**Best things learned from Murray’s course:**

* Factorizing a binary 0/1 variable will screw up emmeans backtransformations later on! Needs to fit as numeric with glm
* Binomial model coefficients can be used to calculate the LD50 for survival data: LD50 = -intercept/slope
* Interactions between continuous variables **REQUIRE** the covariates to be centered first, otherwise they WILL be collinear
* Can keep in the transformation of predictors (e.g., scale(…, scale=FALSE), log(…)) and then the original variables can be used as inputs in emmeans, etc.
* emmeans package requires TRUE and FALSEs to be spelled out to work properly
* Cook's distance is not needed if you only have categorical predictors
* Use emmeans on link scale %>% regrid %>% pairs %>% confint to get absolute differences (X is # units higher than Y) rather than fractional differences