**Notes from phone call with Mike Hanam:**

2/1/17

* Read McMahon & Diez (2007)
* Consider running full random model-see R code added to script; this would have site nested within Region
* But really we want variances to differ among regions, rather than sites for questions #2
* But to deal with problem of variance in questions #1, allow variance to be different among sites
* Way to do both in one model? Look back in Zuur chapter to see if solution
* If not, perhaps just put site one in appendix and state in text
* Also look into nested ANOVA (i.e., fixed effects of Region and site)-look at Quinn and Keough and underwood; issue with this can be sensitivity to differences in sample sizes (which we have), affect heterogeneity of variances; but could try with different variance structures to explore
  + but I think only really this is worthwhile if want to look at/test hypotheses of differences between sites/regions
* When looking at model output, the st.dev. listed under the random effect is the st. dev we’d expect between two site, given the regional random effect (double check ask Brian to make sure I’m interpreting correctly if going to use)
* For the variance differences listed among sites or regions (depending on model) see Zuur for explanation, but basically is multiplication factor with first one as base (1.0)
* Can check this against variation shown in boxplots to make sure is correct
* For doing site specific contrasts
  + Helmut (sp??) contrasts
  + Tukey etc
  + Alternatively, use predict() function for lme: if intervals not overlap, then different
  + But read up understanding that there’s a difference between confidence and prediction intervals…
* For table/output: packages sjmisc and sjplots
* Also want table of model selection: package MuMin (what Mike uses); also AICmodeave
  + want dAIC, AIC, log likelihood, etc.
* Can keep oceanic in model, shouldn’t affect estimates (can read up on/we talked about shrinkage, etc.)
  + put in/take out-can compare and look at residuals
  + not necessarily super helpful, but then at least have in model and can qualitatively/biologically talk about
* Can see estimated random effect for each region (I had this written, but not sure what did I mean by this?)
* Also can put model graphics of residuals with/without variance component in appendix to further support that they are different.
* Random forest: not sure it’s worth it with just 2 variables-would CART be better/simpler since only have two?...look into