Update of penguin model development

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Summary

Since the international workshop in December, work has concentrated on the problem of obtaining an appropriate statistical distribution for the variability of penguin adult mortality about the value suggested by the assumed relationship with pelagic abundance. The initial proposal of the beta distribution has been discarded as it has been shown that this does not work well. This progress is described in the Appendix.

The second important advancement is the incorporation of tag data in the process of estimating survival. Some initial exploratory analysis has been made on the raw data, described in document FISHERIES/2011/SWG-PEL/02.

Feedback concerning hypotheses about the relationships between food available and various penguin life-history parameters has been received. This is to be incorporated into the next stage of modelling.

Adapting the population dynamics model code to incorporate changes recommended by the December international workshop is in progress.

Reference

Robinson W and Butterworth DS. 2011. Proposed timing approach to penguin tag-recapture data. Document FISHERIES/2011/SWG-PEL/02.

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Appendix

Revised statistical model for variability in penguin annual adult mortality

We have found that using the beta distribution for adult survival will not serve our purposes in the Robben Island case, since a unimodal beta distribution can only have a very small variance when the mean is close to the boundary. This gives a high weight to years in which survival values want to go close to the maximum, which itself drives estimates towards the upper boundary. This is undesirable since it implies that when prey biomass is high, survival can only be very close to the maximum. Subsequently, the following approach has been explored and found to work satisfactorily.

Set

$$S_y = e^{-M_y}$$

where M_y is the annual natural mortality rate, modelled as follows:

$$M_y = M_{min} + \left[M_{min}^* + f(B_y) \right] e^{X_y}$$

where X_y is distributed $N\left(0, \sigma_y^2\right)$, and

$$\sigma_y = \sqrt{e^{\tilde{\sigma}^2 / \left(M_{min}^* + f(B_y) \right)^2} - 1}$$

Thus we have a log-normal random effect, but since the σ_y depend on the biomass B_y, the M_y distributions will have exactly the same standard deviation. This is useful since data related to each year receives roughly equal weighting, and, when projecting, high biomass does not force low mortality.

The reason that the M_{min}^* term is introduced is that when calculating M_y the possibility that the term additional to M_{min} could go to zero is excluded. The lower bound on achieved M_y remains M_{min}, but the lower bound on the median of its distribution is $M_{min} + M_{min}^*$.

The model currently uses the following:

$$\tilde{\sigma} = 0.1$$

$$M_{min} = 0.03$$

$$M_{min}^* = 0.02$$

$$f(B_y) = \left(a + \frac{B_y}{b} \right)^{-n}$$, where values tried are $n = 1$ (see Figure 1) and $n = 2$ (see Figure 2).
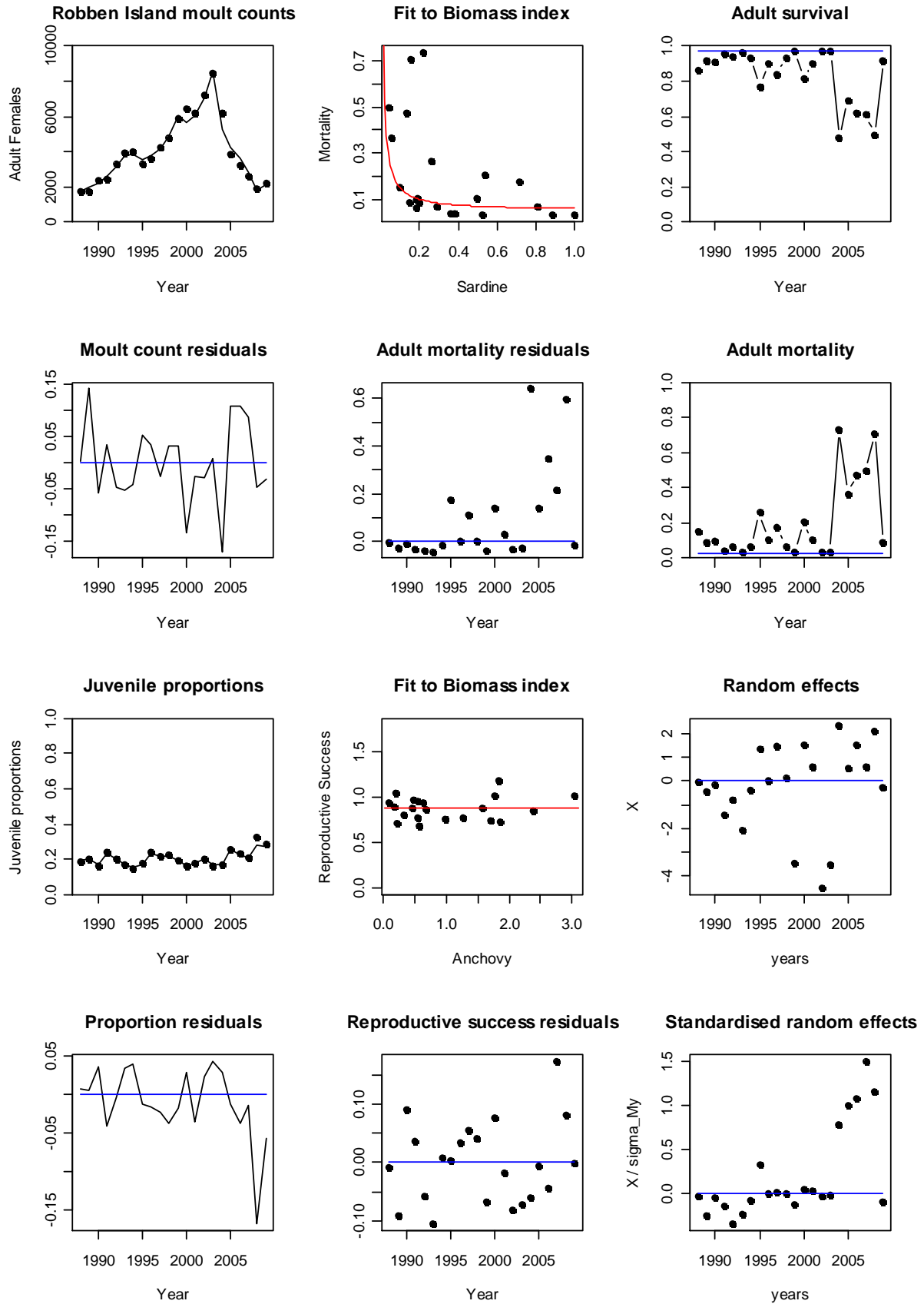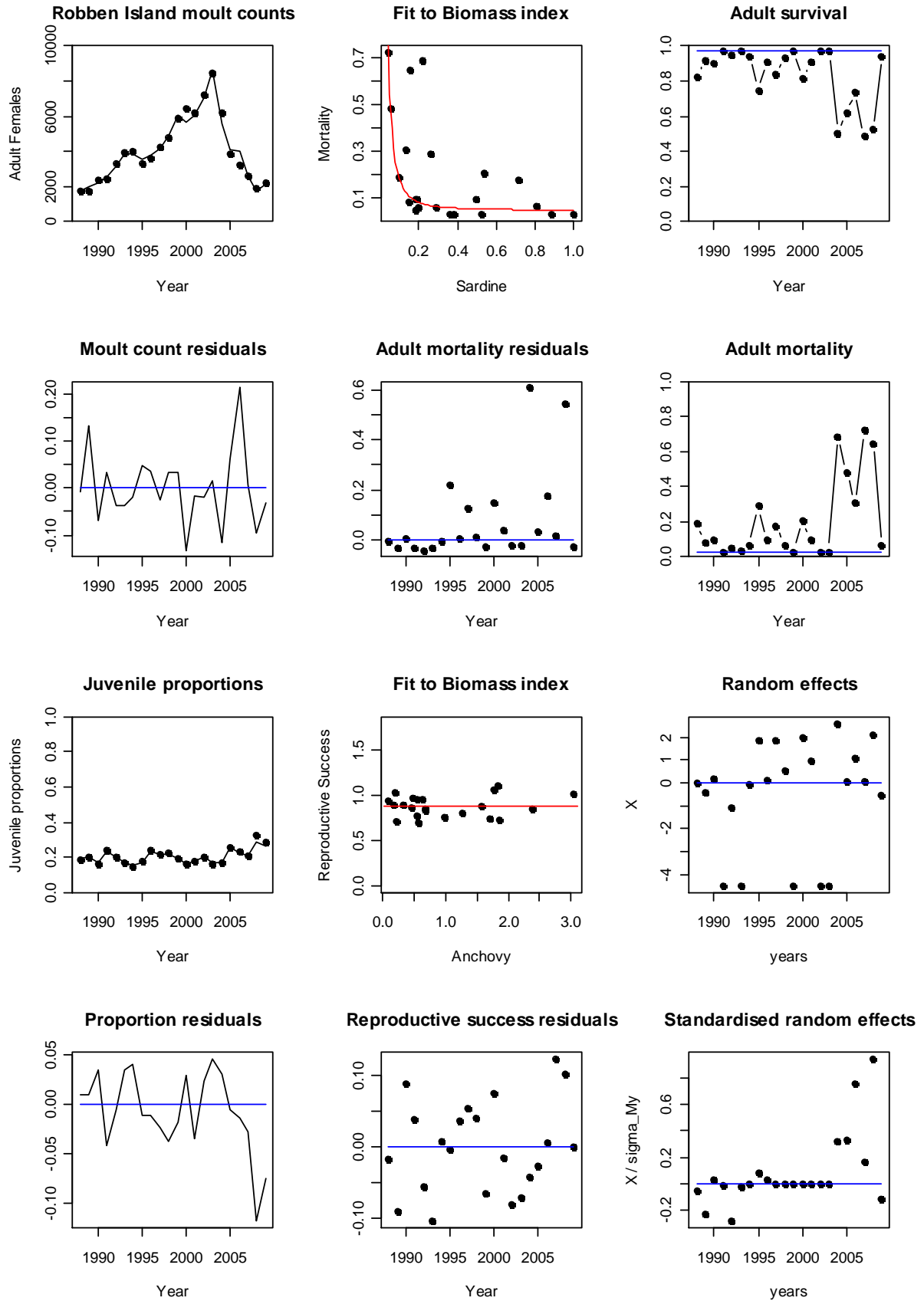
Figure 1: $n = 1$. Random effects are on adult mortality.

Figure 2: $n = 2$. Random effects are on adult mortality.