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1) Bolker describes custom-made analyses based on Maximum Likelihood, which often have a biological, ecological, or mechanistic justification. He contrasts these with the familiar Least Squares, *canned* methods that we typically learn in our first statistics course. Briefly (1 - 2 short paragraphs) describe at least two tradeoffs between the customized ML methods and the canned methods.

>   There are many tradeoffs to consider when developing the statistical model to apply to your data. Custom-made analyses based on Maximum Likelihood are often built to best fit your data, but sometimes provide a similar result as a classical Least Squares approach. One trade off when taking a Maximum Likelihood approach is convincing readers of its plausibility. Least Square approaches are well understood in biology at large, so when you decide to fit your own custom model readers might have more hesitation in understanding and concurring with your approach. Furthermore, a Least Squares approach is much less computationally intense; you don't need to choose starting parameters and are less likely to encounter numerical problems when running your code. On the other hand, doing a model more computationally intense might produce a better model and is worth the effort.

2) Briefly (1 - 2 sentences) describe each of the four key assumptions of the general linear modeling approach

>   The four key assumptions of the general linear modeling approach are that all observed values are independent, there is constant variance (homogeneity), fixed x values, and normality of the residuals. The independent observation assumption means the sampling of one observation should not tell us anything about the next. The constant variance assumption means that variability in the data points does not change as x values increase or decrease. The fixed x value assumption means there is no measurement error. Lastly, the normality assumption means under repeated sampling the data would be normally distributed at each x value, not that the data itself is normally distributed.

3) Explain how the normality assumption can be met in a general linear model, even if the response variable is not normally-distributed. (1 - 2 paragraphs)

>   The normality assumption can be met in a general linear model, even if the response variable is not normally distributed because this assumption is met if the response variable is normally distributed at a given x value upon repeated sampling (normal residuals). An example of this would be in the R penguins dataset. When plotted as a histogram bill length does not appear normal, but when plotted against body mass, if a subset of bill lengths was taken with repeated sampling, the distribution of bill lengths sampled at each body mass would be normally distributed.