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# Appendix S2: Density Calculations

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We calculated the density of our experimental populations as the average length of individuals in a given stage times the number of individuals in that stage, summed across all stages. This is proportional to the population's biomass excluding eggs. Average sizes were calculated for each stage within treatment and each date, pooling individuals and replicates (Wickham 2011). We could not calculate average sizes at the level of replicate within treatment because some stages were not measured on every date in every replicate. Counts of individuals within stages were done on all necessary dates in all replicates of the counting populations, but only on every other necessary date in the sampling populations (Figure B1). To interpolate density estimates to the necessary dates in sampling populations, we took the average of densities from the same population on dates before and after, along with the average of densities of other populations of the same treatment on the same date (Figure B1). This is a combination of linearly interpolating within a population, and extrapolating from counting populations to sampling populations.

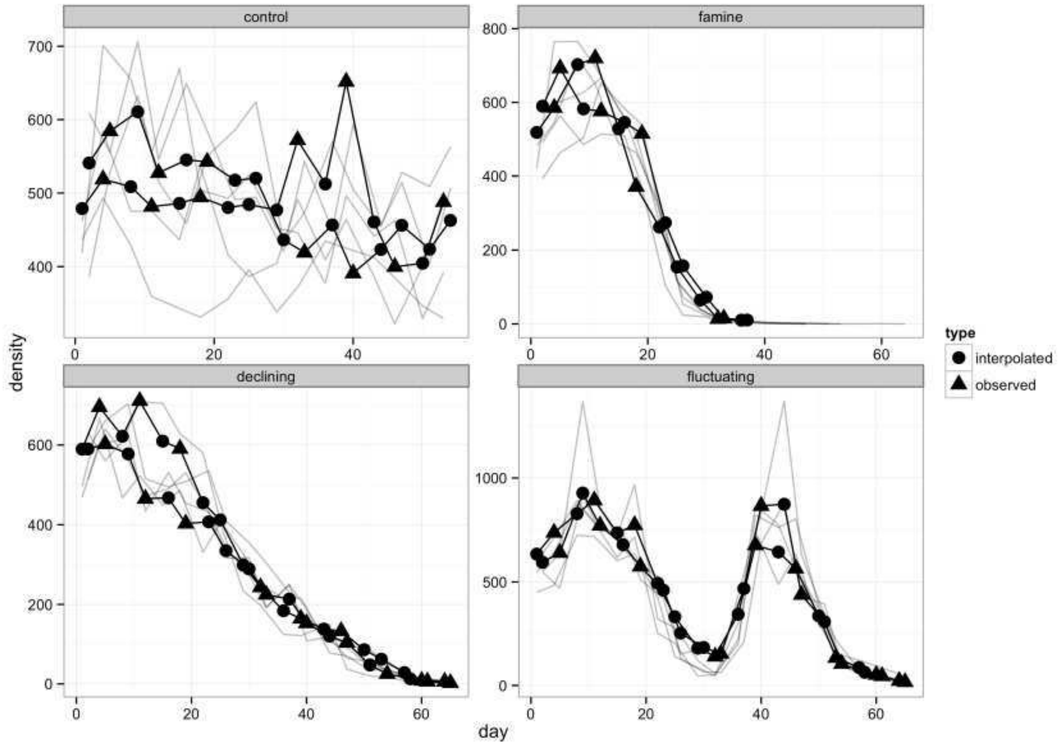

**Figure B1-** Grey lines show observed densities in the counting populations (one line per population). Black lines show densities in the sampling populations, both for observed dates (triangles) and dates for which values were needed but not observed and therefore interpolated (circles).

## Literature Cited

Wickham, H. (2011) The split-apply-combine strategy for data analysis. *Journal of Statistical Software*, **40**, 1–29.