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]:

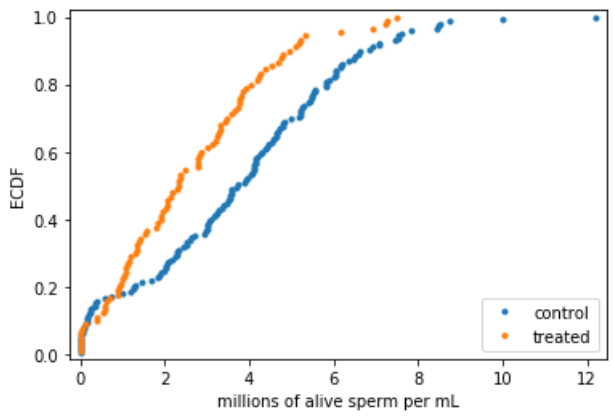
```
# Compute x,y values for ECDFs
x_control, y_control = ecdf(control)
x_treated, y_treated = ecdf(treated)

# 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` .