

Work Log for December

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1 Goals for the Month

As of December 1st.

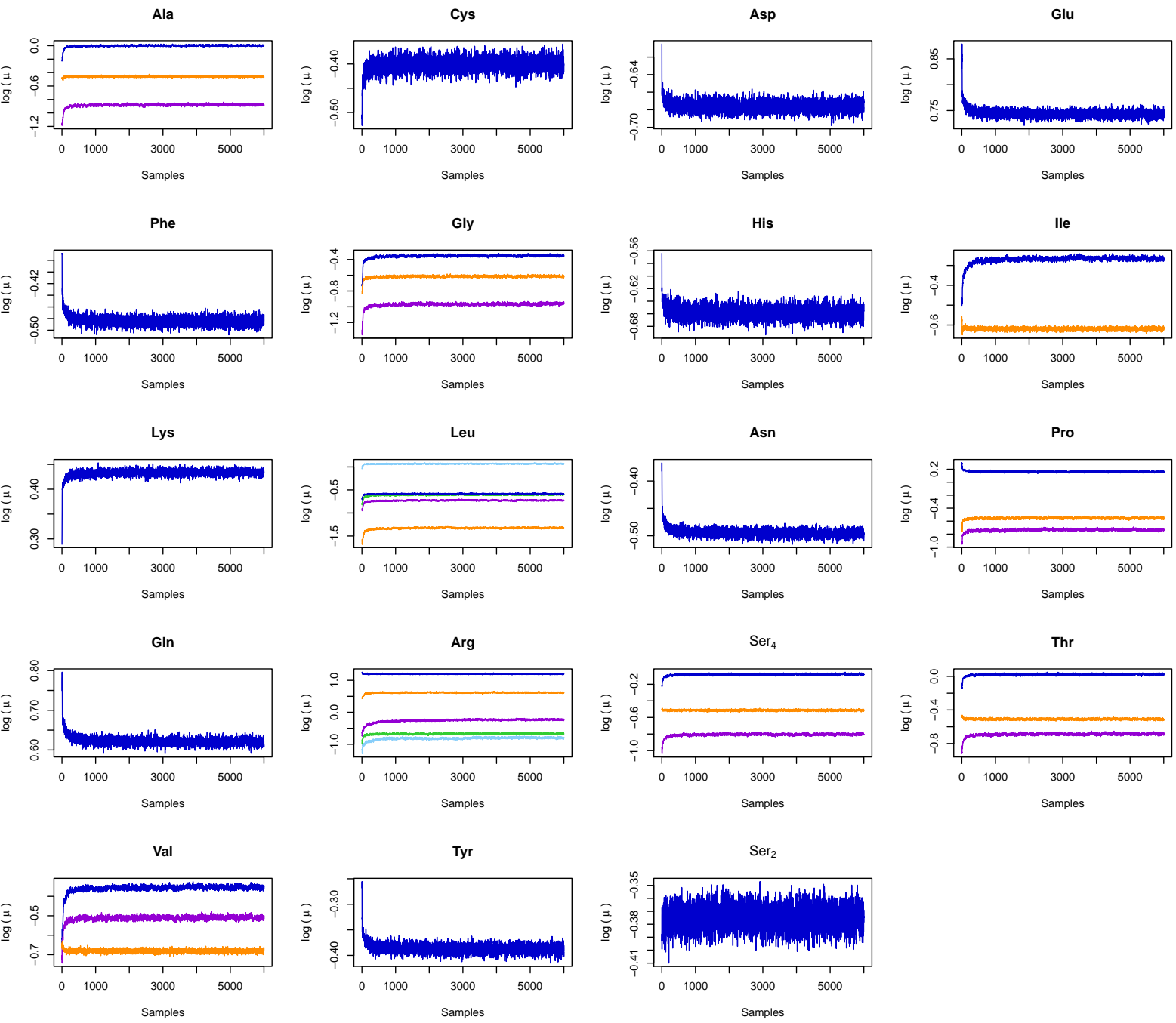
1. Verify logMu Flip by larger runs
2. Investigate Problematic Codons
3. Is it worth it to adjust Delta a₁₂?
4. Fix Names
5. Move to Newton?

2 Progress/Notes

2.1 Verify logMu Flip by larger runs

Verified!

Doing a run of 6000 steps is definitely long enough, especially if you look at the log likelihood trace (not included for brevity). The logMu looks a bit more convincing, and also, it improves the behavior of the hyperparameters like σ_ϵ and σ_ϕ . For the first 300 or so samples, the model has to fit to the negative $\log(\mu)$ value. To its credit, the model does so, but that's not good.



AA parameter trace 11-24
Mon Dec 1 13:14:01 2014

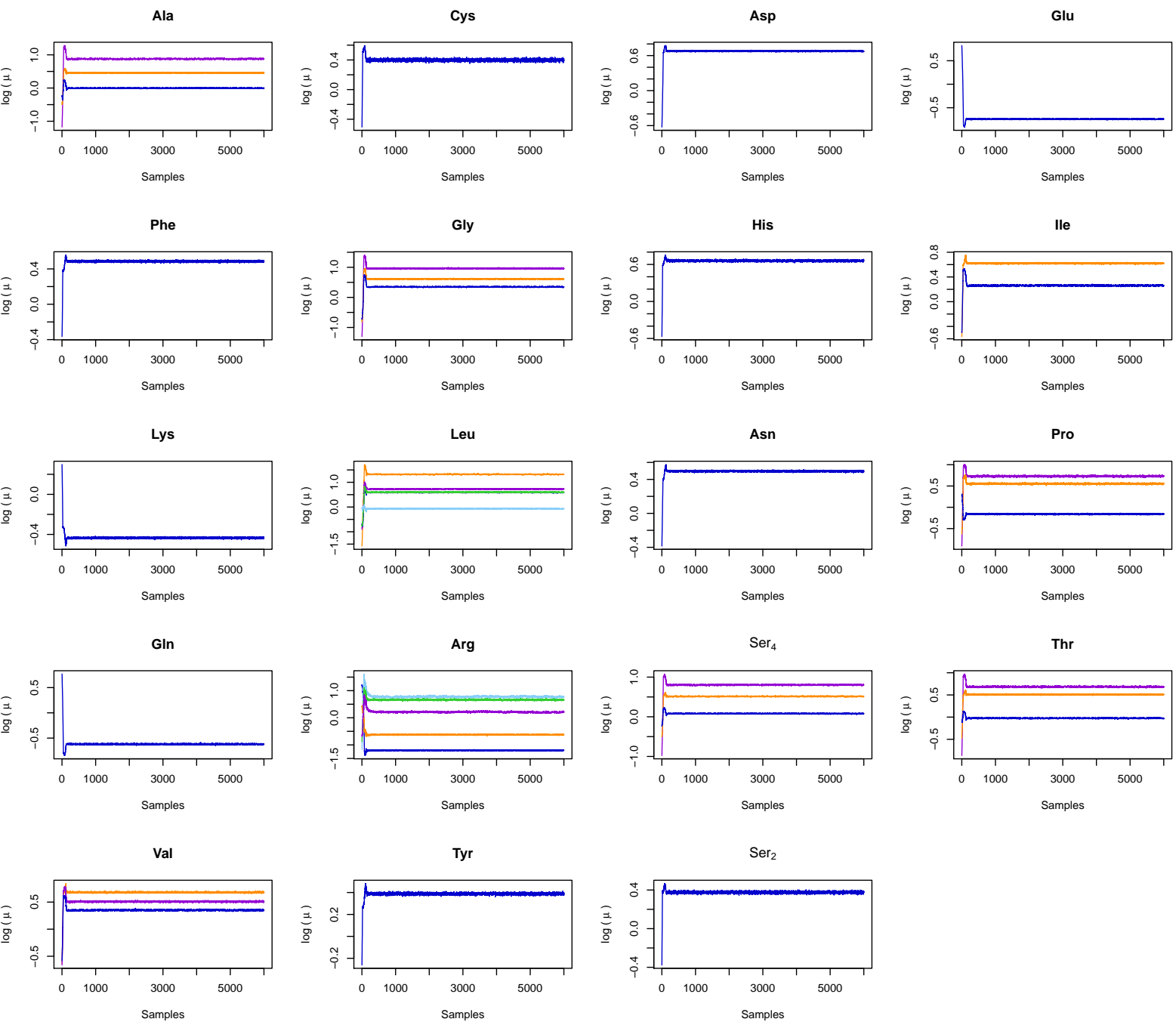
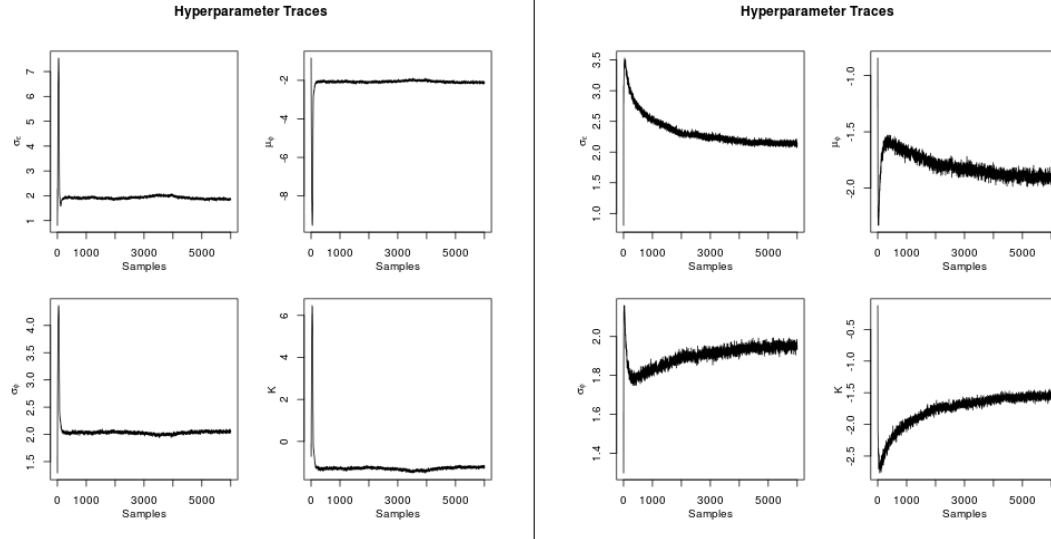


Figure 1: The left figure is a run before the logMu flip. The right is after. You can see that before fixing the logMu flip, the hyperparameters see a huge spike early on, which quickly subsides, while on the right, you simply see them increase at the beginning as the model begins to fit, then fall off slowly as the model converges.



2.2 Investigate Problematic Codons

One thing we were interested in looking at was comparing the problematic ω values to their problematic $\log\mu$ values. Here's a mapping!

Green Square: Leucine CTT

Yellow Diamond: Proline CCG

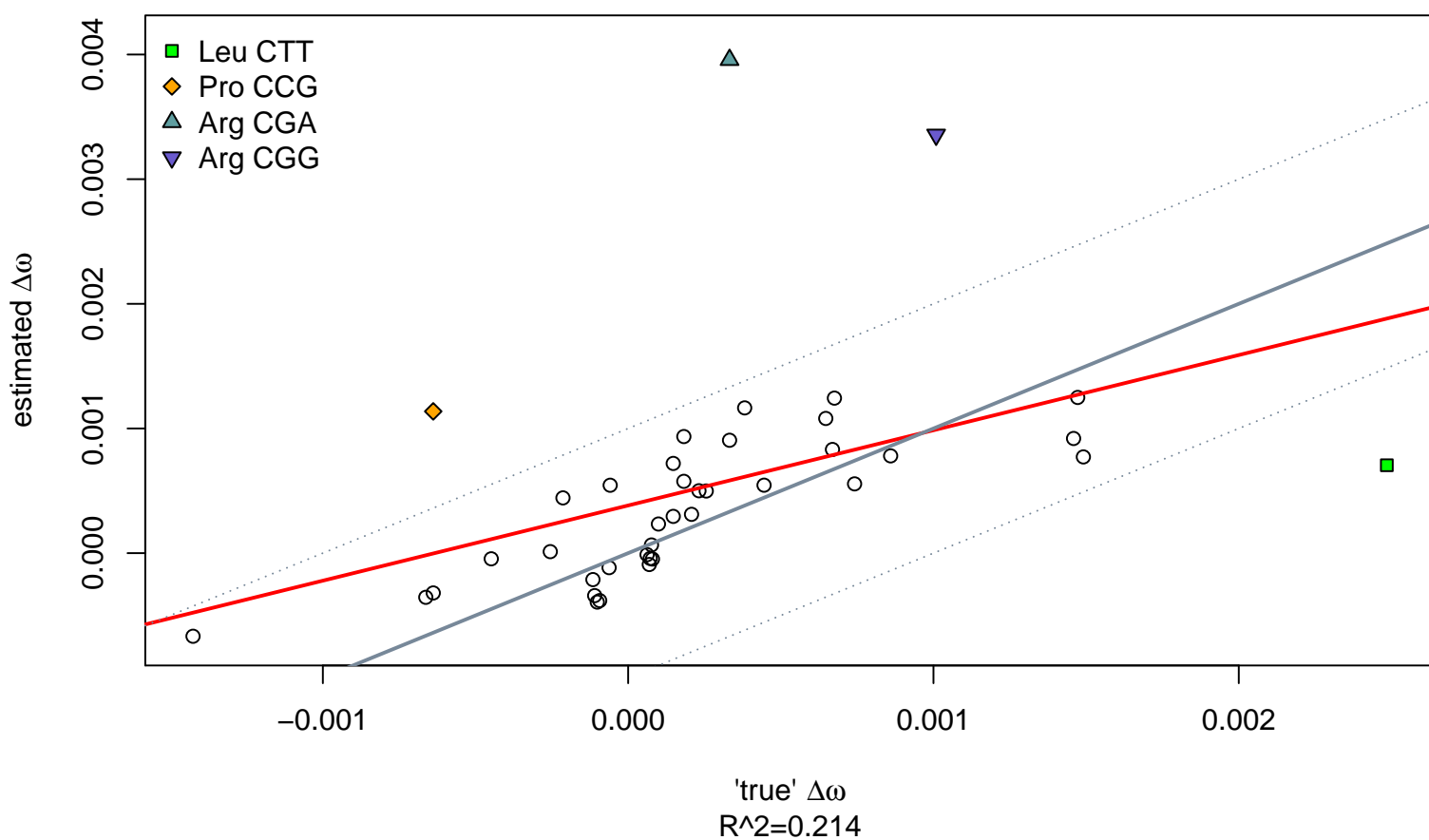
Blue Up Arrow: Arginine CGA

Purple Down Arrow: Arginine CCG

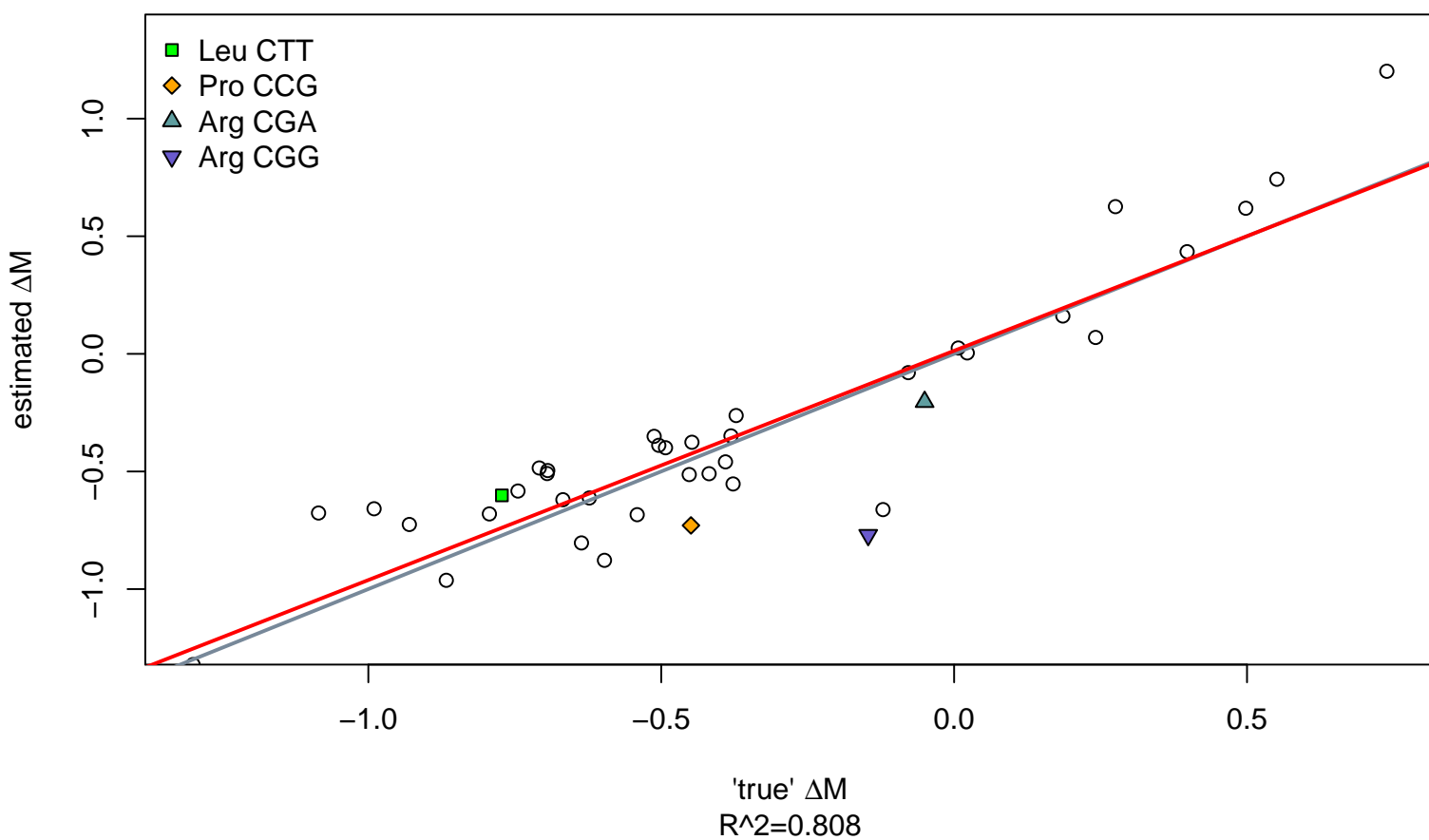
As we anticipated, higher nonsense error rates lead to lower mutation rates, and lower nonsense error rates lead to higher mutation rates. The magnitude is a bit off, the lowest mutation does not cause the highest nonsense errors.

This was also reproduced when using different sections of the Yeast Genome. Here are 3 distinct sections of preston's simulated yeast (they share no genes in common) that produce similar results.

'true' $\Delta\omega$ vs Estimated $\Delta\omega$

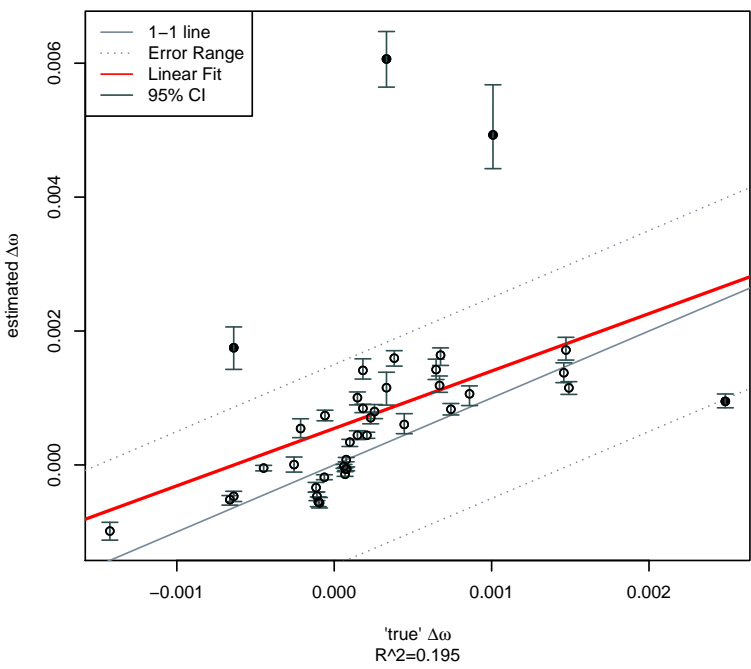


'true' ΔM vs Estimated ΔM

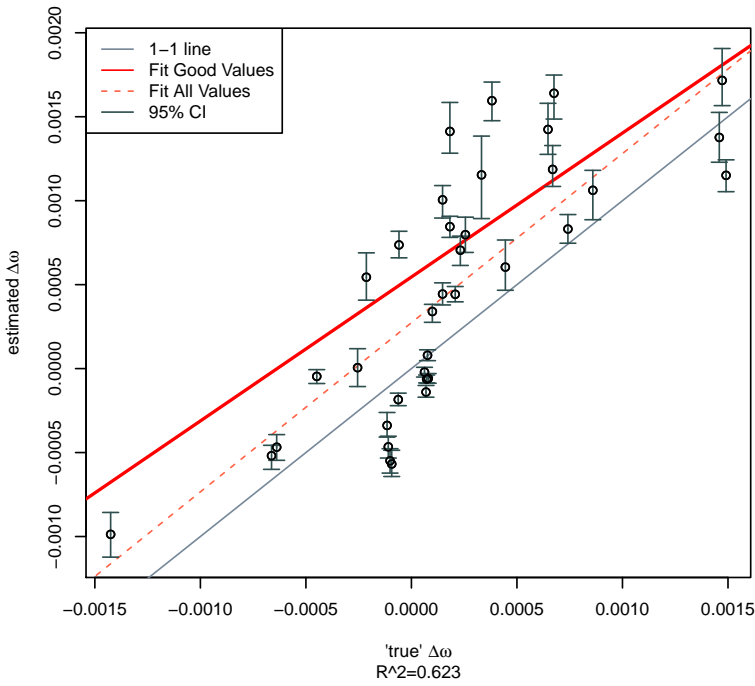


Section 1

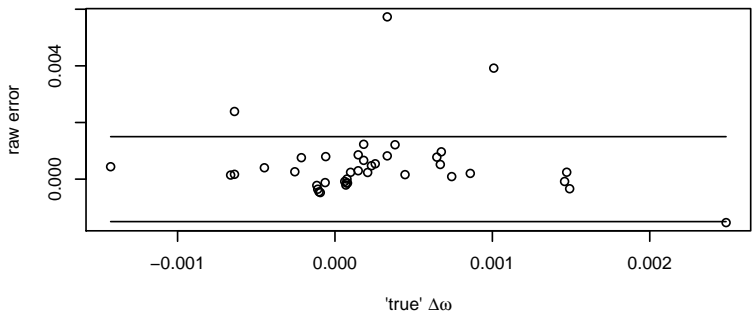
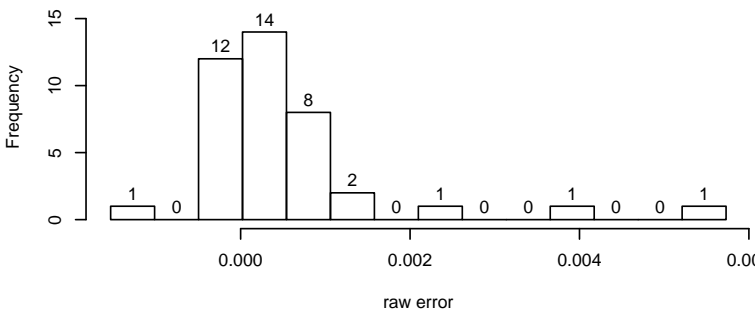
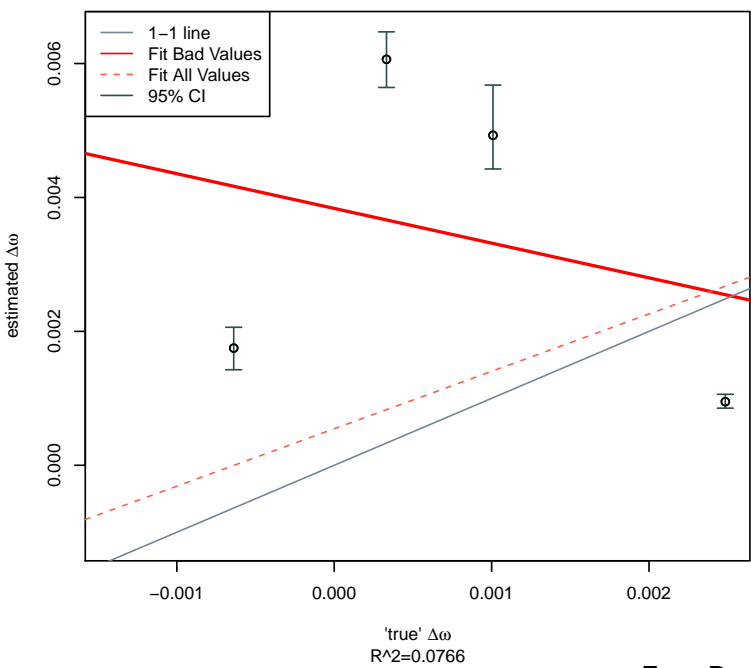
raw error 'true' $\Delta\omega$ vs estimated $\Delta\omega$



raw error $\Delta\omega$ without problem values



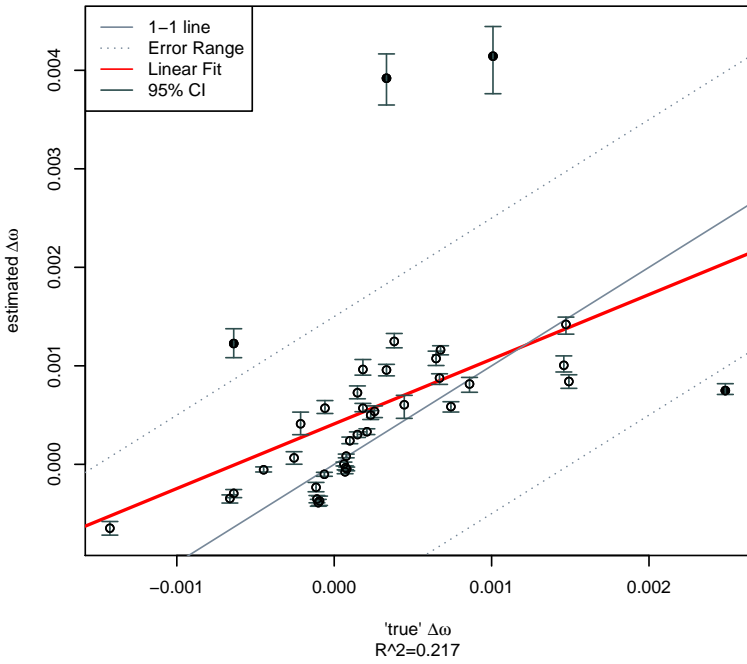
raw error $\Delta\omega$ problem values



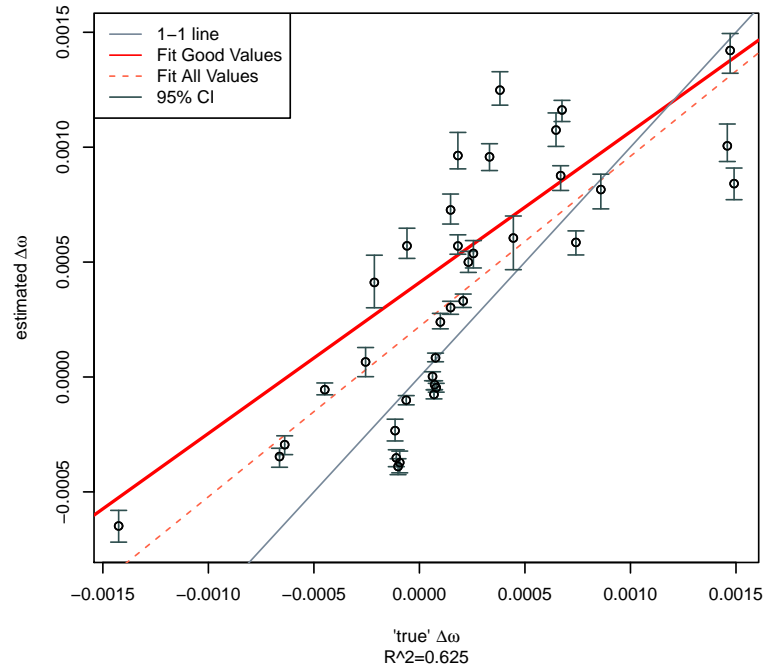
Error Range is +/- 0.0015

Section 3

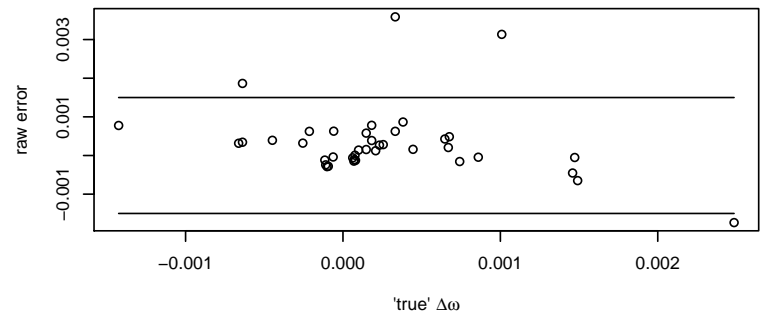
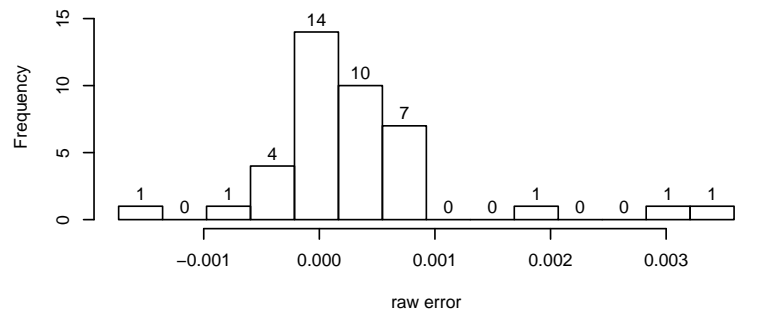
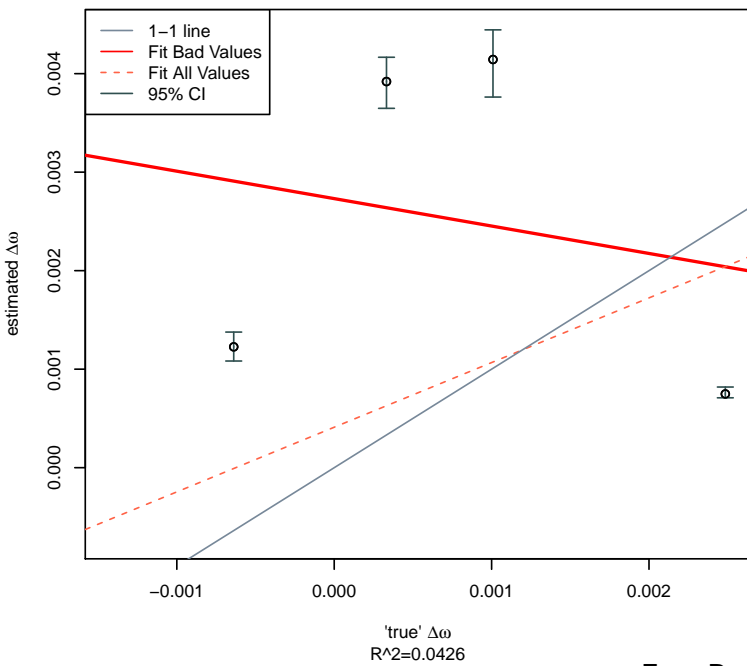
raw error 'true' $\Delta\omega$ vs estimated $\Delta\omega$



raw error $\Delta\omega$ without problem values



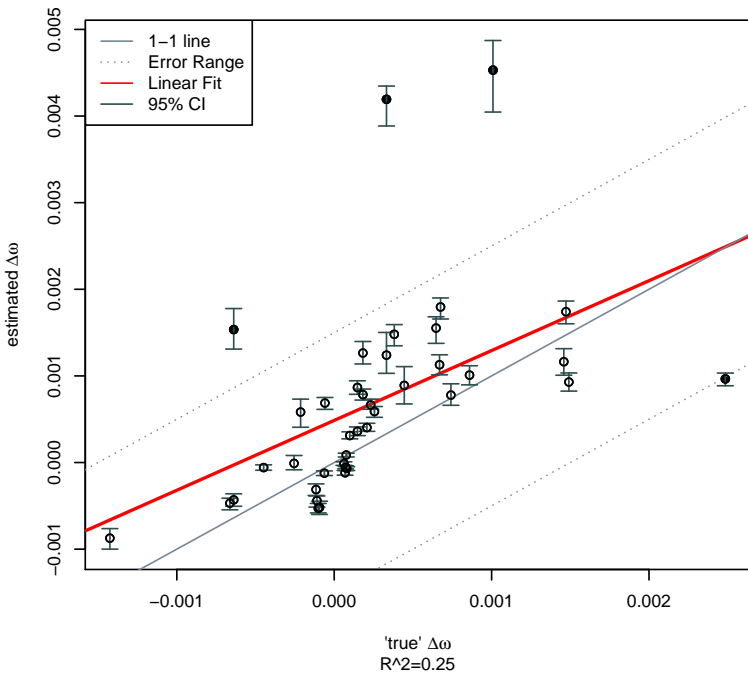
raw error $\Delta\omega$ problem values



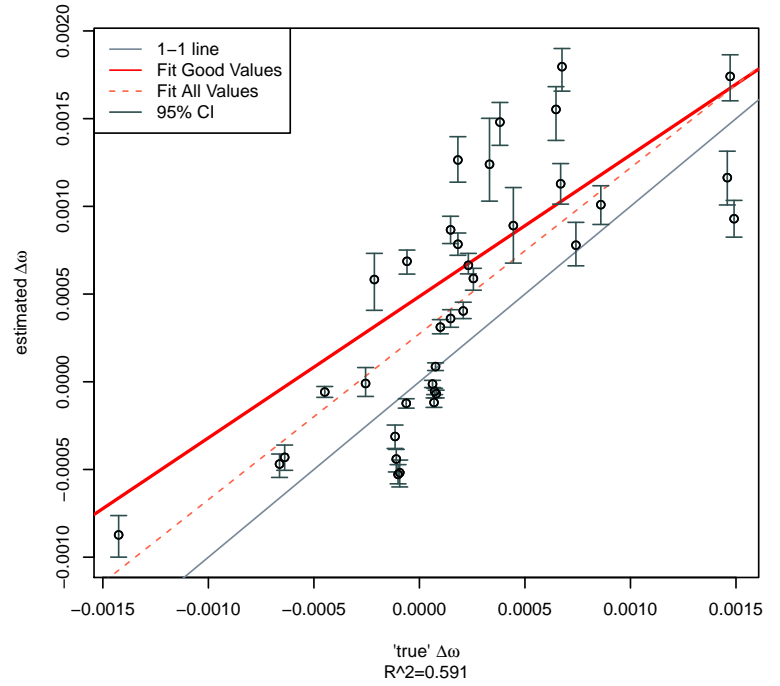
Error Range is ± 0.0015

Section 4

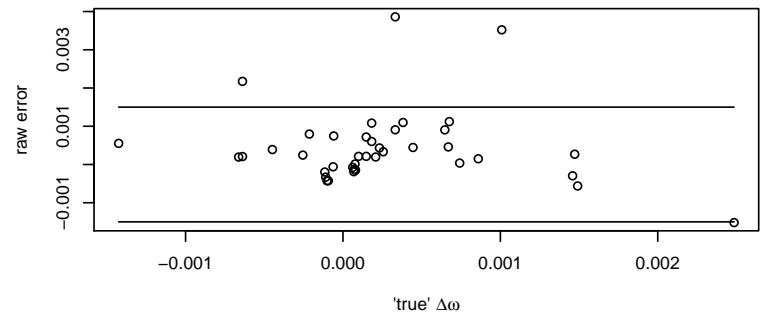
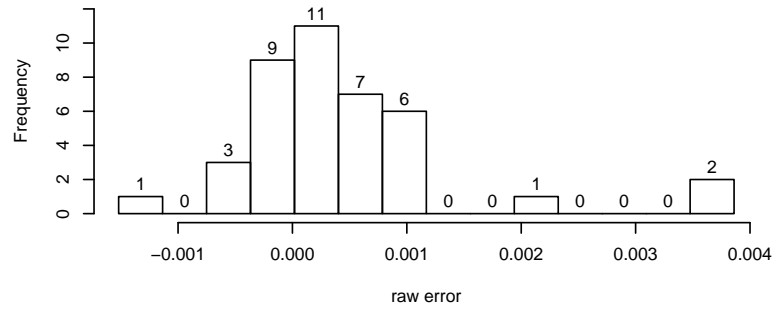
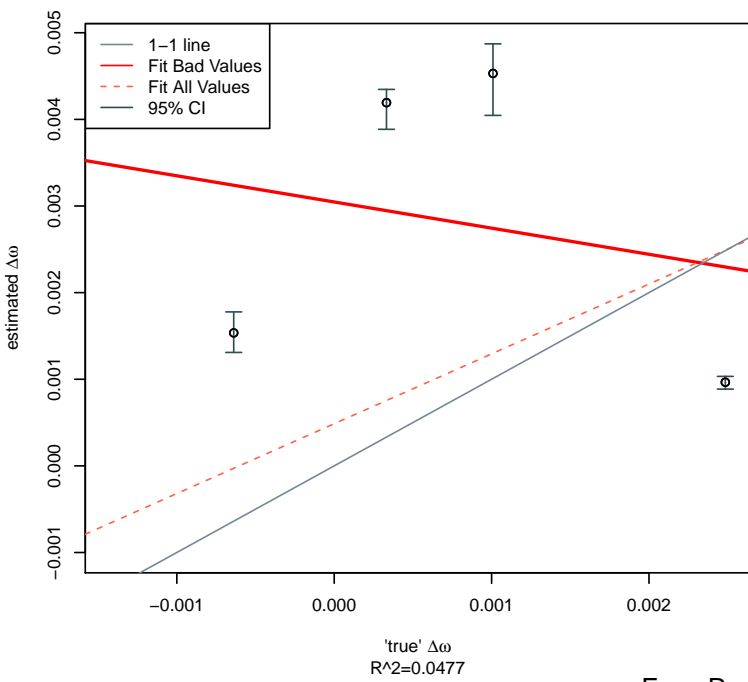
raw error 'true' $\Delta\omega$ vs estimated $\Delta\omega$



raw error $\Delta\omega$ without problem values



raw error $\Delta\omega$ problem values



Error Range is ± 0.0015

2.3 Generate a new Genome

DONE.

By modifying preston's old code, I was able to create two new simulated genomes that used the same inputs as Preston's yeast, but are new and different.

2.4 Is it worth it to adjust Delta a₁₂?

2.5 Fix Names

2.6 Move to Newton?

3 Goals for next Month

1. Future Goal