

Week 1

- Broad goal: Fix code.
 - ☒ Use less filtered dataset
 - Now at 30% with 39 taxa.
 - ☒ Make graphs of parameter values at each iteration
 - Did a lot of graphs, histograms and changes of betas between loops. Need to do final after changes are made.
 - ☒ Try stepwise update
 - Using .1 as a constant. Still doesn't work, so likely a more complicated approach would not be helpful.
 - ☒ Fix problem where R inverse and others not updating in beta loop
 - ☒ Change R-inv function to depend on alpha instead of X and beta since already calculated.
 - ☒ Flip order of beta and phi loops.
 - ☒ Look at residuals in each iteration. (in phi step)
 - ☐ Keep something constant through loop and/or try using identity for R.
 - ☒ Try different dataset? Maybe simulated one from previous paper.
 - Same troubles
 - ☐ Distance matrix argument to dist?
 - Need both forms, so may or may not be useful
 - ☐ Check if phi is correct now, and see how is used
 - ☒ Figure out large alpha problem
 - Seems the + and one loop beta fixed this?
 - ☐ Try a different covariate?
 - ☐ Figure out why geem code uses + instead of - on update
 - I think + is correct. At least it converges.
 - ☐ Identify which covariate is causing the trouble.
 - ☐ Try removing the single OTU that seems to be contributing to problem.
 - ☐ Save everything to list correctly to look at later.
 - Saving rho, omega, phi, beta, diff (abs), num iterations
 - Also do residuals. Which residuals? Cross product ones? Squared ones? Standardized squared ones? Probably standardized but not squared. Should be distributed around zero. ?
 - ☒ Plot lists
 - Plotted rhos, omegas, phis, diffs, not sure what else to plot.
 - ☒ Remove scalar update.
 - Doesn't work. see journal
 - ☐ Write up algorithm for Yuan to go through? Ask to check.
 - ☐ Final run through before meeting of graphs and numbers
 - ☒ Move timing into function

Week 2

Main tasks:

- To-do from sheet
- Prepare presentation

- ☐ Try different covariates (parasite burden/antibiotics/exposure)
- ☐ Think about genus level analysis/ phylogenetic tree for taxonomic units
- ☐ Choose α automatically (simple line search)
- ☐ Think about how to test the significance of β