**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.
* (1|random) is interpreted as ‘do the intercept [‘1’] by [‘|’] the random factor’
* Can fit random slopes using both covariates and factor variables!
* Different random effect structures include correlated vs. non-correlated:
  + Correlated random intercept and slope:   
    x+(x|g) = > 1+x+(1+x|g)
  + Uncorrelated random intercept and slope:   
    x+(x||g) => 1+x+(1|g)+(0+x|g)
* Sometimes models fail to converge using one of the other optimizers, even if they are supposedly better…
* `scales::pseudo\_log\_trans()` is good for dealing with zero-inflated values and still log it!
* When fitting a negative binomial in glmmTMB, use family = **negbinom2**(link = “log”), which is the quadratic parameterization that is more relatable to the Poisson distribution!
* When fitting a random slope model, we should try to keep the random effects slope the same as the fixed effects term. So if the fixed effects was a polynomial, we should keep the random effects term a polynomial too.

GAMs

* The general rule of thumb for wiggliness k.check is that if you need more knot dfs, we should double it.
* edf = 1 suggests just a significant linear term (not curvilinear), edf = 0 suggests no such trend

Bayesian

Priors for sigma:

* *cauchy*(0,5) was a really good prior for sigma prior to the widespread adoption of no U-turn samplers (NUTS); however, now *gamma*(2,1) tends to work the best. *Exp*(1) also is used
* Only baysian stats can say something about where the true mean lies between with their 95% credible intervals. The frequentist cannot, as they assume a single value of the true mean, whereas Bayesian assumes that the true mean is a distribution.
* Evidence ratio = How much evidence is there that the probability is >50 divided by how much evidence is against that
* Priors must be on the link scale – so be careful with their backtransformation!
* Leave one out is the best model.

Extra things to make:

\*\*Package for extracting formula, determining model differences, and filling these in for the AIC table\*\*