Scale-location:

The scale-location plot indicates whether the residuals are spread equally along the ranges of predictors. The plot serves as a method to check for the assumption of homoscedasticity. Heteroscedasticity is a change in residual spread over the range of measured values and can cause misleading results (Long and Ervin 2000). Ideally, the plot will show a horizontal line with data points that are spread equally around it. In this plot, however, there is a cluster of points on the left side of the X-axis, and the residuals become much wider further right along the X-axis. While the data appear to have a generally uniform variance after 1.5 along the X-axis, this substantial slope of the red line indicates that heteroscedasticity exists in this data, which may need to be addressed.

Residuals vs. Leverage:

The plot is useful for identifying specific observations that are influential outliers in the linear regression analysis. These observations could be extreme cases against the regression line that alter the results when excluded. In this plot, influential outliers are in the upper and lower right corners. Since there are no observations located outside of the red dotted line (Cook's distance; Ayinde et al. 2015), there are no influential cases and all residuals are well within the Cook's distance lines, which is barely visible on the plot.

Coefficient plot:

The coefficient plot shows the standard errors and distribution for each coefficient along with confidence intervals. The value of the coefficient indicated how much the response variable's mean changes in response to a one-unit shift in the predictor variable while other variables are kept constant (Brown 2019). The sign of these regression coefficients indicates whether the correlation between the response and predictor variables is positive or negative. This plot indicates that age has a very strong positive effect on my response variable (tarsal length), which is expected. However, hatching spread has a substantially smaller effect that is both negative and overlaps with zero. The variable is expected to have a negative effect but was hoped the effect was larger. This may be due to several things, for example, heteroscedasticity in data remains undealt with or missing predictor variable in equation (e.g. hatch order has been shown to affect offspring growth and may be confounding). Additionally, this plot can be used to compare multiple models simultaneously (although this is not shown here). This can show how the inclusion of a new predictor variable can cause the estimate of another variable to change.

Literature Cited:

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