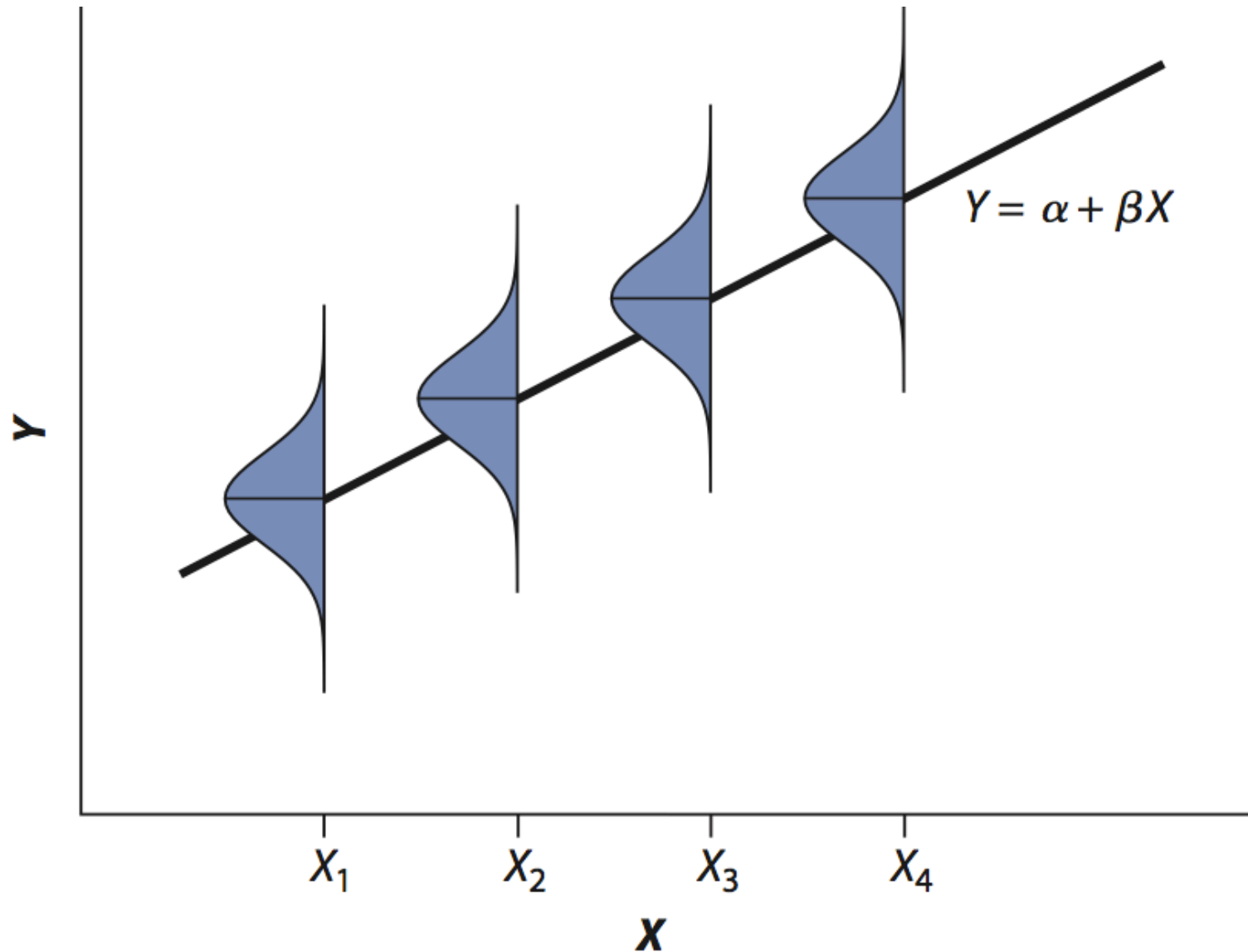


Violations in Assumptions of Regression Analysis

Assumptions of Regression Analysis:



Assumptions of Regression Analysis:

- For each X_i , there is a population of Y values whose mean lies on the ‘true’ regression line
 - For each X_i , the Y are a random sample
 - For each X_i , the Y are normally distributed
- Homoscedasticity
 - For every X_i , the variance of Y is equal
- Nothing is assumed about the distribution of X
 - It doesn’t need to be normally distributed or randomly sampled - they might be fixed by the experimenter

Major types of violation:

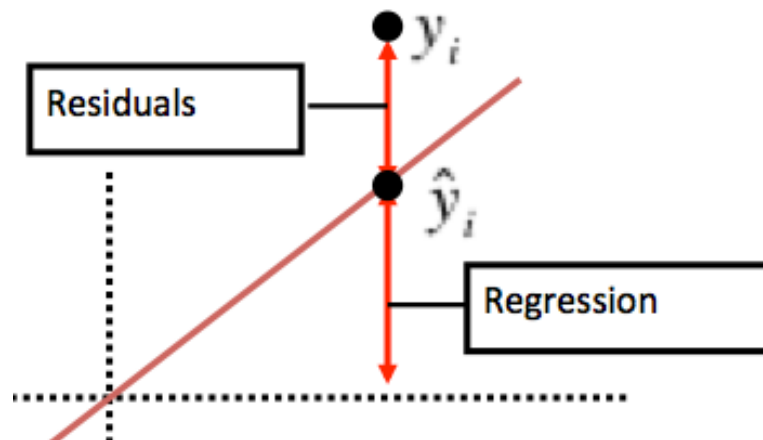
1. Outliers

- Violates homoscedasticity
- Violates normality of Y
- May make regression inappropriate
 - Especially if they occur at the boundaries of X
- Compare results of regression with and without outlier
- Transformation of data ?

2. Non-linearity (we are dealing with linear regression)

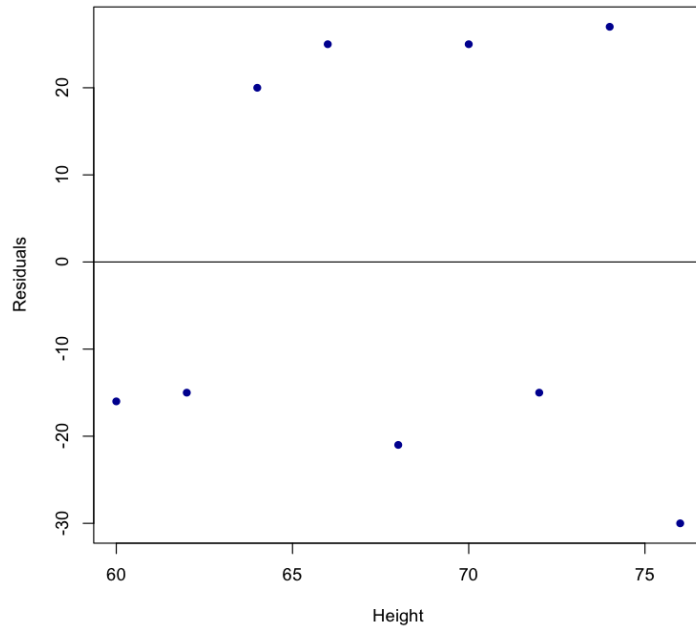
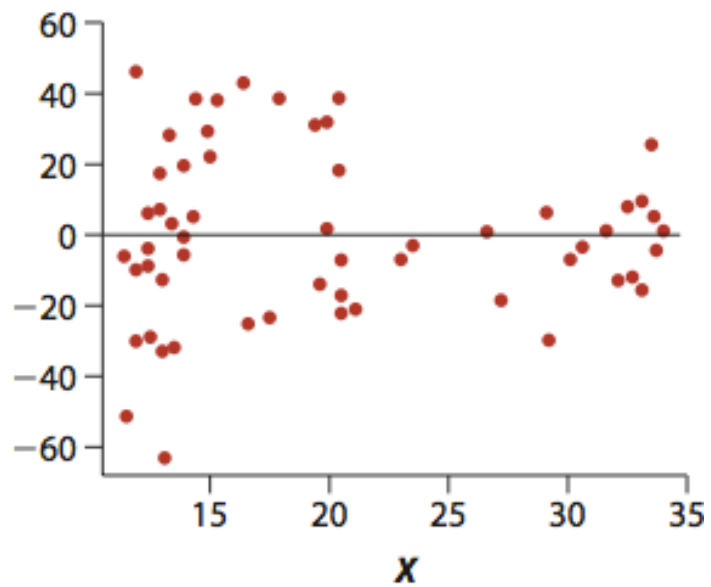
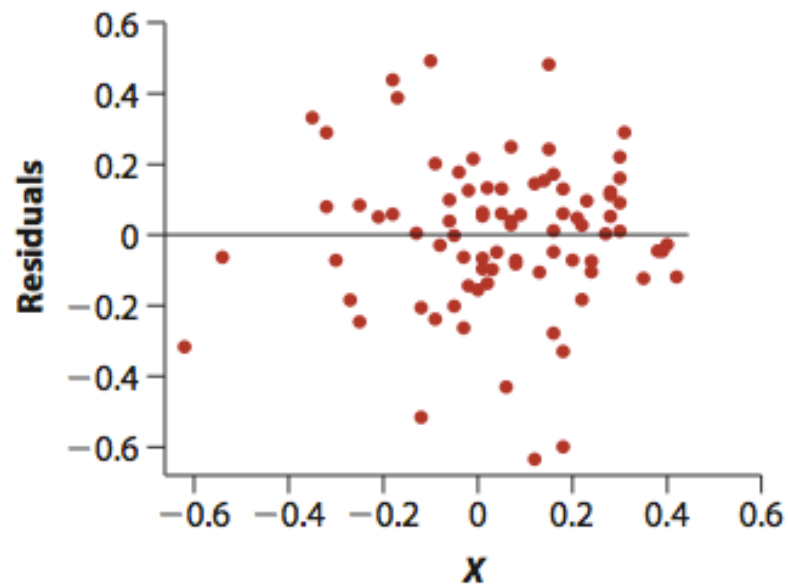
- Usually done by visual inspection of a scatterplot

- Residual plot:
 - Help assess assumptions
 - Residual ($Y_i - \hat{Y}_i$) is plotted against X_i

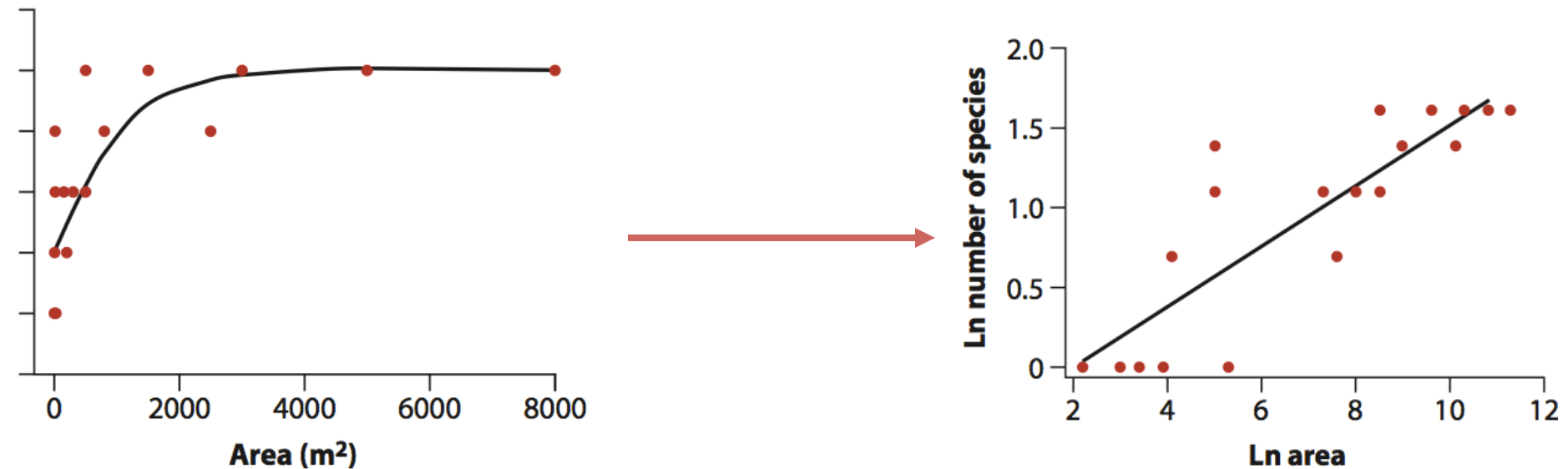


- If assumptions about normality and homoscedasticity are correct:
 - Symmetric cloud of points above and below horizontal line
- Use a computer

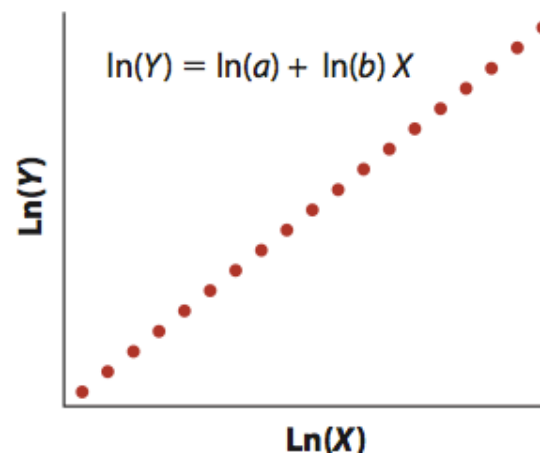
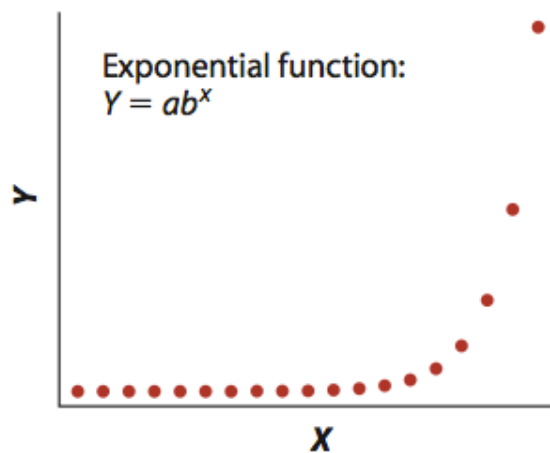
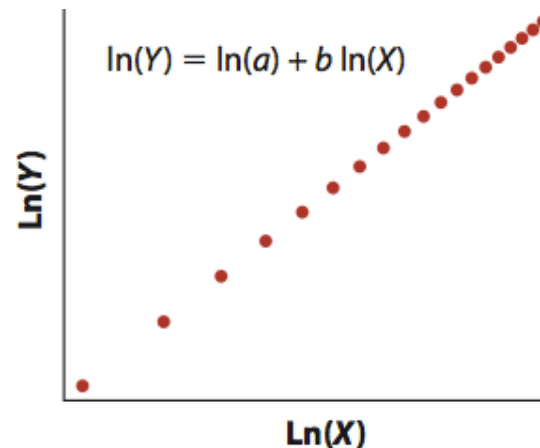
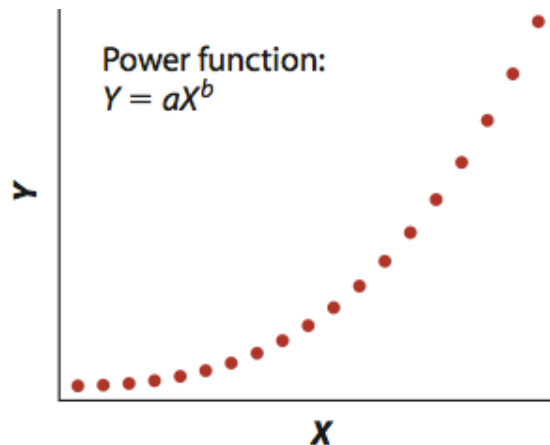
Regression Assumption Violations



- Transformations:
 - Non-linear relationships can sometimes be forced into linearity

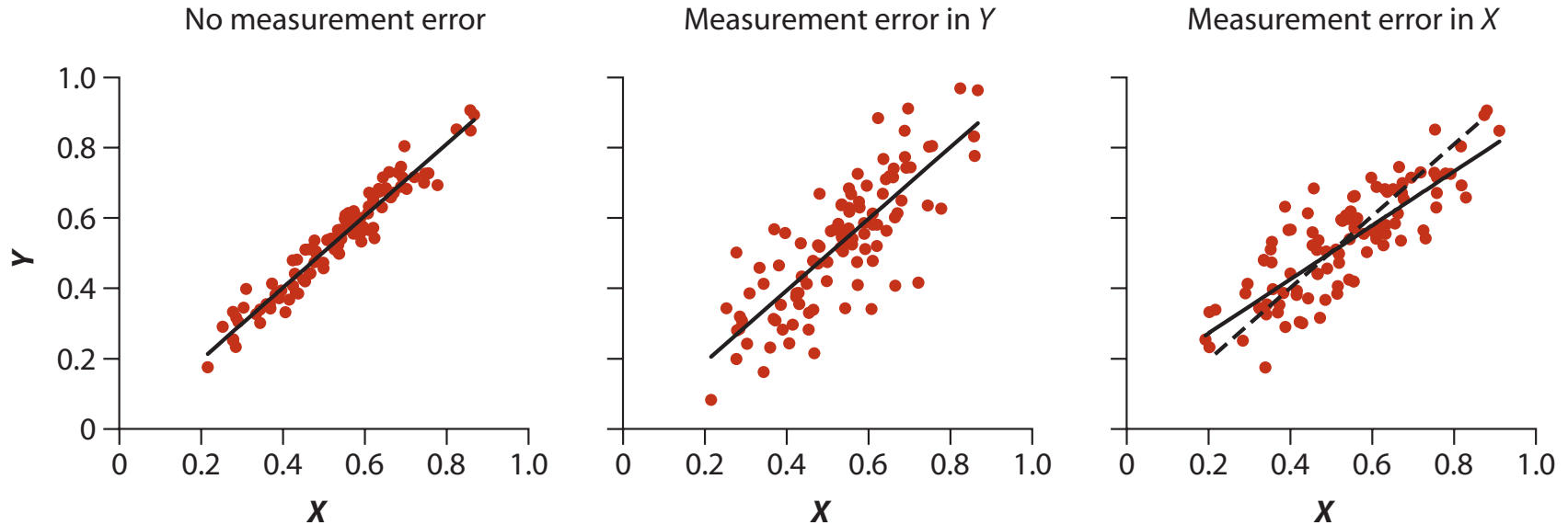


- Transformations:
 - The usual suspects:
 - log transformation for power and exponential relationships



- Measurement error:
 - Biological traits can be difficult to measure accurately
 - Effects of measurement error depends on the variable
 - **If measurement error occurs on Y**
 - Increase variance of residuals
 - Increases SE of slope
 - **If measurement error occurs on X**
 - Increases variance of residuals
 - **Causes bias in estimate of b** (underestimates slope)
 - » b will lie closer to 0 than β
 - » Remember: BIAS is really bad!

- Measurement error:



What happens if transformations don't work?!

Or... linear regression is inappropriate?

Non-linear regression

Non-linear Regression:

- Same assumptions are linear regression but, obviously, doesn't assume a linear relationship
- Keep it simple
- Don't **over fit**
 - It is possible to get a curve that fits each and every point ($MS_{\text{residual}} = 0$) but it will not predict future points since the curve ***doesn't describe a general trend***

Regression Assumption Violations

Curve with Asymptote

$$Y = \frac{aX}{b + X}$$

Quadratic curve

$$Y = a + bX + cX^2$$

Binary response Variable

$$\text{Log-odds}(Y) = a + bX$$

Smoothing

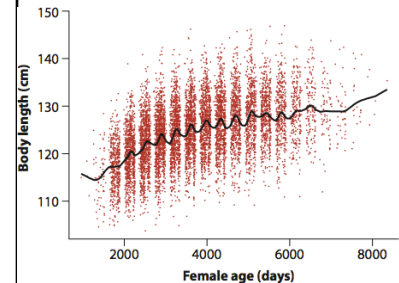
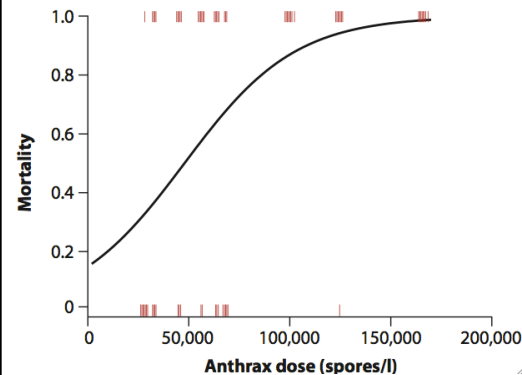
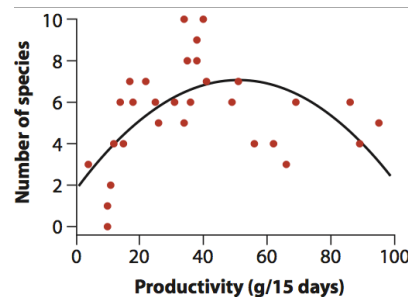
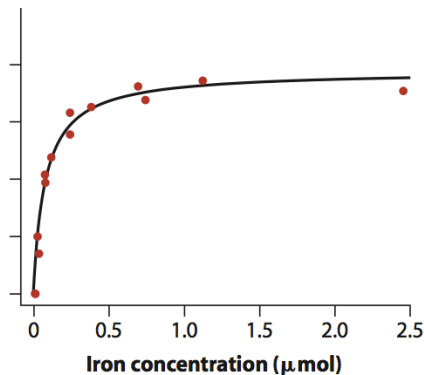
- depends on data

Michaelis-menten eq_n

Parabolic relationships

Dose response curve

Diagnosis of exclusion



Interleaf 11: Using species as data points

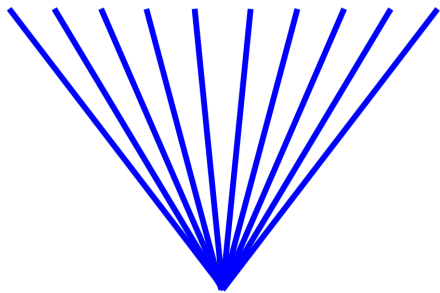
- Species are not ***independent*** because they share a common evolutionary history
- Phylogenies illustrate (hypothesized) ancestor-descendant relationship
 - Phylogenetically independent contrasts (Felsenstein, 1985) – a little like a paired t-test for each node:
 - http://ib.berkeley.edu/courses/ib200b/lect/ib200b_lect08_Ginger_Jui_PICs.pdf
 - <https://slideplayer.com/slide/7838671/>
 - https://biology.ucr.edu/people/faculty/Garland/Garland_JoeFest_1_Upload_Post.pdf
 - Many computer programs to deal with this issue but they all have their own baked-in assumptions that you should understand
 - Most commonly based on “random walk”/”Brownian motion”

Interleaf 11: Using species as data points

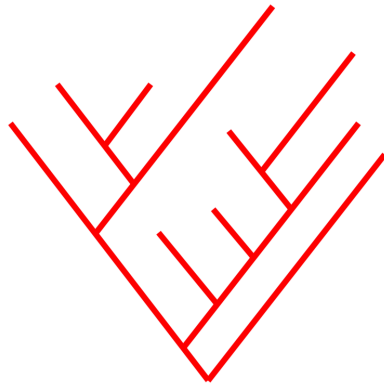
- Species are not *independent* because they share a common evolutionary history

https://biology.ucr.edu/people/faculty/Garland/Garland_JoeFest_1_Upload_Post.pdf

What
Conventional
Statistical
Methods
Assume

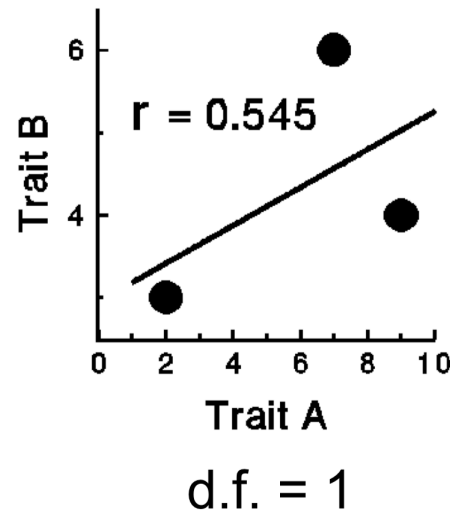


What
Evolution
Provides



It can make a big difference!

Conventional
Statistical Analysis



Phylogenetically
Independent Contrasts

