Statistical Thinking in Python Part 2

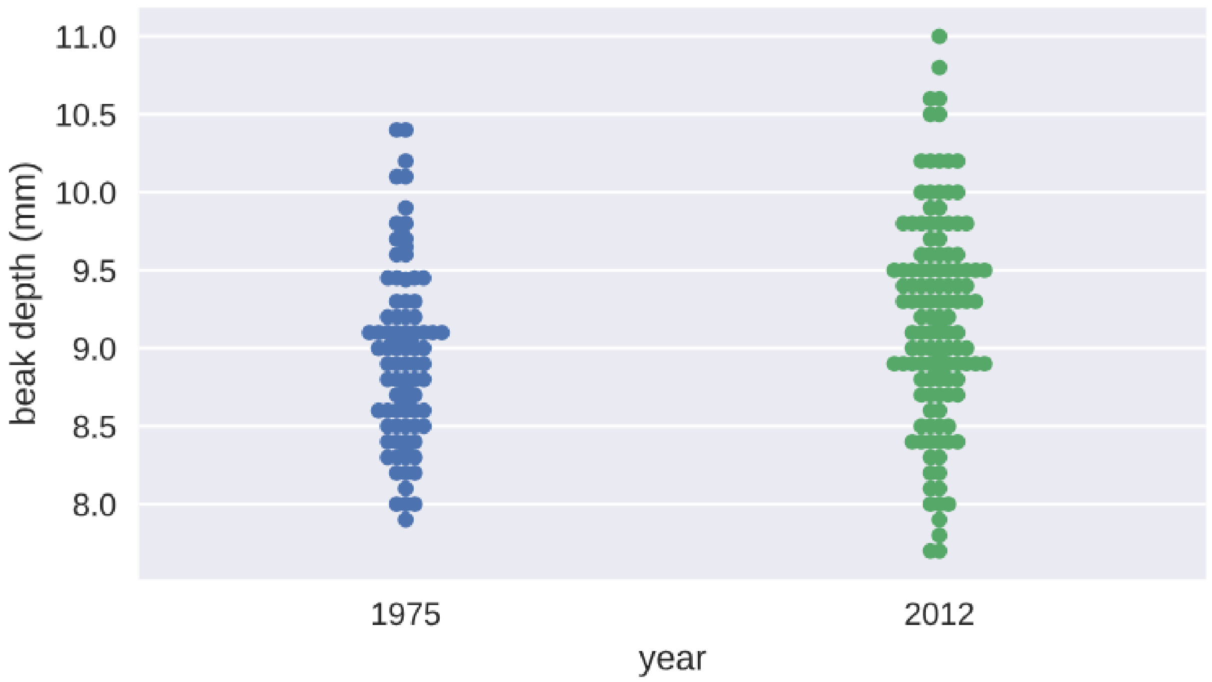
5). Putting it all together: a case study

a). EDA of beak depths of Darwin's finches

```
# 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()
```



b). ECDFs of beak depths

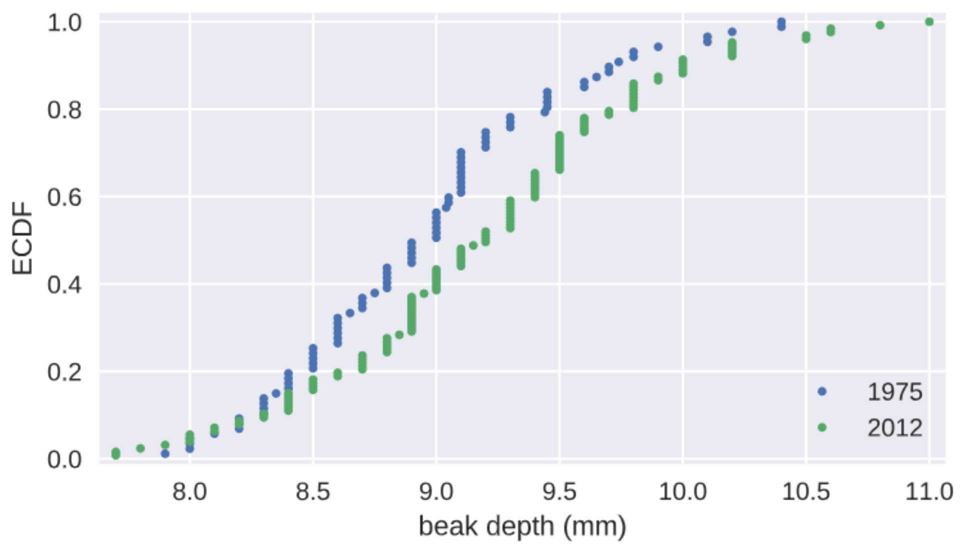
```
# Compute ECDFs
x_1975, y_1975 = ecdf(bd_1975)
x_2012, y_2012 = ecdf(bd_2012)

# 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(0.02)

# 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()
```



c). Parameter estimates of beak depths

```
# 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, size=10000)
bs_replicates_2012 = draw_bs_reps(bd_2012,np.mean, size=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')
```

<script.py> output:

```
    difference of means = 0.226220472441 mm
    95% confidence interval = [ 0.05633521  0.39190544] mm
```

d). <u>Hypothesis test: Are beaks deeper in 2012?</u>

```
# 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)

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

<script.py> output:

```
    p = 0.0034
```

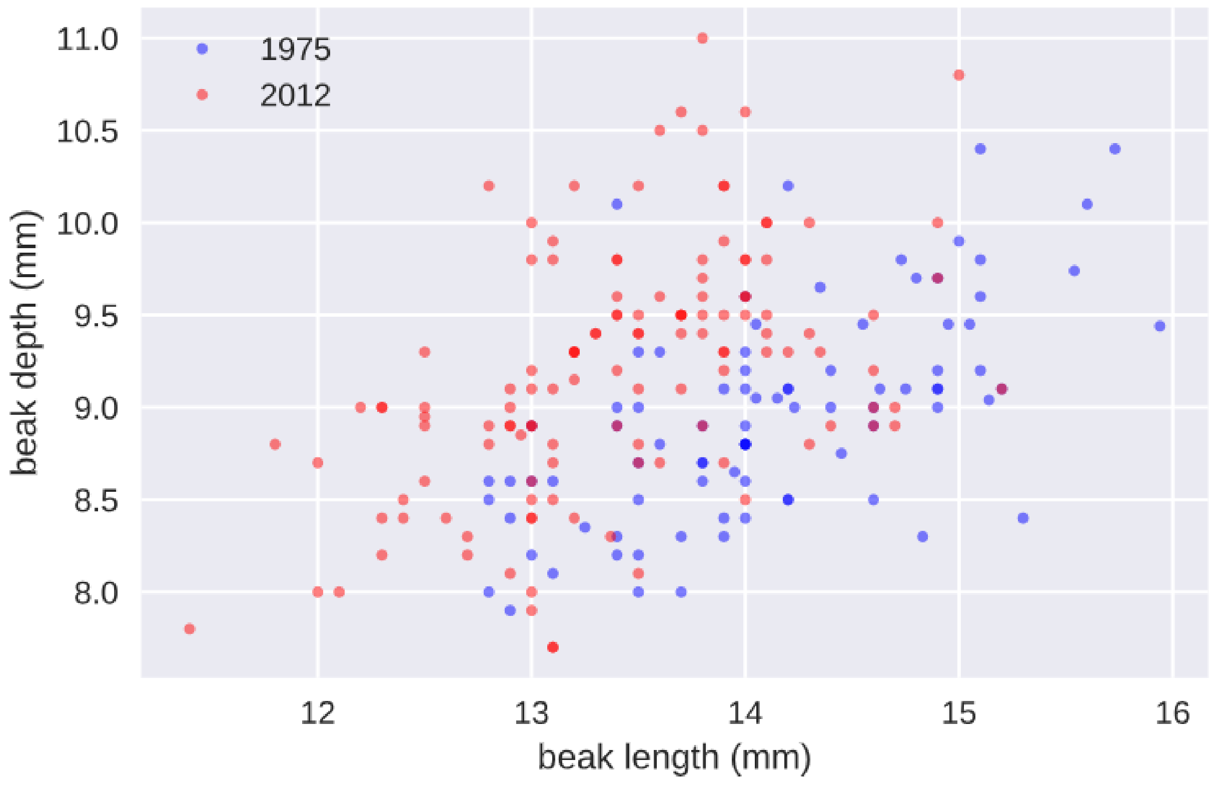
e). EDA of beak length and depth

```
# 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')

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



f). Linear Regression

```
# 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])

# 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)
```

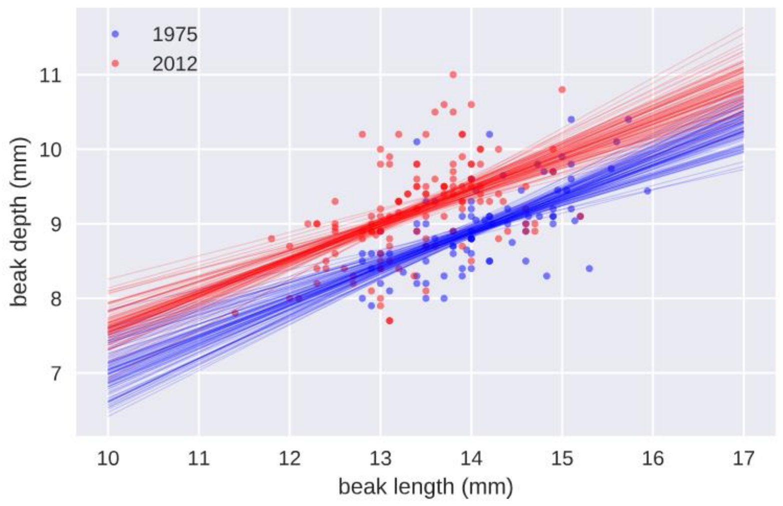
<script.py> output:

```
    1975: slope = 0.465205169161 conf int = [ 0.33851226  0.59306491]
    1975: intercept = 2.39087523658 conf int = [ 0.64892945  4.18037063]
    2012: slope = 0.462630358835 conf int = [ 0.33137479  0.60695527]
    2012: intercept = 2.97724749824 conf int = [ 1.06792753  4.70599387]
```

g). Displaying the linear regression result

```
# 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()
```



h). Beak length to deapth ratio

```
# 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)
```

<script.py> output:

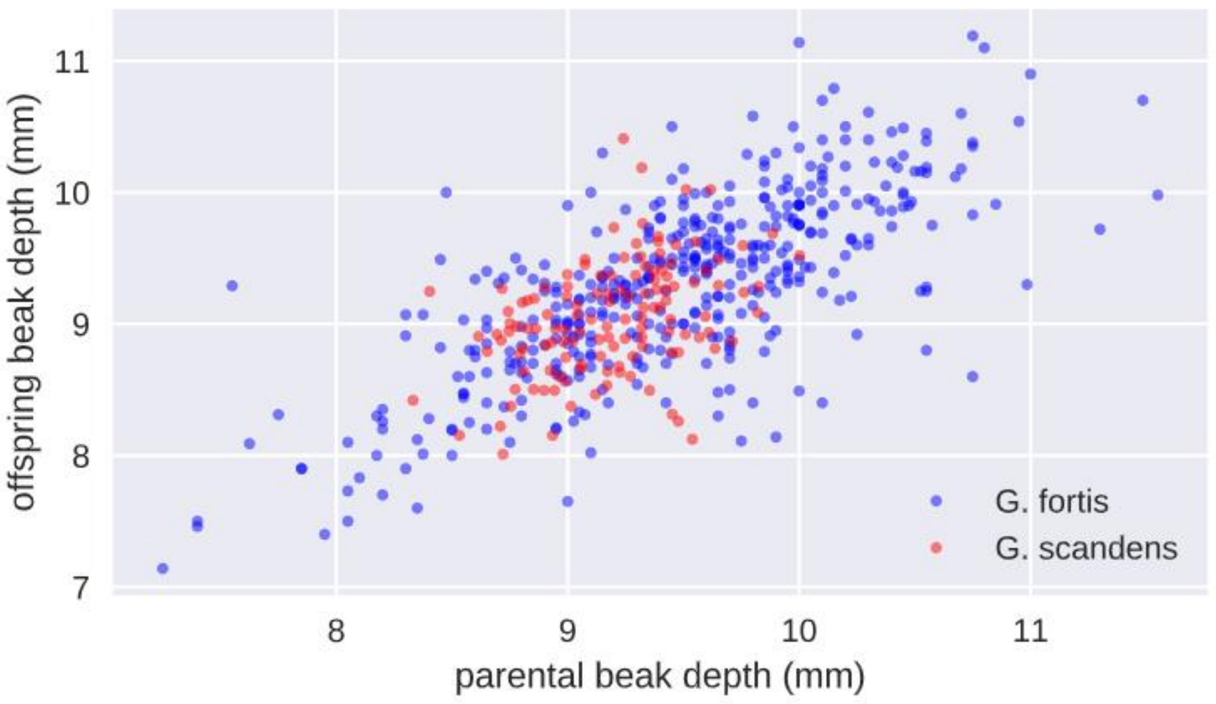
```
    1975: mean ratio = 1.57888237719 conf int = [ 1.55668803  1.60073509]
    2012: mean ratio = 1.46583422768 conf int = [ 1.44363932  1.48729149]
```

i). <u>EDA od hieratibility</u>

```
# 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()
```



j). <u>Corelation of offspring and Parental data</u>

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

k). Pearson correlation of offspring and parental data

```
# 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)
```

<script.py> output:

```
    G. scandens: 0.41170636294 [ 0.26564228  0.54388972]
    G. fortis: 0.728341239552 [ 0.6694112   0.77840616]
```

l). <u>Measuring Heritability</u>

```
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, 1000)

replicates_fortis = draw_bs_pairs(bd_parent_fortis, bd_offspring_fortis, heritability, 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)
```

<script.py> output:

```
    G. scandens: 0.548534086869 [ 0.34395487  0.75638267]
    G. fortis: 0.722905191144 [ 0.64655013  0.79688342]
```

j). <u>Is beak depth heritable at all in G. scandens?</u>

```
# 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)
```

```
<script.py> output:
    p-val = 0.0
```