

Homework 10

The file “zooplankton_size_diversity.csv” contains data from the paper, Ye et al. 2013. The data were collected on 5 cruises in the East China Sea. The researchers counted and identified the zooplankton collected in a 330 μm mesh net; the total number of fish larvae was recorded from the same samples. They also measured chlorophyll concentration, nitrate, silicate, phosphate, and temperature, with each variable averaged over the depth from which the plankton net tow was taken.

The authors used this data to test a number of hypotheses regarding the factors that influence control of phytoplankton by zooplankton (i.e. top-down control). They used the ratio of total zooplankton biomass (estimated from biovolume) to chlorophyll-a as a proxy of top-down control; i.e., if there are more zooplankton relative to phytoplankton then the implication is that zooplankton are more strongly controlling phytoplankton biomass. This ratio was log10-transformed to give an approximately normally distributed response variable.

The authors wanted to test the following 6 hypotheses:

1. Increasing size diversity of zooplankton enhances top-down control, due to more complete consumption of the whole size range of phytoplankton
2. A greater proportion of large zooplankton enhances top-down control, because larger zooplankton are more effective grazers
3. Nutrient enrichment weakens top-down control, by promoting grazing-resistant prey
4. Increasing taxonomic diversity of zooplankton enhances top-down control, through a diversity of feeding modes
5. Greater fish abundance decreases top-down control, via a trophic cascade
6. Increasing temperature enhances top-down control, by accelerating consumption relative to production

The authors test these hypotheses using regression where $\log_{10}(\text{zooplankton:phytoplankton biomass ratio})$ is the response variable, and the predictors are: zooplankton size diversity, proportion of large zooplankton (NBSS slope), zooplankton taxonomic diversity (shannon diversity), #fish larvae ($\log_{10}(x+1)$ -transformed), water temperature (WT), and the concentrations of nitrate, phosphate, and silicate. The NBSS slope measures the size-spectrum of zooplankton, and this number becomes less negative as a greater proportion of large zooplankton are present.

For this assignment you need to test the authors' hypotheses using regression and model selection with this data. There are different ways to do this, so for learning purposes let's try a couple different ways and compare. It would be nice to have six different predictors representing the six different hypotheses. However, there are 3

different nutrients, but these are highly correlated with each other. So just pick one of the nutrients and use that as the predictor representing the nutrient hypothesis.

In order to account for the structure of the sampling (i.e. non-independence of the data), *you should use Cruise as a factor in all models*, regardless of the other predictors you include/exclude. This is because samples from the same cruise are likely to be similar, due to various unmeasured factors. Therefore the cruise factor is a kind of 'structural' predictor separate from the hypotheses we are testing.

1) Make six linear models, each model having one of the six predictors. Plot the raw relationships and fitted lines, and report R^2 . Make a table of AICc, delta-AICc, and Akaike weights for the six models. How do you interpret these results in light of the authors' hypotheses?

2) Testing the hypotheses separately has a nice clarity to it, but the hypotheses are not mutually exclusive, and support for one predictor may change when it is competing against another predictor in the same model. This is especially likely when the predictors are partially correlated (e.g. the different zooplankton diversity measures). Make one model that has all the predictors, and plot the fitted effects as well as residual diagnostics. Test the importance of the predictors using LRTs. How do these results differ from those found in #1? What are the implications for the authors' hypotheses? Why do you think the results might differ?

3) Testing the predictors in one big model is nice, but we might be concerned that this is not the 'best' model and that effect estimates in the 'best' model might differ from those in the full model. Use dredge() and model.sel() to compare all possible models with these predictors. (Note, you can make sure Cruise is in all models by specifying fixed = ~ Cruise, in the dredge() function).

What does the distribution of Akaike weights look like? By comparing the models that have some support from the data, which predictors do you think are important? What are the variable importances calculated from the Akaike weights? Do the effect estimates vary much across models?

4) Creating all possible models with a set of predictors produces complex results, but one way to synthesize the output, while appropriately accounting for model uncertainty, is model averaging. Use model averaging to get average effects for the six predictors representing our six hypotheses. How do your conclusions from this approach compare to your conclusions from #2, where you assumed that one model (with all the predictors) was the appropriate model to use?