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## **Week 9 Reading Questions**

## Q1 (1 pt.): Briefly (1 - 2 short paragraphs) describe at least two tradeoffs between the customized ML methods and the canned methods.

One trade-off is computational speed and stability. Having an established, or 'canned' method allows you to skip choosing starting parameters and go directly into a well-established model. However, a customized model may be able to run its computations faster. Another trade-off is that there are standardized definitions to go with 'canned' models. These definitions may actually allow you more flexibility to play with optimizing the model since they already have established definitions. If they both fit the data equally well, then you can work with an equation that's easier to manipulate to transitions in the data. Plus, if both the custom model and the 'canned' model fit the biology equally well, and you use a 'canned' method, you don't have to have anyone be skeptical of 'fancy' statistics.

## Q2 (1 pt.): Briefly (1 - 2 sentences) describe each of the four key assumptions of the general linear modeling approach.

The first assumption of general linear models is normality, that is that your residuals are normally distributed. Next, the observations in the dataset are independent observations, they aren't linked in some way. Then, there is no major measurement error. Finally, is that there is homoscedasticity, or homogeneity of variance, which essentially means that the variance is equal across your samples.

## Q3 (1 pt.): 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)

Normality is typically addressed in terms of the independent variable, but because there are multiple observations for every independent variable value, there are also residuals for every value of the response variable, or X. Since X is fixed (i.e. – nonrandom, theoretically eliminating extra noise from the data), this means that normality assumes that the variance of every x value is also normally distributed across its residuals. So, because of the assumption that X is fixed, even if it's not actually normally distributed, this should show that you would meet the assumption of normality in a general linear model.