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CHARACTERISATION OF CANADIAN BLUEFIN TUNA CATCH USING COHORT SLICING AND AGE-LENGTH KEYS

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SUMMARY

Bluefin Tuna catch is currently characterized using cohort slicing which attributes a single age to fish of the same length. However, direct ageing of the Canadian catch between 2010 and 2013 has produced enough data that the catch can be characterized using an age-length key. In this analysis, age assignment based on cohort slicing is compared with an age-length key developed from the combined data. Age assignment is also compared between annual keys and a combined key.

RÉSUMÉ

La prise de thon rouge est actuellement définie au moyen du découpage des cohortes qui attribue un âge unique aux poissons de la même longueur. Cependant, la détermination directe de l'âge des prises canadiennes entre 2010 et 2013 a produit suffisamment de données pour que la capture puisse être caractérisée au moyen d'une clé âge-taille. Dans la présente analyse, l'attribution de l'âge sur la base du découpage des cohortes est comparée à une clé âge-taille élaborée à partir des données combinées. L'attribution de l'âge est également comparée avec des clés annuelles et une clé combinée.

RESUMEN

La captura de atún rojo se caracteriza actualmente utilizando el método de separación de cohortes que atribuye una sola edad a peces de la misma talla. Sin embargo, la determinación directa de la edad de la captura canadiense entre 2010 y 2013 ha producido suficientes datos, de tal modo que la captura puede caracterizarse utilizando una clave edad-talla. En este análisis, la asignación de edad basada en separación de cohortes se compara con una clave edad-talla desarrollada a partir de datos combinados. Se compara también la asignación de edad entre las claves anuales y una clave combinada.

KEYWORDS

Age-length key, Cohort slicing, Catch at age, Bluefin tuna

1. Introduction

In support of the Grande Bluefin Year Program's efforts to collect data that will address uncertainties in the stock assessment, many scientists have focused on determining the age composition of the Bluefin tuna population by directly ageing the catch. These direct ages can be used to assign an age to the catch provided associated lengths are also available. The standard approach has been to use cohort slicing which essentially assigns an age to each length. This approach does not recognize that similar sized fish may be quite different in age and as a consequence; dominant cohorts are smeared across the neighbouring ages as the cohort members grow in size. This problem is largely resolved when the catch is characterized using an age-length key. Consequently, it allows cohorts to be tracked through the fishery, improving our knowledge of the age composition and true status of the stock. That is the good news. The bad news is that to achieve this new level of clarity, an age-length key must likely be developed for each year of the fishery (ideally by fleet) unless the age at length assignment is invariant with time.

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Given that the direct ages are only available for the most recent years of fishing, we are obligated to assume that the assignment is time invariant if we wish to conduct the stock assessment using an age-length key. The other option is to use cohort slicing when direct ages are not available but this would likely introduce some interesting and unwanted patterns in the catch at age matrix around the time of the method switch.

In this analysis, the consistency of the age assignment by an age-length key was tested for a small number of years and the difference in age assignment between the standard approach and a key was also examined.

2. Methods

2.1 Data Source

The Bluefin tuna catch from the Canadian fishery was sampled from 2010 to 2013. The heads, labeled with a unique commercial tag number, were stockpiled by fishermen and co-ops, and then sampled by a field technician. Sampling consisted of extracting sagittal otoliths from Atlantic Bluefin tuna heads and taking snout length measurements (Busawon *et al.* 2013).

The preparation and ageing of the otoliths was conducted according to standard protocols (Busawon et al. 2015).

2.2 Analysis

All comparisons were performed using the direct age data from the Canadian catch grouped by 1 cm length bins. Age-length keys were developed for the 2011 to 2013 ages separately and for all years combined (2010 to 2013). There were not enough observations in 2010 to warrant the development of a key.

Each key was applied to the curved fork lengths used to build it, yielding expected ages. The symmetry of age agreement between the expected and corresponding direct ages was assessed using age-bias plots (Muir et al. 2008) and symmetry tests. The three tests used were the “unpooled” or Bowker's test (Hoenig et al. 1995), the “semi-pooled” or Evans-Hoenig test (Evans and Hoenig 1998) and the “pooled” or McNemar's test (Evans and Hoenig 1998). Each test is capable of detecting different forms of asymmetry. Also, the symmetry of the expected ages from each annual key was evaluated against the expected ages from a key based on all years.

The last sets of comparisons were between the expected ages from the four keys described above and the expected age from the growth curve derived by Restrepo *et al*. (2010). This growth curve is currently used to perform the cohort slicing.

The software that provided much of the support for the analysis was the FSA package in R (Ogle, 2015).

3. Results

All three symmetry tests indicated that the expected ages from the annual keys and a single key based on all the data were not symmetrical with the ages estimated using the growth curve ($p<0.001$). However all tests between the annual keys and the single multi-year key indicated that these age assignments were symmetrical ($p>0.2$). Finally, tests of symmetry between the direct ages and the ages estimated by a key could not detect significant differences in age assignment ($p>0.2$).

The bias between the direct age and the age assignment from the corresponding key is shown for individual years of data in **Figure 1**. Although the tests indicate no asymmetry, there is some tendency for the assigned age to be older than the direct age, especially for older fish (>17 y).

The bias between the assigned age from the keys and the age estimated by the growth curve is given in **Figures 2, 4, 6** and **8.** In all cases there is a significant negative bias when the age estimated by the growth curve is greater than 10 or 12 years and an indication of positive bias for ages less than 10 years. Consequently, the growth curve consistently over estimates the age provided by a key when fish are above 10 years and underestimates the age on younger fish. The respective keys are provided in **Figures 3, 5, 7** and **9**. They show a very narrow range of lengths being mapped to each age for the growth curve and a very wide range of potential lengths giving the same age using the keys. The keys are also less regular and can yield an expected modal age for successively greater lengths that do not necessarily increase unlike for the growth curve.

Lastly, the bias in age assignment between annual keys and a multi-year key (**Figure 10**) was negative for older estimated ages. Thus, the age assigned by the multi-year key was older than from the annual key yet as indicated by the tests, the asymmetry was not statistically significant.

4. Discussion

The analysis of the age assignment by an age-length key relative to the assignment by cohort slicing showed that the key provides younger ages than the growth curve with the discrepancy increasing from age 10 on. The performance of the key for younger fish could not be assessed due to their absence in the Canadian catch.

Each key based on a single year of data showed a tendency to over-age and yet these estimates were still younger than those provided by the growth curve. This tendency, while not a source of significant asymmetry, may be a function of a decreasing number of samples with increasing length bin value.

The agreement between the assigned age from the annual keys and those of the multi-year key indicates that it is possible to combine data from several years (3-5 y), though with more samples per year the uniqueness of each year may be more evident.

The very regular progression of ages with increasing length using the growth curve is in sharp contrast with what can be expected from keys based on a single year of data or even three. To some degree this lack of a regular pattern is natural but some of it is due to a lack of samples for some length bins, the small bin width (1 cm) and the presence of outliers. Consequently, additional sampling and tests of the sensitivity of the age estimates to changing bin size and mild smoothing of the age probability distribution at length should be examined.

The multi-year key applied to the historical catch data will lower the average age of the population across time. This has implications with respect to the assessed stock status. With fish reaching a given size at younger ages the intrinsic rate of population growth would need to increase and consequently the overall productivity of the stock as well.

5. Recommendations

1. Extend the analysis to younger fish.
2. Determine the effect of increasing length bin size.
3. Increase the samples for larger fish.
4. Look at the asymmetry in assigned ages for keys in different decades.
5. Look at the asymmetry in assigned ages for keys in different regions.
6. Test the effect of smoothing the age at length distribution.

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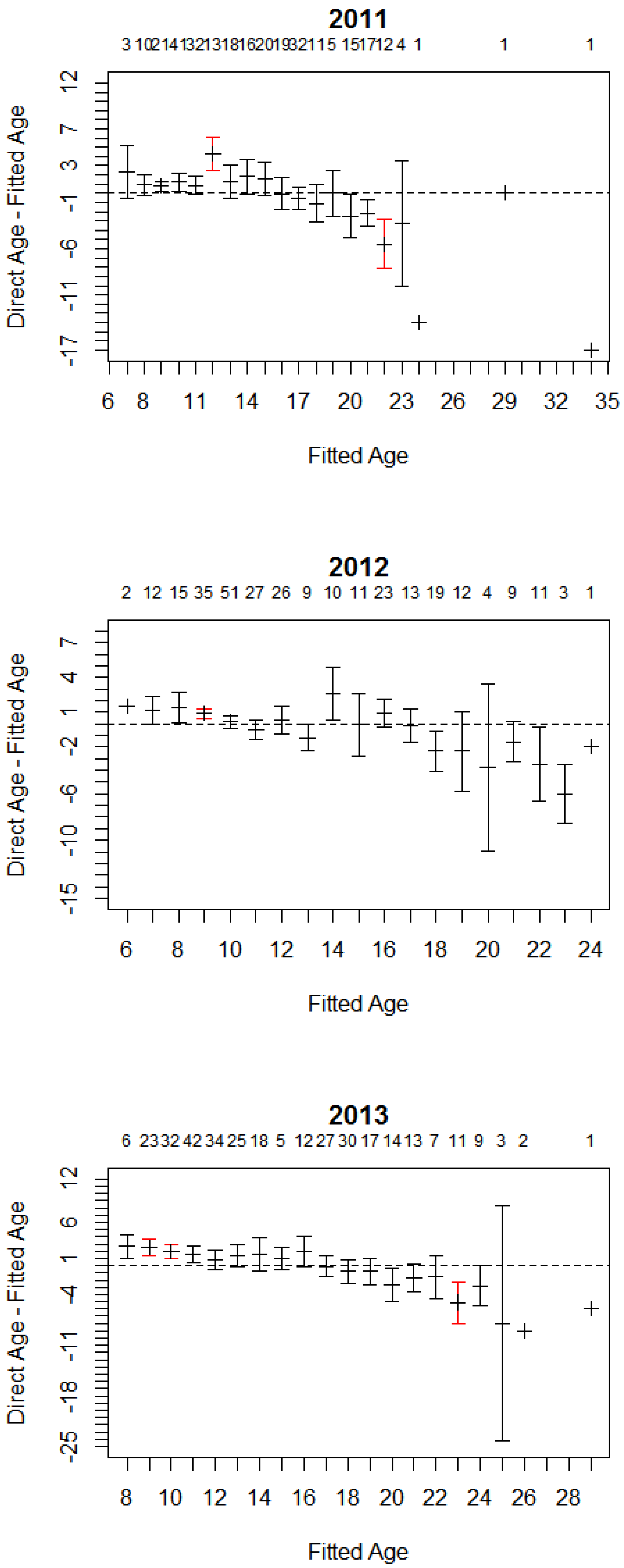


Figure 1. Age assignment bias between each annual key's expected age and the direct ages that generated the key. The plots show the lack of fit relative to the expected values where significant differences are shown in red.

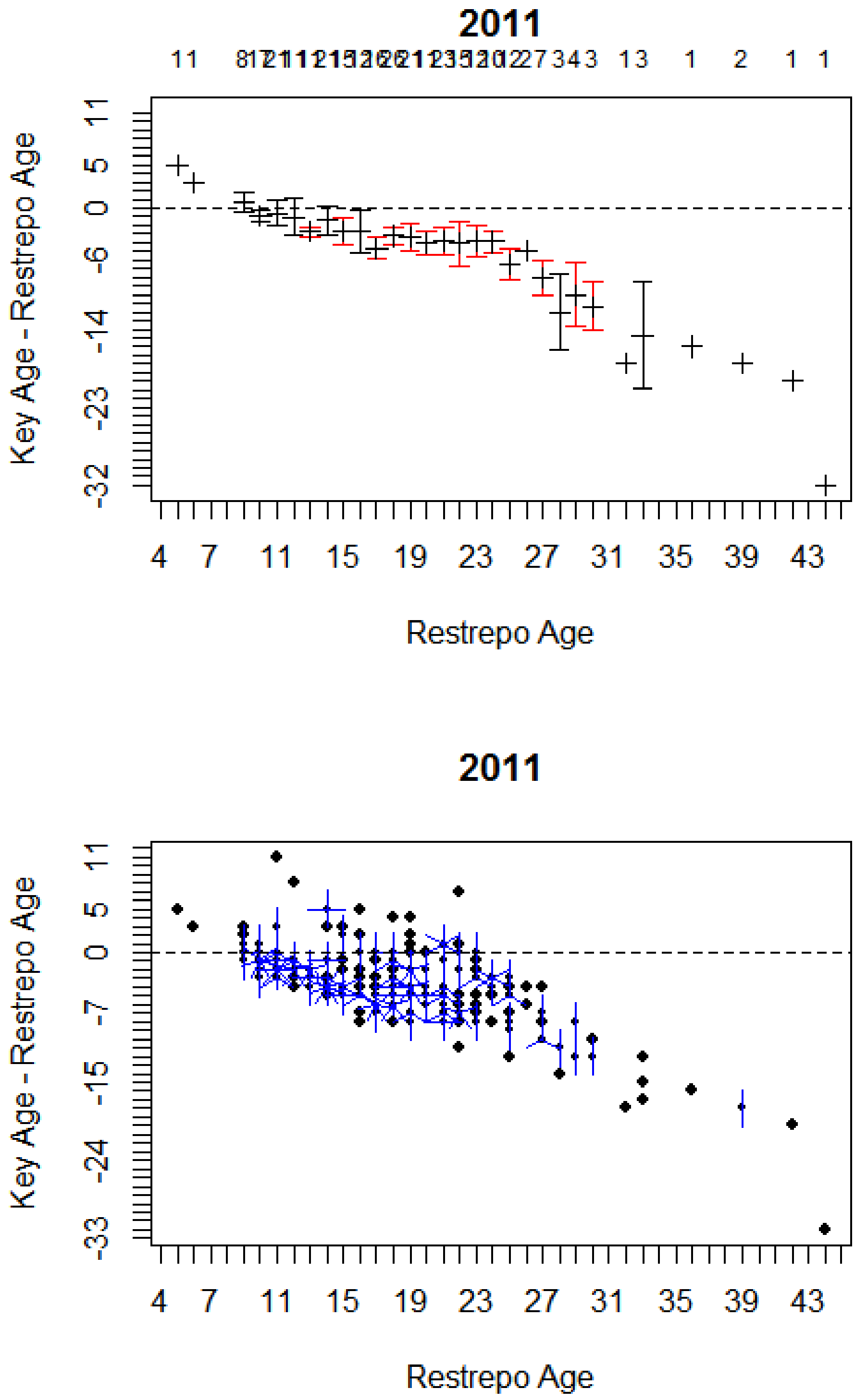


Figure 2. Age bias between the 2011 key ages and the growth curve estimates of age. The upper plot shows the difference in ages relative to the growth curve estimate with significant differences shown in red. The sunflower plot in the bottom panel shows the support in the data for the comparisons with the number of blue petals.

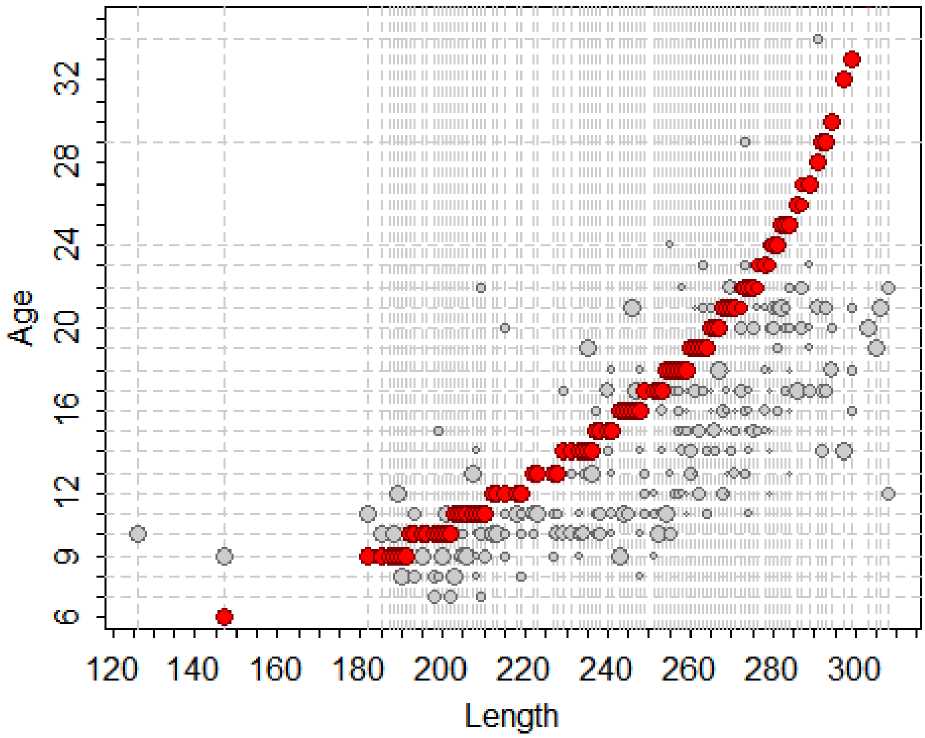


Figure 3. Proportion at age by 1 cm length intervals for the growth model (red) and the 2011 direct ages.

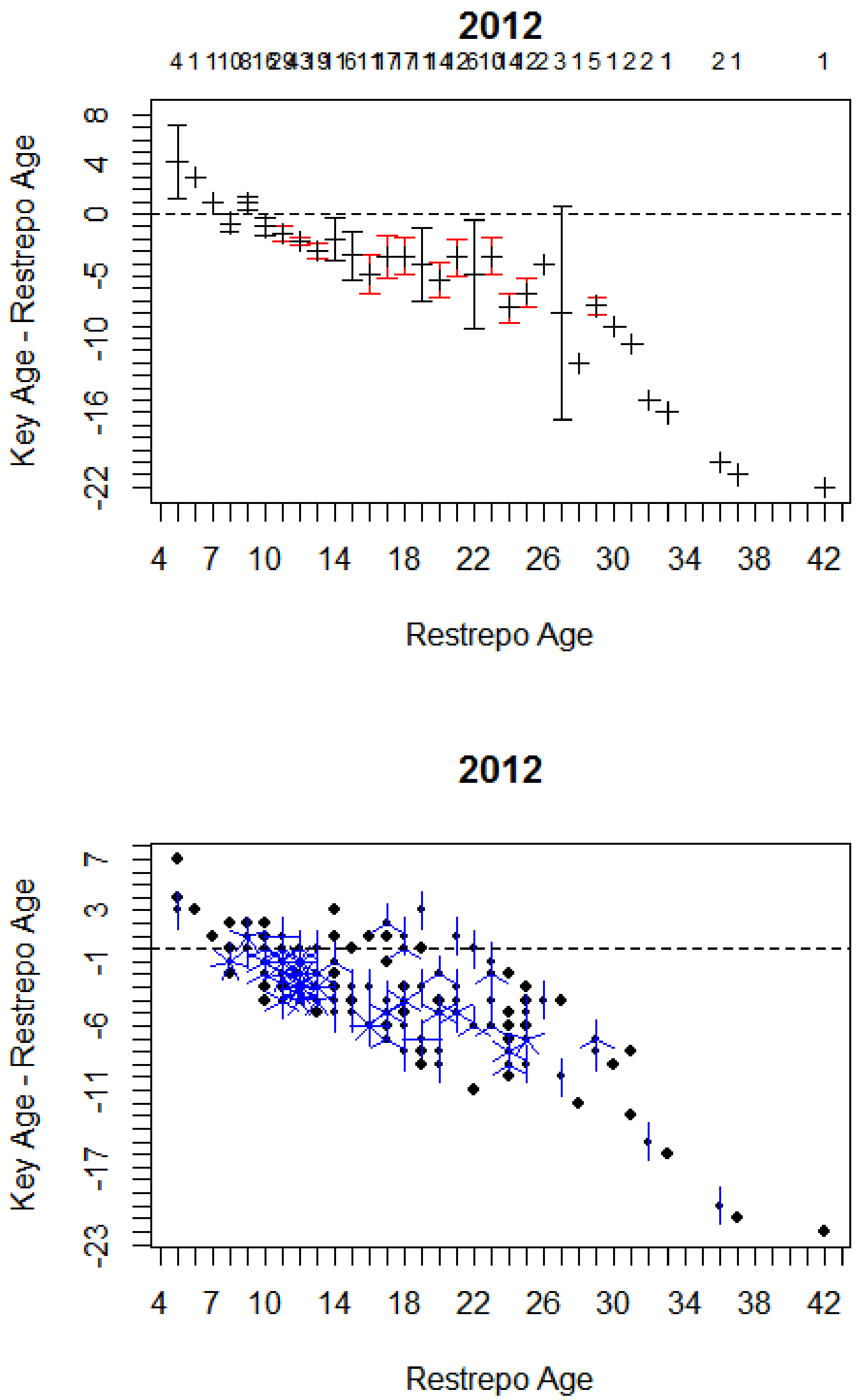


Figure 4. Age bias between the 2012 key ages and the growth curve estimates of age. The upper plot shows the difference in ages relative to the growth curve estimate with significant differences shown in red. The sunflower plot in the bottom panel shows the support in the data for the comparisons with the number of blue petals.

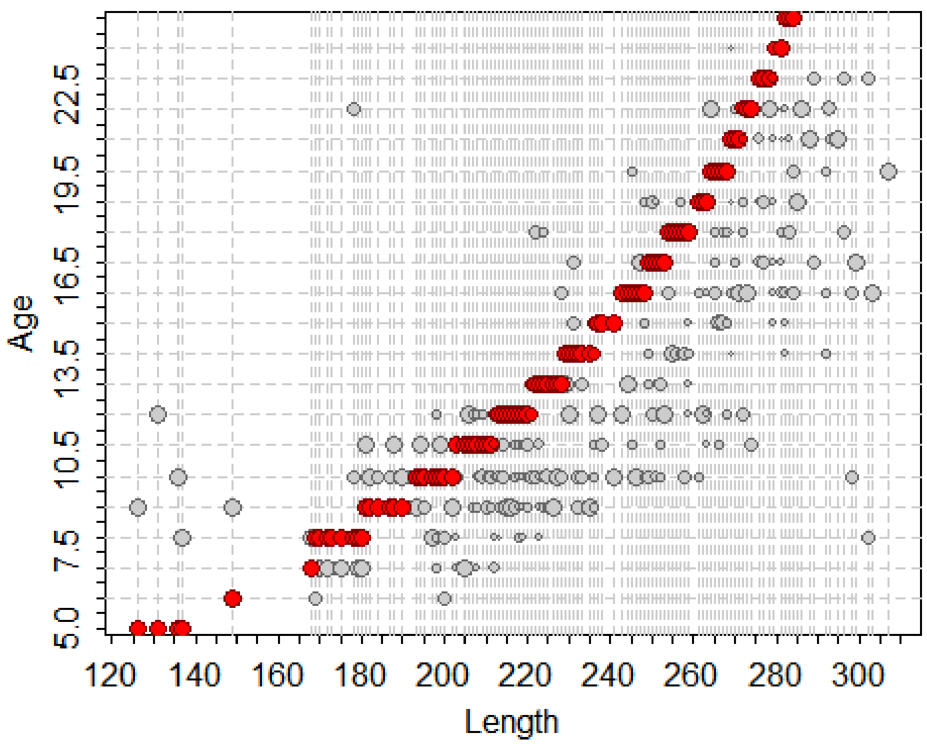


Figure 5. Proportion at age by 1 cm length intervals for the growth model (red) and the 2012 direct ages.

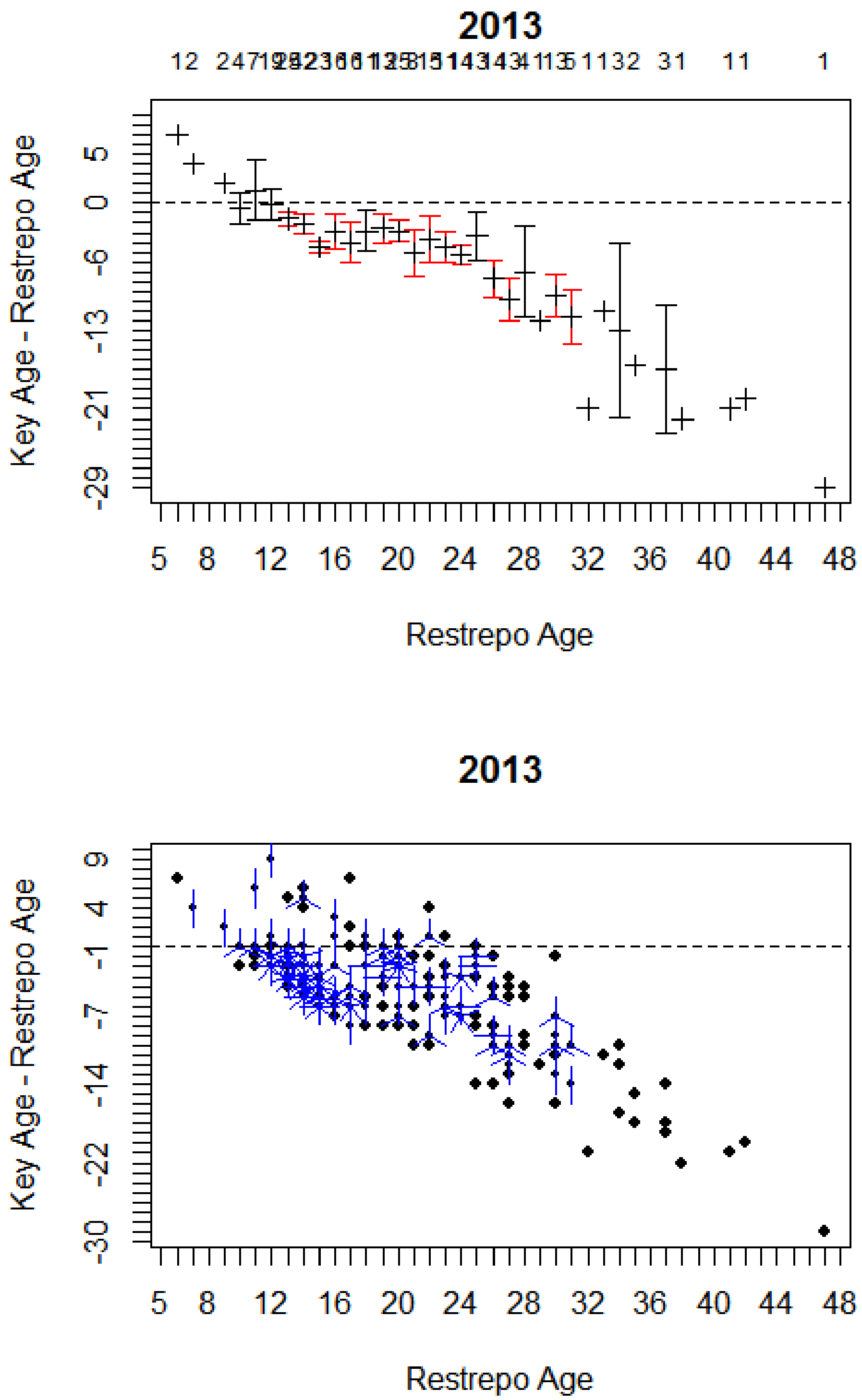


Figure 6. Age bias between the 2013 key ages and the growth curve estimates of age. The upper plot shows the difference in ages relative to the growth curve estimate with significant differences shown in red. The sunflower plot in the bottom panel shows the support in the data for the comparisons with the number of blue petals.

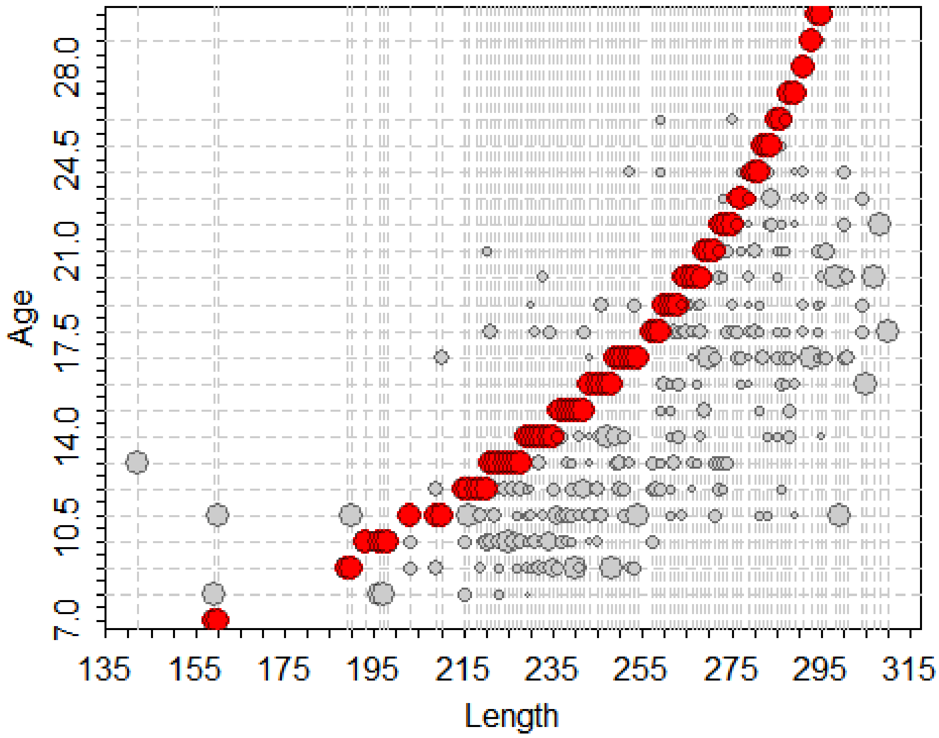
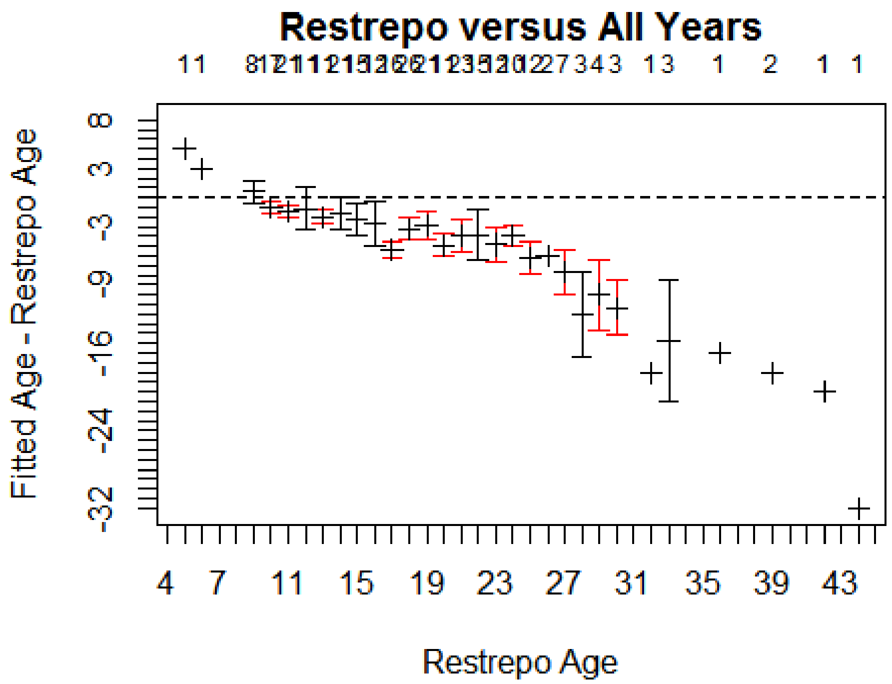


Figure 7. Proportion at age by 1 cm length intervals for the growth model (red) and the 2013 direct ages.



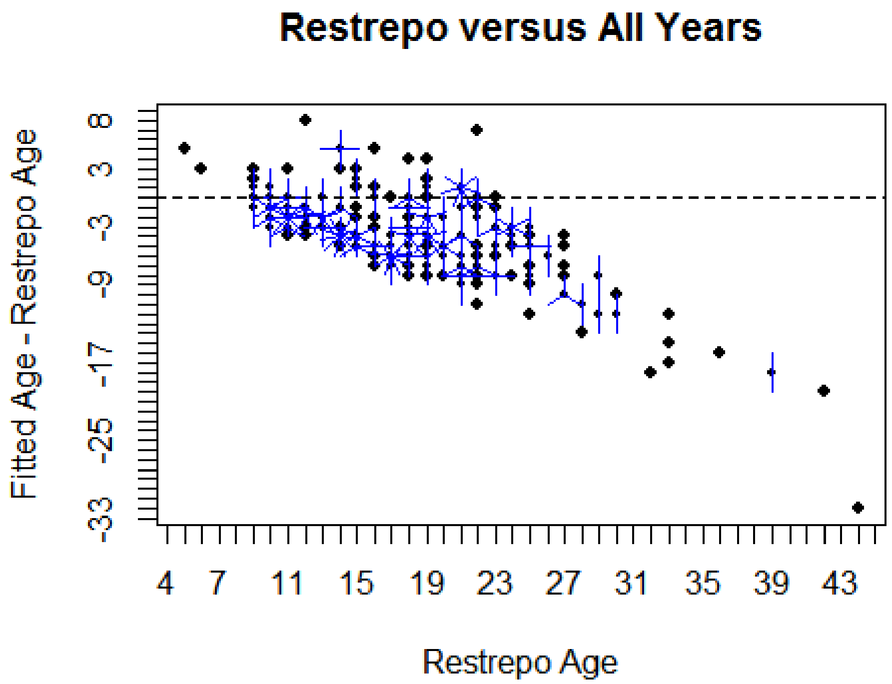


Figure 8. Age bias between the combined key expected ages and the growth curve estimates of age. The upper plot shows the difference in ages relative to the growth curve estimate with significant differences shown in red. The sunflower plot in the bottom panel shows the support in the data for the comparisons with the number of blue petals.

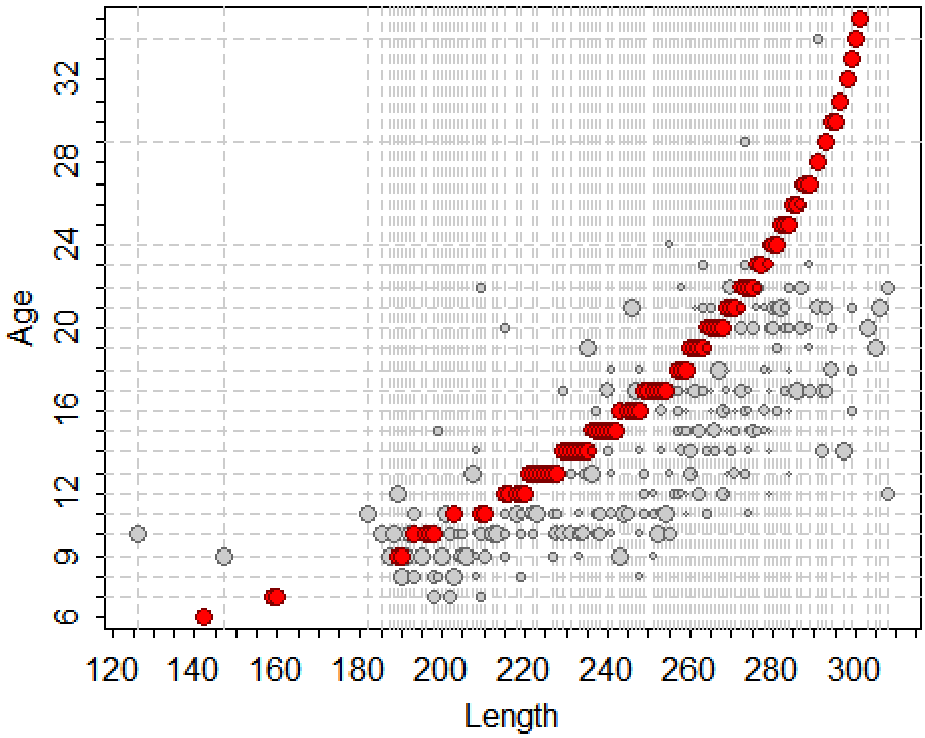


Figure 9. Proportion at age by 1 cm length intervals for the growth model (red) and the 2010 to 2013 direct ages.

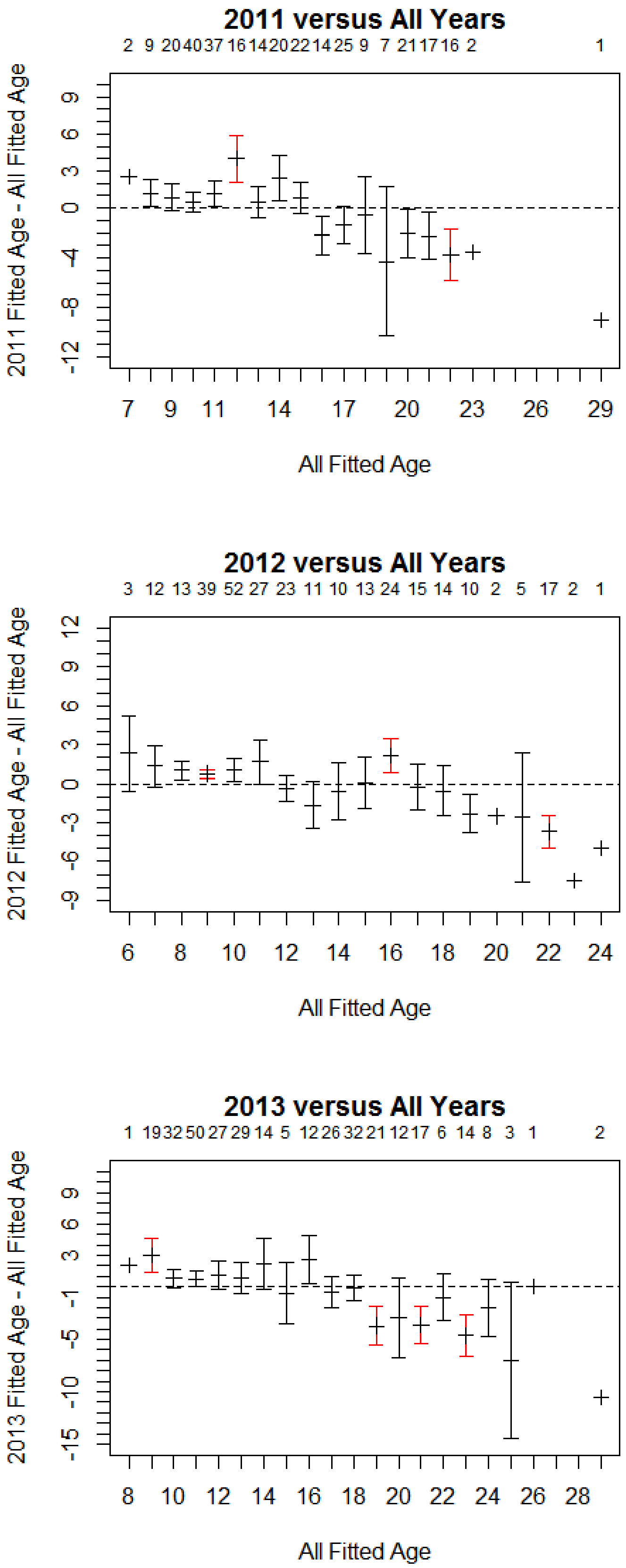


Figure 10. Age bias between the combined key expected ages and the expected ages from annual keys. The plots shows the difference in ages relative to the estimates from the combined data with significant differences shown in red.