**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
* *nlme* was the first way of doing mixed-effect models, it uses quasi-likelihood by re-fitting the models different ways, so isn’t as modern as *lme4* or *glmer*, but these are limited in the families that it supports, including zero-inflated models. Thus *glmmTMB* to fit the broad range of models used in ecology
* 'group' works similar to 'by', just that group is more versatile when it comes to mapping, etc. because it will automatically group by polygon, while by needs a named list as input. Otherwise, they work very similarly.
* Allowing a random slope and intercept model is ok with minimum evidence of non-parallel lines, as the model will tell us if this is unnecessary.