

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

- ☐ Writeup meeting notes
- ☐ Email Tom (response to my email) about more information
- ☐ Look into *resolving nodes*
- ☐ Select one Genus/Family to only have 10 ish ASVs. Filter dataset, and tree.
- ☐ Test against identity, fixed values of ω and ρ .

Week 5

- ✓ Make gamma, lambda values arguments in the functions.
- ✓ Save final residuals in model.
- ✓ Convert initialization to one line list.
- ✓ See if weird jump still happens. figure this out.
 - Seems like jump does not exist anymore.
- ✓ Add model call to result list
- ✓ Create diagnostics plot function
 - Patchwork outputs
- ✓ Clean up old code
- ✓ Save beta values again and look at changes.
- ✓ Run through with bug fixed. See what goes on. Write up results
- ✓ Figure out a way to compare beta values
 - Using a line plot across iterations
- ✓ Add GEE values to plot.
- ✓ Check if gamma = 1 betas are same as gamma = .1 betas
 - They are not.
- ✓ Figure out how to compare betas across different model runs (probably same line function?)
- ☐ Think about how to do simulations, since we need to have something to check against.
- ☐ Try to sum up phylogenetic tree and see if there are any problems.
- ☐ Email Tom about summing up the phylogenetic tree
- ☐ Look at residual matrix (cross residuals). See if close to zero.
- ☐ Use data that is just random common taxa.
- ☐ Try different covariates
- ☐ Consider moving functions to new files
- ☐ Convert all nls functions to matrices to make sure all entries match indeces.
- ☐ Update roxygen skeletons for functions
- ☐ Add final values of omega, rho and phi to patchwork plot
- ✓ Try independence
- ☐ Compare independence to geem beta values.
- ☐ Try fixed values of ω, ρ
- ✓ Figure out why flavo + 30p dataset stops in 2 iterations
 - Figured out where the problem occurs, but not sure why it occurs...

- ☐ See how λ values change beta values.
- ☐ Explore convergence of optim loop.
- ☐ Check variances are correctly between 0 and 1.
- ☐ Compare beta values with a larger/smaller gamma to .1 and see if beta values are different.
- ☐ Implement line search? maybe will work now that bug is found.

Week 6

☐ Do simulation

Week 7

- ☒ Do better with version control!!!
- ☒ Split function into multiple parts: b02e5e9
- ☒ Arrange file structure
- ☒ Add commits to finished todos.
- ☒ Make repo public.
- ☒ Roxygen for all functions. d232743
- ☒ Organize Dirichlet and other simulation files
- ☐ Rename main function
- ☐ Consider moving code to package for roxygen and loading
- ☐ Make sure everything runs with changes
- ☐ Find points in code that were changed in meeting
- ☐ Simulation:
- ☐ Get working on just Dirichlet
- ☐ Fix variance calculated to be true values of alpha.
- ☐ Check on all instances of making a matrix and if it is the byrow correctly or not!
- ☐ Include github and commit info for weekly update