Statistical Thinking in Python

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The following exercises were excerpted from the Data Camp course "Statistical Thinking in Python"

- Major League Baseball No-Hitters
- Sheffield Weather Station
- Literacy vs Fertility
- South American Horned Frogs
- Civil Rights Vote
- Bernoulli Trials and Simulating Bank Loans
- Belmont Stakes
- Bee Reproduction
- Anscombe's Quartet
- Darwin's Finches

Apologies for the rough page breaks. Unfortunately, there are surprising difficulties in outputting Jupyter notebooks into an attractive offline format.

For simplicity, I embedded numpy arrays into the Jupyter notebook, rather than create external datasets that need to be imported.

I found performing the Data Camp exercises in Jupyter to be more beneficial to my learning then working in Data Camp's development environment. The Data Camp course contains a series of videos that give better context to the attached exercises.

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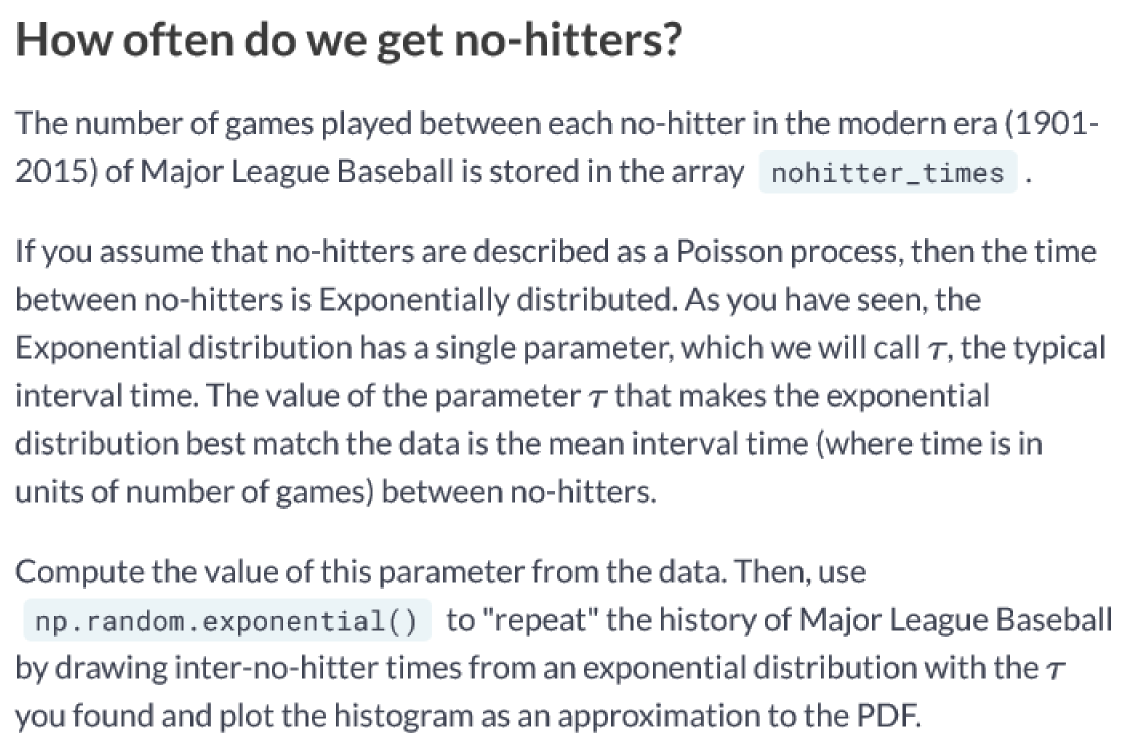
Check out my SQL blog at www.AdvancedSQLPuzzles.com

Enjoy!

Major League Baseball No-Hitters

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"



How often do we get no-hitters?

The number of games played between each no-hitter in the modern era (1901-2015) of Major League Baseball is stored in the array `nohitter_times`.

If you assume that no-hitters are described as a Poisson process, then the time between no-hitters is Exponentially distributed. As you have seen, the Exponential distribution has a single parameter, which we will call τ, the typical interval time. The value of the parameter τ that makes the exponential distribution best match the data is the mean interval time (where time is in units of number of games) between no-hitters.

Compute the value of this parameter from the data. Then, use `np.random.exponential()` to "repeat" the history of Major League Baseball by drawing inter-no-hitter times from an exponential distribution with the τ you found and plot the histogram as an approximation to the PDF.

In [129]:

```python
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

In [130]:

```python
nohitter_times = np.array([843, 1613, 1101,  215,  684,  814,  278,  324,  161,  219,  545,
        715,  966,  624,   29,  450,  107,   20,   91, 1325,  124, 1468,
        104, 1309,  429,   62, 1878, 1104,  123,  251,   93,  188,  983,
        166,   96,  702,   23,  524,   26,  299,   59,   39,   12,    2,
        308, 1114,  813,  887,  645, 2088,   42, 2090,   11,  886, 1665,
       1084, 2900, 2432,  750, 4021, 1070, 1765, 1322,   26,  548, 1525,
         77, 2181, 2752,  127, 2147,  211,   41, 1575,  151,  479,  697,
        557, 2267,  542,  392,   73,  603,  233,  255,  528,  397, 1529,
       1023, 1194,  462,  583,   37,  943,  996,  480, 1497,  717,  224,
        219, 1531,  498,   44,  288,  267,  600,   52,  269, 1086,  386,
        176, 2199,  216,   54,  675, 1243,  463,  650,  171,  327,  110,
        774,  509,    8,  197,  136,   12, 1124,   64,  380,  811,  232,
        192,  731,  715,  226,  605,  539, 1491,  323,  240,  179,  702,
        156,   82, 1397,  354,  778,  603, 1001,  385,  986,  203,  149,
        576,  445,  180, 1403,  252,  675, 1351, 2983, 1568,   45,  899,
       3260, 1025,   31,  100, 2055, 4043,   79,  238, 3931, 2351,  595,
        110,  215,    0,  563,  206,  660,  242,  577,  179,  157,  192,
        192, 1848,  792, 1693,   55,  388,  225, 1134, 1172, 1555,   31,
       1582, 1044,  378, 1687, 2915,  280,  765, 2819,  511, 1521,  745,
       2491,  580, 2072, 6450,  578,  745, 1075, 1103, 1549, 1520,  138,
       1202,  296,  277,  351,  391,  950,  459,   62, 1056, 1128,  139,
        420,   87,   71,  814,  603, 1349,  162, 1027,  783,  326,  101,
        876,  381,  905,  156,  419,  239,  119,  129,  467])
```

In [131]:

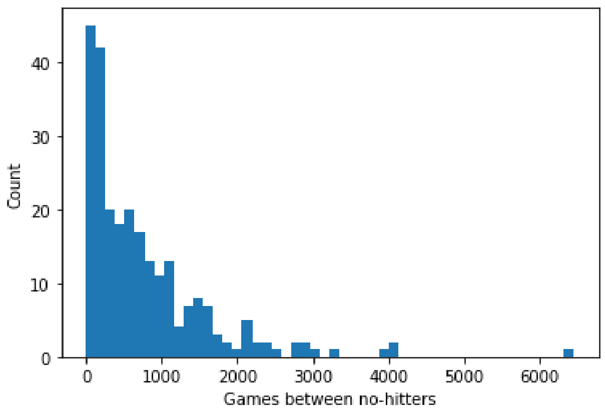
```
#Print summary statistcs
print('The array count is',len(nohitter_times))
print('The mean is',np.mean(nohitter_times))
print('The median is',np.median(nohitter_times))
print('The variance is',np.var(nohitter_times))
print('The standard deviation is',np.std(nohitter_times))
print('The percentiles are',np.percentile(nohitter_times,[2.5, 25, 50, 75, 97.5]))
#np.sort(nohitter_times)
```

```
The array count is 251
The mean is 763.0358565737051
The median is 524.0
The variance is 707938.0664433899
The standard deviation is 841.3905552378098
The percentiles are [  20.75  190.    524.   1063.   2911.25]
```

Visualize the data first

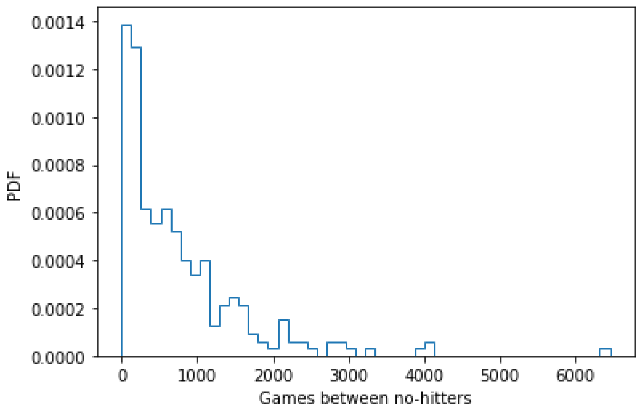
In [132]:

```
# Plot a histogram and label axes
_ = plt.hist(nohitter_times, bins=50)
_ = plt.xlabel('Games between no-hitters')
_ = plt.ylabel('Count')

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



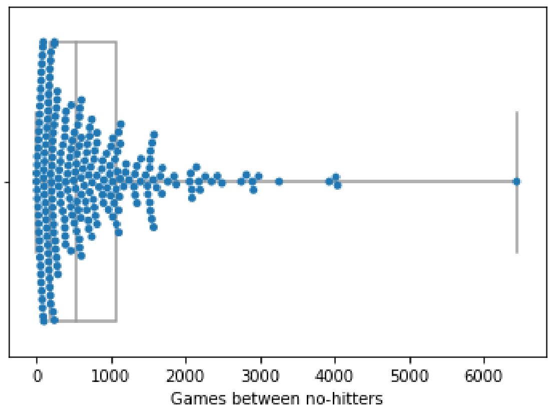
In [133]:

```
# Plot the PDF and label axes
_ = plt.hist(nohitter_times,
             bins=50, density=True, histtype='step')
_ = plt.xlabel('Games between no-hitters')
_ = plt.ylabel('PDF')

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



In [134]:

```
# Plot a combined boxplot and swarmplot
_ = sns.boxplot(x = nohitter_times,whis=np.inf,color='white')
_ = sns.swarmplot(x = nohitter_times)

# Label the axes
_ = plt.xlabel('Games between no-hitters')

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



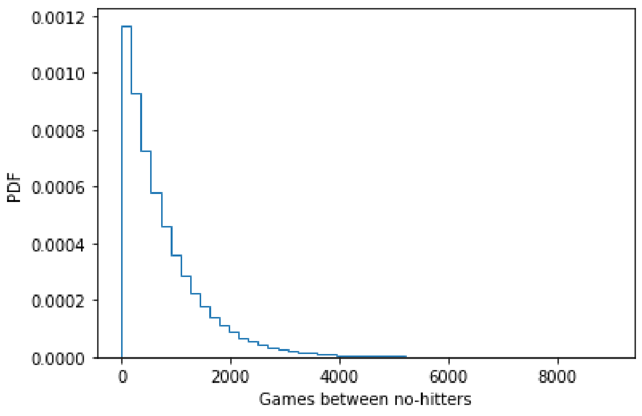
Determine if the time between no-hitters is exponentialy distributed

In [135]:

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

# Compute mean no-hitter time: tau
tau = np.mean(nohitter_times)

# Draw out of an exponential distribution with parameter tau: inter_nohitter_time
inter_nohitter_times = np.random.exponential(tau, 100000)
```

In [136]:

```
# Plot the PDF and label axes
_ = plt.hist(inter_nohitter_times,
             bins=50, density=True, histtype='step')
_ = plt.xlabel('Games between no-hitters')
_ = plt.ylabel('PDF')

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



Nice work! We see the typical shape of the Exponential distribution, going from a maximum at 0 and decaying to the right.

Do the data follow our story?

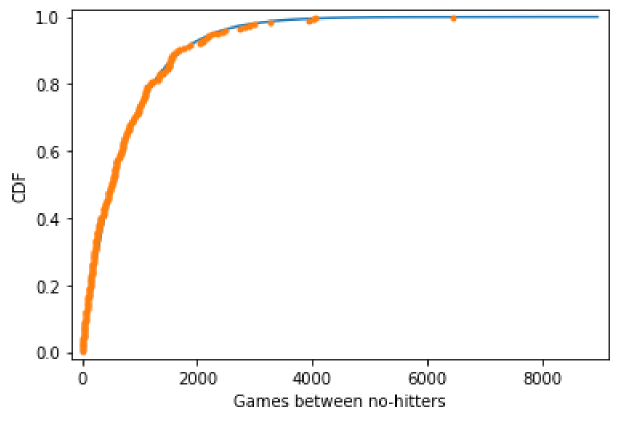
You have modeled no-hitters using an Exponential distribution. Create an ECDF of the real data. Overlay the theoretical CDF with the ECDF from the data. This helps you to verify that the Exponential distribution describes the observed data.

In [137]:

```
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
```

In [138]:

```
# Create an ECDF from real data: x, y
x, y = ecdf(nohitter_times)

# Create a CDF from theoretical samples: x_theor, y_theor
x_theor, y_theor = ecdf(inter_nohitter_times)

# Overlay the plots
plt.plot(x_theor, y_theor)
plt.plot(x, y, marker='.', linestyle='none')

# Margins and axis labels
plt.margins(.02)
plt.xlabel('Games between no-hitters')
plt.ylabel('CDF')

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



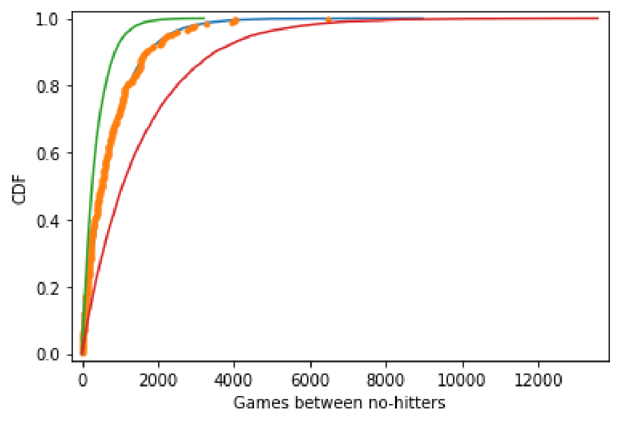
It looks like no-hitters in the modern era of Major League Baseball are Exponentially distributed. Based on the story of the Exponential distribution, this suggests that they are a random process; when a no-hitter will happen is independent of when the last no-hitter was.

How is this parameter optimal?

Now sample out of an exponential distribution with τ being twice as large as the optimal τ. Do it again for τ half as large. Make CDFs of these samples and overlay them with your data. You can see that they do not reproduce the data as well. Thus, the τ you computed from the mean inter-no-hitter times is optimal in that it best reproduces the data.

In [139]:

```
# Plot the theoretical CDFs
plt.plot(x_theor, y_theor)
plt.plot(x, y, marker='.', linestyle='none')
plt.margins(0.02)
plt.xlabel('Games between no-hitters')
plt.ylabel('CDF')

# Take samples with half tau: samples_half
samples_half = np.random.exponential(tau/2,10000)

# Take samples with double tau: samples_double
samples_double = np.random.exponential(2*tau,10000)

# Generate CDFs from these samples
x_half, y_half = ecdf(samples_half)
x_double, y_double = ecdf(samples_double)

# Plot these CDFs as lines
_ = plt.plot(x_half, y_half)
_ = plt.plot(x_double, y_double)

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



Great work! Notice how the value of tau given by the mean matches the data best. In this way, tau is an optimal parameter.

Confidence interval on the rate of no-hitters

Consider again the inter-no-hitter intervals for the modern era of baseball. Generate 10,000 bootstrap replicates of the optimal parameter □$\tau$. Plot a histogram of your replicates and report a 95% confidence interval.

In [140]:

```
def bootstrap_replicate_1d(data, func):
    """Generate bootstrap replicate of 1D data."""
    bs_sample = np.random.choice(data, len(data))
    return func(bs_sample)
```

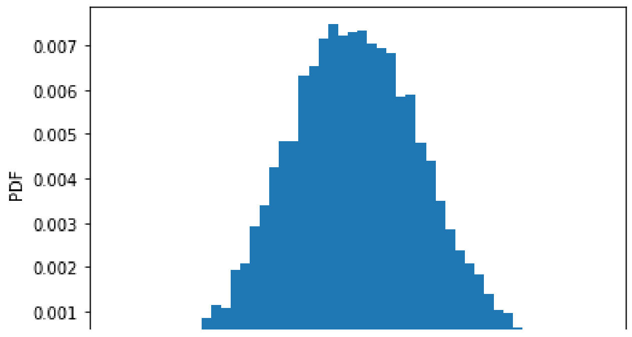
In [141]:

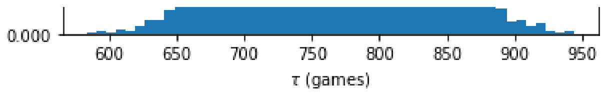
```
def draw_bs_reps(data, func, size=1):
    """Draw bootstrap replicates."""

    # Initialize array of replicates: bs_replicates
    bs_replicates = np.empty(shape=size)

    # Generate replicates
    for i in range(size):
        bs_replicates[i] = bootstrap_replicate_1d(data,func)

    return bs_replicates
```

In [142]:

```
# Draw bootstrap replicates of the mean no-hitter time (equal to tau): bs_replicates
bs_replicates = draw_bs_reps(nohitter_times, np.mean,10000)

# Compute the 95% confidence interval: conf_int
conf_int = np.percentile(bs_replicates,[2.5,97.5])

# Print the confidence interval
print('95% confidence interval of the bootstrap replicates=',conf_int, 'games')

# Plot the histogram of the replicates
_ = plt.hist(bs_replicates, bins=50, density=True)
_ = plt.xlabel(r'$\tau$ (games)')
_ = plt.ylabel('PDF')

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

```
95% confidence interval of the bootstrap replicates= [661.97370518 870.59501992] games
```





This gives you an estimate of what the typical time between no-hitters is. It could be anywhere between 660 and 870 games.

A time-on-website analog

It turns out that you already did a hypothesis test analogous to an A/B test where you are interested in how much time is spent on the website before and after an ad campaign. The frog tongue force (a continuous quantity like time on the website) is an analog. "Before" = Frog A and "after" = Frog B. Let's practice this again with something that actually is a before/after scenario.

We return to the no-hitter data set. In 1920, Major League Baseball implemented important rule changes that ended the so-called dead ball era. Importantly, the pitcher was no longer allowed to spit on or scuff the ball, an activity that greatly favors pitchers. In this problem you will perform an A/B test to determine if these rule changes resulted in a slower rate of no-hitters (i.e., longer average time between no-hitters) using the difference in mean inter-no-hitter time as your test statistic. The inter-no-hitter times for the respective eras are stored in the arrays `nht_dead` and `nht_live`, where "nht" is meant to stand for "no-hitter time."

In [143]:

```
nht_dead = np.array([  -1,  894,   10,  130,    1,  934,   29,    6,  485,  254,  372,
         81,  191,  355,  180,  286,   47,  269,  361,  173,  246,  492,
        462, 1319,   58,  297,   31, 2970,  640,  237,  434,  570,   77,
        271,  563, 3365,   89,    0,  379,  221,  479,  367,  628,  843,
       1613, 1101,  215,  684,  814,  278,  324,  161,  219,  545,  715,
        966,  624,   29,  450,  107,   20,   91, 1325,  124, 1468,  104,
       1309,  429,   62, 1878, 1104,  123,  251,   93,  188,  983,  166,
         96,  702,   23,  524,   26,  299,   59,   39,   12,    2,  308,
       1114,  813,  887])

nht_live = np.array([ 645, 2088,   42, 2090,   11,  886, 1665, 1084, 2900, 2432,  750,
       4021, 1070, 1765, 1322,   26,  548, 1525,   77, 2181, 2752,  127,
       2147,  211,   41, 1575,  151,  479,  697,  557, 2267,  542,  392,
         73,  603,  233,  255,  528,  397, 1529, 1023, 1194,  462,  583,
         37,  943,  996,  480, 1497,  717,  224,  219, 1531,  498,   44,
        288,  267,  600,   52,  269, 1086,  386,  176, 2199,  216,   54,
        675, 1243,  463,  650,  171,  327,  110,  774,  509,    8,  197,
        136,   12, 1124,   64,  380,  811,  232,  192,  731,  715,  226,
        605,  539, 1491,  323,  240,  179,  702,  156,   82, 1397,  354,
        778,  603, 1001,  385,  986,  203,  149,  576,  445,  180, 1403,
        252,  675, 1351, 2983, 1568,   45,  899, 3260, 1025,   31,  100,
       2055, 4043,   79,  238, 3931, 2351,  595,  110,  215,    0,  563,
        206,  660,  242,  577,  179,  157,  192,  192, 1848,  792, 1693,
         55,  388,  225, 1134, 1172, 1555,   31, 1582, 1044,  378, 1687,
       2915,  280,  765, 2819,  511, 1521,  745, 2491,  580, 2072, 6450,
        578,  745, 1075, 1103, 1549, 1520,  138, 1202,  296,  277,  351,
        391,  950,  459,   62, 1056, 1128,  139,  420,   87,   71,  814,
        603, 1349,  162, 1027,  783,  326,  101,  876,  381,  905,  156,
        419,  239,  119,  129,  467])
```

In [144]:

```
def diff_of_means(data_1, data_2):
    """Difference in means of two arrays."""

    # The difference of means of data_1, data_2: diff
    diff = np.mean(data_1) - np.mean(data_2)

    return diff
```

In [145]:

```
def permutation_sample(data1, data2):
    """Generate a permutation sample from two data sets."""

    # Concatenate the data sets: data
    data = np.concatenate((data1,data2))

    # Permute the concatenated array: permuted_data
    permuted_data = np.random.permutation(data)

    # Split the permuted array into two: perm_sample_1, perm_sample_2
    perm_sample_1 = permuted_data[:len(data1)]
    perm_sample_2 = permuted_data[len(data1):]

    return perm_sample_1, perm_sample_2
```

In [146]:

```
def draw_perm_reps(data_1, data_2, func, size=1):
    """Generate multiple permutation replicates."""

    # Initialize array of replicates: perm_replicates
    perm_replicates = np.empty(size)

    for i in range(size):
        # Generate permutation sample
        perm_sample_1, perm_sample_2 = permutation_sample(data_1,data_2)

        # Compute the test statistic
        perm_replicates[i] = func(perm_sample_1, perm_sample_2)

        return perm_replicates
```

In [147]:

```
# Compute the observed difference in mean inter-no-hitter times: nht_diff_obs
nht_diff_obs = diff_of_means(nht_dead,nht_live)
print(nht_diff_obs)
```

```
-345.0011367942402
```

In [148]:

```
# Acquire 10,000 permutation replicates of difference in mean no-hitter time: perm_replicates
perm_replicates = draw_perm_reps(nht_dead,nht_live,diff_of_means,size=10000)
perm_replicates
```

Out[148]:

```
array([1.34282683e+002, 8.95283735e-312, 1.06161801e-051, ...,
       1.03753786e-322, 4.94065646e-324, 9.88131292e-323])
```

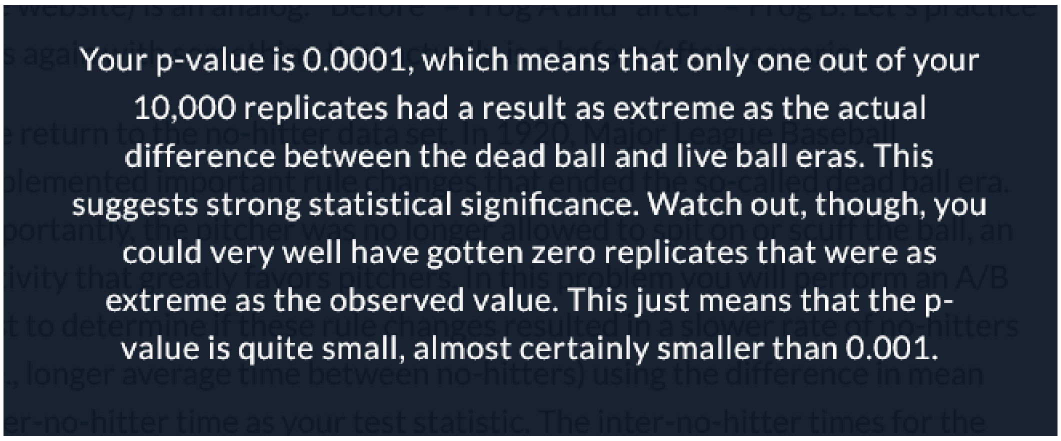
In [149]:

```
# Compute and print the p-value: p
```

```
p = np.sum(perm_replicates <= nht_diff_obs) / len(perm_replicates)

print('p-val =', p)
```

```
p-val = 0.0341
```

```
C:\Users\smpet\Anaconda3\lib\site-packages\ipykernel_launcher.py:2: RuntimeWarning: invalid value
encountered in less_equal
```


Your p-value is 0.0001, which means that only one out of your 10,000 replicates had a result as extreme as the actual difference between the dead ball and live ball eras. This suggests strong statistical significance. Watch out, though, you could very well have gotten zero replicates that were as extreme as the observed value. This just means that the p-value is quite small, almost certainly smaller than 0.001.

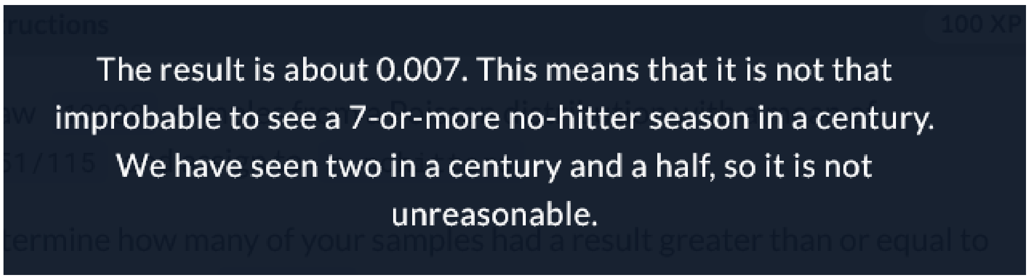
Was 2015 anomalous?

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?

In [150]:

```
# 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)
print(n_large)

# 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)
```

```
70
Probability of seven or more no-hitters: 0.007
```


The result is about 0.007. This means that it is not that improbable to see a 7-or-more no-hitter season in a century. We have seen two in a century and a half, so it is not unreasonable.

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 then* 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.

In [151]:

```
def successive_poisson(tau1, tau2, size=1):
    """Compute time for arrival of 2 successive Poisson processes."""
    # 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
```

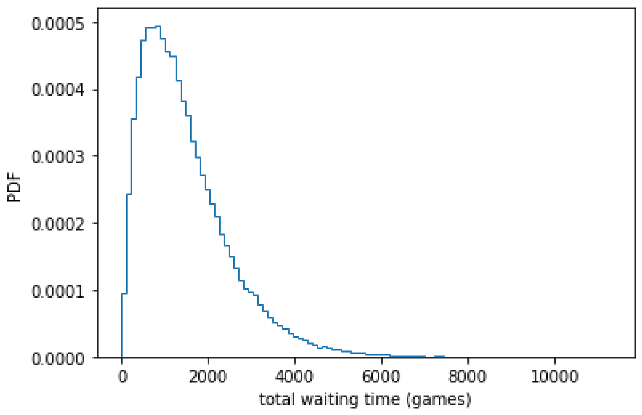
Great work! We'll put the function to use in the next exercise.

Distribution of no-hitters and cycles

Now, you'll use your sampling function to compute the waiting time to observe 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.

In [152]:

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

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

# Label axes
_ = plt.xlabel('total waiting time (games)')
_ = plt.ylabel('PDF')

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



Great work! Notice that the PDF is peaked, unlike the waiting time for a single Poisson process. For fun (and enlightenment), I encourage you to also plot the CDF.

Sheffield Weather Station

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"

> ### Visualizing bootstrap samples
>
> In this exercise, you will generate bootstrap samples from the set of annual rainfall data measured at the Sheffield Weather Station in the UK from 1883 to 2015. The data are stored in the NumPy array `rainfall` in units of millimeters (mm). By graphically displaying the bootstrap samples with an ECDF, you can get a feel for how bootstrap sampling allows probabilistic descriptions of data.

In [6]:

```python
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

In [7]:

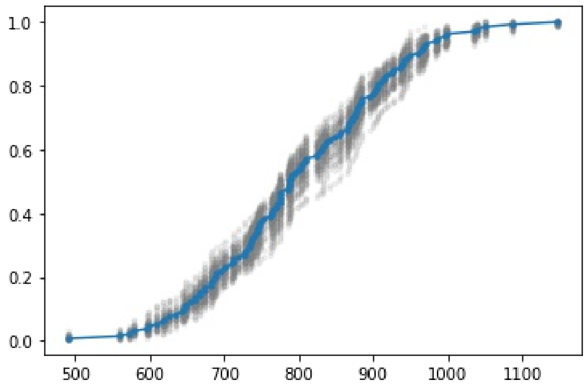
```python
rainfall = np.array([ 875.5,  648.2,  788.1,  940.3,  491.1,  743.5,  730.1,  686.5,
        878.8,  865.6,  654.9,  831.5,  798.1,  681.8,  743.8,  689.1,
        752.1,  837.2,  710.6,  749.2,  967.1,  701.2,  619. ,  747.6,
        803.4,  645.6,  804.1,  787.4,  646.8,  997.1,  774. ,  734.5,
        835. ,  840.7,  659.6,  828.3,  909.7,  856.9,  578.3,  904.2,
        883.9,  740.1,  773.9,  741.4,  866.8,  871.1,  712.5,  919.2,
        927.9,  809.4,  633.8,  626.8,  871.3,  774.3,  898.8,  789.6,
        936.3,  765.4,  882.1,  681.1,  661.3,  847.9,  683.9,  985.7,
        771.1,  736.6,  713.2,  774.5,  937.7,  694.5,  598.2,  983.8,
        700.2,  901.3,  733.5,  964.4,  609.3, 1035.2,  718. ,  688.6,
        736.8,  643.3, 1038.5,  969. ,  802.7,  876.6,  944.7,  786.6,
        770.4,  808.6,  761.3,  774.2,  559.3,  674.2,  883.6,  823.9,
        960.4,  877.8,  940.6,  831.8,  906.2,  866.5,  674.1,  998.1,
        789.3,  915. ,  737.1,  763. ,  666.7,  824.5,  913.8,  905.1,
        667.8,  747.4,  784.7,  925.4,  880.2, 1086.9,  764.4, 1050.1,
        595.2,  855.2,  726.9,  785.2,  948.8,  970.6,  896. ,  618.4,
        572.4, 1146.4,  728.2,  864.2,  793. ])
```

In [8]:

```python
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
```

In [9]:

```python
for _ in range(50):
    # Generate bootstrap sample: bs_sample
    # Generate bootstrap sample: bs_sample
    bs_sample = np.random.choice(rainfall, size=len(rainfall))

    # Compute and plot ECDF from bootstrap sample
    x, y = ecdf(bs_sample)
    _ = plt.plot(x, y, marker='.', linestyle='none',
                 color='gray', alpha=0.1)

# Compute and plot ECDF from original data
x, y = ecdf(rainfall)
_ = plt.plot(x, y, marker='.')
```



Good job! Notice how the bootstrap samples give an idea of how the distribution of rainfalls is spread.

In [10]:

```
def bootstrap_replicate_1d(data, func):
    """Generate bootstrap replicate of 1D data."""
    bs_sample = np.random.choice(data, len(data))
    return func(bs_sample)
```

In [11]:

```
def draw_bs_reps(data, func, size=1):
    """Draw bootstrap replicates."""

    # Initialize array of replicates: bs_replicates
    bs_replicates = np.empty(shape=size)

    # Generate replicates
    for i in range(size):
        bs_replicates[i] = bootstrap_replicate_1d(data,func)

    return bs_replicates
```

Bootstrap replicates of the mean and the SEM

In this exercise, you will compute a bootstrap estimate of the probability density function of the mean annual rainfall at the Sheffield Weather Station. Remember, we are estimating the mean annual rainfall we would get if the Sheffield Weather Station could repeat all of the measurements from 1883 to 2015 over and over again. This is a *probabilistic* estimate of the mean. You will plot the PDF as a histogram, and you will see that it is Normal.

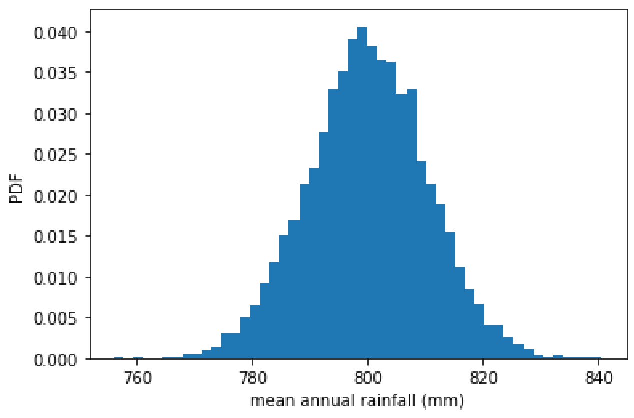
In fact, it can be shown theoretically that under not-too-restrictive conditions, the value of the mean will always be Normally distributed. (This does not hold in general, just for the mean and a few other statistics.) The standard deviation of this distribution, called the **standard error of the mean**, or SEM, is given by the standard deviation of the data divided by the square root of the number of data points. I.e., for a data set, `sem = np.std(data) / np.sqrt(len(data))`. Using hacker statistics, you get this same result without the need to derive it, but you will verify this result from your bootstrap replicates.

The dataset has been pre-loaded for you into an array called `rainfall`.

In [12]:

```
# Take 10,000 bootstrap replicates of the mean: bs_replicates
bs_replicates = draw_bs_reps(rainfall,np.mean,10000)

# Compute and print SEM
sem = np.std(rainfall) / np.sqrt(len(rainfall))
print(sem)

# Compute and print standard deviation of bootstrap replicates
bs_std = np.std(bs_replicates)
print(bs_std)

# Make a histogram of the results

#C:\Users\smpet\Anaconda3\lib\site-packages\ipykernel_launcher.py:13:
MatplotlibDeprecationWarning:
#The 'normed' kwarg was deprecated in Matplotlib 2.1 and will be removed in 3.1. Use 'density' ins
tead.
#  del sys.path[0]

_ = plt.hist(bs_replicates, bins=50, density=True)
_ = plt.xlabel('mean annual rainfall (mm)')
_ = plt.ylabel('PDF')

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

```
10.510549150506188
10.364395840934675
```



Great work! Notice that the SEM we got from the known expression and the bootstrap replicates is the same and the distribution of the bootstrap replicates of the mean is Normal.

Confidence intervals of rainfall data

A *confidence interval* gives upper and lower bounds on the range of parameter values you might expect to get if we repeat our measurements. For named distributions, you can compute them analytically or look them up, but one of the many beautiful properties of the bootstrap method is that you can take percentiles of your bootstrap replicates to get your confidence interval. Conveniently, you can use the `np.percentile()` function.

Use the bootstrap replicates you just generated to compute the 95% confidence interval. That is, give the 2.5th and 97.5th percentile of your bootstrap replicates stored as `bs_replicates` . What is the 95% confidence interval?

In [13]:

```
np.percentile(bs_replicates,[2.5,97.5])
```

Out[13]:

```
array([779.42353383, 820.23086466])
```

Correct! See, it's simple to get confidence intervals using bootstrap!

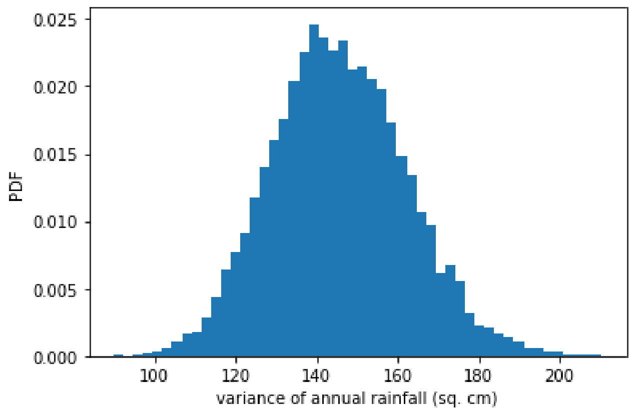
Bootstrap replicates of other statistics

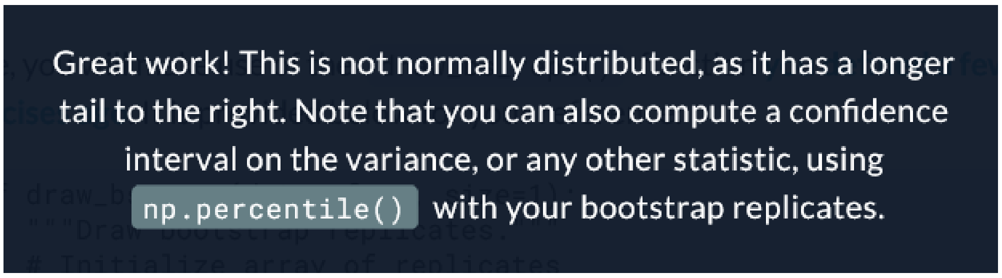
We saw in a previous exercise that the mean is Normally distributed. This does not necessarily hold for other statistics, but no worry: as hackers, we can always take bootstrap replicates! In this exercise, you'll generate bootstrap replicates for the variance of the annual rainfall at the Sheffield Weather Station and plot the histogram of the replicates.

In [14]:

```
# Generate 10,000 bootstrap replicates of the variance: bs_replicates
bs_replicates = draw_bs_reps(rainfall,np.var,10000)

# Put the variance in units of square centimeters
bs_replicates = bs_replicates/100

# Make a histogram of the results
_ = plt.hist(bs_replicates, bins=50, density=True)
_ = plt.xlabel('variance of annual rainfall (sq. cm)')
_ = plt.ylabel('PDF')

# Show the plot
```

```
plt.show()
```




Great work! This is not normally distributed, as it has a longer tail to the right. Note that you can also compute a confidence interval on the variance, or any other statistic, using `np.percentile()` with your bootstrap replicates.

Generating a permutation sample

In the video, you learned that permutation sampling is a great way to simulate the hypothesis that two variables have identical probability distributions. This is often a hypothesis you want to test, so in this exercise, you will write a function to generate a permutation sample from two data sets.

Remember, a permutation sample of two arrays having respectively `n1` and `n2` entries is constructed by concatenating the arrays together, scrambling the contents of the concatenated array, and then taking the first `n1` entries as the permutation sample of the first array and the last `n2` entries as the permutation sample of the second array.

In [15]:

```
def permutation_sample(data1, data2):
    """Generate a permutation sample from two data sets."""

    # Concatenate the data sets: data
    data = np.concatenate((data1,data2))

    # Permute the concatenated array: permuted_data
    permuted_data = np.random.permutation(data)

    # Split the permuted array into two: perm_sample_1, perm_sample_2
    perm_sample_1 = permuted_data[:len(data1)]
    perm_sample_2 = permuted_data[len(data1):]

    return perm_sample_1, perm_sample_2
```

Visualizing permutation sampling

To help see how permutation sampling works, in this exercise you will generate permutation samples and look at them graphically.

We will use the Sheffield Weather Station data again, this time considering the monthly rainfall in June (a dry month) and November (a wet month). We expect these might be differently distributed, so we will take permutation samples to see how their ECDFs *would look if* they were identically distributed.

The data are stored in the Numpy arrays `rain_june` and `rain_november.`

In [16]:

```
rain_june = np.array([ 66.2,  39.7,  76.4,  26.5,  11.2,  61.8,   6.1,  48.4,  89.2,
       104. ,  34. ,  60.6,  57.1,  79.1,  90.9,  32.3,  63.8,  78.2,
        27.5,  43.4,  30.1,  17.3,  77.5,  44.9,  92.2,  39.6,  79.4,
        66.1,  53.5,  98.5,  20.8,  55.5,  39.6,  56. ,  65.1,  14.8,
        13.2,  88.1,   8.4,  32.1,  19.6,  40.4,   2.2,  77.5, 105.4,
        77.2,  38. ,  27.1, 111.8,  17.2,  26.7,  23.3,  77.2,  87.2,
        27.7,  50.6,  60.3,  15.1,   6. ,  29.4,  39.3,  56.3,  80.4,
        85.3,  68.4,  72.5,  13.3,  28.4,  14.7,  37.4,  49.5,  57.2,
        85.9,  82.1,  31.8, 126.6,  30.7,  41.4,  33.9,  13.5,  99.1,
        70.2,  91.8,  61.3,  13.7,  54.9,  62.5,  24.2,  69.4,  83.1,
        44. ,  48.5,  11.9,  16.6,  66.4,  90. ,  34.9, 132.8,  33.4,
       225. ,   7.6,  40.9,  76.5,  48. , 140. ,  55.9,  54.1,  46.4,
        68.6,  52.2, 108.3,  14.6,  11.3,  29.8, 130.9, 152.4,  61. ,
        46.6,  43.9,  30.9, 111.1,  68.5,  42.2,   9.8, 285.6,  56.7,
       168.2,  41.2,  47.8, 166.6,  37.8,  45.4,  43.2])
```

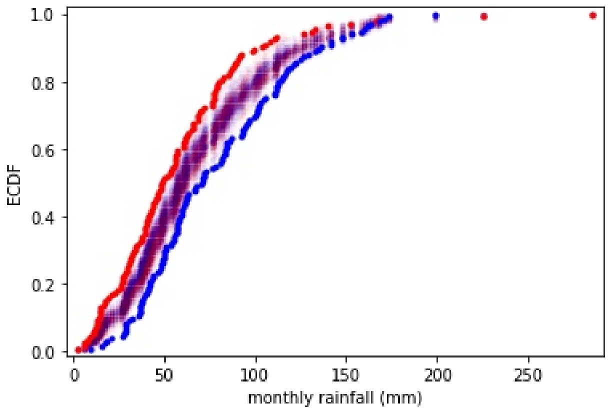
In [17]:

```
rain_november = np.array([ 83.6,  30.9,  62.2,  37. ,  41. , 160.2,  18.2, 122.4,  71.3,
        44.2,  49.1,  37.6, 114.5,  28.8,  82.5,  71.9,  50.7,  67.7,
       112. ,  63.6,  42.8,  57.2,  99.1,  86.4,  84.4,  38.1,  17.7,
       102.2, 101.3,  58. ,  82. , 101.4,  81.4, 100.1,  54.6,  39.6,
        57.5,  29.2,  48.8,  37.3, 115.4,  55.6,  62. ,  95. ,  84.2,
       118.1, 153.2,  83.4, 104.7,  59. ,  46.4,  50. , 147.6,  76.8,
        59.9, 101.8, 136.6, 173. ,  92.5,  37. ,  59.8, 142.1,   9.9,
       158.2,  72.6,  28. , 112.9, 119.3, 199.2,  50.7,  44. , 170.7,
        67.2,  21.4,  61.3,  15.6, 106. , 116.2,  42.3,  38.5, 132.5,
        40.8, 147.5,  93.9,  71.4,  87.3, 163.7, 141.4,  62.6,  84.9,
        28.8, 121.1,  28.6,  32.4, 112. ,  50. ,  96.9,  81.8,  70.4,
       117.5,  41.2, 124.9,  78.2,  93. ,  53.5,  50.5,  42.6,  47.9,
        73.1, 129.1,  56.9, 103.3,  60.5, 134.3,  93.1,  49.5,  48.2,
       167.9,  27. , 111.1,  55.4,  36.2,  57.4,  66.8,  58.3,  60. ,
       161.6, 112.7,  37.4, 110.6,  56.6,  95.8, 126.8])
```

In [18]:

```
for _ in range(50):
    # Generate permutation samples
    perm_sample_1, perm_sample_2 = permutation_sample(rain_june, rain_november)


    # Compute ECDFs
    x_1, y_1 = ecdf(perm_sample_1)
    x_2, y_2 = ecdf(perm_sample_2)

    # Plot ECDFs of permutation sample
    _ = plt.plot(x_1, y_1, marker='.', linestyle='none',
                 color='red', alpha=0.02)
    _ = plt.plot(x_2, y_2, marker='.', linestyle='none',
                 color='blue', alpha=0.02)
```

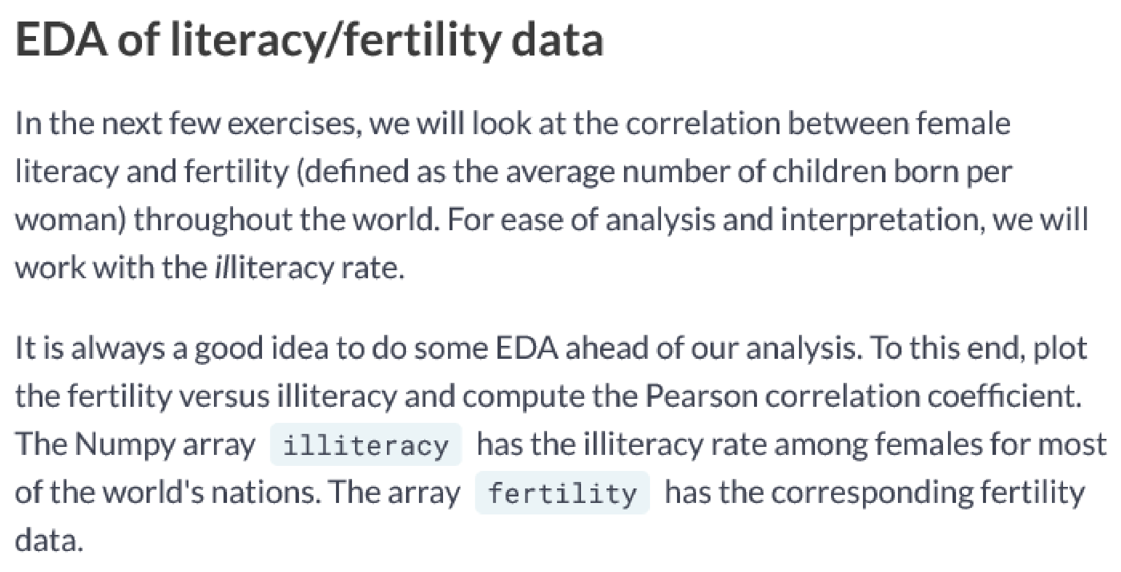
```
# Create and plot ECDFs from original data
x_1, y_1 = ecdf(rain_june)
x_2, y_2 = ecdf(rain_november)
_ = plt.plot(x_1, y_1, marker='.', linestyle='none', color='red')
_ = plt.plot(x_2, y_2, marker='.', linestyle='none', color='blue')

# Label axes, set margin, and show plot
plt.margins(0.02)
_ = plt.xlabel('monthly rainfall (mm)')
_ = plt.ylabel('ECDF')
plt.show()
```



Great work! Notice that the permutation samples ECDFs overlap and give a purple haze. None of the ECDFs from the permutation samples overlap with the observed data, suggesting that the hypothesis is not commensurate with the data. June and November rainfall are not identically distributed.

Literacy vs Fertility

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"



EDA of literacy/fertility data

In the next few exercises, we will look at the correlation between female literacy and fertility (defined as the average number of children born per woman) throughout the world. For ease of analysis and interpretation, we will work with the *il*literacy rate.

It is always a good idea to do some EDA ahead of our analysis. To this end, plot the fertility versus illiteracy and compute the Pearson correlation coefficient. The Numpy array `illiteracy` has the illiteracy rate among females for most of the world's nations. The array `fertility` has the corresponding fertility data.

In [24]:

```
import numpy as np
import matplotlib.pyplot as plt
```

In [25]:

```
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]
```

In [26]:

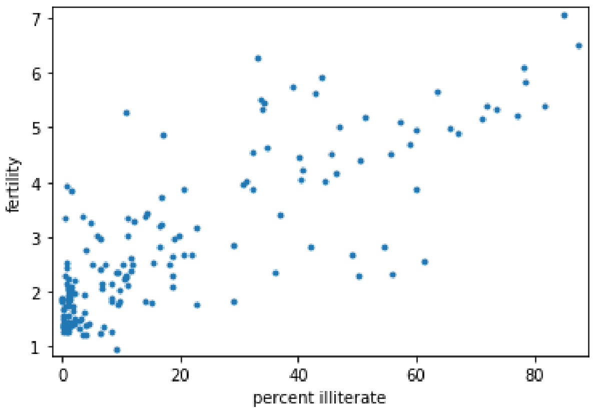
```
illiteracy = np.array([ 9.5, 49.2,  1. , 11.2,  9.8, 60. , 50.2, 51.2,  0.6,  1. ,  8.5,
        6.1,  9.8,  1. , 42.2, 77.2, 18.7, 22.8,  8.5, 43.9,  1. ,  1. ,
        1.5, 10.8, 11.9,  3.4,  0.4,  3.1,  6.6, 33.7, 40.4,  2.3, 17.2,
        0.7, 36.1,  1. , 33.2, 55.9, 30.8, 87.4, 15.4, 54.6,  5.1,  1.1,
       10.2, 19.8,  0. , 40.7, 57.2, 59.9,  3.1, 55.7, 22.8, 10.9, 34.7,
       32.2, 43. ,  1.3,  1. ,  0.5, 78.4, 34.2, 84.9, 29.1, 31.3, 18.3,
       81.8, 39. , 11.2, 67. ,  4.1,  0.2, 78.1,  1. ,  7.1,  1. , 29. ,
        1.1, 11.7, 73.6, 33.9, 14. ,  0.3,  1. ,  0.8, 71.9, 40.1,  1. ,
        2.1,  3.8, 16.5,  4.1,  0.5, 44.4, 46.3, 18.7,  6.5, 36.8, 18.6,
       11.1, 22.1, 71.1,  1. ,  0. ,  0.9,  0.7, 45.5,  8.4,  0. ,  3.8,
        8.5,  2. ,  1. , 58.9,  0.3,  1. , 14. , 47. ,  4.1,  2.2,  7.2,
        0.3,  1.5, 50.5,  1.3,  0.6, 19.1,  6.9,  9.2,  2.2,  0.2, 12.3,
        4.9,  4.6,  0.3, 16.5, 65.7, 63.5, 16.8,  0.2,  1.8,  9.6, 15.2,
       14.4,  3.3, 10.6, 61.3, 10.9, 32.2,  9.3, 11.6, 20.7,  6.5,  6.7,
        3.5,  1. ,  1.6, 20.5,  1.5, 16.7,  2. ,  0.9])
```

In [27]:

```
fertility = np.array([1.769, 2.682, 2.077, 2.132, 1.827, 3.872, 2.288, 5.173, 1.393,
       1.262, 2.156, 3.026, 2.033, 1.324, 2.816, 5.211, 2.1  , 1.781,
       1.822, 5.908, 1.881, 1.852, 1.39 , 2.281, 2.505, 1.224, 1.361,
       1.468, 2.404, 5.52 , 4.058, 2.223, 4.859, 1.267, 2.342, 1.579,
       6.254, 2.334, 3.961, 6.505, 2.53 , 2.823, 2.498, 2.248, 2.508,
       3.04 , 1.854, 4.22 , 5.1  , 4.967, 1.325, 4.514, 3.173, 2.308,
       4.62 , 4.541, 5.637, 1.926, 1.747, 2.294, 5.841, 5.455, 7.069,
       2.859, 4.018, 2.513, 5.405, 5.737, 3.363, 4.89 , 1.385, 1.505,
       6.081, 1.784, 1.378, 1.45 , 1.841, 1.37 , 2.612, 5.329, 5.33 ,
       3.371, 1.281, 1.871, 2.153, 5.378, 4.45 , 1.46 , 1.436, 1.612,
       3.19 , 2.752, 3.35 , 4.01 , 4.166, 2.642, 2.977, 3.415, 2.295,
       3.019, 2.683, 5.165, 1.849, 1.836, 2.518, 2.43 , 4.528, 1.263,
       1.885, 1.943, 1.899, 1.442, 1.953, 4.697, 1.582, 2.025, 1.841,
       5.011, 1.212, 1.502, 2.516, 1.367, 2.089, 4.388, 1.854, 1.748,
       2.978, 2.152, 2.362, 1.988, 1.426, 3.29 , 3.264, 1.436, 1.393,
       2.822, 4.969, 5.659, 3.24 , 1.693, 1.647, 2.36 , 1.792, 3.45 ,
       1.516, 2.233, 2.563, 5.283, 3.885, 0.966, 2.373, 2.663, 1.251,
       2.052, 3.371, 2.093, 2.   , 3.883, 3.852, 3.718, 1.732, 3.928])
```

In [28]:

```python
# Plot the illiteracy rate versus fertility
_ = plt.plot(illiteracy, fertility, marker='.', linestyle='none')

# Set the margins and label axes
plt.margins(.02)
_ = plt.xlabel('percent illiterate')
_ = plt.ylabel('fertility')

# Show the plot
plt.show()

# Show the Pearson correlation coefficient
print(pearson_r(illiteracy, fertility))
```



```
0.8041324026815341
```

You can see the correlation between illiteracy and fertility by eye, and by the substantial Pearson correlation coefficient of 0.8. It is difficult to resolve in the scatter plot, but there are many points around near-zero illiteracy and about 1.8 children/woman.

Linear regression

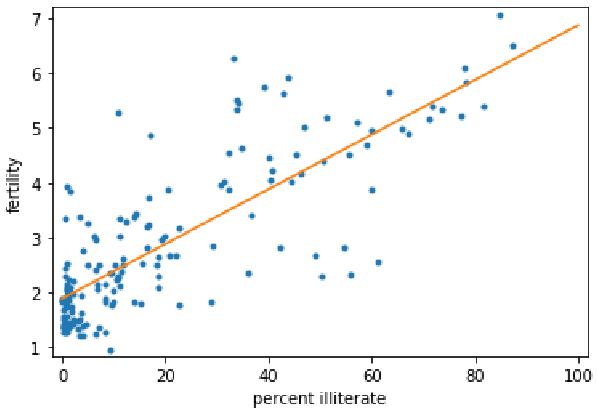
We will assume that fertility is a linear function of the female illiteracy rate. That is, $f = ai + b$, where a is the slope and b is the intercept. We can think of the intercept as the minimal fertility rate, probably somewhere between one and two. The slope tells us how the fertility rate varies with illiteracy. We can find the best fit line using `np.polyfit()` .

Plot the data and the best fit line. Print out the slope and intercept. (Think: what are their units?)

In [29]:

```
# Plot the illiteracy rate versus fertility
_ = plt.plot(illiteracy, fertility, marker='.', linestyle='none')
plt.margins(0.02)

# Perform a linear regression using np.polyfit(): a, b
a, b = np.polyfit(illiteracy, fertility, 1)

# Print the results to the screen
print('slope =', a, 'children per woman / percent illiterate')
print('intercept =', b, 'children per woman')

# Make theoretical line to plot
x = np.array([0,100])
y = a * x + b

# Add regression line to your plot
_ = plt.plot(x, y)
_ = plt.xlabel('percent illiterate')
_ = plt.ylabel('fertility')


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

```
slope = 0.04979854809063423 children per woman / percent illiterate
intercept = 1.888050610636557 children per woman
```



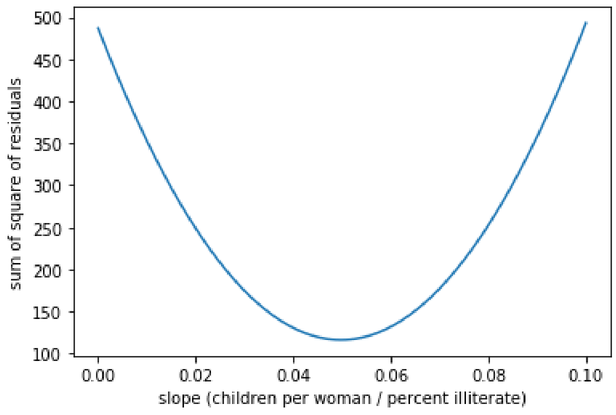
Great work!

How is it optimal?

The function `np.polyfit()` that you used to get your regression parameters finds the *optimal* slope and intercept. It is optimizing the sum of the squares of the residuals, also known as RSS (for residual sum of squares). In this exercise, you will plot the function that is being optimized, the RSS, versus the slope parameter `a` . To do this, fix the intercept to be what you found in the optimization. Then, plot the RSS vs. the slope. Where is it minimal?

In [30]:

```
# Specify slopes to consider: a_vals
a_vals = np.linspace(0, 0.1, 200)

# Initialize sum of square of residuals: rss
rss = np.empty_like(a_vals)

# Compute sum of square of residuals for each value of a_vals
for i, a in enumerate(a_vals):
    rss[i] = np.sum((fertility - a*illiteracy - b)**2)

# Plot the RSS
plt.plot(a_vals, rss, '-')
plt.xlabel('slope (children per woman / percent illiterate)')
plt.ylabel('sum of square of residuals')

plt.show()
```



Great work! Notice that the minimum on the plot, that is the value of the slope that gives the minimum sum of the square of the residuals, is the same value you got when performing the regression.

Pairs bootstrap of literacy/fertility data

Using the function you just wrote, perform pairs bootstrap to plot a histogram describing the estimate of the slope from the illiteracy/fertility data. Also report the 95% confidence interval of the slope. The data is available to you in the NumPy arrays `illiteracy` and `fertility` .

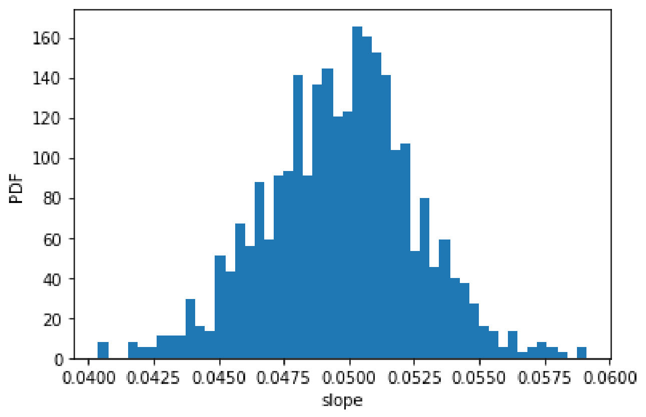
In [31]:

```
def draw_bs_pairs_linreg(x, y, size=1):
    """Perform pairs bootstrap for linear regression."""

    # Set up array of indices to sample from: inds
    inds = np.arange(len(x))

    # Initialize replicates: bs_slope_reps, bs_intercept_reps
    bs_slope_reps = np.empty(size)
    bs_intercept_reps = np.empty(size)

    # Generate replicates
    for i in range(size):
        bs_inds = np.random.choice(inds, size=len(inds))
        bs_x, bs_y = x[bs_inds], y[bs_inds]
        bs_slope_reps[i], bs_intercept_reps[i] = np.polyfit(bs_x,bs_y,1)

    return bs_slope_reps, bs_intercept_reps
```

In [32]:

```
# Generate replicates of slope and intercept using pairs bootstrap
bs_slope_reps, bs_intercept_reps = draw_bs_pairs_linreg(illiteracy, fertility, size=1000)

# Compute and print 95% CI for slope
print(np.percentile(bs_slope_reps, [2.5,97.5]))

# Plot the histogram
_ = plt.hist(bs_slope_reps, bins=50, density=True)
_ = plt.xlabel('slope')
_ = plt.ylabel('PDF')
plt.show()
```

```
[0.04384997 0.05522836]
```



Great work!

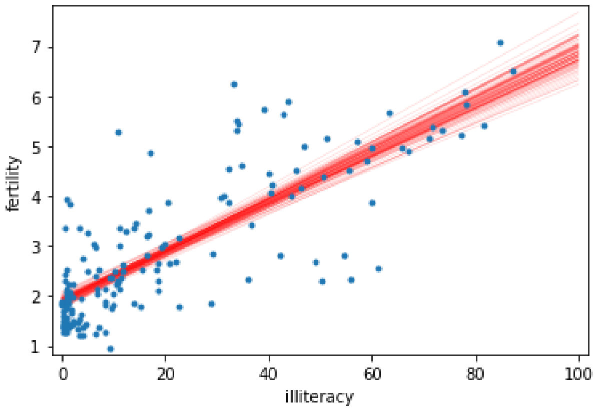
Plotting bootstrap regressions

A nice way to visualize the variability we might expect in a linear regression is to plot the line you would get from each bootstrap replicate of the slope and intercept. Do this for the first 100 of your bootstrap replicates of the slope and intercept (stored as `bs_slope_reps` and `bs_intercept_reps`).

In [33]:

```
# Generate array of x-values for bootstrap lines: x
x = np.array([0,100])
```

```
# Plot the bootstrap lines
for i in range(100):
    _ = plt.plot(x,
                 bs_slope_reps[i] * x + bs_intercept_reps[i],
                 linewidth=0.5, alpha=0.2, color='red')

# Plot the data
_ = plt.plot(illiteracy, fertility, marker='.',linestyle='none')

# Label axes, set the margins, and show the plot
_ = plt.xlabel('illiteracy')
_ = plt.ylabel('fertility')
plt.margins(0.02)
plt.show()
```



Great work! You now have some serious chops for parameter estimation. Let's move on to hypothesis testing!

Hypothesis test on Pearson correlation

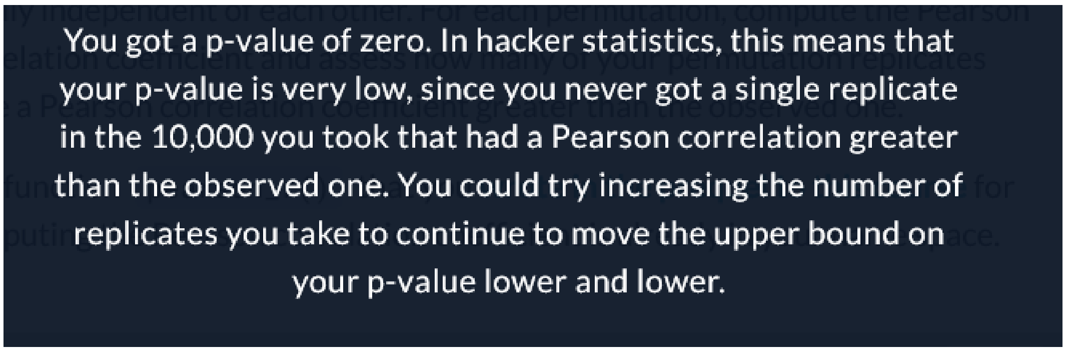
The observed correlation between female illiteracy and fertility may just be by chance; the fertility of a given country may actually be totally independent of its illiteracy. You will test this hypothesis. To do so, permute the illiteracy values but leave the fertility values fixed. This simulates the hypothesis that they are totally independent of each other. For each permutation, compute the Pearson correlation coefficient and assess how many of your permutation replicates have a Pearson correlation coefficient greater than the observed one.

In [34]:

```
# Compute observed correlation: r_obs
r_obs = pearson_r(illiteracy,fertility)

# Initialize permutation replicates: perm_replicates
perm_replicates = np.empty(10000)

# Draw replicates
for i in range(10000):
    # Permute illiteracy measurments: illiteracy_permuted
    illiteracy_permuted = np.random.permutation(illiteracy)

    # Compute Pearson correlation
    perm_replicates[i] = pearson_r(illiteracy_permuted,fertility)
```

```python
# Compute p-value: p
p = np.sum(perm_replicates >= r_obs) / len(perm_replicates)
print('p-val =', p)
```

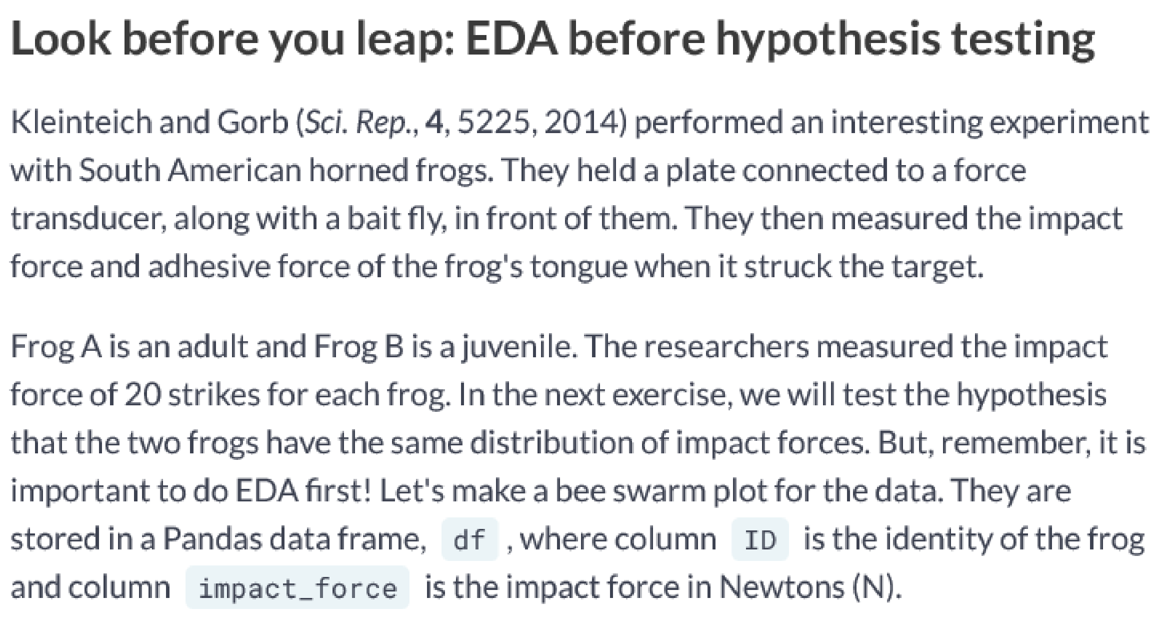
```
p-val = 0.0
```



You got a p-value of zero. In hacker statistics, this means that your p-value is very low, since you never got a single replicate in the 10,000 you took that had a Pearson correlation greater than the observed one. You could try increasing the number of replicates you take to continue to move the upper bound on your p-value lower and lower.

South American Horned Frogs

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"



Look before you leap: EDA before hypothesis testing

Kleinteich and Gorb (*Sci. Rep.*, **4**, 5225, 2014) performed an interesting experiment with South American horned frogs. They held a plate connected to a force transducer, along with a bait fly, in front of them. They then measured the impact force and adhesive force of the frog's tongue when it struck the target.

Frog A is an adult and Frog B is a juvenile. The researchers measured the impact force of 20 strikes for each frog. In the next exercise, we will test the hypothesis that the two frogs have the same distribution of impact forces. But, remember, it is important to do EDA first! Let's make a bee swarm plot for the data. They are stored in a Pandas data frame, `df`, where column `ID` is the identity of the frog and column `impact_force` is the impact force in Newtons (N).

In [19]:

```
import numpy as np
force_a = np.array([1.612,0.605,0.327,0.946,0.541,1.539,0.529,0.628,1.453,0.297,0.703,0.269,0.751,0
.245,1.182,0.515,0.435,0.383,0.457,0.730])
force_b = np.array([0.172,0.142,0.037,0.453,0.355,0.022,0.502,0.273,0.720,0.582,0.198,0.198,0.597,0
.516,0.815,0.402,0.605,0.711,0.614,0.468])
```

In [1]:

```
impact_force = [1.612,0.605,0.327,0.946,0.541,1.539,0.529,0.628,1.453,0.297,0.703,0.269,0.751,0.245
,1.182,0.515,0.435,0.383,0.457,0.730,0.172,0.142,0.037,0.453,0.355,0.022,0.502,0.273,0.720,0.582,0.
198,0.198,0.597,0.516,0.815,0.402,0.605,0.711,0.614,0.468]
ID = ['A','A','A','A','A','A','A','A','A','A','A','A','A','A','A','A','A','A','A','A','B','B','B','B
','B','B','B','B','B','B','B','B','B','B','B','B','B','B','B','B']
```

In [15]:

```
my_dict = {'ID':ID,'impact_force':impact_force,}
```

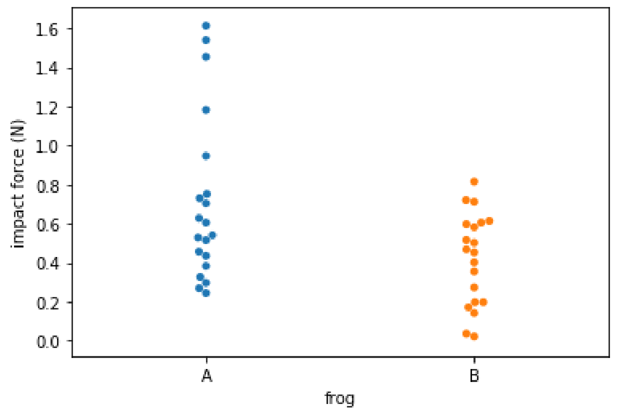
In [8]:

```
import pandas as pd
df = pd.DataFrame(my_dict)
display(df.head())
```

	ID	impact_force
0	A	1.612
1	A	0.605
2	A	0.327
3	A	0.946
4	A	0.541

In [14]:

```
import matplotlib.pyplot as plt
import seaborn as sns

# Make bee swarm plot
_ = sns.swarmplot(data=df,x='ID',y='impact_force')

# Label axes
_ = plt.xlabel('frog')
_ = plt.ylabel('impact force (N)')

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



Eyeballing it, it does not look like they come from the same distribution. Frog A, the adult, has three or four very hard strikes, and Frog B, the juvenile, has a couple weak ones. However, it is possible that with only 20 samples it might be too difficult to tell if they have difference distributions, so we should proceed with the hypothesis test.

Permutation test on frog data

The average strike force of Frog A was 0.71 Newtons (N), and that of Frog B was 0.42 N for a difference of 0.29 N. It is possible the frogs strike with the same force and this observed difference was by chance. You will compute the probability of getting at least a 0.29 N difference in mean strike force under the hypothesis that the distributions of strike forces for the two frogs are identical. We use a permutation test with a test statistic of the difference of means to test this hypothesis.

For your convenience, the data has been stored in the arrays `force_a` and `force_b` .

In [8]:

```python
def diff_of_means(data_1, data_2):
    """Difference in means of two arrays."""

    # The difference of means of data_1, data_2: diff
    diff = np.mean(data_1) - np.mean(data_2)
    #print(diff)
    return diff
```

In [82]:

```python
def permutation_sample(data1, data2):
    """Generate a permutation sample from two data sets."""

    # Concatenate the data sets: data
    data = np.concatenate((data1,data2))

    # Permute the concatenated array: permuted_data
    permuted_data = np.random.permutation(data)

    # Split the permuted array into two: perm_sample_1, perm_sample_2
    perm_sample_1 = permuted_data[:len(data1)]
    perm_sample_2 = permuted_data[len(data1):]

    return perm_sample_1, perm_sample_2
```

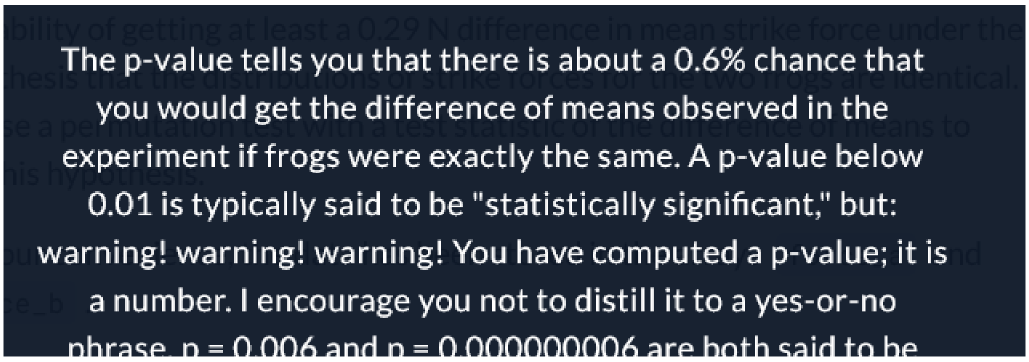
In [83]:

```python
def draw_perm_reps(data_1, data_2, func, size=1):
    """Generate multiple permutation replicates."""

    # Initialize array of replicates: perm_replicates
    perm_replicates = np.empty(size)

    for i in range(size):
        # Generate permutation sample
        perm_sample_1, perm_sample_2 = permutation_sample(data_1,data_2)

        # Compute the test statistic
        perm_replicates[i] = func(perm_sample_1, perm_sample_2)

        return perm_replicates
```

In [87]:

```python
# Compute difference of mean impact force from experiment: empirical_diff_means
empirical_diff_means = diff_of_means(force_a, force_b)

# Draw 10,000 permutation replicates: perm_replicates
perm_replicates = draw_perm_reps(force_a, force_b,diff_of_means, size=10000)

# Compute p-value: p
p = np.sum(perm_replicates >= empirical_diff_means) / len(perm_replicates)

# Print the result
print('p-value =', p)
```

```
p-value = 0.0053
```


The p-value tells you that there is about a 0.6% chance that you would get the difference of means observed in the experiment if frogs were exactly the same. A p-value below 0.01 is typically said to be "statistically significant," but: warning! warning! warning! You have computed a p-value; it is a number. I encourage you not to distill it to a yes-or-no phrase. p = 0.006 and p = 0.000000006 are both said to be

"statistically significant," but they are definitely not the same!

A one-sample bootstrap hypothesis test

Another juvenile frog was studied, Frog C, and you want to see if Frog B and Frog C have similar impact forces. Unfortunately, you do not have Frog C's impact forces available, but you know they have a mean of 0.55 N. Because you don't have the original data, you cannot do a permutation test, and you cannot assess the hypothesis that the forces from Frog B and Frog C come from the same distribution. You will therefore test another, less restrictive hypothesis: The mean strike force of Frog B is equal to that of Frog C.

To set up the bootstrap hypothesis test, you will take the mean as our test statistic. Remember, your goal is to calculate the probability of getting a mean impact force less than or equal to what was observed for Frog B *if the hypothesis that the true mean of Frog B's impact forces is equal to that of Frog C is true*. You first translate all of the data of Frog B such that the mean is 0.55 N. This involves adding the mean force of Frog C and subtracting the mean force of Frog B from each measurement of Frog B. This leaves other properties of Frog B's distribution, such as the variance, unchanged.

In [91]:

```python
def bootstrap_replicate_1d(data, func):
    """Generate bootstrap replicate of 1D data."""
    bs_sample = np.random.choice(data, len(data))
    return func(bs_sample)
```

In [92]:

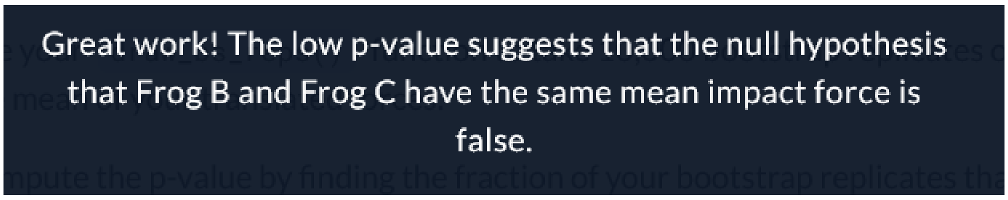
```python
def draw_bs_reps(data, func, size=1):
    """Draw bootstrap replicates."""

    # Initialize array of replicates: bs_replicates
    bs_replicates = np.empty(shape=size)

    # Generate replicates
    for i in range(size):
        bs_replicates[i] = bootstrap_replicate_1d(data,func)

    return bs_replicates
```

In [93]:

```python
# Make an array of translated impact forces: translated_force_b
translated_force_b = force_b - np.mean(force_b) + 0.55

# Take bootstrap replicates of Frog B's translated impact forces: bs_replicates
bs_replicates = draw_bs_reps(translated_force_b, np.mean, 10000)

# Compute fraction of replicates that are less than the observed Frog B force: p
p = np.sum(bs_replicates <= np.mean(force_b)) / 10000

# Print the p-value
```

```
print('p = ', p)
```

```
p =  0.0058
```



Great work! The low p-value suggests that the null hypothesis that Frog B and Frog C have the same mean impact force is false.

A two-sample bootstrap hypothesis test for difference of means

We now want to test the hypothesis that Frog A and Frog B have the same mean impact force, but not necessarily the same distribution, which is also impossible with a permutation test.

To do the two-sample bootstrap test, we shift *both* arrays to have the same mean, since we are simulating the hypothesis that their means are, in fact, equal. We then draw bootstrap samples out of the shifted arrays and compute the difference in means. This constitutes a bootstrap replicate, and we generate many of them. The p-value is the fraction of replicates with a difference in means greater than or equal to what was observed.

The objects `forces_concat` and `empirical_diff_means` are already in your namespace.

In [96]:

```
forces_concat = np.array([1.612, 0.605, 0.327, 0.946, 0.541, 1.539, 0.529, 0.628, 1.453,
       0.297, 0.703, 0.269, 0.751, 0.245, 1.182, 0.515, 0.435, 0.383,
       0.457, 0.73 , 0.172, 0.142, 0.037, 0.453, 0.355, 0.022, 0.502,
       0.273, 0.72 , 0.582, 0.198, 0.198, 0.597, 0.516, 0.815, 0.402,
       0.605, 0.711, 0.614, 0.468])
```

In [98]:

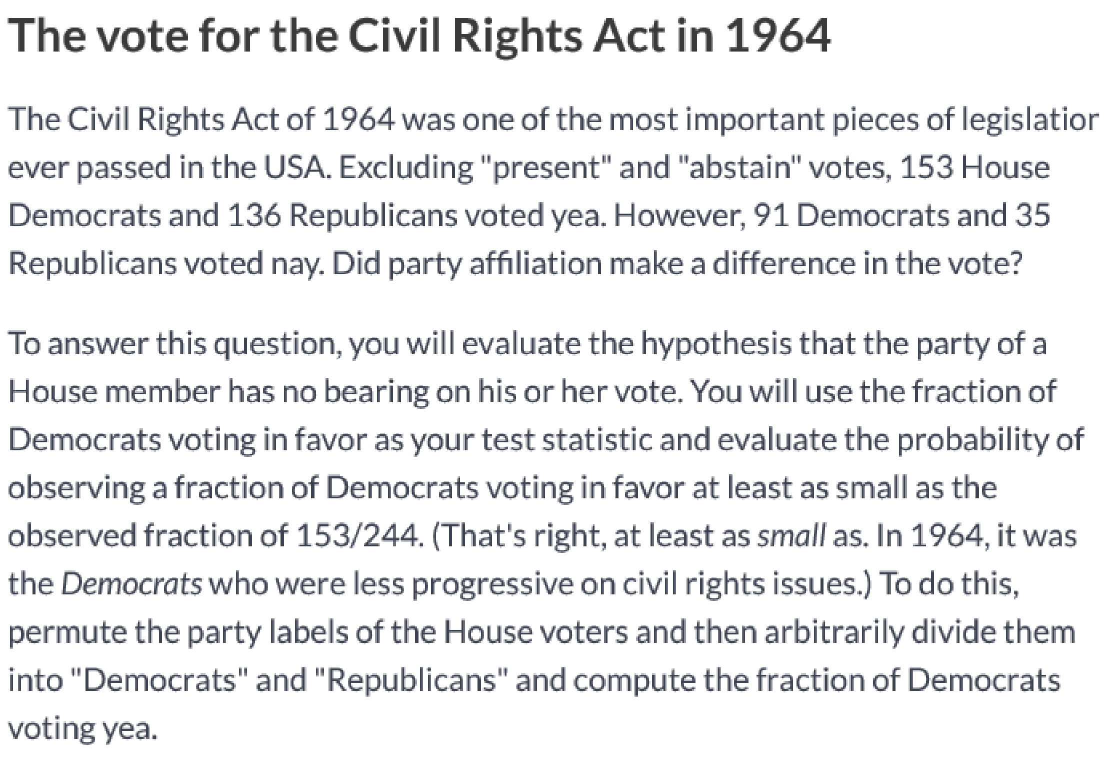
```
# Compute mean of all forces: mean_force
mean_force = np.mean(forces_concat)

# Generate shifted arrays
force_a_shifted = force_a - np.mean(force_a) + mean_force
force_b_shifted = force_b - np.mean(force_b) + mean_force

# Compute 10,000 bootstrap replicates from shifted arrays
bs_replicates_a = draw_bs_reps(force_a_shifted, np.mean, 10000)
bs_replicates_b = draw_bs_reps(force_b_shifted, np.mean, 10000)

# Get replicates of difference of means: bs_replicates
bs_replicates = bs_replicates_a - bs_replicates_b

# Compute and print p-value: p
p = np.sum(bs_replicates >= empirical_diff_means) / len(bs_replicates)
print('p-value =', p)
```

```
p-value = 0.0054
```

Nice work! You got a similar result as when you did the permutation test. Nonetheless, remember that it is important to carefully think about what question you want to ask. Are you only interested in the mean impact force, or in the distribution of impact forces?

Civil Rights Act of 1964

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"



The vote for the Civil Rights Act in 1964

The Civil Rights Act of 1964 was one of the most important pieces of legislatior ever passed in the USA. Excluding "present" and "abstain" votes, 153 House Democrats and 136 Republicans voted yea. However, 91 Democrats and 35 Republicans voted nay. Did party affiliation make a difference in the vote?

To answer this question, you will evaluate the hypothesis that the party of a House member has no bearing on his or her vote. You will use the fraction of Democrats voting in favor as your test statistic and evaluate the probability of observing a fraction of Democrats voting in favor at least as small as the observed fraction of 153/244. (That's right, at least as *small* as. In 1964, it was the *Democrats* who were less progressive on civil rights issues.) To do this, permute the party labels of the House voters and then arbitrarily divide them into "Democrats" and "Republicans" and compute the fraction of Democrats voting yea.

In [3]:

```
def permutation_sample(data1, data2):
    """Generate a permutation sample from two data sets."""

    # Concatenate the data sets: data
    data = np.concatenate((data1,data2))

    # Permute the concatenated array: permuted_data
    permuted_data = np.random.permutation(data)

    # Split the permuted array into two: perm_sample_1, perm_sample_2
    perm_sample_1 = permuted_data[:len(data1)]
    perm_sample_2 = permuted_data[len(data1):]

    return perm_sample_1, perm_sample_2
```

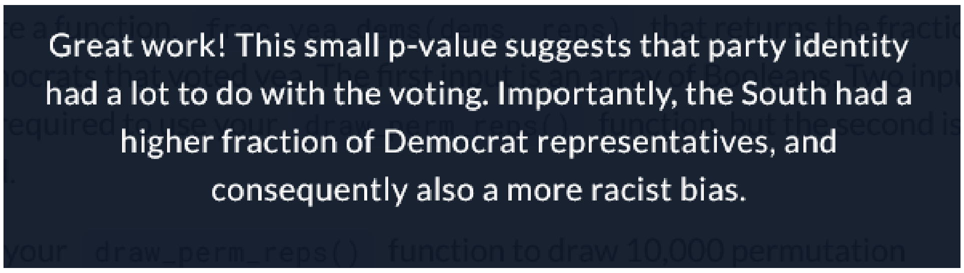
In [8]:

```
def draw_perm_reps(data_1, data_2, func, size=1):
    """Generate multiple permutation replicates."""

    # Initialize array of replicates: perm_replicates
    perm_replicates = np.empty(size)

    for i in range(size):
        # Generate permutation sample
        perm_sample_1, perm_sample_2 = permutation_sample(data_1,data_2)

        # Compute the test statistic
        perm_replicates[i] = func(perm_sample_1, perm_sample_2)

        return perm_replicates
```

```
In [10]:
```

```python
import numpy as np

# Construct arrays of data: dems, reps
dems = np.array([True] * 153 + [False] * 91)
reps = np.array([True] * 136 + [False] * 35)

def frac_yea_dems(dems, reps):
    """Compute fraction of Democrat yea votes."""
    frac = np.sum(dems) / len(dems)
    return frac

# Acquire permutation samples: perm_replicates
perm_replicates = draw_perm_reps(dems, reps, frac_yea_dems, 10000)

# Compute and print p-value: p
p = np.sum(perm_replicates <= 153/244) / len(perm_replicates)
print('p-value =', p)
```

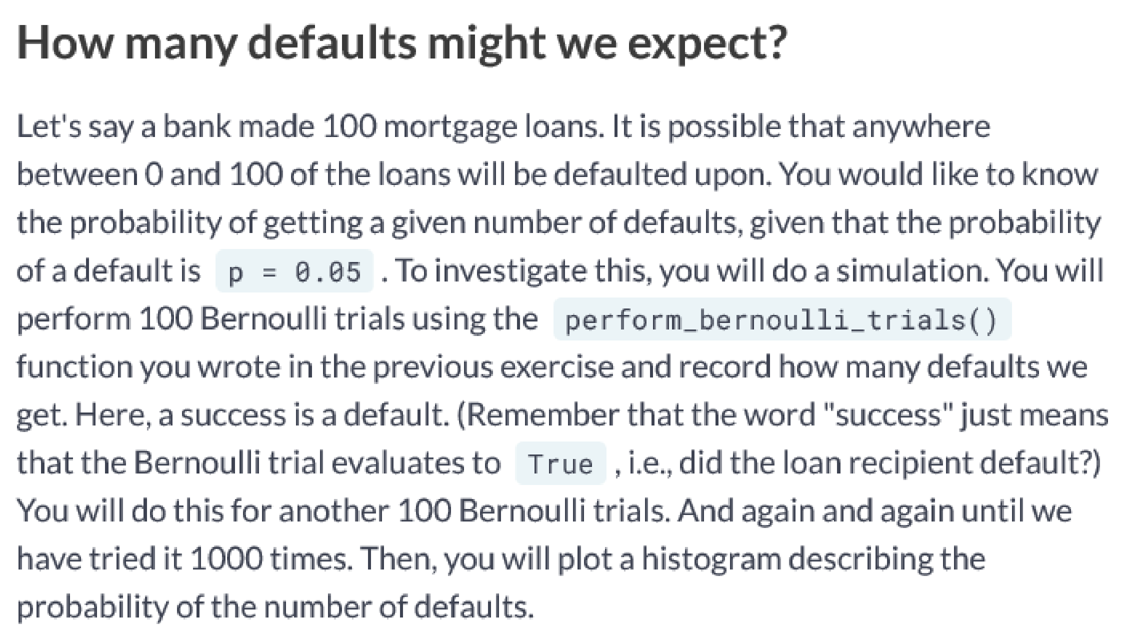
```
p-value = 0.9999
```



Great work! This small p-value suggests that party identity had a lot to do with the voting. Importantly, the South had a higher fraction of Democrat representatives, and consequently also a more racist bias.

Bernoulli Trials - Simulating Bank Loans

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"



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.

In [9]:

```
import numpy as np
import matplotlib.pyplot as plt
```

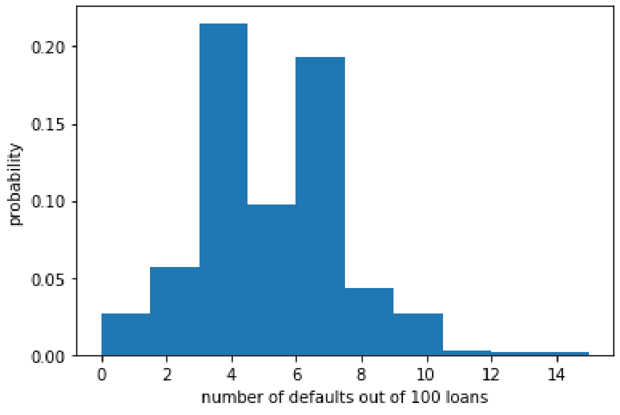
In [5]:

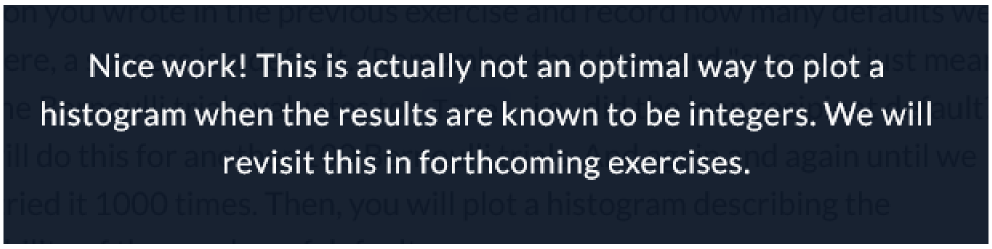
```
def perform_bernoulli_trials(n, p):
    """Perform n Bernoulli trials with success probability p
    and return number of successes."""
    # Initialize number of successes: n_success
    n_success = 0

    # 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
```

In [11]:

```
# 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,.05)
```

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

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




Nice work! This is actually not an optimal way to plot a histogram when the results are known to be integers. We will revisit this in forthcoming exercises.

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?

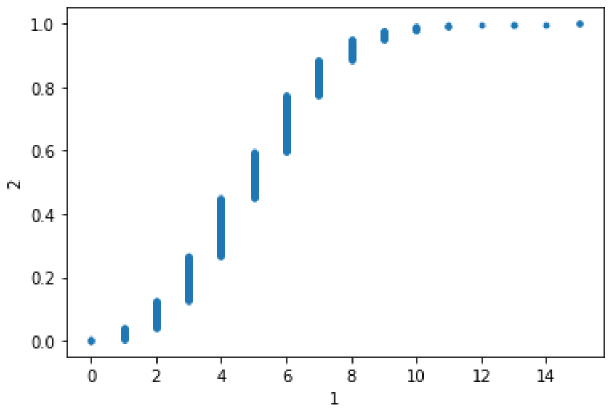
In [14]:

```
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
```

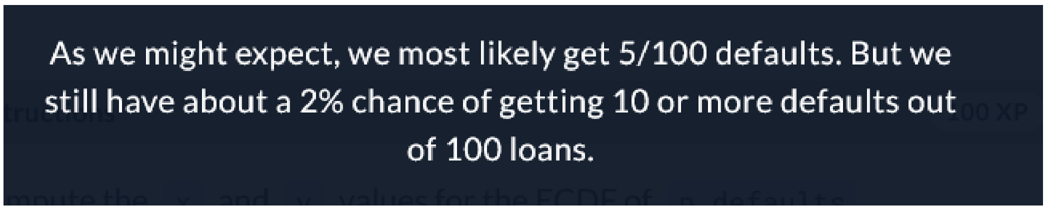
In [15]:

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

```
# Plot the ECDF with labeled axes
_ = plt.plot(x, y, marker='.', linestyle='none')
_ = plt.xlabel('1')
_ = plt.ylabel('2')

# 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))
```



```
Probability of losing money = 0.022
```



As we might expect, we most likely get 5/100 defaults. But we still have about a 2% chance of getting 10 or more defaults out of 100 loans.

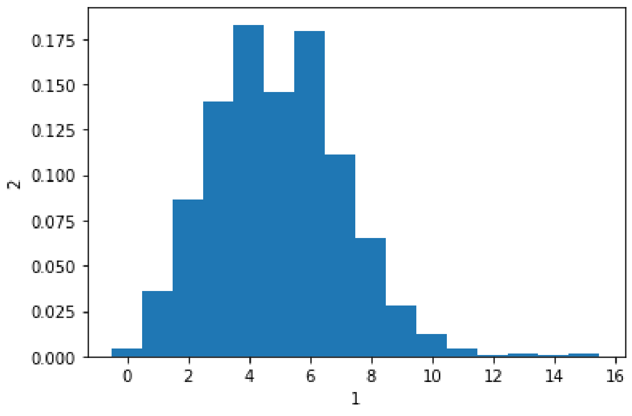
Plotting the Binomial PMF

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`.

In [18]:

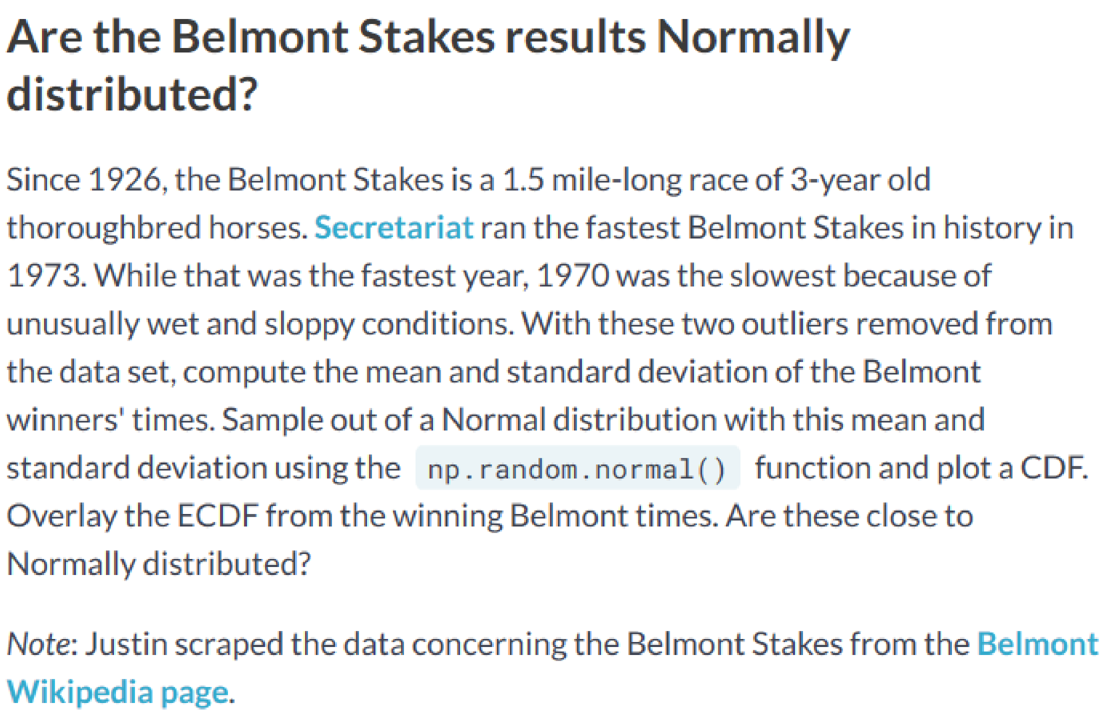
```python
# Compute bin edges: bins
bins = np.arange(0, max(n_defaults) + 1.5) - 0.5

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

# Label axes
_ = plt.xlabel('1')
_ = plt.ylabel('2')


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



Great work!

Belmont Stakes

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"



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.

In [4]:

```
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

In [9]:

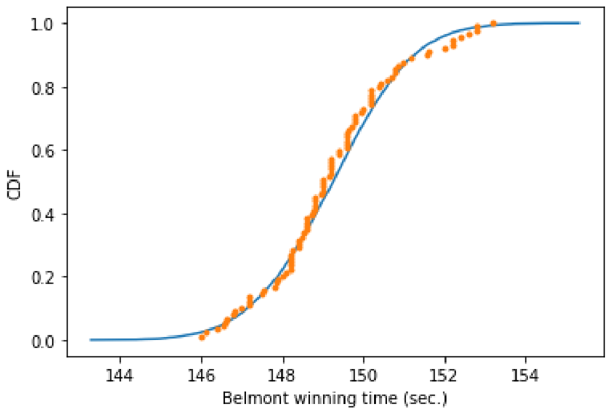
```
belmont_no_outliers = np.array([148.51, 146.65, 148.52, 150.7 , 150.42, 150.88, 151.57, 147.54,
       149.65, 148.74, 147.86, 148.75, 147.5 , 148.26, 149.71, 146.56,
       151.19, 147.88, 149.16, 148.82, 148.96, 152.02, 146.82, 149.97,
       146.13, 148.1 , 147.2 , 146.  , 146.4 , 148.2 , 149.8 , 147.  ,
       147.2 , 147.8 , 148.2 , 149.  , 149.8 , 148.6 , 146.8 , 149.6 ,
       149.  , 148.2 , 149.2 , 148.  , 150.4 , 148.8 , 147.2 , 148.8 ,
       149.6 , 148.4 , 148.4 , 150.2 , 148.8 , 149.2 , 149.2 , 148.4 ,
       150.2 , 146.6 , 149.8 , 149.  , 150.8 , 148.6 , 150.2 , 149.  ,
       148.6 , 150.2 , 148.2 , 149.4 , 150.8 , 150.2 , 152.2 , 148.2 ,
       149.2 , 151.  , 149.6 , 149.6 , 149.4 , 148.6 , 150.  , 150.6 ,
       149.2 , 152.6 , 152.8 , 149.6 , 151.6 , 152.8 , 153.2 , 152.4 ,
       152.2 ])
```

In [10]:

```
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
```

In [13]:

```
# 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.xlabel('Belmont winning time (sec.)')
_ = plt.ylabel('CDF')
plt.show()
```



The theoretical CDF and the ECDF of the data suggest that the winning Belmont times are, indeed, Normally distributed. This also suggests that in the last 100 years or so, there have not been major technological or training advances that have significantly affected the speed at which horses can run this race.

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

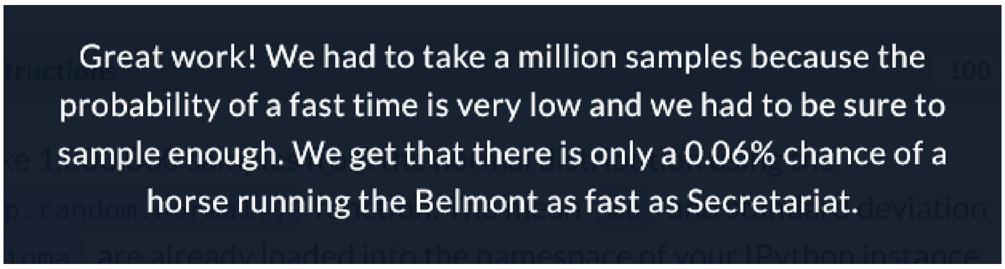
Assume that the Belmont winners' times are Normally distributed (with the 1970 and 1973 years removed), what is the probability that the winner of a given Belmont Stakes will run it as fast or faster than Secretariat?

In [16]:

```
# Take a million samples out of the Normal distribution: samples
```

```python
samples = np.random.normal(mu,sigma,size=1000000)

# Compute the fraction that are faster than 144 seconds: prob
prob = np.sum(samples <= 144)/1000000

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

```
Probability of besting Secretariat: 0.000639
```



Great work! We had to take a million samples because the probability of a fast time is very low and we had to be sure to sample enough. We get that there is only a 0.06% chance of a horse running the Belmont as fast as Secretariat.

Bee Reproduction

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"

> ### Do neonicotinoid insecticides have unintended consequences?
>
> As a final exercise in hypothesis testing before we put everything together in our case study in the next chapter, you will investigate the effects of neonicotinoid insecticides on bee reproduction. These insecticides are very widely used in the United States to combat aphids and other pests that damage plants.
>
> In a recent study, Straub, et al. (*Proc. Roy. Soc. B, 2016*) investigated the effects of neonicotinoids on the sperm of pollinating bees. In this and the next exercise, you will study how the pesticide treatment affected the count of live sperm per half milliliter of semen.
>
> First, we will do EDA, as usual. Plot ECDFs of the alive sperm count for untreated bees (stored in the Numpy array `control`) and bees treated with pesticide (stored in the Numpy array `treated`).

In [13]:

```
import numpy as np
import matplotlib.pyplot as plt
```

In [20]:

```
control = np.array([ 4.159234,  4.408002,  0.172812,  3.498278,  3.104912,  5.164174,
        6.615262,  4.633066,  0.170408,  2.65    ,  0.0875  ,  1.997148,
        6.92668 ,  4.574932,  3.896466,  5.209814,  3.70625 ,  0.      ,
        4.62545 ,  3.01444 ,  0.732652,  0.4     ,  6.518382,  5.225   ,
        6.218742,  6.840358,  1.211308,  0.368252,  3.59937 ,  4.212158,
        6.052364,  2.115532,  6.60413 ,  5.26074 ,  6.05695 ,  6.481172,
        3.171522,  3.057228,  0.218808,  5.215112,  4.465168,  2.28909 ,
        3.732572,  2.17087 ,  1.834326,  6.074862,  5.841978,  8.524892,
        4.698492,  2.965624,  2.324206,  3.409412,  4.830726,  0.1     ,
        0.      ,  4.101432,  3.478162,  1.009688,  4.999296,  4.32196 ,
        0.299592,  3.606032,  7.54026 ,  4.284024,  0.057494,  6.036668,
        2.924084,  4.150144,  1.256926,  4.666502,  4.806594,  2.52478 ,
        2.027654,  2.52283 ,  4.735598,  2.033236,  0.      ,  6.177294,
        2.601834,  3.544408,  3.6045  ,  5.520346,  4.80698 ,  3.002478,
        3.559816,  7.075844, 10.      ,  0.139772,  6.17171 ,  3.201232,
        8.459546,  0.17857 ,  7.088276,  5.496662,  5.415086,  1.932282,
        3.02838 ,  7.47996 ,  1.86259 ,  7.838498,  2.242718,  3.292958,
        6.363644,  4.386898,  8.47533 ,  4.156304,  1.463956,  4.533628,
        5.573922,  1.29454 ,  7.547504,  3.92466 ,  5.820258,  4.118522,
        4.125   ,  2.286698,  0.591882,  1.273124,  0.      ,  0.      ,
        0.      , 12.22502 ,  7.601604,  5.56798 ,  1.679914,  8.77096 ,
        5.823942,  0.258374,  0.      ,  5.899236,  5.486354,  2.053148,
        3.25541 ,  2.72564 ,  3.364066,  2.43427 ,  5.282548,  3.963666,
        0.24851 ,  0.347916,  4.046862,  5.461436,  4.066104,  0.      ,
        0.065   ])
```

In [22]:

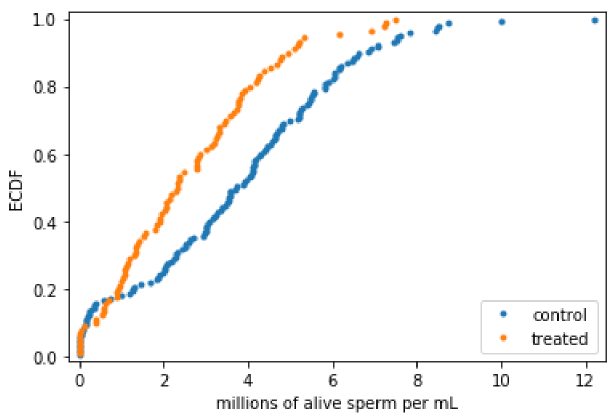
```
treated = np.array([1.342686, 1.058476, 3.793784, 0.40428 , 4.528388, 2.142966,
       3.937742, 0.1375  , 6.919164, 0.      , 3.597812, 5.196538,
       2.78955 , 2.3229  , 1.090636, 5.323916, 1.021618, 0.931836,
       2.78    , 0.412202, 1.180934, 2.8674  , 0.      , 0.064354,
       3.008348, 0.876634, 0.      , 4.971712, 7.280658, 4.79732 ,
       2.084956, 3.251514, 1.9405  , 1.566192, 0.58894 , 5.219658,
       0.977976, 3.124584, 1.297564, 1.433328, 4.24337 , 0.880964,
       2.376566, 3.763658, 1.918426, 3.74    , 3.841726, 4.69964 ,
       4.386876, 0.      , 1.127432, 1.845452, 0.690314, 4.185602,
       2.284732, 7.237594, 2.185148, 2.799124, 3.43218 , 0.63354 ,
       1.142496, 0.586   , 2.372858, 1.80032 , 3.329306, 4.028804,
       3.474156, 7.508752, 2.032824, 1.336556, 1.906496, 1.396046,
       2.488104, 4.759114, 1.07853 , 3.19927 , 3.814252, 4.275962,
       2.817056, 0.552198, 3.27194 , 5.11525 , 2.064628, 0.      ,
       3.34101 , 6.177322, 0.      , 3.66415 , 2.352582, 1.531696])
```

In [18]:

```
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
```

In [23]:

```
# Compute x,y values for ECDFs
x_control, y_control = ecdf(control)
x_treated, y_treated = ecdf(treated)

# Plot the ECDFs
plt.plot(x_control, y_control, marker='.', linestyle='none')
plt.plot(x_treated, y_treated, marker='.', linestyle='none')

# Set the margins
plt.margins(0.02)

# Add a legend
plt.legend(('control', 'treated'), loc='lower right')

# Label axes and show plot
plt.xlabel('millions of alive sperm per mL')
plt.ylabel('ECDF')
plt.show()
```



Nice plot! The ECDFs show a pretty clear difference between the treatment and control; treated bees have fewer alive sperm. Let's now do a hypothesis test in the next exercise.

Bootstrap hypothesis test on bee sperm counts

Now, you will test the following hypothesis: On average, male bees treated with neonicotinoid insecticide have the same number of active sperm per milliliter of semen than do untreated male bees. You will use the difference of means as your test statistic.

In [25]:

```
def bootstrap_replicate_1d(data, func):
    """Generate bootstrap replicate of 1D data."""
    bs_sample = np.random.choice(data, len(data))
    return func(bs_sample)
```

In [26]:

```
def draw_bs_reps(data, func, size=1):
    """Draw bootstrap replicates."""

    # Initialize array of replicates: bs_replicates
    bs_replicates = np.empty(shape=size)

    # Generate replicates
    for i in range(size):
        bs_replicates[i] = bootstrap_replicate_1d(data,func)

    return bs_replicates
```

In [28]:

```
# Compute the difference in mean sperm count: diff_means
diff_means = np.mean(control) - np.mean(treated)

# Compute mean of pooled data: mean_count
mean_count = np.mean(np.concatenate((control, treated)))

# Generate shifted data sets
control_shifted = control - np.mean(control) + mean_count
treated_shifted = treated - np.mean(treated) + mean_count

# Generate bootstrap replicates
bs_reps_control = draw_bs_reps(control_shifted,
                       np.mean, size=10000)
bs_reps_treated = draw_bs_reps(treated_shifted,
                       np.mean, size=10000)

# Get replicates of difference of means: bs_replicates
bs_replicates = bs_reps_control - bs_reps_treated

# Compute and print p-value: p
p = np.sum(bs_replicates >= np.mean(control) - np.mean(treated)) \
            / len(bs_replicates)
print('p-value =', p)
```

```
p-value = 0.0001
```

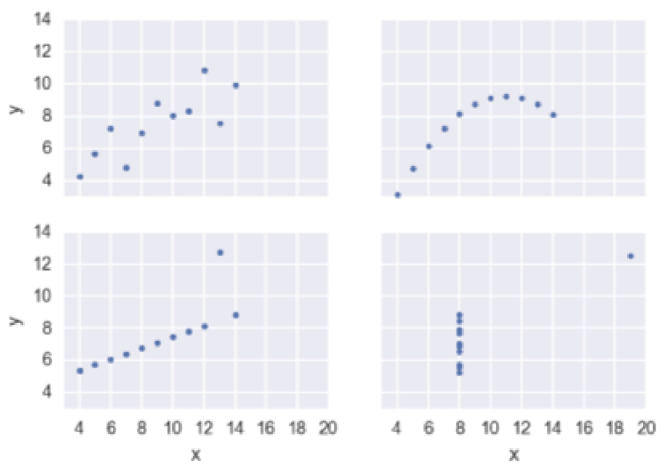
Nice work! The p-value is small, most likely less than 0.0001, since you never saw a bootstrap replicated with a difference of means at least as extreme as what was observed. In fact, when I did the calculation with 10 million replicates, I got a p-value of `2e-05` .

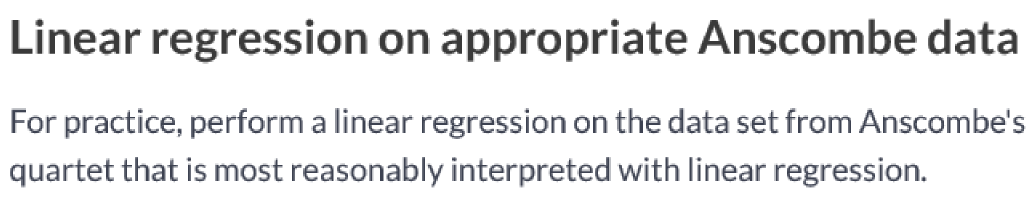
Anscombe's Quartet

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"

https://en.wikipedia.org/wiki/Anscombe%27s_quartet

Anscombe's quartet





Linear regression on appropriate Anscombe data

For practice, perform a linear regression on the data set from Anscombe's quartet that is most reasonably interpreted with linear regression.

In [7]:

```
import numpy as np
import matplotlib.pyplot as plt
```

In [ ]:

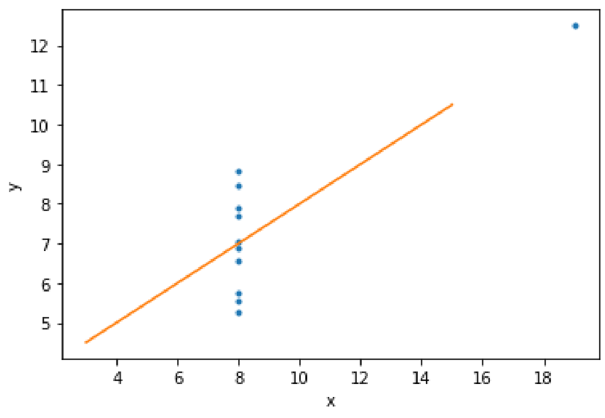
```
x = np.array([10.,  8., 13.,  9., 11., 14.,  6.,  4., 12.,  7.,  5.])
y = np.array([ 8.04,  6.95,  7.58,  8.81,  8.33,  9.96,  7.24,  4.26, 10.84,
        4.82,  5.68])
```

In [18]:

```
# Perform linear regression: a, b
a, b = np.polyfit(x, y, 1)

# Print the slope and intercept
print(a, b)

# Generate theoretical x and y data: x_theor, y_theor
```

```
x_theor = np.array([3, 15])
y_theor = a * x_theor + b

# Plot the Anscombe data and theoretical line
_ = plt.plot(x, y, marker='.', linestyle='none')
_ = plt.plot(x_theor, y_theor)

# Label the axes
plt.xlabel('x')
plt.ylabel('y')

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

```
0.49990909090909064 3.0017272727272735
```



Great work! You're getting to be a linear regression pro!

Linear regression on all Anscombe data

Now, to verify that all four of the Anscombe data sets have the same slope and intercept from a linear regression, you will compute the slope and intercept for each set. The data are stored in lists; `anscombe_x = [x1, x2, x3, x4]` and `anscombe_y = [y1, y2, y3, y4]`, where, for example, `x2` and `y2` are the x and y values for the second Anscombe data set.

In [16]:

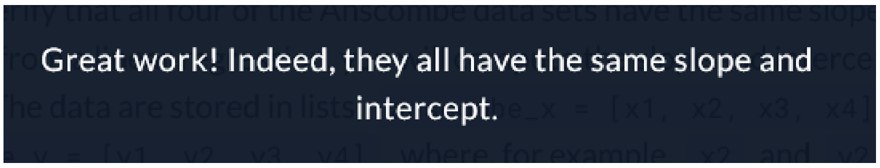
```
anscombe_x = ([10.,  8., 13.,  9., 11., 14.,  6.,  4., 12.,  7.,  5.],
[10.,  8., 13.,  9., 11., 14.,  6.,  4., 12.,  7.,  5.],
[10.,  8., 13.,  9., 11., 14.,  6.,  4., 12.,  7.,  5.],
[ 8.,  8.,  8.,  8.,  8.,  8.,  8., 19.,  8.,  8.,  8.])


anscombe_y = ([ 8.04,  6.95,  7.58,  8.81,  8.33,  9.96,  7.24,  4.26, 10.84,4.82,  5.68],
[9.14, 8.14, 8.74, 8.77, 9.26, 8.1 , 6.13, 3.1 , 9.13, 7.26, 4.74],
[ 7.46,  6.77, 12.74,  7.11,  7.81,  8.84,  6.08,  5.39,  8.15,6.42,  5.73],
[ 6.58,  5.76,  7.71,  8.84,  8.47,  7.04,  5.25, 12.5 ,  5.56,7.91,  6.89])
```

In [17]:

```
# Iterate through x,y pairs
```

```
for x, y in zip(anscombe_x, anscombe_y):
    # Compute the slope and intercept: a, b
    a, b = np.polyfit(x, y, 1)

    # Print the result
    print('slope:', a, 'intercept:', b)
```

```
slope: 0.5000909090909095 intercept: 3.0000909090909076
slope: 0.5000000000000004 intercept: 3.000909090909089
slope: 0.4997272727272731 intercept: 3.0024545454545453
slope: 0.4999090909090909064 intercept: 3.0017272727272735
```


Great work! Indeed, they all have the same slope and intercept.

Darwin's Finches

The following analysis was excerpted from the Data Camp course "Statistical Thinking in Python"

https://en.wikipedia.org/wiki/Darwin%27s_finches

The finches of Daphne Major

Our data source

- Peter and Rosemary Grant
  - 40 Years of Evolution: Darwin's Finches on Daphne Major Island
  - Princeton University Press, 2014
- Data acquired from Dryad Digital Repository
  - http://dx.doi.org/10.5061/dryad.g6g3h

DRYAD

EDA of beak depths of Darwin's finches

For your first foray into the Darwin finch data, you will study how the beak depth (the distance, top to bottom, of a closed beak) of the finch species *Geospiza scandens* has changed over time. The Grants have noticed some changes of beak geometry depending on the types of seeds available on the island, and they also noticed that there was some interbreeding with another major species on Daphne Major, *Geospiza fortis*. These effects can lead to changes in the species over time.

In the next few problems, you will look at the beak depth of *G. scandens* on Daphne Major in 1975 and in 2012. To start with, let's plot all of the beak depth measurements in 1975 and 2012 in a bee swarm plot.

The data are stored in a pandas DataFrame called `df` with columns `'year'` and `'beak_depth'`. The units of beak depth are millimeters (mm).

In [27]:

```
import pandas as pd
import matplotlib.pyplot as plt
import numpy as np
import seaborn as sns
```

In [13]:

```
df2 = pd.read_csv('geospiza_scandens_data.txt')
```

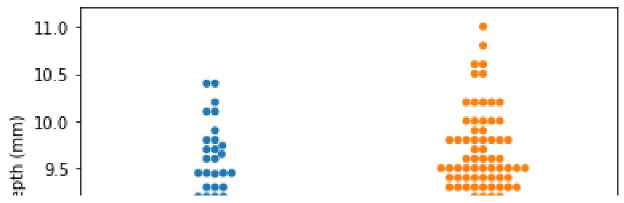
In [102]:

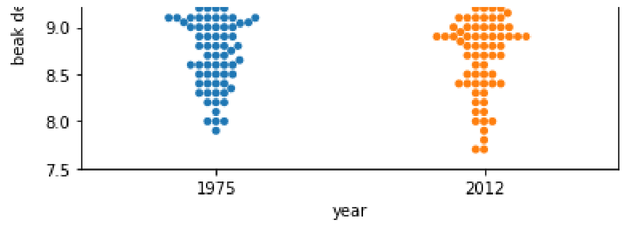
```
display(df2.head())
```

	id	beak_depth	year
0	0	8.4	1975
1	1	8.8	1975
2	2	8.4	1975
3	3	8.0	1975
4	4	7.9	1975

In [23]:

```
# Create bee swarm plot
_ = sns.swarmplot(x='year',y='beak_depth',data=df)

# Label the axes
_ = plt.xlabel('year')
_ = plt.ylabel('beak depth (mm)')

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





It is kind of hard to see if there is a clear difference between the 1975 and 2012 data set. Eyeballing it, it appears as though the mean of the 2012 data set might be slightly higher, and it might have a bigger variance.

ECDFs of beak depths

While bee swarm plots are useful, we found that ECDFs are often even better when doing EDA. Plot the ECDFs for the 1975 and 2012 beak depth measurements on the same plot.

For your convenience, the beak depths for the respective years has been stored in the NumPy arrays `bd_1975` and `bd_2012` .

In [39]:

```
bd_1975 = np.array([ 8.4 ,  8.8 ,  8.4 ,  8.  ,  7.9 ,  8.9 ,  8.6 ,  8.5 ,  8.9 ,
        9.1 ,  8.6 ,  9.8 ,  8.2 ,  9.  ,  9.7 ,  8.6 ,  8.2 ,  9.  ,
        8.4 ,  8.6 ,  8.9 ,  9.1 ,  8.3 ,  8.7 ,  9.6 ,  8.5 ,  9.1 ,
        9.  ,  9.2 ,  9.9 ,  8.6 ,  9.2 ,  8.4 ,  8.9 ,  8.5 , 10.4 ,
        9.6 ,  9.1 ,  9.3 ,  9.3 ,  8.8 ,  8.3 ,  8.8 ,  9.1 , 10.1 ,
        8.9 ,  9.2 ,  8.5 , 10.2 , 10.1 ,  9.2 ,  9.7 ,  9.1 ,  8.5 ,
        8.2 ,  9.  ,  9.3 ,  8.  ,  9.1 ,  8.1 ,  8.3 ,  8.7 ,  8.8 ,
        8.6 ,  8.7 ,  8.  ,  8.8 ,  9.  ,  9.1 ,  9.74,  9.1 ,  9.8 ,
       10.4 ,  8.3 ,  9.44,  9.04,  9.  ,  9.05,  9.65,  9.45,  8.65,
        9.45,  9.45,  9.05,  8.75,  9.45,  8.35])
```

In [73]:

```
bl_1975 = np.array([13.9 , 14.  , 12.9 , 13.5 , 12.9 , 14.6 , 13.  , 14.2 , 14.  ,
       14.2 , 13.1 , 15.1 , 13.5 , 14.4 , 14.9 , 12.9 , 13.  , 14.9 ,
       14.  , 13.8 , 13.  , 14.75, 13.7 , 13.8 , 14.  , 14.6 , 15.2 ,
       13.5 , 15.1 , 15.  , 12.8 , 14.9 , 15.3 , 13.4 , 14.2 , 15.1 ,
       15.1 , 14.  , 13.6 , 14.  , 14.  , 13.9 , 14.  , 14.9 , 15.6 ,
       13.8 , 14.4 , 12.8 , 14.2 , 13.4 , 14.  , 14.8 , 14.2 , 13.5 ,
       13.4 , 14.6 , 13.5 , 13.7 , 13.9 , 13.1 , 13.4 , 13.8 , 13.6 ,
       14.  , 13.5 , 12.8 , 14.  , 13.4 , 14.9 , 15.54, 14.63, 14.73,
       15.73, 14.83, 15.94, 15.14, 14.23, 14.15, 14.35, 14.95, 13.95,
       14.05, 14.55, 14.05, 14.45, 15.05, 13.25])
```

In [48]:

```
bd_2012 = np.array([ 9.4 ,  8.9 ,  9.5 , 11.  ,  8.7 ,  8.4 ,  9.1 ,  8.7 , 10.2 ,
        9.6 ,  8.85,  8.8 ,  9.5 ,  9.2 ,  9.  ,  9.8 ,  9.3 ,  9.  ,
       10.2 ,  7.7 ,  9.  ,  9.5 ,  9.4 ,  8.  ,  8.9 ,  9.4 ,  9.5 ,
        8.  , 10.  ,  8.95,  8.2 ,  8.8 ,  9.2 ,  9.4 ,  9.5 ,  8.1 ,
        9.5 ,  8.4 ,  9.3 ,  9.3 ,  9.6 ,  9.2 , 10.  ,  8.9 , 10.5 ,
        8.9 ,  8.6 ,  8.8 ,  9.15,  9.5 ,  9.1 , 10.2 ,  8.4 , 10.  ,
       10.2 ,  9.3 , 10.8 ,  8.3 ,  7.8 ,  9.8 ,  7.9 ,  8.9 ,  7.7 ,
        8.9 ,  9.4 ,  9.4 ,  8.5 ,  8.5 ,  9.6 , 10.2 ,  8.8 ,  9.5 ,
        9.3 ,  9.  ,  9.2 ,  8.7 ,  9.  ,  9.1 ,  8.7 ,  9.4 ,  9.8 ,
        8.6 , 10.6 ,  9.  ,  9.5 ,  8.1 ,  9.3 ,  9.6 ,  8.5 ,  8.2 ,
        8.  ,  9.5 ,  9.7 ,  9.9 ,  9.1 ,  9.5 ,  9.8 ,  8.4 ,  8.3 ,
        9.6 ,  9.4 , 10.  ,  8.9 ,  9.1 ,  9.8 ,  9.3 ,  9.9 ,  8.9 ,
        8.5 , 10.6 ,  9.3 ,  8.9 ,  8.9 ,  9.7 ,  9.8 , 10.5 ,  8.4 ,
       10.  ,  9.  ,  8.7 ,  8.8 ,  8.4 ,  9.3 ,  9.8 ,  8.9 ,  9.8 ,
        9.1 ])
```

In [74]:

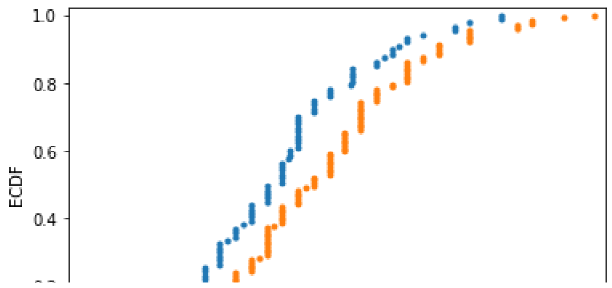
```python
bl_2012 = np.array([14.3 , 12.5 , 13.7 , 13.8 , 12.  , 13.  , 13.  , 13.6 , 12.8 ,
       13.6 , 12.95, 13.1 , 13.4 , 13.9 , 12.3 , 14.  , 12.5 , 12.3 ,
       13.9 , 13.1 , 12.5 , 13.9 , 13.7 , 12.  , 14.4 , 13.5 , 13.8 ,
       13.  , 14.9 , 12.5 , 12.3 , 12.8 , 13.4 , 13.8 , 13.5 , 13.5 ,
       13.4 , 12.3 , 14.35, 13.2 , 13.8 , 14.6 , 14.3 , 13.8 , 13.6 ,
       12.9 , 13.  , 13.5 , 13.2 , 13.7 , 13.1 , 13.2 , 12.6 , 13.  ,
       13.9 , 13.2 , 15.  , 13.37, 11.4 , 13.8 , 13.  , 13.  , 13.1 ,
       12.8 , 13.3 , 13.5 , 12.4 , 13.1 , 14.  , 13.5 , 11.8 , 13.7 ,
       13.2 , 12.2 , 13.  , 13.1 , 14.7 , 13.7 , 13.5 , 13.3 , 14.1 ,
       12.5 , 13.7 , 14.6 , 14.1 , 12.9 , 13.9 , 13.4 , 13.  , 12.7 ,
       12.1 , 14.  , 14.9 , 13.9 , 12.9 , 14.6 , 14.  , 13.  , 12.7 ,
       14.  , 14.1 , 14.1 , 13.  , 13.5 , 13.4 , 13.9 , 13.1 , 12.9 ,
       14.  , 14.  , 14.1 , 14.7 , 13.4 , 13.8 , 13.4 , 13.8 , 12.4 ,
       14.1 , 12.9 , 13.9 , 14.3 , 13.2 , 14.2 , 13.  , 14.6 , 13.1 ,
       15.2 ])
```

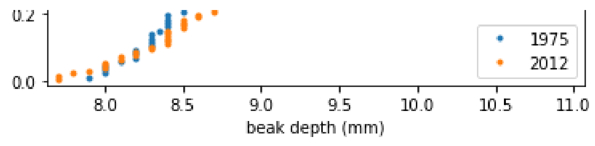
In [49]:

```python
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
```

In [52]:

```python
# Compute ECDFs
x_1975, y_1975 = ecdf(bd_1975)
x_2012, y_2012 = ecdf(bd_2012)

# Plot the ECDFs
_ = plt.plot(x_1975, y_1975, marker='.', linestyle='none')
_ = plt.plot(x_2012, y_2012, marker='.', linestyle='none')

# Set margins
plt.margins(.02)

# Add axis labels and legend
_ = plt.xlabel('beak depth (mm)')
_ = plt.ylabel('ECDF')
_ = plt.legend(('1975', '2012'), loc='lower right')

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





The differences are much clearer in the ECDF. The mean is larger in the 2012 data, and the variance does appear larger as well.

Parameter estimates of beak depths

Estimate the *difference* of the mean beak depth of the *G. scandens* samples from 1975 and 2012 and report a 95% confidence interval.

Since in this exercise you will use the `draw_bs_reps()` function you wrote in chapter 2, it may be helpful to **refer back to it**.

In [53]:

```
def bootstrap_replicate_1d(data, func):
    """Generate bootstrap replicate of 1D data."""
    bs_sample = np.random.choice(data, len(data))
    return func(bs_sample)
```

In [58]:

```
def draw_bs_reps(data, func, size=1):
    """Draw bootstrap replicates."""

    # Initialize array of replicates: bs_replicates
    bs_replicates = np.empty(shape=size)

    # Generate replicates
    for i in range(size):
        bs_replicates[i] = bootstrap_replicate_1d(data,func)

    return bs_replicates
```

In [60]:

```
# Compute the difference of the sample means: mean_diff
mean_diff = np.mean(bd_2012) - np.mean(bd_1975)

# Get bootstrap replicates of means
bs_replicates_1975 = draw_bs_reps(bd_1975,np.mean,10000)
bs_replicates_2012 = draw_bs_reps(bd_2012,np.mean,10000)

# Compute samples of difference of means: bs_diff_replicates
bs_diff_replicates = bs_replicates_2012 - bs_replicates_1975

# Compute 95% confidence interval: conf_int
conf_int = np.percentile(bs_diff_replicates, [2.5,97.5])

# Print the results
print('difference of means =', mean_diff, 'mm')
print('95% confidence interval =', conf_int, 'mm')
```

```
difference of means = 0.22622047244094645 mm
```

```
95% confidence interval = [0.05955249 0.39191499] mm
```

Great work!

Hypothesis test: Are beaks deeper in 2012?

Your plot of the ECDF and determination of the confidence interval make it pretty clear that the beaks of *G. scandens* on Daphne Major have gotten deeper. But is it possible that this effect is just due to random chance? In other words, what is the probability that we would get the observed difference in mean beak depth if the means were the same?

Be careful! The hypothesis we are testing is *not* that the beak depths come from the same distribution. For that we could use a permutation test. The hypothesis is that the means are equal. To perform this hypothesis test, we need to shift the two data sets so that they have the same mean and then use bootstrap sampling to compute the difference of means.

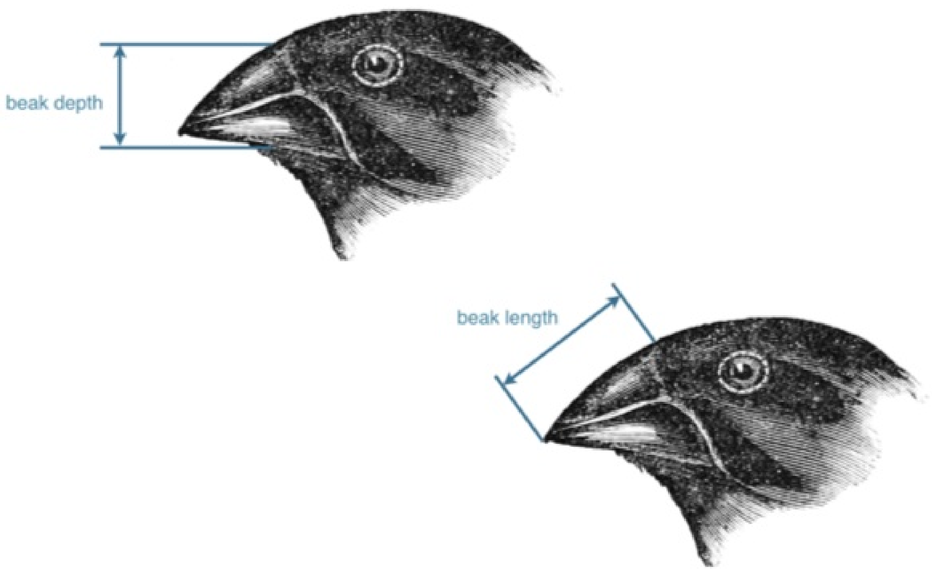
In [62]:

```python
# Compute mean of combined data set: combined_mean
combined_mean = np.mean(np.concatenate((bd_1975, bd_2012)))

# Shift the samples
bd_1975_shifted = bd_1975 - np.mean(bd_1975) + combined_mean
bd_2012_shifted = bd_2012 - np.mean(bd_2012) + combined_mean

# Get bootstrap replicates of shifted data sets
bs_replicates_1975 = draw_bs_reps(bd_1975_shifted,np.mean,10000)
bs_replicates_2012 = draw_bs_reps(bd_2012_shifted,np.mean,10000)

# Compute replicates of difference of means: bs_diff_replicates
bs_diff_replicates = bs_replicates_2012 - bs_replicates_1975

# Compute the p-value
p = np.sum(bs_diff_replicates >= mean_diff) / len(bs_diff_replicates)
#p = np.sum(perm_replicates <= 153/244) / len(perm_replicates)

# Print p-value
print('p =', p)
```

```
p = 0.0035
```

We get a p-value of 0.0034, which suggests that there is a statistically significant difference. But remember: it is very important to know how different they are! In the previous exercise, you got a difference of 0.2 mm between the means. You should combine this with the statistical significance. Changing by 0.2 mm in 37 years is substantial by evolutionary standards. If it kept changing at that rate, the beak depth would double in only 400 years.

Beak geometry

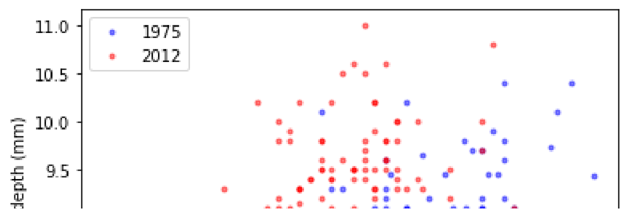


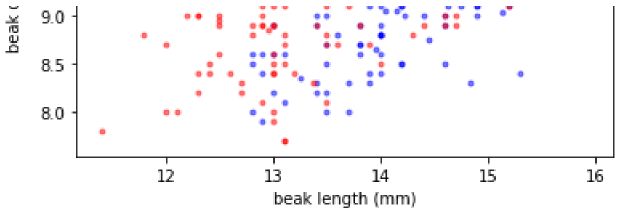
EDA of beak length and depth

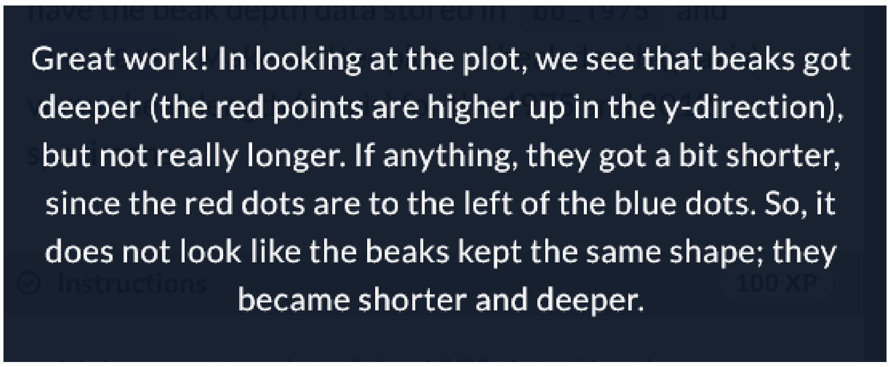
The beak length data are stored as `bl_1975` and `bl_2012`, again with units of millimeters (mm). You still have the beak depth data stored in `bd_1975` and `bd_2012`. Make scatter plots of beak depth (y-axis) versus beak length (x-axis) for the 1975 and 2012 specimens.

In [75]:

```python
# Make scatter plot of 1975 data
_ = plt.plot(bl_1975, bd_1975, color='blue', marker='.',
             linestyle='None', alpha=0.5)

# Make scatter plot of 2012 data
_ = plt.plot(bl_2012, bd_2012, color='red', marker='.',
             linestyle='None', alpha=0.5)

# Label axes and make legend
_ = plt.xlabel('beak length (mm)')
_ = plt.ylabel('beak depth (mm)')
_ = plt.legend(('1975', '2012'), loc='upper left')

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






Great work! In looking at the plot, we see that beaks got deeper (the red points are higher up in the y-direction), but not really longer. If anything, they got a bit shorter, since the red dots are to the left of the blue dots. So, it does not look like the beaks kept the same shape; they became shorter and deeper.

Linear regressions

Perform a linear regression for both the 1975 and 2012 data. Then, perform pairs bootstrap estimates for the regression parameters. Report 95% confidence intervals on the slope and intercept of the regression line.

In [76]:

```python
def draw_bs_pairs_linreg(x, y, size=1):
    """Perform pairs bootstrap for linear regression."""

    # Set up array of indices to sample from: inds
    inds = np.arange(len(x))

    # Initialize replicates: bs_slope_reps, bs_intercept_reps
    bs_slope_reps = np.empty(size)
    bs_intercept_reps = np.empty(size)

    # Generate replicates
    for i in range(size):
        bs_inds = np.random.choice(inds, size=len(inds))
        bs_x, bs_y = x[bs_inds], y[bs_inds]
        bs_slope_reps[i], bs_intercept_reps[i] = np.polyfit(bs_x,bs_y,1)

    return bs_slope_reps, bs_intercept_reps
```

In [77]:

```python
# Compute the linear regressions
slope_1975, intercept_1975 = np.polyfit(bl_1975,bd_1975,1)
slope_2012, intercept_2012 = np.polyfit(bl_2012,bd_2012,1)


# Perform pairs bootstrap for the linear regressions
bs_slope_reps_1975, bs_intercept_reps_1975 = \
        draw_bs_pairs_linreg(bl_1975, bd_1975, 1000)
bs_slope_reps_2012, bs_intercept_reps_2012 = \
        draw_bs_pairs_linreg(bl_2012, bd_2012, 1000)

# Compute confidence intervals of slopes
slope_conf_int_1975 = np.percentile(bs_slope_reps_1975, [2.5,97.5])
slope_conf_int_2012 = np.percentile(bs_slope_reps_2012, [2.5,97.5])
intercept_conf_int_1975 = np.percentile(bs_intercept_reps_1975, [2.5,97.5])
intercept_conf_int_2012 = np.percentile(bs_intercept_reps_2012, [2.5,97.5])
```

```python
# Print the results
print('1975: slope =', slope_1975,
      'conf int =', slope_conf_int_1975)
print('1975: intercept =', intercept_1975,
      'conf int =', intercept_conf_int_1975)
print('2012: slope =', slope_2012,
      'conf int =', slope_conf_int_2012)
print('2012: intercept =', intercept_2012,
      'conf int =', intercept_conf_int_2012)
```

```
1975: slope = 0.4652051691605937 conf int = [0.33555971 0.59272975]
1975: intercept = 2.3908752365842263 conf int = [0.59166199 4.21468578]
2012: slope = 0.462630358835313 conf int = [0.34429233 0.61470456]
2012: intercept = 2.9772474982360198 conf int = [0.97085306 4.58622387]
```

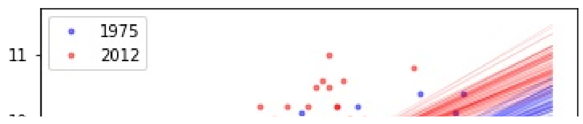
Nicely done! It looks like they have the same slope, but different intercepts.

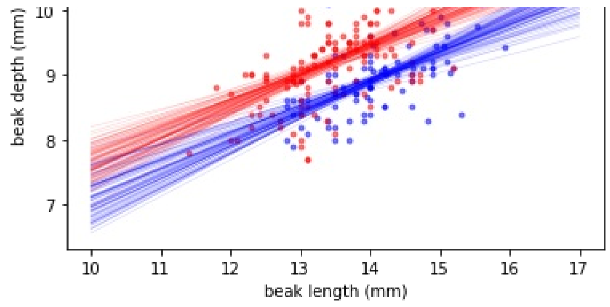
Displaying the linear regression results

Now, you will display your linear regression results on the scatter plot, the code for which is already pre-written for you from your previous exercise. To do this, take the first 100 bootstrap samples (stored in `bs_slope_reps_1975` , `bs_intercept_reps_1975` , `bs_slope_reps_2012` , and `bs_intercept_reps_2012`) and plot the lines with `alpha=0.2` and `linewidth=0.5` keyword arguments to `plt.plot()` .

In [80]:

```python
# Make scatter plot of 1975 data
_ = plt.plot(bl_1975, bd_1975, marker='.',
             linestyle='none', color='blue', alpha=0.5)

# Make scatter plot of 2012 data
_ = plt.plot(bl_2012, bd_2012, marker='.',
             linestyle='none', color='red', alpha=0.5)

# Label axes and make legend
_ = plt.xlabel('beak length (mm)')
_ = plt.ylabel('beak depth (mm)')
_ = plt.legend(('1975', '2012'), loc='upper left')

# Generate x-values for bootstrap lines: x
x = np.array([10, 17])

# Plot the bootstrap lines
for i in range(100):
    plt.plot(x, bs_slope_reps_1975[i] * x + bs_intercept_reps_1975[i],
            linewidth=0.5, alpha=0.2, color='blue')
    plt.plot(x, bs_slope_reps_2012[i] * x + bs_intercept_reps_2012[i],
             linewidth=0.5, alpha=0.2, color='red')
# Draw the plot again
plt.show()
```





Great work!

Beak length to depth ratio

The linear regressions showed interesting information about the beak geometry. The slope was the same in 1975 and 2012, suggesting that for every millimeter gained in beak length, the birds gained about half a millimeter in depth in both years. However, if we are interested in the shape of the beak, we want to compare the *ratio* of beak length to beak depth. Let's make that comparison.

In [81]:

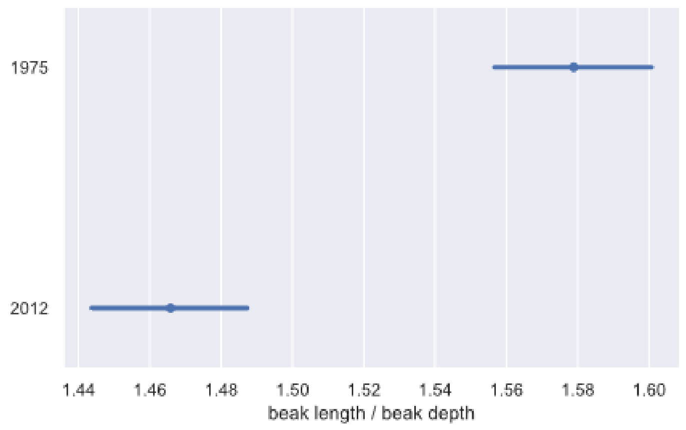
```
# Compute length-to-depth ratios
ratio_1975 = bl_1975 / bd_1975
ratio_2012 = bl_2012 / bd_2012

# Compute means
mean_ratio_1975 = np.mean(ratio_1975)
mean_ratio_2012 = np.mean(ratio_2012)

# Generate bootstrap replicates of the means
bs_replicates_1975 = draw_bs_reps(ratio_1975, np.mean, size=10000)
bs_replicates_2012 = draw_bs_reps(ratio_2012, np.mean, size=10000)

# Compute the 99% confidence intervals
conf_int_1975 = np.percentile(bs_replicates_1975, [0.5, 99.5])
conf_int_2012 = np.percentile(bs_replicates_2012, [0.5, 99.5])

# Print the results
print('1975: mean ratio =', mean_ratio_1975,
      'conf int =', conf_int_1975)
print('2012: mean ratio =', mean_ratio_2012,
      'conf int =', conf_int_2012)
```

```
1975: mean ratio = 1.5788823771858533 conf int = [1.55779266 1.60172738]
2012: mean ratio = 1.4658342276847767 conf int = [1.44401643 1.48741846]
```

Great work! You will interpret these results in the next exercise.

How different is the ratio?

In the previous exercise, you computed the mean beak length to depth ratio with 99% confidence intervals for 1975 and for 2012. The results of that calculation are shown graphically in the plot accompanying this problem. In addition to these results, what would you say about the ratio of beak length to depth?



[✓ The mean beak length-to-depth ratio decreased by about 0.1, or 7%, from 1975 to 2012. The 99% confidence intervals are not even close to overlapping, so this is a real change. The beak shape changed.]

Great work!

EDA of heritability

The array `bd_parent_scandens` contains the average beak depth (in mm) of two parents of the species `G. scandens`. The array `bd_offspring_scandens` contains the average beak depth of the offspring of the respective parents. The arrays `bd_parent_fortis` and `bd_offspring_fortis` contain the same information about measurements from *G. fortis* birds.

Make a scatter plot of the average offspring beak depth (y-axis) versus average parental beak depth (x-axis) for both species. Use the `alpha=0.5` keyword argument to help you see overlapping points.

In [83]:

```
bd_parent_fortis = np.array([10.1  ,  9.55 ,  9.4  , 10.25 , 10.125,  9.7  ,  9.05 ,  7.4  ,
        9.   ,  8.65 ,  9.625,  9.9  ,  9.55 ,  9.05 ,  8.35 , 10.1  ,
       10.1  ,  9.9  , 10.225, 10.   , 10.55 , 10.45 ,  9.2  , 10.2  ,
        8.95 , 10.05 , 10.2  ,  9.5  ,  9.925,  9.95 , 10.05 ,  8.75 ,
        9.2  , 10.15 ,  9.8  , 10.7  , 10.5  ,  9.55 , 10.55 , 10.475,
        8.65 , 10.7  ,  9.1  ,  9.4  , 10.3  ,  9.65 ,  9.5  ,  9.7  ,
       10.525,  9.95 , 10.1  ,  9.75 , 10.05 ,  9.9  , 10.   ,  9.1  ,
        9.45 ,  9.25 ,  9.5  , 10.   , 10.525,  9.9  , 10.4  ,  8.95 ,
        9.4  , 10.95 , 10.75 , 10.1  ,  8.05 ,  9.1  ,  9.55 ,  9.05 ,
       10.2  , 10.   , 10.55 , 10.75 ,  8.175,  9.7  ,  8.8  , 10.75 ,
        9.3  ,  9.7  ,  9.6  ,  9.75 ,  9.6  , 10.45 , 11.   , 10.85 ,
       10.15 , 10.35 , 10.4  ,  9.95 ,  9.1  , 10.1  ,  9.85 ,  9.625,
        9.475,  9.   ,  9.25 ,  9.1  ,  9.25 ,  9.2  ,  9.95 ,  8.65 ,
        9.8  ,  9.4  ,  9.   ,  8.55 ,  8.75 ,  9.65 ,  8.95 ,  9.15 ,
        9.85 , 10.225,  9.825, 10.   ,  9.425, 10.4  ,  9.875,  8.95 ,
        8.9  ,  9.35 , 10.425, 10.   , 10.175,  9.875,  9.875,  9.15 ,
        9.45 ,  9.025,  9.7  ,  9.7  , 10.05 , 10.3  ,  9.6  , 10.   ,
        9.8  , 10.05 ,  8.75 , 10.55 ,  9.7  , 10.   ,  9.85 ,  9.8  ,
        9.175,  9.65 ,  9.55 ,  9.9  , 11.55 , 11.3  , 10.4  , 10.8  ,
        9.8  , 10.45 , 10.   , 10.75 ,  9.35 , 10.75 ,  9.175,  9.65 ,
        8.8  , 10.55 , 10.675,  9.95 ,  9.55 ,  8.825,  9.7  ,  9.85 ,
        9.8  ,  9.55 ,  9.275, 10.325,  9.15 ,  9.35 ,  9.15 ,  9.65 ,
       10.575,  9.975,  9.55 ,  9.2  ,  9.925,  9.2  ,  9.3  ,  8.775,
        9.325,  9.175,  9.325,  8.975,  9.7  ,  9.5  , 10.225, 10.025,
        8.2  ,  8.2  ,  9.55 ,  9.05 ,  9.6  ,  9.6  , 10.15 ,  9.875,
       10.485, 11.485, 10.985,  9.7  ,  9.65 ,  9.35 , 10.05 , 10.1  ,
        9.9  ,  8.95 ,  9.3  ,  9.95 ,  9.45 ,  9.5  ,  8.45 ,  8.8  ,
        8.525,  9.375, 10.2  ,  7.625,  8.375,  9.25 ,  9.4  , 10.55 ,
        8.9  ,  8.8  ,  9.   ,  8.575,  8.575,  9.6  ,  9.375,  9.6  ,
        9.95 ,  9.6  , 10.2  ,  9.85 ,  9.625,  9.025, 10.375, 10.25 ,
        9.3  ,  9.5  ,  9.55 ,  8.55 ,  9.05 ,  9.9  ,  9.8  ,  9.75 ,
       10.25 ,  9.1  ,  9.65 , 10.3  ,  8.9  ,  9.95 ,  9.5  ,  9.775,
        9.425,  7.75 ,  7.55 ,  9.1  ,  9.6  ,  9.575,  8.95 ,  9.65 ,
        9.65 ,  9.65 ,  9.525,  9.85 ,  9.05 ,  9.3  ,  8.9  ,  9.45 ,
       10.   ,  9.85 ,  9.25 , 10.1  ,  9.125,  9.65 ,  9.1  ,  8.05 ,
        7.4  ,  8.85 ,  9.075,  9.   ,  9.7  ,  8.7  ,  9.45 ,  9.7  ,
        8.35 ,  8.85 ,  9.7  ,  9.45 , 10.3  , 10.   , 10.45 ,  9.45 ,
        8.5  ,  8.3  , 10.   ,  9.225,  9.75 ,  9.15 ,  9.55 ,  9.   ,
        9.275,  9.35 ,  8.95 ,  9.875,  8.45 ,  8.6  ,  9.7  ,  8.55 ,
        9.05 ,  9.6  ,  8.65 ,  9.2  ,  8.95 ,  9.6  ,  9.15 ,  9.4  ,
        8.95 ,  9.95 , 10.55 ,  9.7  ,  8.85 ,  8.8  , 10.   ,  9.05 ,
        8.2  ,  8.1  ,  7.25 ,  8.3  ,  9.15 ,  8.6  ,  9.5  ,  8.05 ,
        9.425,  9.3  ,  9.8  ,  9.3  ,  9.85 ,  9.5  ,  8.65 ,  9.825,
        9.   , 10.45 ,  9.1  ,  9.55 ,  9.05 , 10.   ,  9.35 ,  8.375,
        8.3  ,  8.8  , 10.1  ,  9.5  ,  9.75 , 10.1  ,  9.575,  9.425,
        9.65 ,  8.725,  9.025,  8.5  ,  8.95 ,  9.3  ,  8.85 ,  8.95 ,
        9.8  ,  9.5  ,  8.65 ,  9.1  ,  9.4  ,  8.475,  9.35 ,  7.95 ,
        9.35 ,  8.575,  9.05 ,  8.175,  9.85 ,  7.85 ,  9.85 , 10.1  ,
        9.35 ,  8.85 ,  8.75 ,  9.625,  9.25 ,  9.55 , 10.325,  8.55 ,
        9.675,  9.15 ,  9.   ,  9.65 ,  8.6  ,  8.8  ,  9.   ,  9.95 ,
        8.4  ,  9.35 , 10.3  ,  9.05 ,  9.975,  9.975,  8.65 ,  8.725,
        8.2  ,  7.85 ,  8.775,  8.5  ,  9.4  ])
```

In [84]:

```
bd_offspring_fortis = np.array([10.7 ,  9.78,  9.48,  9.6 , 10.27,  9.5 ,  9.  ,  7.46,  7.65,
        8.63,  9.81,  9.4 ,  9.48,  8.75,  7.6 , 10.  , 10.09,  9.74,
        9.64,  8.49, 10.15, 10.28,  9.2 , 10.01,  9.03,  9.94, 10.5 ,
        9.7 , 10.02, 10.04,  9.43,  8.1 ,  9.5 ,  9.9 ,  9.48, 10.18,
       10.16,  9.08, 10.39,  9.9 ,  8.4 , 10.6 ,  8.75,  9.46,  9.6 ,
        9.6 ,  9.95, 10.05, 10.16, 10.1 ,  9.83,  9.46,  9.7 ,  9.82,
       10.34,  8.02,  9.65,  9.87,  9.  , 11.14,  9.25,  8.14, 10.23,
        8.7 ,  9.8 , 10.54, 11.19,  9.85,  8.1 ,  9.3 ,  9.34,  9.19,
        9.52,  9.36,  8.8 ,  8.6 ,  8.  ,  8.5 ,  8.3 , 10.38,  8.54,
        8.94, 10.  ,  9.76,  9.45,  9.89, 10.9 ,  9.91,  9.39,  9.86,
        9.74,  9.9 ,  9.09,  9.69, 10.24,  8.9 ,  9.67,  8.93,  9.3 ,
        8.67,  9.15,  9.23,  9.59,  9.03,  9.58,  8.97,  8.57,  8.47,
        8.71,  9.21,  9.13,  8.5 ,  9.58,  9.21,  9.6 ,  9.32,  8.7 ,
       10.46,  9.29,  9.24,  9.45,  9.35, 10.19,  9.91,  9.18,  9.89,
        9.6 , 10.3 ,  9.45,  8.79,  9.2 ,  8.8 ,  9.69, 10.61,  9.6 ,
        9.9 ,  9.26, 10.2 ,  8.79,  9.28,  8.83,  9.76, 10.2 ,  9.43,
        9.4 ,  9.9 ,  9.5 ,  8.95,  9.98,  9.72,  9.86, 11.1 ,  9.14,
       10.49,  9.75, 10.35,  9.73,  9.83,  8.69,  9.58,  8.42,  9.25,
       10.12,  9.31,  9.99,  8.59,  8.74,  8.79,  9.6 ,  9.52,  8.93,
       10.23,  9.35,  9.35,  9.09,  9.04,  9.75, 10.5 ,  9.09,  9.05,
        9.54,  9.3 ,  9.06,  8.7 ,  9.32,  8.4 ,  8.67,  8.6 ,  9.53,
        9.77,  9.65,  9.43,  8.35,  8.26,  9.5 ,  8.6 ,  9.57,  9.14,
       10.79,  8.91,  9.93, 10.7 ,  9.3 ,  9.93,  9.51,  9.44, 10.05,
       10.13,  9.24,  8.21,  8.9 ,  9.34,  8.77,  9.4 ,  8.82,  8.83,
        8.6 ,  9.5 , 10.2 ,  8.09,  9.07,  9.29,  9.1 , 10.19,  9.25,
        8.98,  9.02,  8.6 ,  8.25,  8.7 ,  9.9 ,  9.65,  9.45,  9.38,
       10.4 ,  9.96,  9.46,  8.26, 10.05,  8.92,  9.5 ,  9.43,  8.97,
        8.44,  8.92, 10.3 ,  8.4 ,  9.37,  9.91, 10.  ,  9.21,  9.95,
        8.84,  9.82,  9.5 , 10.29,  8.4 ,  8.31,  9.29,  8.86,  9.4 ,
        9.62,  8.62,  8.3 ,  9.8 ,  8.48,  9.61,  9.5 ,  9.37,  8.74,
        9.31,  9.5 ,  9.49,  9.74,  9.2 ,  9.24,  9.7 ,  9.64,  9.2 ,
        7.5 ,  7.5 ,  8.7 ,  8.31,  9.  ,  9.74,  9.31, 10.5 ,  9.3 ,
        8.12,  9.34,  9.72,  9.  ,  9.65,  9.9 , 10.  , 10.1 ,  8.  ,
        9.07,  9.75,  9.33,  8.11,  9.36,  9.74,  9.9 ,  9.23,  9.7 ,
        8.2 ,  9.35,  9.49,  9.34,  8.87,  9.03,  9.07,  9.43,  8.2 ,
        9.19,  9.  ,  9.2 ,  9.06,  9.81,  8.89,  9.4 , 10.45,  9.64,
        9.03,  8.71,  9.91,  8.33,  8.2 ,  7.83,  7.14,  8.91,  9.18,
        8.8 ,  9.9 ,  7.73,  9.25,  8.7 ,  9.5 ,  9.3 ,  9.05, 10.18,
        8.85,  9.24,  9.15,  9.98,  8.77,  9.8 ,  8.65, 10.  ,  8.81,
        8.01,  7.9 ,  9.41, 10.18,  9.55,  9.08,  8.4 ,  9.75,  8.9 ,
        9.07,  9.35,  8.9 ,  8.19,  8.65,  9.19,  8.9 ,  9.28, 10.58,
        9.  ,  9.4 ,  8.91,  9.93, 10.  ,  9.37,  7.4 ,  9.  ,  8.8 ,
        9.18,  8.3 , 10.08,  7.9 ,  9.96, 10.4 ,  9.65,  8.8 ,  8.65,
        9.7 ,  9.23,  9.43,  9.93,  8.47,  9.55,  9.28,  8.85,  8.9 ,
        8.75,  8.63,  9.  ,  9.43,  8.28,  9.23, 10.4 ,  9.  ,  9.8 ,
        9.77,  8.97,  8.37,  7.7 ,  7.9 ,  9.5 ,  8.2 ,  8.8 ])
```

In [86]:

```
bd_parent_scandens = np.array([ 8.3318,  8.4035,  8.5317,  8.7202,  8.7089,  8.7541,  8.773 ,
        8.8107,  8.7919,  8.8069,  8.6523,  8.6146,  8.6938,  8.7127,
        8.7466,  8.7504,  8.7805,  8.7428,  8.7164,  8.8032,  8.8258,
        8.856 ,  8.9012,  8.9125,  8.8635,  8.8258,  8.8522,  8.8974,
        8.9427,  8.9879,  8.9615,  8.9238,  8.9351,  9.0143,  9.0558,
        9.0596,  8.9917,  8.905 ,  8.9314,  8.9465,  8.9879,  8.9804,
        9.0219,  9.052 ,  9.0407,  9.0407,  8.9955,  8.9992,  8.9992,
        9.0747,  9.0747,  9.5385,  9.4781,  9.4517,  9.3537,  9.2707,
        9.1199,  9.1689,  9.1425,  9.135 ,  9.1011,  9.1727,  9.2217,
        9.2255,  9.2821,  9.3235,  9.3198,  9.3198,  9.3198,  9.3273,
        9.3725,  9.3989,  9.4253,  9.4593,  9.4442,  9.4291,  9.2632,
        9.2293,  9.1878,  9.1425,  9.1275,  9.1802,  9.1765,  9.2481,
        9.2481,  9.1991,  9.1689,  9.1765,  9.2406,  9.3198,  9.3235,
        9.1991,  9.2971,  9.2443,  9.316 ,  9.2934,  9.3914,  9.3989,
        9.5121,  9.6176,  9.5535,  9.4668,  9.3725,  9.3348,  9.3763,
        9.3839,  9.4216,  9.4065,  9.3348,  9.4442,  9.4367,  9.5083,
        9.448 ,  9.4781,  9.595 ,  9.6101,  9.5686,  9.6365,  9.7119,
        9.8213,  9.825 ,  9.7609,  9.6516,  9.5988,  9.546 ,  9.6516,
        9.7572,  9.8854, 10.0023,  9.3914])
```

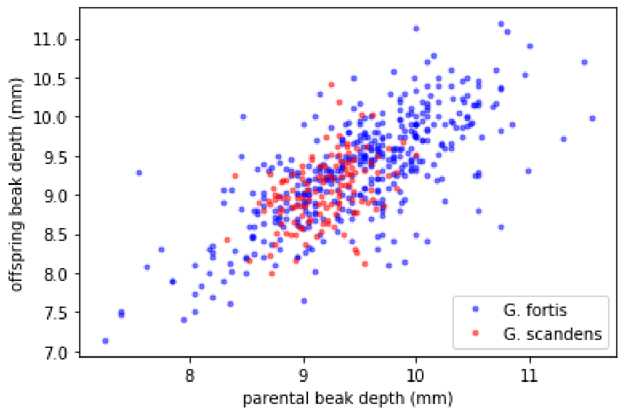
In [87]:

```
bd_offspring_scandens = np.array([ 8.419 ,  9.2468,  8.1532,  8.0089,  8.2215,  8.3734,  8.5025,
        8.6392,  8.7684,  8.8139,  8.7911,  8.9051,  8.9203,  8.8747,
        8.943 ,  9.0038,  8.981 ,  9.0949,  9.2696,  9.1633,  9.1785,
        9.1937,  9.2772,  9.0722,  8.9658,  8.9658,  8.5025,  8.4949,
        8.4949,  8.5633,  8.6013,  8.6468,  8.1532,  8.3734,  8.662 ,
        8.6924,  8.7456,  8.8367,  8.8595,  8.9658,  8.9582,  8.8671,
        8.8671,  8.943 ,  9.0646,  9.1405,  9.2089,  9.2848,  9.3759,
        9.4899,  9.4519,  8.1228,  8.2595,  8.3127,  8.4949,  8.6013,
        8.4646,  8.5329,  8.7532,  8.8823,  9.0342,  8.6392,  8.6772,
        8.6316,  8.7532,  8.8291,  8.8975,  8.9734,  9.0494,  9.1253,
        9.1253,  9.1253,  9.1785,  9.2848,  9.4595,  9.3608,  9.2089,
        9.2544,  9.3684,  9.3684,  9.2316,  9.1709,  9.2316,  9.0342,
        8.8899,  8.8291,  8.981 ,  8.8975, 10.4089, 10.1886,  9.7633,
        9.7329,  9.6114,  9.5051,  9.5127,  9.3684,  9.6266,  9.5354,
       10.0215, 10.0215,  9.6266,  9.6038,  9.4063,  9.2316,  9.338 ,
        9.262 ,  9.262 ,  9.4063,  9.4367,  9.0342,  8.943 ,  8.9203,
        8.7835,  8.7835,  9.057 ,  8.9354,  8.8975,  8.8139,  8.8671,
        9.0873,  9.2848,  9.2392,  9.2924,  9.4063,  9.3152,  9.4899,
        9.5962,  9.6873,  9.5203,  9.6646])
```

In [88]:

```
# Make scatter plots
_ = plt.plot(bd_parent_fortis, bd_offspring_fortis,
             marker='.', linestyle='none', color='blue', alpha=0.5)
_ = plt.plot(bd_parent_scandens, bd_offspring_scandens,
             marker='.', linestyle='none', color='red', alpha=0.5)

# Label axes
```

```
_ = plt.xlabel('parental beak depth (mm)')
_ = plt.ylabel('offspring beak depth (mm)')

# Add legend
_ = plt.legend(('G. fortis', 'G. scandens'), loc='lower right')

# Show plot
plt.show()
```



It appears as though there is a stronger correlation in *G. fortis* than in *G. scandens*. This suggests that beak depth is more strongly inherited in *G. fortis*. We'll quantify this correlation next.

Correlation of offspring and parental data

In an effort to quantify the correlation between offspring and parent beak depths, we would like to compute statistics, such as the Pearson correlation coefficient, between parents and offspring. To get confidence intervals on this, we need to do a pairs bootstrap.

You have **already written** a function to do pairs bootstrap to get estimates for parameters derived from linear regression. Your task in this exercise is to make a new function with call signature `draw_bs_pairs(x, y, func, size=1)` that performs pairs bootstrap and computes a single statistic on pairs samples defined. The statistic of interest is computed by calling `func(bs_x, bs_y)`. In the next exercise, you will use `pearson_r` for `func`.

In [95]:

```
def draw_bs_pairs(x, y, func, size=1):
    """Perform pairs bootstrap for a single statistic."""

    # Set up array of indices to sample from: inds
    inds = np.arange(len(x))

    # Initialize replicates: bs_replicates
    bs_replicates = np.empty(size)
    # Generate replicates
    for i in range(size):
        bs_inds = np.random.choice(inds, len(inds))
        bs_x, bs_y = x[bs_inds], y[bs_inds]
        bs_replicates[i] = func(bs_x, bs_y)

    return bs_replicates
```

Great work!

Pearson correlation of offspring and parental data

The Pearson correlation coefficient seems like a useful measure of how strongly the beak depth of parents are inherited by their offspring. Compute the Pearson correlation coefficient between parental and offspring beak depths for *G. scandens*. Do the same for *G. fortis*. Then, use the function you wrote in the last exercise to compute a 95% confidence interval using pairs bootstrap.

In [90]:

```
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]
```

In [97]:

```
# Compute the Pearson correlation coefficients
r_scandens = pearson_r(bd_parent_scandens,bd_offspring_scandens)
r_fortis = pearson_r(bd_parent_fortis,bd_offspring_fortis)

# Acquire 1000 bootstrap replicates of Pearson r
bs_replicates_scandens = draw_bs_pairs(bd_parent_scandens, bd_offspring_scandens, pearson_r, 1000)

bs_replicates_fortis = draw_bs_pairs(bd_parent_fortis, bd_offspring_fortis, pearson_r, 1000)


# Compute 95% confidence intervals
conf_int_scandens = np.percentile(bs_replicates_scandens,[2.5,97.5])
conf_int_fortis = np.percentile(bs_replicates_fortis,[2.5,97.5])

# Print results
print('G. scandens:', r_scandens, conf_int_scandens)
print('G. fortis:', r_fortis, conf_int_fortis)
```

```
G. scandens: 0.4117063629401258 [0.26374327 0.53895073]
G. fortis: 0.7283412395518486 [0.66854281 0.77955708]
```

It is clear from the confidence intervals that beak depth of the offspring of *G. fortis* parents is more strongly correlated with their offspring than their *G. scandens* counterparts.

Measuring heritability

Remember that the Pearson correlation coefficient is the ratio of the covariance to the geometric mean of the variances of the two data sets. This is a measure of the correlation between parents and offspring, but might not be the best estimate of heritability. If we stop and think, it makes more sense to define heritability as the ratio of the covariance between parent and offspring to the *variance of the parents alone*. In this exercise, you will estimate the heritability and perform a pairs bootstrap calculation to get the 95% confidence interval.

This exercise highlights a very important point. Statistical inference (and data analysis in general) is not a plug-n-chug enterprise. You need to think carefully about the questions you are seeking to answer with your data and analyze them appropriately. If you are interested in how heritable traits are, the quantity we defined as the heritability is more apt than the off-the-shelf statistic, the Pearson correlation coefficient.

In [99]:

```python
def heritability(parents, offspring):
    """Compute the heritability from parent and offspring samples."""
    covariance_matrix = np.cov(parents, offspring)
    return covariance_matrix[0,1] / covariance_matrix[0,0]

# Compute the heritability
heritability_scandens = heritability(bd_parent_scandens,
                                     bd_offspring_scandens)
heritability_fortis = heritability(bd_parent_fortis,
                                   bd_offspring_fortis)

# Acquire 1000 bootstrap replicates of heritability
replicates_scandens = draw_bs_pairs(
        bd_parent_scandens, bd_offspring_scandens, heritability, size=1000)
replicates_fortis = draw_bs_pairs(
        bd_parent_fortis, bd_offspring_fortis, heritability, size=1000)

# Compute 95% confidence intervals
conf_int_scandens = np.percentile(replicates_scandens, [2.5, 97.5])
conf_int_fortis = np.percentile(replicates_fortis, [2.5, 97.5])

# Print results
print('G. scandens:', heritability_scandens, conf_int_scandens)
print('G. fortis:', heritability_fortis, conf_int_fortis)
```

```
G. scandens: 0.5485340868685982 [0.35707581 0.74281168]
G. fortis: 0.7229051911438155 [0.64155927 0.79732078]
```

Here again, we see that *G. fortis* has stronger heritability than *G. scandens*. This suggests that the traits of *G. fortis* may be strongly incorporated into *G. scandens* by introgressive hybridization.

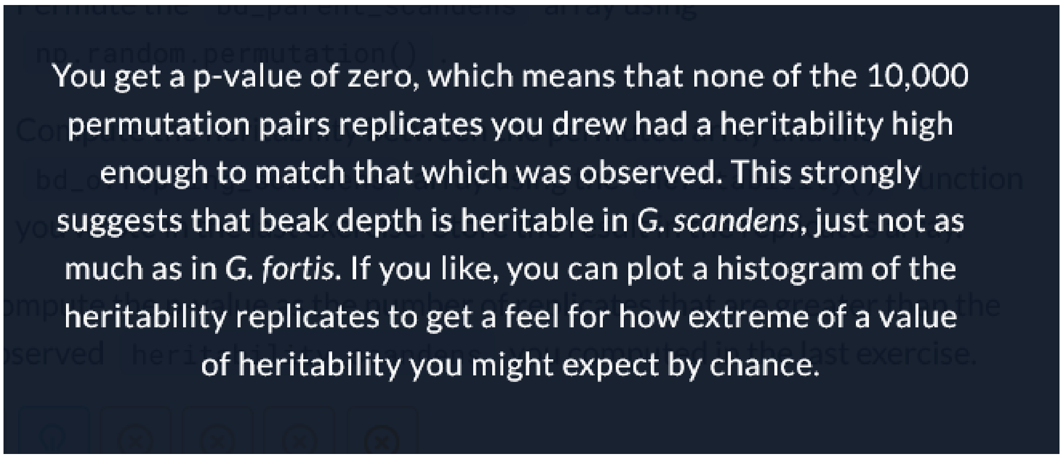
Is beak depth heritable at all in G. scandens?

The heritability of beak depth in *G. scandens* seems low. It could be that this observed heritability was just achieved by chance and beak depth is actually not really heritable in the species. You will test that hypothesis here. To do this, you will do a pairs permutation test.

In [101]:

```python
# Initialize array of replicates: perm_replicates
perm_replicates = np.empty(10000)

# Draw replicates
for i in range(10000):
    # Permute parent beak depths
    bd_parent_permuted = np.random.permutation(bd_parent_scandens)
    perm_replicates[i] = heritability(bd_parent_permuted,
                                      bd_offspring_scandens)

# Compute p-value: p
p = np.sum(perm_replicates >= heritability_scandens) / len(perm_replicates)

# Print the p-value
print('p-val =', p)
```

```
p-val = 0.0
```



You get a p-value of zero, which means that none of the 10,000 permutation pairs replicates you drew had a heritability high enough to match that which was observed. This strongly suggests that beak depth is heritable in *G. scandens*, just not as much as in *G. fortis*. If you like, you can plot a histogram of the heritability replicates to get a feel for how extreme of a value of heritability you might expect by chance.