***Estimation of growth parameters integrating tag-recapture, length-frequency, and direct aging data using likelihood and Bayesian methods for the tropical deepwater snapper Pristipomoides filamentous in Hawaii***

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***Abstract***

*Pristipomoides filamentosus* is an economically and culturally important species of deepwater snapper found throughout the Indo-Pacific. From 1989 to 1993, the State of Hawaii initiated a tagging program with scientists and fishers opportunistically recapturing fish to quantify regional growth and other life history parameters for the species. Over approximately 10 years, 10.5% of 4,179 tagged fish were recaptured. We used this data to compare von Bertalanffy growth parameters estimated using Bayesian and likelihood approaches. Next, we defined an objective cost function to estimate growth parameters that integrated the tagging data with direct aging and length frequency data used in previous regional growth studies. Our results reconcile 30+ years of effort from various methods to estimate growth parameters for *P. filametosus* in Hawaii (=68.14 cm FL 95% [95% Confidence Interval (CI): 65.42–69.54] and K=0.22 [CI: 0.20–0.25]), demonstrate the importance of individual variability in the species due primarily to the asymptotic length parameter , and suggest the effects of sexual dimorphism on growth as a focus of future inquiry. These results have direct management implications for the species as growth is a critical input for age-based stock assessment models and often used as a proxy for other life history traits.

***1. Introduction***

*Pristipomoides filamentosus* (Valenciennes, 1830) is a species of long-lived deepwater snapper distributed throughout the tropical Indo-Pacific (Allen, 1985; Gaither et al., 2011). The species constitutes a significant fraction of Hawaii’s commercial bottomfish fishery where it is colloquially known as opakapaka (Ralston and Polovina 1982, Langseth et al. 2018). Opakapaka is one of seven management unit species pooled for stock assessment of Hawaii’s bottomfish, however there is interest in the potential use of species-specific, age-structured assessments for this fishery which require accurate life history estimates of growth and other life history parameters (Langseth et al., 2018; Mauder et al., 2015, Oyafuso et al. 2017).

A number of studies have used different approaches to estimate growth parameters for *P. filamentosus* in Hawaii and elsewhere in the Indo-Pacific (Table 2). Early estimates were obtained using direct aging approaches with length-at-age data from otolith reads interpreted as a proxy for age (Ralston & Miyamoto, 1983; Uchiyama & Tagami, 1984; Radtke, 1987; DeMartini, Landgraf & Ralston, 1994, Ralston & Williams, 1988). These methods relied on the integration of daily otolith bands which can bias age estimates due to episodic growth and poor increment resolution in early (< 5 years) life stages (Wakefield et al., 2017). Revised parameter estimates using the direct aging approach were obtained by supplementing datasets from those previous studies with additional length-at-age data where ages were estimated using bomb radiocarbon and lead-radium ratios (Andrews et al., 2012). In addition, a length frequency approach was used to estimate growth parameters by tracking the modal length progression of juvenile cohorts caught in nursery habitat in Kaneohe Bay, Hawaii. However, this study used a previous estimate of where individual variability was not considered; this omission can result in biased parameter estimates (Sainsbury, 1980, Moffitt and Parrish, 1996). Estimation of growth estimates from an ongoing mark-recapture study (separate from the results reported here) has attempted using growth increment approaches but preliminary results have been limited by the size distribution of recaptured individuals and the use of a parameterization of von Bertalanffy’s growth function (VBGF) that is not compatible with direct aging and length frequency approaches (R. I. C. C. Francis, 1988; O’Malley, 2015). While the methods of each aforementioned studies produced individual estimates of growth parameters, none of the studies attempted to integrate all three classes of data (i.e., direct aging, modal progression, growth increment from tagging) to explicitly evaluate the parameter values and sources of uncertainty.

Analytical and statistical advances for estimating growth have developed to account for sources of variability and permit parameter comparisons across length-at-age, length frequency, and tagging based approaches (Eveson et al., 2004; R. I.C.C. Francis, 1988; Wang et al., 1995). Structural modifications to Fabens (1965) parameterization of the VBGF address issues of compatibility between growth parameters from direct aging and length frequency approaches with those derived from tagging studies (Maller and Deboer 1988, James 1991, Palmer et al. 1991, Laslett et al. 2002, Eveson et al. 2004, 2007, Zhang et al. 2009). These methods use maximum likelihood and Bayesian frameworks to accommodate individual variability by describing population parameters using probability distributions (R. I.C.C. Francis, 1988; Kimura et al., 1993; Wang et al., 1995; Zhang et al., 2009). Bayesian approaches allow and to be sampled in this manner and can account for prior information when estimating parameters (Zhang et al. 2009). Maximum likelihood approaches typically estimate once for the entire population (henceforth referred to as “fixed”) but flexibility in their implementation has allowed for the development of model structures that can estimate a single set of growth parameters from direct aging, length frequency, and growth increment data simultaneously (Wang et al. 1995, Laslett et al. 2002, Eveson et al. 2004).

Here, we derive growth parameters using Bayesian and maximum likelihood methods applied to a previously unreported dataset from a cooperative tagging program for *P. filamentosus* in the Main Hawaiian Islands (MHI) with fishers opportunistically recapturing fish and reporting to the State of Hawaii’s Division of Aquatic Resources. Parameters estimated from these data using a Bayesian framework are compared to a maximum likelihood approach integrating tagging data with length-at-age and length frequency data previously used to describe growth in *P. filamentosus* in the Main Hawaiian Islands (MHI) and Northwestern Hawaiian Islands (NWHI). These new growth estimates are compared to those previously reported for *P. filamentosus* the Hawaiian Archipelago.

***2. Materials and Methods***

*2.1 Opakapaka Tagging Program*

Tagging data used for this analysis were obtained by biologists from Hawaii’s Division of Aquatic Resources (DAR) within the state’s Department of Land and Natural Resources (DLNR). Between 1989 and 1993 the Opakapaka Tagging Program (OTP), led by staff biologist Henry Okamoto operated from fishing vessels contracted out of Honolulu Harbor, tagging and releasing 4,179 *P. filamentosus* in total. All tagging occurred in the MHI with coarse location data for the site of tagging and recapture recorded using the commercial statistical reporting grid (Table 1, Figure 1). Tagging effort concentrated primarily around the island of Oahu and the Maui Nui complex which includes the islands of Maui, Molokai, Lanai and Kahoolawe. Since 1990, these areas have accounted for approximately 67.7% of Hawaii’s commercial bottomfish harvest. Fewer than 1% of fish in this study were tagged offshore of the islands of Niihau and Hawaii (Big Island).

Fish were caught with hook-and-line gear and brought to the surface at a rate of 2-5 feet per second. Prior to tagging, each fish was placed in a holding container with aerated seawater to assess their likelihood of surviving. Fish appearing lively and upright were deemed suitable candidates for tagging. If the stomach was inverted and full of gas, it was punctured using a small sharp instrument (e.g., scalpel, hypodermic needle, fishhook). A few scales were carefully removed and a small surgical incision (~1 cm) was made near the fish’s anal opening to assist in expelling gas from the body cavity. A uniquely identifiable monofilament streamer tag was anchored within and protruded from this incision. The fork length of each fish was recorded to the nearest ¼ inch in addition to the location and time of capture before returning the fish to the to sea headfirst with downward momentum attempting to counteract buoyancy due to any residual gas.

Local commercial and recreational fishers were made aware of the program through fliers distributed at the local fish markets, to fish dealers, at fishing supply outlets, and posted at small boat harbors and recaptured fish were reported up to a decade after they were tagged (Kobayashi et al., 2008; Okamoto, 1993). Fishers were incentivized with a $10 reward to report the date, location, and depth that each fish was landed and the fish’s fork length. When recaptured by OTP personnel, tagged fish were fitted with an additional tag and released again.

*2.2 Tagging Data Management*

The data collected by OTP was entered into a spreadsheet and subsequent analysis was performed using R (R Core Team, 2014), the Bayesian statistical software JAGS (Plummer, 2003), and the R package R2Jags (Su and Yajima, 2012). The dataset was filtered to remove records of individuals that were never recaptured, individuals for which the tagging date, recapture date, or tag ID was not recorded, and individuals that were not the species of interest. Fork lengths for the remaining fish recorded at tagging and recapture were linearly transformed from inches to centimeters prior to model fitting for consistency with growth parameters estimated elsewhere. Incremental growth () and time at liberty () were calculated for each fish. When individuals were recaptured on more than one occasion, and were only calculated between the first marking event and the final recapture so as to not violate model assumptions of independence. Fish with less than 60 days were excluded from the dataset.

*2.3 Parameter Estimation from Tagging Data: Bayesian Approach*

Growth parameters were estimated for the *P. filamentosus* tagging data following the Bayesian methodology of Zhang et al. (2009). This approach uses a Fabens version of the VBGF but allows the parameters to vary among individuals. Hence the predicted length of a captured individual is expressed as:

This is parameterized such that is the length of individual *i* when the individual is captured (that is, when an individual is initially captured and marked and again during the final recapture event), is the time-at-liberty (time between initial capture and the last recapture) for the *ith* individual when it was recaptured. This term is zero when the equation is used to calculate the individual’s length at capture. is the relative age of *ith* individual at tagging (age minus ). Parameters and are the VBGF parameters for the *ith* individual drawn from Gaussian distributions defining the population means. Prior growth parameter estimates reported by Andrews et al. (2012) were used to inform model priors for and parameters. Uninformative priors were used for all other input parameters, using Gaussian, gamma, beta, and uniform distributions following the approach of Zhang et al. (2009). The JAGS code for specifying these parameters and performing this analysis is provided in Appendix 1.

The hierarchical Bayesian model which allowed both the and parameters to vary across individuals, by sampling these parameters from the distribution of hyperparameters, as described above is henceforth referred to as Model 1. This model was compared to three additional models fit with various constraints to and . Model 2 estimated the parameter once for the entire population (henceforth referred to as “fixed”) while accounting for variation across individuals by sampling from hyperparameter distributions. Model 3 treated as a fixed parameter while sampling parameter from hyperparameter distributions, and both parameters were fixed under Model 4.

Evaluating the restrictive assumptions of models 2-4 was accomplished by comparing growth parameters to those estimated by Model 1. Model 1 is the presumptive best estimate for *P. filamentosus* VBGF parameters, since it allows the most flexible incorporation of individual variability by sampling both and from hyperparameters. If a given parameter is relatively stable when the parameter varies across individuals and when it was treated as fixed for the population, then it might be inferred that treating this parameter on an individual basis is not warranted. However, if parameter estimates differed when the parameter was fixed, then it might be inferred that treating this parameter on an individual basis is necessary. Model 4 would *a priori* be most similar to the Fabens approach, with both fixed and , but with the added feature of estimating ages at initial tagging, . It is the inclusion of this term that models growth as a function of age, rather than length, allowing for direct comparison between parameters estimated using tagging data and those obtained from direct-age and length frequency approaches (Wang et al., 1995).

For each Bayesian model, the first 150,000 samples from the posterior distribution were treated as burn-in and discarded from the Monte Carlo simulation. Additional samples were thinned at an interval of 1/50 (number kept = 30,000) to reduce potential autocorrelation between sequential values or strings of values in the posterior distributions. Initial starting estimates of and were obtained from Andrews et al. (2012) with two additional chains run simultaneously with initial starting values 50% lower and 100% higher. This resulted in nearly identical solutions as shown in Table 3. The mean and values from the posterior distribution were used as metrics of population values. Median values deviated from mean values by less than one half of 1 percent (Table 3), indicative of symmetrical distributions easily characterized by any descriptor of value tendency (i.e., mean, median, or mode). Convergence was also ascertained by examination of the Gelman-Rubin statistic (Gelman and Rubin, 1992).

The fit of each model was assessed by calculating a Bayesian p-value from the posterior predictive distribution. Bayesian p-values were simulated using the model’s posterior distribution and test whether simulated data is more extreme than the observed data. Bayesian P-values range between 0 and 1 where values approaching 0.5 indicate the model is a good fit to the data, while extreme values near 0 or 1 indicate that the model does not adequately represent the data (Meng, 1994). The deviance information criterion (DIC) was used to compare between models.

*2.4 Parameter Estimation from Tagging Data: Maximum Likelihood Approach*

The maximum likelihood approach of Laslett et al. (2002) was used to fit Model 5 using the following equation,

This method derives growth parameters from the joint distribution of an individual’s length at tagging and recapture. This is most similar in approach to Model 2 of the Bayesian approach in that asymptotic length, , is treated as a normal random effect , accounting for differences between an individual the total population, while is treated as a fixed unknown parameter. Rather than using length increments to fit observed growth, a bivariate normal joint distribution of lengths recorded at marking and recapture is used to estimate each individual’s age at tagging . The distribution of across all individuals is treated as a random effect with a lognormal distribution . Measurement error is also treated as a random normal distribution . An unconditional joint density is then derived for each individual by integrating their individual joint distribution with respect to . This process is described in greater detail by Laslett et al. (2002).

This approach was used to estimate values of the growth parameters , , , , , and by minimizing of the negative log-likelihood cost function obtained from summing the unconditional joint density of each individual (E3).

Two-sided 95% confidence intervals (2.5%, Median, 97.5%) were estimated for each parameter through a bootstrapping procedure repeated for 10,000 iterations. During each bootstrap iteration, the model was refit using data randomly resampled with replacement from the original tagging data.

*2.5 Estimation of Integrated Growth Parameters using sources of growth data*

Datasets previously used by other studies to quantify the growth of *P. filamentosus* in the MHI and NWHI were combined with OTP tagging data to produce a single set of integrated parameter estimates using a modified form of the method proposed by Eveson, Laslett, and Polachek (2004). Additional datasets that were included represent both direct aging and length frequency approaches and are briefly described below. In total, 6 candidate models (Models 6-11) were fit using this approach (Table 4).

*2.6 Parameter Estimation: Length Frequency Data*

Length frequency data consisted of the size distributions of juvenile *P. filamentosus* sampled over 13 months between October 1989 and February 1991 as reported by Moffitt and Parrish (1996). The reported fork lengths of captured fish were binned in 1 cm increments and presented in 13 histograms corresponding to each month of sampling. The data was reconstructed by overlaying a series of evenly spaced horizontal lines across the Y-axis of each histogram corresponding to the addition of a single fish. The reconstructed data contained 1,048 observations, one more than was reported by the original study (Moffitt and Parrish, 1996).

The reconstructed length frequency data were incorporated into integrated models by following the two-step method described in Laslett et al. 2004. In the first step, a Gaussian mixture model was fit using maximum likelihood and used to decompose the distribution of fork lengths for each recruitment cohort present for each month of data. This was done using the normalmixEM function from the mixtools package in R (Benaglia et al., 2009) by assuming the mean of each distribution corresponded to the observed mode. A bimodal Gaussian mixture model was fit for the data collected between the months of October-February, as the original study reported that two cohorts were present during this period. A single cohort was present the remainder of the year. In the second step, estimated mean fork length, and standard error, , of each cohort during each month of sampling was used to estimate growth parameters using the following parameterization of the VBGF (E4).

With this parameterization, and reflect the fishing year, month, and age cohort, respectively. The estimated age of each cohort at each sampling period is denoted by . Ages were estimated relative to the month of July when peak spawning of *P. filamentosus* occurs, resulting in age estimates between 3 and 19 months (Luers et al., 2017).. Sampling and residual model errors were described using random normal distributions. In contrast to tagging and direct aging methods, length frequency approaches lack the information to estimate the variance component of asymptotic length (), so this term was modeled as fixed effect, . From this, the expected mean fork length of each cohort (E6), and associated variability during each sampling period (E7) were used to minimize the model’s negative log-likelihood cost function (E8). The rationale for these approximations is discussed to greater depth in Eveson et al. 2004.

*2.7 Parameter Estimation: Direct Aging Data*

Sources of direct ageing data included four length-at-age datasets from three prior growth studies. Approaches for estimating age differed between study and included analytical integration of otolith bands (Ralston and Miyamoto, 1983, n = 65), counts of otolith micro increments (DeMartini et al., 1994, n = 35), comparison of otolith derived bomb radiocarbon ratios (Δ14C) relative to a standard reference obtained from hermatypic coral cores from the Hawaiian Archipelago (Andrews et al., 2012, n = 33), and otolith derived lead-radium ratios pooled by size class (Andrews et al., 2012, n = 3).

The details of the method used to estimate growth parameters from direct aging data are described in detail in Eveson et al. 2004. Briefly summarized, parameters are modeled using the VBGF parametrization described by equation E9.

Expected length for each individual and the variance of the measurement error is described by equations E10 and E11.

Where denotes the length of the fish*,* at age and is a fixed parameter analogous to when a fish has a hypothetical length of zero. As with the model for tagging data, is the individual asymptotic length of thefish drawn from the random normal distribution . represents the distribution of individual measurement error and is similarly random, drawn from the distribution . The log-likelihood cost function derived from these equations is described by the following equation (E12).

*2.8 Defining an objective cost function and estimating integrated growth parameters*

To derive integrated growth parameters across tag-recapture, direct aging, length frequency, and growth increment data sources, we developed an appropriate integrated cost function, defined from the sum of the cost functions for each data source and a set of scaling constants, *βi* (E13). The single set of growth parameters best describing all data sources is obtained through minimization of the integrated cost function, (E13).

The six candidate model structures (Models 6-11) for estimating growth in *P. filamentosus* were developed and evaluated by permutating the value of scaling constants, the pooling of datasets using similar approaches, and whether length-at-age data where age estimates were obtained through integration of daily otolith bands were included (Table 4). Two approaches were used for the value of scaling constants (*βi*). The first weighted scaling constants for every data source so that each source contributed equally to the resulting parameter estimates while the second weighted each source proportionate to its number of observations. Other differences between integrated models included whether the four direct aging data sources contributed individually to the integrated cost function or if they were first pooled. Omitting direct aging data where ages were estimated by integrating daily growth increments was also considered as this method is likely to underestimate age (Table 4; Wakefield et al 2017).

*2.9 Model Evaluation*

The six candidate integrated models (Models 6-11) were evaluated using a repeated cross validation procedure to determine the model structure that best predicted the growth observed in the OTP data (Burman, 1989). During each iteration of this procedure, two thirds of fish in the OTP dataset (n = 258) were randomly selected without replacement for model training while the remaining third (n = 129) were used to test model performance. Performance was assessed by the ability of each parameter set, fit using the training data, to predict the expected length at recapture for fish in the test data by calculating the root mean squared error (RMSE) between the predicted and observed growth. The preferred model was the one who’s structure most frequently resulted in the lowest RMSE over 10,000 iterations. To determine if incorporating additional data sources improved predictive performance, RMSE for the preferred integrated model was then compared to the structure of Model 5 which included only tagging data.

Once the structure of the preferred integrated model was determined, two-sided 95% confidence intervals were estimated for each parameter from 10,000 bootstrap iterations. As with tagging data, the procedure for resampling direct aging data was straightforward and involved random sampling with replacement to construct synthetic datasets with an equal number of observations as the original data. Bootstrapping length frequency data was done by hierarchical sampling such that the study periods in each bootstrapped dataset were resampled from the corresponding periods of the original data.

*2.10 Sensitivity Analysis*

The accuracy of growth parameters can be affected by the distribution of individuals sampled relative to that of the total population (Bolser et al., 2018, Calliet and Tanaka 1990). Gear selectivity, sampling location, variation in annual recruitment, and other factors can lead to under representation of select size and age classes in the sample population (Goodyear 2019, Kapur et al., 2020).

A sensitivity analysis was performed to quantify the effect of the sampled distribution on parameter estimates with an approach inspired by the approach of Bolser et al. (2018). This was done by first segmenting the OTP data in 5-cm increment bins by the length of each individual recorded during tagging. Then a synthetic dataset was constructed for each model by simulating additional individuals using the mean of each bin and the standard deviation within that bin calculated from the tagging data, until all bins contained the same number of observations (200). Growth in synthetic data was estimated using parameters obtained for each model and the mean time at liberty for all fish in the OTP study. Each model was then refit using its corresponding synthetic dataset. The influence of sampling distribution on parameters and was quantified as the amount synthetic estimates differed from estimates from observed data. This type of approach does not explicitly account for differences in selectivity or differences between the sampled and true population structure, but it can fill critical gaps caused by these issues by flattening the number of observations across size classes (Bolser 2018).

***3. Results***

*3.1 Opakapaka Tagging Program*

In total, 487 recaptures were recorded for 439 unique individuals for a recapture rate of 10.5% (Table 1). Mortality of fish upon release appeared to be generally low, likely due to the selection of healthy fish in good condition. Some immediate mortality was observed due to capture stress and predation by sharks and cetaceans (4 individuals). Long-term mortality was thought to be relatively low based upon the high rates of tag return spanning many years. Hydra (small cnidarian polyps) biofouling of the tags was observed for some individuals with large times at liberty, with some lesions apparent around the opening where the tag exited the body cavity. This was not thought to be a serious health issue since the fish appeared to be feeding and swimming normally.

Initial fork length at capture across all individuals ranged in size from 16.5 to 53.3 cm (mean = 31.9 cm, standard deviation (s.d.) = 5.5) and ranged from 19.1 cm and 52.8 cm (mean = 32.8, s.d. = 5.1) for fish that were later recaptured. For those fish that were later recaptured, fork length measured at recapture was between 22.9 cm and 76.2 cm (mean = 41.9, s.d. = 8.7). The minimum time at liberty for any fish between tagging and recapture was a single day while the maximum time at liberty was 10.3 years (3,748 days) (Figure 2). The mean time at liberty was 1.82 years or 666 days (s.d. = 625).

One fish was excluded from further analysis as its initial fork length at capture was not recorded so growth could not be calculated. Seven fish were removed because the recapture date was not properly recorded and therefore their time at liberty could not be determined. Of the remaining 432 fish recaptured, 351 were recaptured a single time, 33 fish were recaptured a total of two times, one fish recaptured 3 times, and two fish were recaptured 4 times. We also excluded from analysis 45 individuals for whom time at liberty was less than 60 days to minimize the influence of any short-term tagging effects. This process yielded a data set consisting of 387 unique individuals.

*3.2 Estimating Growth Parameters from Tagging Data: Bayesian Approach*

The Bayesian hierarchical approach produced mean estimates of and for Models 1–4 (Table 3). Model 1, which incorporated individual variability in both and , yielded mean parameter estimates of = 61.4 cm (coefficient of variation [c.v.] = 2.56) and = 0.30 (c.v. = 8.33). and parameter estimates for Model 2, where was fixed, were 61.61 cm (c.v. = 2.72) and 0.29 (c.v. = 45.6) respectively. Under Model 3, where was fixed and was fit freely = 72.0 cm (c.v. = 41.0) and = 0.19 (c.v. = 8.67) and = 74.82 cm (c.v. = 42.71) and = 0.17 (c.v. = 72.91) for Model 4, where both parameters were fixed. Additional parameters for each of the four models are presented in Table 3. The Gelman-Rubin convergence criteria indicated that the model solutions were credible, with asymptotic convergence clearly occurring after ~4000 iterations, well within the burn-in phase of the Bayesian modeling runs. All 4 models appeared to fit the the data well; the mean Bayesian P-values from all retained posterior samples for all models ranged between 0.500 and 0.501. Model 4 had the lowest DIC (4780.7) followed by Model 3 (5216.3), and Model 2 (8644.5), while Model 1 had the highest DIC (8826.8), however treating model parameters as fixed under models 2-4 resulted in large coefficients of variation suggesting that accounting for individual variability is important, with perhaps variability in being more important based upon the low coefficient of variation in from the base case of Model 1 and the large coefficients seen in Model 3 and Model 4 (Figure 3).

*3.3 Parameter estimation using maximum likelihood*

The maximum likelihood approach used for Model 5 converged to produce estimates of , , , , , and (Table 5). Bootstrap confidence intervals of parameters and overlapped and parameters from Bayesian models 1 and 2 (Table 2). From these results, it was concluded that estimates produced by maximum likelihood approaches were satisfactorily similar to estimates from the Bayesian approach. Model residuals appeared homoskedastic and normally distributed around zero for all but the largest fish. For fish with recapture lengths exceeding 60 cm, growth models underestimated observed recapture lengths (Figure 4).

*3.4 Comparing model performance*

Across all 10,000 cross validation iterations to determine the preffered integrated model structure, the six candidate models produced RMSE values that ranged between 2.78 and 4.95 (mean = 3.9, s.d. = 0.3) with lower values indicating a better fit to the data. The structure of Model 11 outperformed competing models during cross validation (2,192 of 10,000 iterations ). RMSE for this model ranged between 2.9 and 4.9 (mean = 3.9, s.d. = 0.3).

The inclusion of additional growth data improved the predictive capability of growth models compared to tagging data alone. The structure of Model 11 performed better than the structure of Model 5 during cross validation (5,672 of 10,000 iterations). Differences in RMSE between the competing structures of Model 11 and Model 5 ranged between -1.2 and 0.1 (mean = -0.1, s.d. = 0.1) with structure of Model 5, fit exclusively using tagging data, producing RMSE values that ranged between 2.8 and 5.3 (mean = 3.9, s.d. = 0.3). Bootstrapped parameter estimates refit using the structure of the prefered integrated model (Model 11) and the tagging only structure of Model 5 are summarized in Table 2 and all parameters for models 5-11 are reported in full in Table 5.

*3.5 Sensitivity Analysis*

Parameters estimated using the observed and synthetic data differed by as much as 95.74% but was generally less than 3.30%. For all models, the paramer differed more between the synthetic and observed data than the parameter . Estimates of and from the preferred integrated model (Model 11) estimated from synthetic data differed from the observed data by 0.69% and 2.46% respectively. These differences between the observed and synthetic data were smaller than those for all other maximum likelihood models and second smallest overall. Parameter estimates for Model 1, the Bayesian model that accounted for individual differences in each parameterand had the lowest coefficient of variation across both parameters, differed by 1.23% for the parameter and 4.09% for . Parameters for Model 4, the Bayesian model with the lowest DIC score, differed between observed and synthetic data by 0.22% in the parameter and by 1.04% in , the lowest of any model. Sensitivity results for all models are reported in full for all models in table 6.

***4. Discussion***

Our integrated model results reconcile 30+ years of effort to quantify growth for *P. filamentosus* in the Hawaiian Archipelago and provides robust support for some previously estimated parameter values. Growth parameters derived using integrated models incorporating additional length frequency and length-at-age data were better able to predict the growth observed in recaptured fish compared to those fit using only tagging data. These parameters were in agreement with direct aging studies where ages were estimated using 1) the fit of only integrated daily growth increments from otoliths collected in the NWHI without constraining (Ralston and Miyamoto, 1983), 2) integrated daily growth increments and microincrement counts (DeMartini et al. 1994), and 3) the radioisotopic composition of otolith material and counts of otolith increments from the MHI and NWHI (Andrews et al. 2012) and support the implicit assumption that tagging individuals did not significantly disrupt their growth trajectory. integrated parameters differed from estimates from an ongoing mark recapture study in the MHI which reported faster growth and smaller asymptotic lengths (O’Malley, 2015). These differences could arise from real changes in growth rate between the periods fish were collected, methodological differences in model interpretation, and/or that thus far, none of the fish recaptured during the ongoing study have been of the largest size classes (maximum size reported = 47.6 cm FL).

Compared to growth studies across their broader distribution, parameters obtained from the Hawaiian archipelago indicate that *P. filamentosus* were generally slower growing but obtained a larger asymptotic length than those from the Mariana Archipelago (Ralston and Williams, 1988) and Papua New Guinea (Fry et al. 2006, Andrews et al. 2012) and were faster growing but smaller in their asymptotic length when compared to estimates from the Seychelles (Hardman-Mountford et al., 1997; Mees, 1993; Mees and Rousseau, 1997; Pilling, 2000). These differences may represent genetic or phenotypic differences between these populations, or differences in the methods and sampling distribution between studies.

Of the Bayesian models, Model 1 was presumed optimal because it incorporated individual variability in both and *K* parameters, however this model performed the worst of all Bayesian models during sensitivity testing. Models 2-4 suggest that individual variability in both and parameters is important, with perhaps variability in being more important based on the similar parameter estimates obtained from Models 1 and 2 and comparison of relatively small the coefficient of variation for from the base case of Model 1 to the larger coefficients of variation under assumptions of constrained individual variability in Model 3 and Model 4 (Figure 3). Based upon these parameter estimates and pattern of large standard deviations, it is likely Models 3 and 4 were not credible despite lower DIC values and performing well during sensitivity testing. Similar parameter estimates obtained from Models 1 and 2 suggested that the primary source of individual variability was due to variability in the parameter. This is consistent with other studies where the best models accounted for individual variability in both terms but accounting for individual variation in the term alone was sufficient to describe growth while significantly reducing computational complexity (Eveson et al. 2007, Zhang et al. 2009).

The treatement of individual variability in parameters for Model 2 were identical to those used to fit Model 5 (OTP data only). Comparing growth parameter estimates from these models indicate that Bayesian and maximum likelihood fitting methods performed similarly. Parameter estimates for Models 1 and 2 were contained within the 95% confidence intervals of Model 5. These results suggest that treatment of *K* as a fixed effect was unlikely to bias estimates in integrated models, fit using maximum likelihood, which were evaluated under the same assumptions as models 2 and 5.

Of all models presented, Model 11 appears to be the most predictive and robust. Across all candidate integrated growth models, the parameters estimated by Model 11 were best predictive of length at recapture during cross validation. This model was also the second most robust to the sensitivity analysis, with parameter estimates differing by less than 2.5%. While information from older/larger fish from direct aging datasets was very important for grounding the upper end of integrated growth curves and resulted in parameters that better predicted length at recapture, these additional data sources were less influential to this model than for the model otherwise identical in structure (Model 10) that placed a greater emphasis on these data sources. This suggests that the inclusion of additional data was important for obtaining accurate results but were most helpful when their influence was limited.

Additional data sources included here represent collections spanning several decades from the MHI and NWHI. When incorporating these additional data sources, it is an inherent assumption that growth within the population did not differ significantly with time or region. This is not the first study to make these assumptions; with the exception of Ralston and Miyamoto (1983), all subsequent studies of growth for *P. filamentosus* in the Hawaiian archipelago have included datasets or parameter estimates from one or more previous studies in their calculations without regard to the time and place the data was collected (DeMartini et al. 1994, Moffitt and Parrish 1996, Andrews et al. 2012). Genetic homogeneity between NWHI and MHI stocks provides some justification pooling data across both regions, however these spatial and temporal assumptions may not reflect phenotypic realities and further work is required to resolve whether differences in growth exist between the two regions (Gaither et al. 2010, Gaither et al. 2011).

Sexual size dimorphism may explain the tendency of parameters obtained here and elsewhere to underestimate the length at recapture observed for the largest fish in the OTP dataset (approximate fork length > 50 cm) (Figure 4). For sex agnostic models, parameters are essentially averaged between sexes. In smaller sizes classes where the sex ratio of individuals is similar to that of the total population, this averaging of parameters between sexes results in increased estimates of variance. However, if dimorphic differences in growth are present and one sex disproportionately attains a greater asymptotic length than the other, that sex is likely to be overrepresented in the largest size classes relative to the total population. Growth estimated for these individuals continues to represent an average of both sexes and will result in the underestimation of lengths at recapture, while growth in the underrepresented sex will be overestimated. This produces a residual pattern resembling the one seen in the OTP data.

While not pronounced, dimorphic size differences have been observed in a number of lutjanid species (Grimes, 1987; Mees, 1993; Newman et al., 2000; Newman and Dunk, 2002; Nichols, 2019; Taylor et al., 2018; Williams et al., 2017). Elsewhere in their distribution, larger asymptotic lengths have been reported for male *P. filamentosus* in the Seychelles while during research fishing in the Northwestern Hawaiian Islands, the number of females outnumbered males almost 2:1 in the largest size classes, and in Guam no differences between sexes were observed(Kami, 1973; Kikkawa, 1984; Mees, 1993)*.* These differences may be true sexual dimorphism or discrepancies between the structure of the sampled and true populations. Estimation of growth parameters for *P. filamentosus* in the Central Pacific have thus far remained sex agnostic and a method for non-invasive sexing of this species was unknown until recently (Luers et al. 2017). More work addressing sex specific differences is required to adequately test for dimorphism in this region.

Accurate estimates of von Bertalanffy growth parameters are very important for management. Growth parameters are often used directly or indirectly in stock assessment and fisheries management (Haight et al., 1993; Polovina et al., 1987). These efforts are sensitive to both growth parameters and the model used to estimate those parameters. For example, the rate of instantaneous natural mortality *M* is a value of interest often inferred from *K* using empirical relationships (Jensen, 1996; Ralston, 1987; Thorson et al., 2017). Underestimating will underestimate *M*, characterizing a stock as less productive than it actually is while overestimating *K* will have the opposite effect. If a management regime is linked to such a flawed estimate of stock productivity, then the stock is likely to be mismanaged and under or over harvested, respectively, relative to its true biological potential. Future work to refine these estimates for *P. filamentosus* should consider the role that dimorphic differences that may exist between males and females may have on their respective life histories.

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***Competing Interests***

The authors declare that they have no competing interests.

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**Tables**

**Table 1.** Summary of tagging and recapture locations for *P. filamentosus* used for growth increment approaches as referenced to reporting grids in Figure 1. Adapted from Kobayashi, Okamoto & Oishi (2008).

**Table 2.** Estimates (and 95% confidence intervals when available) of von Bertalanffy growth parameters , *K*, and *to* reported by the present and prior studies.

**Table 3.** Von Bertalanffy growth parameter estimates from Bayesian hierarchical growth models (Models 1-4).

**Table 4.** A reference for the candidate model structures used to determine the preferred model structure from integrated maximum likelihood growth models (Models 5-11).

**Table 5.** Sample and Population Parameter Estimates (with bootstrapped confidence intervals) from Maximum Likelihood Growth Models (Models 5-11).

**Table 6.** Parameter estimates obtained from a sensitivity analysis where tagging data was divided into 5 cm bins and then synthetic data was added so that each bin contained 200 observations. Comparing parameter estimates fit to synthetic data against those from the original dataset provide a metric to compare the effect of the sampling distribution on the estimates obtained.

**Figure Captions**

**Figure 1. Reporting Grid Map.**

*Map showing the location and number of the State of Hawaii’s statistical reporting grids corresponding to the reported location of tagging and recaptured for fish summarized in Table 5.2.*

**Figure 2. Length and Time at Liberty for OTP and Additional Data.**

*The length of P. filamentosus recaptured and included in analysis of OTP tagging data and the distribution of times at liberty are presented in subplots a and b respectively. The fork length of fish during tagging is highlighted in blue while length at recapture is shown in red. Subplot c shows the measured fork length and estimated ages from the various sources of length at age data included in models 6 – 10 while subplot d tracks the mode fork length for cohorts included in the length frequency data originally presented by Moffitt and Parrish (1996), also used to supplement OTP data in models 6-10.*

**Figure 3. Coefficient of Variation for von Bertalanffy Growth Function Parameters.**

*Coefficient of variation for 2 von Bertalanffy growth function parameters (Brody growth coefficient, K and mean asymptotic length, L∞) for P. filamentosus. Individual variability was examined incorporating individual variability in both parameters, in either one of the parameters in series, or in neither parameter.*

**Figure 4. Plots Comparing Predicted and Observed Length at Recapture.**

*Predicted lengths at recapture compared to the observed lengths at recapture for tagged P. filamentosus. Length at recapture was predicted as a function of length at marking, time at liberty, and parameter point estimates. The 1:1 line indicates where points* *would fall if model parameters perfectly predicted length at recapture.*