FITTING DYNAMIC ENERGY BUDGET MODELS: PARAMETER COVARIATION

I have done some initial simulation recovery experiments, and I want to explore the results of those efforts here. Note that the correlations among parameters for the four different parameter sets that have been fitted can be found in "Correlation_among_parameters.pdf". In this file, I am exploring the first parameter set.

I begin by looking at all of the estimated values for the fitted parameters, plotted as pairwise scatterplots to look for obvious correlations between the estimates. I focus only on those parameter sets where the log-likelihood was within 20 units of the minimum log-likelihood (note that subplex had not converged for any of these parameter sets - yikes). Points colored red are within 5 log-likelihood units of the minimum. I will focus my attention initially on the energy allocation parameters, and show the energy ingestion parameters and initial condition parameters next. Note that ν is on the logarithmic scale.

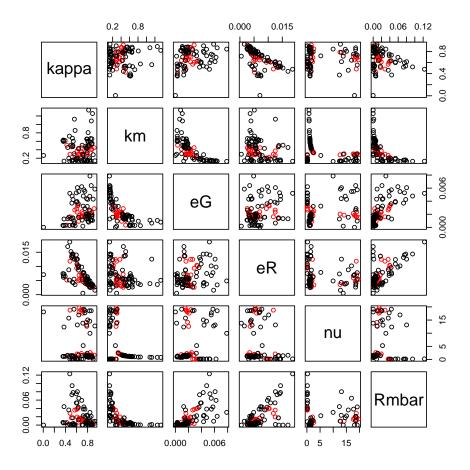
These show considerable correlation among the parameters. For example, the estimate of the energy requirement for maturation \bar{R}_m is positively correlated with the estimate of the cost of reproduction ϵ_R , and the cost of growth ϵ_G is negatively correlated with the somatic maintenance rate k_m . This correlation is unsurprising, given that the DEB model, like all biological models, is overparameterized. Morever, the energy budget creates constraints that may allow parameters to trade-off against one another, producing similar growth trajectories. It may be that, although individual parameters cannot be well-estimated, certain parameter combinations can be, and the model can be reparameterized in terms of these estimable *compound* parameters.

The ingestion parameters are, on the whole, badly identified. This can be seen from the fact that most of the estimates of assimilation efficiency ϵ_A are clustered near unity, when the truth was 0.7, and by the fact that maximum surface-area specific assimilation rate p_{am} and half-saturation constant F_h have to be plotted on the log scale.

Many of the estimates of p_{am} and F_h are clustered appear to cluster; unfortunately, this cluster is not actually at the true parameter values, as can be seen in a scatterplot of just p_{am} and F_h , with the truth plotted in red.

Given that the ingestion parameters seem to be difficult to estimate, a problem that is unsurprising given that we are only considering data at a single food level, I will focus my attention on the energy allocation parameters only.

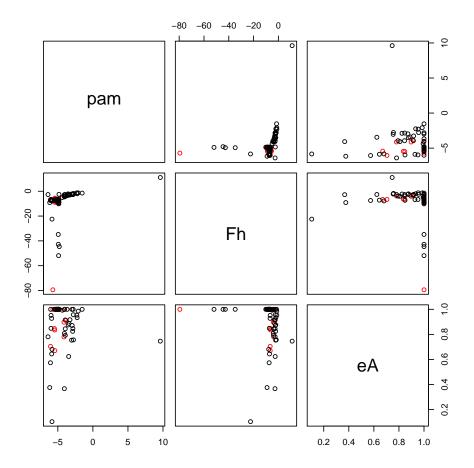
Let's first look at the estimates for each parameter by creating a histogram of the ratio of the estimates to the true value - a histogram with peak at, or near, unity inidicates that the parameter was well-estimated. The red line indicates the truth, the blue line indicates the mean parameter estimate, and the green line the median estimate. This will



allow us to focus our attention on only those parameters that might need to be looked as ratios or products with other parameters.

It is clear that some of the parameters are actually not very badly estimated, in that many of the parameter sets seem to be converging to the truth. Interestingly, the means for some of the parameters are very close to the truth - I wonder if this is some incarnation of the Central Limit Theorem that we can leverage? Energy conductance ν is clearly just very difficult to estimate; it has been log-transformed to be possible to visualize. The mean of these, surprisingly, is still actually quite close to the truth. I had expected ν to be difficult to estimate based on Martin et al.'s work - it works a lot like selection strength in phylogenetic comparative hypothesis testing. The stronger the strength of selection, the less influence the phylogenetic history has on current traits; the larger the energy conductance, the less influence reserve dynamics have on growth and reproduction. As ν goes to infinity, the model becomes reserveless.

Looking at the parameter values from all of the datasets, it is clear that the fitting algorithm has a lot of degrees of freedom to adjust parameters relative to one another. For example, one parameter set that had a lower log-likelihood than the cutoff, but which is still illustrative, fit a half-saturation constant value of $F_h = 2e5$, compared to a true



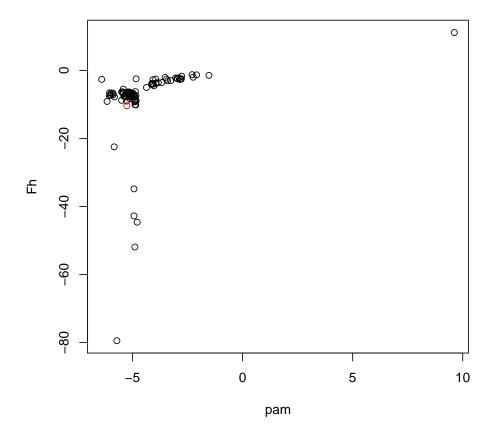
value of 3e-5. It made this work by having $p_{am} = 6.7e4$, compared to a true value of 5.1e-3, and $\nu = 2.4e6$, compared to a true value of 18.1.

Another interesting example actually has an okay log-likelihood (about 10 log-likelihood units worse than the best). The estimate of κ was 0.96, implying almost no energy going to reproduction. The algorithm surmounts this problem by having a very low cost of growth and reproduction and the energy threshold for sexual maturity happened at incredibly low amounts of energy.

All of these really brings the question of whether we can find parameter combinations that are better identified into sharp focus. Even better, are there parameter combinations that appear in the DEB model that are well-estimated? For example, the mobilization rate of reserve and the growth rate in length are

$$p_C = L^3 \left(\frac{\nu}{L} + k_m\right) \frac{E/L^3}{1 + \frac{\kappa}{\epsilon_G} \frac{E}{L^3}} \tag{1}$$

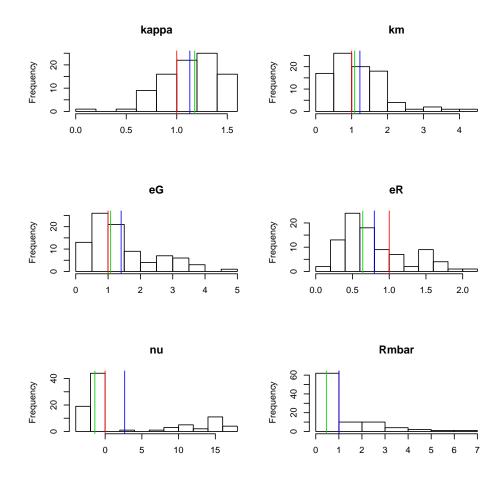
$$\frac{dL}{dt} = \frac{\frac{\kappa}{\epsilon_G} p_C - kmL^3}{3L^2}.$$
 (2)



In both p_C and dL/dt, the parameter combination κ/ϵ_G appears. Is this parameter combination well estimated, even if κ and ϵ_G are not? Again, showing a histogram with the red line indicating the truth, the blue line indicating the mean estimate, and the green line indicating the median estimate, you can see that, indeed, the ratio is well-estimated (the mean is skewed upward by some datasets that estimated very tiny, tiny values of e_G . This is at least suggestive of the fact that the model can profitably be reparameterized in terms of a new parameter $\alpha = \kappa/eG$.

Another parameter combination that appears to be pretty well-estimated is $k_m \epsilon_G$. Interestingly, in the derivation of the standard DEB model, these two parameters together are the total somatic maintenance rate p_M .

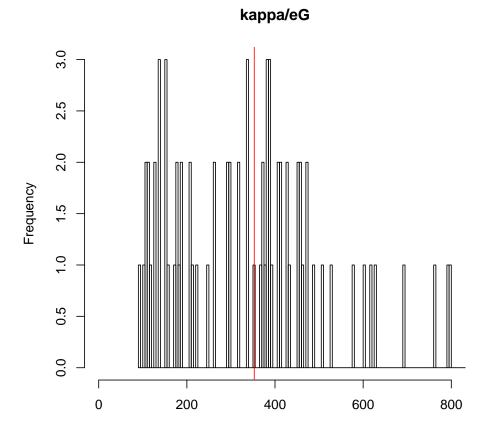
Another possibility is the ratio \bar{R}_m/e_R . Both of these parameters deal with reproduction only. They appear nowhere else in the DEB dynamics. Interestingly, looking back at the pairwise scatterplot, there almost seem to be two different lines of correlation, with the correlation between parameters lower for parameter sets with higher likelihood (red points). This is just a trick of the eye, however, as you can see by overlaying histograms for all of the data, and only the data with low likelihood score.

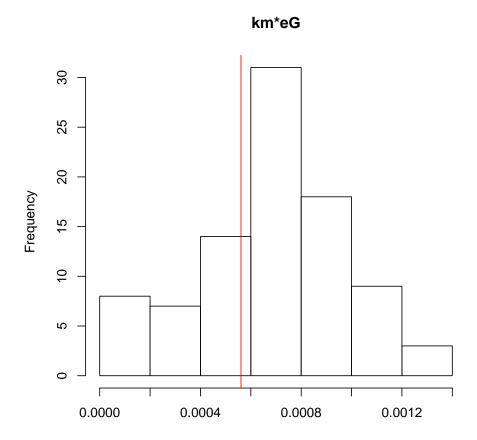


It's hard to tell initially with κ/ϵ_R , because there are a number of parameter sets where κ is north of 0.96, which forces ϵ_R to be less than 10^{-5} (the most extreme is a parameter set where $\kappa = 0.99999$ and $\epsilon_R = 6.5e - 8$). If I exclude these parameter sets, the histogram is much easier to visualize, and it is clear that the estimates come very close to the truth.

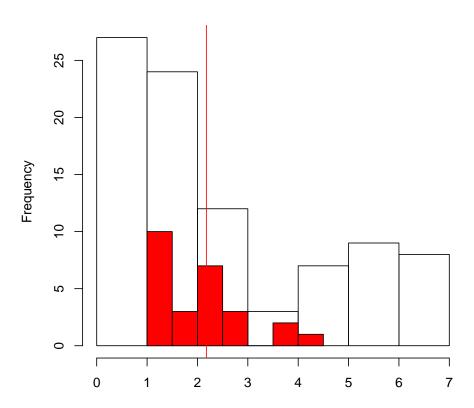
All of this is making me wonder whether it might not be better to combine more than two parameters at the same time. In particular, I wonder if the non-dimensionalized parameters that Bill and I were playing around with might not be well-estimated too.

DEB theory makes use of a number of compound parameters - are any of these well-estimated?

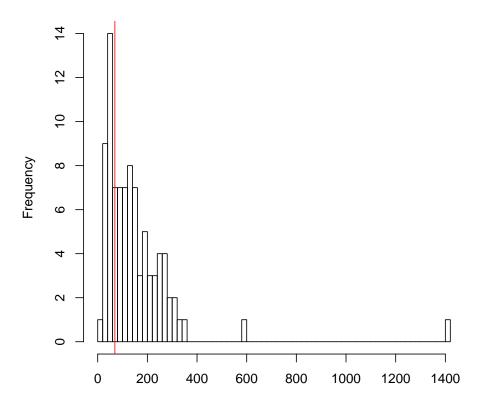




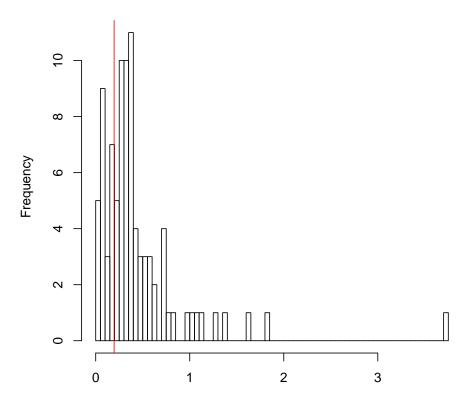




kappa/eR







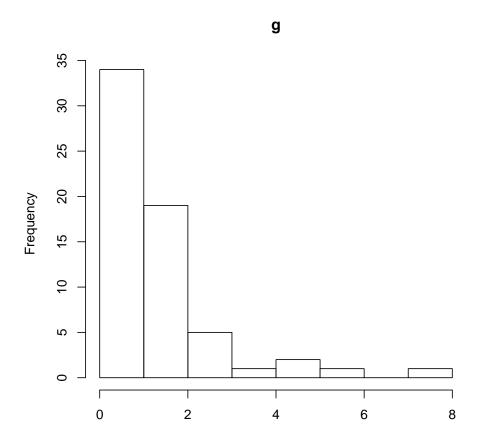


FIGURE 1. Estimates of the DEB compound parameter $g=\frac{\epsilon_G \nu}{\kappa p_{am}},$ the energy investment ratio.

```
> thres <- res[-which(res[,'pam']/res[,'nu'] > 0.01),]
> hist(thres[,'pam']/thres[,'nu'],
+ main='Em', xlab='')
> abline(v=true.pars['pam']/true.pars['nu'],col=2)
```

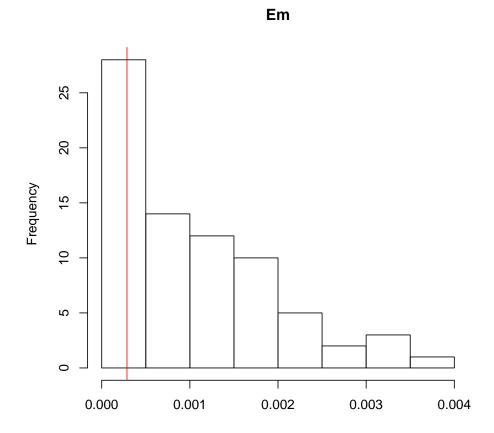


FIGURE 2. Estimates of the DEB compound parameter $E_m = p_{am}/\nu$, the maximum reserve density.

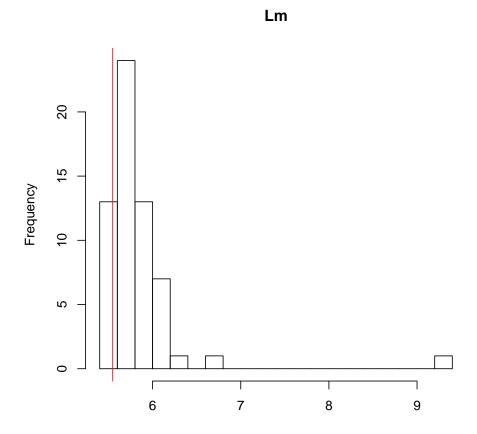


FIGURE 3. Estimates of the DEB compound parameter $L_m = \frac{\kappa p_{am}}{k_m \epsilon_G}$, the maximum length.