**FISH 9898 REVIEW**

**Overview**

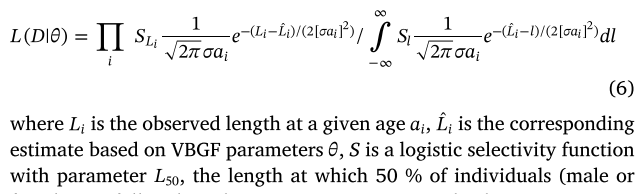
This paper seeks to estimate von Bertalanffy growth parameters for a commercially valuable Hawaiian bottomfish species, *P.* *filamentosus*. It uses tag-recapture data from a 10-year study which involved fisher participation. The study compares MLE and Bayesian approaches for growth parameter estimation and investigates incorporating multiple datasets into the MLE estimation procedure, which they refer to as as an “integrated estimate”. The Bayesian models are compared using model selectigion, and the best estimates are like those found using bomb radiocarbon dating methods for this same sp.

Considering the value of this fishery, and importance of quality VB estimates for use in stock assessment, the paper would benefit from a closer discussion of the implications of their findings. If the estimates are very similar to previous studies, what does this add to the literature? (Confirmation/increased confidence in parameter estimates are both worthy causes). It would also be valuable to touch on the future for assessment of this species, which I recall was previously assessed in a surplus production model as part of a complex.

**Major Comments**

There were many aspects of the writing and presentation which made interpretation difficult, which I describe briefly in minor comments. Setting this aside, there were two major concerns with the technical approach which must be addressed before the work can be re-considered for publication.

The first concern is with respect to fishery selectivity. The tagging program was fishery-dependent and used hook-and-line gear, which likely selectively samples various size classes of fish; I didn’t see this accounted for in your description of your likelihood function. An example of this penalty is pasted below from Kapur et al. (2019) – there is TMB code for estimation available online which accompanies this paper.



Kapur, M., Haltuch, M., Connors, B., Rogers, L., Berger, A., Koontz, E., Cope, J., Echave, K., Fenske, K., Hanselman, D., Punt, A.E., 2020. Oceanographic features delineate growth zonation in Northeast Pacific sablefish. Fish. Res. 222. https://doi.org/10.1016/j.fishres.2019.105414

The second concern regards the implementation and presentation of the Bayesian model. Considering the previous work on growth for this species, it is strange that uninformative priors were used for all input parameters (line 120). Even a moderately broad prior (ie to account for sexual dimorphism) would be acceptable, but we do have a sense for the general range for this species. It is unsurprising that the MLE & Bayes methods performed similarly based on this setup, considering they used the same data source.

It would simplify the reader’s understanding of Model 1 vs Model 2 if you would use the language for hierarchical Bayesian models, whereby individual growth parameters are sampled from a distribution. Please remove the line 125 where k is referred to as fixed, and simply state outright that k is estimated once for the entire population, same story for L129 regarding L infinity. This pops up several times (L171, “k is treated as fixed unknown parameter”) – just say it was estimated for the entire population.

Finally, it isn’t clear to me if/how the MLE and Bayesian methods were compared aside from the bootstrapped intervals overlapping. You mention “cross validation iterations to determine model structure” L349, with no prior description of what this is or what it does – nor a definition of “mssr”. Once the corrections above are made, it would be useful to directly compare the best-fit model estimates from each approach.

**Minor Comments**

The title and abstract are somewhat misleading – the study focuses on estimating parameters of the VB growth curve for this species; there was insufficient mention of maximum age, dimorphism in age etc. to warrant this being classified as an age AND growth study,

L33 is this the same dataset considered in the present study?

I found many sentences could benefit from the addition of some punctuation or being broken up to ease readability. Eg L31 “…focused on early growth in juvenile fish, but individual variability was not considered…, which can result…”. Line 68 is another example.

Other minor typos should be caught by a close proofread. E.g L57 “applied to a previously unreported tagging data…”

Equation 1 you state that Lij is the length at the jth recapture, but previously state you only worked with the “last” recapture, which I took to mean “final”. Please clarify whether your dataset did or did not use multiple recaptures for individuals. If not, I don’t see the necessity for the j subscript.

L137 “…presumptive best estimate” – be careful here. You may end up with very imprecise estimates, which does not really mean the “best”.

At least in the abstract, present the uncertainty of parameter estimates.

Some of the language used to describe the methods is vague and confuses the reader who is otherwise familiar with Bayesian vs. MLE approaches. For example, an “integrated model” is typically one that fits to multiple datasets (via a joint NLL), which it appears to me is model 5. Indeed, the term “integrated” is used loosely throughout the whole manuscript (eg line 29) when there is likely a more specific term not confused with a mathematical concept. I found the phrase “Integrative growth parameters” similarly confusing.

Please label the models 6-12 in the MLE methods section.

L349 define “Mssr”

Similar to proofreading for readability above: L147 “samples…was tabulated into the posterior distribution”. There are simpler ways of stating that the total 1.4 million samples were thinned at an interval of 1/50 to reduce autocorrelation.

Fig2 make these colors transparent so it is clearer the purple zone is overlap, not a third color.