Meta-analysis:Code\_meta\_data

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Updated: 20200626 ~~~ GOAL: Meta-analysis on soil organic amendment impact on soil carbon pools > 20cm in depth ~~~ STATS OVERVIEW: mixed model for meta-analysis (regression?) with maximum likelihood (hierarchical w study and depth as groups) OR I could run different analyssis every 20cm -need mixed effect to account for studies with multiple amendments in 1 study (autocorrelated)

parameter = carbon stock moderators = initial soil conditions, other environmental factors, management covariate = length of study (months)?? ~~~ WORKING ON: glmulti - get the df.c\_ratio\_all data to work -> make sure thh cf and zf dataframes are combinging correctly

Bootstrap Qb values for different parameters - how can this incorporate ACC (strata?)? Autocorrelation w depth? -if depth is just another parameter, no testing of how the other parameters vary with depth…

Need to bias correct bootstrap - <50% of distribution above mean I2 test of each moderator instead of Qb value? Must I down weight studies with imputed error? Can I bootstrap to check distribution of the variances? Which moderators best explain the variance? Qw and Qb calculations (how do I get a p-value? = CIs?) ~~~ STATS QUESTIONS: a. Is the effect different from zero? (are there outliers of effect sizes?) -YES, bootrapped mean effect sizes for the global meta-analysis b. Examine degree of heterogeneity of effect sizes -Account for between study varition (2nd source of heterogeneity) -USE either Qt, or I2 is more accurate between meta-analysis comparison c. Estimate standard deviation of studies (1) assume normal and S = 1 ; (2) impute from studies with data (SD/mean ratio for complete studies AND (3) regression S = alpha +beta\*n) d. Calculate weight of each study (based on sample size of control and trt) (p205)

1. Make statistical inference to derive estimates, test hypothese, make deicions based on the model -calculate Q for each moderator? Or calucate I2 (pg 112) -bootstrappping and 95% CI on factors (p 123)
2. Meta regression (random effect = study), specifically a mixed model, & test factor influence on the effective size (see list below of 16 factors extracted) -metafor mods<-cbind(a, b, c) ; mima (yi, vi, mods, method = “REML”)
3. Check assumptions
   1. fit assumptions of statisitcal models
   2. test publicaiton bias (p219)
   3. check stat power of tests
   4. test sensitivity of results to inclusion/exlustion of data - does it change main conclusions -imputed SD, estimated 1, only complete studies -w and w/out the outliers -leave one out (studies or categories)
   5. check manuscripts (Ch 20)
4. Discuss generaliziability and limitations -SE assumed rather than SD when not recorded (more conservative)
5. Gaps where more primary studies are needed? ~~~ RESEARCH QUESTIONS: Is the overall effect of amendments positive (different from zero) on soil carbon stocks? How does amendment stabilizaiton of SC change with depth? with time? Do effects differ between minimum controls vs fertilzed controls?

0 \*\*\* Assess correlation of moderators\*\*\* -> find a group where moderators are not confounded and run analysis -results are different than the global effects? Do the following moderators help predict change in soil carbon stocks: 1. Amendment type 2. Amendment rate 3. Amendment C:N ratio 4. C pool  
5. Time since amendment start

Environmental factors 6. MAP 7. MAT 8. MAP/MAT 9. XXXXX place holder… 10. **Lattitude**

Initial soil proerpties 11. Texture 12. Initial SOC 13. pH

Management 14. Crop System 15. Irrigation type 16. Fertilizer input ~~~ NOTES: echo=false supresses code; include=false supressed output ~~~ COMPLETED: 1) Make categories for each variable = cropping system (monocrop, rotation), crop type (grain, row, legume, forage), years of application, type of amendment, soil pH, SOC content intial, clay content, latitute, C rate applied, dry weight, N rate 2) convert SE (sm) to SD (large) (assumed it was SE (small) and convert to SD = make larger) 3) Calculated stocks for the df.c data frame only -> no need to calculate the response ratios again, as the BD did not change and they are the same as the C concentraiton ratios 4) Imputed error in the form of SD with ratios (SD/X’mean’) and regrssion SD= alpha +beta (N) ; 36% have errors reported 5) Checked heterogeneity within meta-analysis due to different studies (section 8); calculated I2 statistic 6) Remove correlated factors: pH and MAT = .98 and MAT/MAP; elevation and time.n.mos (.97); elevation and MAT.MAP .76, lat and Nfert.rate .333 =remove elevation and MAT (keep MAT/MAP) 7) analyze fertilized and zero controls #to combine datasets - use fertilized controls when possible= had a lower effect size (will not overestimate the effect?)

~~ Code that did not get rJava and glmulti to work: ################################ #in Terminal # sudo R CMD javareconf # sudo R #install.packages(‘rJava’,,‘<http://www.rforge.net/>’) #did not work #install.packages(‘rJava’) ,repos = “<http://cran.us.r-project.org>”)

# additional attempts

# a

#dyn.load(‘/Library/Java/JavaVirtualMachines/jdk1.8.0\_241.jdk/Contents/Home/jre/lib/server/libjvm.dylib’)

# b

#packurl<-“<https://cran.r-project.org/src/contrib/Archive/rJava/rJava_0.9-9.tar.gz>” #install.packages(packurl, repos=NULL, type=“source”)