

FITTING DYNAMIC ENERGY BUDGET MODELS: NOTES

I have fit all of Adriana's data and determined the best fitting parameter set for each animal of each genotype. For each animal of each genotype, I have also recorded the observed age at death, the observed mean daily egg rate, and Adriana's fitted von Bertalanffy L_{inf} value. Additionally, I have used the best fit parameter values to compute growth and reproduction trajectories, and then calculated a predicted mean daily egg rate and L_{max} (maximum predicted length, distinct from von Bertalanffy L_{inf}). I also used NLS to fit von Bertalanffy growth curves to each trajectory, as Adriana did, and recorded the best fit k and L_{inf} parameters. I then went back and refit all the individual trajectories, fitting only L_{inf} , with k held at the mean k for all of the previous fittings. I then calculated $\kappa_1 = L_{inf}\bar{k}$ so I could compare it against Adriana's κ_1 , where she had estimated $\bar{k} = 0.161$.

The first thing I want to look at is the correlation between Adriana's κ_1 and the predicted κ_1 , and between the observed and predicted mean daily egg rates. I also show the correlation between life history characteristics (growth rate κ_1 , mean daily egg rate, and age at death) as computed by Adriana, and using the predicted trajectories. Adriana's life history characteristics are shown as red squares in each panel, and the predicted life history characteristics are shown as black circles.

The next figure shows the partial correlation coefficients between each life history characteristic, both observed and predicted using the best fit parameter sets. The partial correlation is the correlation between the residuals of two variables, after regressing against the third, e.g., regress growth rate and egg rate against age at death and then compute the correlation between the residuals.

I also want to see if the empirically-observed high fliers have parameter values that cluster together. To show this, I am going to plot the distributions of the estimated parameters, and I will color those parameter estimates that came from individuals with mean daily egg rates in the top 25% red (Figs. 3-6). I also show these distributions with individuals with L_{inf} values in the top 25% colored red (Figs. 7-10).

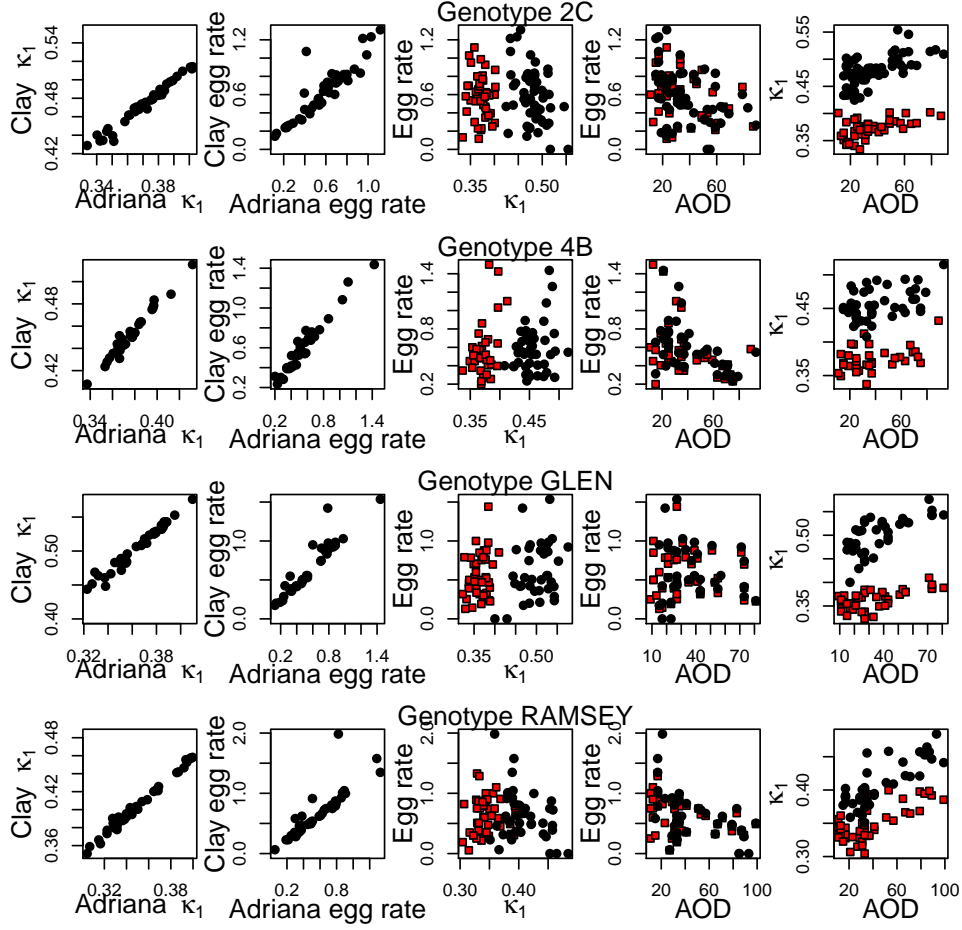


FIGURE 1. Comparison of empirically-derived κ_1 growth rate measure and mean daily egg rate and the growth and egg rates calculated using the growth and reproduction trajectories from the best-fit parameter values.

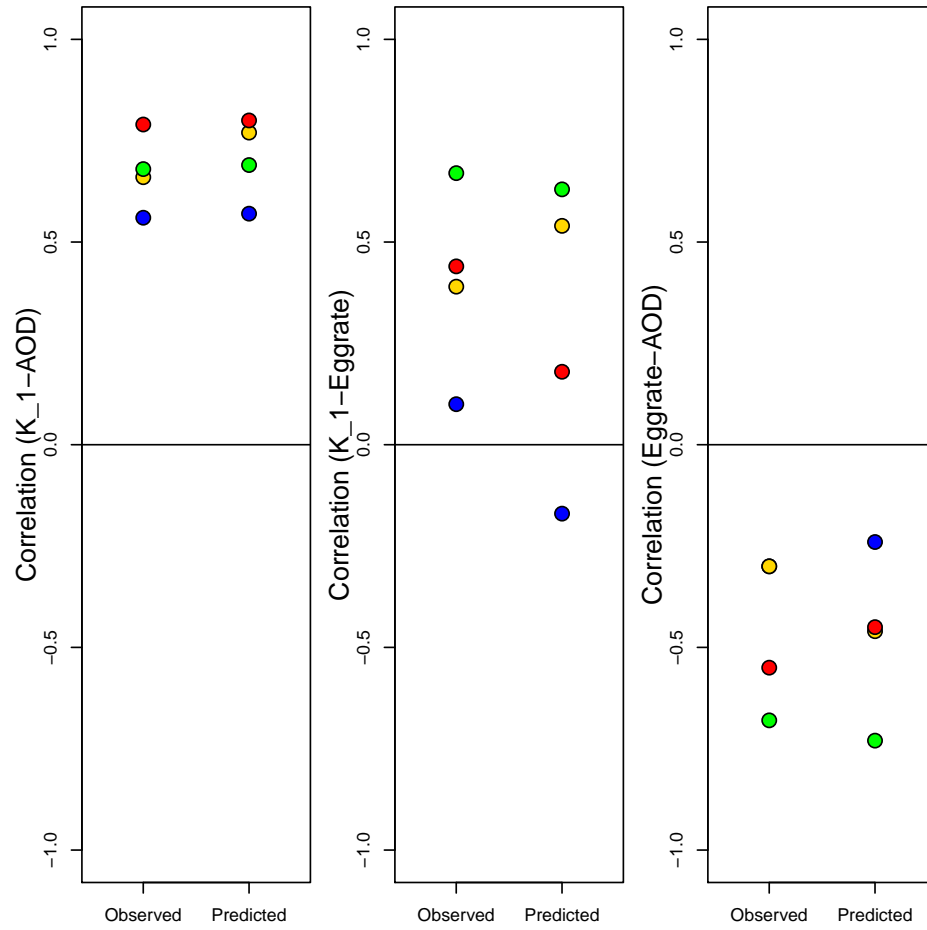


FIGURE 2. Partial correlation coefficients between life history characteristics observed in the data and predicted using the trajectories generated by the best fit parameter values.

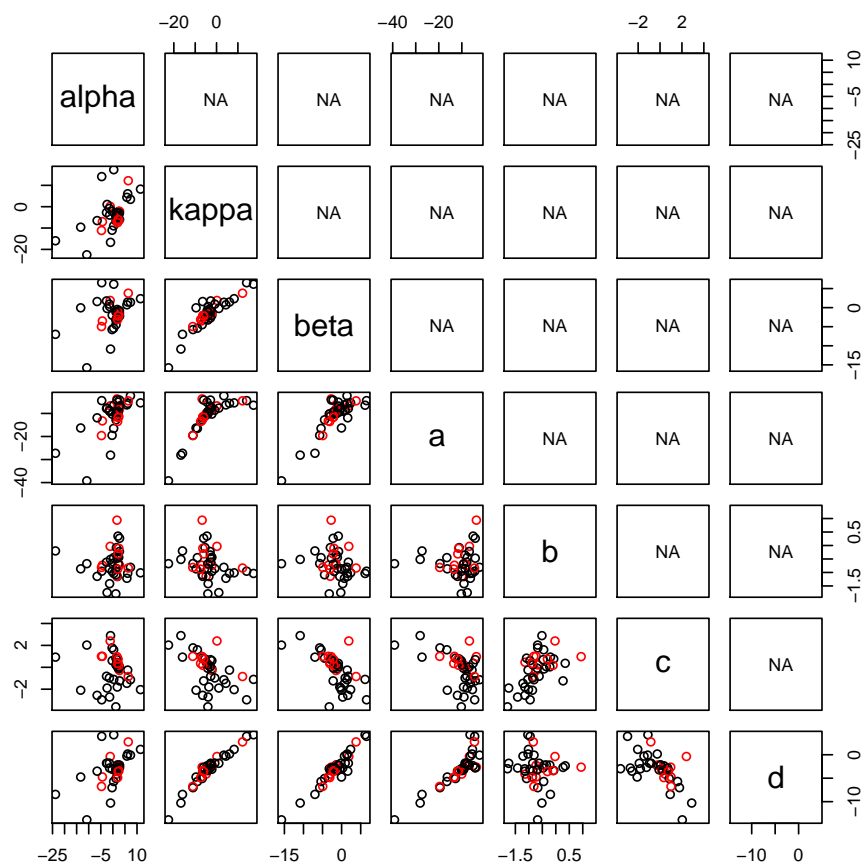


FIGURE 3. For genotype 2C, the correlations amongst the best fit parameter values. The top 25% of reproducers are shown in red.

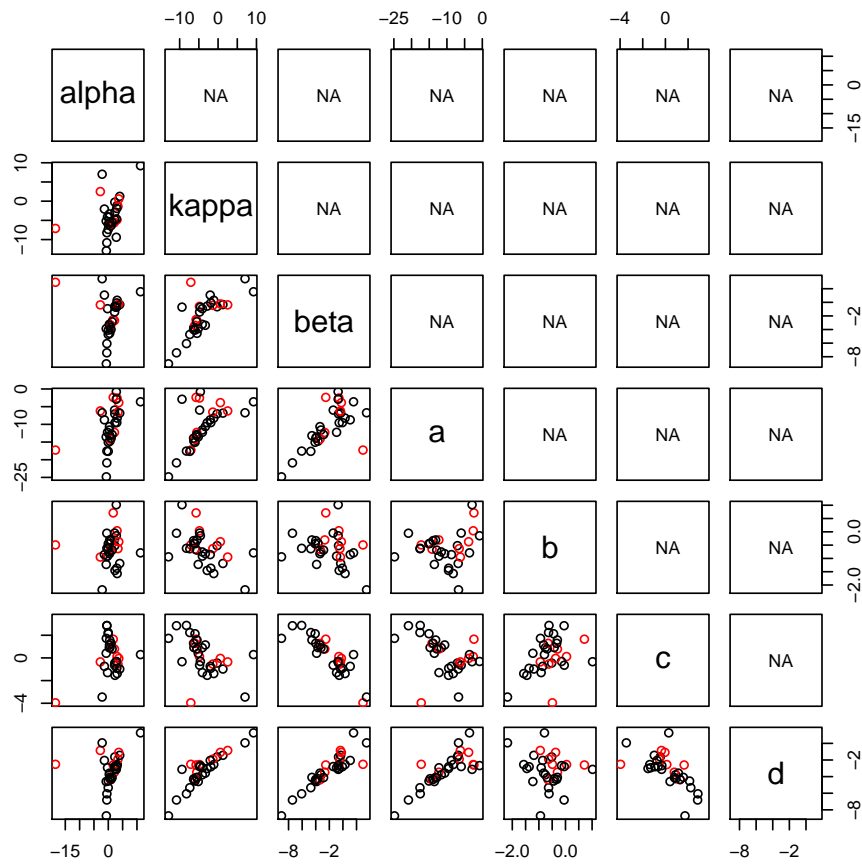


FIGURE 4. For genotype 4B, the correlations amongst the best fit parameter values. The top 25% of reproducers are shown in red.

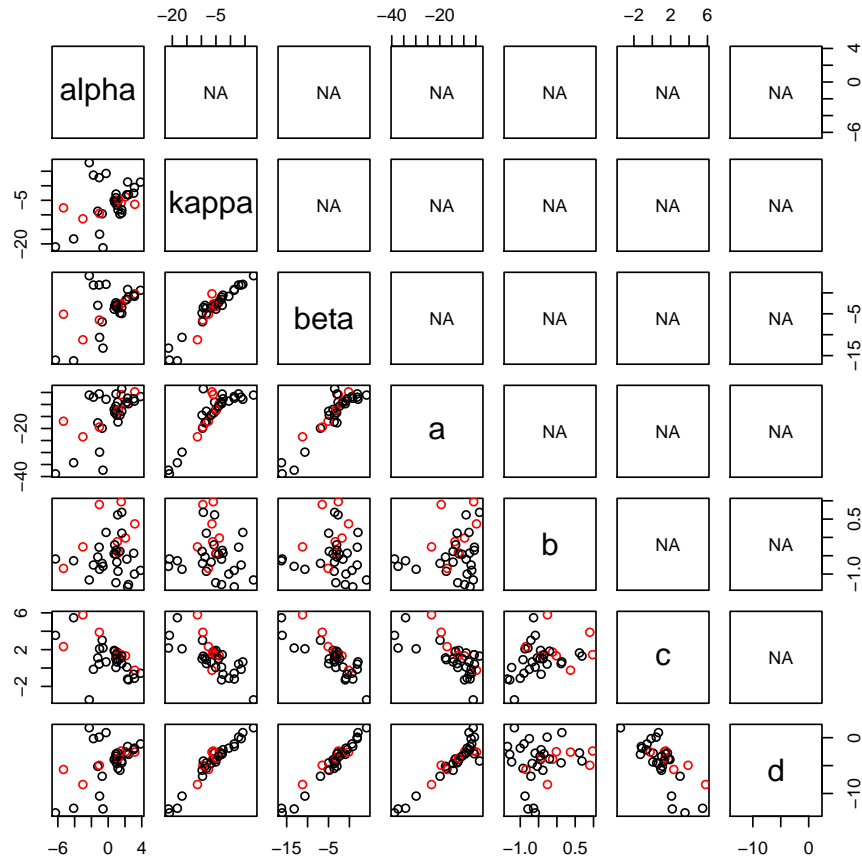


FIGURE 5. For genotype GLEN, the correlations amongst the best fit parameter values. The top 25% of reproducers are shown in red.

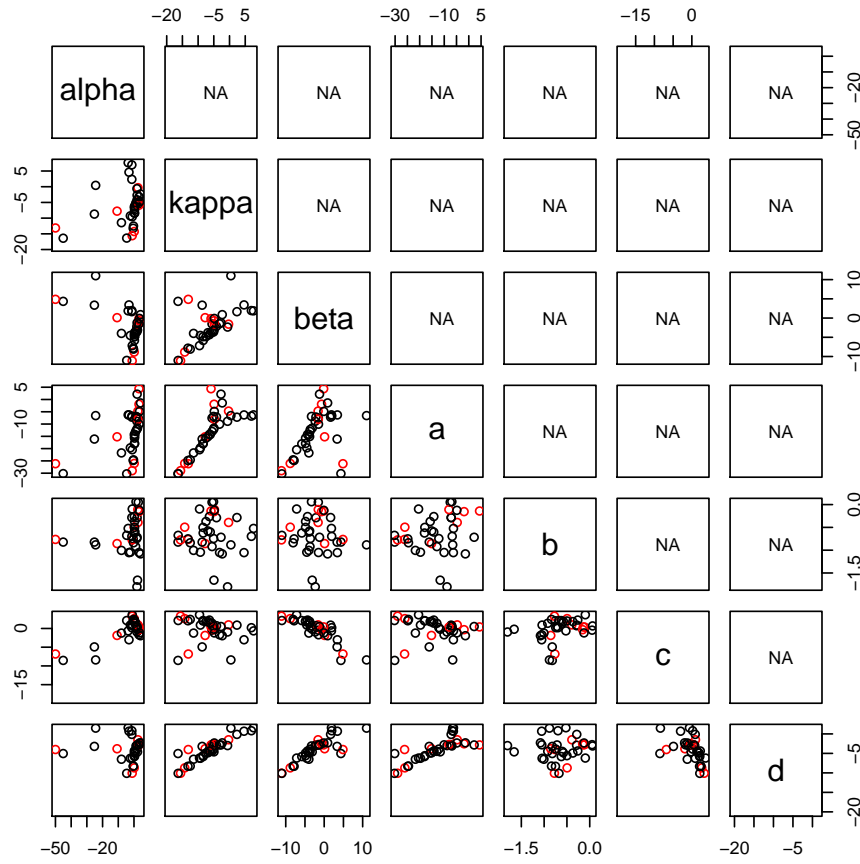


FIGURE 6. For genotype RAMSEY, the correlations amongst the best fit parameter values. The top 25% of reproducers are shown in red.

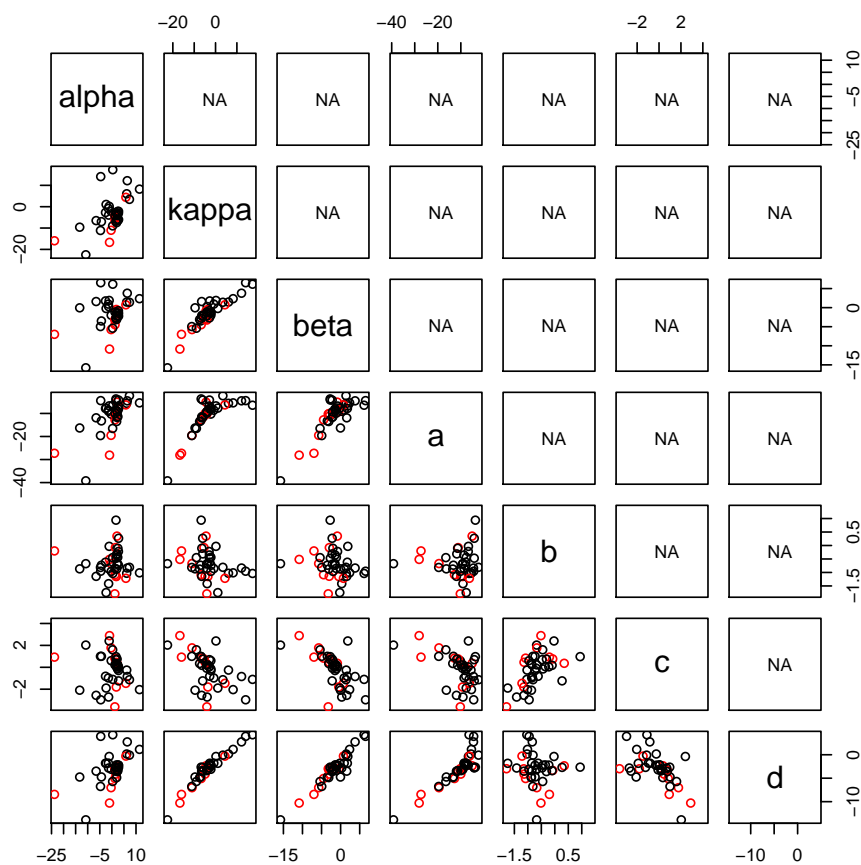


FIGURE 7. For genotype 2C, the correlations amongst the best fit parameter values. The top 25% of growers are shown in red.

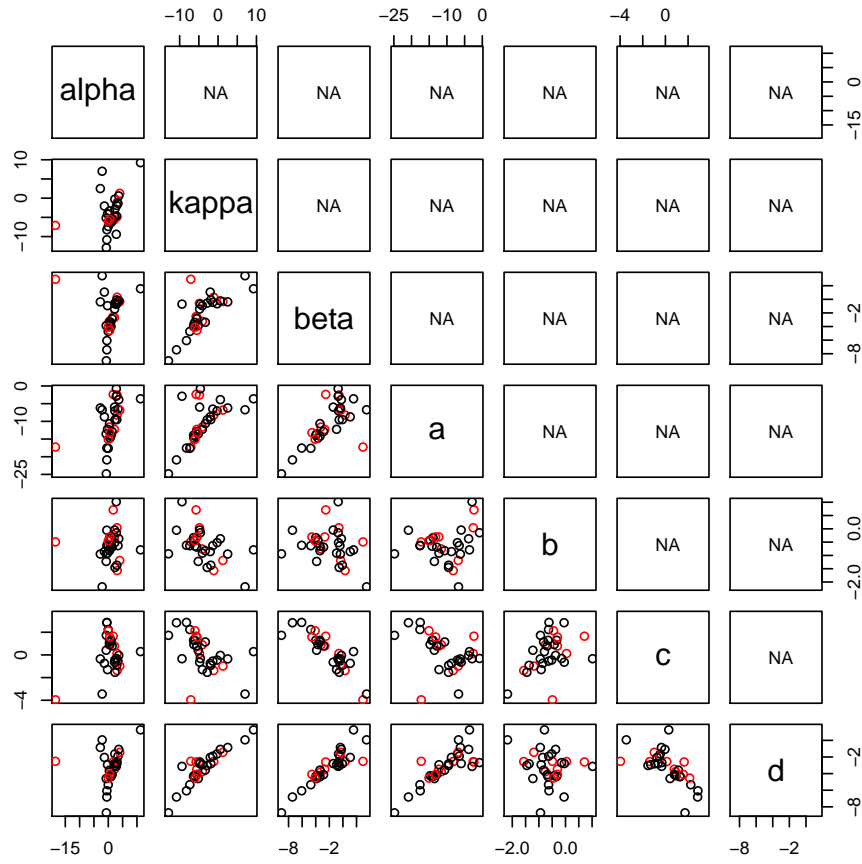


FIGURE 8. For genotype 4B, the correlations amongst the best fit parameter values. The top 25% of growers are shown in red.

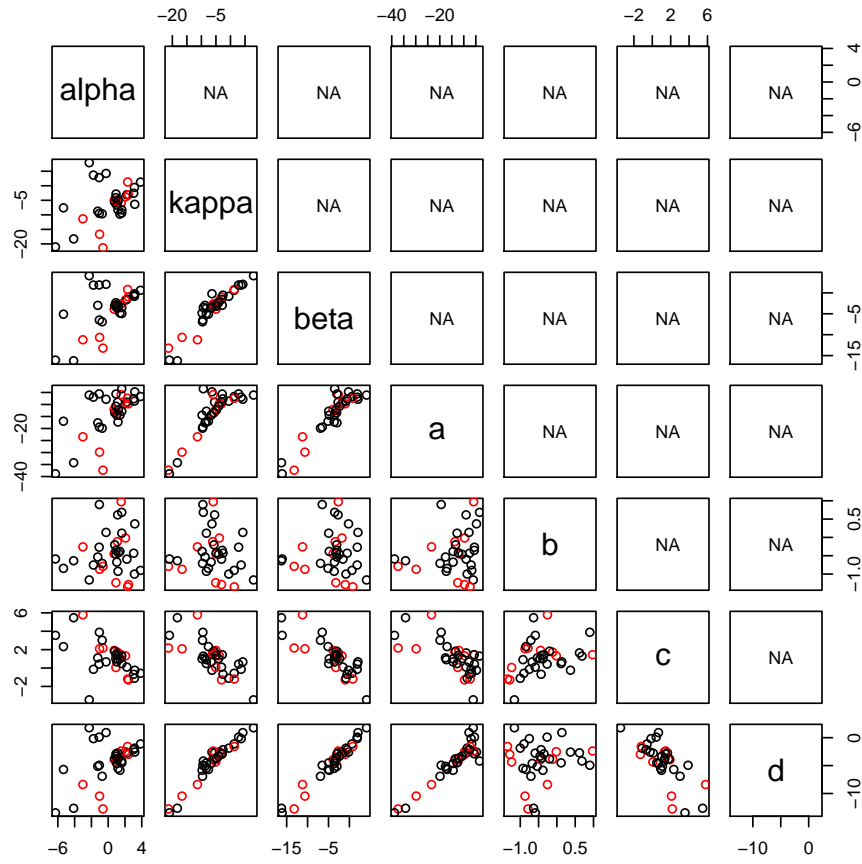


FIGURE 9. For genotype GLEN, the correlations amongst the best fit parameter values. The top 25% of growers are shown in red.

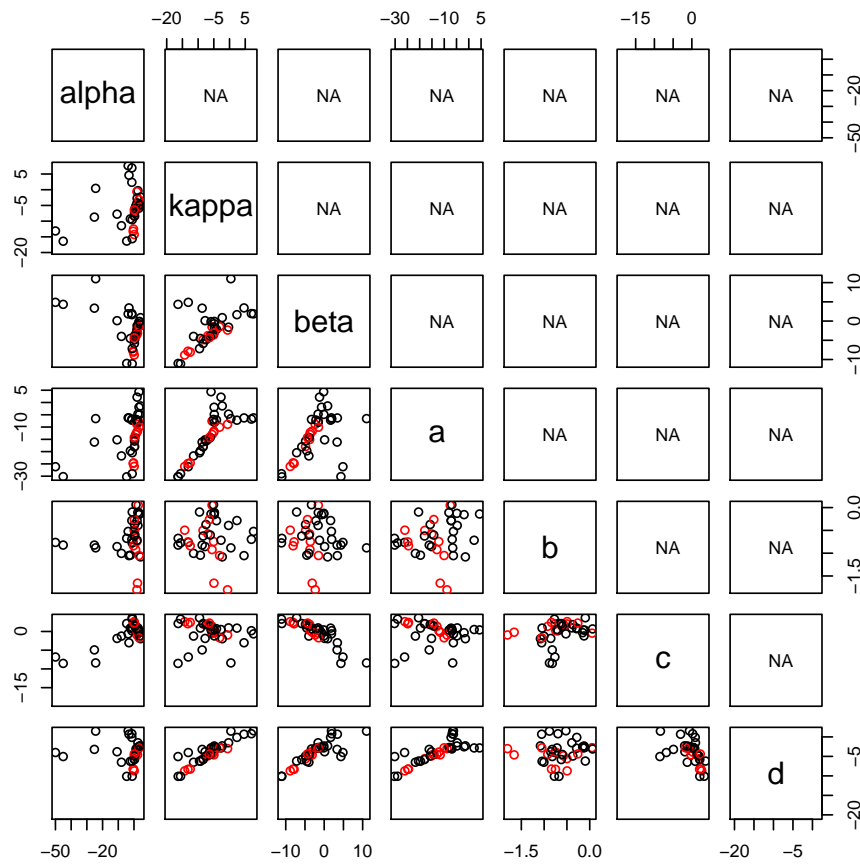


FIGURE 10. For genotype RAMSEY, the correlations amongst the best fit parameter values. The top 25% of growers are shown in red.