Hackathon 8/21 goals

1. ~~Make sure we have a shared github repo to work on, that we can both push and pull to~~
2. Load in data, visualize data and uncertainty. For ALL HOOH DATA:
   1. Plot unlogged standard deviation vs. unlogged mean and
   2. Plot logged standard deviation vs logged mean

In a single graph

* Tidy up graphs, make it so that the ylim/xlim is the same for logged and unlogged mean vs. standard deviation
  + Calculating ratios right now but ‘stretch’ of smaller one isn’t working
* Do histograms of pearson r correlation for logged vs. unlogged standard deviation
  + Working on some abiotic and one set of *Prochlorococcus* data
* Somehow mark in fig (e.g. with horizontal bar) the assumption we make about the standard deviation of replicates (across the board)

1. ~~Define the model~~
2. ~~Define priors~~
   1. ~~Init file added with strain specific values (strain and org column in init file)~~
3. Find ‘initial’ parameter guesses – deltaH is negative\_\_\_\_\_\_\_?
4. ~~Fit with ODElib and look at posterior distributions, comparing to priors~~

Hackathon sept 5th goals

Katie TODO

Ordering and formatting - priority

1. Structure and comment all code that is being used
   1. Ongoing with *Prochlorococcus* and media src
2. ~~Remove all code that is not being used into a ‘dump’ folder or similar~~
3. ~~Decide which figs and formats will be either in paper or supplement. Format these figs and finalize, and delete ALL OTHER figs~~
4. For main paper or supplement figs, label all axes, properly format in general

~~Items 1,3,4 to David by Friday 15~~~~th~~ ~~(in the form of an updated github)~~

1. Add in plots of:
   1. Random walk trace plots from different initial conditions
      1. Is it possible to do within one file run? Need multiple init files?
   2. Scatter plots of random walks from different initial conditions, with x and y axes being random walks of the same parameter from different initial conditions. Could do regressions (OLS type II, ask Eric Carr) increasing burnin from a very low value to close to what we currently use (half the iterations)
   3. Sensitivity of modeled dynamics to step size (no need to use MCMC for this)
      1. Have on hepes 3.35? trial that also looks at biotic H intro?
      2. Or with mu and mu, alpha dynamic plot?

Aim to have done by Thursday Sept 28th

1. Finalize these in the github (comment, organize, structure code)

Stats stuff (least priority)

1. Visualize residuals

Rest of paper

1. HEPES dynamics – graphing currently
2. Biotic HOOH spike assays – 2 data sets 0, H+ assays? Run at same time?