

A flag for specimen not to be aged available in the Age_View

It is not worth ageing specimens that do not have complete data or data with errors. In the Age_view in the longline survey database under the field “ErrorDescription” that defines whether a specimen has the appropriate data that determines if a specimen should be aged. Here is a description of the responses in this column and their definitions.

“No error”

All biological data is available and length-weight combination is reasonable.

“Incomplete Specimen”

Specimen is either missing a weight, length, or sex.

“Above Standard” or “Below Standard”

This error means that there is a large deviation from the sablefish length-weight relationship fit from over 14 years of randomly sampled specimens (Figure 1). The deviation (residual) from this length-weight relationship is calculated as,

-
- If standardized residual is below (-0.0303), then weight is too large 99.9% of the time
 - If standardized residual is above 0.02617, then weight is too small 99.9% of the time

Justification

The pooled allometric relationship was calculated from ages from 1997-2010 ($n = 31,369$). The residuals were calculated as illustrated above because they showed the least tendency to select toward small or large fish. A plot of these residuals with the percentile intervals is shown in Figure 2. This method on average will select ~2 specimens per year as outliers.

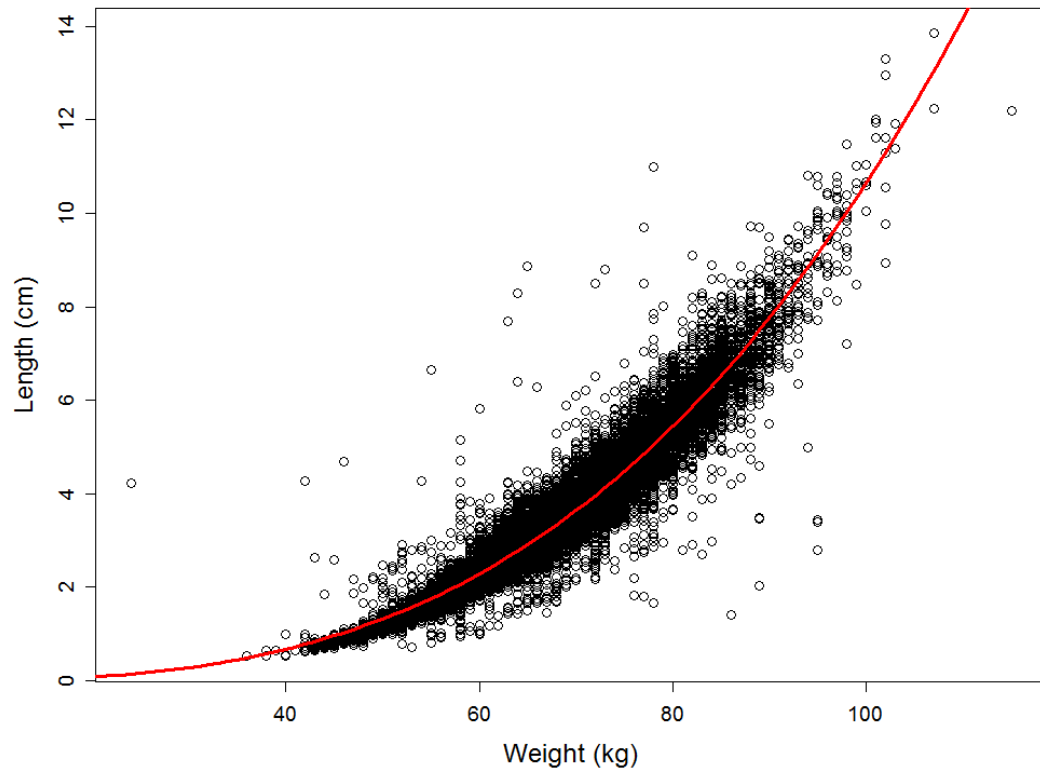


Figure 1. Pooled length-weight relationship from 1997-2010 for sablefish.

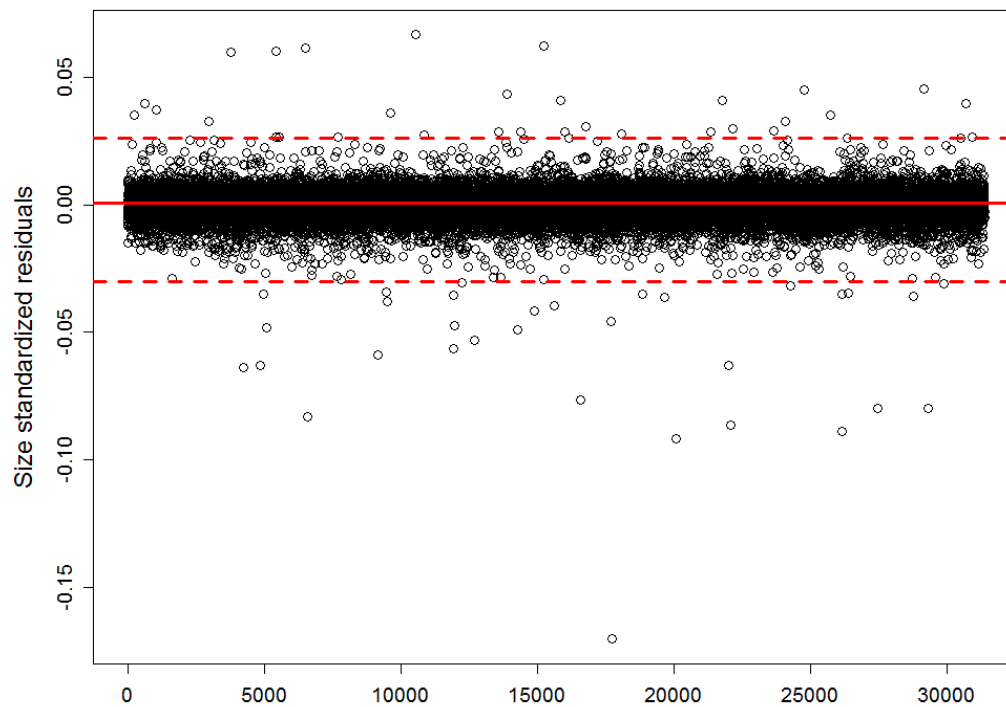


Figure 2. Distribution of size-standardized residuals from sablefish length-weight relationship from 1997-2010. Dashed redlines are the 0.1% and 99.9% percentiles, and the solid red line is the median.