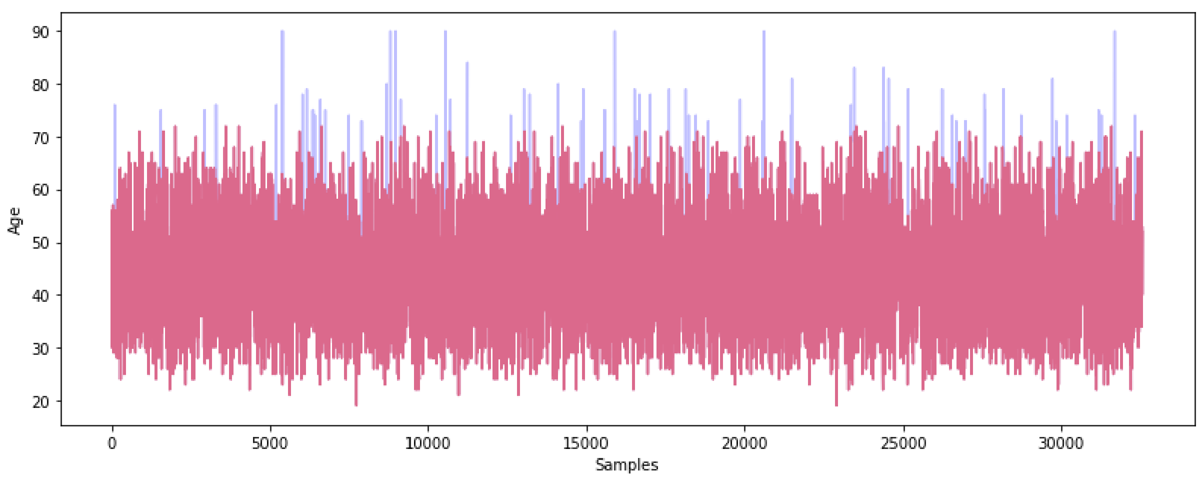
In [38]:
```
print 'The mean difference with outliers is: %4.2f.' % (ml_age.mean() - fm_age.mean())
print "The mean difference without outliers is: %4.2f." % (ml2_age.mean() - fm2_age.mean(
```

```
The mean difference with outliers is: 2.58.
The mean difference without outliers is: 2.44.
```

Let's compare visually the age distributions before and after removing the outliers:

In [39]:
```
plt.figure(figsize=(13.4,5))

df.age[(df.income == '>50K\n')].plot(alpha=.25, color='blue')
df2.age[(df2.income == '>50K\n')].plot(alpha=.45,color='red')

plt.ylabel('Age')
plt.xlabel('Samples')
```

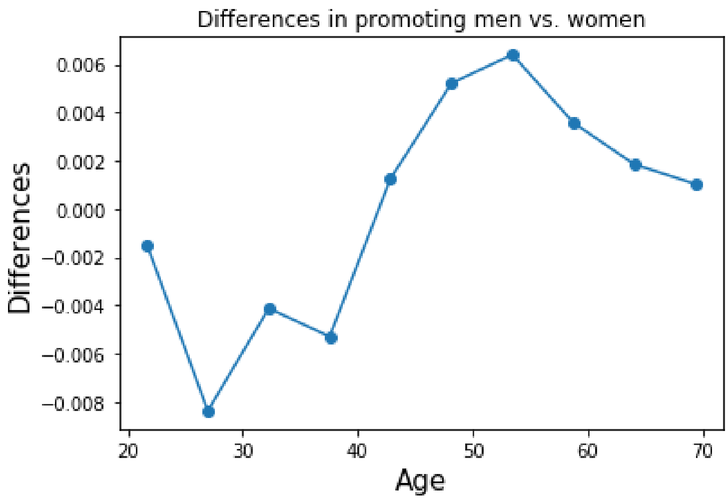
Out[39]:
```
Text(0.5,0,u'Samples')
```



Let's see what is happening near the mode:

In [40]:
```
import numpy as np

countx,divisionx = np.histogram(ml2_age, normed=True)
county,divisiony = np.histogram(fm2_age, normed=True)
```

In [41]:
```
import matplotlib.pyplot as plt

val = [(divisionx[i]+divisionx[i+1])/2 for i in range(len(divisionx)-1)]
plt.plot(val, countx-county, 'o-')
plt.title('Differences in promoting men vs. women')
plt.xlabel('Age',fontsize=15)
plt.ylabel('Differences',fontsize=15)
plt.show()
```



There is still some evidence for our hypothesis!

In [42]:
```
print "Remember:\n We have the following mean values for men, women and the difference:\r
print "For high-income: ", ml1_age.mean(), fm1_age.mean(), ml1_age.mean()- fm1_age.mean()
print "After cleaning: ", ml2_age.mean(), fm2_age.mean(), ml2_age.mean()- fm2_age.mean()

print "\nThe same for the median:"
print ml_age.median(), fm_age.median(), ml_age.median()- fm_age.median() # The difference
print ml1_age.median(), fm1_age.median(), ml1_age.median()- fm1_age.median() # The differ
print ml2_age.median(), fm2_age.median(), ml2_age.median()- fm2_age.median(), # The diffe
```

```
Remember:
 We have the following mean values for men, women and the difference:
Originally:  39.4335474989 36.8582304336 2.57531706528
For high-income:  44.6257880516 42.1255301103 2.50025794137
After cleaning:  44.3179821239 41.877028181 2.44095394288

The same for the median:
38.0 35.0 3.0
44.0 41.0 3.0
44.0 41.0 3.0
```

2.5 Measuring asymmetry (optional).

Skewness is a statistic that measures the asymmetry of set of n data samples x_i:

$$g_1 = \frac{\frac{1}{n}\sum_i (x_i - \mu)^2}{\frac{1}{n}\sum_i (x_i - \mu)^3}$$

The numerator is the mean squared deviation (or variance) and the denominator the mean cubed deviation.

Negative deviation indicates that the distribution "skews left" (it extends farther to the left than to the right).

Skewness can be affected by outliers!!! A simpler alternative is to look at the relationship between mean (μ) and median ($\mu_{\frac{1}{2}}$).

In [ ]:

In [43]:
```
def skewness(x):
    res=0
    m=x.mean()
    s=x.std()
    for i in x:
        res+=(i-m)*(i-m)*(i-m)
    res/=(len(x)*s*s*s)
    return res

print "The skewness of the male population is:", skewness(ml2_age)
print "The skewness of the female population is:", skewness(fm2_age)
```

```
The skewness of the male population is: 0.266444383843
The skewness of the female population is: 0.386333524913
```

2.6 Pearson's median skewness coefficient is a more robust alternative:

$$g_p = \frac{3(\mu - \mu_{\frac{1}{2}})}{\sigma}$$

Exercise: Write a function to compute g_1 and g_p of the pregnancy length.

In [44]:
```
def pearson(x):
    return 3*(x.mean()-x.median())*x.std()

print "The Pearson's coefficient of the male population is:", pearson(ml2_age)
print "The Pearson's coefficient of the female population is:", pearson(fm2_age)
```

```
The Pearson's coefficient of the male population is: 9.55830402221
The Pearson's coefficient of the female population is: 26.4067269073
```

2.6 Relative Risk

Let's say that a person is "early" promoted if he/she is promoted before the age of 41, "on time" if he/she is promoted of age 41, 42, 43 or 44, and "late" promoted if he/she is ascended to get income bigger than 50K after being 44 years old. Let us compute the probability of being early, on time and late promoted for men and women:

In [45]:
```
#ml1 = df[(df.sex == 'Male')&(df.income=='>50K\n')]

ml2 = ml1.drop(ml1.index[(ml1['age'] > df['age'].median() + 35) & (ml1['age'] > df['age']
fm2 = fm1.drop(fm1.index[(fm1['age'] > df['age'].median() + 35) & (fm1['age'] > df['age']

print ml2.shape, fm2.shape
```

```
(6601, 15) (1171, 15)
```

In [46]:
```
print "Men grouped in 3 categories:"
print "Young:",int(round(100*len(ml2_age[ml2_age<41])/float(len(ml2_age.index)))),"%."
print "Elder:", int(round(100*len(ml2_age[ml2_age >44])/float(len(ml2_age.index)))),"%."
print "Average age:", int(round(100*len(ml2_age[(ml2_age>40) & (ml2_age< 45)])/float(len(
```

```
Men grouped in 3 categories:
Young: 38 %.
Elder: 48 %.
Average age: 14 %.
```

In [47]:
```
print "Women grouped in 3 categories:"
print "Young:",int(round(100*len(fm2_age[fm2_age <41])/float(len(fm2_age.index)))),"%."
print "Elder:", int(round(100*len(fm2_age[fm2_age >44])/float(len(fm2_age.index)))),"%."
print "Average age:", int(round(100*len(fm2_age[(fm2_age>40) & (fm2_age< 45)])/float(len(
```

```
Women grouped in 3 categories:
Young: 48 %.
Elder: 37 %.
Average age: 15 %.
```

The **relative risk** is the ratio of two probabilities. In order to get the relative risk \cite{Downey} of early promotion, we need to consider the fraction of both probabilities.

In [48]:
```
print "The male mean:", ml2_age.mean()
print "The female mean:", fm2_age.mean()
```

```
The male mean: 44.3179821239
The female mean: 41.877028181
```

In [49]:
```
ml2_young = len(ml2_age[(ml2_age<41)])/float(len(ml2_age.index))
fm2_young  = len(fm2_age[(fm2_age<41)])/float(len(fm2_age.index))
print "The relative risk of female early promotion is: ", 100*(1-ml2_young/fm2_young)
```

```
The relative risk of female early promotion is:  21.1254400822
```

That means that women are 21% more likely to get high gains before 41 years than men.

In [50]:
```
ml2_elder = len(ml2_age[(ml2_age>44)])/float(len(ml2_age.index))
fm2_elder  = len(fm2_age[(fm2_age>44)])/float(len(fm2_age.index))
print "The relative risk of male late promotion is: ", 100*ml2_elder/fm2_elder
```

```
The relative risk of male late promotion is:  128.971570897
```

That means that men are 29% more likely to get high gains after 44 years than women.

Discussions.

After exploring the data, we obtained some apparent effects that seem to support our first assumption:

- **Data description:** The mean age for ascending male professionals is 44 years old while for female professionals it is 41 years.
- **Relative risk:** Female professionals are 21% more likely to be ascended before 41 years of age, while men are 29% more likely to be ascended being at least 45 years old.

3.4 Continous distributions

So far, we have built **empirical distributions** (which represent the distributions of values in a sample), based on observations, but many real problems are well approximated by fitting **continous distributions functions (CDF)**.

They are called in this way because the distribution is described by an analytical continous function.

3.4.1 The exponential distribution

The CDF of the exponential distribution is:

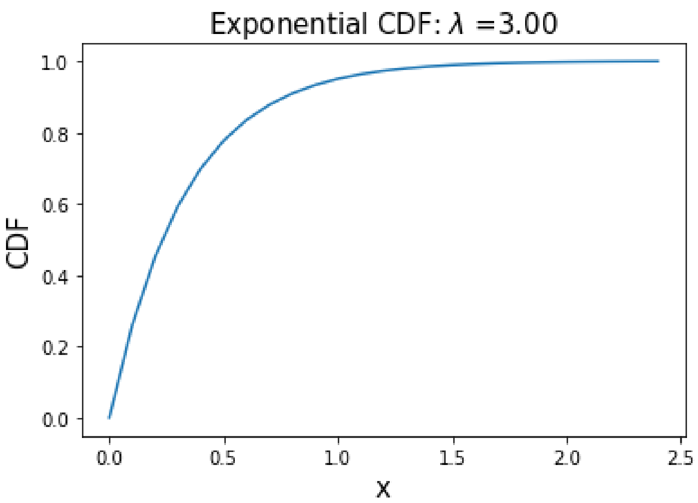
$$CDF(x) = 1 - \exp^{-\lambda x}$$

And its PDF is:

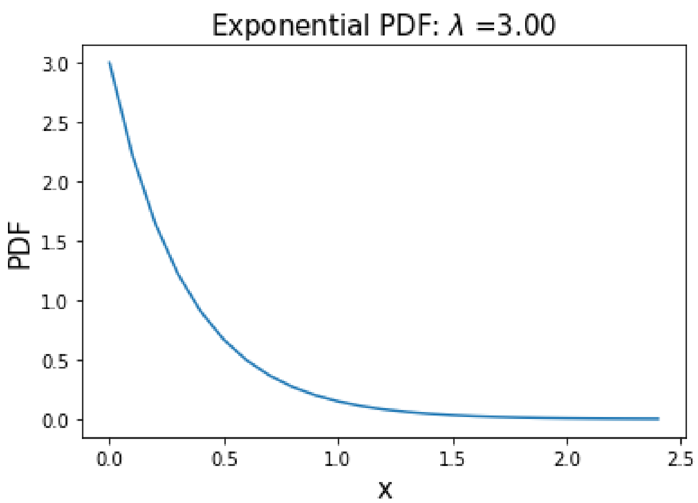
$$PDF(x) = \lambda \exp^{-\lambda x}$$

The parameter λ determines the shape of the distribution, the mean of the distribution is $1/\lambda$ and its variance is $1/\lambda^2$. The median is $ln(2)/\lambda$.

In [51]:
```
l = 3
x=np.arange(0,2.5,0.1)
y= 1 - np.exp(-l*x)
plt.plot(x,y,'-')
plt.title('Exponential CDF: $\lambda$ =%.2f' % l ,fontsize=15)
plt.xlabel('x',fontsize=15)
plt.ylabel('CDF',fontsize=15)
plt.show()
```



In [52]:
```
from __future__ import division

import scipy.stats as stats
i

l = 3
x=np.arange(0,2.5,0.1)
y= l * np.exp(-l*x)
plt.plot(x,y,'-')
plt.title('Exponential PDF: $\lambda$ =%.2f' % l, fontsize=15)
plt.xlabel('x', fontsize=15)
plt.ylabel('PDF', fontsize=15)
plt.show()
```



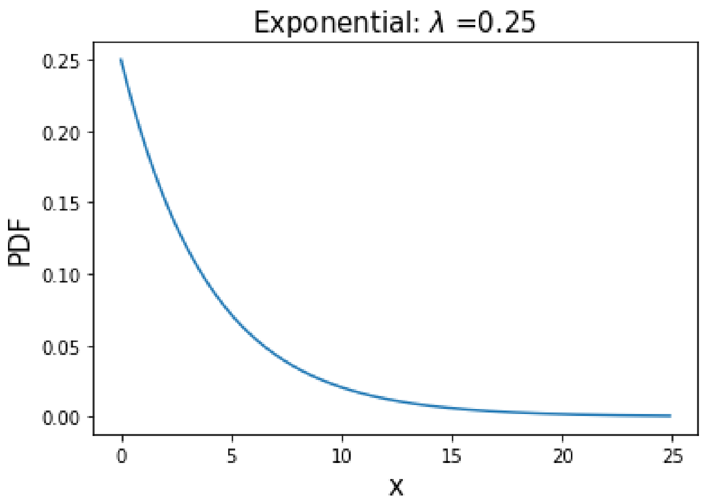
There are a lot of real world events that can be described with this distribution.

- The time until a radioactive particle decays,
- The time it takes before your next telephone call,
- The time until default (on payment to company debt holders) in reduced form credit risk modeling.

The random variable X of the lifelengths of some batteries is associated with a probability density function of the form:

$$PDF(x) = \frac{1}{4}\exp^{-\frac{x}{4}}$$

In [53]:
```
l = 0.25
x=np.arange(0,25,0.1)
y= l * np.exp(-l*x)
plt.plot(x,y,'-')
plt.title('Exponential: $\lambda$ =%.2f' % l ,fontsize=15)
plt.xlabel('x',fontsize=15)
plt.ylabel('PDF',fontsize=15)
plt.show()
```



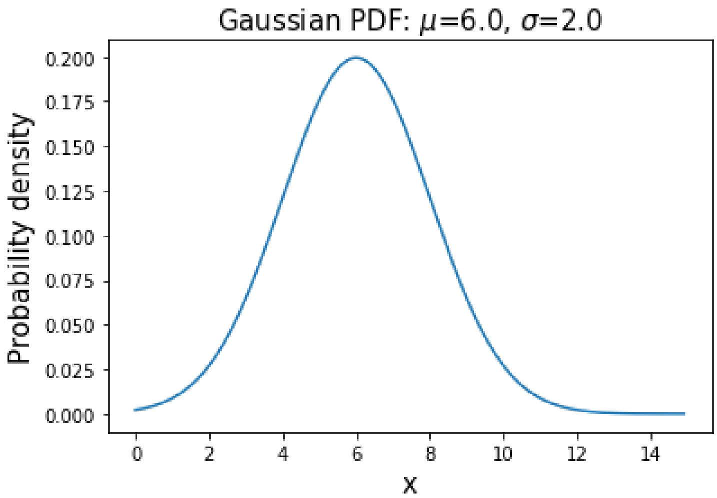
3.4.2 The normal distribution

The **normal, or Gaussian distribution** is the most used one because it describes a lot of phenomena and because it is amenable for analysis.

Its CDF has no closed-form expression and its more common representation is the PDF:

$$PDF(x) = \frac{1}{\sqrt{2\pi\sigma^2}}\exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right)$$

In [54]:
```
u=6 # mean
s=2 # standard deviation
x=np.arange(0,15,0.1)
y=(1/(np.sqrt(2*np.pi*s*s)))*np.exp(-(((x-u)**2)/(2*s*s)))
plt.plot(x,y,'-')
plt.title('Gaussian PDF: $\mu$=%.1f, $\sigma$=%.1f' % (u,s),fontsize=15)
plt.xlabel('x',fontsize=15)
plt.ylabel('Probability density',fontsize=15)
plt.show()
```



Examples:

```
* Measures of size of living tissue (length, height, skin area, weight);
* The length of inert appendages (hair, claws, nails, teeth) of biological speci
mens, in the direction of growth; presumably the thickness of tree bark also fal
ls under this category;
* Certain physiological measurements, such as blood pressure of adult humans.
```

3.5 Central Limit Theorem

The normal distribution is also important, because it is involved in the Central Limit Theorem:

> Take the mean of n random samples from ANY arbitrary distribution with a $well\ defined$ standard deviation σ and mean μ. As n gets bigger the **distribution of the sample mean** will always converge to a Gaussian (normal) distribution with mean μ and standard deviation $\frac{\sigma}{\sqrt{n}}$.

Colloquially speaking, the theorem states the distribution of an average tends to be normal, even when the distribution from which the average is computed is decidedly non-normal. This explains the ubiquity of the Gaussian distribution in science and statistics.

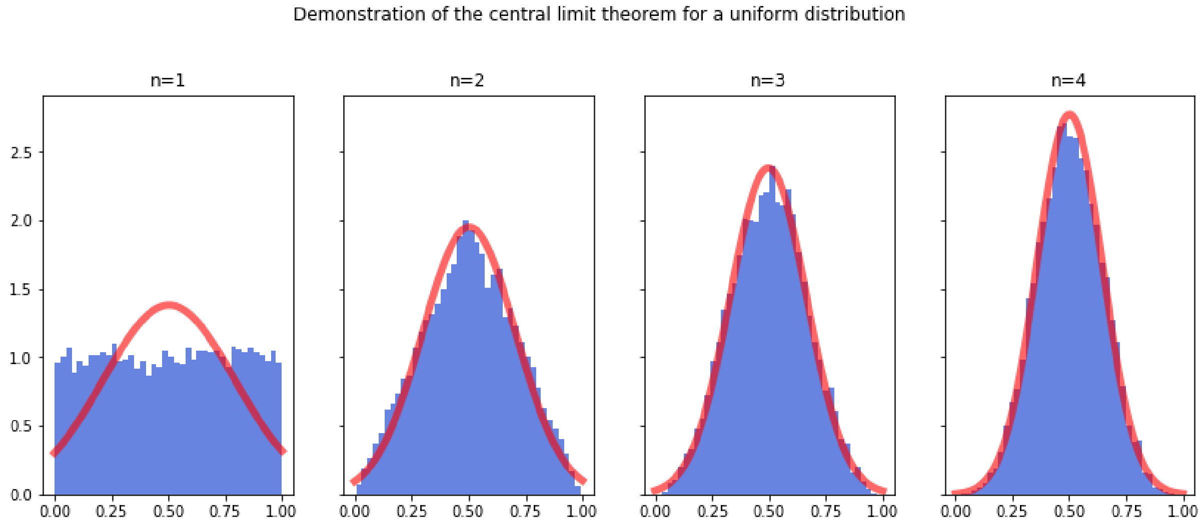
Example: Uniform Distribution

The uniform distribution is obviously non-normal. Let's call it the $parent\ distribution$.

To compute an average, two samples are drawn ($n = 2$), at random, from the parent distribution and averaged. Then another sample of two is drawn and another value of the average computed. This process is repeated, over and over, and averages of two are computed.

Repeatedly taking more elements ($n = 3, 4...$) from the parent distribution, and computing the averages, produces a normal probability density.

In [55]:
```
fig, ax = plt.subplots(1, 4, sharey=True, squeeze=True, figsize=(14, 5))
x = np.linspace(0, 1, 100)
for i in range(4):
    f = np.mean(np.random.random((10000, i+1)), 1)
    m, s = np.mean(f), np.std(f, ddof=1)
    fn = (1/(s*np.sqrt(2*np.pi)))*np.exp(-(x-m)**2/(2*s**2))  # normal pdf
    ax[i].hist(f, 40, normed=True, color=[0, 0.2, .8, .6])
    ax[i].set_title('n=%d' %(i+1))
    ax[i].plot(x, fn, color=[1, 0, 0, .6], linewidth=5)
plt.suptitle('Demonstration of the central limit theorem for a uniform distribution', y=1
plt.show()
```

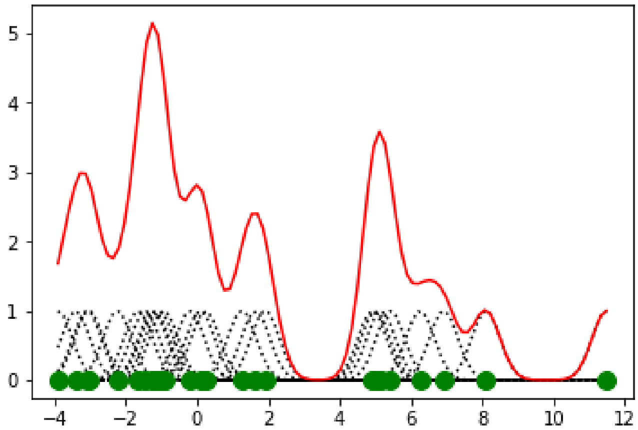


3.6 Kernel density estimates

In some instances, we may not be interested in the parameters of a particular distribution of data, but just a **continous representation** of the data at hand. In this case, we can estimate the distribution non-parametrically (i.e. making no assumptions about the form of the underlying distribution) using kernel density estimation.

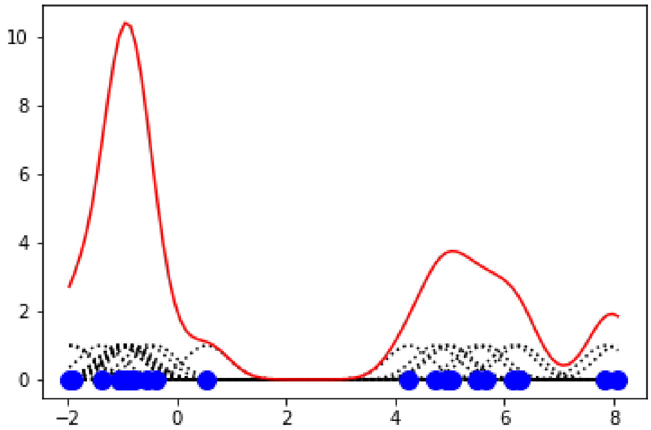
In [56]:
```
from scipy.stats.distributions import norm

# Some random data
y = np.random.random(15) * 10
x = np.linspace(0, 10, 100)

x1 = np.random.normal(-1, 2, 15) # parameters: (loc=0.0, scale=1.0, size=None)
x2 = np.random.normal(6, 3, 10)
y = np.r_[x1, x2] # r_ Translates slice objects to concatenation along the first axis.
x = np.linspace(min(y), max(y), 100)


# Smoothing parameter
s = 0.4

# Calculate the kernels
kernels = np.transpose([norm.pdf(x, yi, s) for yi in y])

plt.plot(x, kernels, 'k:')
plt.plot(x, kernels.sum(1), 'r')
plt.plot(y, np.zeros(len(y)), 'go', ms=10)
```

Out[56]:
```
[<matplotlib.lines.Line2D at 0x136241d0>]
```



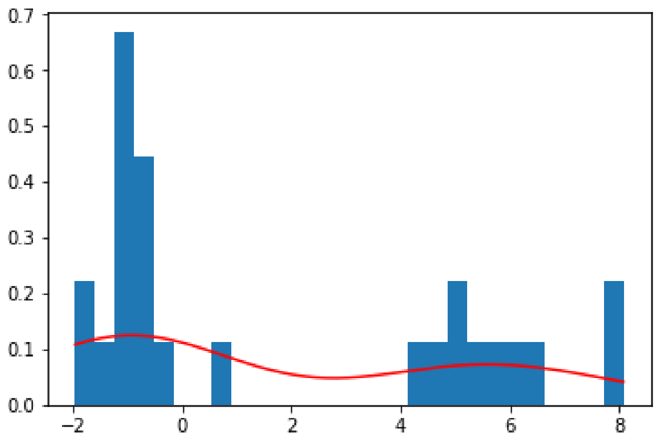
In [57]:
```
from scipy.stats import kde

x1 = np.random.normal(-1, 0.5, 15) # parameters: (loc=0.0, scale=1.0, size=None)
x2 = np.random.normal(6, 1, 10)
y = np.r_[x1, x2] # r_ Translates slice objects to concatenation along the first axis.
x = np.linspace(min(y), max(y), 100)

s = 0.4 # Smoothing parameter

kernels = np.transpose([norm.pdf(x, yi, s) for yi in y]) # Calculate the kernels
density = kde.gaussian_kde(y)

plt.plot(x, kernels, 'k:')
plt.plot(x, kernels.sum(1), 'r')
plt.plot(y, np.zeros(len(y)), 'bo', ms=10)
```

Out[57]:
```
[<matplotlib.lines.Line2D at 0x13891ac8>]
```



In [58]:
```
xgrid = np.linspace(x.min(), x.max(), 200)
plt.hist(y, bins=28, normed=True)
plt.plot(xgrid, density(xgrid), 'r-')
```

Out[58]:
```
[<matplotlib.lines.Line2D at 0x112ea748>]
```

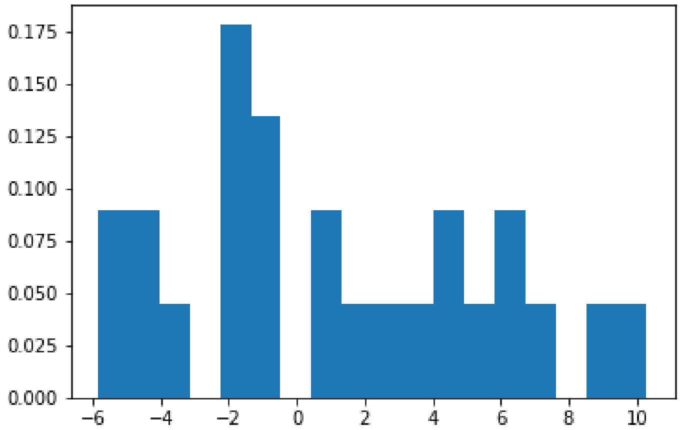


SciPy implements a Gaussian KDE that automatically chooses an appropriate bandwidth. Let's create a bi-modal distribution of data that is not easily summarized by a parametric distribution:

In [60]:
```
# Create a bi-modal distribution with a mixture of Normals.
x1 = np.random.normal(-1, 2, 15) # parameters: (loc=0.0, scale=1.0, size=None)
x2 = np.random.normal(6, 3, 10)

# Append by row
x = np.r_[x1, x2] # r_ Translates slice objects to concatenation along the first axis.
```

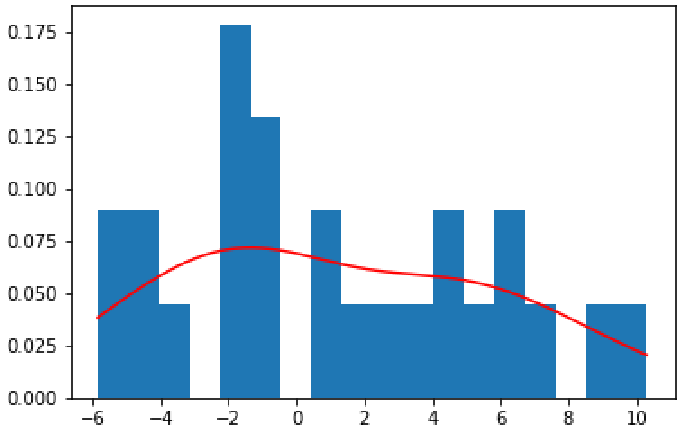
In [61]:
```
plt.hist(x, bins=18, normed=True)
```

Out[61]:
```
(array([ 0.08920786,  0.08920786,  0.04460393,  0.        ,  0.17841571,
         0.13381178,  0.        ,  0.08920786,  0.04460393,  0.04460393,
         0.04460393,  0.08920786,  0.04460393,  0.08920786,  0.04460393,
         0.        ,  0.04460393,  0.04460393]),
 array([ -5.83994087,  -4.94315887,  -4.04637686,  -3.14959486,
         -2.25281285,  -1.35603085,  -0.45924884,   0.43753316,
          1.33431517,   2.23109717,   3.12787918,   4.02466118,
          4.92144319,   5.81822519,   6.7150072 ,   7.6117892 ,
          8.50857121,   9.40535321,  10.30213522]),
 <a list of 18 Patch objects>)
```



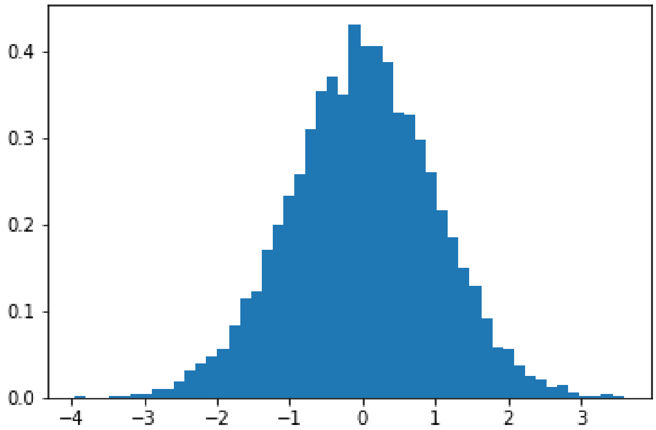
In [62]:
```
density = kde.gaussian_kde(x)
xgrid = np.linspace(x.min(), x.max(), 200)
plt.hist(x, bins=18, normed=True)
plt.plot(xgrid, density(xgrid), 'r-')
```

Out[62]:
```
[<matplotlib.lines.Line2D at 0x10c49ac8>]
```



4 Estimation

In [63]:
```
x = np.random.normal(0.0, 1.0, 10000)
a = plt.hist(x,50,normed='True')
```



Definition: *Estimation* is the process of inferring the parameters (e.g. mean) of a distribution from a statistic of samples drown from a population.

For example: What is the estimated mean $\hat{\mu}$ of the following normal data?

We can use our definition of empirical mean:

In [64]:
```
print 'The empirical mean of the sample is ', x.mean()
```

```
The empirical mean of the sample is  0.0059001026532
```

4.1 Sample mean

- The process is called **estimation** and the statistic we used **estimator**.
- The median is also an estimator (more robust to outliers).
- "Is median better than sample mean?" is a question with at least two different answers. We can use two different objectives to answer this question: the minimization of error or the maximization to get the right answer.
- If there are no outliers, we can use the **sample mean** to minimize **mean squared error** (where m is the number of times you play the estimation game, not the size of the sample!):

$$MSE = \frac{1}{m}\sum(\hat{\mu} - \mu)^2$$

In [65]:
```
NTs=200
mu=0.0
var=1.0
err = 0.0
NPs=1000
for i in range(NTs):
    x = np.random.normal(mu, var, NPs)
    err += (x.mean()-mu)**2

print 'MSE: ', err/NTs
```

```
MSE:  0.00107615617685
```

4.2 Variance

We can also estimate the variance with:

$$\hat{\sigma}^2 = \frac{1}{n}\sum_i (x_i - \mu)^2$$

This estimator works for large samples, but it is biased for small samples. We can use this one:

$$\hat{\sigma}^2_{n-1} = \frac{1}{n-1}\sum_i (x_i - \mu)^2$$

4.3 Other concepts: Standard scores

$$z_i = \frac{x_i - \mu}{\sigma}$$

This measure is dimensionless and its distribution has mean 0 and variance 1.

It inherits the "shape" of X: if it is normally distributed, so is Z. If X is skewed, so is Z.

4.4 Covariance

Covariance is a measure of the tendency of two variables to vary together.

If we have two series X and Y with $X = \{x_i\}$ and $Y = \{y_i\}$, and they vary together, their deviations $x_i - \mu_X$ and $y_i - \mu_Y$ tend to have the same sign.

If we multiply them together, the product is positive, when the deviations have the same sign, and negative, when they have the opposite sign. So adding up the products gives a measure of the tendency to vary together.

Covariance is the mean of the products:

$$Cov(X, Y) = \frac{1}{n}\sum_{i=1}^{n}(x_i - \mu_X) * (y_i - \mu_Y),$$

where n is the length of the two series.

It is a measure that is difficult to interpret.

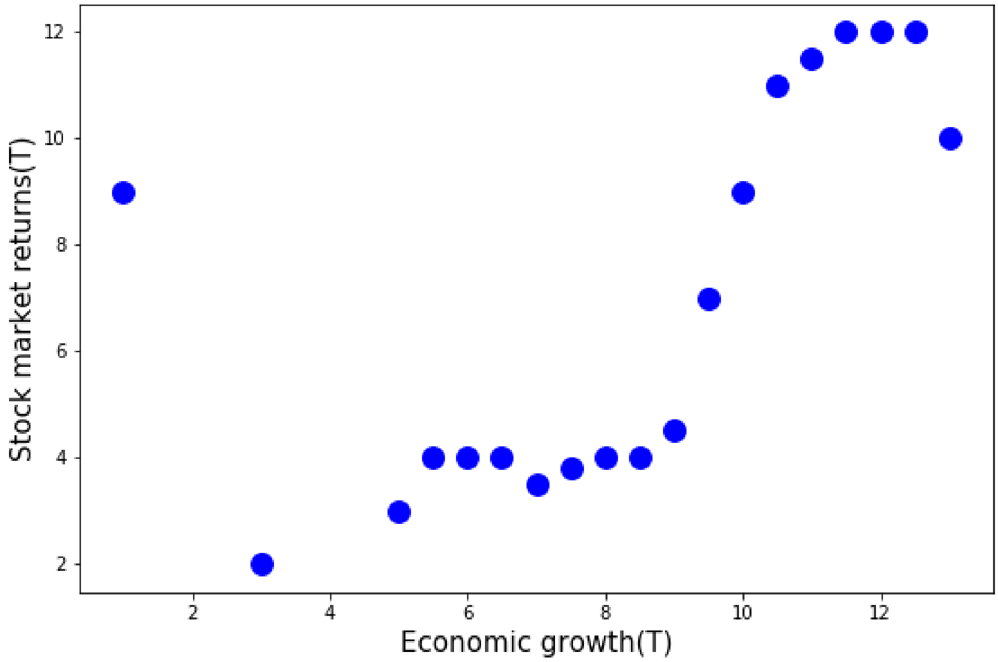
In [66]:
```
def Cov(X, Y):
    def _get_dvis(V):
        return [v - np.mean(V) for v in V]
    dxis = _get_dvis(X)
    dyis = _get_dvis(Y)
    return np.sum([x * y for x, y in zip(dxis, dyis)])/len(X)


X = [5, -1, 3.3, 2.7, 12.2]
X= np.array(X)
Y = [10, 12, 8, 9, 11]

print "Cov(X, X) = %.2f" % Cov(X, X)
print "Var(X) = %.2f" % np.var(X)

print "Cov(X, Y) = %.2f" % Cov(X, Y)
```

```
Cov(X, X) = 18.89
Var(X) = 18.89
Cov(X, Y) = 0.18
```

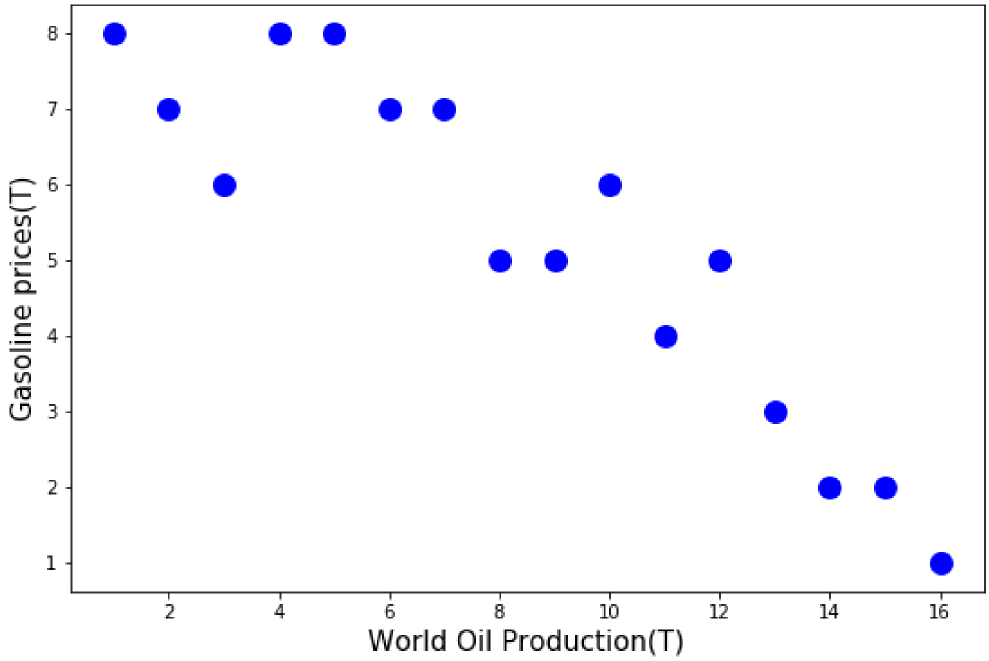
Let us create some examples of positive and negative correlations like those showing the relations of stock market with respect to the economic growth or the gasoline prices with respect to the world oil production:

In [67]:
```
MAXN=100

MAXN=40
X=np.array([[1,9],[3, 2], [5,3],[5.5,4],[6,4],[6.5,4],[7,3.5],[7.5,3.8],[8,4],
            [8.5,4],[9,4.5],[9.5,7],[10,9],[10.5,11],[11,11.5],[11.5,12],[12,12],[12.5,12
```

In [68]:
```
plt.subplot(1,2,1)
plt.scatter(X[:,0],X[:,1],color='b',s=120, linewidths=2,zorder=10)
plt.xlabel('Economic growth(T)',fontsize=15)
plt.ylabel('Stock market returns(T)',fontsize=15)
plt.gcf().set_size_inches((20,6))
```



In [69]:
```
X=np.array([[1,8],[2, 7], [3,6],[4,8],[5,8],[6,7],[7,7],[8,5],[9,5],[10,6],[11,4],[12,5],
plt.subplot(1,2,1)
plt.scatter(X[:,0],X[:,1],color='b',s=120, linewidths=2,zorder=10)
plt.xlabel('World Oil Production(T)',fontsize=15)
plt.ylabel('Gasoline prices(T)',fontsize=15)
plt.gcf().set_size_inches((20,6))
```



4.5 Pearson's Correlation

Shell we take into account the variance? An alternative is to divide the deviations by σ, which yields standard scores, and compute the product of standard scores:

$$p_i = \frac{(x_i - \mu_X)}{\sigma_X} \frac{(y_i - \mu_Y)}{\sigma_Y}$$

The mean of these products is:

$$\rho = \frac{1}{n} \sum p_i = \frac{1}{n} \sum \frac{(x_i - \mu_X)}{\sigma_X} \frac{(y_i - \mu_Y)}{\sigma_Y}$$

Or we can rewrite ρ by factoring out σ_X and σ_Y:

$$\rho = \frac{Cov(X, Y)}{\sigma_X \sigma_Y}$$

In [70]:
```
def Corr(X, Y):
    assert len(X) == len(Y)
    return Cov(X, Y) / np.prod([np.std(V) for V in [X, Y]])

print "Corr(X, X) = %.5f" % Corr(X, X)

Y=np.random.random(len(X))

print "Corr(X, Y) = %.5f" % Corr(X, Y)
```

```
Corr(X, X) = 2.00000
Corr(X, Y) = 0.26278
```

When $\rho = 0$, we cannot say that there is no relationship between the variables!

Pearson's coefficient only measures **linear** correlations!

4.6 Spearman’s rank correlation

Pearson’s correlation works well if the relationship between variables is linear and if the variables are roughly normal. But it is not robust in the presence of **outliers**.

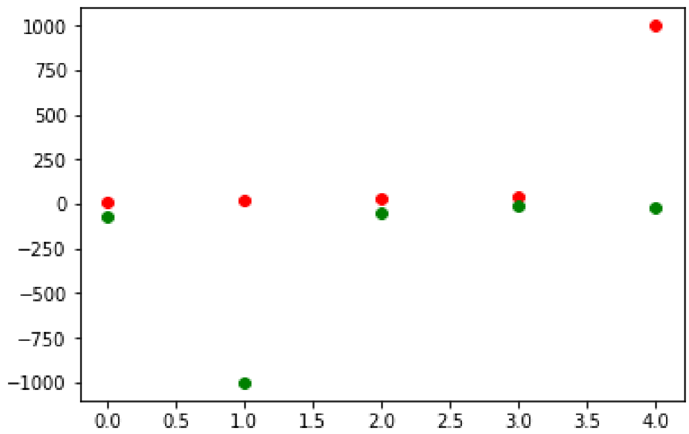
Spearman’s rank correlation is an alternative that mitigates the effect of outliers and skewed distributions. To compute Spearman’s correlation, we have to compute the rank of each value, which is its index in the sorted sample.

For example, in the sample {7, 1, 2, 5} the rank of the value 5 is 3, because it appears third if we sort the elements.

Then, we compute the Pearson’s correlation, **but for the ranks**.

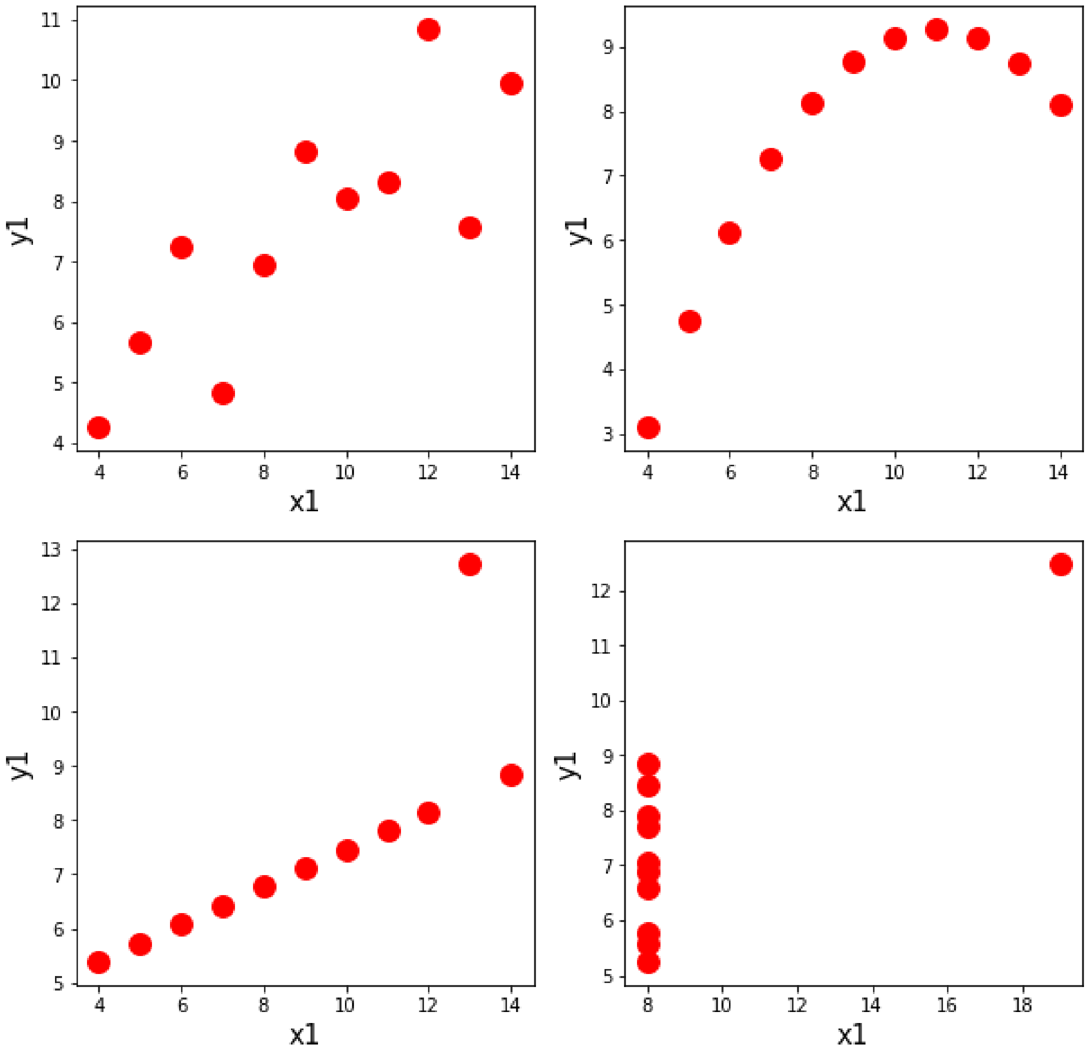
In [71]:
```
def list2rank(l):
    #l is a list of numbers
    # returns a list of 1-based index; mean when multiple instances
    return [np.mean([i+1 for i, sorted_el in enumerate(sorted(l)) if sorted_el == el]) fo

l = [7, 1, 2, 5]
print "ranks: ", list2rank(l)

def spearmanRank(X, Y):
    # X and Y are same-length lists
    print list2rank(X)
    print list2rank(Y)
    return Corr(list2rank(X), list2rank(Y))

X = [10, 20, 30, 40, 1000]
Y = [-70, -1000, -50, -10, -20]
plt.plot(X,'ro')
plt.plot(Y,'go')

print "Pearson rank coefficient: %.2f" % Corr(X, Y)
print "Spearman rank coefficient: %.2f" % spearmanRank(X, Y)
```

```
ranks:  [4.0, 1.0, 2.0, 3.0]
Pearson rank coefficient: 0.28
[1.0, 2.0, 3.0, 4.0, 5.0]
[2.0, 1.0, 3.0, 5.0, 4.0]
Spearman rank coefficient: 0.80
```



Exercise: Obtain for the Anscombe's quartet [2] given in the figures bellow, the different estimators (mean, variance, covariance for each pair, Pearson's correlation and Spearman's rank correlation.

In [72]:
```
X=np.array([[10.0, 8.04, 10.0, 9.14, 10.0, 7.46, 8.0, 6.58],
[8.0, 6.95, 8.0, 8.14, 8.0, 6.77, 8.0, 5.76],
[13.0,7.58,13.0,8.74,13.0,12.74,8.0,7.71],
[9.0,8.81,9.0,8.77,9.0,7.11,8.0,8.84],
[11.0,8.33,11.0,9.26,11.0,7.81,8.0,8.47],
[14.0,9.96,14.0,8.10,14.0,8.84,8.0,7.04],
[6.0,7.24,6.0,6.13,6.0,6.08,8.0,5.25],
[4.0,4.26,4.0,3.10,4.0,5.39,19.0,12.50],
[12.0,10.84,12.0,9.13,12.0,8.15,8.0,5.56],
[7.0,4.82,7.0,7.26,7.0,6.42,8.0,7.91],
[5.0,5.68,5.0,4.74,5.0,5.73,8.0,6.89]])


plt.subplot(2,2,1)
plt.scatter(X[:,0],X[:,1],color='r',s=120, linewidths=2,zorder=10)
plt.xlabel('x1',fontsize=15)
plt.ylabel('y1',fontsize=15)

plt.subplot(2,2,2)
plt.scatter(X[:,2],X[:,3],color='r',s=120, linewidths=2,zorder=10)
plt.xlabel('x1',fontsize=15)
plt.ylabel('y1',fontsize=15)

plt.subplot(2,2,3)
plt.scatter(X[:,4],X[:,5],color='r',s=120, linewidths=2,zorder=10)
plt.xlabel('x1',fontsize=15)
plt.ylabel('y1',fontsize=15)

plt.subplot(2,2,4)
plt.scatter(X[:,6],X[:,7],color='r',s=120, linewidths=2,zorder=10)
plt.xlabel('x1',fontsize=15)
plt.ylabel('y1',fontsize=15)
plt.gcf().set_size_inches((10,10))
```



5. Main reference

[1] *Think Stats: Probability and Statistics for Programmers*, by Allen B. Downey, published by O'Reilly Media. http://www.greenteapress.com/thinkstats/ (http://www.greenteapress.com/thinkstats/)

[2] Anscombe's quartet, https://en.wikipedia.org/wiki/Anscombe%27s_quartet (https://en.wikipedia.org/wiki/Anscombe%27s_quartet)

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