

Week 1

- Broad goal: Fix code.
 - ☒ Use less filtered dataset
 - ☐ 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
- ☒ Wednesday email research update.
- ☒ Include more taxa: more zero-inflation
 - Not great results. see journal $\omega = .99$, $\rho = .1$
 - runtime of 20 min.
- ☒ Add computation time in model.
- ☒ Make presentation
- ☒ Figure out why adding the minus sign changes the code.

- Pretty sure this is because we are then adding or subtracting the λI incorrectly.
- ✓ Try changing the minus sign on larger dataset.
 - Either immediate convergence or infinite alpha values on 1st iteration.....
- ✓ Set up automatic save outputs along with description
- ✓ Try with a medium sized dataset, like prevalence of .2?
- ✓ Save test datasets to files for easy loading
- ✓ Only include last beta output?
- ☐ Try different covariates (parasite burden/antibiotics/exposure)
- ☐ Think about genus level analysis/ phylogenetic tree for taxonomic units
- ☐ Choose α automatically (simple line search)
- ☐ Write up line-search steps and goals
- ☐ Understand how Hessian is calculated and expected values equal zero.
- ☐ Run on previous dataset from original paper.
- ☐ Rename file with algorithm
- ☐ Compare to independence GEE written already geeglm?
- ☐ Calculate sandwich variance estimators for asymptotic significance tests
- ☐ See if new shared tree that Tom had is the same?
- ☐ Add residuals to output and look at plots
- ☐ Change initial value to something different?
 - change initial rho to 10. Changes results (of at least ests of rho and omega)
 - Try previous iterations rho and omega.
 - See how beta estimates change
 - Run code with initial value of 1 again to compare.
- ☐ Read numerical optimization book.
- ☐ Save convergence results of nls optim
- ☐ Make sure subtraction in ϕ is correct

Week 3

- General
 - *☐ Read numerical optimization book.
 - *☐ Understand how Hessian is calculated and expected values equal zero.
 - *☐ Run on previous dataset from original paper.
 - *☐ Rename file with algorithm
 - ☒ Take pictures of meeting notes.
 - ☐ Figure out how to send jobs to server
- Line search
 - *☐ Choose α automatically (simple line search)
 - *☐ Write up line-search steps and goals
 - ☐ Add condition if infinity or NA to halve gamma
 - ☐ Clean up code for speed and remove redundancy.
 - ☐ Look at notes from meeting about (different?) conditions
 - ☐ Code was set up incorrectly. Fix. Shouldnt be updating betas each time, just checking.
 - ☐ Save sum of absolute G for each iteration.
- Convergence
 - *☐ Save convergence results of nls optim
 - ☐ Change λ to be based on eigenvalues.
 - ☐ Save eigenvalues and look at ratio.
 - ☐ Test to see difference within iterations of if starting values (eg rho = 10) give different results.
- Correlation: Importance of ρ, ω
 - *☐ Compare to independence GEE written already geeglm?
 - *☐ Calculate sandwich variance estimators for asymptotic significance tests.
 - ☐ Keep ρ or ω the same throughout the algorithm
- Other
 - *☐ See if new shared tree that Tom had is the same?
 - *☐ Try different covariates (parasite burden/antibiotics/exposure)
 - *☐ Think about genus level analysis/ phylogenetic tree for taxonomic units
 - ☐ Add condition to make sure ρ, ω also converge
 - ☐ Email Tom with questions
 - ☐ Think about how hypothesis tests work
 - ☐ Read about GEE hypothesis tests

Week 4