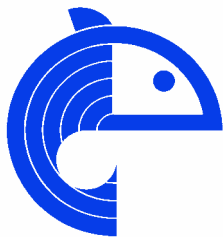


Cross-validations of a diffusion approximation approach to risk estimation for salmonids

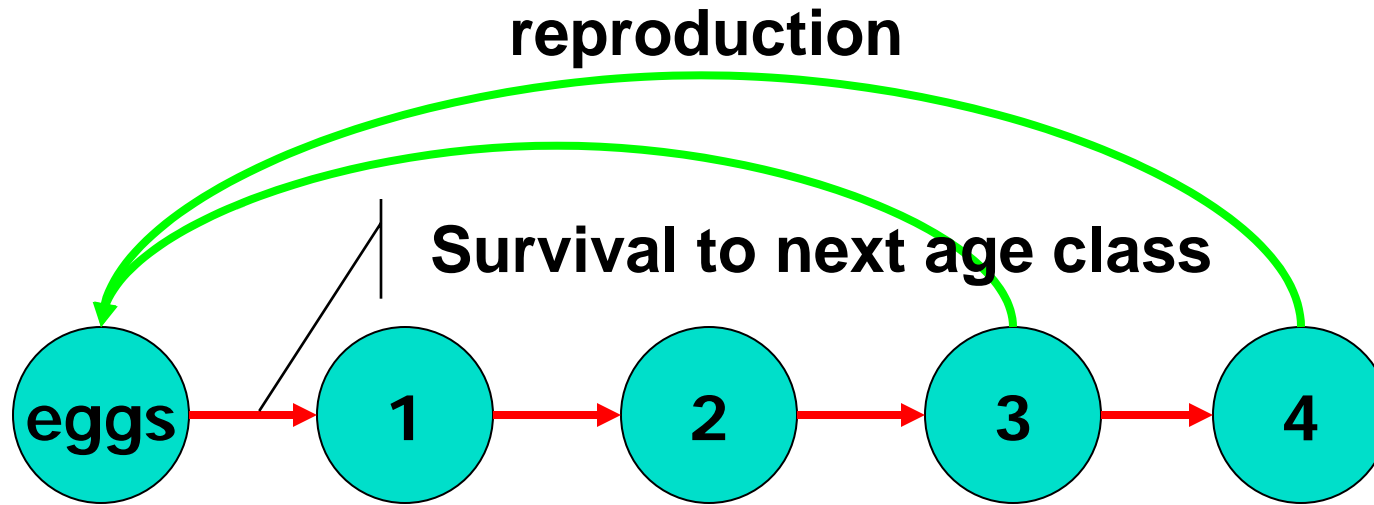
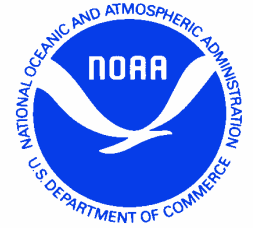
Eli Holmes

Northwest Fisheries Science Center

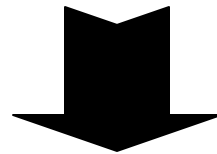
Eli.Holmes@noaa.gov



Diffusion approximations



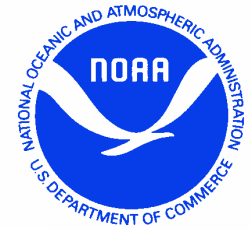
Let reproduction and survival vary yearly



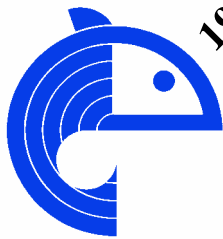
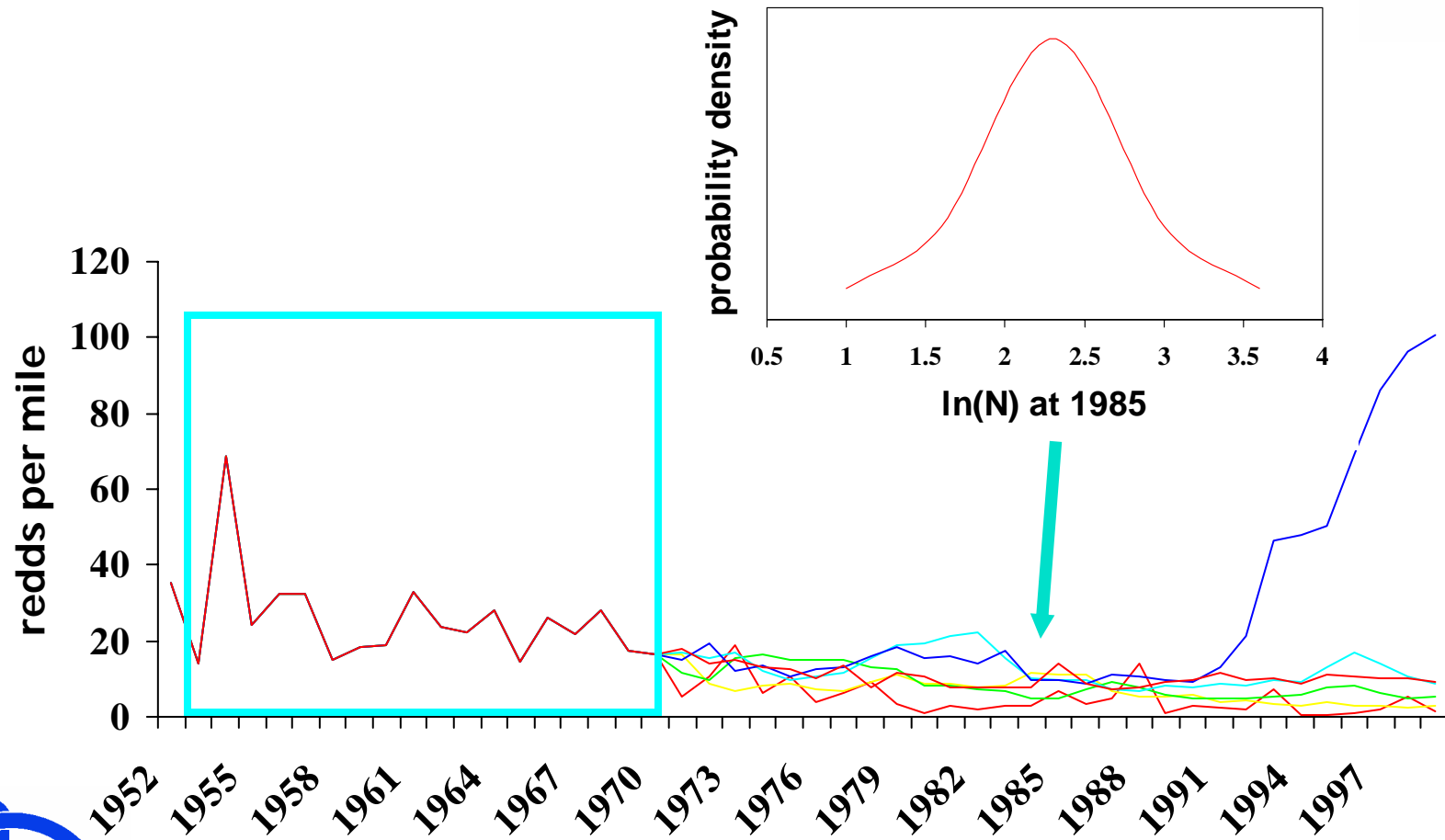
$$N_t = N_0 \exp(\mu t + \varepsilon t)$$

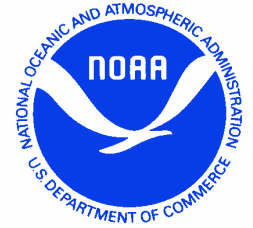
where $\varepsilon \sim \text{Normal}(0, \sigma)$





Basic Idea of DA PVA





Parameters of a DA model

$$N_t = N_0^* \exp(\mu t + \varepsilon t) \text{ where } \varepsilon \sim N(0, \sigma)$$

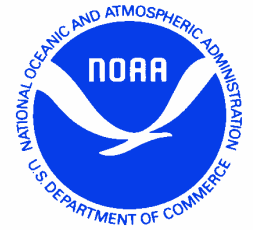
$$O_t = N_t^* \exp(\varepsilon_{np}) \text{ where } \varepsilon_{np} \sim N(0, \sigma_{np})$$

Parameter that governs the median rate of decline.

“Process error”:
parameter that describes the long-term variability of the process.

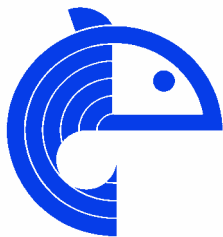
“Non-process error”:
parameter that describes the extra short-term variability of the process.





Overview of research

- ▶ #1 Does a diffusion approximation model work for salmon population processes and the sorts of salmon data we have in the Pacific NW.
- ▶ #2 What are the best ways to estimate the parameters of such a model.
- ▶ #3 How can we express the uncertainty in our risk estimates using DA models.

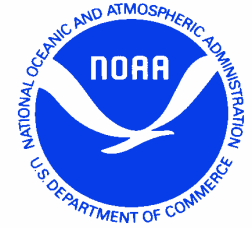




#1 Cross-validation overview

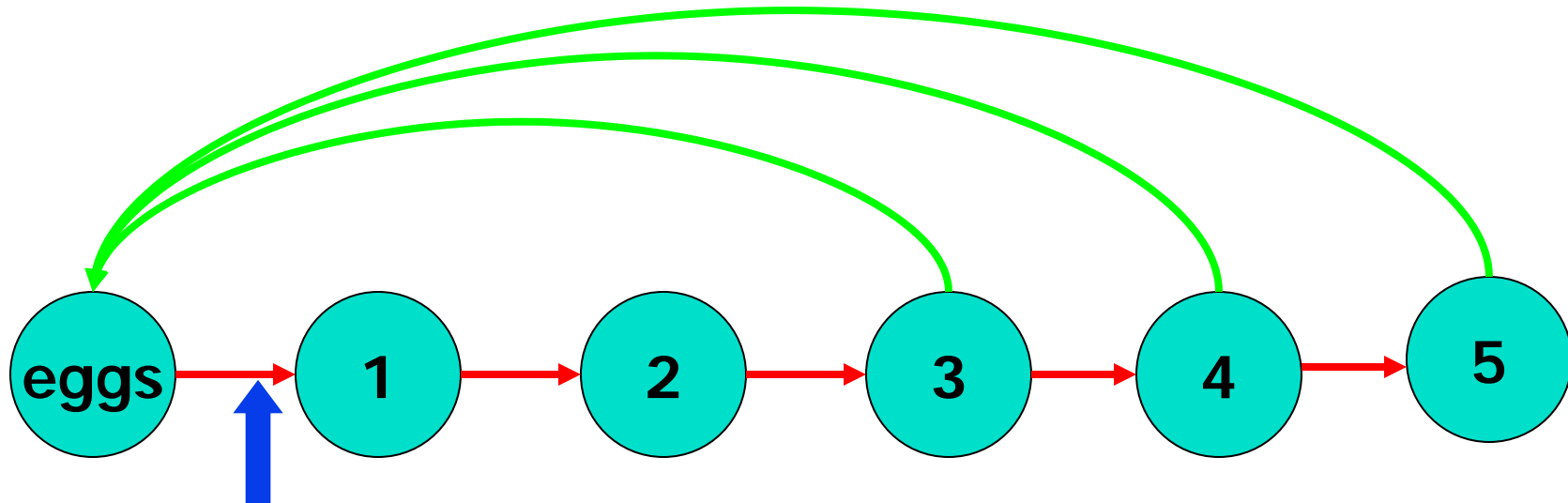
- ▶ Validating the diffusion approximation using salmon life-history models
- ▶ Testing the diffusion approximation approach using a database of actual salmon time series





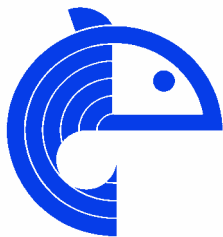
Cross-validation with models

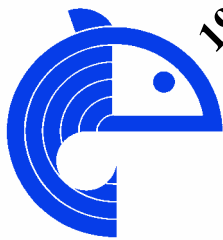
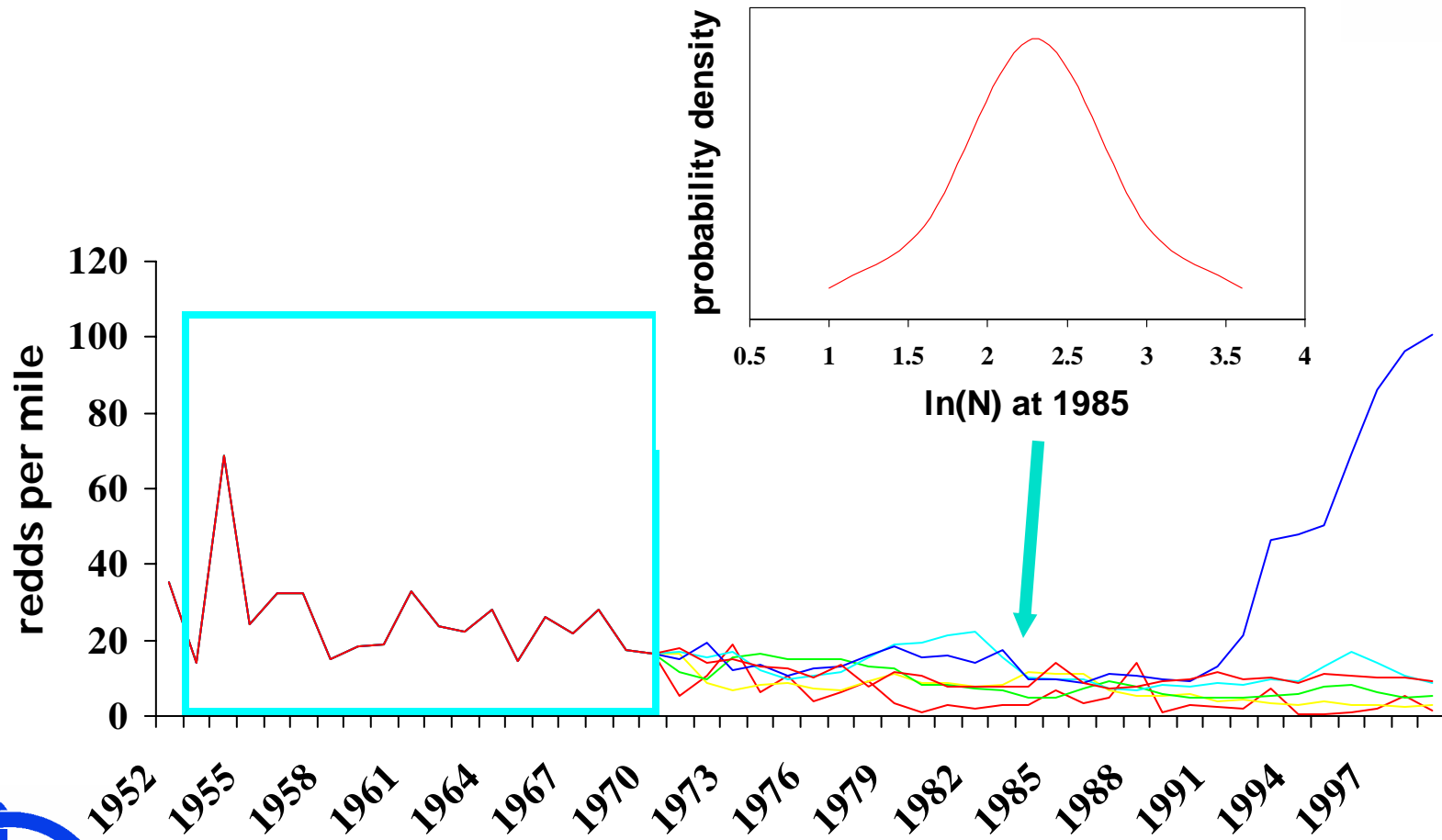
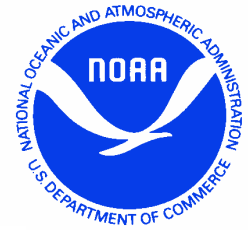
Matrix life-history model for salmon

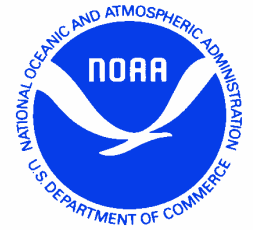


Density-dependence
in egg-to-parr survival

Models prepared for
Snake R spg/sum chinook
Snake R fall chinook
U Columbia R steelhead







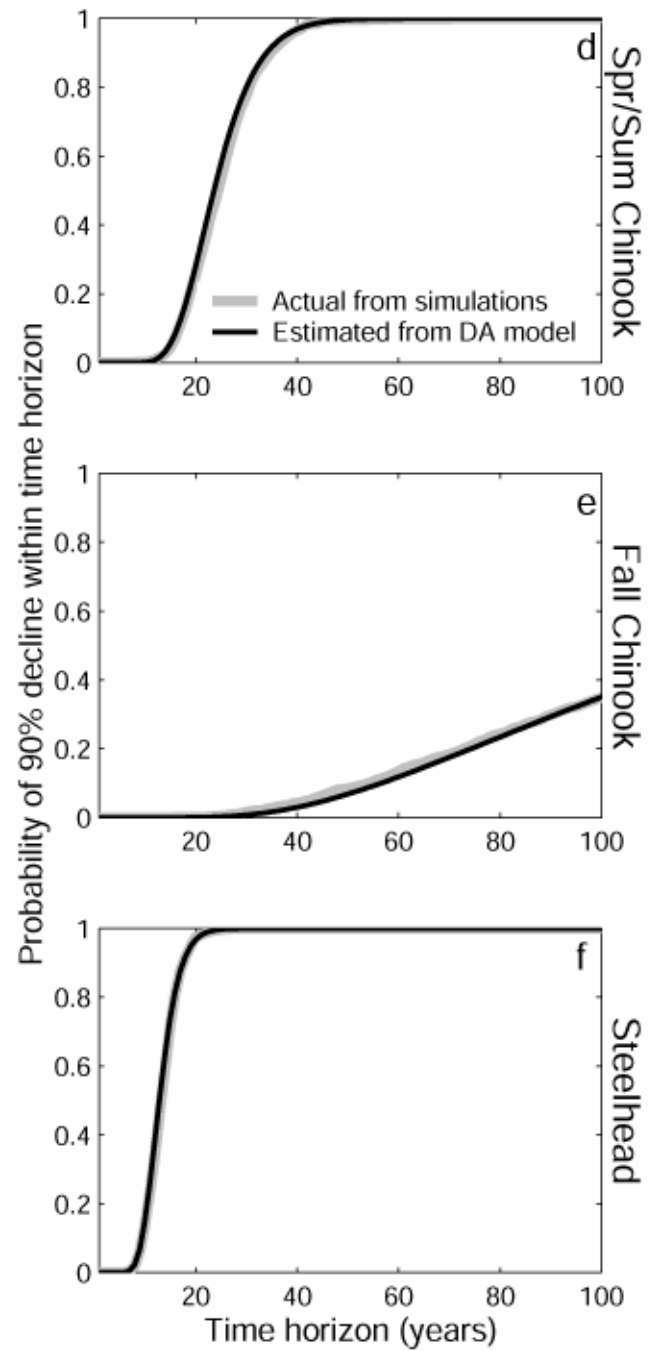
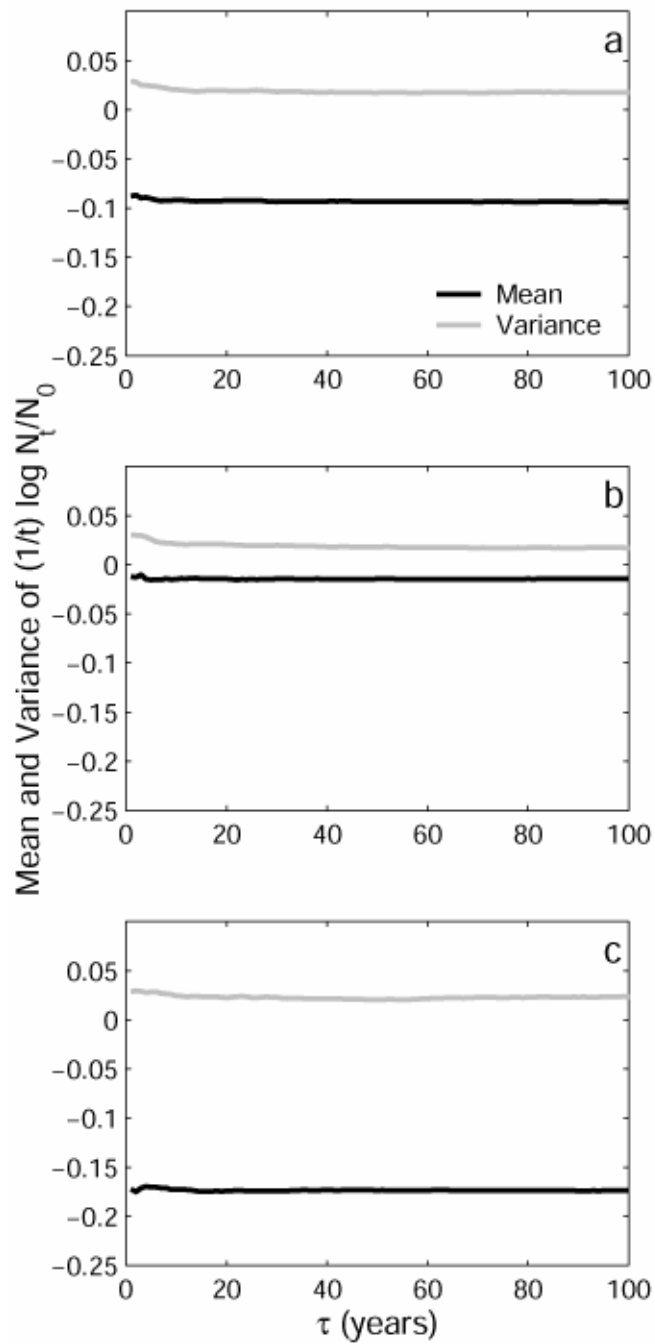
Characteristics of DA model

Mean and variance of the population sizes increases linearly

- ▶ $(1/t) \times \text{mean of } \log(N(t)/N(0)) = \text{a constant \#1}$
- ▶ $(1/t) \times \text{variance of } \log(N(t)/N(0)) = \text{a constant \#2}$

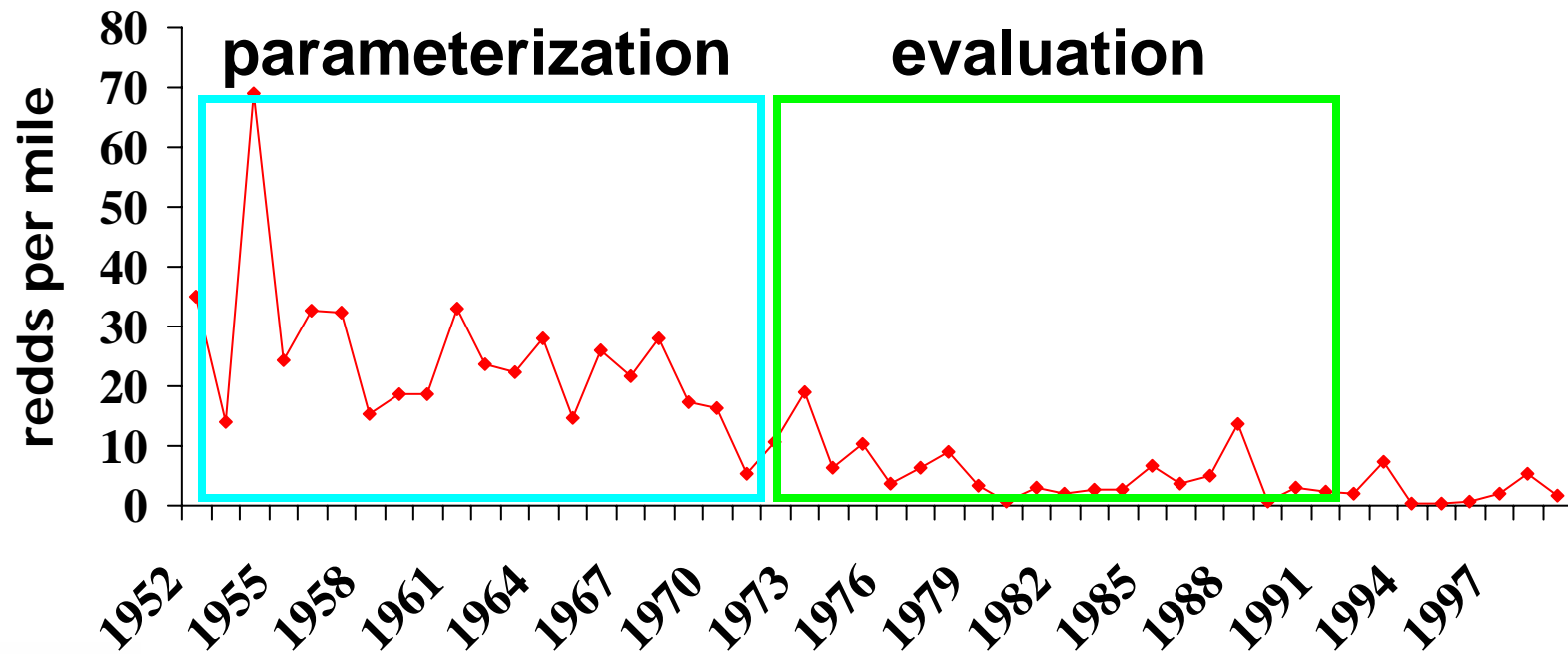
Probability of crossing thresholds has a specific relationship to these 2 constants

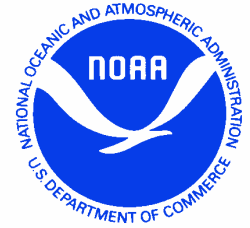




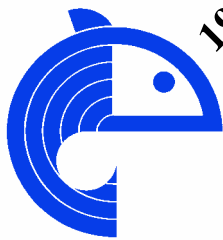
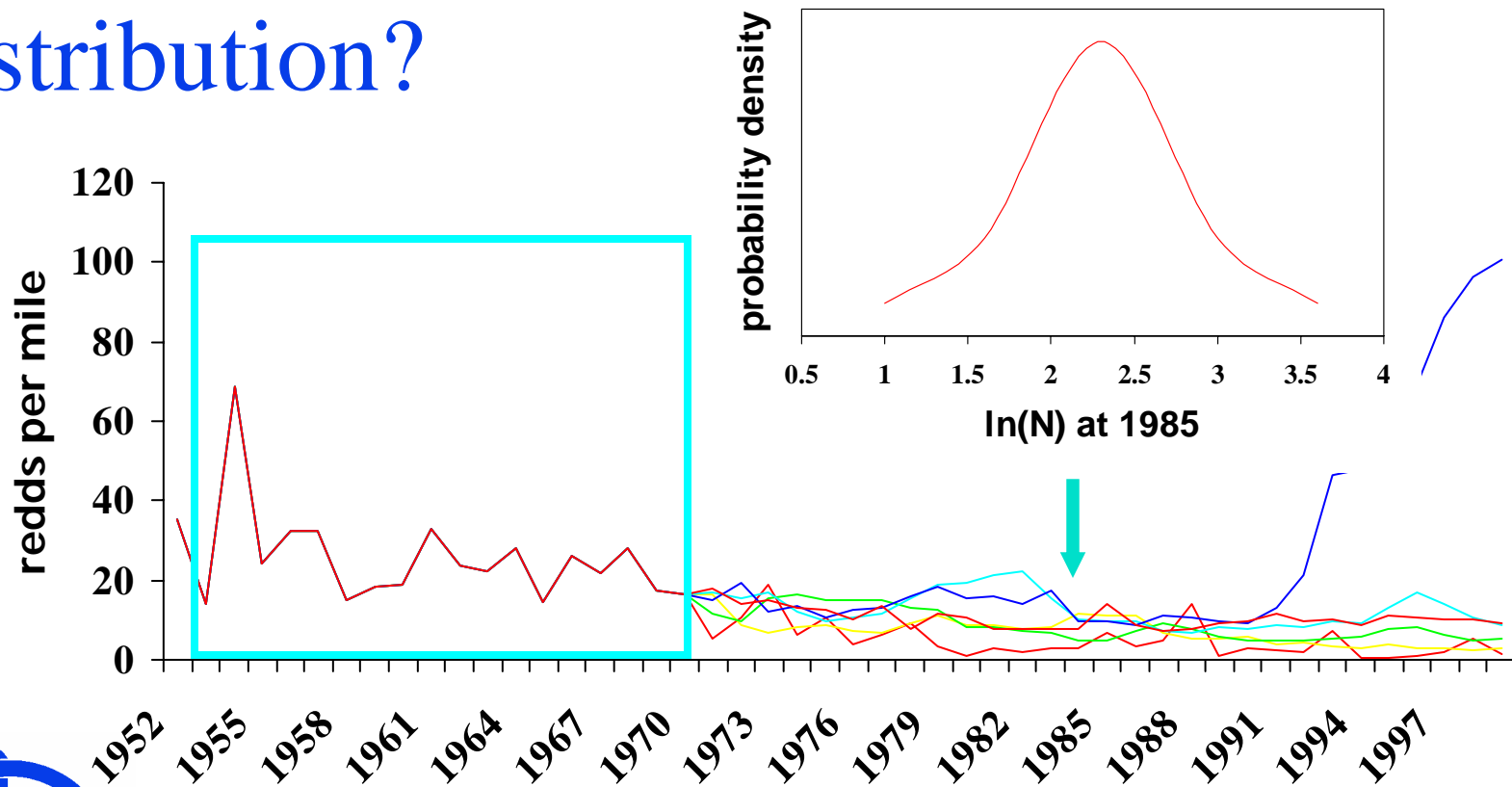
Cross-validation with data

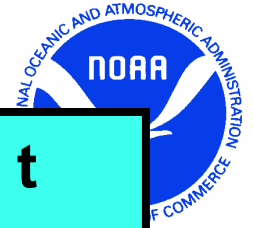
- 147 chinook and 42 steelhead 30-70 year time series from ESUs in WA, OR, and CA





Do the projected population sizes follow the expected theoretical distribution?

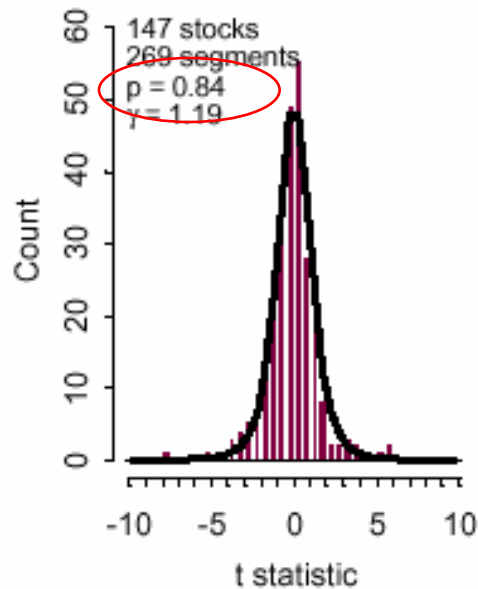




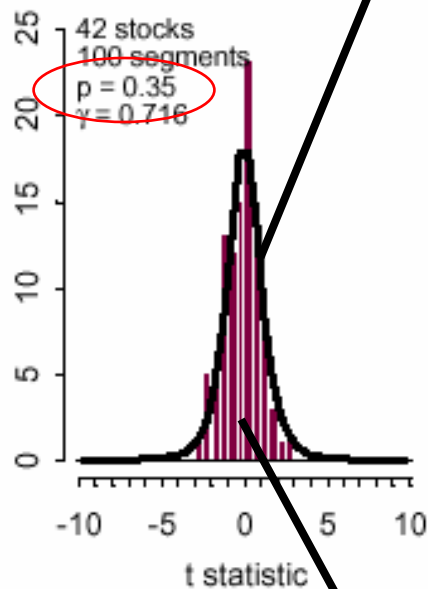
Results for population distribution

Predicted t distribution

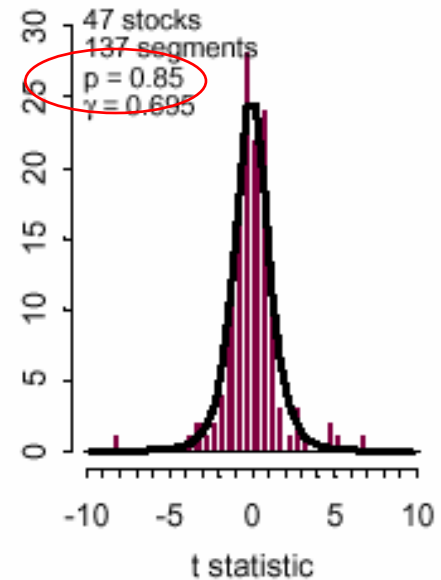
Chinook



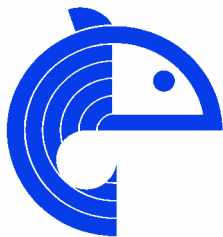
Steelhead

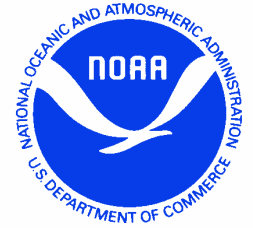


Snake R Spr/Sum



Histogram of actual t statistics

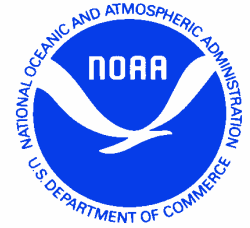




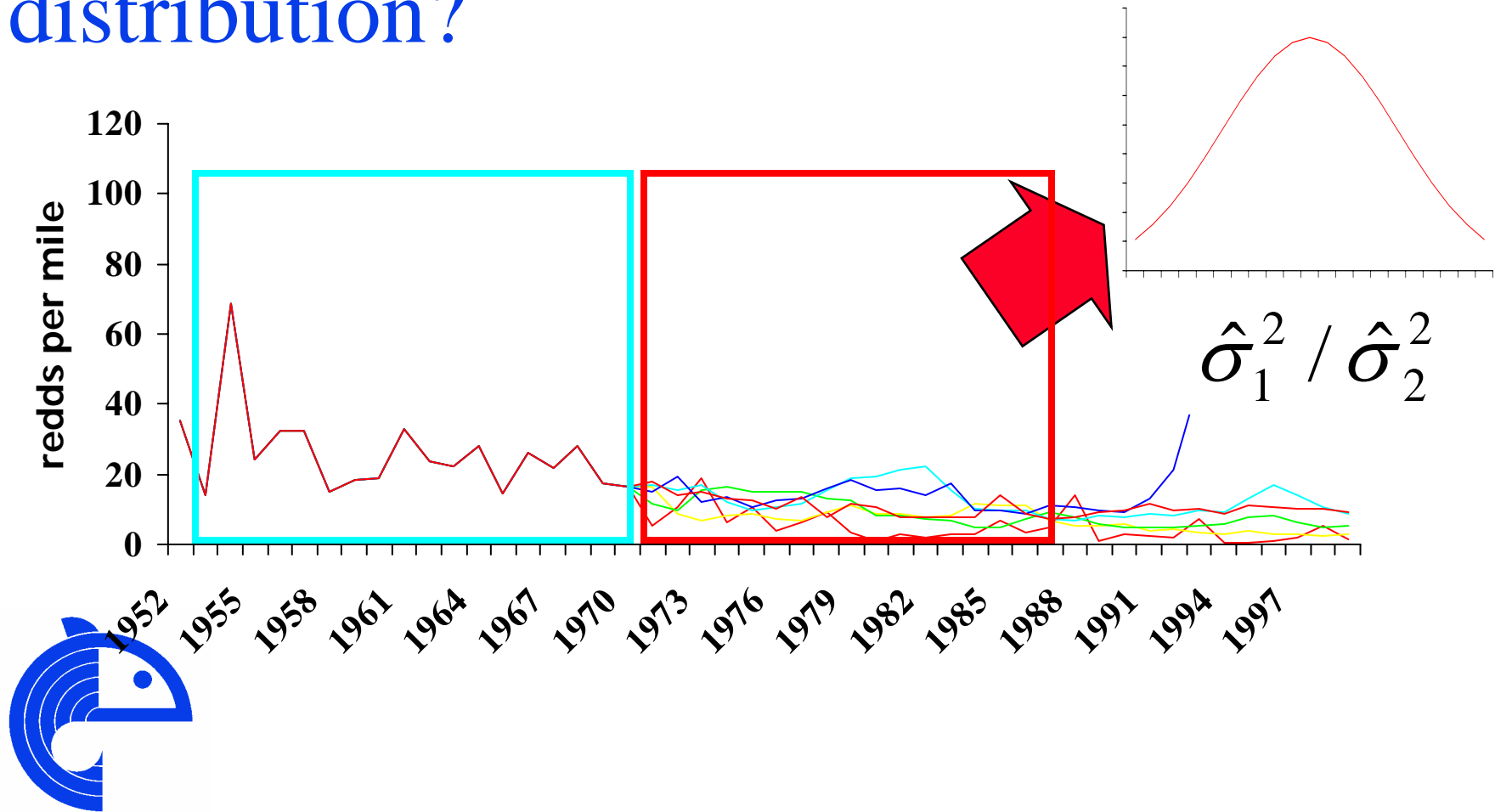
Trend in the rate of decline?

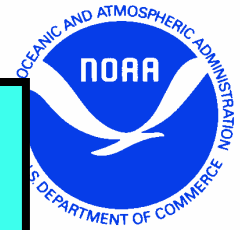
- ▼ Fluctuating or declining stocks
 - ▼ No significant trend
- ▼ Rapidly increasing stocks
 - ▼ Significant negative trend
 - ▼ Estimate of μ lower for bigger population size





Does the estimated process error follow the expected theoretical distribution?

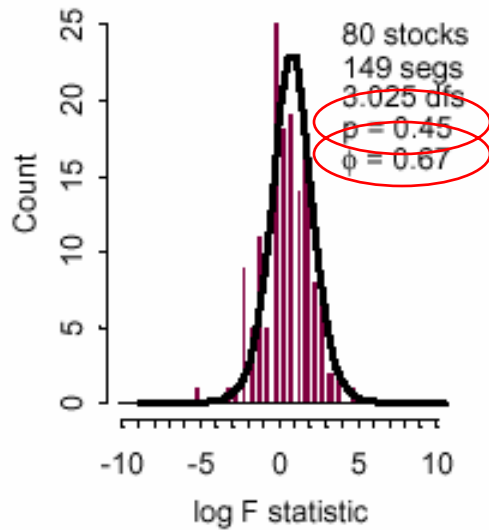




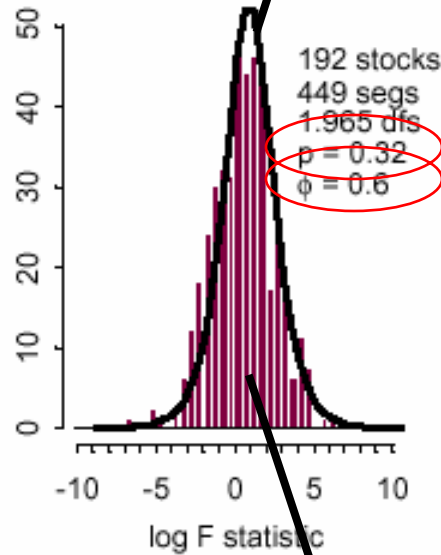
Results for σ

Predicted F distribution

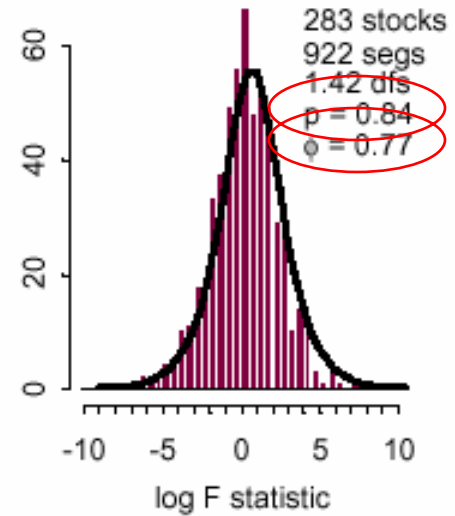
20 years



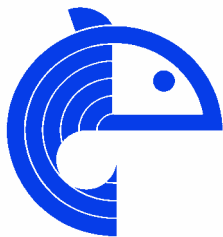
15 years

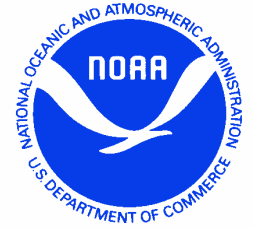


10 years



Histogram of actual F statistics





Trend in σ ?

- ▼ Estimate of σ was higher when counts were really small

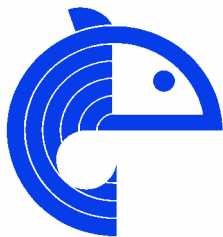
- ▼ Demographic stochasticity?

- ▼ Sampling effect?

Estimate of σ sensitive to percent of sampling error in the observation

Percent error tends to be larger when counts are small

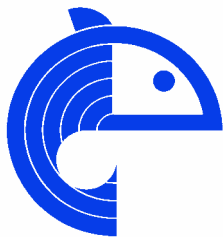
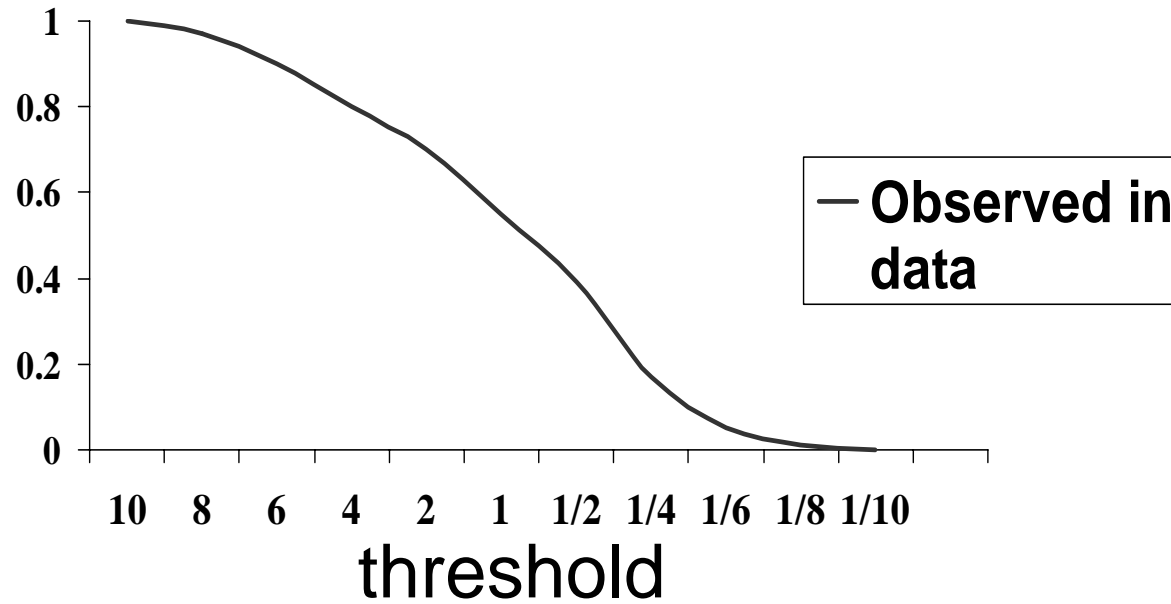
e.g. Dunham and Rieman. 2001. Sources and magnitudes of sampling error in redd counts for Bull Trout. *North American Journal of Fisheries Management* 21:343–352



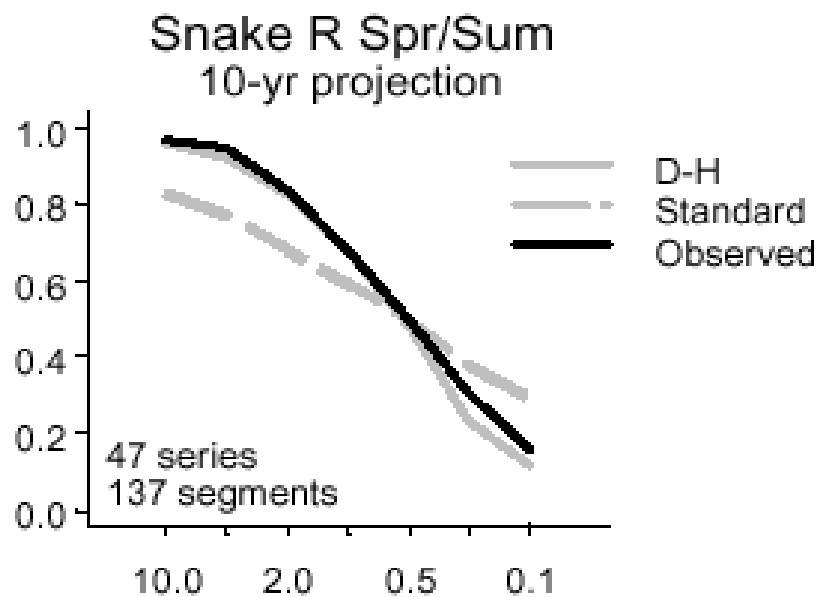
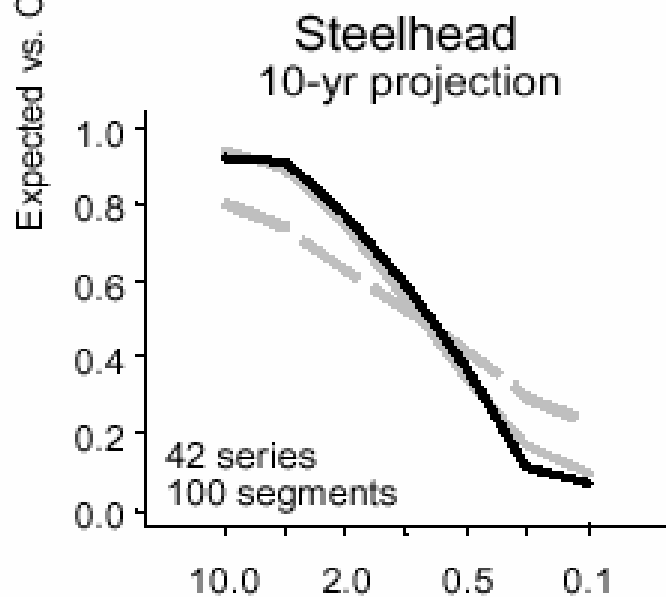
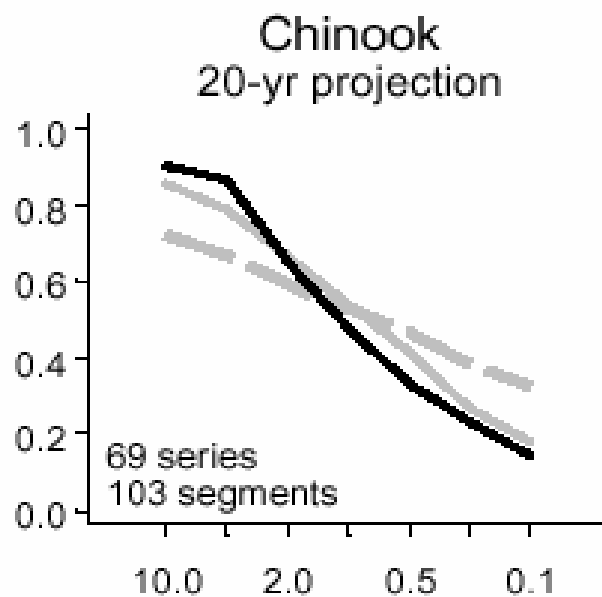
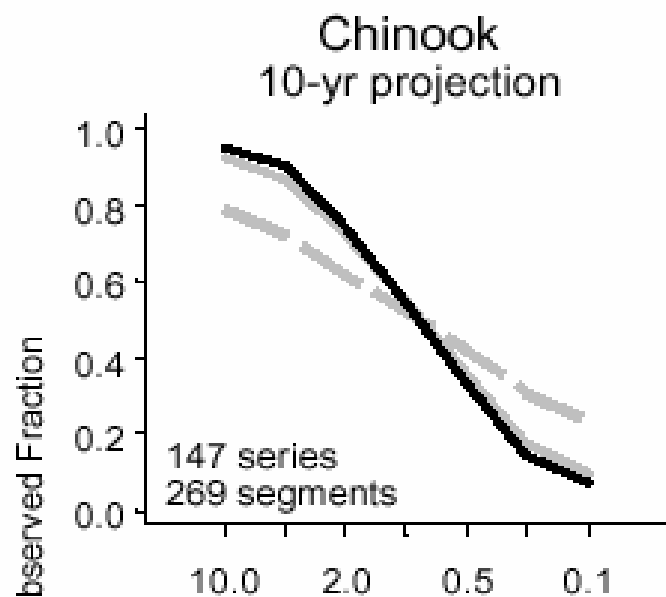


Does the DA model predict the frequency of actual declines?

fraction of stocks that dip below a threshold

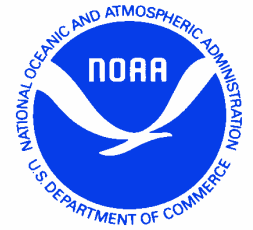


(rel. to size at the start of the eval. period)



— D-H
- - Standard
— Observed

Population Size Threshold (x)



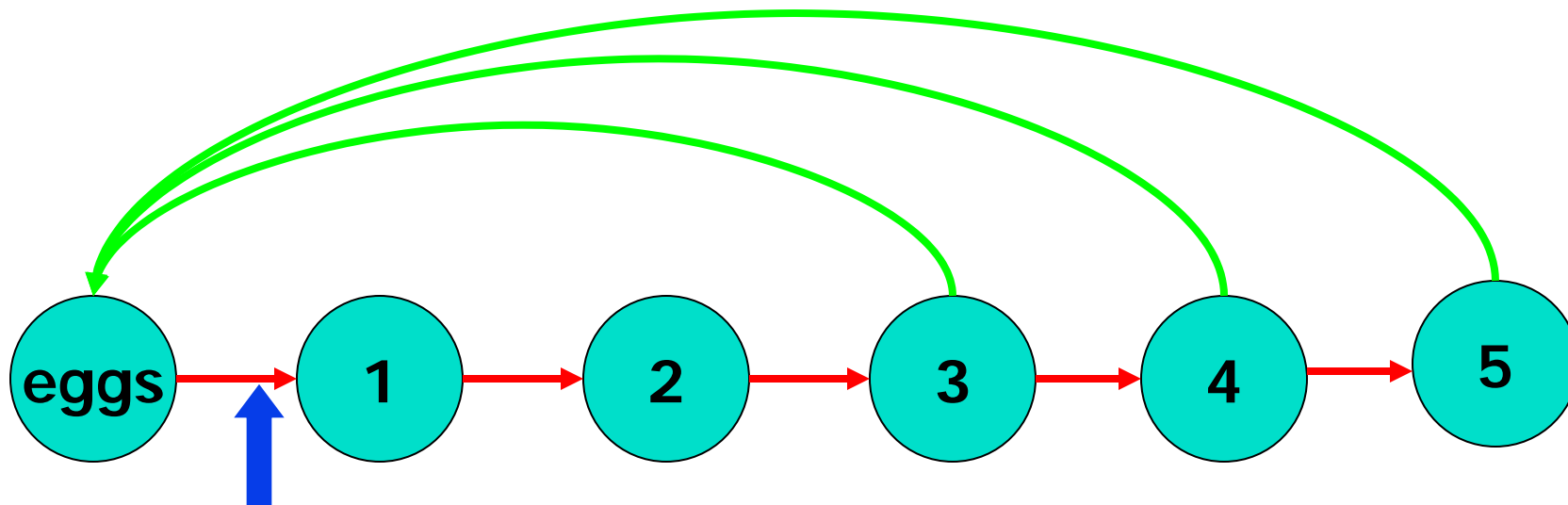
#2 Parameter estimation

A DA model may exist that models a salmon population, but we still have to estimate that model.

- ▼ Dennis methods (assume no non-process error)
- ▼ Runsum (used in the Biop)
- ▼ Heyde-Cohen (not based on DA)
- ▼ State-space approaches using Kalman filters
- ▼ Slope methods (used in Biop)



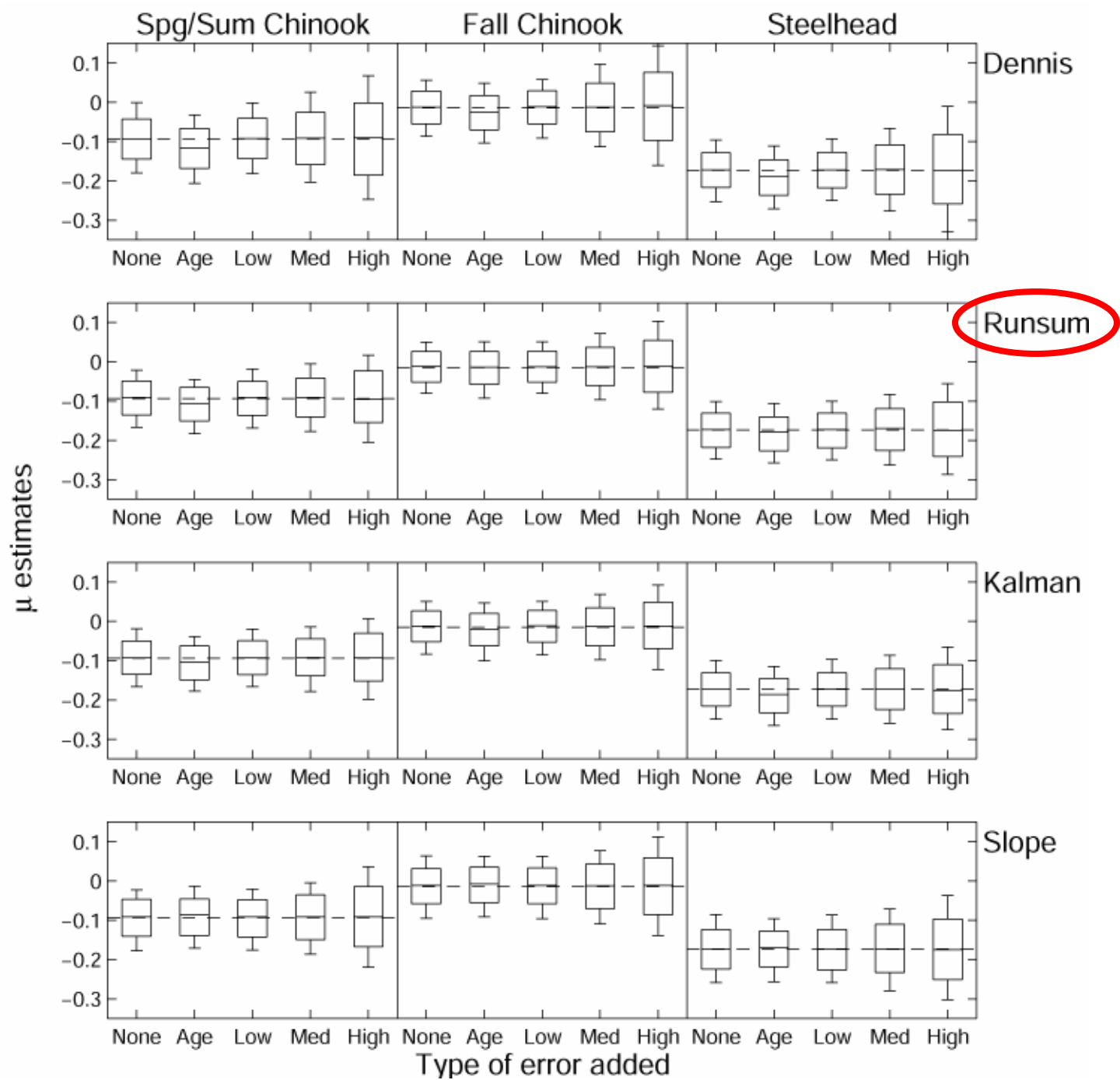
Testing parameterization methods with models

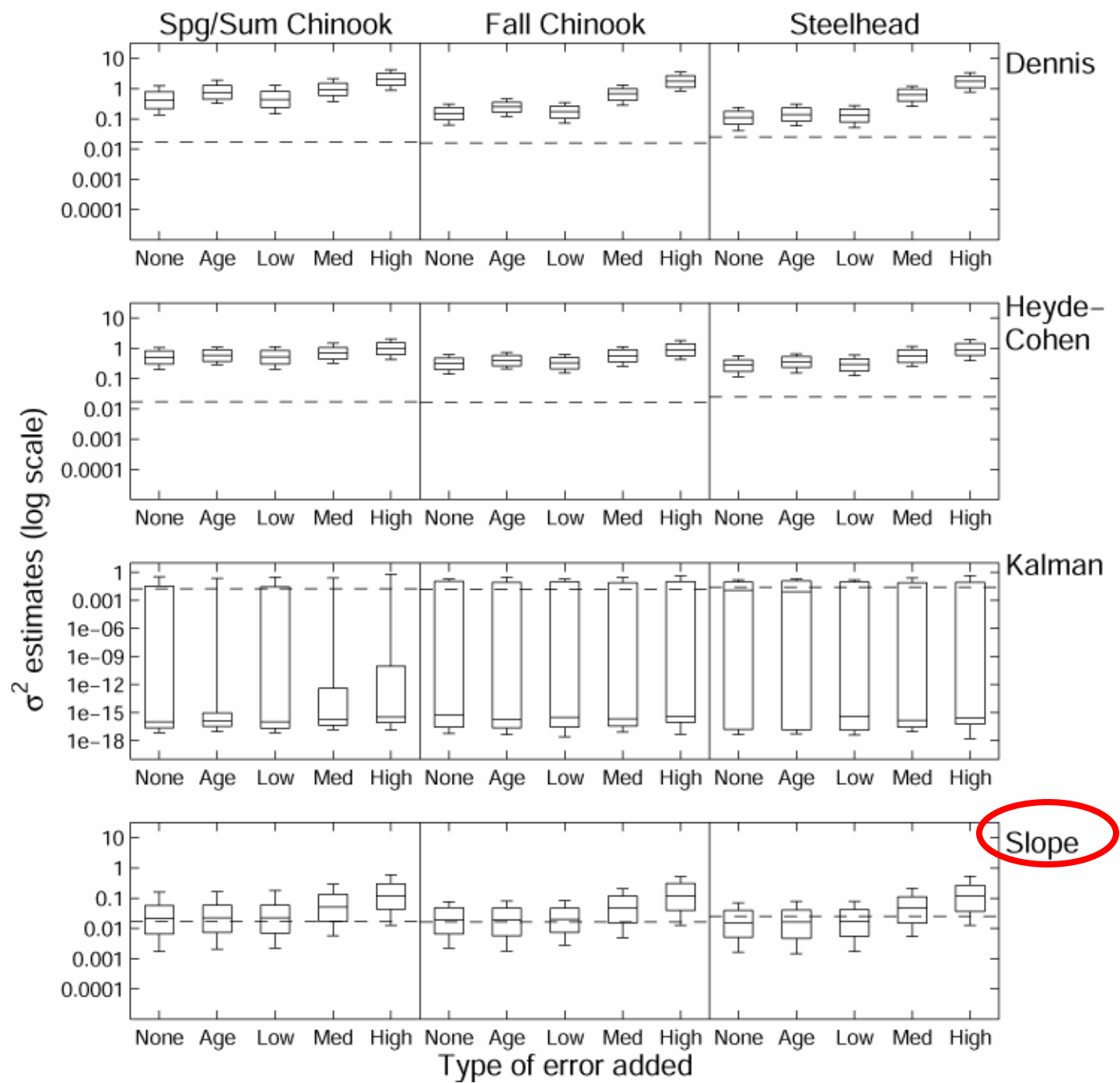


Density-
dependence
in egg-to-
parr survival

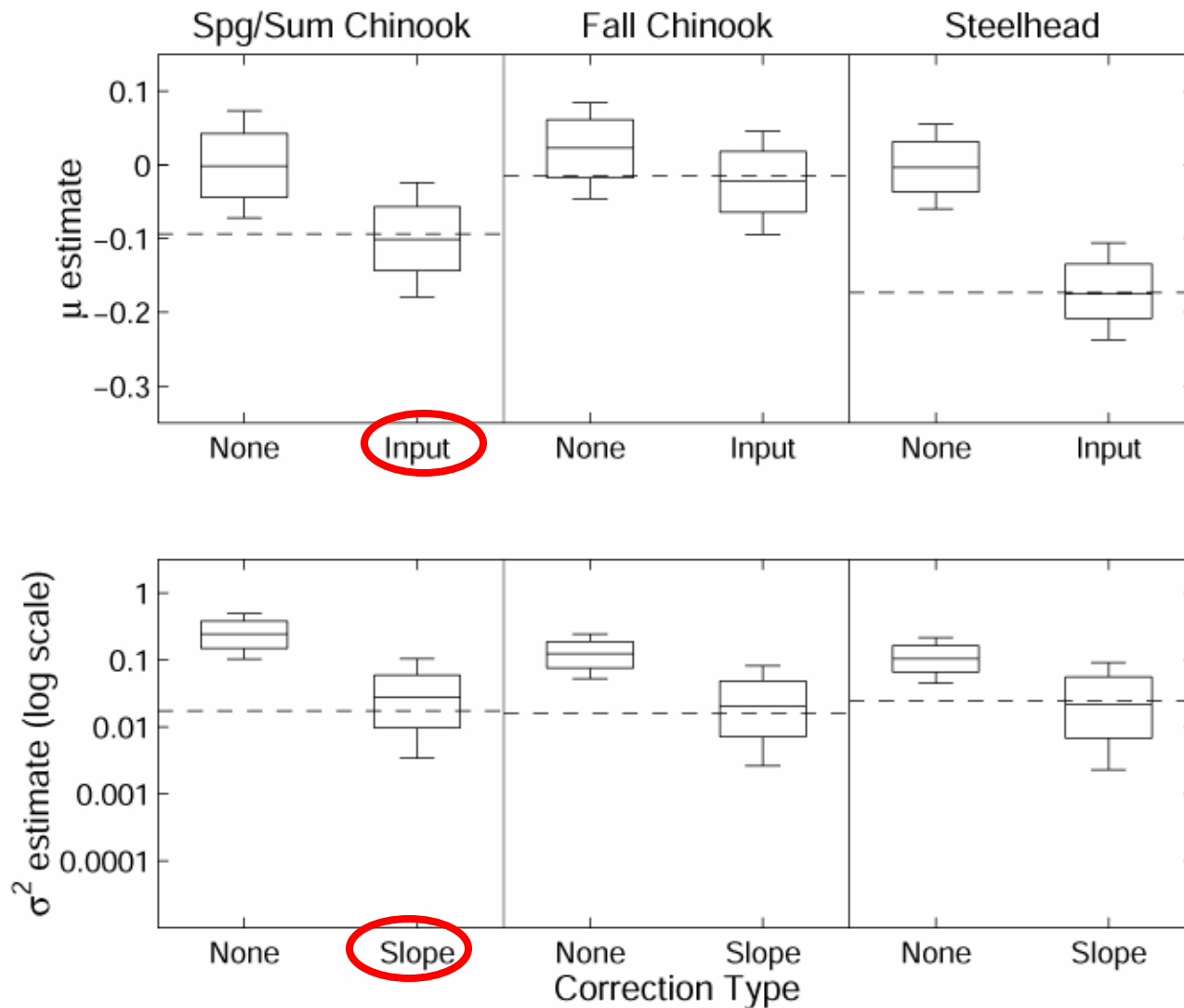


1000s of 20 yr replicates
Different types of error added to
simulated data
Parameters estimated from each
replicate

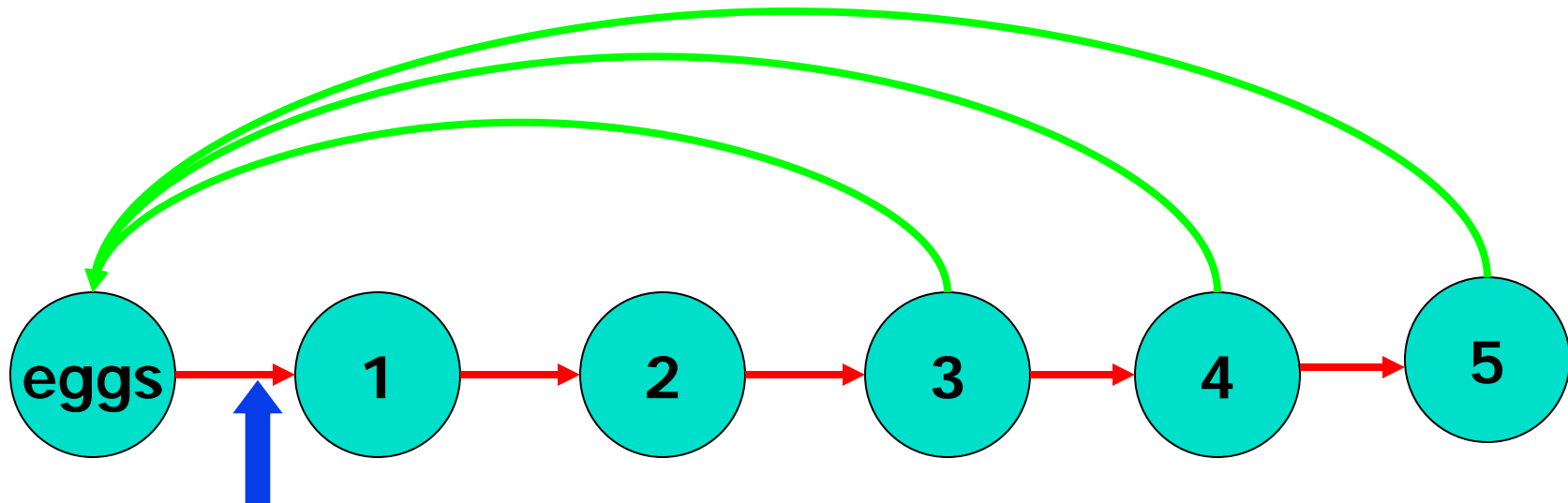




Hatchery correction



#3 Expressing the uncertainty associated with estimates



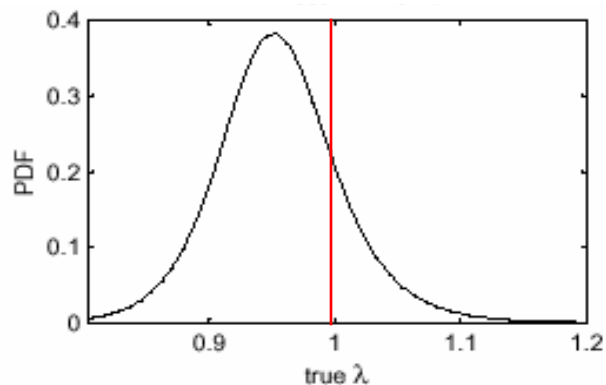
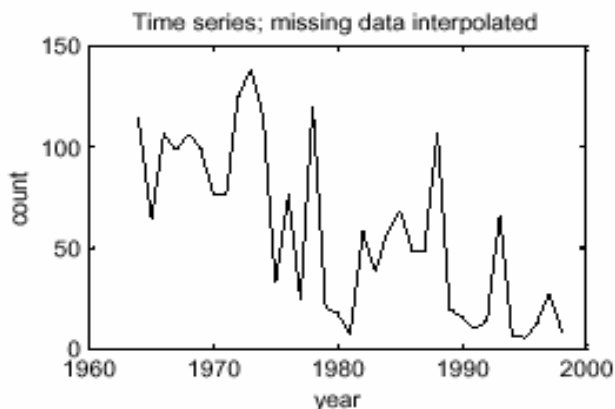
Density-
dependence
in egg-to-
parr survival



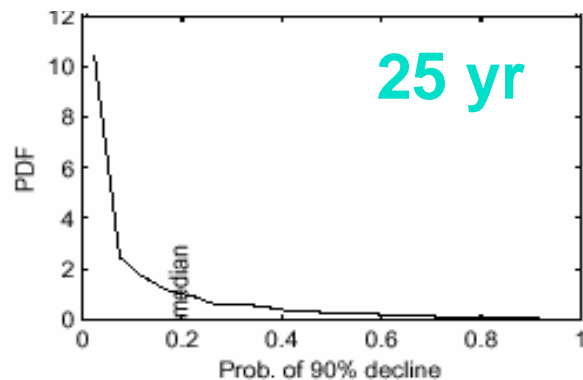
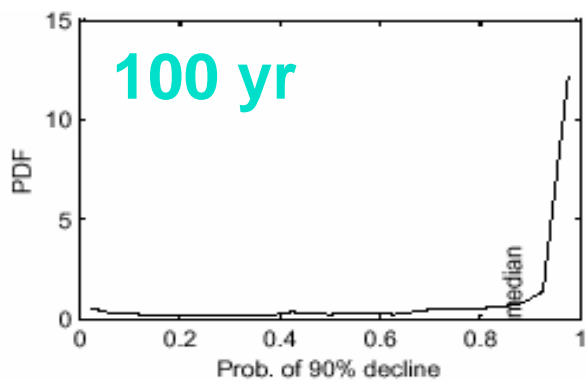
1000s of 20 yr replicates
Different types of error added to
simulated data
Parameters estimated from each
replicate

Lostine River 1964-1998

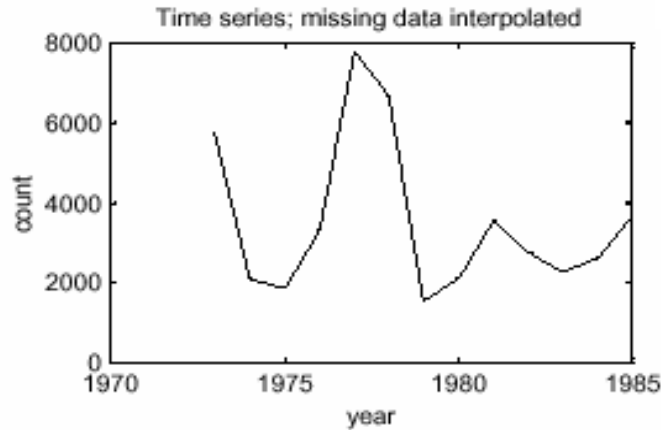
support for different λ 's



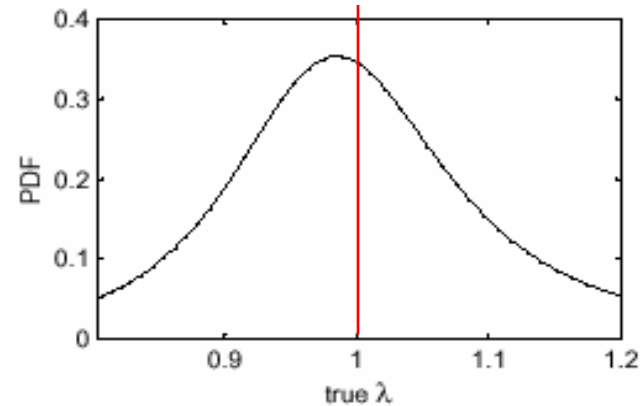
support for different probs of 90% decline



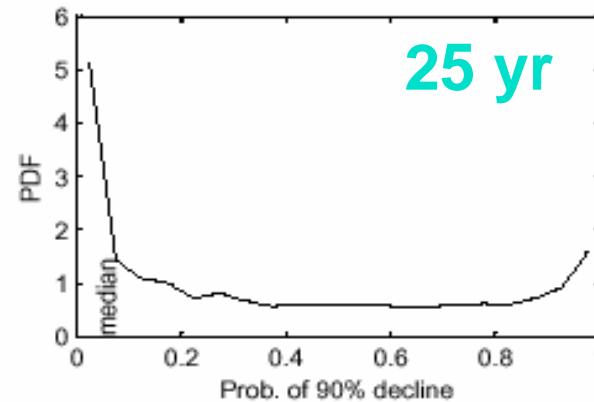
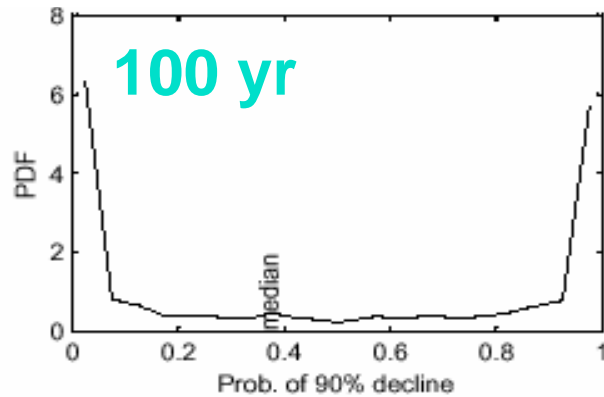
Clearwater River 1973-1985



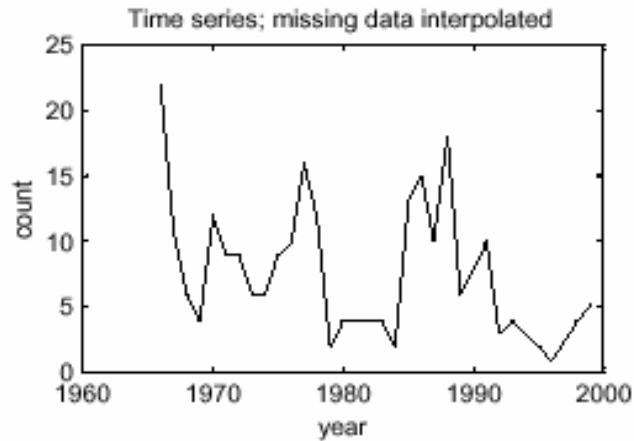
support for different λ 's



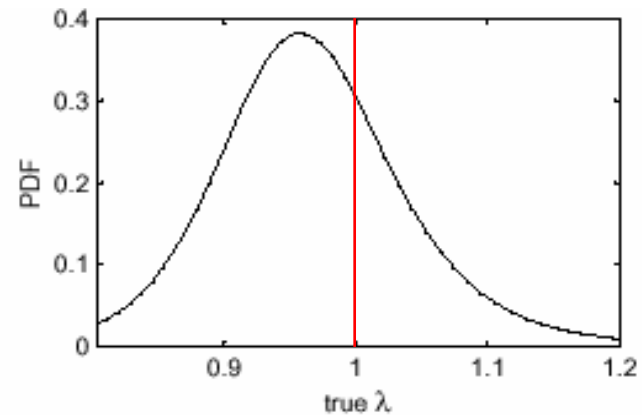
support for different probs of 90% decline



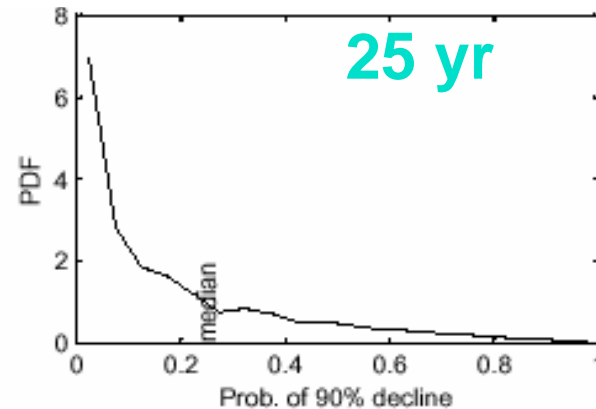
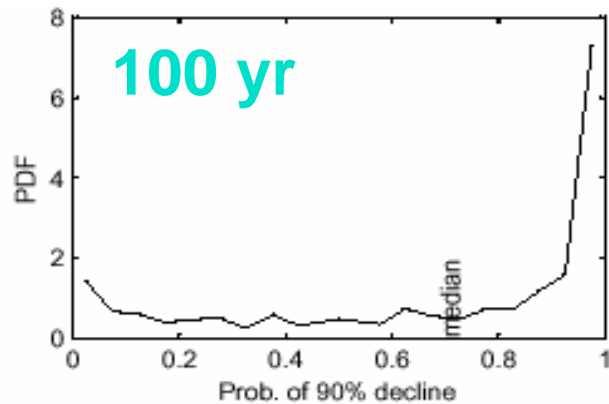
Camp Creek 1966-1999

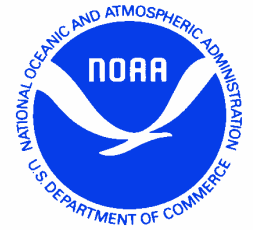


support for different λ 's



support for different probs of 90% decline





Areas for future research

- ▶ Improving estimation via Kalman filter approaches with life-history model 'priors'
- ▶ Improving estimation via priors on the process error by using data from multiple stocks to estimate process error, i.e. an ESU-level process-error estimate rather than stock-by-stock estimates

