#### Modeling growth while fitting simultaneously to direct aging and tag-recapture data: example with bigeye tuna

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# Background



- Two most common ways of estimating fish growth
  - Age-at-length data (direct readings of skeletal parts)

$$L = L_{\infty} \left[ 1 - e^{-K(t-t_0)} \right]$$

Length increment data from tag-recapture experiments (Fabens 1965)

$$\Delta L = (L_{\infty} - L)(1 - e^{-K\Delta T})$$

- Growth parameters generated from both methods are not comparable (Sainsbury 1980; Francis 1988)
  - Curves are fitted using different error structures
  - L@A: residuals between observed L@A and expected L@A
  - Tagging: residuals between observed size inc. and expected at different time intervals



# An integrated model



- Maximum likelihood approaches exist that can model the joint density of the release and recapture lengths (Laslett et al. 2002; Eveson 2004)
- For example, if we use the VB the assumed growth curve for the fish is:

$$L_t = L_{\infty} \left[ 1 - e^{-K(\mathbf{A} - t_0)} \right]$$

A = t, is the age of each fish and treated as a random variable with density p(.) and whose parameters will be estimated in the model





 For a fish *i* tagged at time t<sub>1</sub> with released length L<sub>1</sub> and recaptured at t<sub>2</sub> with L<sub>2</sub>

$$L_{1,i} = L_{\infty} \left[ 1 - e^{-K(\mathbf{A}_{i} - t_{0})} \right]$$

$$L_{2,i} = L_{\infty} \left[ 1 - e^{-K(\mathbf{A}_{i} + \mathbf{t}_{2,i} - \mathbf{t}_{1,i} - \mathbf{t}_{0})} \right]$$

• The joint distribution of  $L_{1,i}$  and  $L_{2,i}$  can be integrated over A:

$$h(L_{1,i}, L_{2,i}) = \int h(L_{1,i}, L_{2,i}|a)p(a)da$$

This can be done using AD Model Builder!









#### Example with BET







### Alternative approaches



- Random effects
- Bayesian (MCMC)
- Penalized likelihood approach







- Use new curve in Stock Synthesis
- Request implementation of penalized likelihood approach in Stock Synthesis

