

# Estimating size-transition matrices in statistical catch-at-size methods

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# Objectives

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1. Develop an approach for computing size-transition matrices that explicitly allows for individual variation in growth. ✓
2. Estimate size-transition matrices for golden king crab in the Aleutian Islands.
3. Use simulation to evaluate:
  - a. the bias in assessment outcomes caused by ignoring individual variation and stochasticity in growth,
  - b. the relationship between bias / precision and sample size for assessments based on size-transition matrices, and
  - c. the implications of the choice of the number of size-classes when conducting size-structured stock assessments,
4. Develop recommendations for best practices when conducting size-structured stock assessments.
5. Implementing in GMACS. !



# Stage 1: Deterministic analysis-I

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It is common to base the size-transition matrix on a formula such as:

$$X_{i,j} = (L_j)^{\alpha_i} e^{-\beta L_j} / \sum_k (L_k)^{\alpha_i} e^{-\beta L_k}$$

where  $\alpha_i$  is the expected growth increment based on a length at the midpoint of size-class  $i$ ,  $\beta$  is the rate parameter (and depends on the CV), and  $L_k$  is upper bound of size-class  $j$ .

The likelihood for this case is:

$$\prod_k [X]_{i_k, j_k}^{T_k}$$

# Stage 1: Deterministic analysis-II

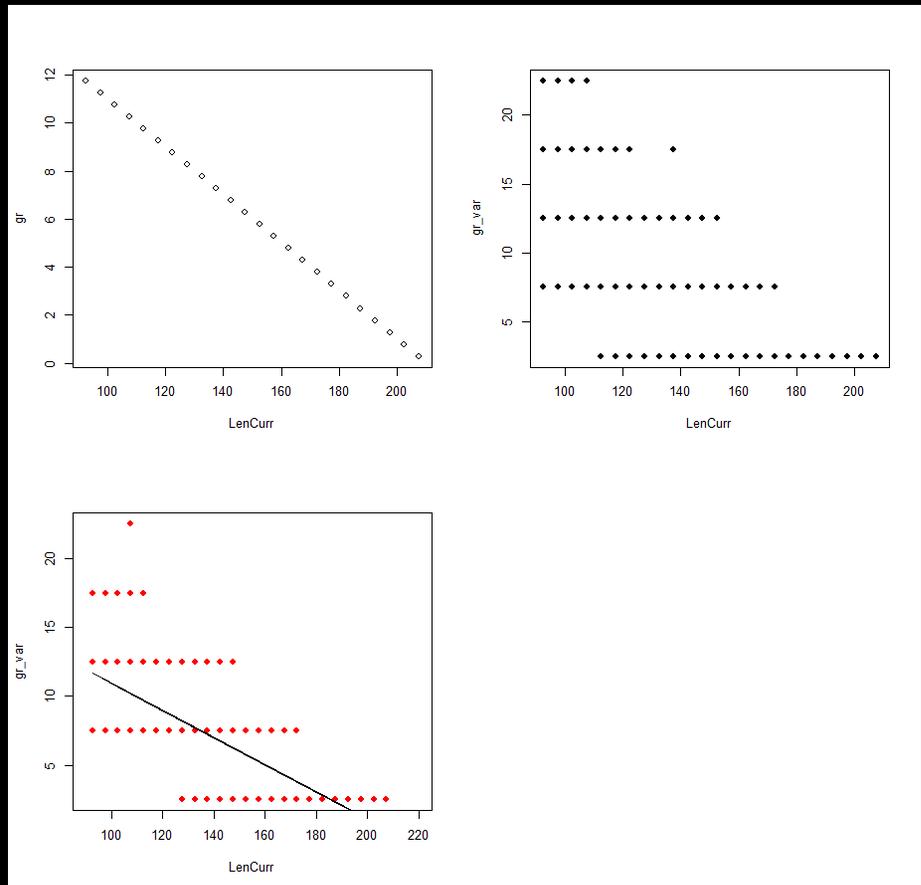
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To test the overall approach, we conducted a “deterministic” analysis, i.e. generated a very large number of data points (100,000), and evaluated whether the estimator can replicate the parameters of the size-transition matrix.

# Results-I

Case 1: All releases at the mid-point of the size-class and the growth increments are all multiplies of the size-class width

This case works fairly well. The values for the parameters of the size-transition matrix (two to define the expected growth increment and one to define the CV of the growth increment) are returned almost exactly.



# Results-II

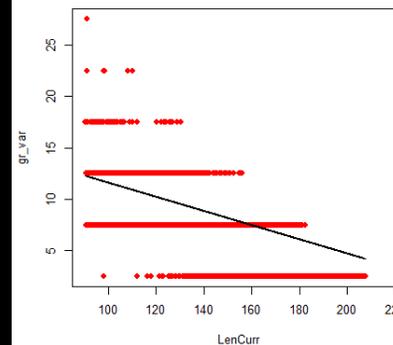
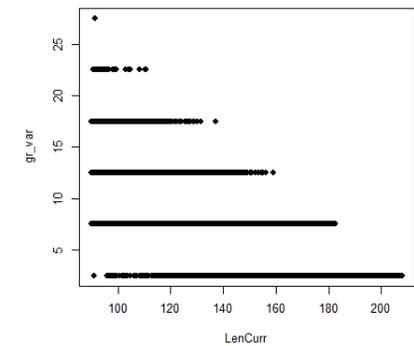
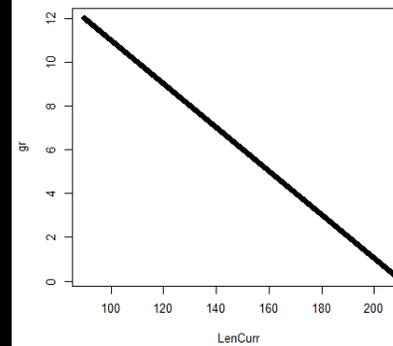
Case 2: All releases are random within the release size-class and the growth increments are all multiples of the size-class width

There is now bias:

True / estimated  $L_\infty$ : 210.41; 267.66

True / estimated  $\kappa$ : 0.105; 0.07255

True / estimated CV: 0.2617; 0.4089



# Results-III

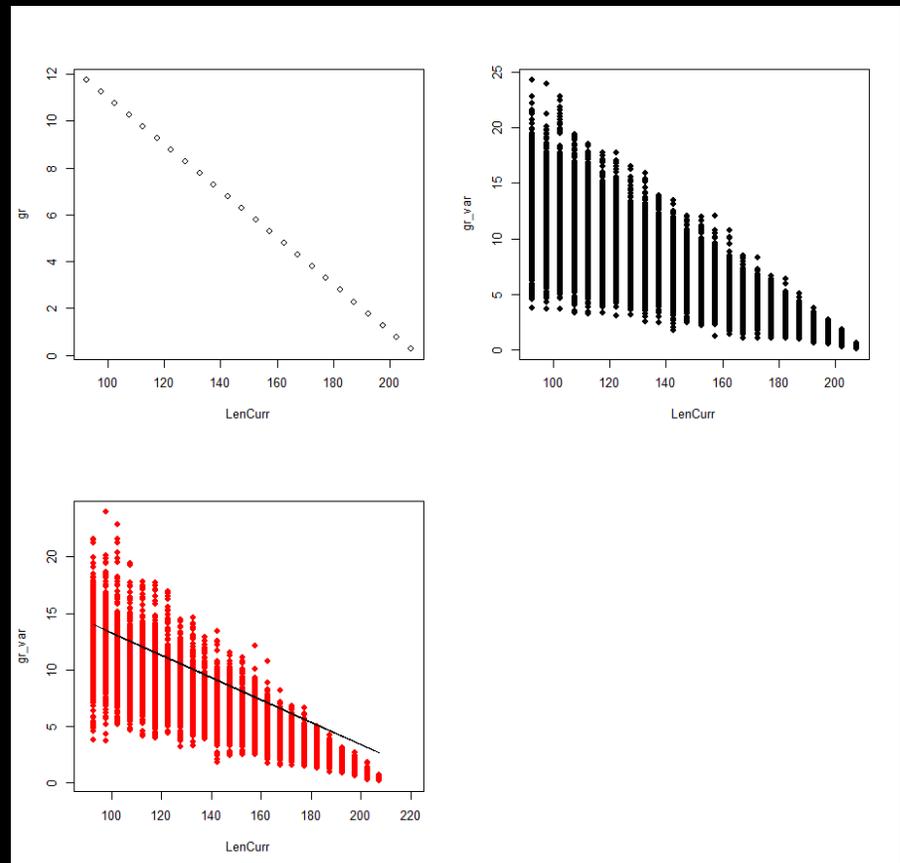
Case 3: All releases at the mid-point of the size-class and the growth increments are random from a gamma distribution

There is now bias:

True / estimated  $L_\infty$ : 210.41; 233.76

True / estimated  $\kappa$ : 0.105; 0.104

True / estimated CV: 0.2617; 0.2607



# Results-IV

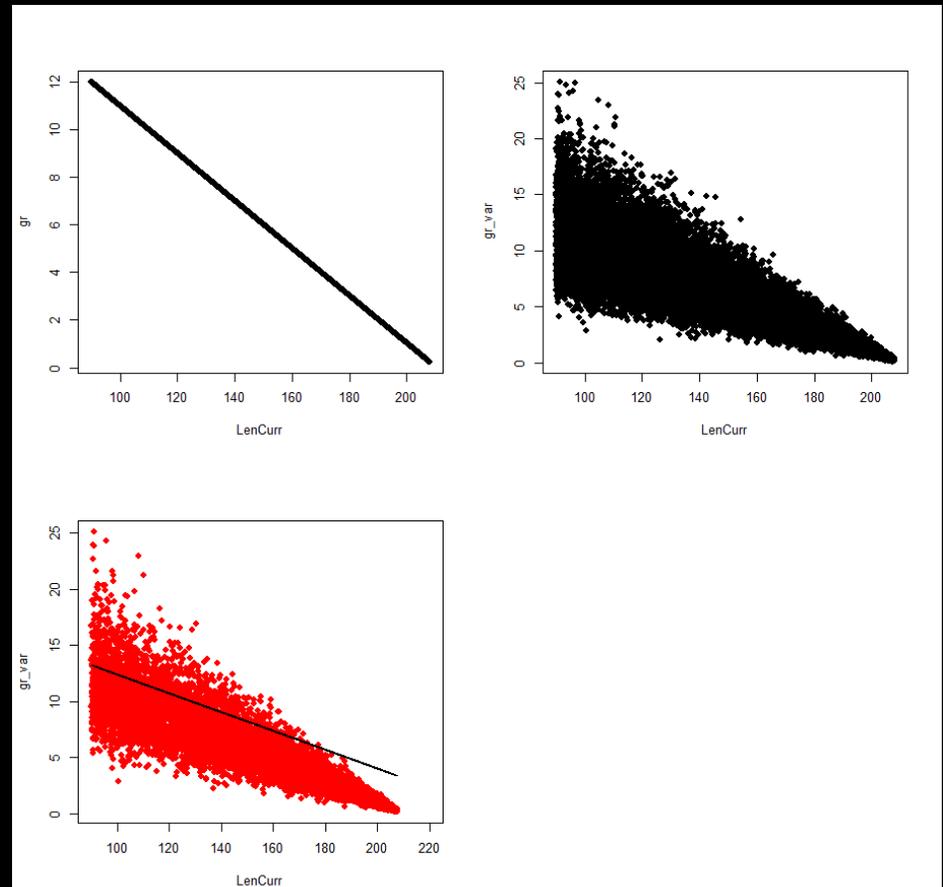
Case 4: All releases are random within the release size-class and the growth increments are gamma samples

There is now bias:

True / estimated  $L_\infty$ : 210.41; 248.38

True / estimated  $\kappa$ : 0.105; 0.08725

True / estimated CV: 0.2617; 0.3316



# Stage 1: Deterministic analysis

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Initial conclusions / comments:

- Assuming all animals are at the mid-point of the size-class of release may be the main cause of bias.
- We do not know if the **size-transition matrix entries** are biased.
- Ignoring that increments are continuous leads to bias, but (perhaps) less than assuming all animals are at the mid-point of the release size-class.
- This analysis ignores selectivity (at release and recapture) and tags that are out for multiple years.
- We haven't tried an estimator that integrates over the size-class of release and recapture.

# Stage 2: Full simulation analysis

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The steps for generating a single release-recapture data point are:

1. Generate the animals'  $L_{\infty}$  and  $\kappa$ .
2. Generate an initial size (well below the size at which animals will be tagged)
3. Compute the selectivity of the animal and see if it was “released”, if so mark it as released, if not got to step 1.
4. Grow the animal (deterministic when there is individual variation in growth, but we can also allow for stochasticity) for one year
5. Generate whether the animal dies of natural causes. If so STOP.
6. Compute the selectivity of the animal and see if it was “recaptured”, if so mark it as recaptured, save the record and STOP.
7. Go to step 4.

# Stage 3: Full simulation analysis

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We will test the following estimation methods

- All individuals follow the same curve with error; initial size is the midpoint of the size class
- All individuals follow one of three growth curves with error through the platoon method; initial size is the same as before
- All individuals have their own growth curve by letting  $L_{\infty}$  vary; variation in initial size
- All individuals have their own growth curve by letting  $\kappa$  vary; variation in initial size
- All individuals have their own growth curve by letting  $\kappa$  and  $L_{\infty}$  vary; variation in initial size

# If you are bored with crab assessments (and hence life itself)

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[https://puntapps.shinyapps.io/tagtest/?](https://puntapps.shinyapps.io/tagtest/)

It is not YouTube but what is?

P.S. No cat videos..