*Other information:*

including otoliths, scales, spines, and/or vertebrae structures *(TK).*

*Underestimation of growth in orange roughy brought NZ’s fishery the brink of collapse and Sebastes spp fisheries off eastern and western Canada.*

*Pristipomoides filamentosus* is a species of long lived snapper distributed throughout the tropical Pacific and Indian Oceans from east Africa to Hawaii and Tahiti, southern Japan to Northern Australia (Allen, 1985; Andrews et al., 2012). In Hawaii, *P. filamentosus* constitutes a significant fraction of harvest from the Deep 7 bottomfish fishery [Kimberlee Harding DLNR/PIFSC-JIMAR Report Email from Uncle Roy (RNVFISHING)].

Lasslet proposed a similar model term a, accounting for variability in age at .

TALK ABOUT ALTERNATIVE MODELS HERE

*Errors during measurement during marking and recapture are often hard to distinguish from individual variability and can further bias growth estimates (TK).*

*Non-linear least squares, maximum likelihood and Bayesian inference are all improved methodologies for fitting individual K and Linf while accounting for individual variation.* As Faben initially proposed, only point estimates are fit.

assumes a constant variability in modeled residual error across all size classes. However, as initial capture size increases, the change in size for individuals recaptured declines as does the residual error.

NLS – Pros: Produces a distribution parameter estimates as a distribution.

Cons: assumes constant variability in model residual error across all size classes.

MLE – Pros: Allows for alternative model structures to be fit

Cons:

Bayesian - ???

To determine which model best predicted observed growth, two-sided 95% confidence intervals were calculated for each of the parameter sets estimated from the two ensemble models. For each model, confidence intervals were computed from 10,000 successful bootstrap iterations. For each iteration, all three data sources were resampled with replacement. As with tagging data, the procedure for resampling direct aging data was straightforward and involved random sampling with replacement from the dataset to construct pseudo data sets with an equal number of observations as the original data. Bootstrapping length frequency data was slightly more complicated with each study period in the pseudo data resampled from the corresponding period of the extrapolated study data. Additionally, each study period in the pseudo dataset contained the same number of observations as in corresponding study period the original study data. Median values and 95% confidence intervals were obtained from the distribution of each bootstrap parameter. Each model was said to differ from the others when bootstrapped confidence intervals did not overlap. Median values of each model’s bootstrapped confidence interval were used to predict growth of each fish in the validation data set using equation 5. The best performing model was said to be the one with the highest correlation between predicted and observed recapture lengths fit to the validation data. Parameter estimates from the best fit ensemble model was compared to Bayesian and maximum likelihood models fit to the full data set and to estimates from preexisting literature.

*Parameter Estimation using Maximum Likelihood*

Francis’ model was fit using the mle and mle2 functions from the bbmle package in R (Bolker & Team, 2017). Model parameters were estimated by minimize the normal likelihood function:

During model fitting, a normal error structure was used but with modifications to the variance structure, , as follows:

*Constant standard deviation*

The initial model was fit with constant variance across all observations, equivalent to the mean difference between the observed and predicted change in fork length calculated for each individual. Using this method, parameters estimated are the same as those fit using a non-linear least squares method.

*Inverse linear relationship between expected ΔL and standard deviation*

With the addition of the parameter (nu), the variance is allowed to vary among individual observations and is proportional to the expected change in length for each individual given its length at marking and time at liberty.

*Exponentially declining residual standard deviations*

In this formula for residual standard deviation, the deviation the introduction of a fourth parameter, (tau), the residual deviation exponentially declines. Larger standard deviations are predicted for individuals with greater expected growth.

*Residual standard deviation as a function of Power law*

Similar to the exponentially declining residual standard deviations formula, this deviation structure follows a power law, again with larger deviations for individuals with greater predicted growth increments.

The fit of each maximum likelihood model compared using the respective values of their Akaike Information Criterion (AIC). Using AIC, the model with the lowest score is thought to be the most parsimonious. Models within 2 AIC values from the lowest value are said to be strongly supported. While AIC provides a statistical methodology for comparing models on the basis of their goodness of fit and the number of parameters used to obtain each fit, it is not a particularly biologically relevant metric. Furthermore, by incorporating unequal variance among individuals prior to calculating the log likelihood of the data set, parameter estimates could be biased with greater weighting of outlier individuals contributing to overall likelihood estimates. As a model’s AIC score is calculated on the fitted log-likelihood, this influence would not be detectible from the AIC metric. Therefore, for each model, the proportion of individuals for whom their predicted growth, determined from their length at tagging and time at liberty, was less than or equal to their observed growth +- was also determined under parameter estimates from each of the models. This provided a second metric to compare the explanatory power of each model.