**Variation in growth among individuals and over time: a case study and simulation experiment involving tagged Antarctic toothfish**

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**Abstract**

Organisms in the marine environment are likely to exhibit variation in growth rates among individuals, and this variation may be persistent (particular individuals growing faster/slower throughout their entire lifetime) or transient (particular individuals growing faster in one year than another year). Understanding variation in growth is necessary when interpreting data regarding size (length or weight) in population models, or when estimating growth given data for tagged individuals. In this study, we explicitly model persistent and transient variation in growth rates among individuals in a wild marine population of Antarctic toothfish (*Dissostichus mawsoni*) in the Ross Sea, in addition to sex-specific differences in average growth rates. The model is implemented using maximum marginal likelihood estimation and validated using a simulation study. The code is distributed as a publicly available package *TagGrowth* in the R statistical environment. Using simulated data, we show that we can accurately estimate parameters representing the magnitude of persistent and transient variation in growth rates, and that parameters estimated in these models are reasonably precise given the case study sample sizes (315 individuals tagged and recaptured over 10 years). The case study application suggests that transient variation among individuals accounts for up to half of the total variability in Antarctic tootfish. We conclude by recommending further research to additionally estimate temporal and spatial variation in growth rates. Estimating the relative magnitude of multiple sources of growth variation will improve our ability to assess the sensitivity of existing population models to growth variation, as well as to understand the range of variation exhibited by wild marine populations.

**Keywords:** Antarctic toothfish; time-varying growth; random effect; von Bertalanffy growth

## 1 Introduction

Variation in growth rates has been discussed for over 100 years for fish populations. Growth in fishes arises from complex behavioral trade-offs for each individual in a population. Growth (measured as an increase in standard length) arises from the allocation of energy between increased size (length) and increased condition (i.e., weight at length). Individuals can also increase their rate of energy acquisition via increased foraging activity, but increased foraging may also cause changes in the risk of predation. Environmental conditions modify the potential for growth, as well as the trade-offs faced by individual fish. For example, increases in water temperature are associated with increased activity levels but also increased energetic demands for maintaining existing body tissue, such that the net effect of changing temperature on growth may vary among individuals (Shelton et al., 2013). Similarly, changes in survival rates (via fishery harvest) may favor earlier maturation, thus affecting the relative allocation of energy between growth and reproduction.

Many recent studies of captive or wild populations have demonstrated persistent differences in behavioral or phenotypic traits among individuals (termed differences in “personality”, Wolf and Weissing, 2012). Persistent differences in activity level or tolerance of predation risk (i.e., a tendency to forage in high vs. low-quality habitat) will likely lead to persistent differences in growth rates among individuals. For example, persistent differences in growth rate, combined with size-selective harvest, will result in older individuals being composed primarily of slow-growing individuals (termed “Rosa Lee’s Phenomenon”), and has been demonstrated to occur in small-lake mesocosm experiments (Biro and Post, 2008). Failure to account for persistent differences in growth rate can lead to biased estimation of average growth rates in wild populations, and population dynamics models are increasingly developed to account for these effects (Taylor and Methot, 2013).

In addition, individuals are likely to experience transient variation in growth rates. Transient variation could be caused by many different processes including movement between warmer/colder ambient temperatures (and hence transient variation in metabolic rates), periodic access to improved feeding (Armstrong and Schindler, 2011), and year-specific decisions regarding the allocation of resources between growth and reproduction (Jørgensen and Fiksen, 2006). Finally, sex-specific differences in behavior can result in differences in average growth rates between males and females (Biro and Sampson, 2015). Sex-specific differences in growth rate are commonly included in population models for marine species (Methot and Wetzel, 2013). We therefore hypothesize that most marine populations will have multiple sources of variability in individual growth rates, including:

1. Persistent variation among individuals (i.e., some individuals grow faster or to a larger size than others)
2. Transient variation over time for a given individual (i.e., individuals will have spurts and drops in growth rates).
3. Variation in average growth rates between males and females

Estimation of growth rates among individuals and over time therefore requires partitioning variation among multiple potential types, and mixed-effects models are generally advocated for this task (Thorson and Minto, In press). Mixed-effects models partition variation among multiple sources by estimating true size at age as a latent variable, which is integrated across during estimation of growth parameters. True growth rates can therefore vary among individuals, and the magnitude of this variation can be explained by multiple putative sources. Hierarchical models are increasingly advocated as a strategy to partition variability into multiple sources, and hence to interpret which source of variance is worth further study (Gelman, 2005; Larsen et al., 2001).

Growth rates in natural populations are generally estimated using capture-mark-recapture (CMR) models. In CMR studies for marine fishes, thousands of individuals are typically captured and marked with a persistent and unique tag, and then measured and released. If a tagged individual is recaptured, it is often killed and its age at recapture identified via analysis of hard parts (e.g., otoliths). Given the known time between capture and recapture, its size and age at both times can be calculated. This study design allows a model for growth increments to be fitted to size and age data for two times for each individual in a data set. Many studies have examined the impact of persistent or transient growth variation on estimation of growth patterns using CMR data for wild marine populations (Francis, 1988; Sainsbury, 1980). However, few studies have explicitly modeled multiple sources of variability in growth rates. One exception is Shelton et al. (2013), which modeled persistent, temporal, and transient variation in growth rates in the analysis of data from a growth experiment for steelhead trout.

In this study, we present a model for partitioning variation in growth into persistent, transient, and sex-specific factors, and parameters are then estimated using maximum marginal likelihood methods. The code is distributed as a publicly available package *TagGrowth* in the R statistical environment, and is illustrated using CMR data for Antarctic toothfish (*Dissostichus mawsoni*). Using these data, we show that we can accurately estimate parameters for a model that includes multiple sources of individual variation in growth, and that estimates are reasonably precise given a feasible number of individual recaptures (250 or more). Our case study application suggests that transient variation over time accounts for up to half of the total variability in Antarctic toothfish in the Ross Sea.

**2 Methods**

We start with the specialized von Bertalanffy growth function:

(1)

where *dL/dt* is change in length *L* as a function of time *t*, *a* scales with energy acquisition, and *k* represents metabolic upkeep costs. Persistent variation among individuals can be estimated by treating each individual's demographic parameters as a random effect that arises from a population-level distribution (Thorson and Minto, In press). Here, we treat average metabolic upkeep costs *ki* as varying among individuals (where subscript *i* signifies the upkeep rate for the *i­-*th individual), due to differences in ambient temperature, intrinsic variation in activity levels, and other factors:

(2)

where , *μk* is the median *ki* among individuals in the population, and is the variance of individual upkeep cost deviations ().

Individuals that are more highly active may obtain more food (increased *a*) and simultaneously have greater upkeep costs (increased *k*). Following Shelton et al. (2013), we include this association via the following equation:

(3)

where *Ψ* determines whether upkeep costs (*ki*) and energy acquisition rate (*ai*) are highly correlated (*Ψ=1*) or independent among individuals (*Ψ=0*), and *γ* controls the average energy acquisition rate among individuals.

We also assume that environmental conditions experienced by each individual will vary over time, such that each individual will have “transient” variation over time in their upkeep costs (*ki*), in turn affecting their access to food (*ai*). In particular, we assume that upkeep costs for a given individual *i* for a short time interval *t* can be approximated by a constant value (*ki,t*), which will vary around the average value for this individual (*ki*). In the proceeding, we use a time interval of one week (7 days), while confirming that results are similar for other small time intervals. Integration then yields:

(4)

where

where *Δt* is the number of time-periods (weeks) elapsed between two times (e.g., tagging and subsequent recapture) and *nΔ* is the number of time-periods per year (52.15), such that *k* is the Brody growth coefficient (with units years-1), and *σz* is the magnitude of transient growth variation (see Appendix A for derivation of , derived from Shelton et al., 2013). In this study, we use a time interval of one week (7 days). We confirm that results are similar for other small time intervals (i.e., days or months), but found that an annual time interval resulted in parameter estimates yielding biased high growth schedules. We assume that all age-0 individuals have a length *L0,s* that differs between males *(s=0*) and females *(s=1*), and estimate length-at-birth for each sex. Eq. 4 can then be used to calculate the predicted length at of first capture *L(t1)* and upon recapture *L(t1+t2*), where *t2* is the time between first tagging and recapture (time at liberty), and *t1+t2* is the age at recapture as determined from conventional ageing methods.

The observed length for each individual upon first tagging *Lobs(t1)* and upon recapture *Lobs(t1+t2*) is assumed to follow a normal distribution with a fixed coefficient of variation (c.v., representing observation error caused by at-sea length measurements) given the estimated length at that age *L(t)*:

(5)

where , and and *cobs* is the c.v. of observed growth.

## 2.1 Estimation

We estimate the value of fixed effects in this model (*L0*, *μk*, *σk*, *γ*, *σz*, *cobs*) using maximum marginal likelihood while integrating across the probability of all random variables representing persistent and transient variation among individuals (Thorson and Minto, In press). Preliminary exploration using data for the case study (explained below) suggested that *Ψ* was not estimable for our data set, so we proceed by fixing *Ψ=0*. Parameter estimation is conducted using Template Model Builder (TMB; Kristensen, 2014; Kristensen et al., In press;available from: <https://github.com/kaskr/adcomp>) software called from the R statistical environment (R Core Development Team, 2013) and all code necessary for replicating the case study and simulation experiment are publicly available (<https://github.com/quantifish/TagGrowth>; Appendix B). The marginal likelihood is then maximized using conventional nonlinear minimization tools in R, while using the gradient of the marginal likelihood with respect to fixed effects as calculated by TMB. Standard errors are then estimated via the information matrix and delta-method.

After fixed effects have been estimated, the median asymptotic length () for individuals in the population can be calculated as:

(6)

which is obtained by setting Eqn. 1 equal to zero, substituting in Eqn. 3, and rearranging. Readers are referred to Shelton et al. (2013) for an expanded model that also incorporates variability in average energy acquisition rates (*γ*) for all individuals in a given time period. All of the variables used in this paper are outlined in Table 1.

**2.2 Case study application**

Antarctic toothfish are large Nototheniids native to the Southern Ocean. They can grow to be more than 2m in length, weighing over 100kg, and can live for up to 50 years of age. The exploratory toothfish fishery in the Ross Sea region began in 1997 and is managed by The Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR). Since then the fishery has increased to about 3000 tonnes per year. Fishing is restricted to the summer months (December usually until to March), once the ice shelf recedes allowing vessels access to the region. The Antarctic toothfish tagging programme was initiated in the in the 2001 fishing season by New Zealand vessels involved in the fishery. In 2004, toothfish tagging was made compulsory for all vessels participating in the fishery. Currently toothfish are required to be double tagged at a rate of 1 fish per tonne landed. The tagging programme records information on the date, depth, location, sex, and size of each tagged/recaptured fish. A small subset of the recaptured fish are aged by reading their otolith.

We identified those fish that had been tagged, recaptured and aged upon recapture. This yielded 315 individuals of which 166 were female and 149 male. All individuals were originally tagged between 2001 and 2008, and were subsequently recaptured between 2002 and 2013. These data allowed us to identify the observed length (cm) at first capture *Lobs(t1)* and recapture *Lobs(t1+t2)*. The time at liberty (*t2*) and the measured age of the fish at recapture (*t1+t2*) was used to calculate the age of the fish at tagging (*t1*). We fit several different versions of the model to these data, these included: no random-effects, random-effects for the persistent differences in upkeep costs (*ki,s* only) for each sex, transient variation in growth ( only), and random-effects representing both persistent and transient variation in growth (*ki,s* and ).

Length at birth (*L0,s*), average upkeep costs (*μk,s*), the magnitude of persistent variation in growth (*σk,s*) and average energy acquisition rates (*γs*) were all assumed to be sex-specific in the application of this model. The magnitude of transient variation in growth (*σz*) and the magnitude of error when measuring length (*c*obs) were assumed to be constant for males and females. The simulation study illustrated that the model had little ability to identify the value of *Ψ*. We therefore fixed the value of *Ψ*=0. Preliminary exploration indicated that seasonal effects could not be explored because all tagging and recaptures are observed during a few months (December-March and a few in May) and hence seasonal and annual effects are confounded.

## 2.1 Simulation

A simulation study was done to ensure that the model could generate estimates of growth rates that are unbiased and reasonably precise. Four different scenarios were simulated including: no random-effects, random-effects for persistent individual variation in upkeep costs (*ki,s* only) for each sex, transient variation in growth ( only), and both persistent and transient variation in growth (both *ki,s* and ). A power analysis was done for each of the four scenarios where data were simulated for 50, 100, 250 and 500 recaptured individuals. This yielded 16 different simulation experiments. We did 200 replicates for each of the 16 combinations of scenario and sample size (*n*).

Average age at length zero (*t0,s*), average upkeep costs (*k­s*), and asymptotic maximum length (*L∞,s*) were taken from Dunn et al. (2006) and used to derive the values of the length at birth (*L0,s*) and average energy acquisition rate (*γs*) parameters used in the simulation study. These can be calculated as:

(7)

and

(8)

The length at birth (*L0,s*), average upkeep cost (*μk,s*), magnitude of persistent variation in growth (*σk,s*) and average energy acquisition rate (*γs*) parameters were all assumed to be sex-specific in the simulation study, the magnitude of transient variation in growth (*σz*) and the magnitude of error when measuring length (*c*obs) were not (Table 2, Table 3). The c.v. of observed growth (*cobs*) was set at the value in Dunn et al. 2006 in the scenario with no random-effects. In the remaining scenarios, the c.v. of observed growth (*cobs*), magnitude of persistent variation among individuals (*σk,s*) and magnitude of transient variation(*σz*,) were set at values that resulted in reasonable variation in individual length trajectories (*Table* 3).

For each individual in each of the scenario/power simulations, sex was sampled with replacement from the observed sex of individuals in the toothfish data set. The age at release, age at recapture and time at liberty were sampled independently from the observed individuals in the toothfish data set also, then one of the three variables was chosen at random and calculated using the other two variables and rounded to the nearest integer. For instance:

1. if age at first capture (*t1*) was chosen at random it was calculated as the age at recapture (*t1+t2*) minus the time at liberty (*t2*), i.e., *t1 = (t1+t2) - t2*;
2. if age at recapture (*t1+t2*) was chosen it was calculated as the age at first capture (*t1*) plus the time at liberty (*t2*), i.e., *(t1+t2) = t1 + t2*;
3. if time at liberty (*t2*) was chosen it was calculated as the age at recapture (*t1+t2*) minus the age at first capture (*t1*), i.e., *t2 = (t1+t2) - t1*.

Sampling in this way ensured that the distribution of each of the variables approximated those observed the real-world data set, without the need for sampling from complex joint distributions (e.g., copulas). The model was fit to the data for each of the 200 replicates in each of the 16 simulation experiments. Instead of reporting average energy acquisition rate (*γs*) we present the derived value median asymptotic length () which is calculated using Eqn. 6.

## 3 Results

## 3.1 Case study application

When applied to data for Antarctic toothfish in Ross Sea, the model without random-effects looks much like a standard von Bertalanffy growth curve for both females and males (*Figure 1*). The residual fit of this model is poor, given that many individuals have a positive/negative residual at both tagging and resighting, and therefore residuals are correlated for a given individual (*Figure 2*). The model without persistent or transient growth variation was the least parsimonious model of the four according to the Akaike information criterion (AIC; Akaike 1998; Table 4). Compared to Dunn et al. (2006) this model estimated a larger size at birth (*L0,s*) and larger median asymptotic maximum length (). Using Eqn. 7, the length at birth (*L0,s*) from Dunn et al. (2006) is -0.34cm and 3.98cm for females and males, respectively. Here the length at birth (*L0,s*) was estimated to be 46.51cm and 51.54cm (*Table 4*). Using Eqn. 6, the median asymptotic maximum length () was 216cm and 177cm for females and males, respectively (compared with 180.20cm and 169.07cm in Dunn et al. 2006). Our estimate of the magnitude of residual variation (*cobs*) was very similar at 0.111 (compared to 0.102 in Dunn et al. 2006).

The most parsimonious model (which has AIC 160 lower than the model without random effects; *Table 4*), included transient individual variation in growth rates (, *Figure 3*). In this model, the standard deviation in log-space of transient variation (*σz*) was 0.632, representing a 70% coefficient of variation in transient growth rates for each individual in each week. This model produced a tighter fit than the model described above (*Figure 4*). The distribution of residuals for each individual at tagging and recapture are approximately uncorrelated, with the exception of a few males that are either smaller than expected at tagging and larger than expected at resighting (or vice versa, Figure 4). Values for most estimated parameters were similar to those estimated in the model without the inclusion of any random-effects, however, the estimated c.v. of residual errors is lower (AIC-selected model: *cobs*=0.05 vs. model without random effects: *cobs* = 0.102) as over half of the variability is apportioned into the time-varying individual variation (*σz*, Table 4).

The model that included both persistent and transient variation in individual growth rates (*ks,i* and also ) resulted in no decrease in marginal likelihood, and hence was deemed to not be parsimonious by AIC. This occurred because the maximum likelihood estimate of the magnitude of persistent variation (*σk,s*) approached zero for both sexes.

## 3.2 Simulation

In the simulation study, estimates of average upkeep costs (*μk,s*) and average asymptotic maximum length () are unbiased in each of the four estimation models, and the precision (i.e., the distribution of estimates around the true value) gets tighter as the sample size (*n*) is increased from 50 to 500 individuals (Figure 5 and Figure 6). The size at birth (*L0,s*) is also unbiased for all sample sizes, but has very high imprecision (i.e., an SD of 15.1 and 15.7, for females and males respectively, when estimated with both transient and persistent variation in growth rates) given low sample sizes (i.e., *n=50* individuals). The precision improves markedly with increasing sample size (Figure 7), and has an SD of 2.6 and 2.7, for females and males respectively, for large sample sizes when estimating both persistent and transient variation (*n=500* individuals).

The magnitude of persistent variation among individuals (*σk,s*) parameter was approximately unbiased for all sample sizes, and relatively precise at sample sizes above *n=100*, with a small proportion of parameter estimates hitting the lower bound when sample sizes were small (Figure 8). Finally, the magnitude of transient variation (*σz*) was estimated to approach 0 for the majority of simulation replicates when sample sizes were low (*n=50)*, and particularly when estimating both persistent and transient variation (estimating variation in *ks,i* and ). However, by large sample sizes (*n=500*), the magnitude of residual variation was estimated well for either model (Figure 9).

Not all fits to simulated data had a positive definite Hessian, signifying that some combinations of simulation replicate and estimation model had parameters that were either (1) not converged or (2) not uniquely identifiable. When the estimation model included no random-effects, or random-effects for upkeep costs (*ki,s*) only, almost all model fits were positive definite. Fewer simulation replicates were positive definite when the model incorporated transient individual random effects (), particularly at lower sample sizes (see Figures 5, 6, 7, 8, and 9). However, we conclude that most models were positive definite for sample sizes above 250 individuals, and that non-positive definite models can be used as indication that the model is likely to be overfitted relative to the available data.

## 4 Discussion

In this study, we have used a case study application for Antarctic toothfish and a simulation experiment to demonstrate that it is feasible to simultaneously estimate persistent and transient variation in growth among individuals, as well as differences in growth rate between males and females and residual (measurement error) variation. Early studies incorporated variability in growth via individual variation in growth parameters (Sainsbury, 1980) or both time-dependent and time-independent variation in growth increments (Francis, 1988). Recent studies have developed mixed-effect models for estimating variation in growth rates over time and/or among individuals in wild or experimental settings involving fish (Shelton et al., 2013; Stawitz et al., In review; Thorson and Minte-Vera, In press; Vincenzi et al., 2014). Variation in growth rates is also an active area of research and method development in other ecological taxa (Brooks et al., 2013). However, our study is the first to our knowledge to apply these methods to a wild marine population. Our case study application suggests that transient variation among individuals accounts for up to half of the total variability in Antarctic toothfish.

By estimating persistent and transient variation among individuals and between sexes, we have largely eliminated the correlations in residual size between tagging and recapture, as was seen in the toothfish data set for the model without random effects. However, we have neglected two obvious types of variation in growth rates: persistent variation over space, and synchronous variation that is similar among individuals (i.e., annual variation). Populations may experience synchronous variation in growth rates for several reasons. For example, annual variation in water temperature may drive changes in metabolic costs as well as food availability in upwelling systems such as the California Current (Black et al., 2010), and this may cause all individuals to have elevated or depressed growth rates in a given year. Recent meta-analytic work supports the hypothesis that time-variation in average growth rates is the rule rather than the exception for marine populations (Thorson and Minte-Vera, In press). Similarly, many studies have illustrated persistent spatial differences in growth rates (Gertseva et al., 2010), e.g., where populations often have a smaller maximum size in warmer waters. Previous research has demonstrated the prevalence of spatial variation in growth (Gertseva et al., 2010) and condition (Thorson, In press). The modelling framework we present here could easily be modified to include spatial variation in growth rates, either among spatial strata or using geostatistical techniques (Shelton et al., 2014; Thorson et al., In press), but in this study we have chosen instead to focus on testing the individual, temporal, and sex-specific variation that we presented here. We hypothesize that including spatial variation would decrease the magnitude of among-individual variation in growth rates, because spatial variation would explain some portion of individual-level variation.

We note that our model (and results for Antarctic toothfish in the Ross Sea) does not account for the effects of fish handling and tagging on growth rates. Growth rates for untagged individuals may be higher because tagging is likely to cause physiological stress that depresses activity and metabolic levels (Dubula et al., 2005; Santos and Groeneveld, 2015; Xiao, 1994). Future studies could estimate the impact of tagging on growth rates by jointly analyzing CMR and other fishery data types (termed “integrated growth models”; Eveson et al. 2004). In particular, the length-frequency of fishery and survey catches and the direct ageing of hard parts from catches provide a separate source of information regarding size at age. These latter two sources of information do not generally provide information to discriminate between persistent and transient variation in growth rates (because each involves measuring size only once for each individual). However, both sources can provide complementary information regarding average growth rates for untagged individuals. We therefore believe that estimating persistent and transient variation in growth rates within integrated growth models is an important topic for future research.

Information regarding the magnitude of persistent and transient variation in growth is important for at least three reasons. First, stock assessment models and fisheries management strategies are routinely evaluated using simulation experiments (termed “management strategy evaluation”; Sainsbury et al., 2000). However, simulation experiments depend upon having information regarding plausible states-of-nature, which are used to simulate available data (Punt, 2008). Models estimating time-variation in growth can be used to simulate more plausible data for use in testing assessment methods. Second, estimation the magnitude of persistent variation in growth will lead to improved methods for approximating growth in population models. In particular, persistent individual variation in growth has recently been approximated by tracking individual platoons of fishes having the same age but different average growth rates (Taylor and Methot, 2013). Tracking abundance by platoon then allows stock assessment models to account for the impact of size-selective fishing on average growth rates. In particular, improved accounting for growth is likely to be important for models that are highly dependent upon growth information, e.g., length-based spawning potential ratio assessments (Hordyk et al., 2015). Third, previous research has indicated that growth estimates are biased when variation estimated via models that do not account for variation in growth (Sainsbury, 1980), and that these biases can in turn result in biased estimates of stock status and productivity (Punt et al., In review). We therefore hypothesize that improved treatment of transient and persistent individual variation in growth will improve estimates of growth rates obtained from CMR data sets, and that this improvement may result in improved estimates of fishery productivity.

## 5 Conclusions

In this study, we have estimated the magnitude of persistent and transient variation in growth rates among individuals in a wild marine population of Antarctic toothfish in the Ross Sea during 2001-2013, in addition to differences in average growth rates between males and females. Model selection suggests that transient variation is more significant than persistent variation among individuals during these years. Estimating transient variation decreased the coefficient of variation of residual (measurement error) variation by nearly half. Our simulation study corroborates that all models provide parameters estimates that are approximately unbiased and reasonably precise given sample sizes similar to those available here. Finally, we provide an R package *TagGrowth*, containing code to applying our estimation model to other data sets. We encourage future research comparing the magnitude of persistent and transient variation in growth among marine populations in different taxa and environments.

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Table 1: List and definition of symbols used in the text and equations with their units.

Table 2: Sex-specific parameter values used in all four scenarios in the simulation experiment.

Table 3: Sex-specific parameter values that vary among each of the four scenarios in the simulation experiment.

Table 4: Estimated parameter values in each of the four case study models by sex (s). **∆**AIC is the difference in Akaike Information Criterion between the current model and the most parsimonious model. Values marked with an asterisks (\*) are hitting the lower bound.

Figure 1: Observed and expected length (cm) at age (years) for individual female and male Antarctic toothfish using the model with no random-effects.

Figure 2: Standardized residual in length at tagging vs. the standardized residual in length at recapture (cm) for individual female and male Antarctic toothfish using the model with no random-effects. The standardized residual is calculated as where SD is the standard deviation.

Figure 3: Observed and expected length (cm) at age (years) for individual female and male Antarctic toothfish using the model with transient variation in growth ( only).

Figure 4: Standardized residual in length at tagging vs. the standardized residual in length at recapture (cm) for individual female and male Antarctic toothfish using the model with transient variation in growth. The standardized residual is calculated as where SD is the standard deviation.

Figure 5: Estimated value of the median upkeep cost (μk,s, years-1) in each of the simulation study experiments. The vertical red lines show the true simulated values of the parameter, the number of fits that are positive definite Hessian (pdH) are given in the top right of each panel.

Figure 6: Estimated value of the median asymptotic length (, cm) in each of the simulation study experiments (derived using Eqn. 6). The vertical red lines show the true simulated values of the parameter, the number of fits that are positive definite Hessian (pdH) are given in the top right of each panel.

Figure 7: Estimated value of the length at birth (L0,s, cm) in each of the simulation study experiments. The vertical red lines show the true simulated values of the parameter, the number of fits that are positive definite Hessian (pdH) are given in the top right of each panel.

Figure 8: Estimated value of the magnitude of persistent variation among individuals (σk,s) in each of the simulation study experiments. The vertical red lines show the true simulated values of the parameter, the number of fits that are positive definite Hessian (pdH) are given in the top right of each panel.

Figure 9: Estimated value of the magnitude of transient variation among individuals (σz) in each of the simulation study experiments. The vertical red lines show the true simulated values of the parameter, the number of fits that are positive definite Hessian (pdH) are given in the top right of each panel.