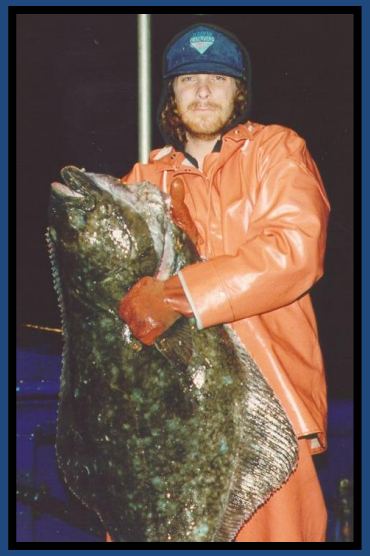
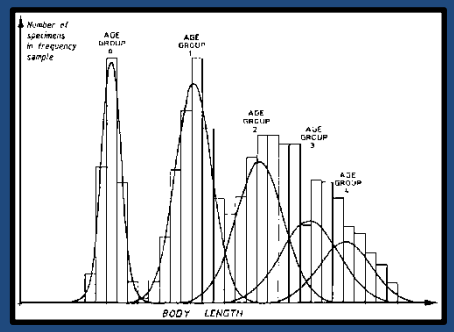
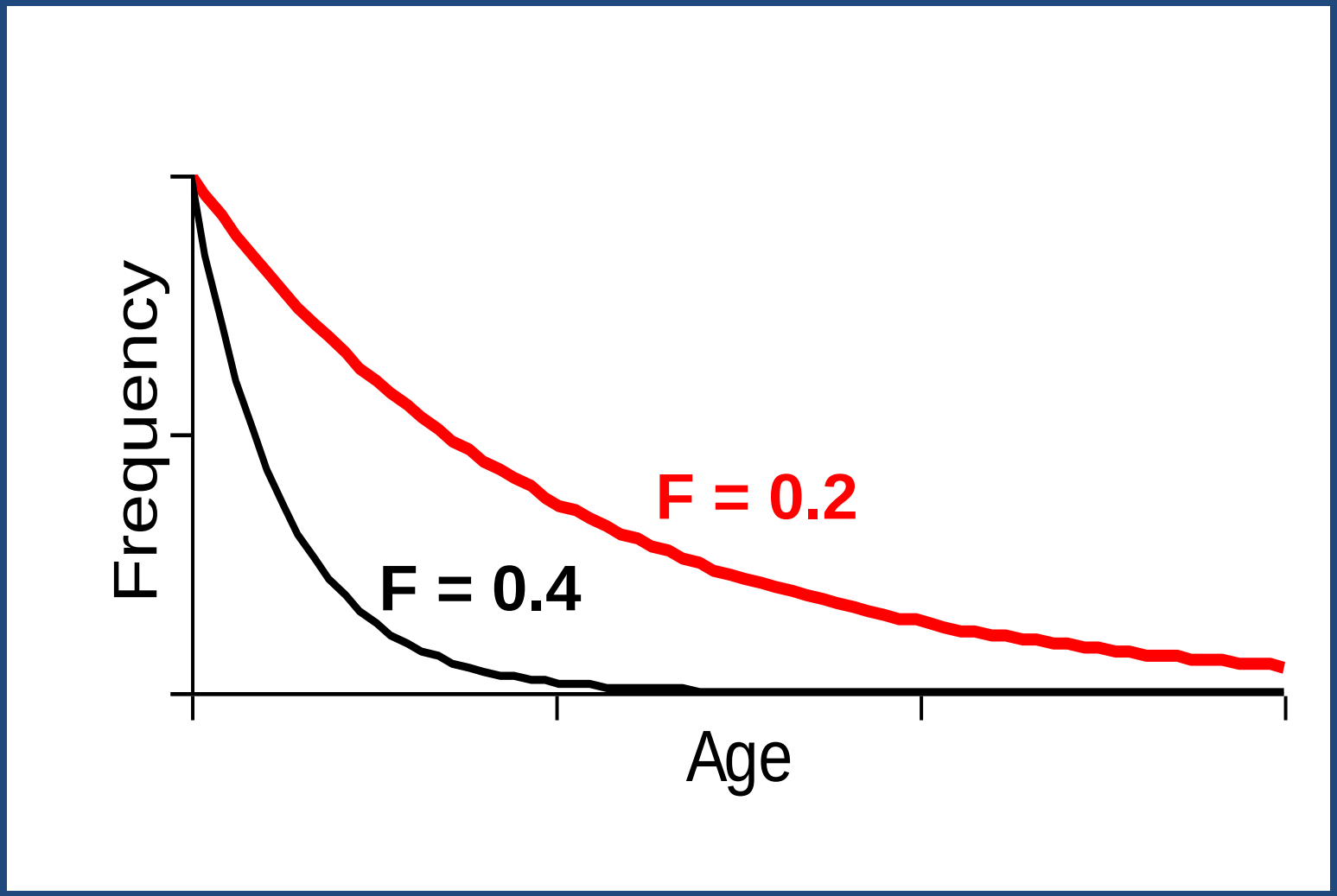
Assessment & Management of Fisheries Based on Mean-Size Statistics: an expansive methodology



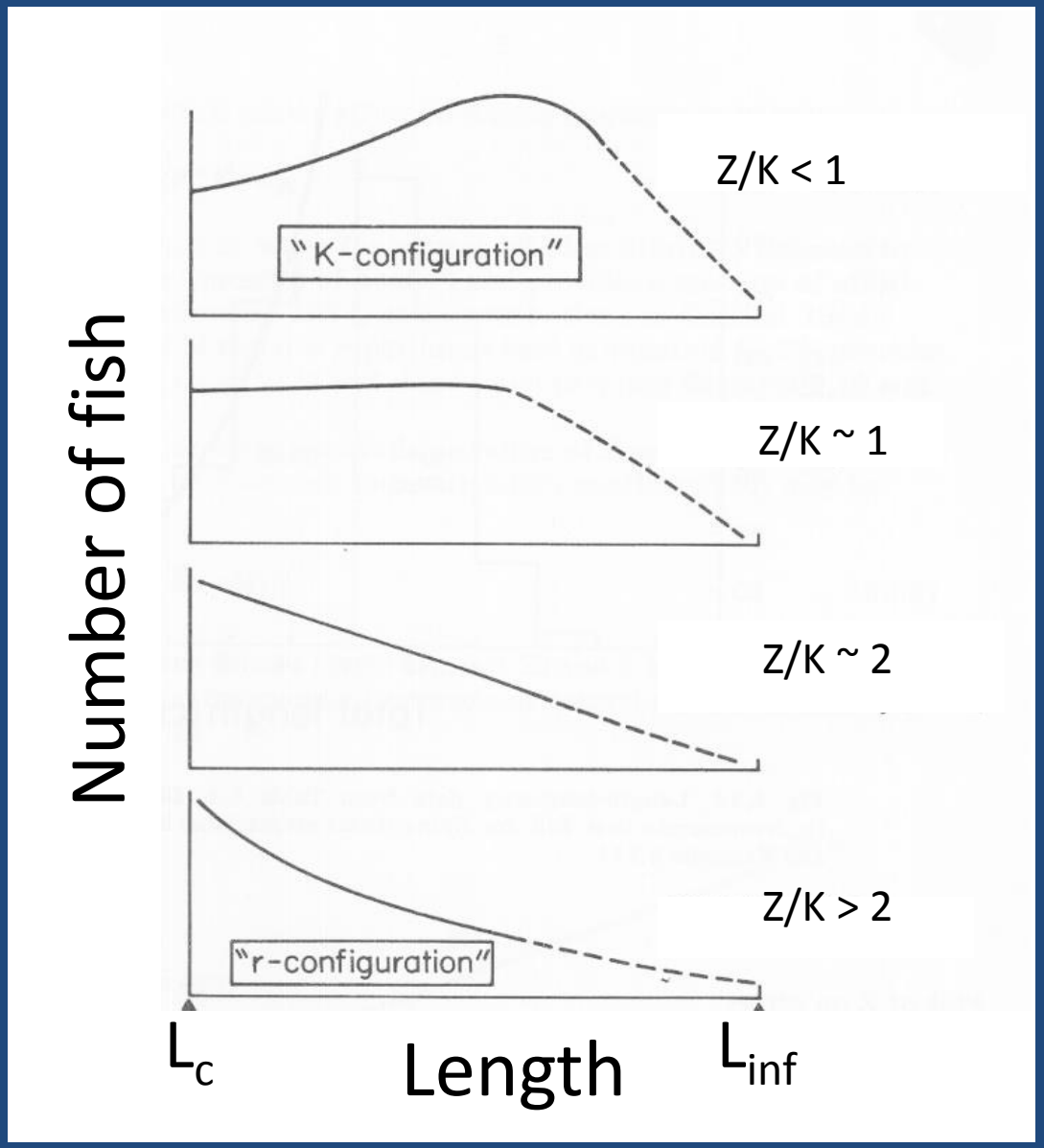


John M. Hoenig, Amy Y.-H. Then, & Todd Gedamke, Meaghan Bryan, Jon Brodziak, Quang C. Huynh, John F. Walter and Clay Porch

More Fishing → Less Older Fish



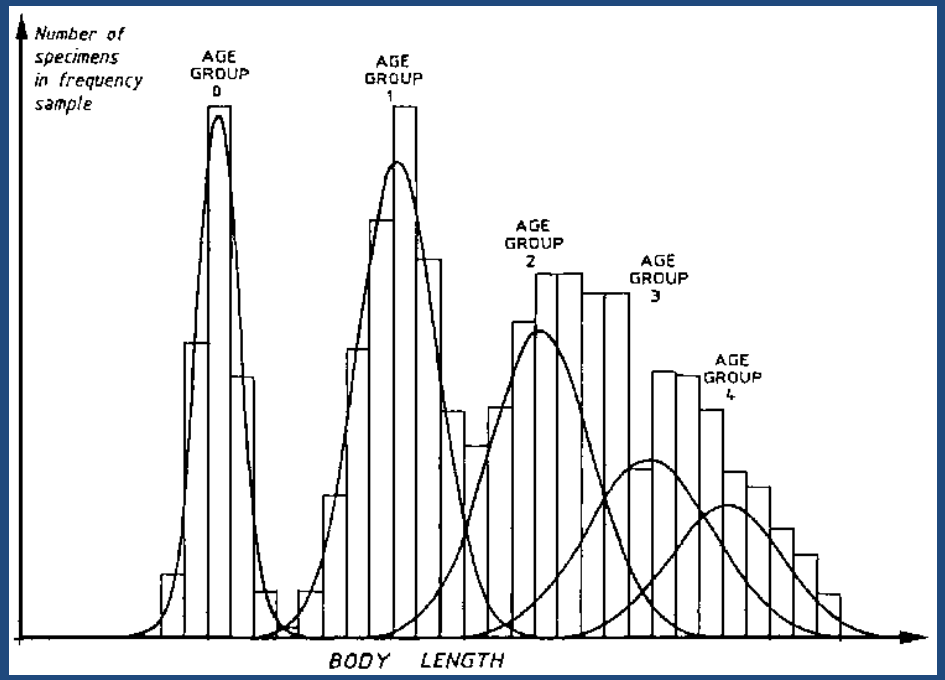
More Fishing → Less Large Fish



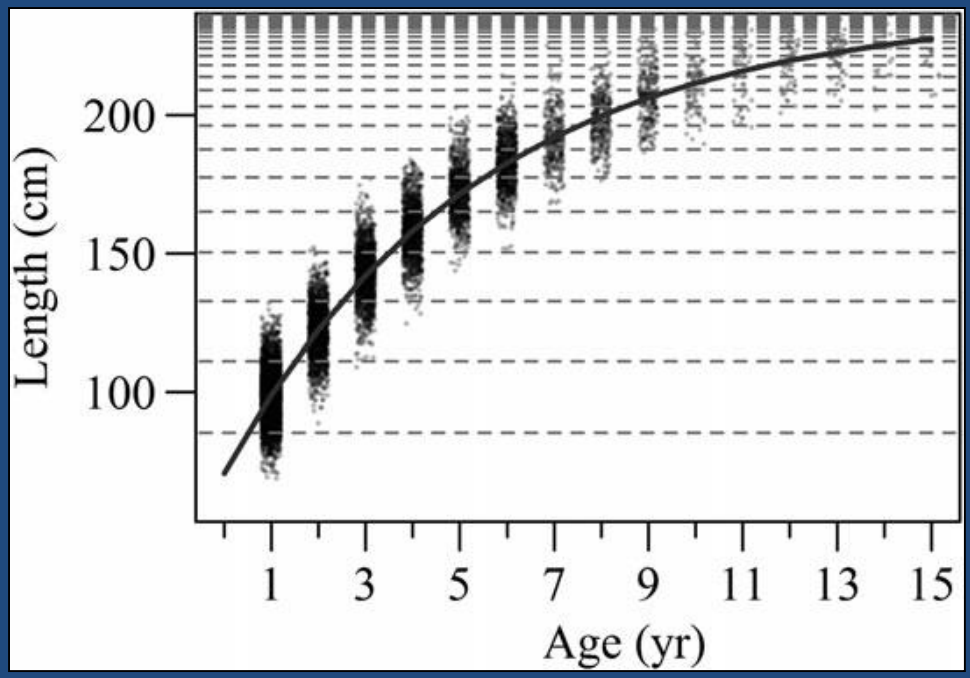
Pauly (1984 p. 71)
after Powell (1979)

What to do with length composition data?

- Convert to ages, then analyze age data



Mixture analysis



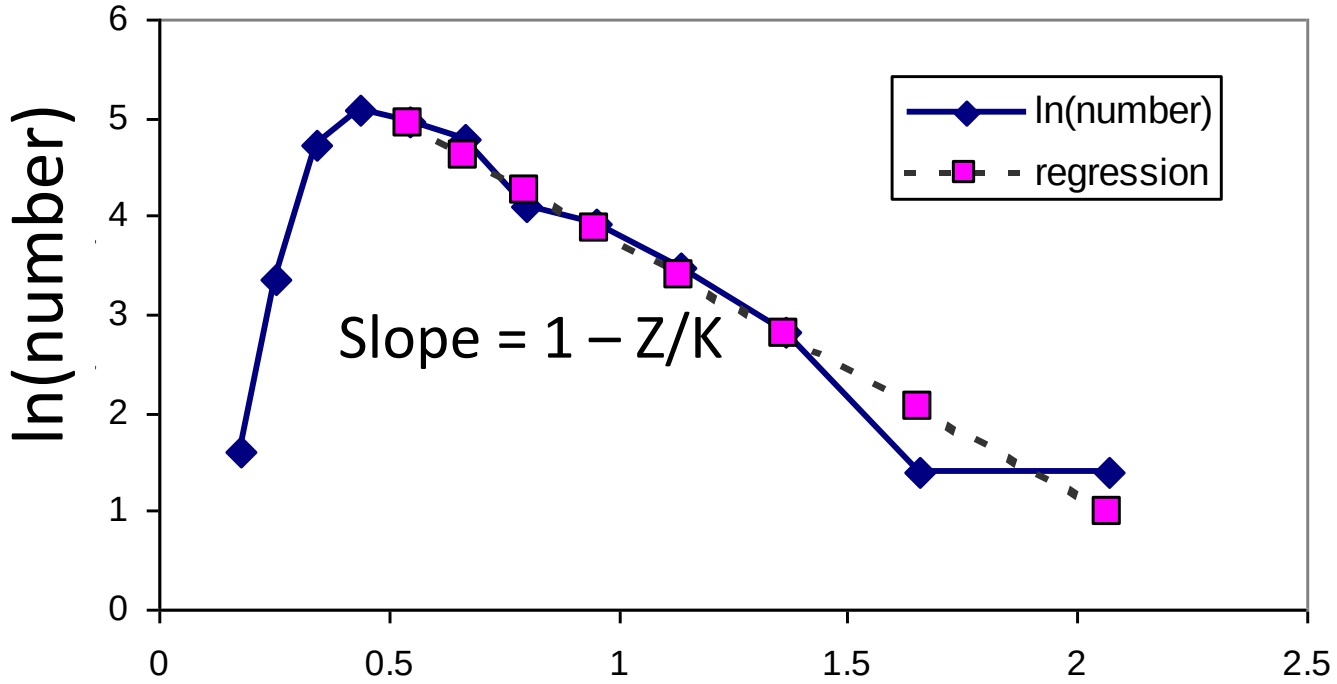
Cohort slicing
(Ailloud et al. 2015)

What to do with length composition data?

- Convert to ages, then analyze age data

banded grouper (*Epinephelus sexfasciatus*)

Pauly (1984)



Relative age $t' = -\log(1 - \frac{L}{L_{\inf}})$

What to do with length composition data?

- Convert to ages, then analyze age data

- Analyze multiple years simultaneously in integrated stock assessment model

What to do with length composition data?

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These approaches look at *SHAPE* of the length frequency distribution

Alternative:

Look at (just) a summary, the mean length

Beverton-Holt mean length mortality estimator

$$\bar{L} = \frac{\int_{t_c}^{\infty} N_t L_t \, dt}{\int_{t_c}^{\infty} N_t \, dt} \rightarrow \bar{L} = L_\infty \left(1 - \frac{Z}{Z+K} \frac{L_\infty - L_c}{L_\infty} \right)$$

growth rate

maximum length

$$Z = \frac{K(L_\infty - \bar{L})}{\bar{L} - L_c}$$

total mortality

mean length

length where all animals fully vulnerable

Tradeoffs

More	Less
Assumptions,	Data & poorer quality,
Sophistication,	Complex,
Detail	Sensitive to assumptions

Desiderata for mean-length-based methods

- Relaxing assumptions
- Diagnostics
- Incorporating more types of data
- Bridges to (more) data-rich methods

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Assumptions

- Growth known
- No variability in size-at-age
- Z constant w/age
- Z constant w/ time
- constant recruitment

Desiderata for mean-length-based methods

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- Bridges to (more) data-rich methods

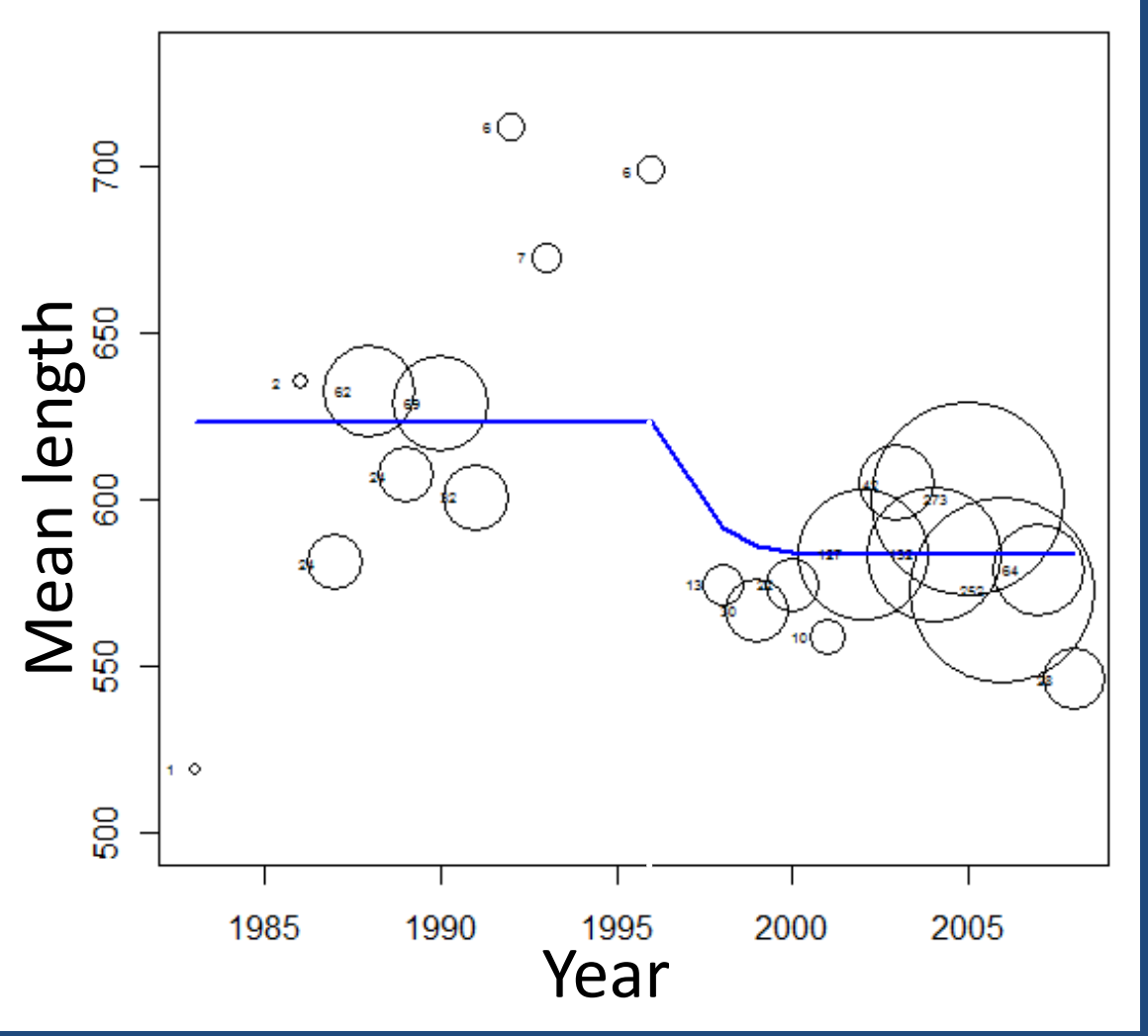
Data Types
• **mean length** • catch rate (cpue) • recruit index (cpue by size) • effort • catch & cpue • other species

Beverton-Holt mean length mortality estimator

$$Z = \frac{K(L_\infty - \bar{L})}{\bar{L} - L_c}$$

5 assumptions:

1. **Asymptotic growth, *K* and L_∞ known & constant over time**
2. **No individual variability in growth**
3. **Mortality constant with age (Selectivity, M)**
4. **Mortality constant over time → Population in equilibrium (mean length reflects mortality)**
5. **'Constant' & continuous recruitment over time**



Growth known:

What if life history parameters questionable??

<u>Queen Snapper</u>

(hook and line in Puerto Rico)

Parameter	Lower bound	Base	Upper bound
L_c	335mm	365mm	465mm
VBK	0.25	0.45	0.65
L_∞	846mm	888mm	906mm

Using Proportional Change in Mortality

$$\text{Proportional Change in Z} = \frac{Z_2 - Z_1}{Z_1}$$

$$Z_1 = \frac{K(L_\infty - \bar{L}_1)}{\bar{L}_1 - L_c}$$

$$Z_2 = \frac{K(L_\infty - \bar{L}_2)}{\bar{L}_2 - L_c}$$

$$Z_{\text{prop. change}} = \frac{\dfrac{\cancel{K}(L_\infty - \bar{L}_2)}{\bar{L}_2 - L_c} - \dfrac{\cancel{K}(L_\infty - \bar{L}_1)}{\bar{L}_1 - L_c}}{\dfrac{\cancel{K}(L_\infty - \bar{L}_1)}{\bar{L}_1 - L_c}}$$

Beverton-Holt mean length mortality estimator

$$Z = \frac{K(L_\infty - \bar{L})}{\bar{L} - L_c}$$

5 assumptions:

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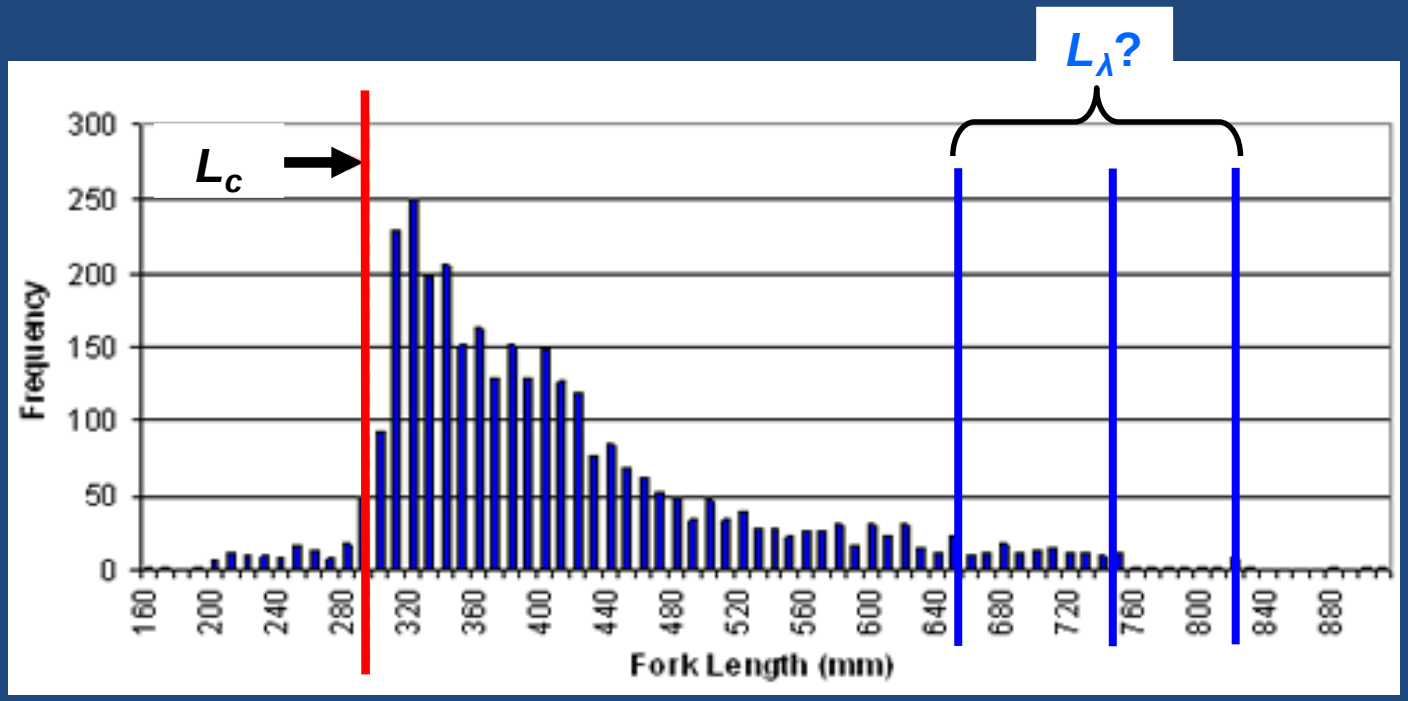
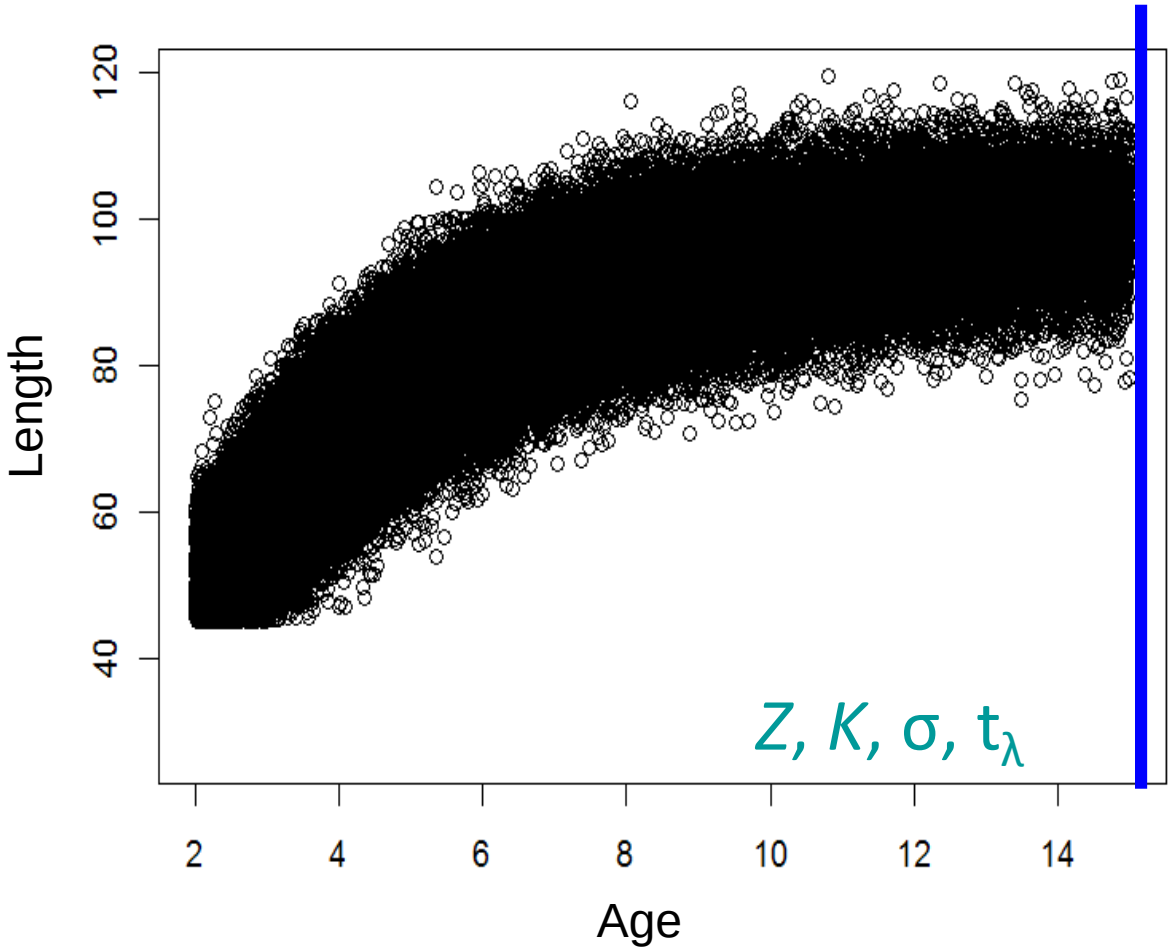
Ehrhardt-Ault (EA) mortality estimator

$$\bar{L} = \frac{\int_{t_c}^{t_\lambda} N_t L_t \, dt}{\int_{t_c}^{t_\lambda} N_t \, dt}$$



EA: Varying imposed L_λ

Age:
'Actual' t_λ



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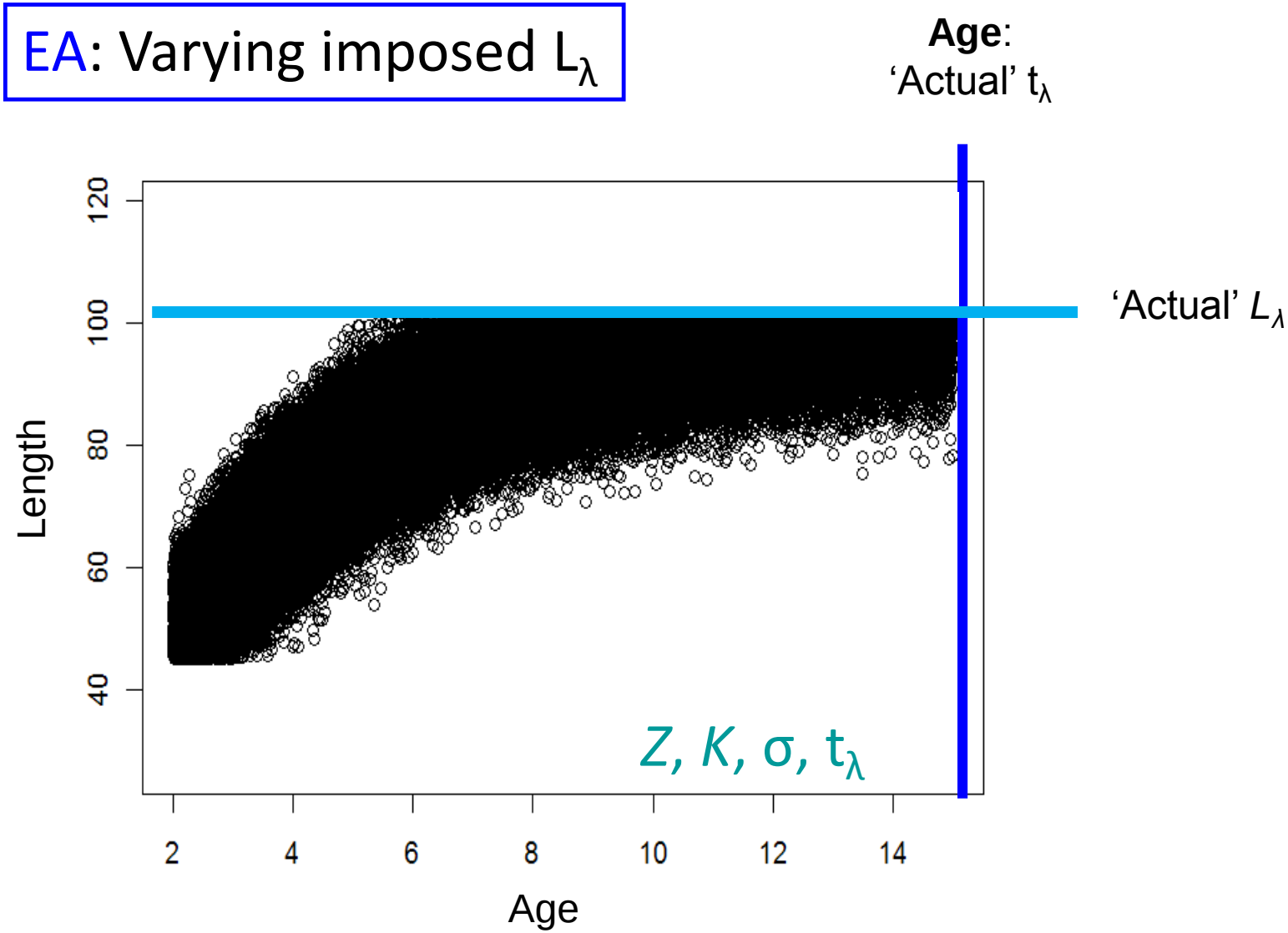
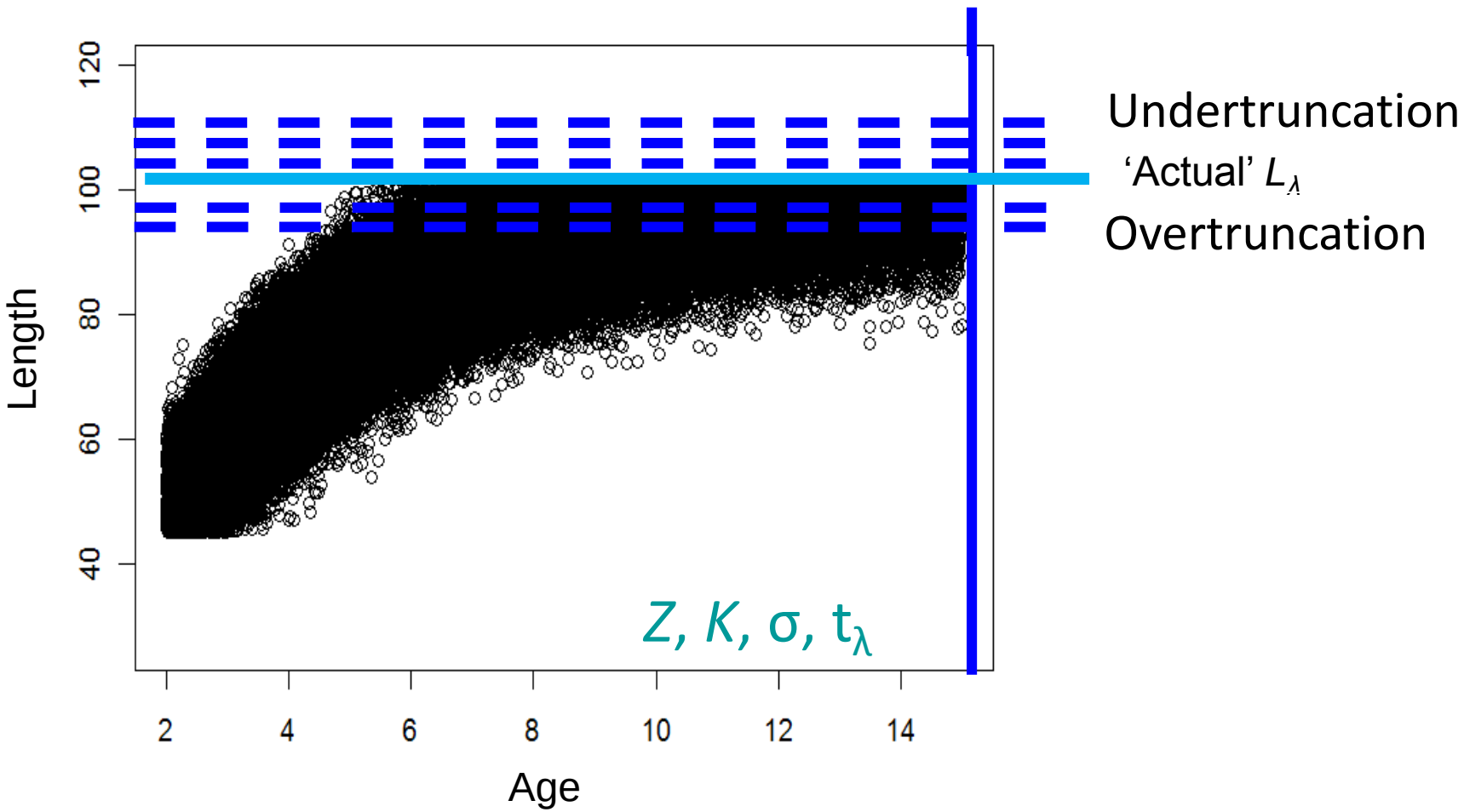
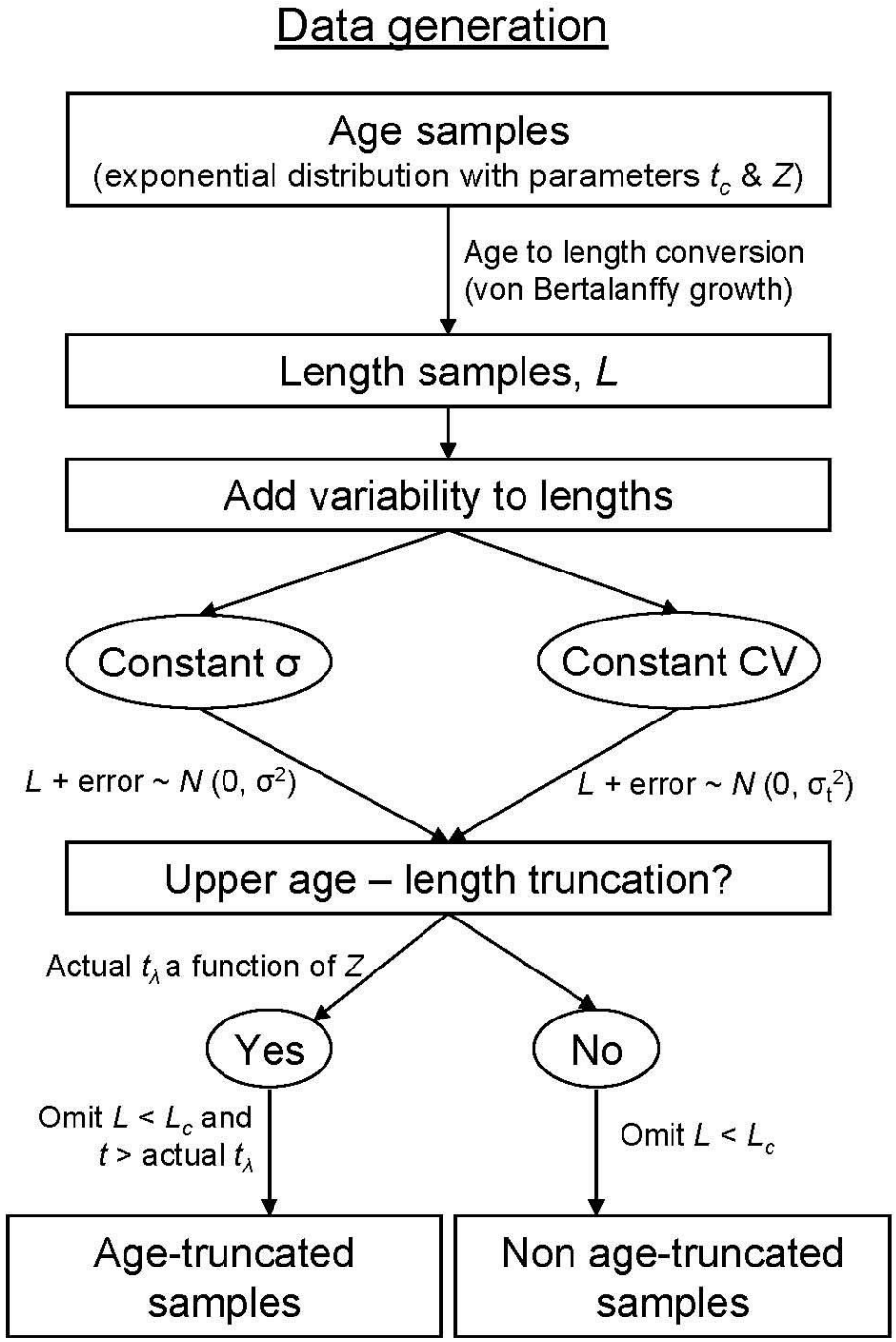
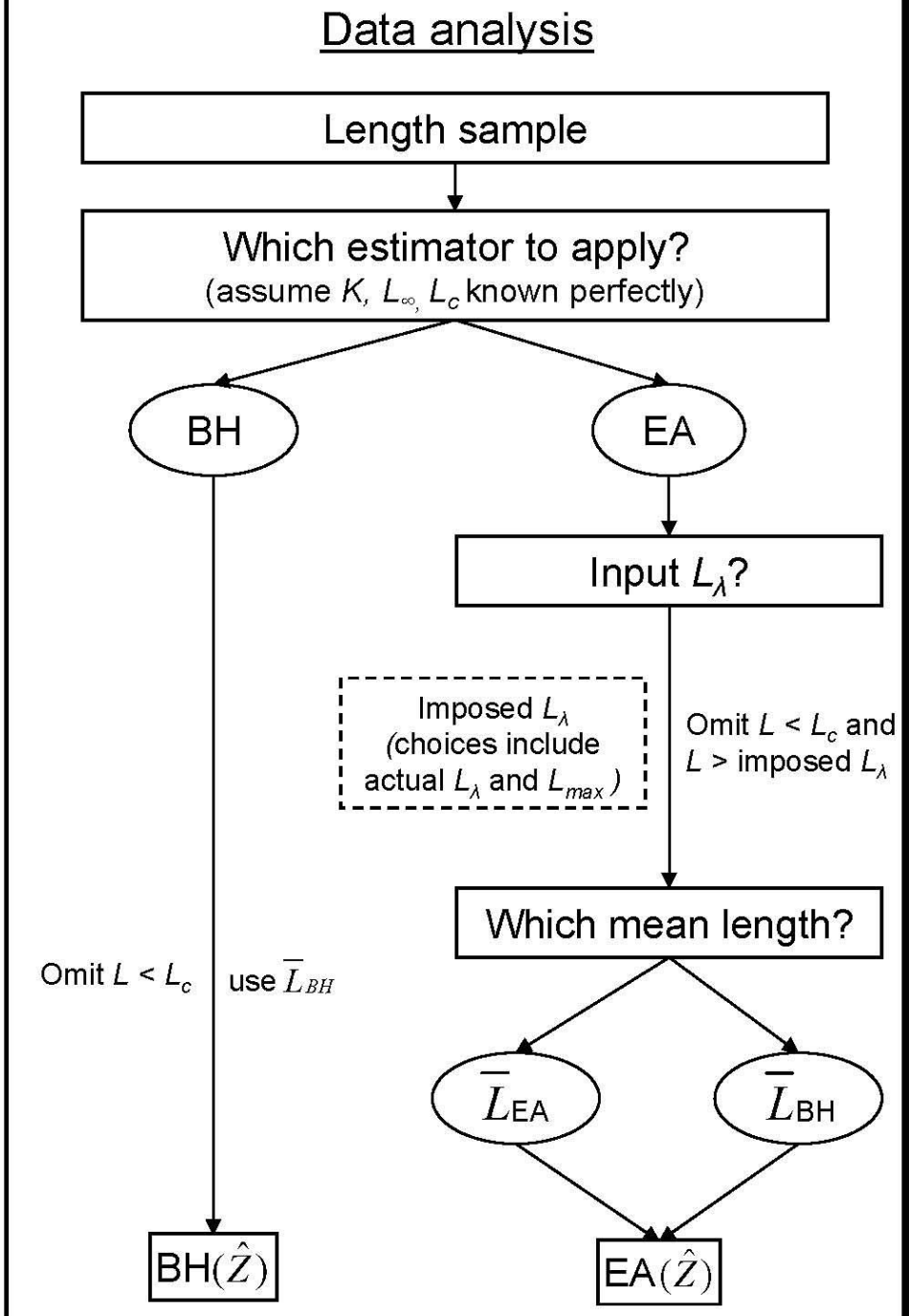


EA: Varying imposed L_λ

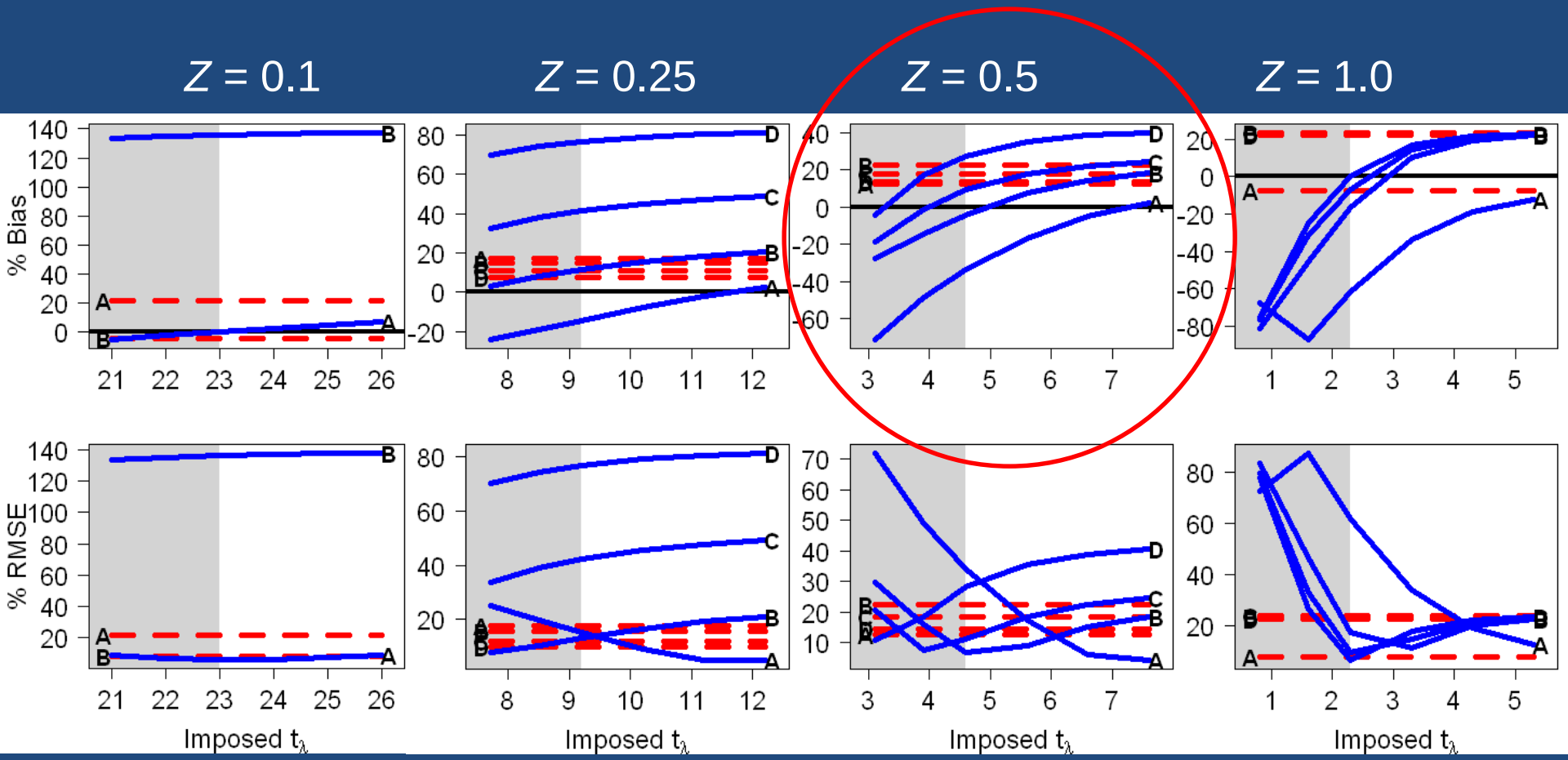



Data generation
Age samples
(exponential distribution with parameters t_c & Z)
Age to length conversion
(von Bertalanffy growth)
Length samples, L
Add variability to lengths
Constant σ
Constant CV
L + error ~ N (0, σ^2)
L + error ~ N (0, σ_t^2)
Upper age – length truncation?
Actual t_λ a function of Z
Yes
No
Omit $L < L_c$ and
$t >$ actual t_λ
Omit $L < L_c$
Age-truncated samples
Non age-truncated samples


Data analysis
Length sample
Which estimator to apply?
(assume K, L_∞, L_c known perfectly)
BH
EA
Input L_λ?
Imposed L_λ
(choices include
actual L_λ and L_{max})
Omit $L < L_c$ and
$L >$ imposed L_λ
Which mean length?
Omit $L < L_c$
use $\overline{L}_{BH}$
$\overline{L}_{EA}$
$\overline{L}_{BH}$
BH($\hat{Z}$)
EA($\hat{Z}$)

Data analyst specifies a t_λ which corresponds to an L_λ

varying imposed L_λ, Z & K (σ = 7)



K = 0.1, 0.4, 0.7, 1.0

A, B, C, D

BH

EA

Take Home Message :

growth variability not a problem for BH;

Truncation → overestimate of Z

EA Model:

- complex behavior, unpredictable bias
- RMSE much better or much worse than BH, depending on Z, σ, & L_λ
- Use not advised (Then et al. in revision)

Dome-shaped selectivity

no general solution

- Live with positive bias
- Evaluate sensitivity to suspected selectivity pattern
- Treat as Index of Z & Look at relative change in Z
- Incorporate selectivity into the model

Beverton-Holt mean length mortality estimator

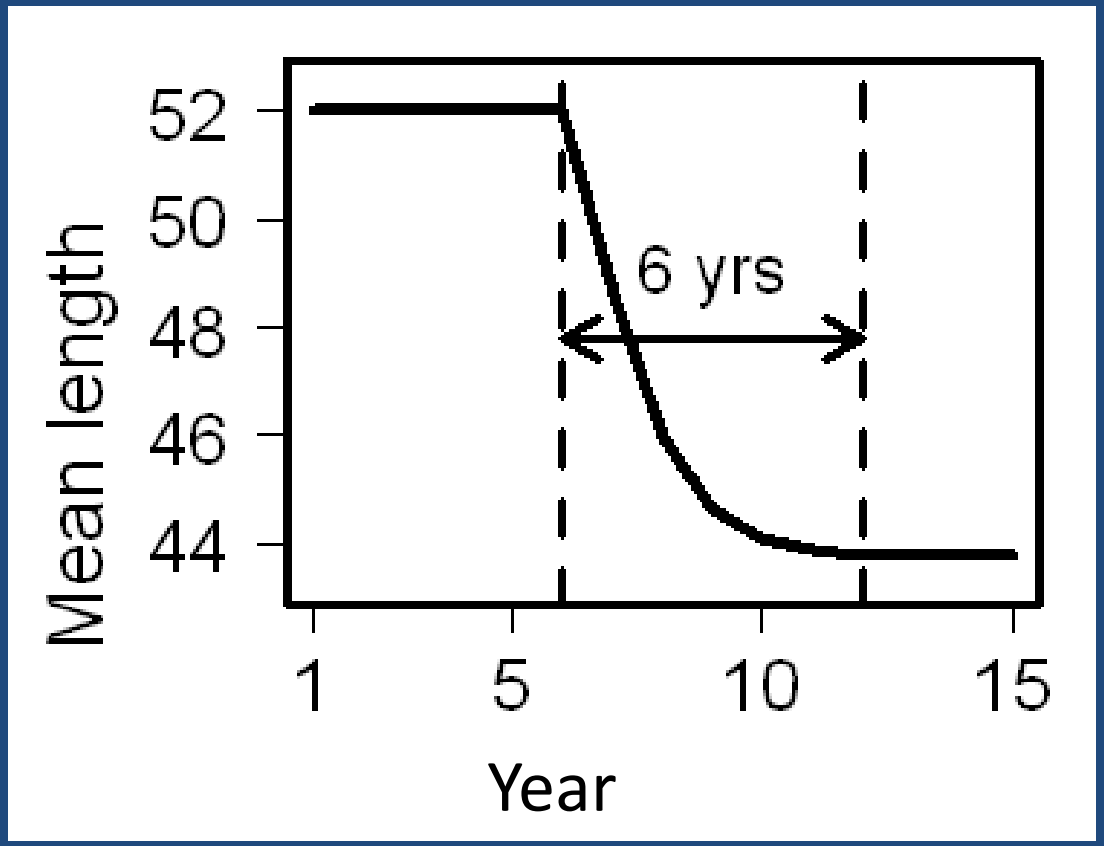
$$Z = \frac{K(L_\infty - \bar{L})}{\bar{L} - L_c}$$

5 assumptions:

1. Asymptotic growth, *K* and L_∞ known & constant over time
2. No individual variability in growth
3. Mortality constant with age (eg. Selectivity, M)
4. Mortality constant over time → Population in equilibrium (mean length reflects mortality)
5. 'Constant' & continuous recruitment over time

First expansion: multiple years

Change in Z causes *gradual* (transitional) change in mean length to new equilibrium value



The derivation

$$\bar{L}_d = \frac{\int_{t_c}^{g} N_o \exp(-Z_2(t-t_c))L_t dt + \int_{g}^{\infty} N_o \exp(-Z_2 d)\exp(-Z_1(t-g))L_t dt}{\int_{t_c}^{g} N_o \exp(-Z_2(t-t_c))dt + \int_{g}^{\infty} N_o \exp(-Z_2 d)\exp(-Z_1(t-g))dt}$$

Younger animals Older animals

In English:

Mean Length =

$$\frac{\text{SUM \# of younger animals at each age } (Z_2 \text{ only}) \cdot \text{Length at age} + \text{SUM \# of older animals at each age (both } Z_1 \text{ and } Z_2) \cdot \text{Length at age}}{\text{SUM \# of younger animals at each age } (Z_2 \text{ only}) + \text{SUM \# of older animals at each age (both } Z_1 \text{ and } Z_2)}$$

Simplified Equation (at least relatively)

$$\bar{L}_d = L_\infty - \frac{Z_1 Z_2 (L_\infty - L_c)\{Z_1 + K + (Z_2 - Z_1)\exp(-(Z_2 + K)d)\}}{(Z_1 + K)(Z_2 + K)(Z_1 + (Z_2 - Z_1)\exp(-Z_2 d))}$$

d = number of years since change in mortality

Maximum likelihood estimation

Means distributed normally (Central Limit Theorem)

"simplified equation"

$$\ln(\Lambda) \propto -n \cdot (\ln \sigma) - \frac{1}{2\sigma^2} \cdot \sum_{y=1}^{n} m_y \cdot [\bar{L}_y - L_{pred,y}]^2$$

Objective or Likelihood Function

"is proportional to"

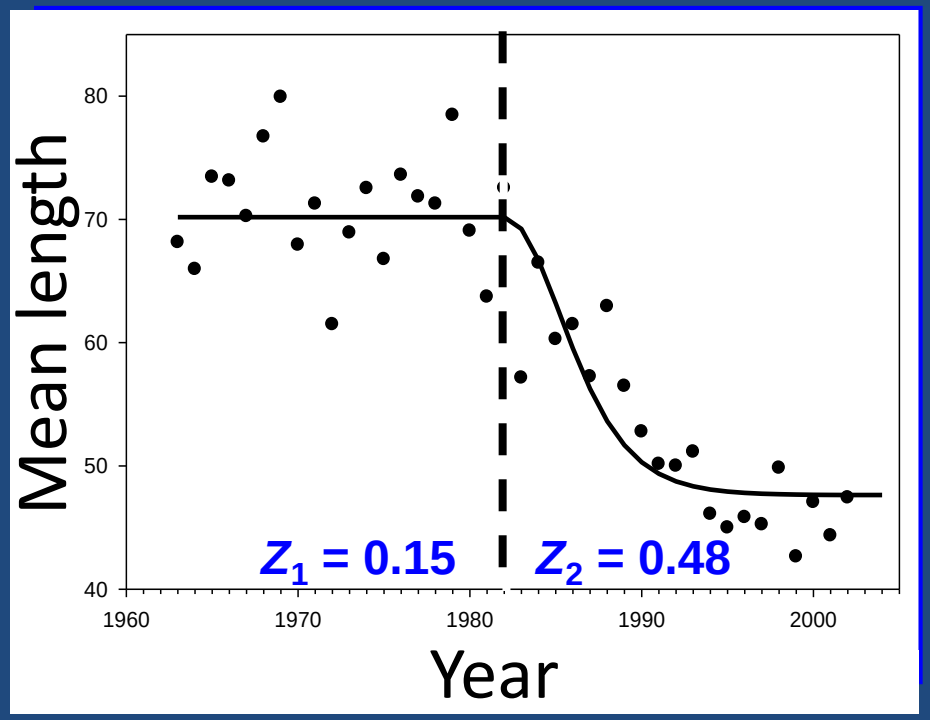
Number of years in time series

Variance

Sample size each year

Observed minus Predicted

Goosefish (*Lophius americanus*)
Gedamke and Hoenig (2006)



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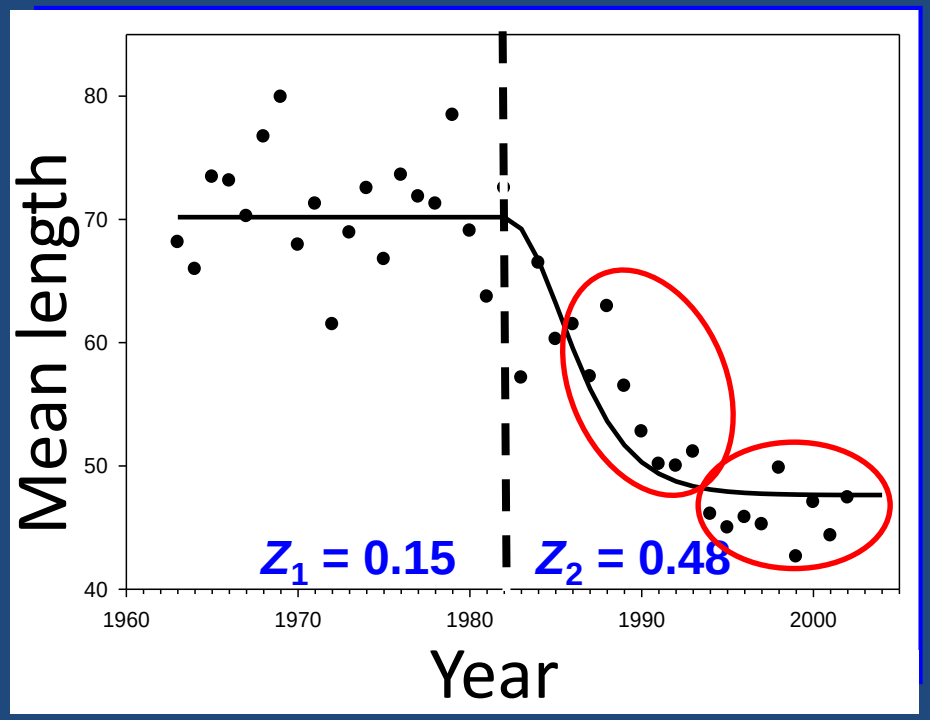
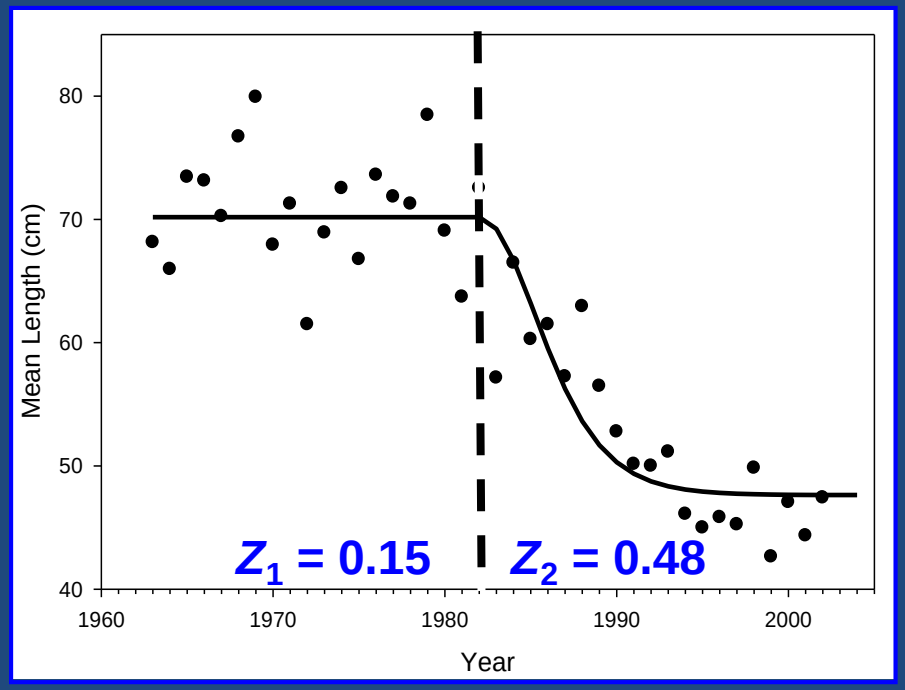
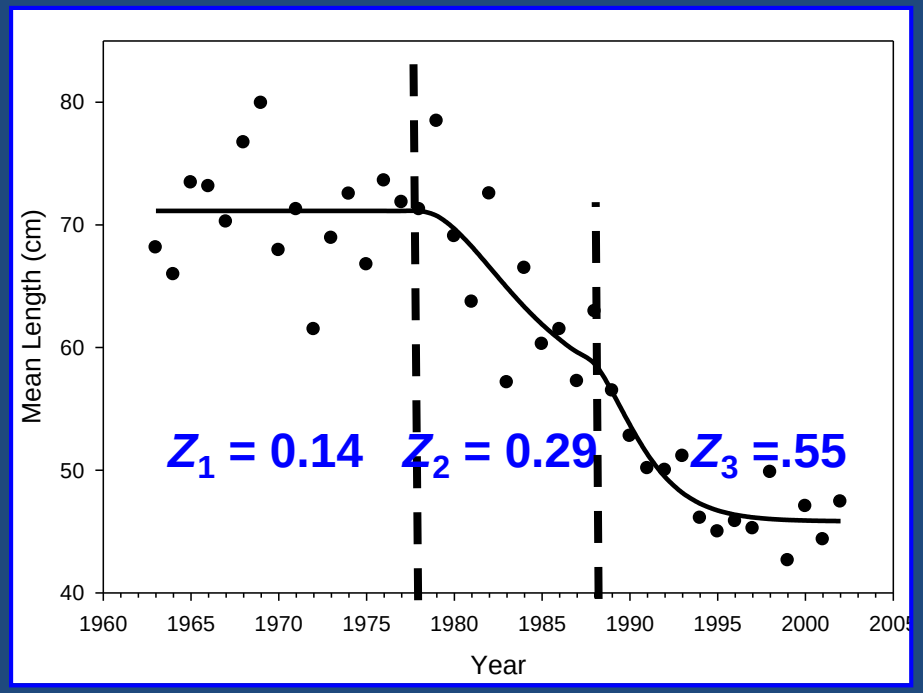


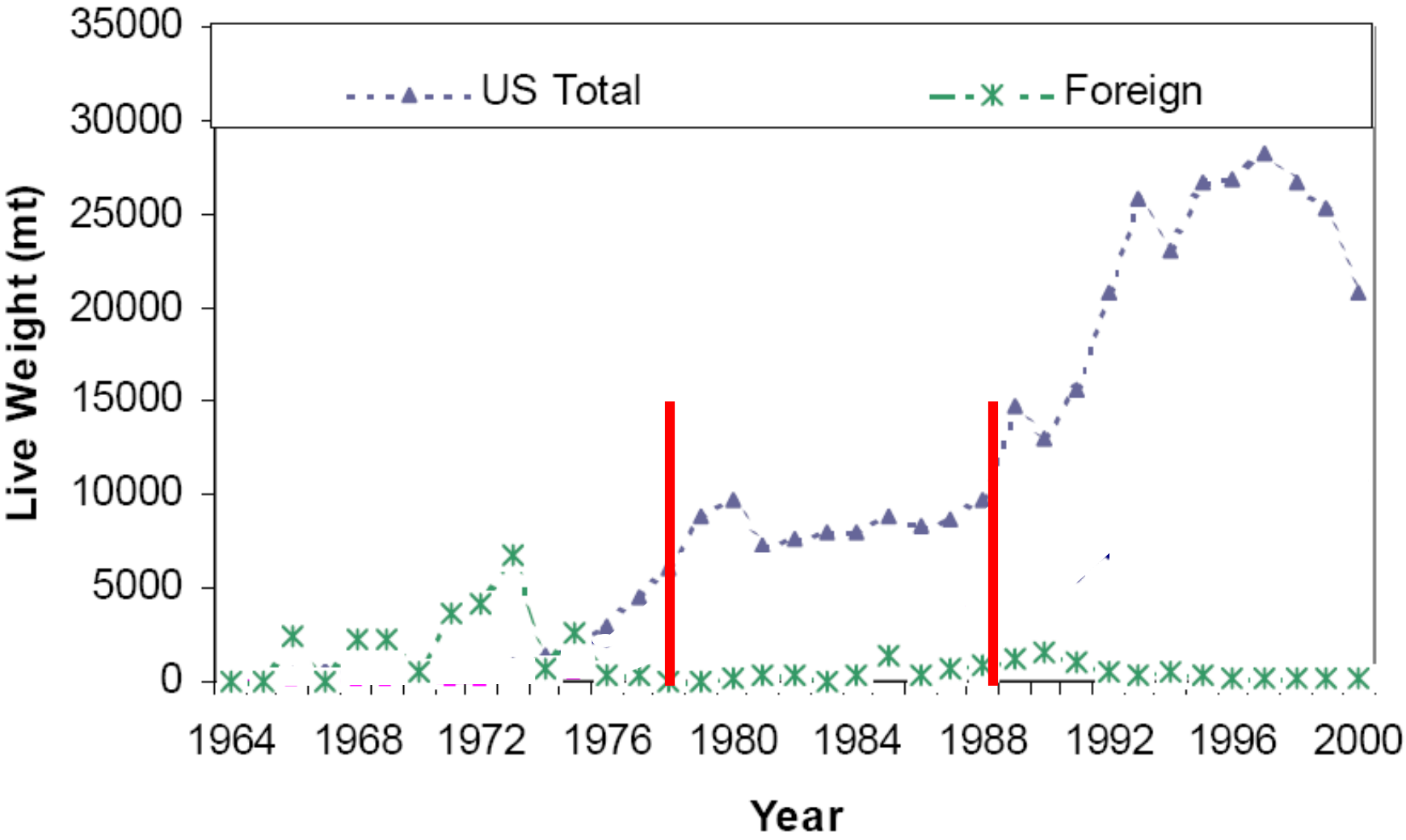
Diagnostic – pattern to residuals

Goosefish (*Lophius americanus*) Gedamke and Hoenig (2006)

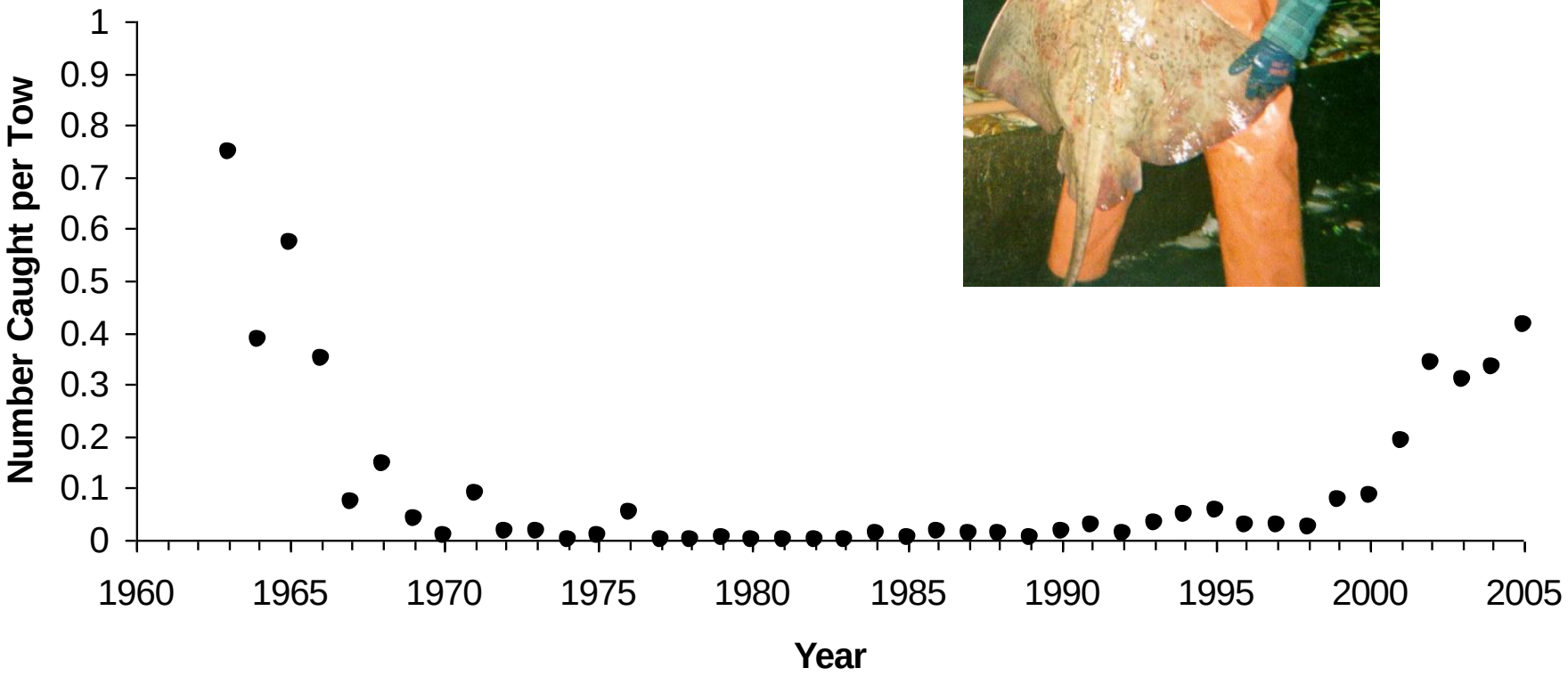




Commercial Landings Northern Management Region



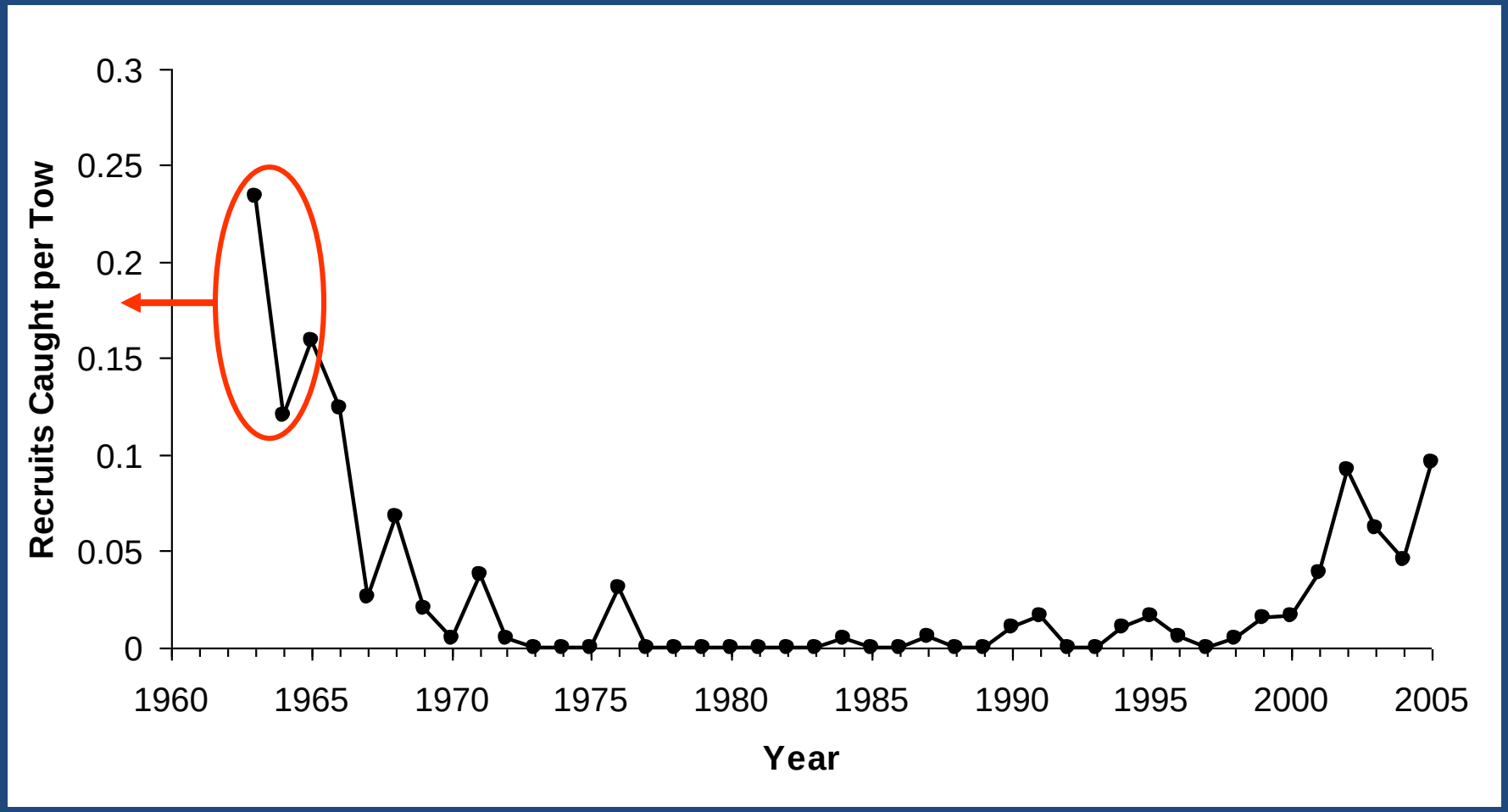
Barndoor skate NMFS survey



Barndoor skate (*Dipturus laevis*) Gedamke et al. (2008)

2nd expansion: Using an index of recruitment

Equate observed mean length with predicted; predicted computed as sum (not integral) and constant recruitment replaced by year-specific index



What if you don’t have an index of recruitment?

Overestimate Z when recruitment is increasing & underestimate when declining

3rd expansion: Incorporating effort data

THoG model (Then, Hoenig, Gedamke)

Simply replace Z by $q\,f_t + M$ *in* "simplified equation"

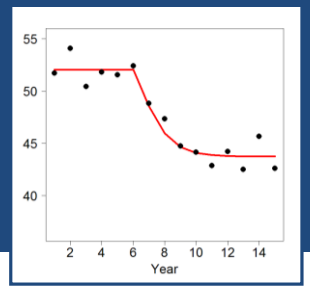
same likelihood function $$\sum\left(\bar{L}_{pred} - \bar{L}_{obs}\right)^2$$

Estimate catchability, q, & natural mortality, M → year-specific fishing & total mortality rates, F & Z

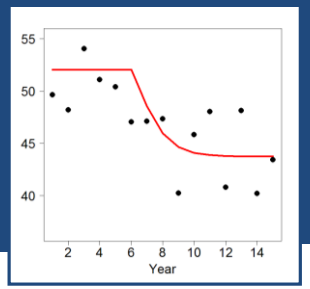
Example: Z_1 = 0.6, Z_2 = 1.0, K = 0.4, Linf = 100

Base Case: *q* & *M* estimates

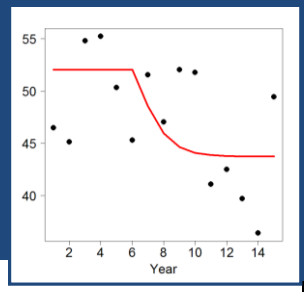
σ' = 1

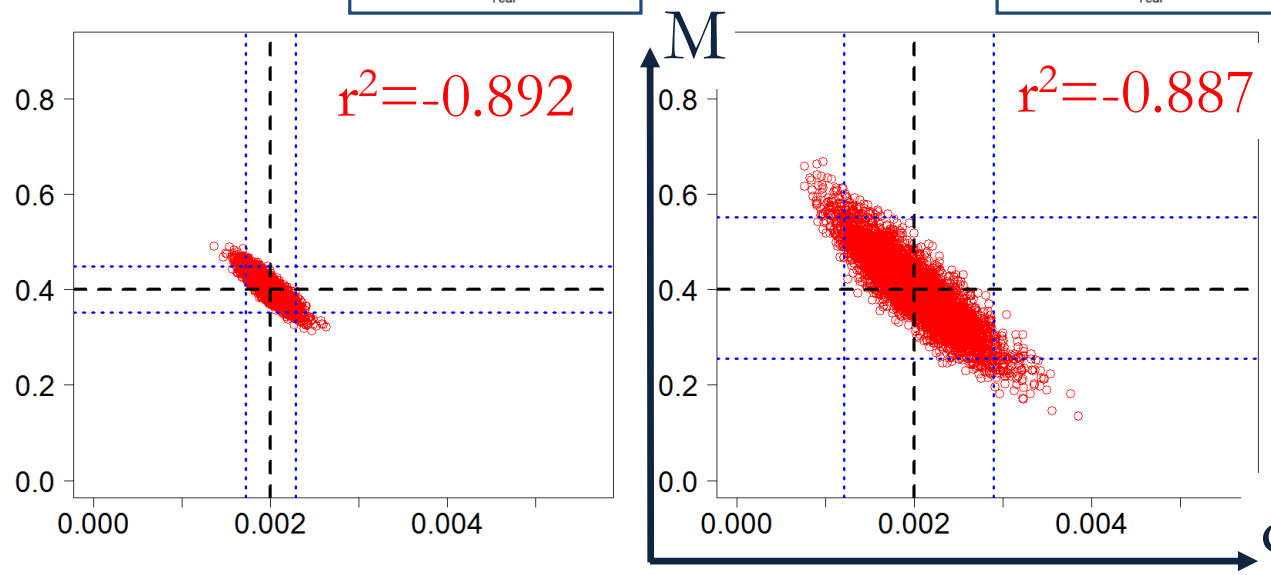


σ' = 3



σ' = 5



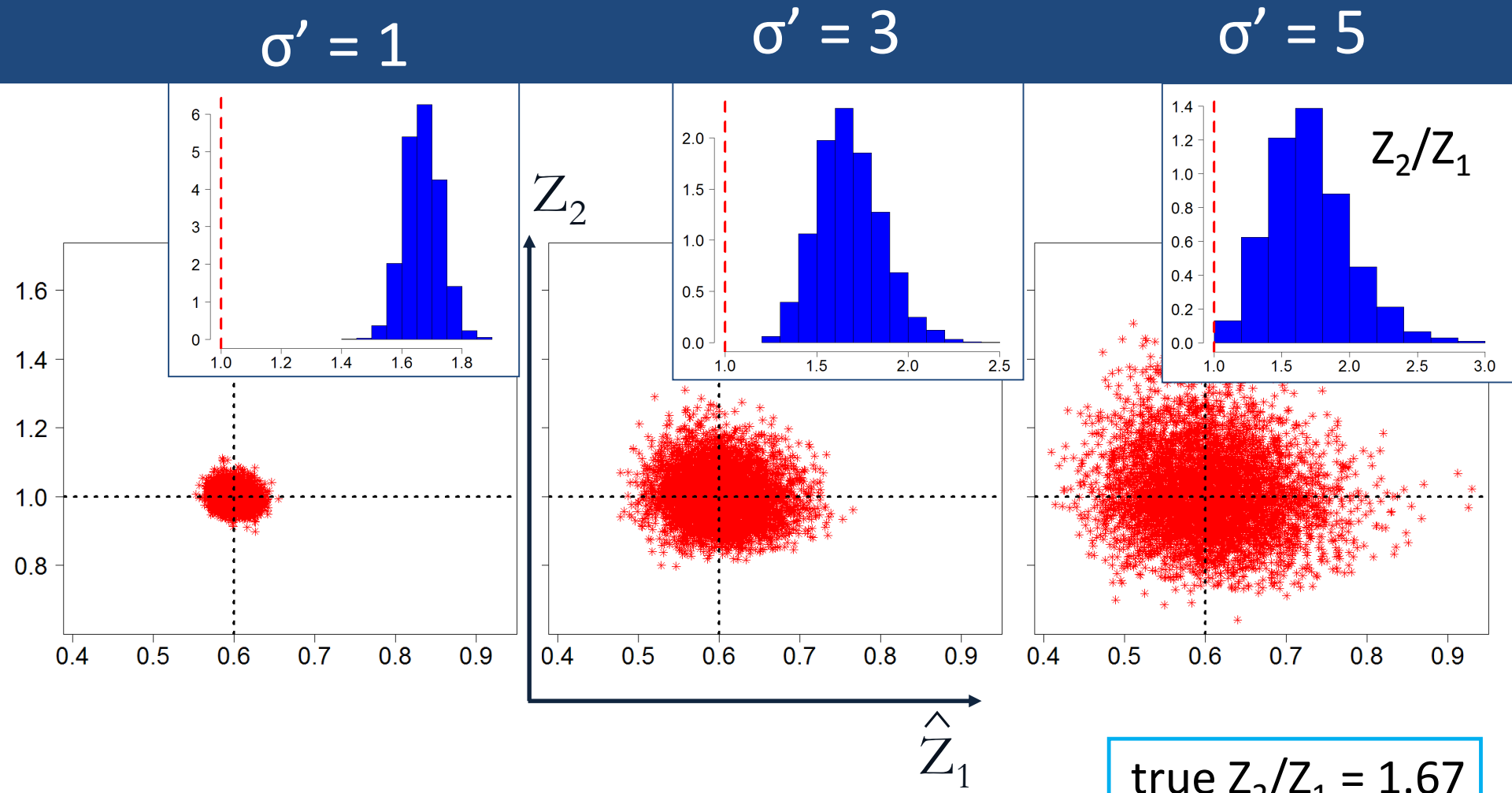


σ' depends on sample size & recruitment variability

True Values

0.025, 0.975 Quantiles

Base Case: Z_1 & Z_2 estimates & ratios



true Z_2/Z_1 = 1.67

4th expansion – use total catch & cpue data

fishing effort → Then-Hoenig-Gedamke (THoG) → q, M, F_t, Z_t

effort = f = catch/cpue →

$Z = q$ catch/cpue + M

total catch, cpue → THoG → q, M, F_t, Z_t

THoG → more years → abundance = cpue/q

THoG → more years → surplus production model → MSY, B_{MSY}, F_{MSY}, F_t, B_t

5th expansion – use of cpue data

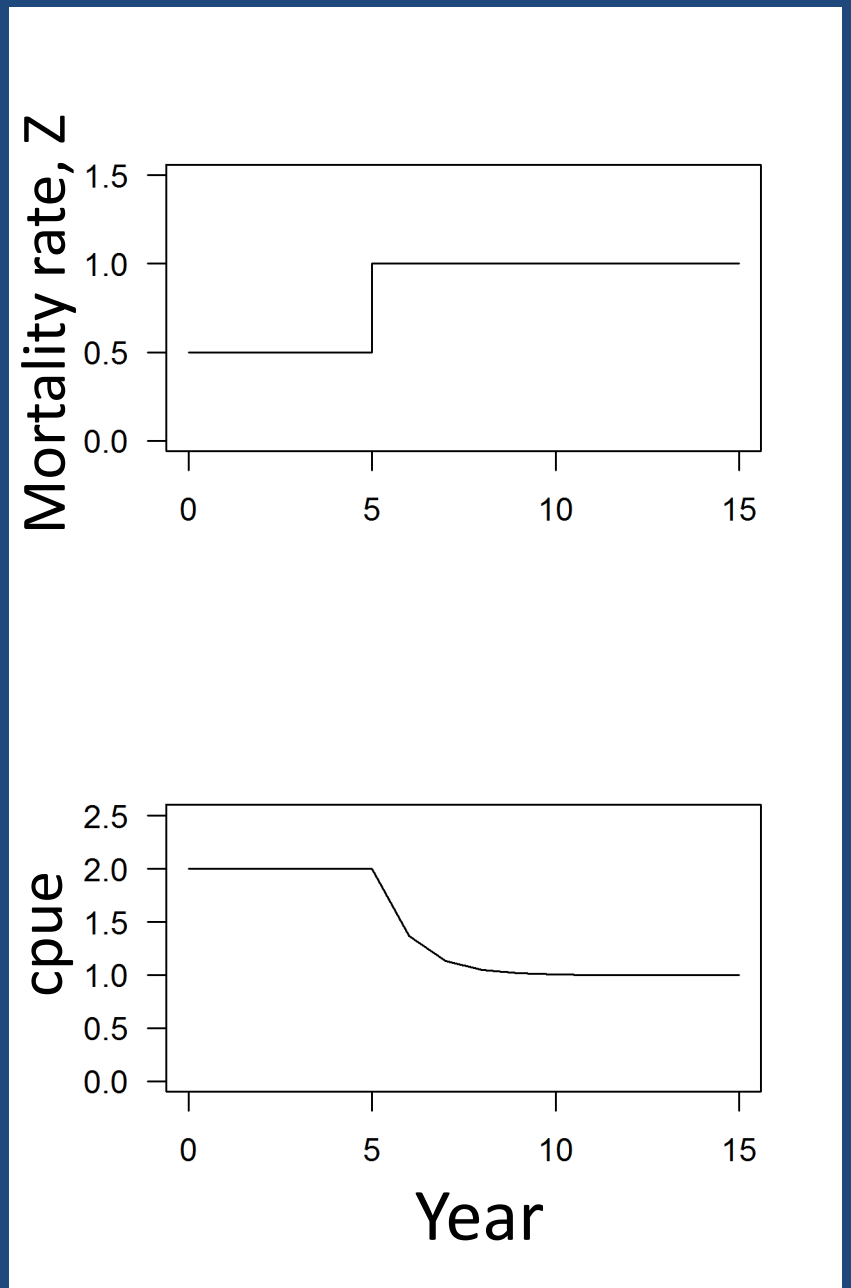
mortality increases → fewer fish

Ratio of observed CPUE inverse to relative change in Z

$$\frac{CPUE_2}{CPUE_1} = \frac{Z_1}{Z_2}$$

cpue → same transitional behavior as mean length

(denominator in derivation of "simplified equation")



Fit model to data

- Estimate total mortality in stanzas
- Specify number of changes in mortality
- Obtain maximum likelihood estimates of Z, year(s) of change:

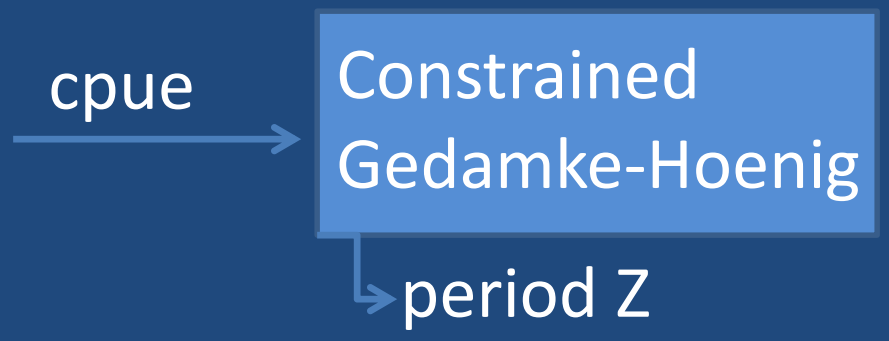
$$\log \Lambda = \log \Lambda_{\bar{L}} + \log \Lambda_{CPUE}$$

both parts have Σ(observed – predicted)^2

- use AIC to find the best fitting model.

$cpue_2 / cpue_1 = Z_1 / Z_2$ in equilibrium

cpue constrains magnitude of change in Z, not absolute levels

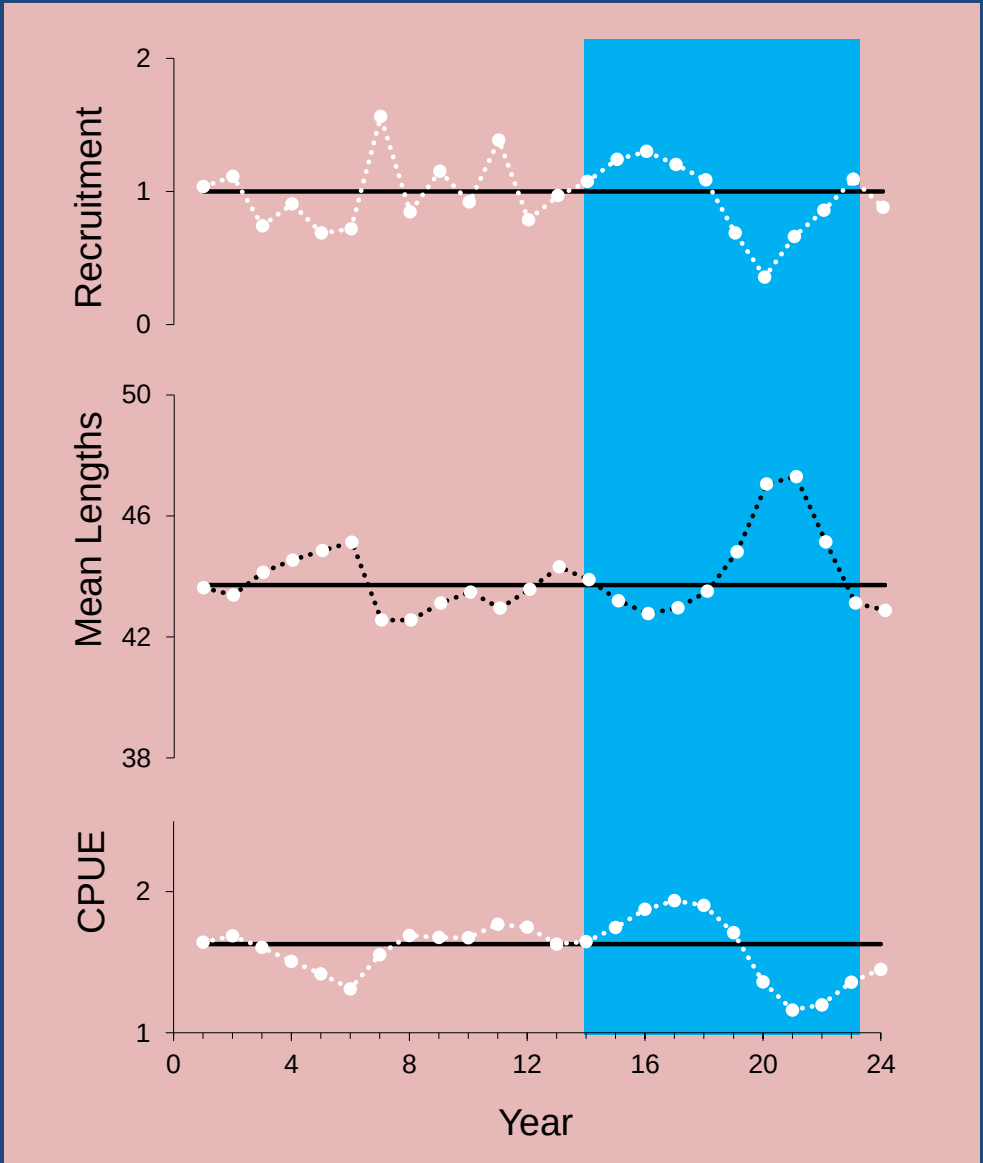


Effects of recruitment

- Change in recruitment changes mean length & cpue

Expect:

Negative correlation of residuals & long runs



6th expansion – multi-species approach

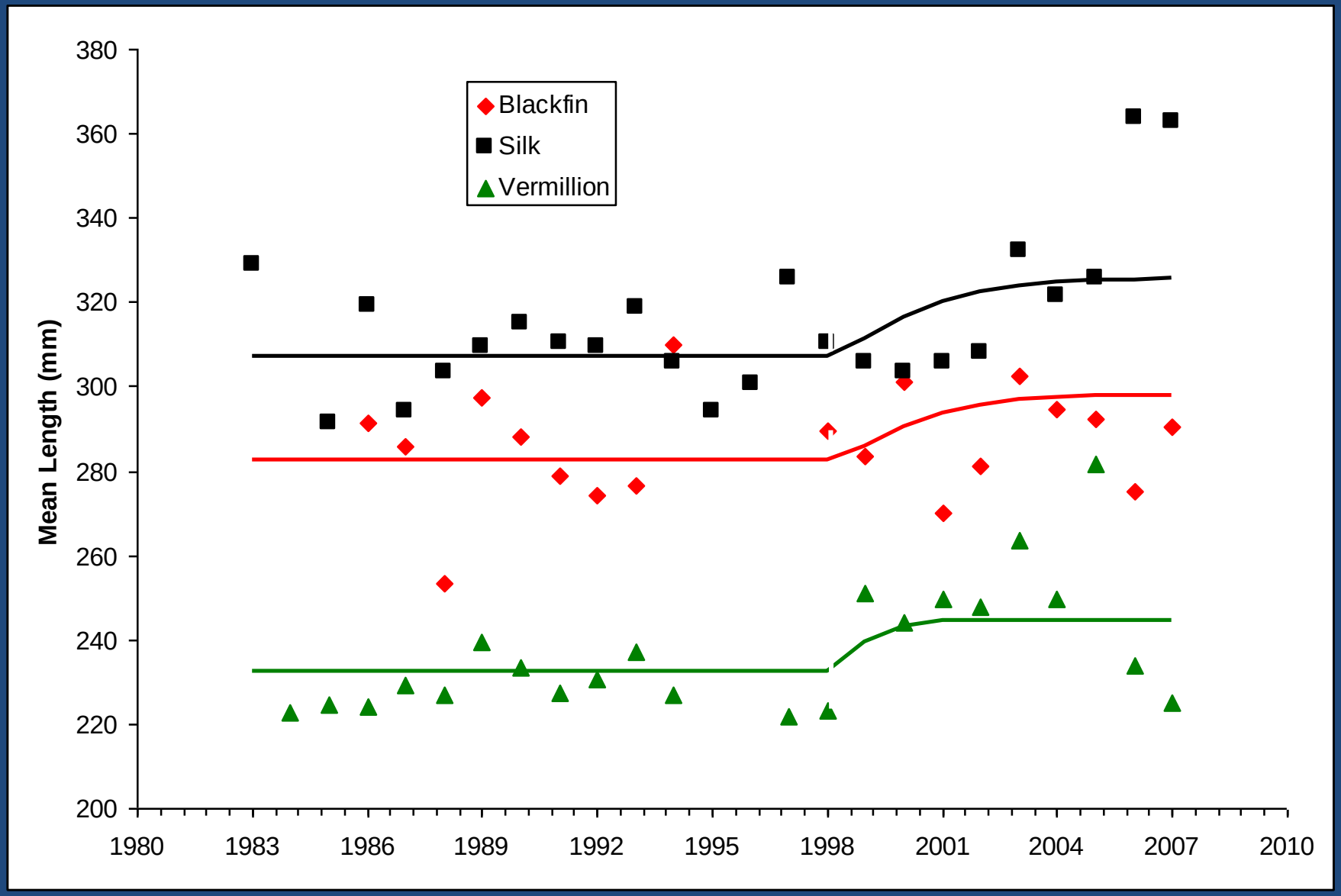
- Multiple species → information on shared parameters
- Species ‘complexes’ subject to similar effort patterns

Example: 4 species w/ 3 changes in mortality

- Each species individually → 32 parameters
- Common change years → 23 parameters
- Common change years & proportional changes in *F* → 14 parameters

Multispecies w/ Common Proportional Change in F

Common Year of Change = 1998.03
Common Proportional change in F = 0.57



Derivation of overfishing limit (OFL)

(1) $$OFL = F_{MSY} N_{current}$$

- F_{MSY} & $N_{current}$ difficult to obtain
- If recent (reference) average catch & *F* known:

(2) $C_{ref} = F_{ref} N_{ref}$ → $N_{ref} = C_{ref} / F_{ref}$

(3) $$OFL = F_{MSY} \frac{C_{ref}}{F_{ref}}$$

- Use a per-recruit statistic as proxy for F_{MSY}:

(4) $$OFL = \frac{F_{benchmark}}{F_{ref}} C_{ref}$$

Flow diagram of approach

External values:
M, w_a, age-length, fecundity

$\bar{L}$, L_c, k, L_∞ → Mean length Z (Gedamke-Hoenig) → Per recruit analysis

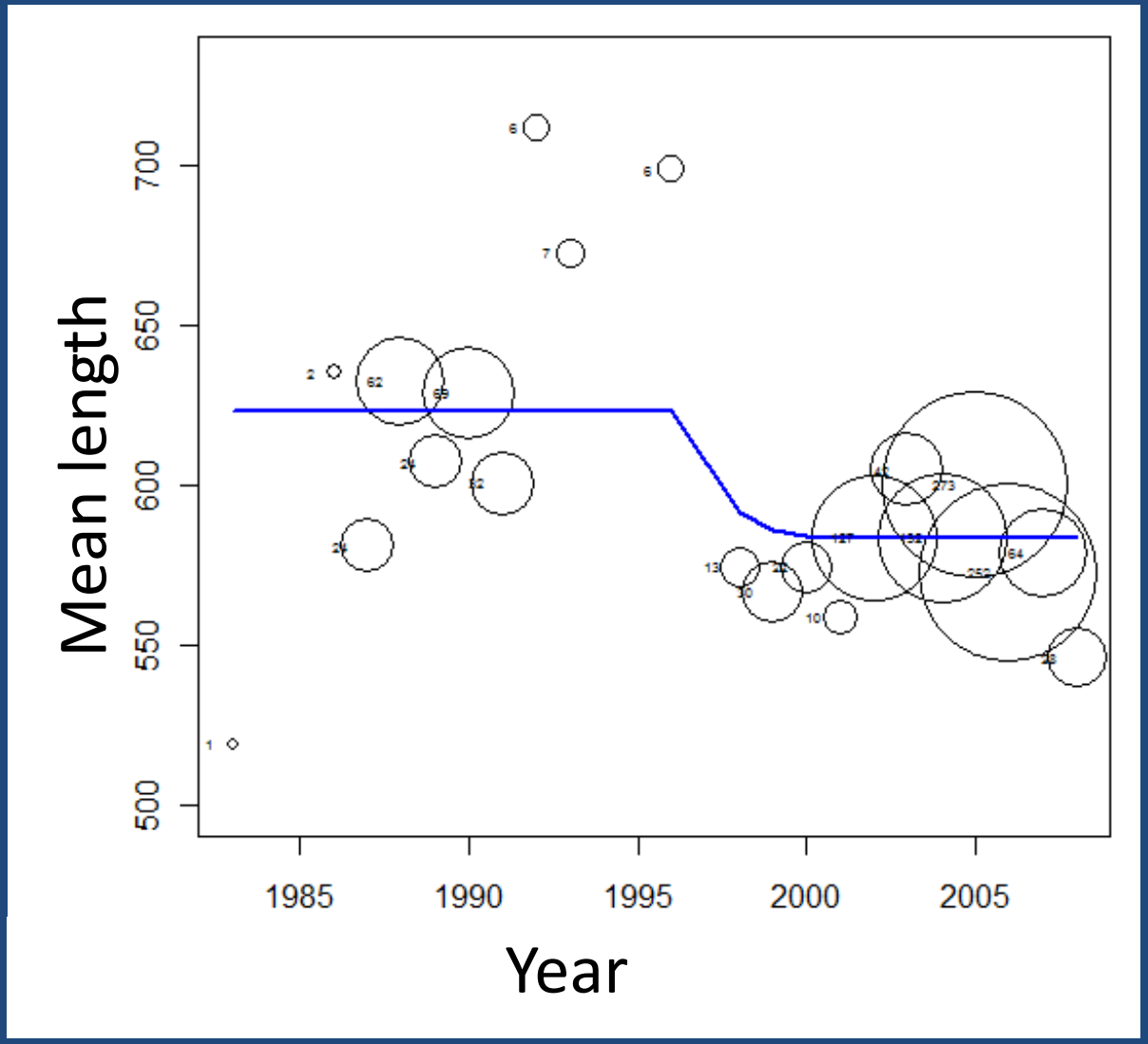
Z by period,
External M

F_{ref} & C_{ref}
(Most recent year of change to present)

$F_{benchmark}$ (e.g., $F_{0.1}$, F_{max}, $F_{30\%}$)

$$OFL = \frac{F_{benchmark}}{F_{ref}} C_{ref}$$

Example: Queen snapper in Puerto Rico

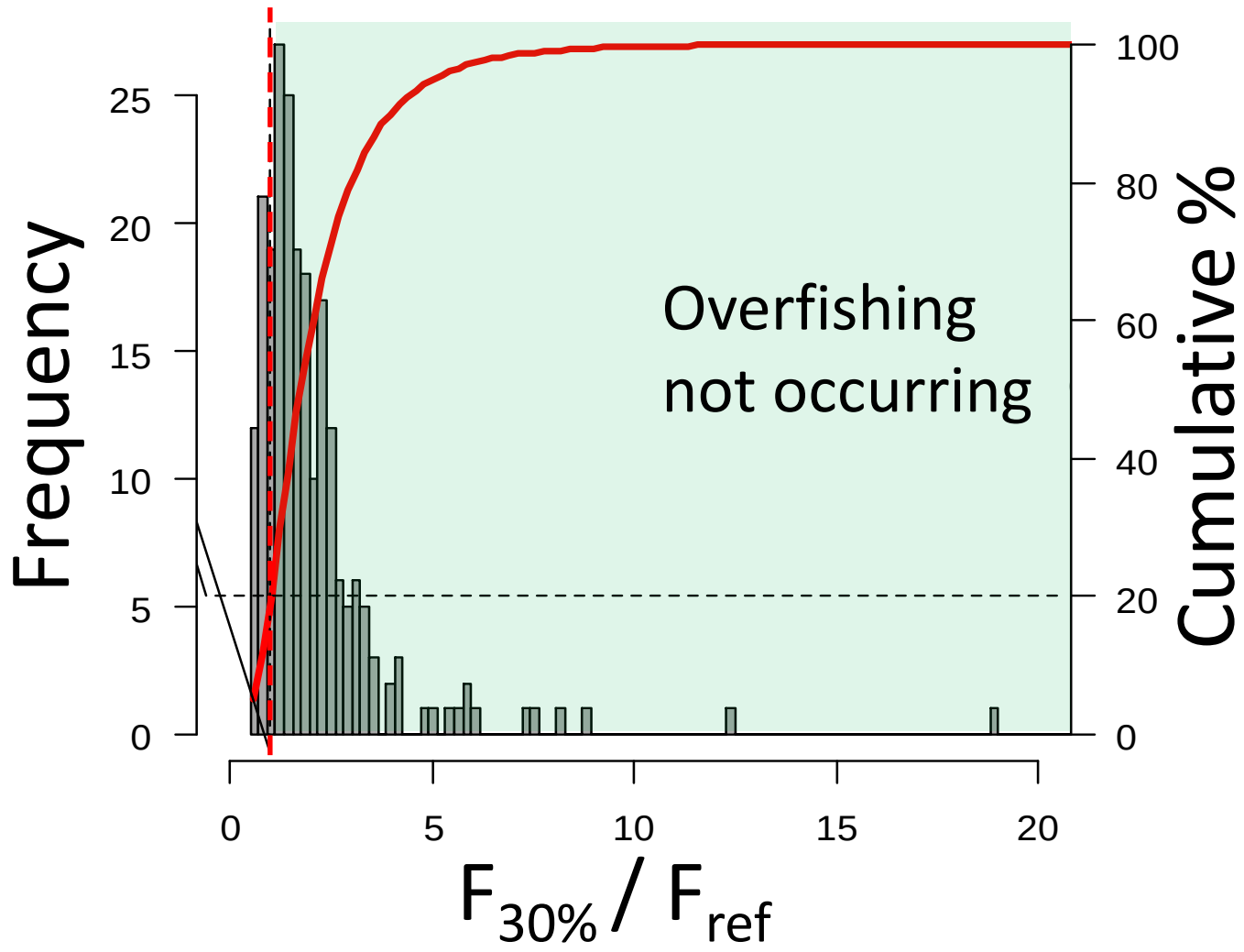


Data:

lengths

catches

Describe uncertainty in growth by simulation



Bottom line:

- Mean length → BH-Z → multiple years → GH (changing Z)

- Add additional data:
  - recruit index
  - effort
  - catch rate (cpue)
  - catch & cpue
  - other species

- Estimate q, M, F_t, Z_t; relax assumptions, obtain diagnostics
- Combine results with other analyses: yield per recruit, abundance estimation → OFL
- Bridge to production models & other models

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Thank you!