Manually edited output file “length\_weight\_par\_output.csv” and created “length\_weight\_par\_output\_supplement.csv” for supplement.

Editing steps included:

* organizing row order hierarchically by taxon (e.g. so that the row for Myctophidae family comes right before the row for Benthosema genus and Benthosema glaciale species)
* remove rows with “spc” as we would instead use the parameter values listed under that genus for any species that are only identified to genus level. This is an artifact from the WoRMS aphiaID (and parameter values were very similar in any case for “Cyclothone” and “Cyclothone spc” for example). Also removed “Myctophidae gen” row as the parameter values were essentially the same as “Myctophidae”.
* Removed the columns NoGenus and NoSpecies (number of genera and number of species) because these are no longer essential information and they are also not correct because I removed “species” such as “Cyclothone spc” which are not truly species
* Instead of leaving the row for Cyclothone genus with NAs for Family, I added Gonostomatidae in this row (as the parent taxon is known, not truly an NA)
* Changed Nannobrachium spc to Nannobrachium (in the genus column). Deleted Scopelogadus spc (very similar parameter estimates to Scopelogadus genus) and Lampanyctus spc
* Changed all genus names (e.g. Cyclothone) to have sp. at end (e.g. Cyclothone sp.) to match the IDs given for Sarmiento fish measured in lab (a few of these fish have a missing weight, but a more specific ID than just to family level than the smaller Sarmiento fish or Cook fish that had lengths measured from photos using ImageJ, which were IDed only to family level)
* deleted duplicate rows: two rows had the lowest taxon of Nannobrachium sp. and parameter estimates were extremely similar for these duplicate rows anyway