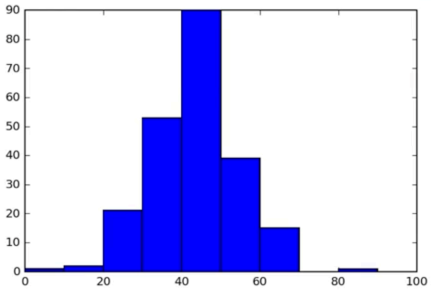
Chapter 1)

Note)

Setting the bins of a histogram

```
In [1]: bin_edges = [0, 10, 20, 30, 40, 50,
   ...:              60, 70, 80, 90, 100]

In [2]: _ = plt.hist(df_swing['dem_share'], bins=bin_edges)

In [3]: plt.show()
```



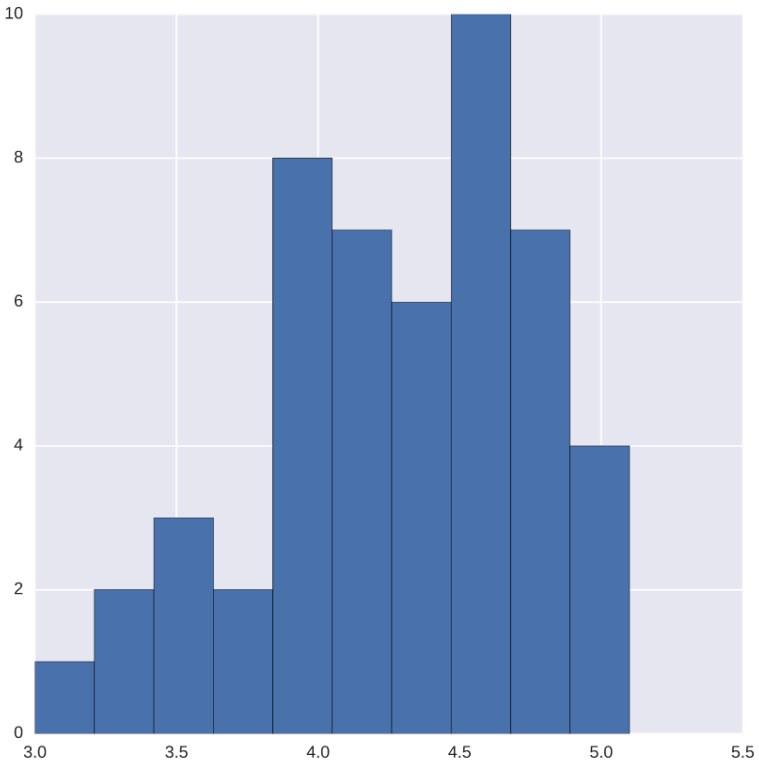
Setting Seaborn styling

```
In [1]: import seaborn as sns

In [2]: sns.set()

In [3]: _ = plt.hist(df_swing['dem_share'])

In [4]: _ = plt.xlabel('percent of vote for Obama')

In [5]: _ = plt.ylabel('number of counties')

In [6]: plt.show()
```

1)

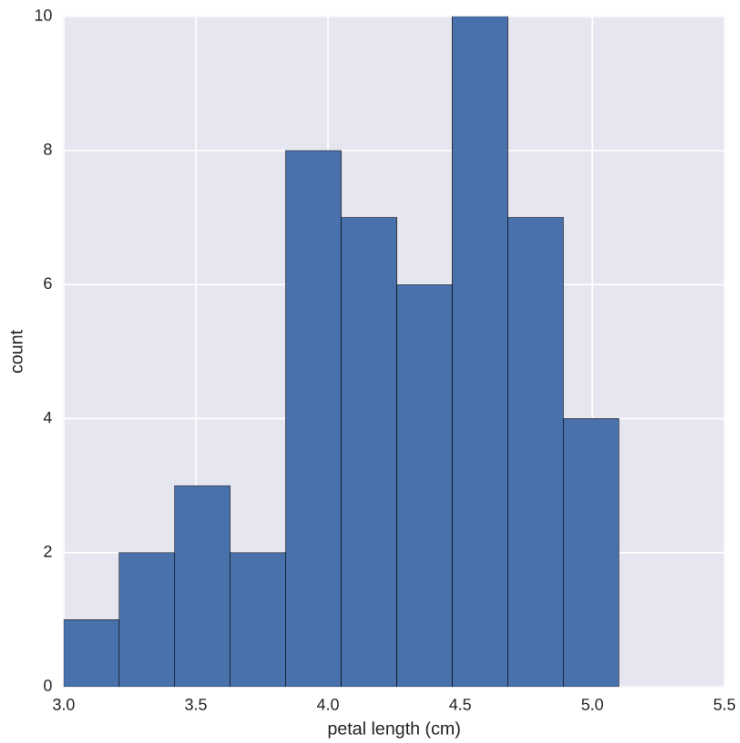
```
# Import plotting modules
import matplotlib.pyplot as plt
import seaborn as sns


# Set default Seaborn style
sns.set()

# Plot histogram of versicolor petal lengths
plt.hist(versicolor_petal_length)

# Show histogram
```

plt.show()



2)

```
# Plot histogram of versicolor petal lengths
_ = plt.hist(versicolor_petal_length)

# Label axes
plt.xlabel('petal length (cm)')

plt.ylabel('count')
# Show histogram
plt.show()
```



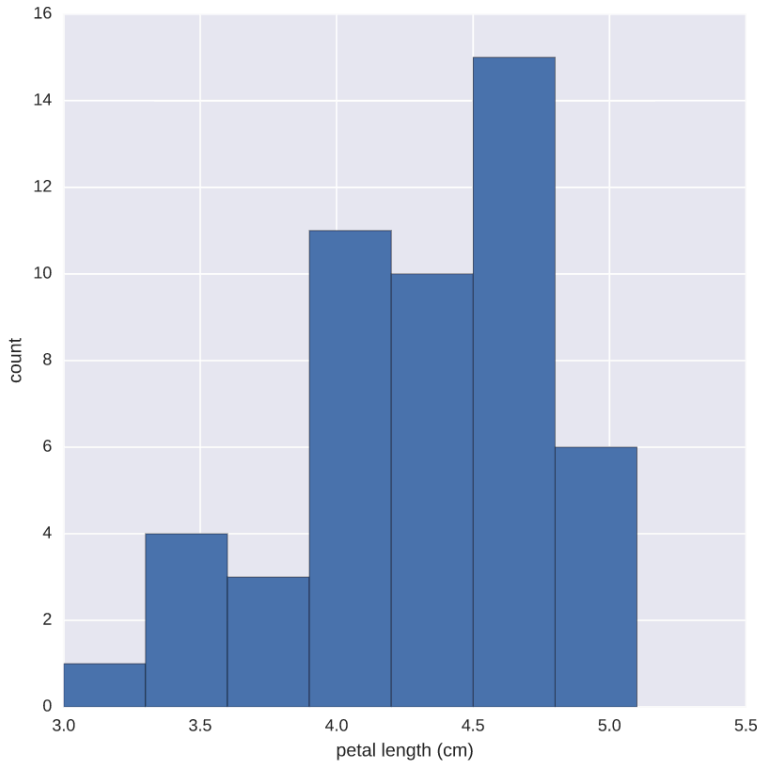
3)

Adjusting the number of bins in a histogram

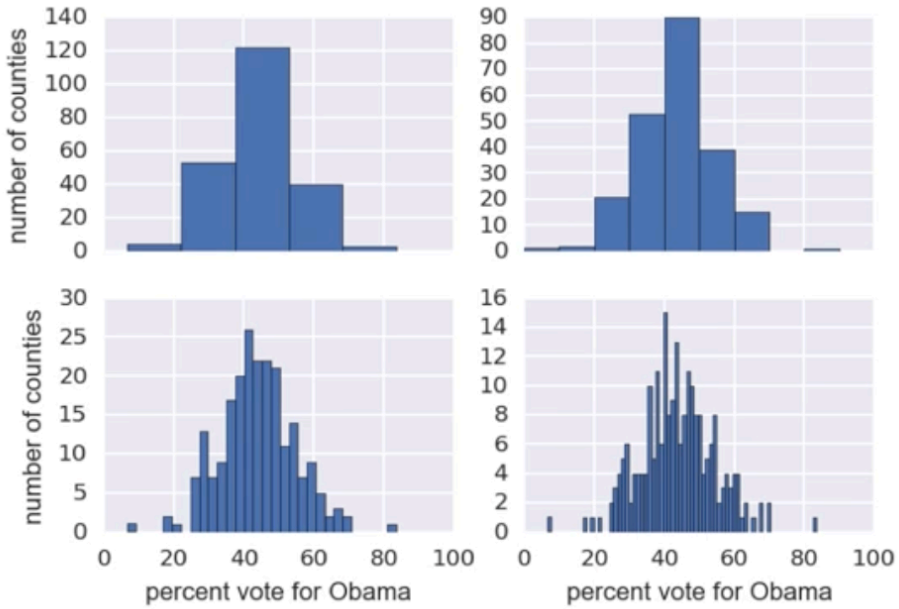
The histogram you just made had ten bins. This is the default of matplotlib. The "square root rule" is a commonly-used rule of thumb for choosing number of bins: choose the number of bins to be the square root of the number of samples. Plot the histogram of *Iris versicolor* petal lengths again, this time using the square root rule for the number of bins. You specify the number of bins using the `bins`keyword argument of `plt.hist()`.
The plotting utilities are already imported and the seaborn defaults already set. The variable you defined in the last exercise, `versicolor_petal_length`, is already in your namespace.

- Import `numpy` as `np`. This gives access to the square root function, `np.sqrt()`.
- Determine how many data points you have using `len()`.

- Compute the number of bins using the square root rule.
- Convert the number of bins to an integer using the built in `int()` function.
- Generate the histogram and make sure to use the `bins` keyword argument

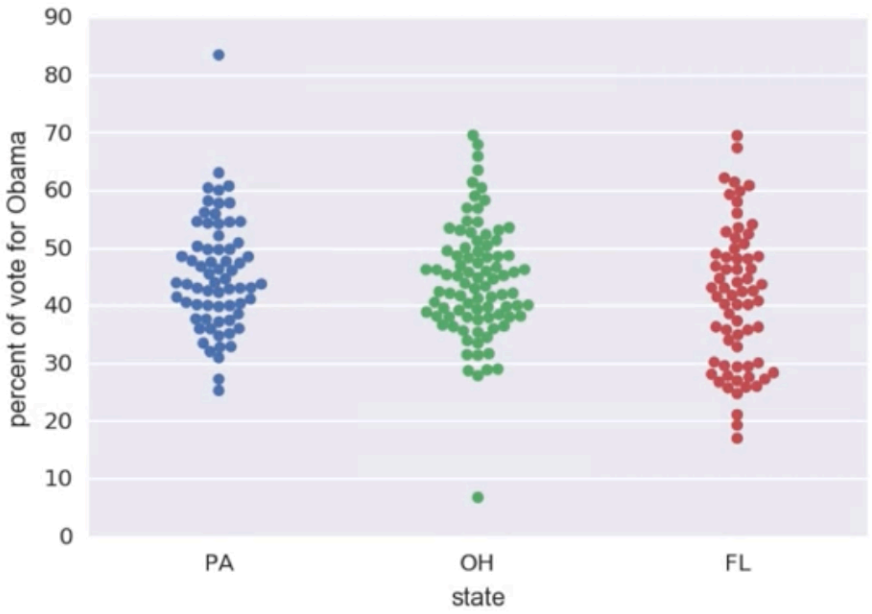


Note) Different Bins, different visualization



Generating a bee swarm plot

```
In [1]: _ = sns.swarmplot(x='state', y='dem_share', data=df_swing)

In [2]: _ = plt.xlabel('state')

In [3]: _ = plt.ylabel('percent of vote for Obama')

In [4]: plt.show()
```



4)

Make a bee swarm plot of the iris petal lengths. Your x-axis should contain each of the three species, and the y-axis the petal lengths. A data frame containing the data is in your namespace as `df`.

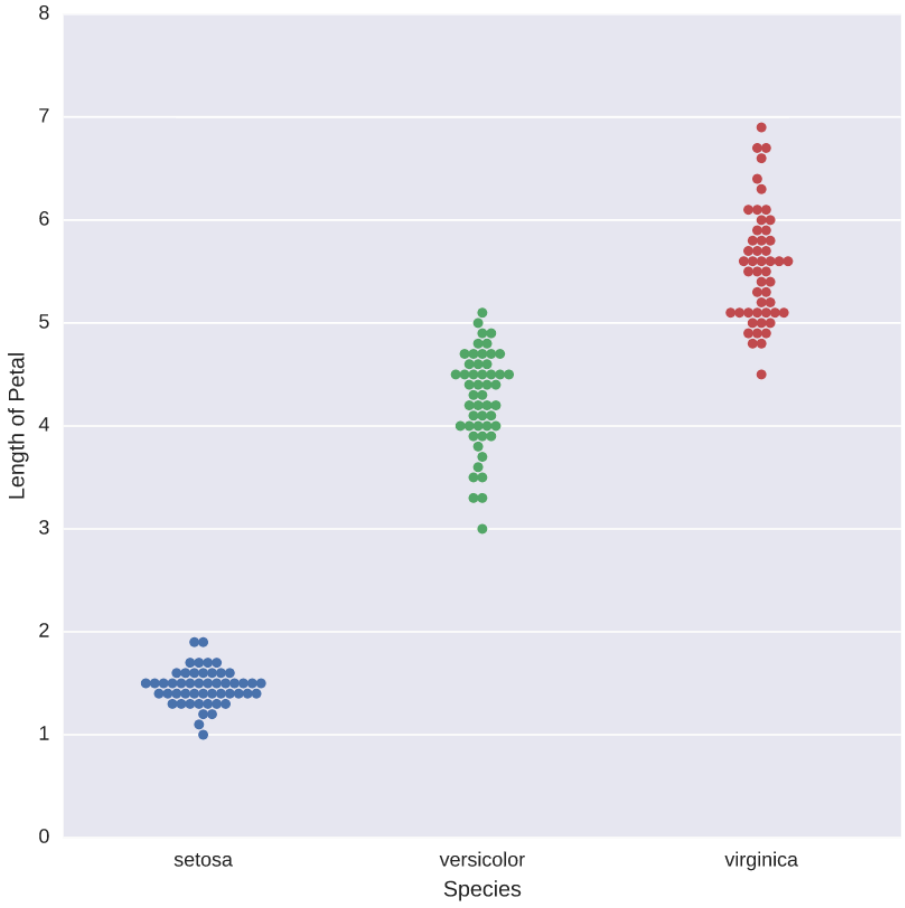
For your reference, the code Justin used to create the bee swarm plot in the video is provided below:

```
_ = sns.swarmplot(x='state', y='dem_share', data=df_swing)
_ = plt.xlabel('state')
_ = plt.ylabel('percent of vote for Obama')
plt.show()
```

In the IPython Shell, you can use `sns.swarmplot?` or `help(sns.swarmplot)` for more details on how to make bee swarm plots using seaborn.

- In the IPython Shell, inspect the DataFrame `df` using `df.head()`. This will let you identify which column names you need to pass as the `x` and `y` keyword arguments in your call to `sns.swarmplot()`.
- Use `sns.swarmplot()` to make a bee swarm plot from the DataFrame containing the Fisher iris data set, `df`. The x-axis should contain each of the three species, and the y-axis should contain the petal lengths.

```
# Create bee swarm plot with Seaborn's default settings
_ = sns.swarmplot(x = 'species',y='petal length (cm)',data=df)

# Label the axes
_ = plt.xlabel('Species')
_ = plt.ylabel('Length of Petal')
# Show the plot
plt.show()
```



Note)

How to Draw the CDF

The best way to learn how to plot the CDF is by an example. Consider the following dataset.

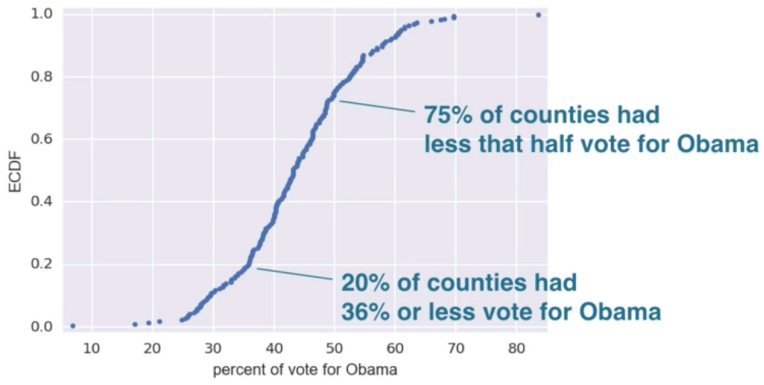
4 0 3 2 2

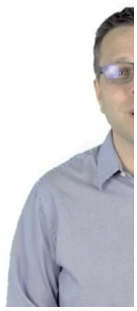
The task is to find the empirical CDF. The first step, when making calculations by hand is to order the data which has been done for the table below. The next step is to find the value of the CDF at the given points. The formula for the CDF is

$$F_n(t) = \frac{\text{\# of sample values } \leq t}{n}$$

Let's begin with $t = 0$. How many observations are less than or equal to 0? The answer is 1. Next, for $t = 2$, how many observations are less than or equal to 2? The answer is 3. If we keep going, we will find the values of $F_n(t)$ in the table below.

Empirical cumulative distribution function (ECDF)



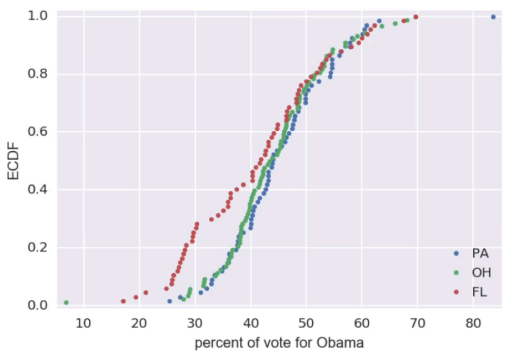


Bản chất là, giả sử tổng số counties là 100. Thì số couties mà bỏ phiếu cho Obama với tỉ lệ <=36% là 20 couties. Vì đã được normalize nên còn 20%.

Making an ECDF

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

In [2]: x = np.sort(df_swing['dem_share'])

In [3]: y = np.arange(1, len(x)+1) / len(x)

In [4]: _ = plt.plot(x, y, marker='.', linestyle='none')

In [5]: _ = plt.xlabel('percent of vote for Obama')

In [6]: _ = plt.ylabel('ECDF')

In [7]: plt.margins(0.02) # Keeps data off plot edges

In [8]: plt.show()
```

2008 US swing state election ECDFs



5)
Computing the ECDF

In this exercise, you will write a function that takes as input a 1D array of data and then returns the `x` and `y` values of the ECDF. You will use this function over and over again throughout this course and its sequel. ECDFs are among the most important plots in statistical analysis. You can write your own function, `foo(x,y)` according to the following skeleton:

```
def foo(a,b):
    """State what function does here"""
    # Computation performed here
    return x, y
```

The function `foo()` above takes two arguments `a` and `b` and returns two values `x` and `y`. The function header `def foo(a,b):` contains the function signature `foo(a,b)`, which consists of the function name, along with its parameters. For more on writing your own functions, see DataCamp's course **Python Data Science Toolbox (Part 1) here**!

- Define a function with the signature `ecdf(data)`. Within the function definition,
  - Compute the number of data points, `n`, using the `len()` function.
  - The xx-values are the sorted data. Use the `np.sort()` function to perform the sorting.
  - The yy data of the ECDF go from `1/n` to `1` in equally spaced increments. You can construct this using `np.arange()`. Remember, however, that the end value in `np.arange()` is not inclusive. Therefore, `np.arange()` will need to go from `1` to `n+1`. Be sure to divide this by `n`.
  - The function returns the values `x` and `y`.

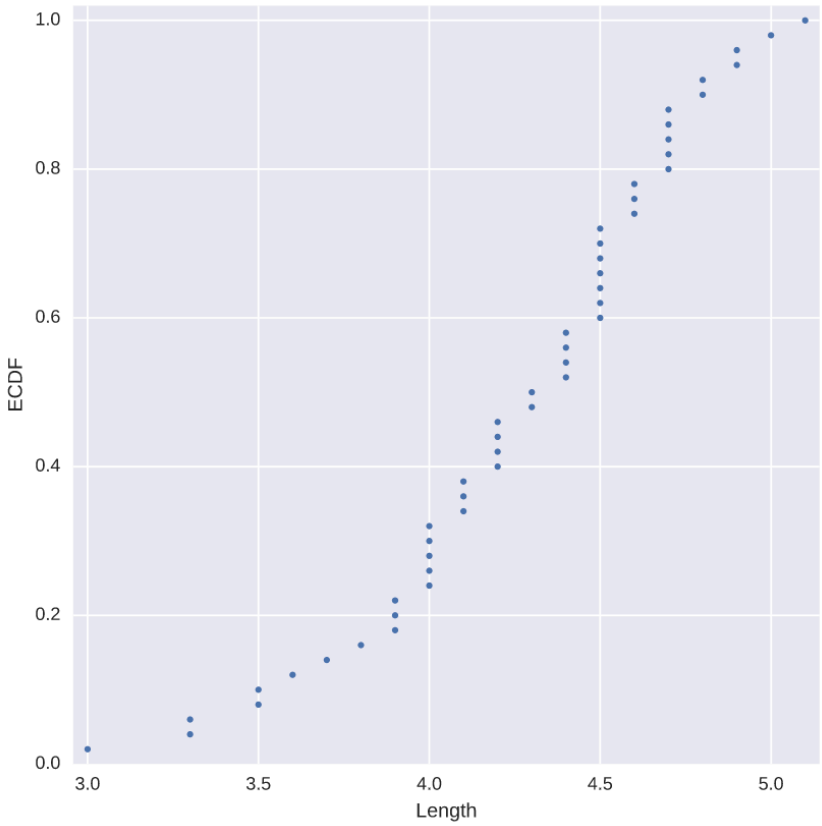
```
def ecdf(data):
    """Compute ECDF for a one-dimensional array of measurements."""

    # Number of data points: n
    n = len(data)

    # x-data for the ECDF: x
    x = np.sort(data)

    # y-data for the ECDF: y
    y = np.arange(1, n+1) / n

    return x, y
```

6)
Plotting the ECDF

You will now use your `ecdf()` function to compute the ECDF for the petal lengths of Anderson's *Iris versicolor* flowers. You will then plot the ECDF. Recall that your `t()` function returns two arrays so you will need to unpack them. An example of such unpacking is `x, y = foo(data)`, for some function `foo()`.

- Use `ecdf()` to compute the ECDF of `versicolor_petal_length`. Unpack the output into `x_vers` and `y_vers`.
- Plot the ECDF as dots. Remember to include `marker = '.'` and `linestyle = 'none'` in addition to `x_vers` and `y_vers` as arguments inside `plt.plot()`.
- Set the margins of the plot with `plt.margins()` so that no data points are cut off. Use a 2% margin.
- Label the axes. You can label the y-axis `'ECDF'`.

```
# Compute ECDF for versicolor data: x_vers, y_vers
x_vers, y_vers = ecdf(versicolor_petal_length)

# Generate plot
plt.plot(x_vers,y_vers,marker='.',linestyle='none')

# Make the margins nice
plt.margins(0.02)

# Label the axes
plt.xlabel('Length')
plt.ylabel('ECDF')


# Display the plot

plt.show()
```



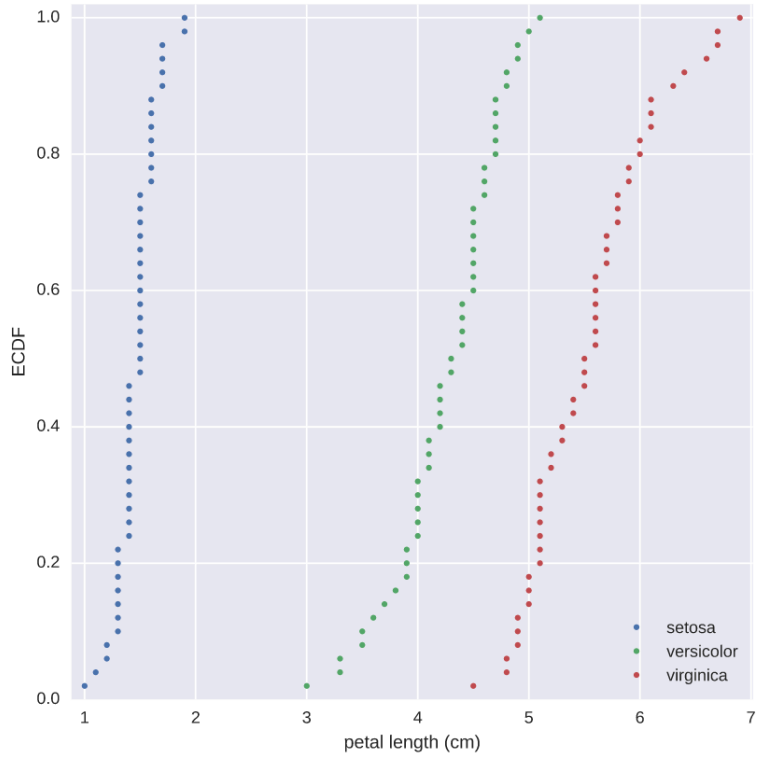
7)

Comparison of ECDFs

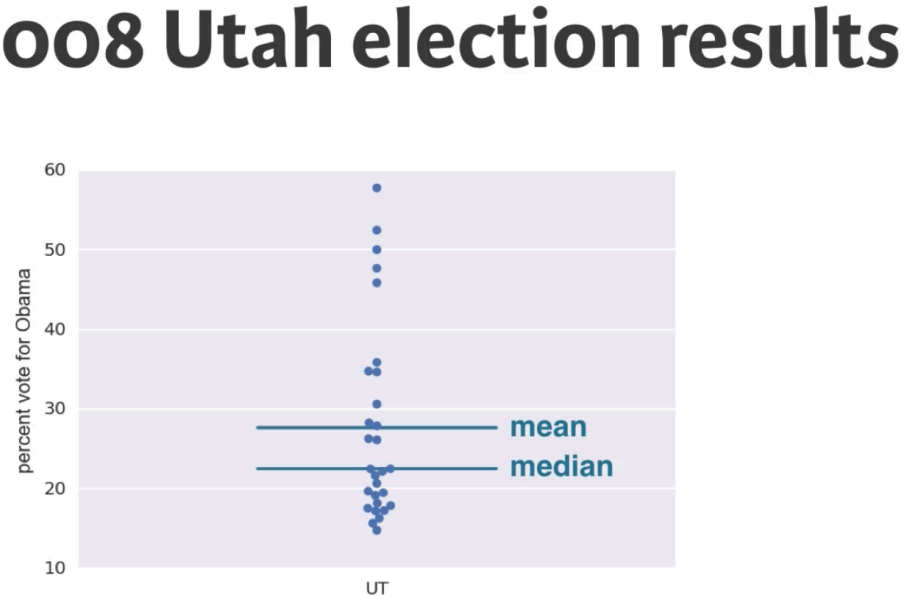
ECDFs also allow you to compare two or more distributions (though plots get cluttered if you have too many). Here, you will plot ECDFs for the petal lengths of all three iris species. You already wrote a function to generate ECDFs so you can put it to good use! To overlay all three ECDFs on the same plot, you can use `plt.plot()` three times, once for each ECDF. Remember to include `marker='.'` and `linestyle='none'` as arguments inside `plt.plot()`.

- Compute ECDFs for each of the three species using your `ecdf()` function. The variables `setosa_petal_length`, `versicolor_petal_length`, and `virginica_petal_length` are all in your namespace. Unpack the ECDFs into `x_set, y_set`, `x_vers, y_vers` and `x_virg, y_virg`, respectively.
- Plot all three ECDFs on the same plot as dots. To do this, you will need three `plt.plot()` commands. Assign the result of each to `_`.
- Specify 2% margins.

```
# Compute ECDFs
x_set, y_set = ecdf(setosa_petal_length)
x_vers,y_vers = ecdf(versicolor_petal_length)
x_virg,y_virg = ecdf(virginica_petal_length)



# Plot all ECDFs on the same plot
plt.plot(x_set,y_set,marker='.',linestyle='none')
plt.plot(x_vers,y_vers,marker='.',linestyle='none')
plt.plot(x_virg,y_virg,marker='.',linestyle='none')



# Make nice margins
plt.margins(0.02) # Để thừa ra phần trên đầu (>1.0)

# Annotate the plot
plt.legend(('setosa', 'versicolor', 'virginica'), loc='lower right')
_ = plt.xlabel('petal length (cm)')
_ = plt.ylabel('ECDF')

# Display the plot
plt.show()
```

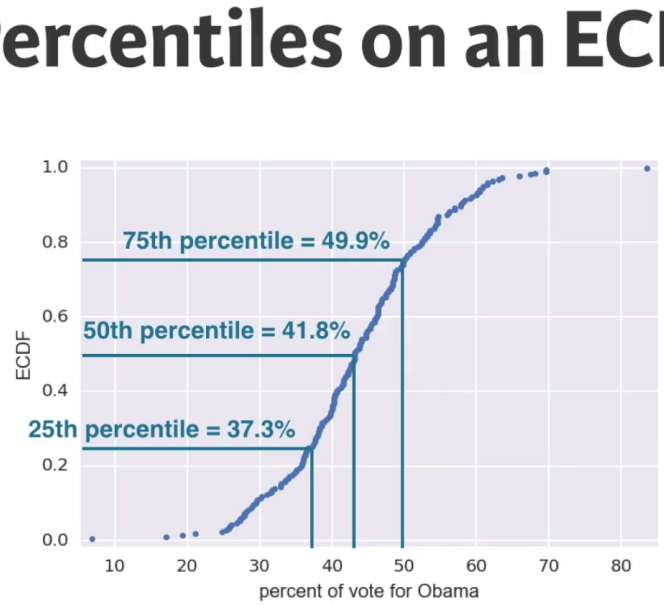


Note)

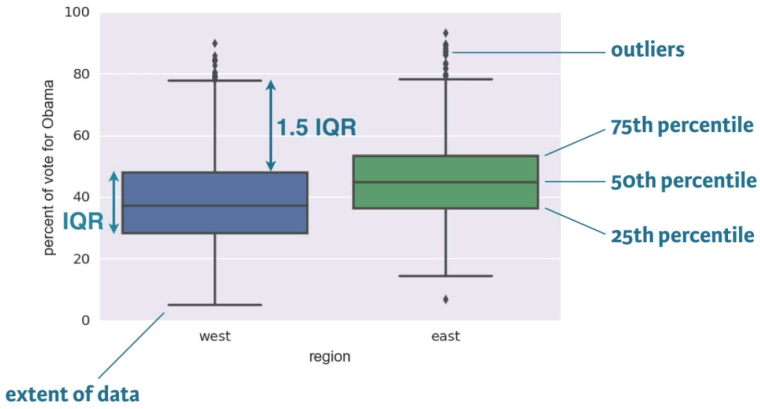


Chapter 2)

Note)



2008 US election box plot



Generating a box plot

```
In [1]: import matplotlib.pyplot as plt

In [2]: import seaborn as sns

In [3]: _ = sns.boxplot(x='east_west', y='dem_share',
   ...:                 data=df_all_states)

In [4]: _ = plt.xlabel('region')

In [5]: _ = plt.ylabel('percent of vote for Obama')

In [6]: plt.show()
```

1)

Computing percentiles

In this exercise, you will compute the percentiles of petal length of *Iris versicolor*.

- Create `percentiles`, a NumPy array of percentiles you want to compute. These are the 2.5th, 25th, 50th, 75th, and 97.5th. You can do so by creating a list containing these ints/floats and convert the list to a NumPy array using `np.array()`. For example, `np.array([30, 50])` would create an array consisting of the 30th and 50th percentiles.
- Use `np.percentile()` to compute the percentiles of the petal lengths from the *Iris versicolor* samples. The variable `versicolor_petal_length` is in your namespace.

# Specify array of percentiles: percentiles
percentiles = np.array([2.5,25,50,75,97.5])

```
# Compute percentiles: ptiles_vers
ptiles_vers = np.percentile(versicolor_petal_length,percentiles)

# Print the result
print (ptiles_vers)
```
```
[ 3.3    4.     4.35   4.6    4.9775]
```

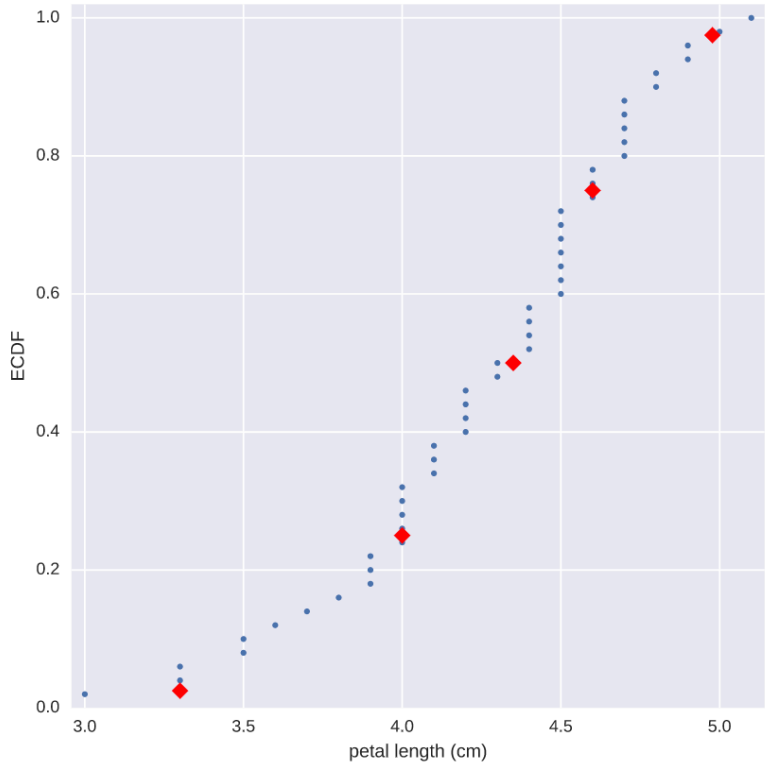
2)

Comparing percentiles to ECDF

To see how the percentiles relate to the ECDF, you will plot the percentiles of *Iris versicolor* petal lengths you calculated in the last exercise on the ECDF plot you generated in chapter 1. The percentile variables from the previous exercise are available in the workspace as `ptiles_vers` and `percentiles`.
Note that to ensure the Y-axis of the ECDF plot remains between 0 and 1, you will need to rescale the `percentiles` array accordingly - in this case, dividing it by 100.

- Plot the percentiles as red diamonds on the ECDF. Pass the x and y co-ordinates - `ptiles_vers` and `percentiles/100` - as positional arguments and specify the `marker='D'`, `color='red'` and `linestyle='none'` keyword arguments. The argument for the y-axis - `percentiles/100` has been specified for you.

```
# Plot the ECDF
_ = plt.plot(x_vers, y_vers, '.')
plt.margins(0.02)
_ = plt.xlabel('petal length (cm)')
_ = plt.ylabel('ECDF')

# Overlay percentiles as red diamonds.
_ = plt.plot(ptiles_vers, percentiles/100, marker='D', color='red',
         linestyle='None')

# Show the plot
plt.show()
```



3)
Box-and-whisker plot

Making a box plot for the petal lengths is unnecessary because the iris data set is not too large and the bee swarm plot works fine. However, it is always good to get some practice. Make a box plot of the iris petal lengths. You have a pandas DataFrame, `df`, which contains the petal length data, in your namespace. Inspect the data frame `df` in the IPython shell using `df.head()` to make sure you know what the pertinent columns are.
For your reference, the code used to produce the box plot in the video is provided below:

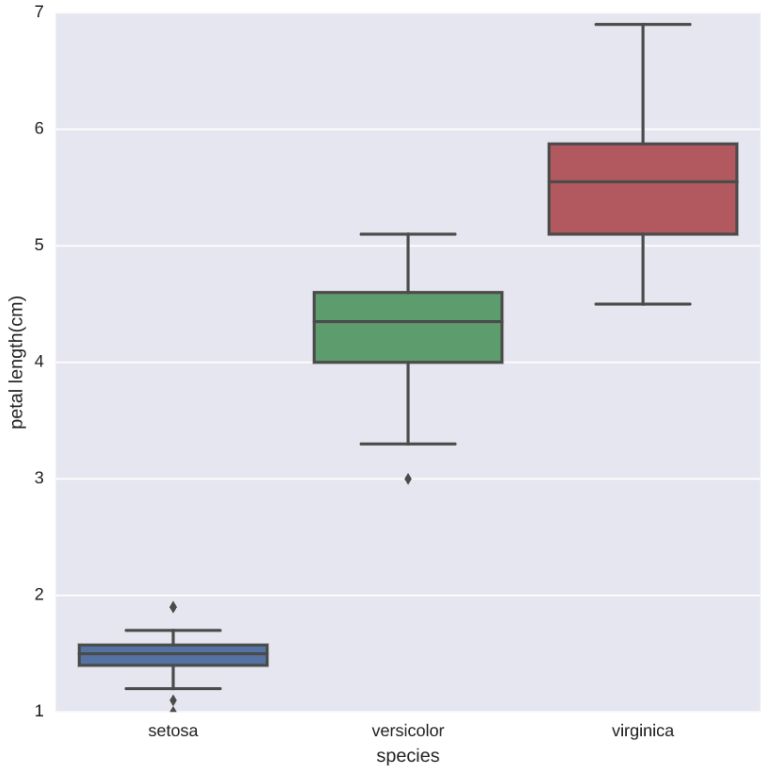
```
_ = sns.boxplot(x='east_west', y='dem_share', data=df_all_states)
_ = plt.xlabel('region')
_ = plt.ylabel('percent of vote for Obama')
```

In the IPython Shell, you can use `sns.boxplot?` or `help(sns.boxplot)` for more details on how to make box plots using seaborn.

- The set-up is exactly the same as for the bee swarm plot; you just call `sns.boxplot()` with the same keyword arguments as you would `sns.swarmplot()`. The x-axis is `'species'` and y-axis is `'petal length (cm)'`.
- Don't forget to label your axes!

# Create box plot with Seaborn's default settings
sns.boxplot(x= 'species',y ='petal length (cm)',data = df)

```
# Label the axes
plt.xlabel('species')
plt.ylabel('petal length(cm)')

# Show the plot
plt.show()
```



4)

Computing the variance

It is important to have some understanding of what commonly-used functions are doing under the hood. Though you may already know how to compute variances, this is a beginner course that does not assume so. In this exercise, we will explicitly compute the variance of the petal length of *Iris veriscolor* using the equations discussed in the videos. We will then use `np.var()` to compute it.

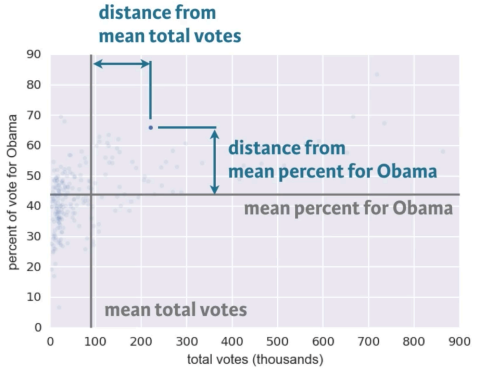
- Create an array called `differences` that is the difference between the petal lengths (`versicolor_petal_length`) and the mean petal length. The variable `versicolor_petal_length` is already in your namespace as a NumPy array so you can take advantage of NumPy's vectorized operations.
- Square each element in this array. For example, `x**2` squares each element in the array `x`. Store the result as `diff_sq`.
- Compute the mean of the elements in `diff_sq` using `np.mean()`. Store the result as `variance_explicit`.
- Compute the variance of `versicolor_petal_length` using `np.var()`. Store the result as `variance_np`.

```
# Array of differences to mean: differences
differences = versicolor_petal_length - np.mean(versicolor_petal_length)

# Square the differences: diff_sq
diff_sq = differences**2

# Compute the mean square difference: variance_explicit
variance_explicit = np.mean(diff_sq)

# Compute the variance using NumPy: variance_np
variance_np = np.var(versicolor_petal_length)

# Print the results
print (variance_explicit,variance_np)
```

0.2164 0.2164

Note)

Calculation of the covariance



$$\text{covariance} = \frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})$$

Pearson correlation coefficient

$$\rho = \text{Pearson correlation} = \frac{\text{covariance}}{(\text{std of } x)\,(\text{std of } y)}$$

$$= \frac{\text{variability due to codependence}}{\text{independent variability}}$$

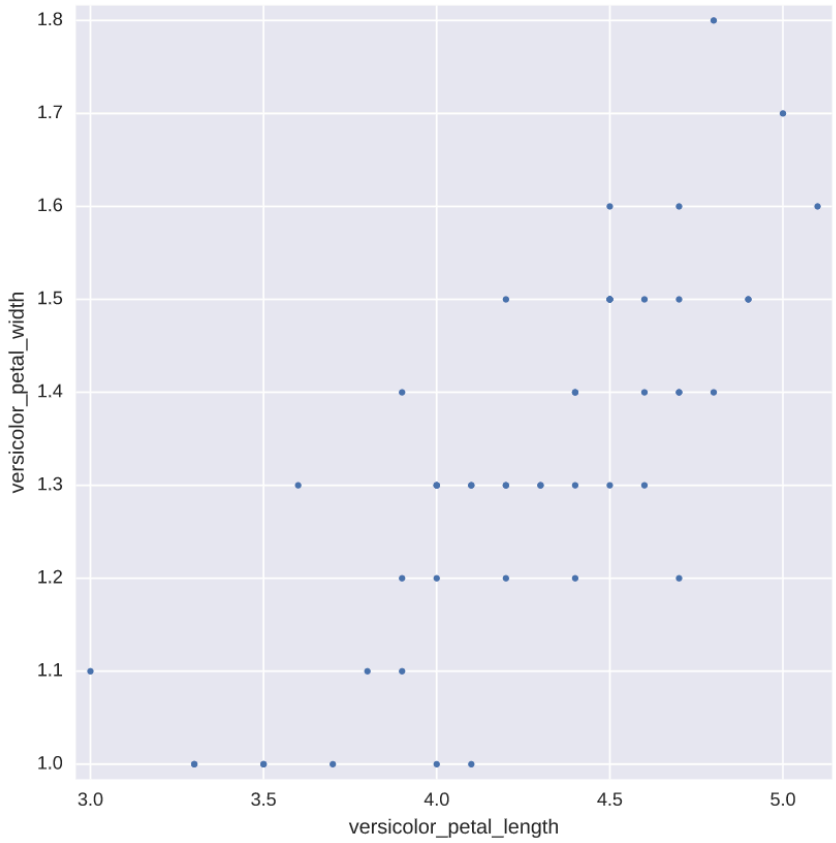
5)
Scatter plots

When you made bee swarm plots, box plots, and ECDF plots in previous exercises, you compared the petal lengths of different species of iris. But what if you want to compare two properties of a single species? This is exactly what we will do in this exercise. We will make a **scatter plot** of the petal length and width measurements of Anderson's *Iris versicolor* flowers. If the flower scales (that is, it preserves its proportion as it grows), we would expect the length and width to be correlated. For your reference, the code used to produce the scatter plot in the video is provided below:

```
_ = plt.plot(total_votes/1000, dem_share, marker='.', linestyle='none')
_ = plt.xlabel('total votes (thousands)')
_ = plt.ylabel('percent of vote for Obama')
```

- Use `plt.plot()` with the appropriate keyword arguments to make a scatter plot of *versicolor* petal length (x-axis) versus petal width (y-axis). The variables `versicolor_petal_length` and `versicolor_petal_width` are already in your namespace. Do not forget to use the `marker='.'` and `linestyle='none'` keyword arguments.
- Specify 2% margins so no data are cut off.

```
# Make a scatter plot

plt.plot(versicolor_petal_length,versicolor_petal_width,marker='.',linestyle='none')

# Set margins
plt.margins(0.02)

# Label the axes
plt.xlabel('versicolor_petal_length')
plt.ylabel('versicolor_petal_width')

# Show the result
plt.show()
```



6)
Computing the covariance

The covariance may be computed using the Numpy function `np.cov()`. For example, we have two sets of data `x` and `y`, `np.cov(x, y)` returns a 2D array where entries `[0,1]` and `[1,0]` are the covariances. Entry `[0,0]` is the variance of the data in `x`, and entry `[1,1]` is the variance of the data in `y`. This 2D output array is called the **covariance matrix**, since it organizes the self- and covariance.
To remind you how the *I. versicolor* petal length and width are related, we include the scatter plot you generated in a previous exercise.

- Use `np.cov()` to compute the covariance matrix for the petal length (`versicolor_petal_length`) and width (`versicolor_petal_width`) of *I. versicolor*.

- Print the covariance matrix.
- Extract the covariance from entry `[0,1]` of the covariance matrix. Note that by symmetry, entry `[1,0]` is the same as entry `[0,1]`.

```
# Compute the covariance matrix: covariance_matrix
covariance_matrix = np.cov(versicolor_petal_length,versicolor_petal_width)

# Print covariance matrix
print (covariance_matrix)
```

```
[[ 0.22081633  0.07310204]
 [ 0.07310204  0.03910612]]
```

```
# Extract covariance of length and width of petals: petal_cov
petal_cov = covariance_matrix[0,1]

# Print the length/width covariance
print (petal_cov)
```

```
0.0731020408163
```

7)

Computing the Pearson correlation coefficient

As mentioned in the video, the Pearson correlation coefficient, also called the Pearson r, is often easier to interpret than the covariance. It is computed using the `np.corrcoef()` function. Like `np.cov()`, it takes two arrays as arguments and returns a 2D array. Entries `[0,0]` and `[1,1]` are necessarily equal to `1`(can you think about why?), and the value we are after is entry `[0,1]`.
In this exercise, you will write a function, `pearson_r(x, y)` that takes in two arrays and returns the Pearson correlation coefficient. You will then use this function to compute it for the petal lengths and widths of *I. versicolor*.
Again, we include the scatter plot you generated in a previous exercise to remind you how the petal width and length are related.

- Define a function with signature `pearson_r(x, y)`.
  - Use `np.corrcoef()` to compute the correlation matrix of `x` and `y` (pass them to `np.corrcoef()` in that order).
  - The function returns entry `[0,1]` of the correlation matrix.
- Compute the Pearson correlation between the data in the arrays `versicolor_petal_length` and `versicolor_petal_width`. Assign the result to `r`

```
def pearson_r(x, y):
    """Compute Pearson correlation coefficient between two arrays."""
    # Compute correlation matrix: corr_mat
    corr_mat=np.corrcoef(x,y)

    # Return entry [0,1]
    return corr_mat[0,1]

# Compute Pearson correlation coefficient for I. versicolor: r
r = pearson_r(versicolor_petal_length,versicolor_petal_width)

# Print the result
print (r)
```

```
0.786668088523
```

Chapter 3)

Note)

Simulating 4 coin flips

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

In [2]: np.random.seed(42)

In [3]: random_numbers = np.random.random(size=4)

In [4]: random_numbers
Out[4]: array([ 0.37454012,  0.95071431,  0.73199394,
0.59865848])

In [5]: heads = random_numbers < 0.5

In [6]: heads
Out[6]: array([ True, False, False, False], dtype=bool)

In [7]: np.sum(heads)
Out[7]: 1
```

Simulating 4 coin flips

```
In [1]: n_all_heads = 0  # Initialize number of 4-heads trials

In [2]: for _ in range(10000):
    ...:     heads = np.random.random(size=4) < 0.5
    ...:     n_heads = np.sum(heads)
    ...:     if n_heads == 4:
    ...:         n_all_heads += 1
    ...:
    ...:

In [3]: n_all_heads / 10000
Out[3]: 0.0621
```

1)

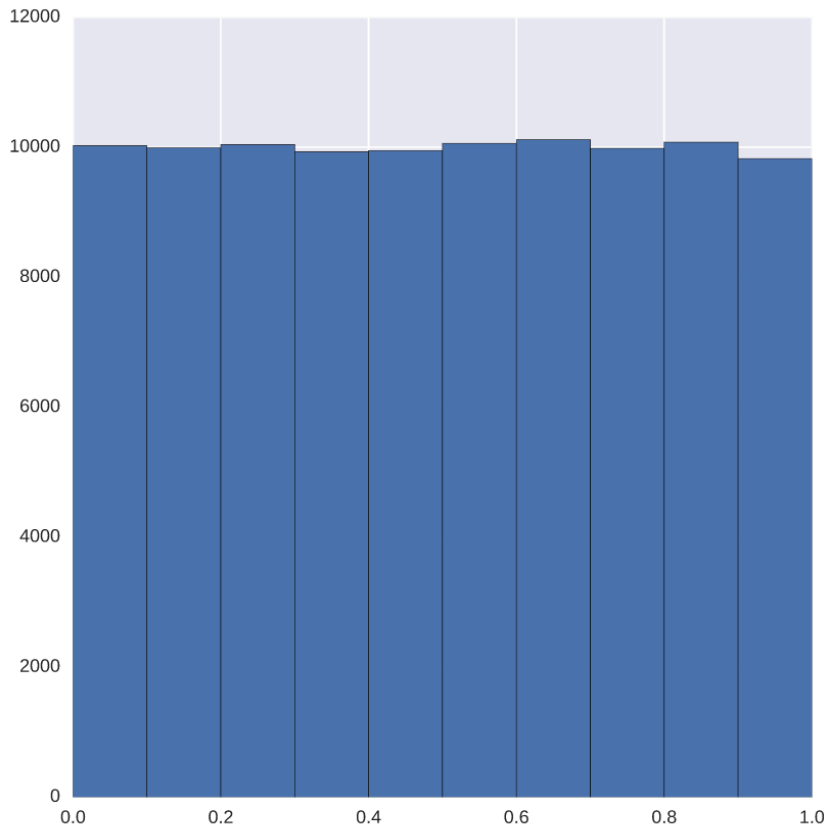
Generating random numbers using the np.random module

We will be hammering the `np.random` module for the rest of this course and its sequel. Actually, you will probably call functions from this module more than any other while wearing your hacker statistician hat. Let's start by taking its simplest

function, `np.random.random()` for a test spin. The function returns a random number between zero and one. Call `np.random.random()` a few times in the IPython shell. You should see numbers jumping around between zero and one.
In this exercise, we'll generate lots of random numbers between zero and one, and then plot a histogram of the results. If the numbers are truly random, all bars in the histogram should be of (close to) equal height.
You may have noticed that, in the video, Justin generated 4 random numbers by passing the keyword argument `size=4` to `np.random.random()`. Such an approach is more efficient than a `for` loop: in this exercise, however, you will write a `for` loop to experience hacker statistics as the practice of repeating an experiment over and over again.

- Seed the random number generator using the seed `42`.
- Initialize an empty array, `random_numbers`, of 100,000 entries to store the random numbers. Make sure you use `np.empty(100000)` to do this.
- Write a `for` loop to draw 100,000 random numbers using `np.random.random()`, storing them in the `random_numbers` array. To do so, loop over `range(100000)`.
- Plot a histogram of `random_numbers`. It is not necessary to label the axes in this case because we are just checking the random number generator

```
# Seed the random number generator
np.random.seed(42)

# Initialize random numbers: random_numbers
random_numbers = np.empty(100000)

# Generate random numbers by looping over range(100000)
for i in range(100000):
    random_numbers[i] = np.random.random()

# Plot a histogram
_ = plt.hist(random_numbers)

# Show the plot
plt.show()
```



2)

The np.random module and Bernoulli trials

You can think of a Bernoulli trial as a flip of a possibly biased coin. Specifically, each coin flip has a probability pp of landing heads (success) and probability $1-p$1–pof landing tails (failure). In this exercise, you will write a function to perform `n`Bernoulli trials, `perform_bernoulli_trials(n, p)`, which returns the number of successes out of `n` Bernoulli trials, each of which has probability `p` of success. To perform each Bernoulli trial, use the `np.random.random()` function, which returns a random number between zero and one.

- Define a function with signature `perform_bernoulli_trials(n, p)`.
    - Initialize to zero a variable `n_success` the counter of `True`s, which are Bernoulli trial successes.
    - Write a `for` loop where you perform a Bernoulli trial in each iteration and increment the number of success if the result is `True`.
      Perform `n`iterations by looping over `range(n)`.
        - To perform a Bernoulli trial, choose a random number between zero and one using `np.random.random()`. If the number you chose is less than `p`, increment `n_success` (use the `+= 1` operator to achieve this).
    - The function returns the number of successes `n_success`.

```
def perform_bernoulli_trials(n, p):
    """Perform n Bernoulli trials with success probability p
    and return number of successes."""
    # Initialize number of successes: n_success
    n_success = 0


    # Perform trials
    for i in range(n):
        # Choose random number between zero and one: random_number
        random_number = np.random.random()

        # If less than p, it's a success so add one to n_success
        if random_number<p:
            n_success +=1

    return n_success
```

3)

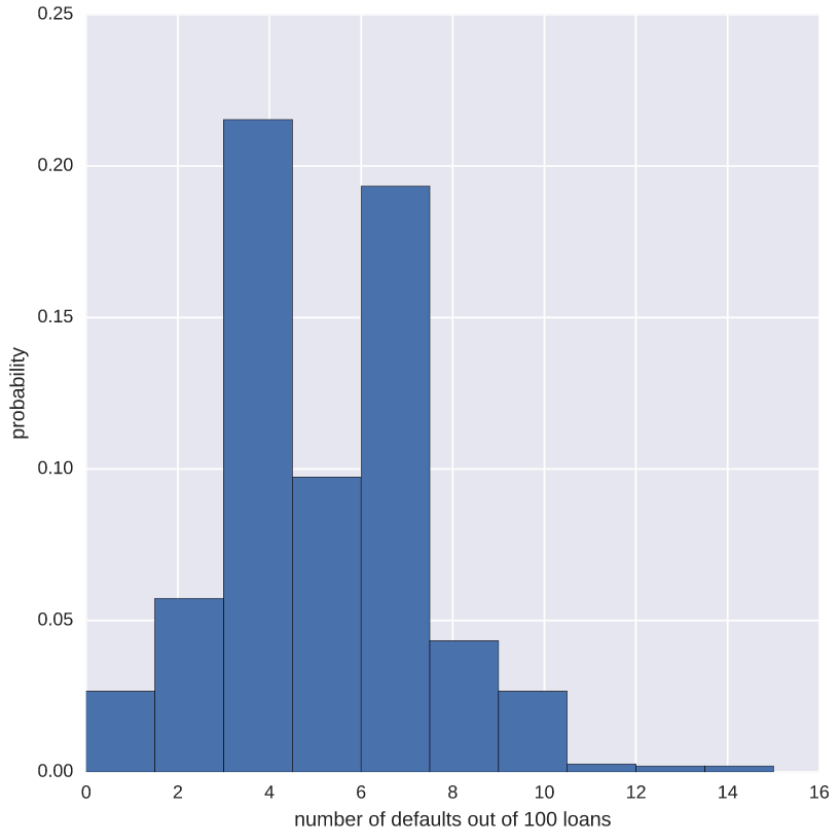
How many defaults might we expect?

Let's say a bank made 100 mortgage loans. It is possible that anywhere between 0 and 100 of the loans will be defaulted upon. You would like to know the probability of getting a given number of defaults, given that the probability of a default is `p = 0.05`. To investigate this, you will do a simulation. You will perform 100 Bernoulli trials using the `perform_bernoulli_trials()` function you wrote in the previous exercise and record how many defaults we get. Here, a success is a default. (Remember that the word "success" just means that the Bernoulli trial evaluates to `True`, i.e., did the loan recipient default?) You will do this for another 100 Bernoulli trials. And again and again until we have tried it 1000 times. Then, you will plot a histogram describing the probability of the number of defaults.

- Seed the random number generator to 42.
- Initialize `n_defaults`, an empty array, using `np.empty()`. It should contain 1000 entries, since we are doing 1000 simulations.
- Write a `for` loop with `1000` iterations to compute the number of defaults per 100 loans using the `perform_bernoulli_trials()` function. It accepts two arguments: the number of trials `n` - in this case 100 - and the probability of success `p` - in this case the probability of a default, which is `0.05`. On each iteration of the loop store the result in an entry of `n_defaults`.
- Plot a histogram of `n_defaults`. Include the `normed=True` keyword argument so that the height of the bars of the histogram indicate the probability.

```
# Seed random number generator
np.random.seed(42)
```

```
# Initialize the number of defaults: n_defaults
n_defaults = np.empty(1000)

# Compute the number of defaults
for i in range(1000):
    n_defaults[i] = perform_bernoulli_trials(100,0.05)


# Plot the histogram with default number of bins; label your axes
_ = plt.hist(n_defaults, normed=True)
_ = plt.xlabel('number of defaults out of 100 loans')
_ = plt.ylabel('probability')

# Show the plot

plt.show()
```



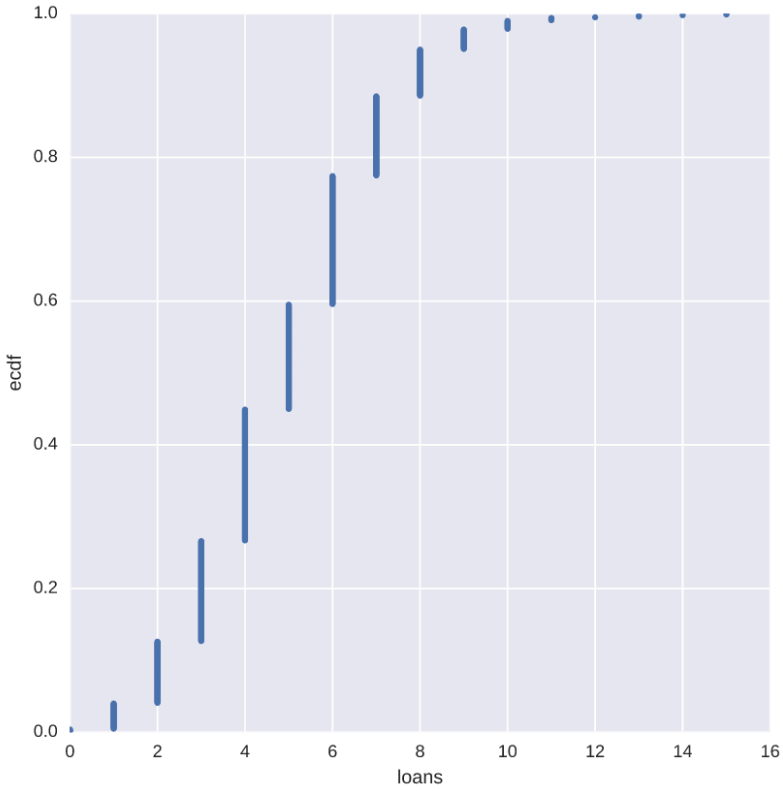
4)
Will the bank fail?

Plot the number of defaults you got from the previous exercise, in your namespace as `n_defaults`, as a CDF. The `ecdf()` function you wrote in the first chapter is available.
If interest rates are such that the bank will lose money if 10 or more of its loans are defaulted upon, what is the probability that the bank will lose money?

- Compute the `x` and `y` values for the ECDF of `n_defaults`.
- Plot the ECDF, making sure to label the axes. Remember to include `marker = '.'` and `linestyle = 'none'` in addition to `x` and `y` in your call `plt.plot()`.

- Show the plot.
- Compute the total number of entries in your `n_defaults` array that were greater than or equal to 10. To do so, compute a boolean array that tells you whether a given entry of `n_defaults` is `>= 10`. Then sum all the entries in this array using `np.sum()`. For example, `np.sum(n_defaults <= 5)` would compute the number of defaults with 5 or *fewer* defaults.
- The probability that the bank loses money is the fraction of `n_defaults` that are greater than or equal to 10

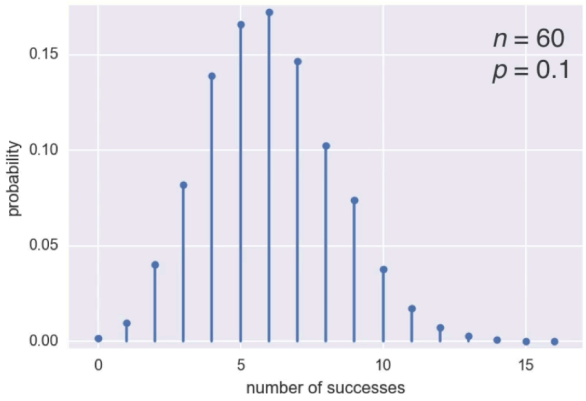
```
# Compute ECDF: x, y
x,y = ecdf(n_defaults)

# Plot the ECDF with labeled axes
plt.plot(x,y,marker ='.',linestyle='none')
plt.xlabel('loans')
plt.ylabel('ecdf')


# Show the plot
plt.show()

# Compute the number of 100-loan simulations with 10 or more defaults:
n_lose_money
n_lose_money = np.sum(n_defaults>=10)

# Compute and print probability of losing money
print('Probability of losing money =', n_lose_money / len(n_defaults))
```



Note)

The Binomial PMF

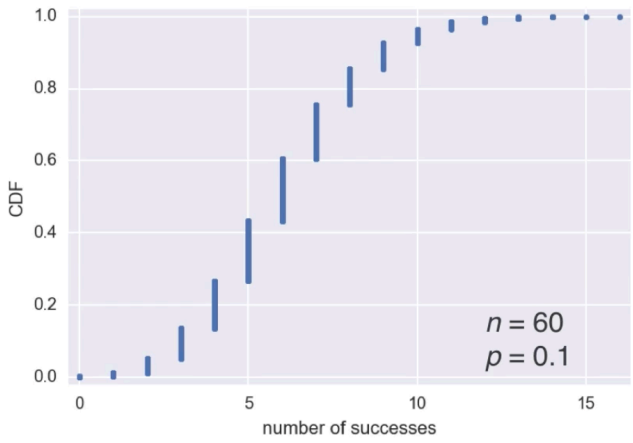
```
In [1]: samples = np.random.binomial(60, 0.1, size=10000)
```



The Binomial CDF

```
In [1]: import matplotlib.pyplot as plt

In [2]: import seaborn as sns

In [3]: sns.set()

In [4]: x, y = ecdf(samples)

In [5]: _ = plt.plot(x, y, marker='.', linestyle='none')

In [6]: plt.margins(0.02)

In [7]: _ = plt.xlabel('number of successes')

In [8]: _ = plt.ylabel('CDF')

In [9]: plt.show()
```

The Binomial CDF



5)
Sampling out of the Binomial distribution

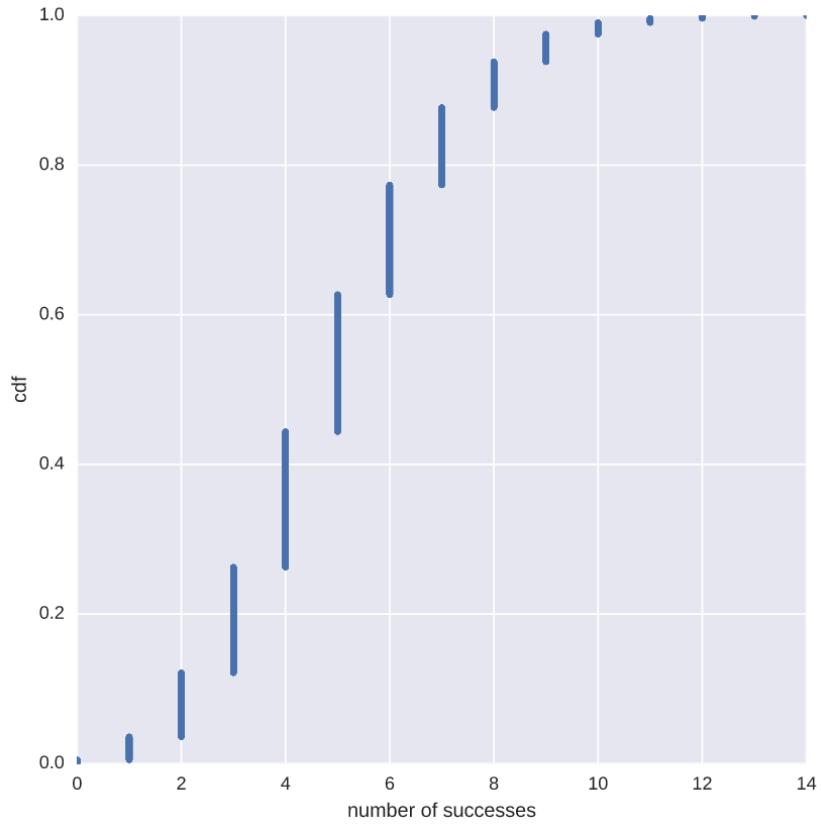
Compute the probability mass function for the number of defaults we would expect for 100 loans as in the last section, but instead of simulating all of the Bernoulli trials, perform the sampling using `np.random.binomial()`. This is identical to the calculation you did in the last set of exercises using your custom-written `perform_bernoulli_trials()` function, but far more computationally efficient. Given this extra efficiency, we will take 10,000 samples instead of 1000. After taking the samples, plot the CDF as last time. This CDF that you are plotting is that of the Binomial distribution.

Note: For this exercise and all going forward, the random number generator is pre-seeded for you (with `np.random.seed(42)`) to save you typing that each time.

- Draw samples out of the Binomial distribution using `np.random.binomial()`. You should use parameters `n = 100` and `p = 0.05`, and set the `size`keyword argument to `10000`.
- Compute the CDF using your previously-written `ecdf()` function.

- Plot the CDF with axis labels. The x-axis here is the number of defaults out of 100 loans, while the y-axis is the CDF.

```
# Take 10,000 samples out of the binomial distribution: n_defaults
n_defaults = np.random.binomial(100,0.05,size=10000)

# Compute CDF: x, y
x,y = ecdf(n_defaults)

# Plot the CDF with axis labels
plt.plot(x,y,marker='.',linestyle='none')
plt.xlabel('number of successes')
plt.ylabel('cdf')


# Show the plot
plt.show()
```



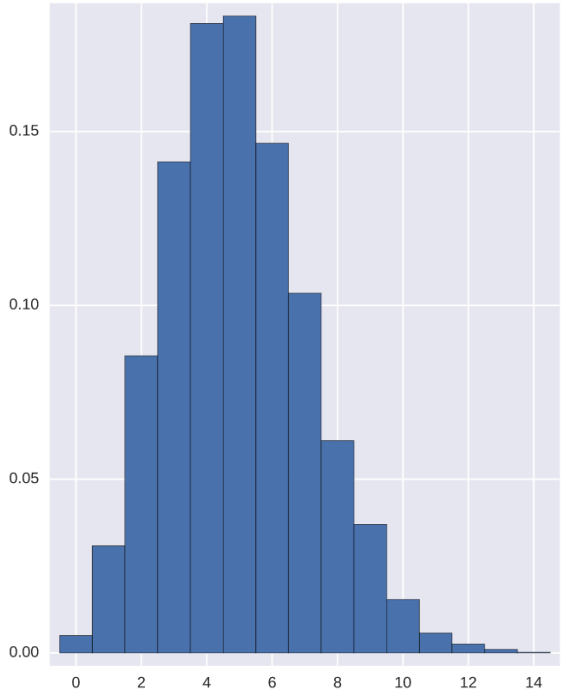
6)
Plotting the Binomial PMF

As mentioned in the video, plotting a nice looking PMF requires a bit of matplotlib trickery that we will not go into here. Instead, we will plot the PMF of the Binomial distribution as a histogram with skills you have already learned. The trick is setting up the edges of the bins to pass to `plt.hist()` via the `bins` keyword argument. We want the bins centered on the integers. So, the edges of the bins should be `-0.5, 0.5, 1.5, 2.5, ...` up to `max(n_defaults) + 1.5`. You can generate an array like this using `np.arange()` and then subtracting `0.5` from the array.
You have already sampled out of the Binomial distribution during your exercises on loan defaults, and the resulting samples are in the NumPy array `n_defaults`.

- Using `np.arange()`, compute the bin edges such that the bins are centered on the integers. Store the resulting array in the variable `bins`.
- Use `plt.hist()` to plot the histogram of `n_defaults` with the `normed=True` and `bins=bins` keyword arguments.

- Leave a 2% margin and label your axes.

```
# Compute bin edges: bins
bins = np.arange(0, max(n_defaults) + 2) - 0.5

# Generate histogram
plt.hist(n_defaults,normed=True,bins=bins)

# Set margins
plt.margins(0.02)

# Label axes

plt.xlabel('')
plt.ylabel('')

# Show the plot
plt.show()
```



Note)

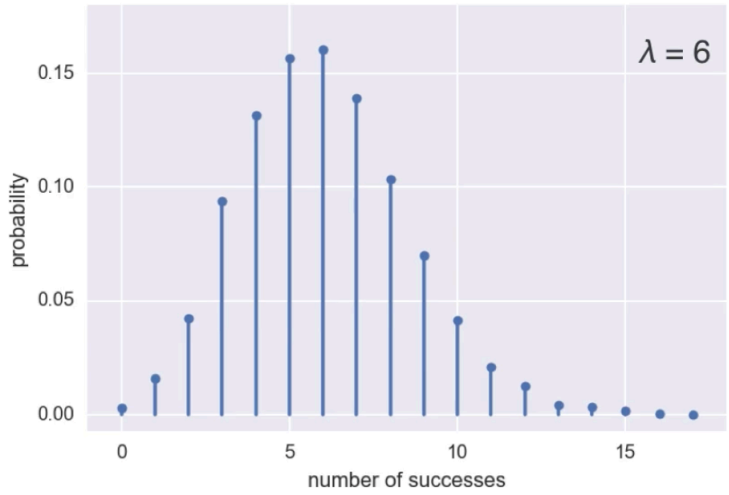
Examples of Poisson processes

- Natural births in a given hospital
- Hit on a website during a given hour
- Meteor strikes
- Molecular collisions in a gas
- Aviation incidents
- Buses in Poissonville

Poisson distribution

- The number *r* of arrivals of a Poisson process in a given time interval with average rate of λ arrivals per interval is Poisson distributed.
- The number *r* of hits on a website in one hour with an average hit rate of 6 hits per hour is Poisson distributed.

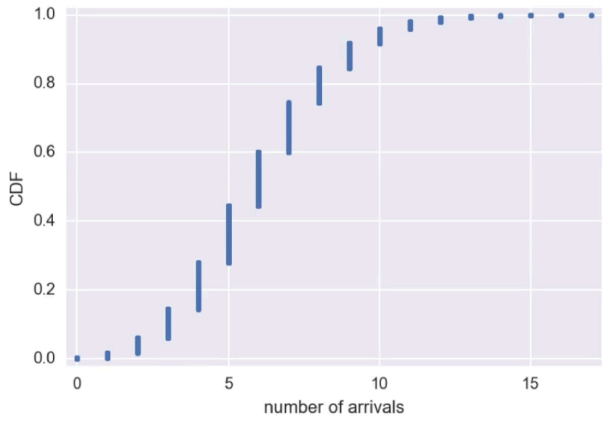
Poisson PMF



The Poisson CDF

```
In [1]: samples = np.random.poisson(6, size=10000)

In [2]: x, y = ecdf(samples)

In [3]: _ = plt.plot(x, y, marker='.', linestyle='none')

In [4]: plt.margins(0.02)

In [5]: _ = plt.xlabel('number of successes')

In [6]: _ = plt.ylabel('CDF')

In [7]: plt.show()
```

The Poisson CDF



7)
Relationship between Binomial and Poisson distributions

You just heard that the Poisson distribution is a limit of the Binomial distribution for rare events. This makes sense if you think about the stories. Say we do a Bernoulli trial every minute for an hour, each with a success probability of 0.1. We would do 60 trials, and the number of successes is Binomially distributed, and we would expect to get about 6 successes. This is just like the Poisson story we discussed in the video, where we get on average 6 hits on a website per hour. So, the Poisson distribution with arrival rate equal to npnp approximates a Binomial distribution for nn Bernoulli trials with probability pp of success (with $n$nlarge and pp small). Importantly, the Poisson distribution is often simpler to work with because it has only one parameter instead of two for the Binomial distribution.
Let's explore these two distributions computationally. You will compute the mean and standard deviation of samples from a Poisson distribution with an arrival rate of 10. Then, you will compute the mean and standard deviation of samples from a Binomial distribution with parameters nn and pp such that $np=10$np=10.

- Using the `np.random.poisson()` function, draw `10000` samples from a Poisson distribution with a mean of `10`.
- Make a list of the `n` and `p` values to consider for the Binomial distribution. Choose `n = [20, 100, 1000]` and `p = [0.5, 0.1, 0.01]` so that npnp is always 10.
- Using `np.random.binomial()` inside the provided `for` loop, draw `10000`samples from a Binomial distribution with each `n, p` pair and print the mean and standard deviation of the samples. There are 3 `n, p` pairs: `20, 0.5`, `100, 0.1`, and `1000, 0.01`. These can be accessed inside the loop as `n[i], p[i]`.

```
# Draw 10,000 samples out of Poisson distribution: samples_poisson
samples_poisson = np.random.poisson(10,size = 10000)

# Print the mean and standard deviation
print('Poisson:     ', np.mean(samples_poisson),
                     np.std(samples_poisson))

# Specify values of n and p to consider for Binomial: n, p
n = [20,100,1000]
p = [0.5,0.1,0.01]

# Draw 10,000 samples for each n,p pair: samples_binomial
for i in range(3):
    samples_binomial = np.random.binomial(n[i],p[i],10000)
```

```
# Print results
print('n =', n[i], 'Binom:', np.mean(samples_binomial),
                            np.std(samples_binomial))
```

```
Poisson:      10.0186 3.14481383233
n = 20 Binom: 9.9637 2.21634435727
n = 100 Binom: 9.9947 3.01358124331
n = 1000 Binom: 9.9985 3.13937856112
```

8)

How many no-hitters in a season?

In baseball, a no-hitter is a game in which a pitcher does not allow the other team to get a hit. This is a rare event, and since the beginning of the so-called modern era of baseball (starting in 1901), there have only been 251 of them through the 2015 season in over 200,000 games. The ECDF of the number of no-hitters in a season is shown to the right. Which probability distribution would be appropriate to describe the number of no-hitters we would expect in a given season?
Note: The no-hitter data set was scraped and calculated from the data sets available at **retrosheet.org**(**license**).

Possible Answers

- Discrete uniform
- Binomial
- Poisson
- **Both Binomial and Poisson, though Poisson is easier to model and compute.**
- Both Binomial and Poisson, though Binomial is easier to model and compute.

Correct! When we have rare events (low p, high n), the Binomial distribution is Poisson. This has a single parameter, the mean number of successes per time interval, in our case the mean number of no-hitters per season

9)

Was 2015 anomalous?

1990 and 2015 featured the most no-hitters of any season of baseball (there were seven). Given that there are on average 251/115 no-hitters per season, what is the probability of having seven or more in a season?

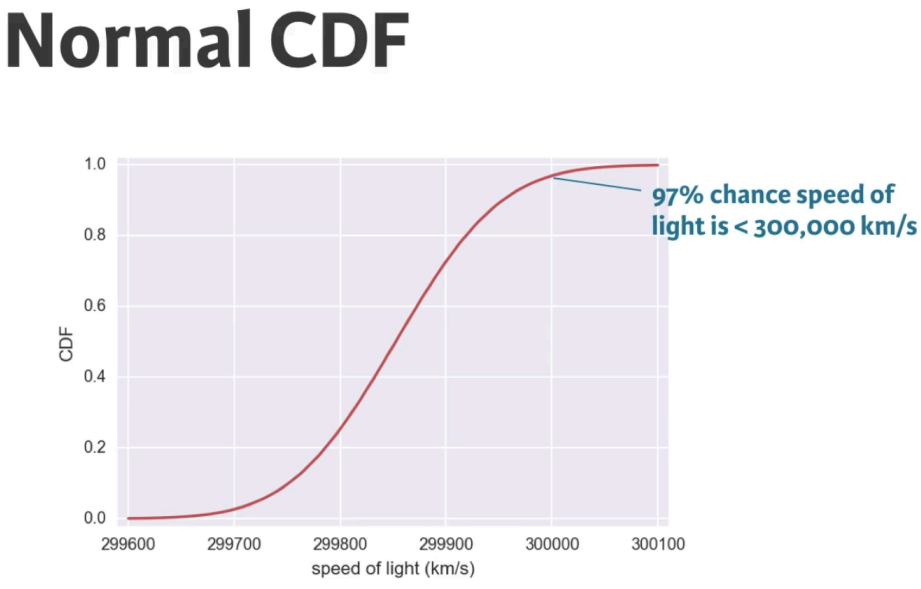
- Draw `10000` samples from a Poisson distribution with a mean of `251/115`and assign to `n_nohitters`.
- Determine how many of your samples had a result greater than or equal to `7`and assign to `n_large`.
- Compute the probability, `p_large`, of having `7` or more no-hitters by dividing `n_large` by the total number of samples (`10000`).

```
# Draw 10,000 samples out of Poisson distribution: n_nohitters
n_nohitters = np.random.poisson(251/115,size=10000)

# Compute number of samples that are seven or greater: n_large
n_large = np.sum(n_nohitters>=7)

# Compute probability of getting seven or more: p_large
p_large = n_large/10000

# Print the result
print('Probability of seven or more no-hitters:', p_large)
```

```
Probability of seven or more no-hitters: 0.0067
```

Chapter 4)

Note)



Parameter		Calculated from data
mean of a Normal distribution	≠	mean computed from data
st. dev. of a Normal distribution	≠	standard deviation computed from data

Checking Normality of Michelson data

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

In [2]: mean = np.mean(michelson_speed_of_light)

In [3]: std = np.std(michelson_speed_of_light)

In [4]: samples = np.random.normal(mean, std, size=10000)

In [5]: x, y = ecdf(michelson_speed_of_light)

In [6]: x_theor, y_theor = ecdf(samples)
```

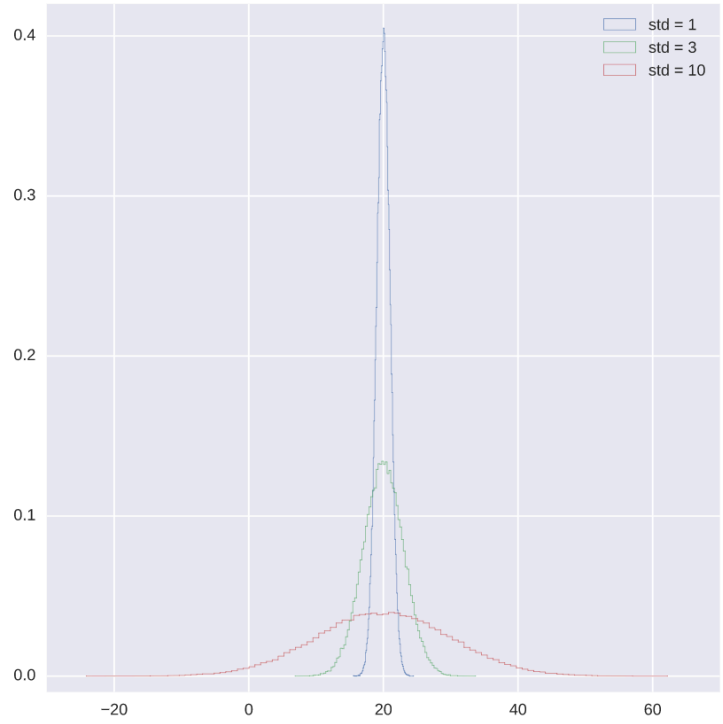
1)
The Normal PDF

In this exercise, you will explore the Normal PDF and also learn a way to plot a PDF of a known distribution using hacker statistics. Specifically, you will plot a Normal PDF for various values of the variance.

- Draw 100,000 samples from a Normal distribution that has a mean of `20` and a standard deviation of `1`. Do the same for Normal distributions with standard deviations of `3` and `10`, each still with a mean of `20`. Assign the results to `samples_std1`, `samples_std3` and `samples_std10`, respectively.
- Plot a histograms of each of the samples; for each, use 100 bins, also using the keyword arguments `normed=True` and `histtype='step'`. The latter keyword argument makes the plot look much like the smooth theoretical PDF. You will need to make 3 `plt.hist()` calls.

# Draw 100000 samples from Normal distribution with stds of interest: samples_std1, samples_std3, samples_std10
samples_std1 = np.random.normal(20,1,size=100000)
samples_std3 = np.random.normal(20,3,size=100000)
samples_std10 = np.random.normal(20,10,size=100000)

```
# Make histograms
plt.hist(samples_std1,bins=100,normed=True,histtype='step')
plt.hist(samples_std3,bins=100,normed=True,histtype='step')
plt.hist(samples_std10,bins=100,normed=True,histtype='step')


# Make a legend, set limits and show plot
_ = plt.legend(('std = 1', 'std = 3', 'std = 10'))
plt.ylim(-0.01, 0.42)
plt.show()
```



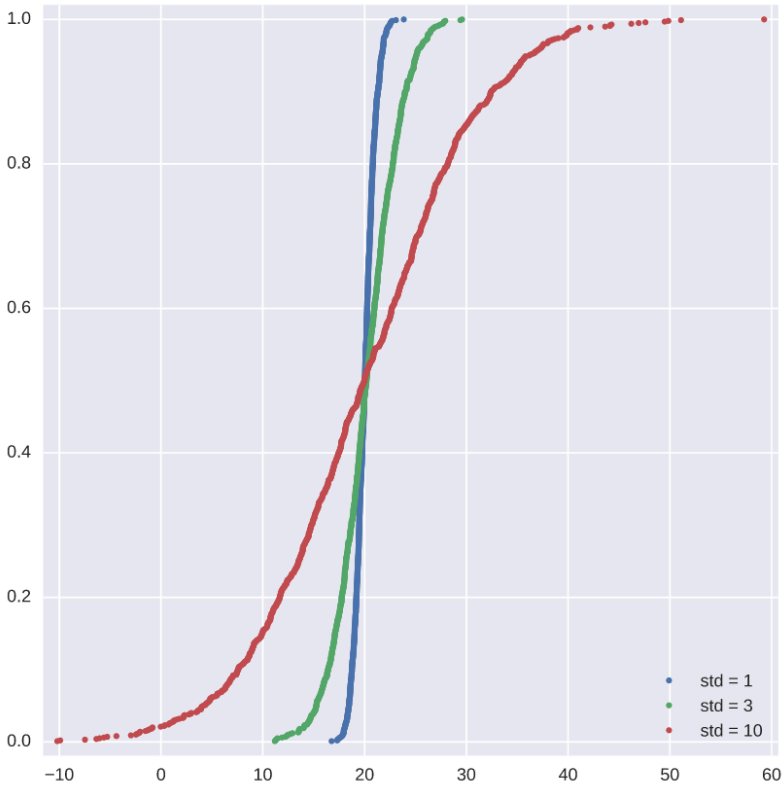
2)
The Normal CDF

Now that you have a feel for how the Normal PDF looks, let's consider its CDF. Using the samples you generated in the last exercise (in your namespace as `samples_std1`, `samples_std3`, and `samples_std10`), generate and plot the CDFs.

- Use your `ecdf()` function to generate x and y values for CDFs: `x_std1, y_std1`, `x_std3, y_std3` and `x_std10, y_std10`, respectively.
- Plot all three CDFs as dots (do not forget the `marker` and `linestyle`keyword arguments!).

- Make a 2% margin in your plot.

```
# Generate CDFs
x_std1,y_std1 = ecdf(samples_std1)
x_std3,y_std3 = ecdf(samples_std3)
x_std10,y_std10 = ecdf(samples_std10)



# Plot CDFs
plt.plot(x_std1,y_std1,marker='.',linestyle='none')
plt.plot(x_std3,y_std3,marker='.',linestyle='none')
plt.plot(x_std10,y_std10,marker='.',linestyle='none')


# Make 2% margin
plt.margins(0.02)

# Make a legend and show the plot
_ = plt.legend(('std = 1', 'std = 3', 'std = 10'), loc='lower right')
plt.show()
```

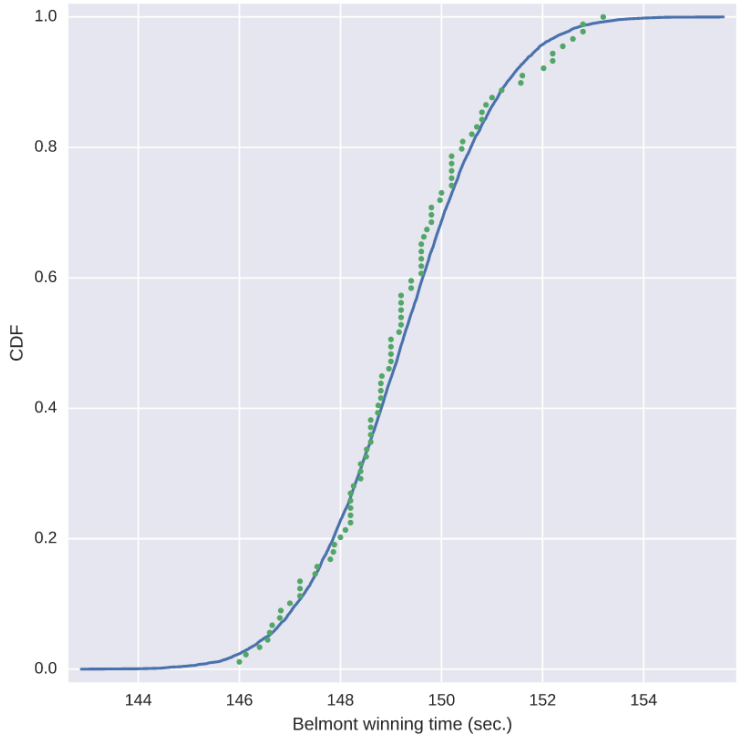


3)
Are the Belmont Stakes results Normally distributed?

Since 1926, the Belmont Stakes is a 1.5 mile-long race of 3-year old thoroughbred horses. **Secretariat** ran the fastest Belmont Stakes in history in 1973. While that was the fastest year, 1970 was the slowest because of unusually wet and sloppy conditions. With these two outliers removed from the data set, compute the mean and standard deviation of the Belmont winners' times. Sample out of a Normal distribution with this mean and standard deviation using the `np.random.normal()` function and plot a CDF. Overlay the ECDF from the winning Belmont times. Are these close to Normally distributed?
Note: Justin scraped the data concerning the Belmont Stakes from the **Belmont Wikipedia page**.

- Compute mean and standard deviation of Belmont winners' times with the two outliers removed. The NumPy array `belmont_no_outliers` has these data.
- Take 10,000 samples out of a normal distribution with this mean and standard deviation using `np.random.normal()`.
- Compute the CDF of the theoretical samples and the ECDF of the Belmont winners' data, assigning the results to `x_theor, y_theor` and `x, y`, respectively.

```
# Compute mean and standard deviation: mu, sigma

mu = np.mean(belmont_no_outliers)
sigma = np.std(belmont_no_outliers)

# Sample out of a normal distribution with this mu and sigma: samples
samples = np.random.normal(mu,sigma,size=10000)

# Get the CDF of the samples and of the data
x_theor,y_theor = ecdf(samples)
x,y = ecdf(belmont_no_outliers)


# Plot the CDFs and show the plot
_ = plt.plot(x_theor, y_theor)
_ = plt.plot(x, y, marker='.', linestyle='none')
plt.margins(0.02)
_ = plt.xlabel('Belmont winning time (sec.)')
_ = plt.ylabel('CDF')
plt.show()
```



4)

What are the chances of a horse matching or beating Secretariat's record?

Assume that the Belmont winners' times are Normally distributed (with the 1970 and 1973 years removed), what is the probability that the winner of a given Belmont Stakes will run it as fast or faster than Secretariat?

- Take 1,000,000 samples from the normal distribution using the `np.random.normal()` function. The mean `mu` and standard deviation `sigma` are already loaded into the namespace of your IPython instance.
- Compute the fraction of samples that have a time less than or equal to Secretariat's time of 144 seconds.

```
# Take a million samples out of the Normal distribution: samples
samples = np.random.normal(mu,sigma,size=1000000)

# Compute the fraction that are faster than 144 seconds: prob
prob = (np.sum(samples <= 144))/len(samples)

# Print the result
print('Probability of besting Secretariat:', prob)
```

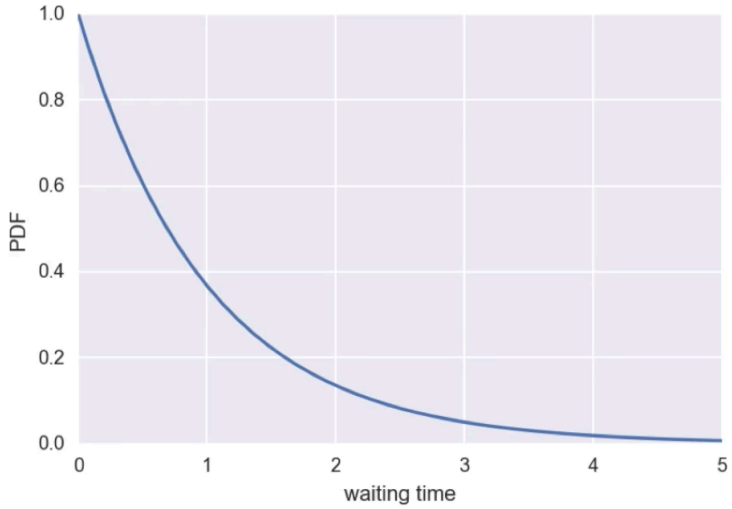
Probability of besting Secretariat: 0.000635

Note)

The Exponential distribution

- The waiting time between arrivals of a Poisson process is Exponentially distributed

The Exponential PDF



5)

If you have a story, you can simulate it!

Sometimes, the story describing our probability distribution does not have a named distribution to go along with it. In these cases, fear not! You can always simulate it. We'll do that in this and the next exercise.

In earlier exercises, we looked at the rare event of no-hitters in Major League Baseball. *Hitting the cycle* is another rare baseball event. When a batter hits the cycle, he gets all four kinds of hits, a single, double, triple, and home run, in a single game. Like no-hitters, this can be modeled as a Poisson process, so the time between hits of the cycle are also Exponentially distributed.

How long must we wait to see both a no-hitter *and* a batter hit the cycle? The idea is that we have to wait some time for the no-hitter, and then after the no-hitter, we have to wait for hitting the cycle. Stated another way, what is the total waiting time

for the arrival of two different Poisson processes? The total waiting time is the time waited for the no-hitter, plus the time waited for the hitting the cycle.
Now, you will write a function to sample out of the distribution described by this story.

- Define a function with call signature `successive_poisson(tau1, tau2, size=1)` that samples the waiting time for a no-hitter and a hit of the cycle.
    - Draw waiting times `tau1` (`size` number of samples) for the no-hitter out of an exponential distribution and assign to `t1`.
    - Draw waiting times `tau2` (`size` number of samples) for hitting the cycle out of an exponential distribution and assign to `t2`.
    - The function returns the sum of the waiting times for the two events.

```
def successive_poisson(tau1, tau2, size=1):
    # Draw samples out of first exponential distribution: t1
    t1 = np.random.exponential(tau1, size=size)

    # Draw samples out of second exponential distribution: t2
    t2 = np.random.exponential(tau2, size=size)

    return t1 + t2
```

6)
Distribution of no-hitters and cycles

Now, you'll use your sampling function to compute the waiting time to observer a no-hitter and hitting of the cycle. The mean waiting time for a no-hitter is 764 games, and the mean waiting time for hitting the cycle is 715 games.

- Use your `successive_poisson()` function to draw 100,000 out of the distribution of waiting times for observing a no-hitter and a hitting of the cycle.
- Plot the PDF of the waiting times using the step histogram technique of a previous exercise. Don't forget the necessary keyword arguments. You should use `bins=100`, `normed=True`, and `histtype='step'`.

```
# Draw samples of waiting times: waiting_times
waiting_times = successive_poisson(764,715,100000)

# Make the histogram
plt.hist(waiting_times,bins=100,normed=True,histtype='step')


# Label axes
```

```
plt.xlabel('times')
plt.ylabel('prob')

# Show the plot
plt.show()
```