Simulation of Simpson's Paradox With Palmer Penguin Data

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Background

Simpson's paradox occurs when a bivariate association is reversed in a multivariate model. This example using the Palmer Penguins Data was inspired by a tweet by Andrew Heiss.

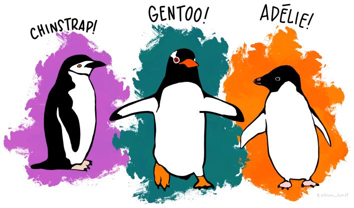


Figure 1: Palmer Penguins Illustration from @allison_horst

To begin, a little definition of penguin terminology is in order. Note the diagram defining culmen depth below.

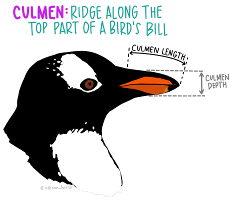


Figure 2: Culmen Depth from @allison_horst

Setup

```
. clear all

. cd "/Users/agrogan/Desktop/newstuff/simpsons-paradox-palmer-penguins"
/Users/agrogan/Desktop/newstuff/simpsons-paradox-palmer-penguins

. use "penguins.dta"
```

Bivariate

```
. twoway (scatter culmen_depth_mm body_mass_g) ///
```

```
> (lfit culmen_depth_mm body_mass_g), ///
> title("Culmen Depth by Body Mass") ///
> caption("Palmer Penguin Data") ///
> scheme(michigan)

. graph export mygraph1.png, width(1000) replace
(file /Users/agrogan/Desktop/newstuff/simpsons-paradox-palmer-penguins/mygraph1.png
> written in PNG format)
```

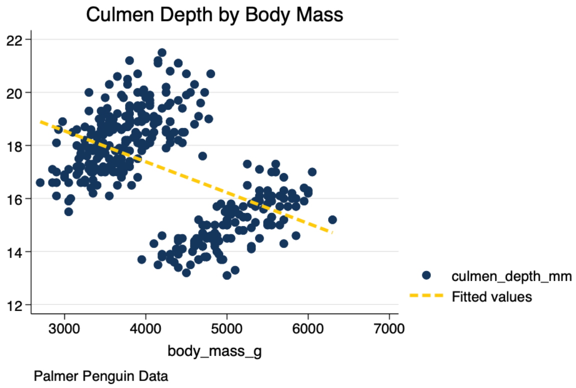


Figure 3: Scatterplot and Linear Fit

```
. regress culmen_depth_mm body_mass_g

      Source |       SS           df       MS      Number of obs   =       342
-------------+----------------------------------   F(1, 340)       =     97.41
       Model |  296.15994         1   296.15994   Prob > F        =    0.0000
    Residual |  1033.67459       340  3.04021939   R-squared       =    0.2227
-------------+----------------------------------   Adj R-squared   =    0.2204
       Total |  1329.83453       341  3.89980801   Root MSE        =    1.7436

------------------------------------------------------------------------------
culmen_dep~m |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
 body_mass_g |  -.0011621   .0001177    -9.87   0.000    -.0013937   -.0009305
       _cons |   22.03395   .5036206    43.75   0.000     21.04334    23.02455
------------------------------------------------------------------------------
```

Multivariate

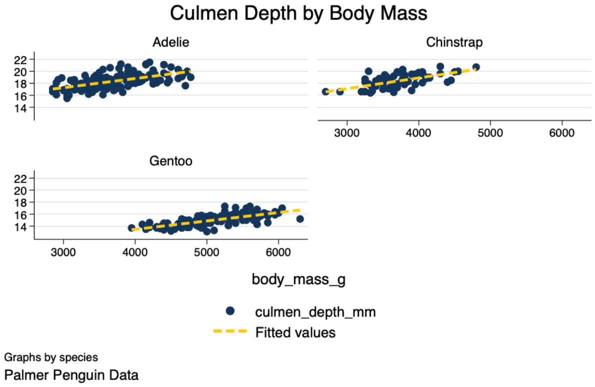
```
. twoway (scatter culmen_depth_mm body_mass_g) ///
> (lfit culmen_depth_mm body_mass_g), ///
> by(species, title("Culmen Depth by Body Mass") caption("Palmer Penguin Data")) ///
> scheme(michigan)

. graph export mygraph2.png, width(1000) replace
(file /Users/agrogan/Desktop/newstuff/simpsons-paradox-palmer-penguins/mygraph2.png
> written in PNG format)
```

The association is reversed when we take into account multiple variables.

```
. regress culmen_depth_mm body_mass_g species

      Source |       SS           df       MS      Number of obs   =       342
-------------+----------------------------------   F(2, 339)       =    225.41
       Model |  759.047284         2  379.523642   Prob > F        =    0.0000
    Residual |  570.787248       339   1.6837382   R-squared       =    0.5708
-------------+----------------------------------   Adj R-squared   =    0.5683
             |
```


Culmen Depth by Body Mass

Adelie

Chinstrap

Gentoo

Palmer Penguin Data

Figure 4: Scatterplot and Linear Fit

```
       Total |  1329.83453       341  3.89980801   Root MSE        =    1.2976
------------------------------------------------------------------------------
culmen_dep~m |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
 body_mass_g |   .0004877   .0001326     3.68   0.000     .0002269    .0007485
     species |  -1.974985   .1191142   -16.58   0.000    -2.209281   -1.740689
       _cons |   18.89014   .4200224    44.97   0.000     18.06396    19.71631
------------------------------------------------------------------------------
```