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

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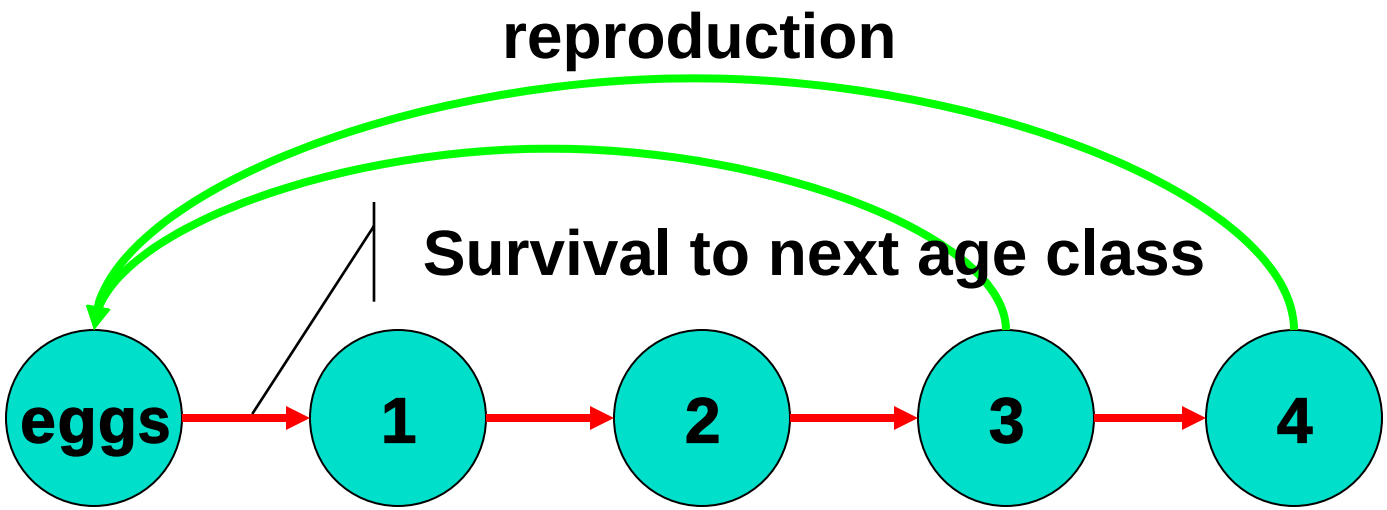
Diffusion approximations

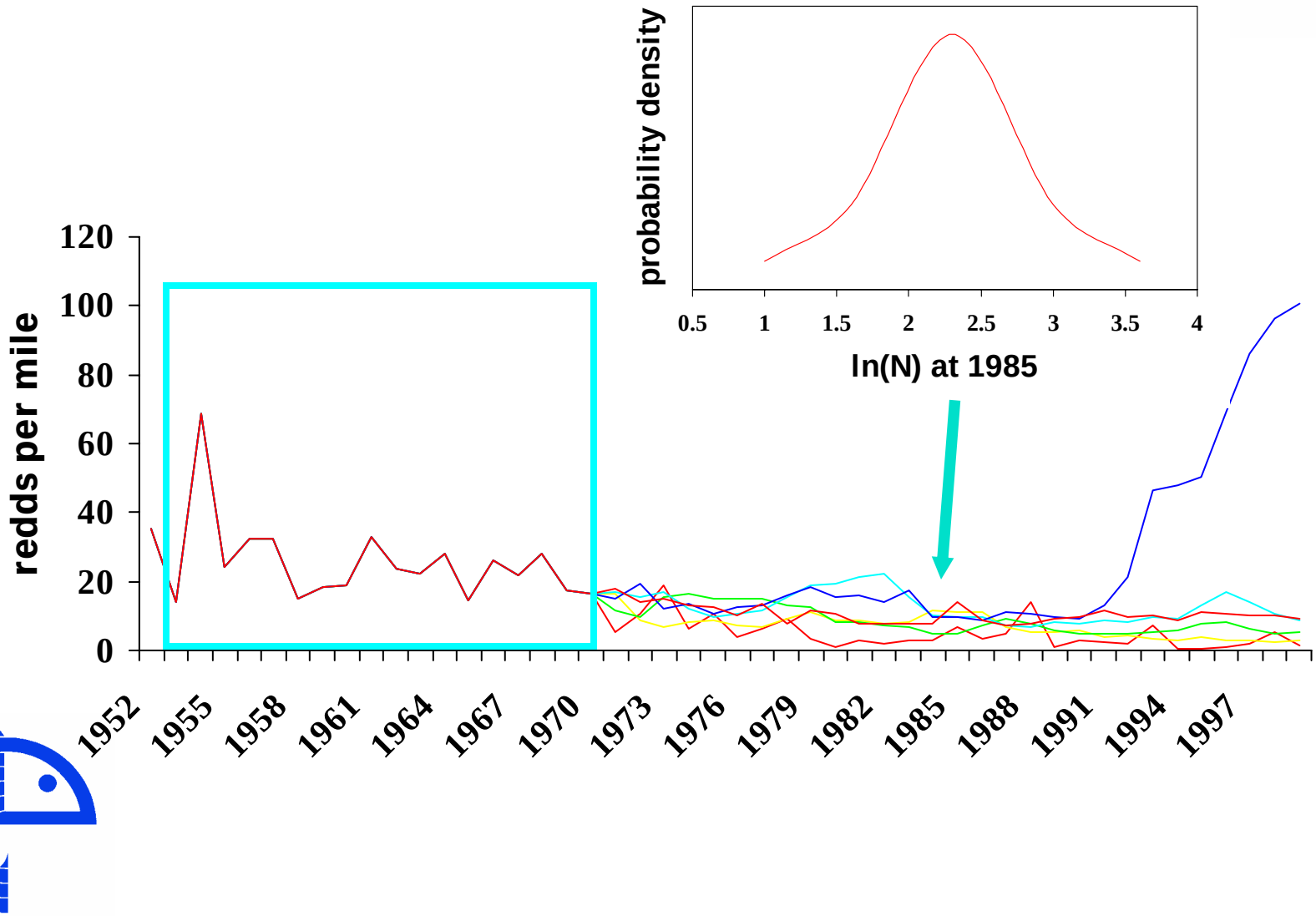


Let reproduction and survival vary yearly

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

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

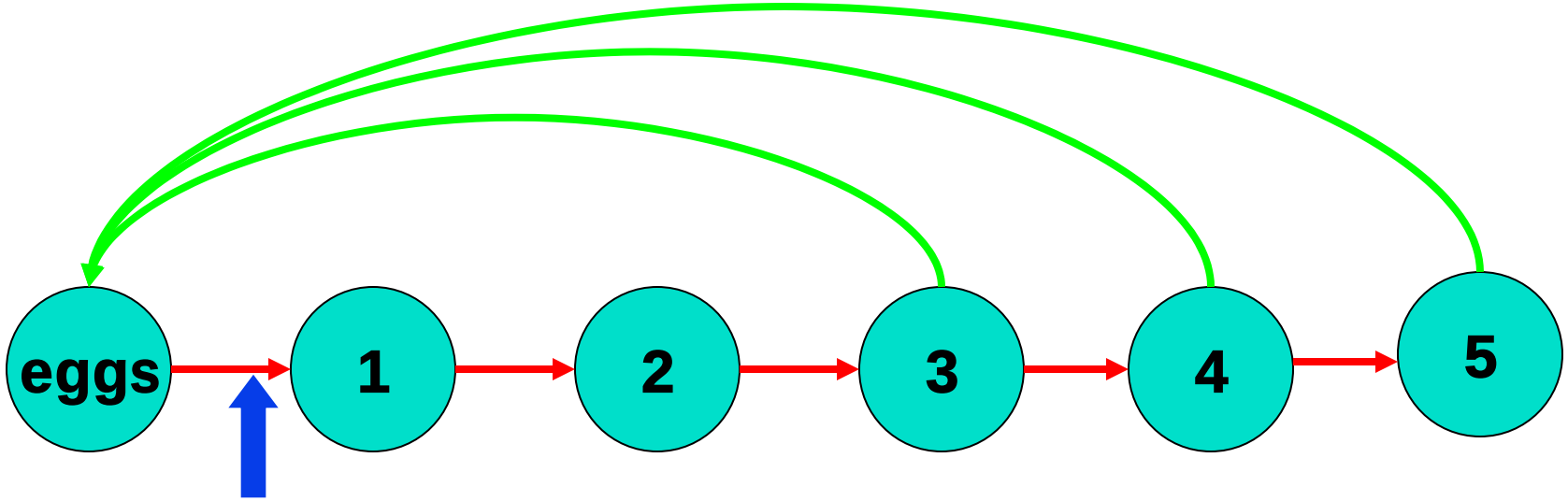
- #1 Does a diffusion approximation model work for salmon population processes and the sorts of salmon data we have in the Pacific NW.
- #2 What are the best ways to estimate the parameters of such a model.
- #3 How can we express the uncertainty in our risk estimates using DA models.

#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



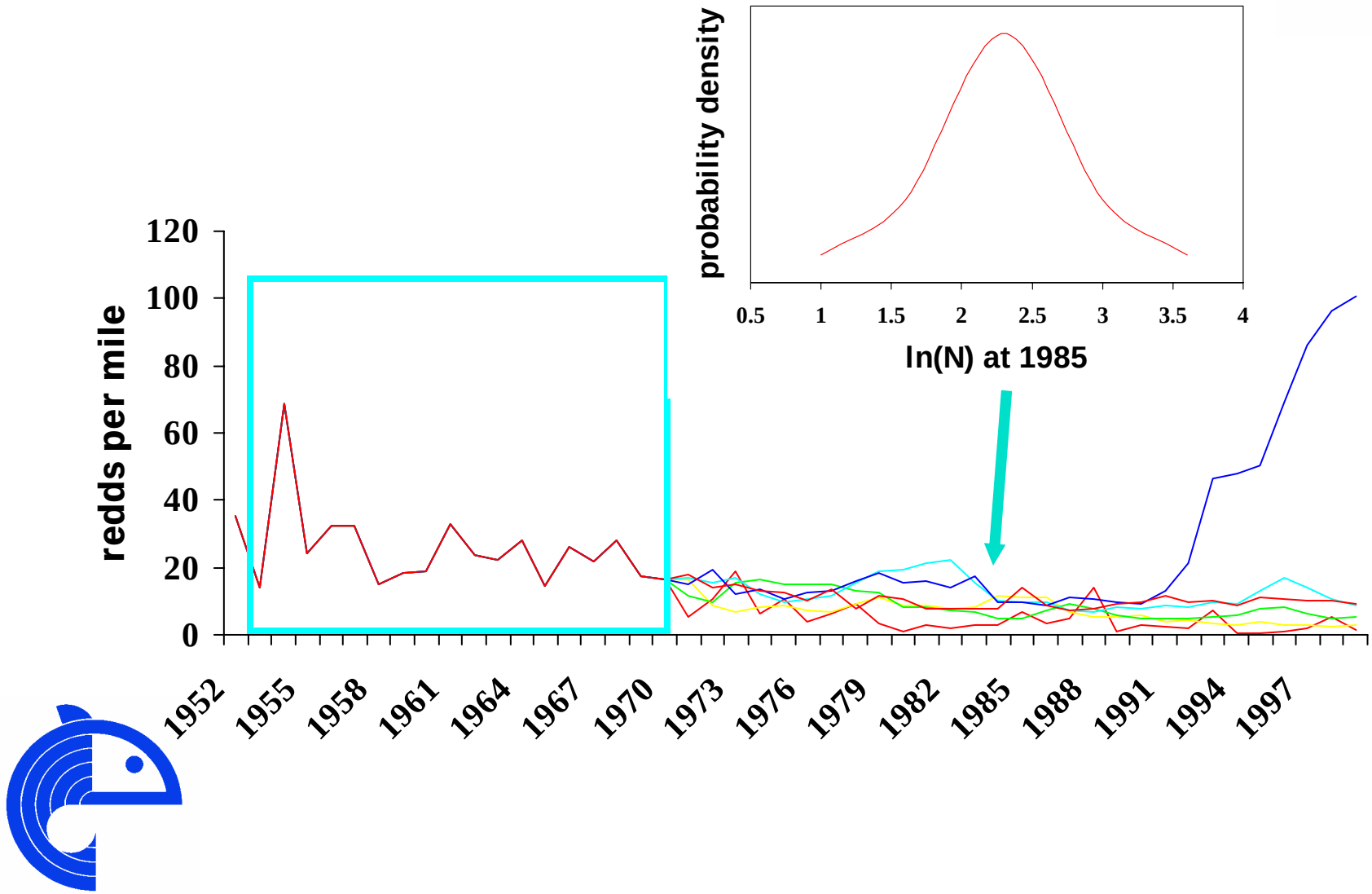
Density-dependence in egg-to-parr survival

Models prepared for

Snake R spg/sum chinook

Snake R fall chinook

U Columbia R steelhead

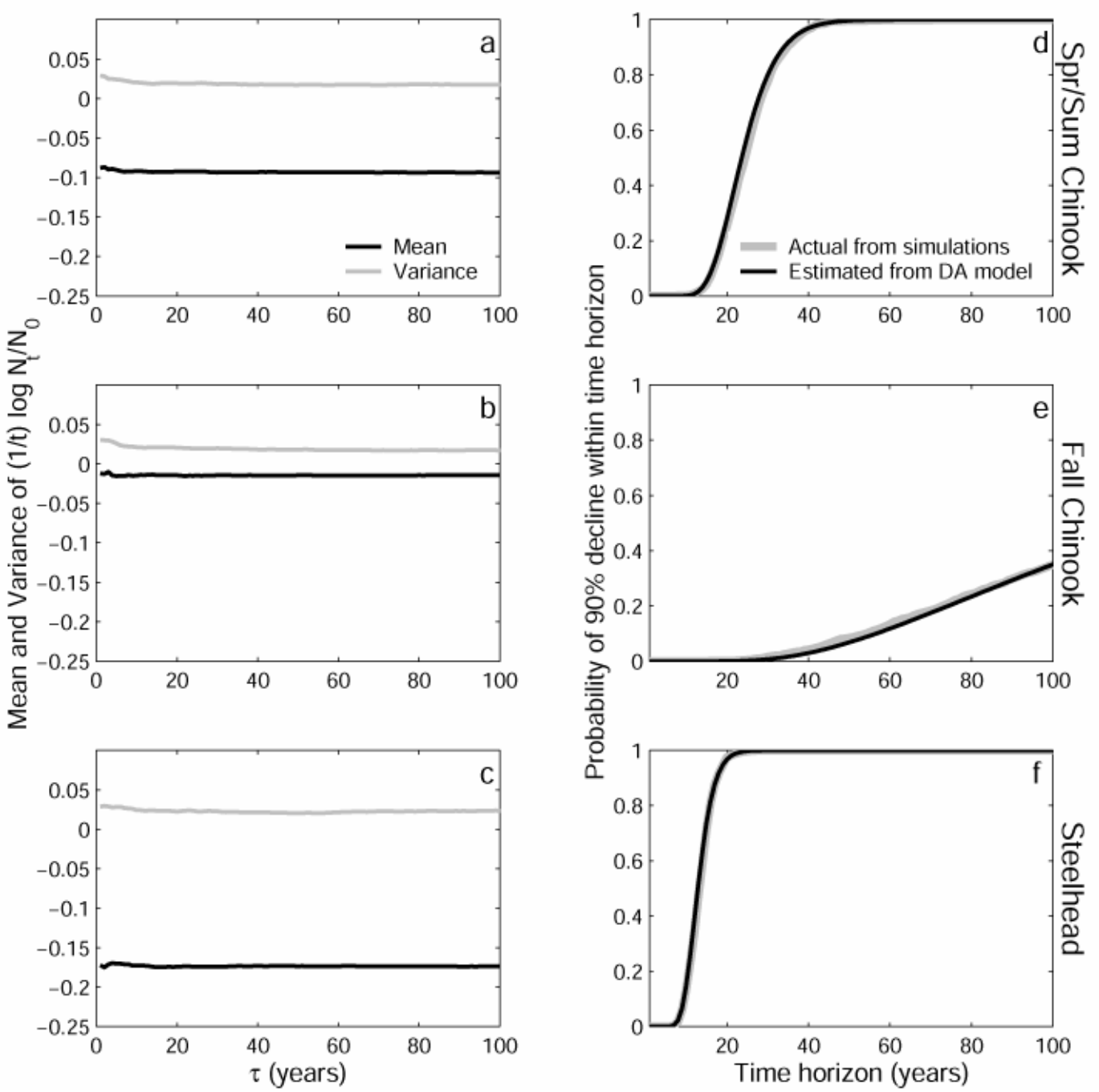

probability density
0.5
1
1.5
2
2.5
3
3.5
4
ln(N) at 1985
redds per mile
120
100
80
60
40
20
0
1952
1955
1958
1961
1964
1967
1970
1973
1976
1979
1982
1985
1988
1991
1994
1997

Characteristics of DA model

Mean and variance of the population sizes increases linearly

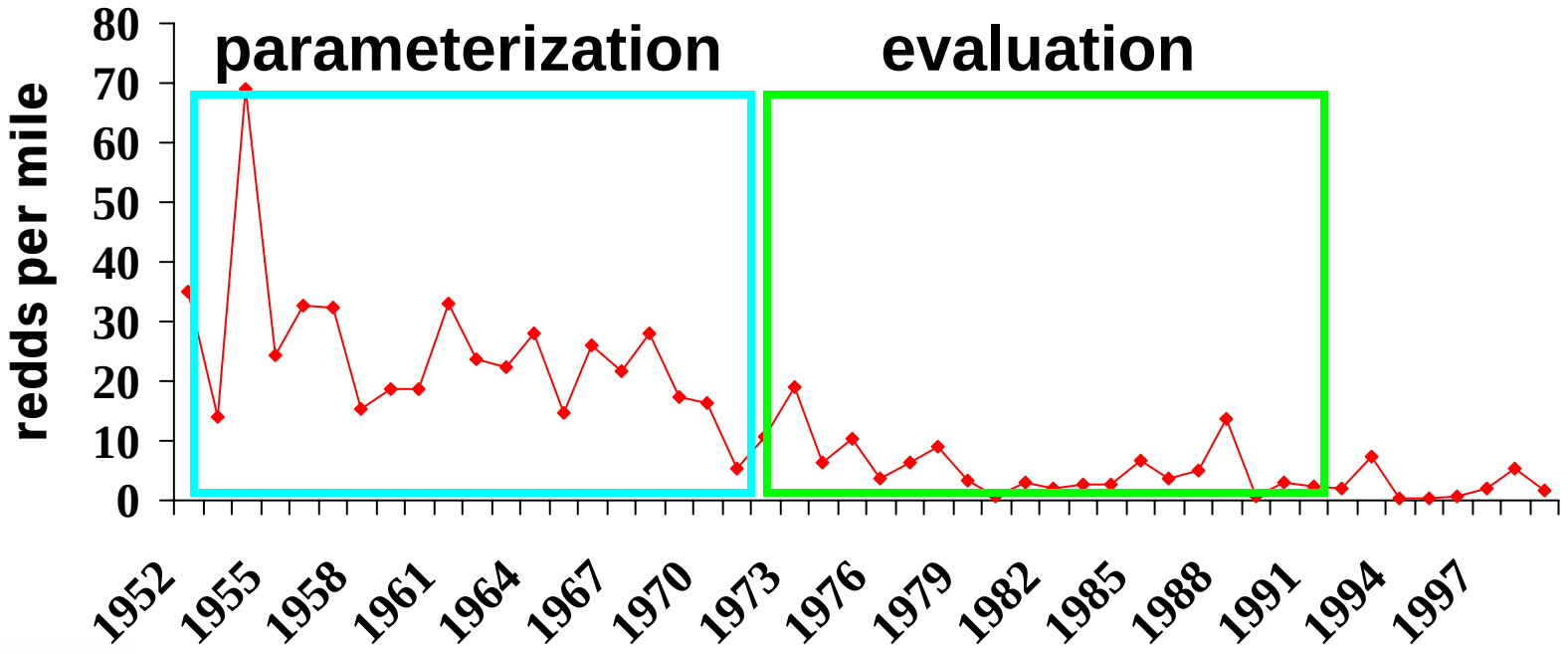
- (1/t) x mean of log(N(t)/N(0)) = a constant #1
- (1/t) x variance of log(N(t)/N(0)) = a constant #2

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

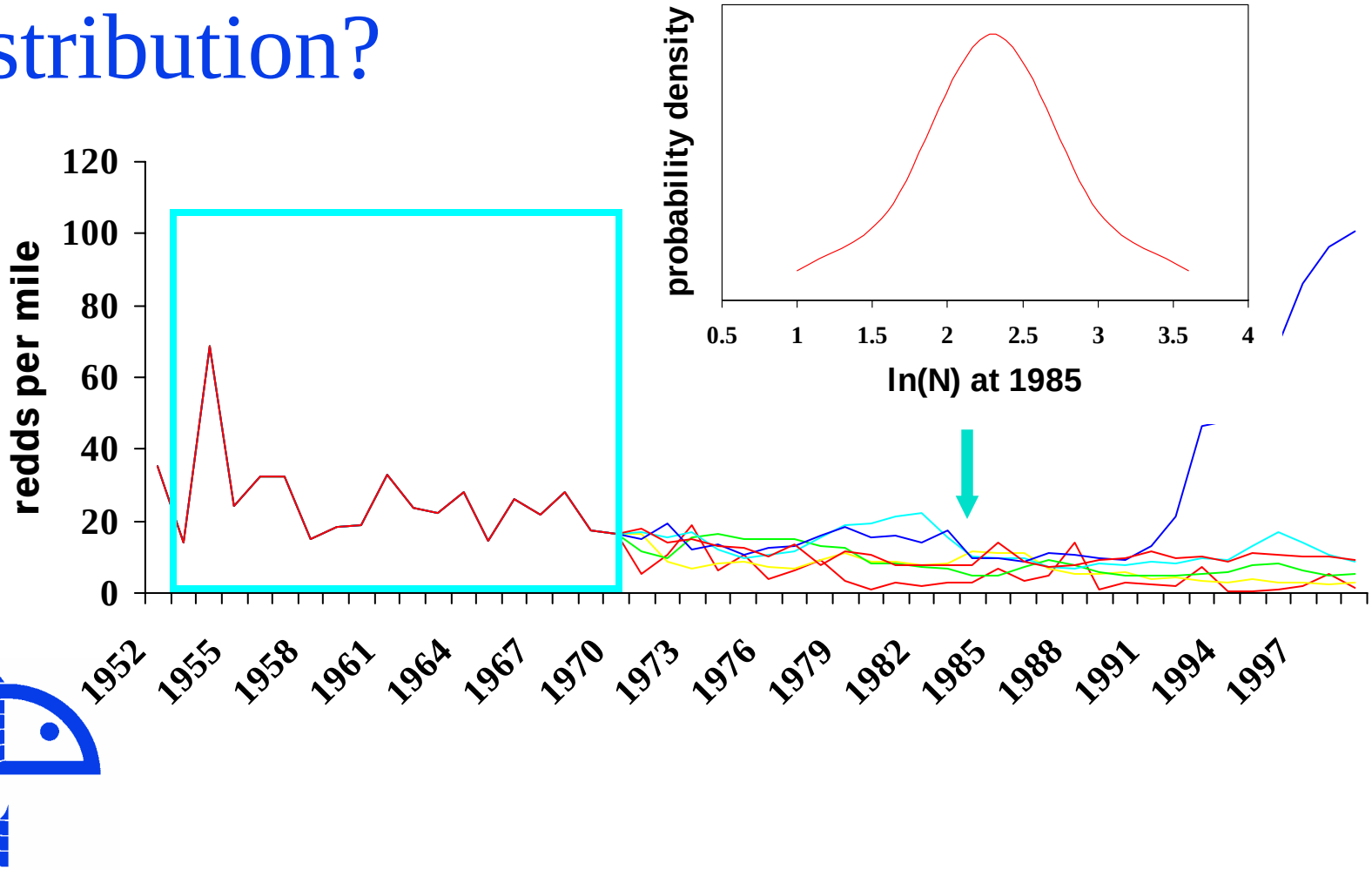

a
b
c
d
e
f
Mean
Variance
Actual from simulations
Estimated from DA model
Mean and Variance of (1/t) log N_t/N_0
Probability of 90% decline within time horizon
τ (years)
Time horizon (years)
Spr/Sum Chinook
Fall Chinook
Steelhead

Cross-validation with data

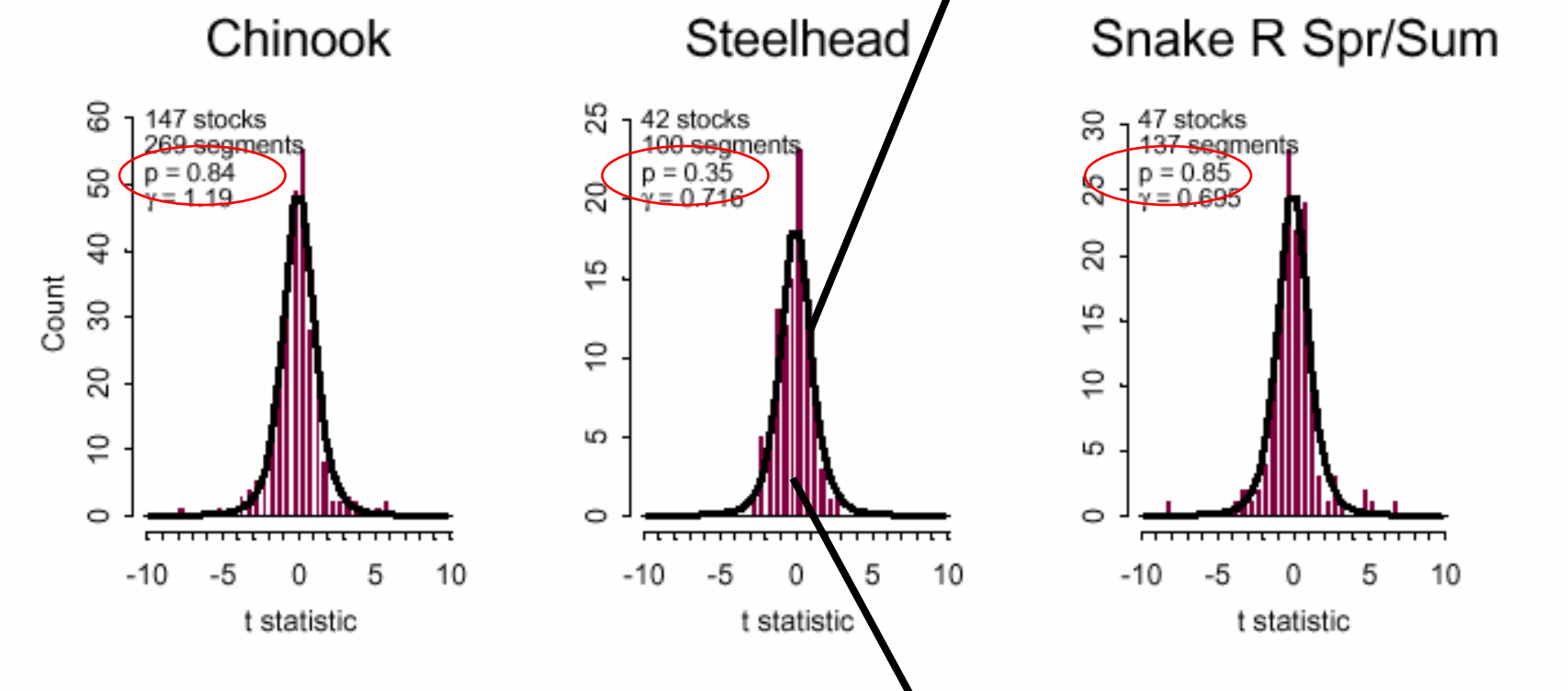
- 147 chinook and 42 steelhead 30-70 year time series from ESUs in WA, OR, and CA



Do the projected population sizes follow the expected theoretical distribution?



Results for population distribution



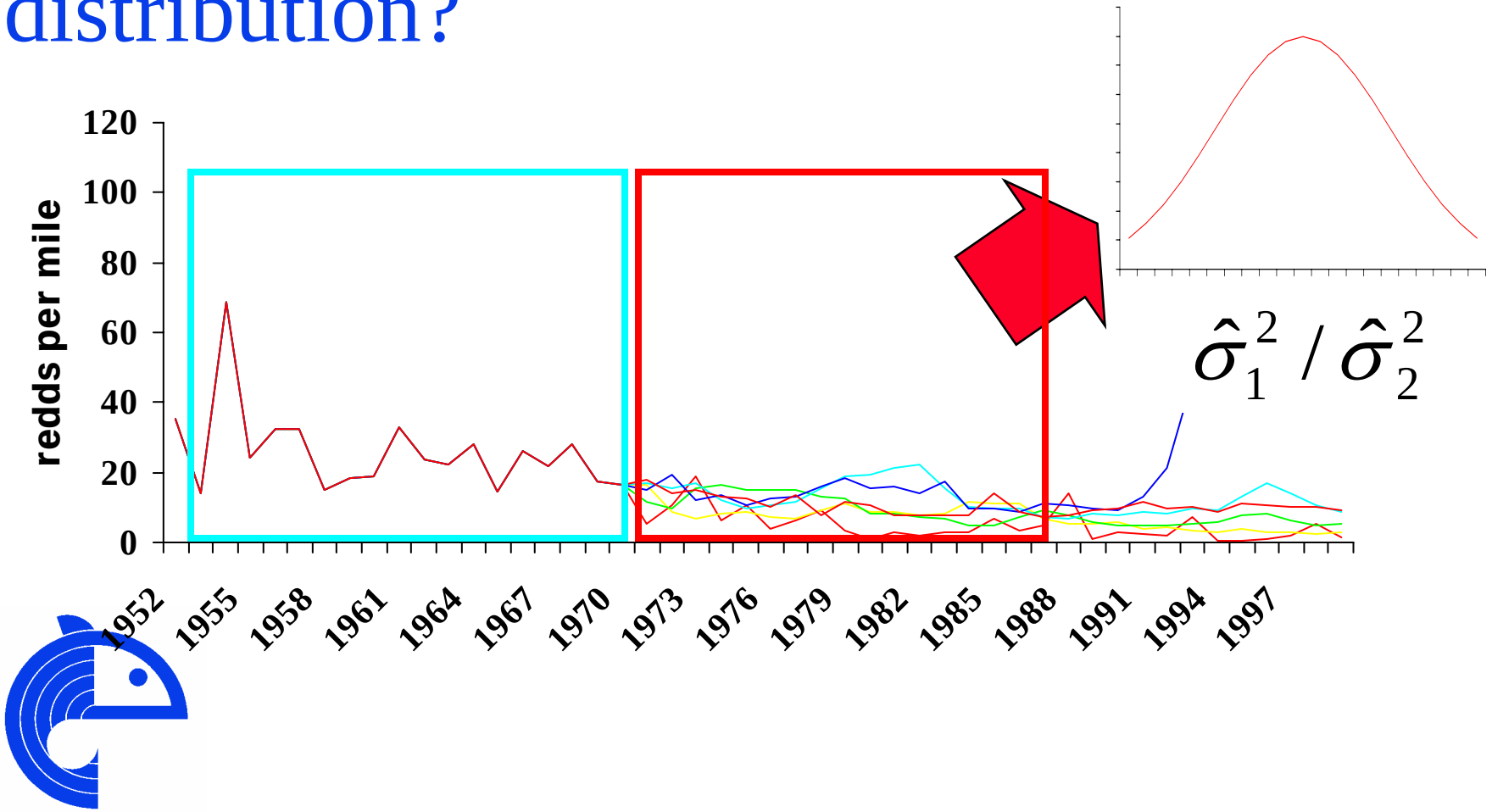
Predicted t distribution

Histogram of actual t statistics

Trend in the rate of decline?

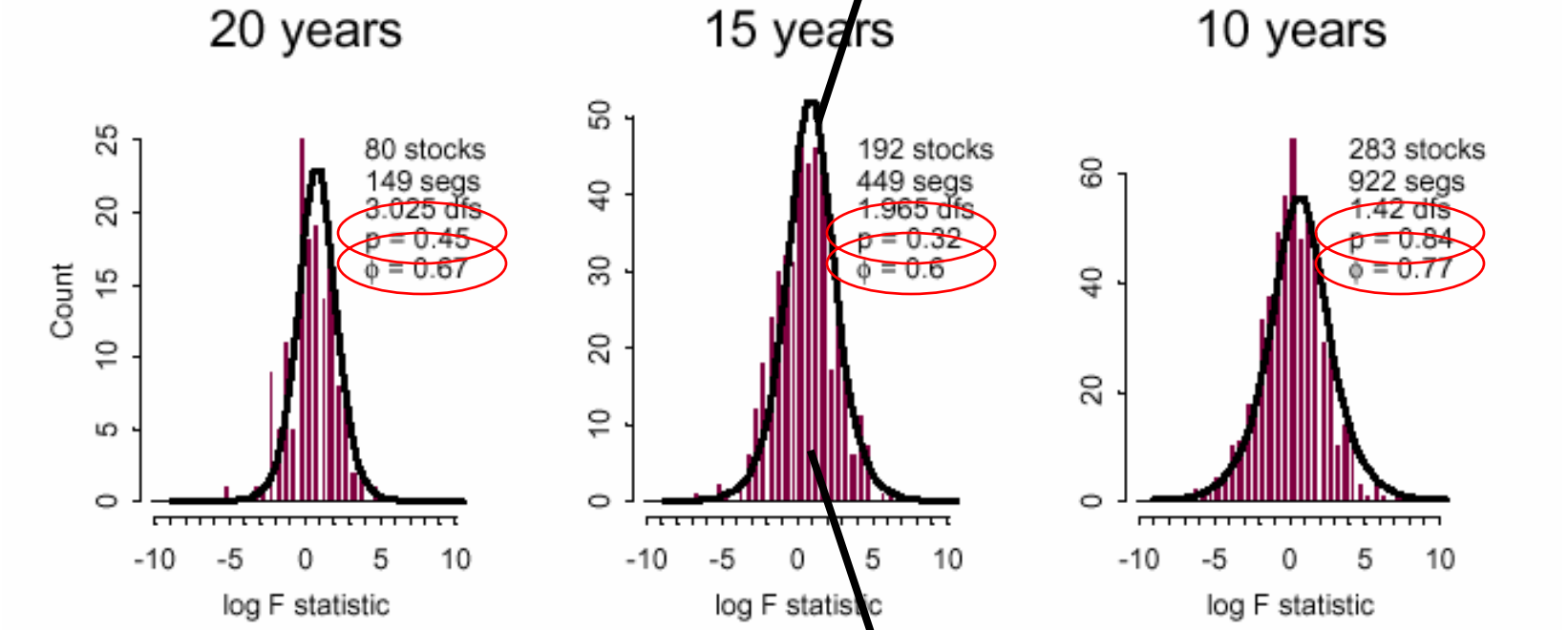
- Fluctuating or declining stocks
  - No significant trend
- Rapidly increasing stocks
  - Significant negative trend
  - Estimate of μ lower for bigger population size

Does the estimated process error follow the expected theoretical distribution?



Results for σ

Predicted F distribution



Histogram of actual F statistics

Trend in σ?

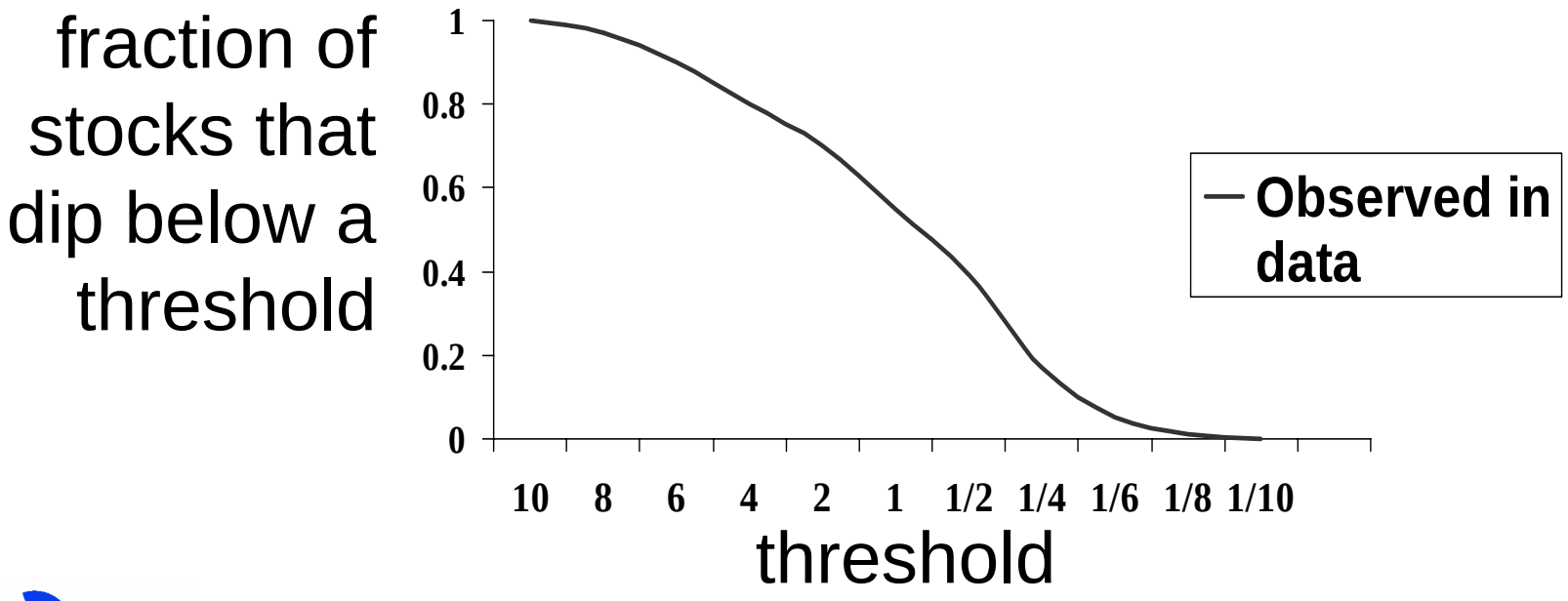
- Estimate of σ was higher when counts were really small
  - Demographic stochasticity?
  - Sampling effect?

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

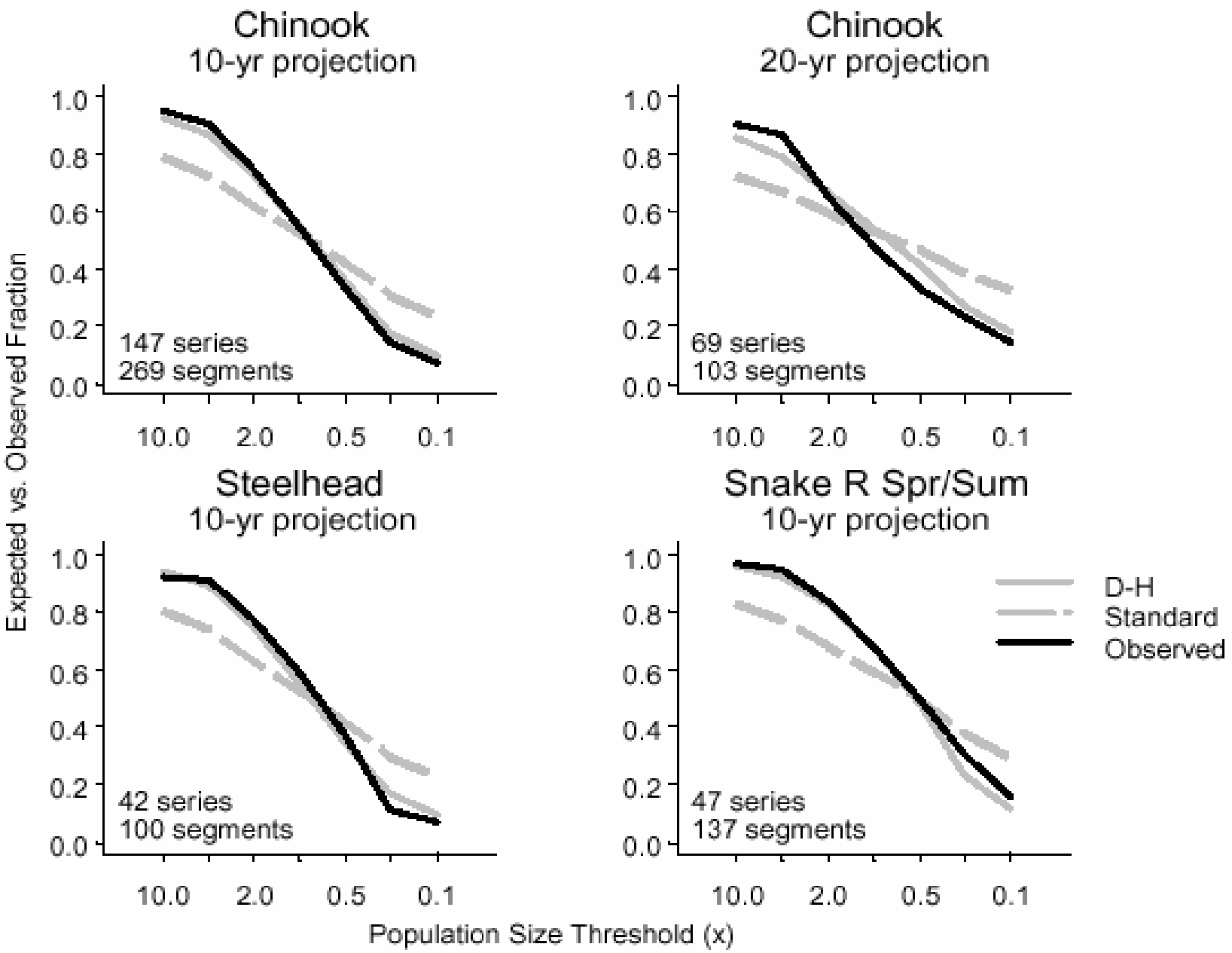
    Percent error tends to be larger when counts are small

    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?



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

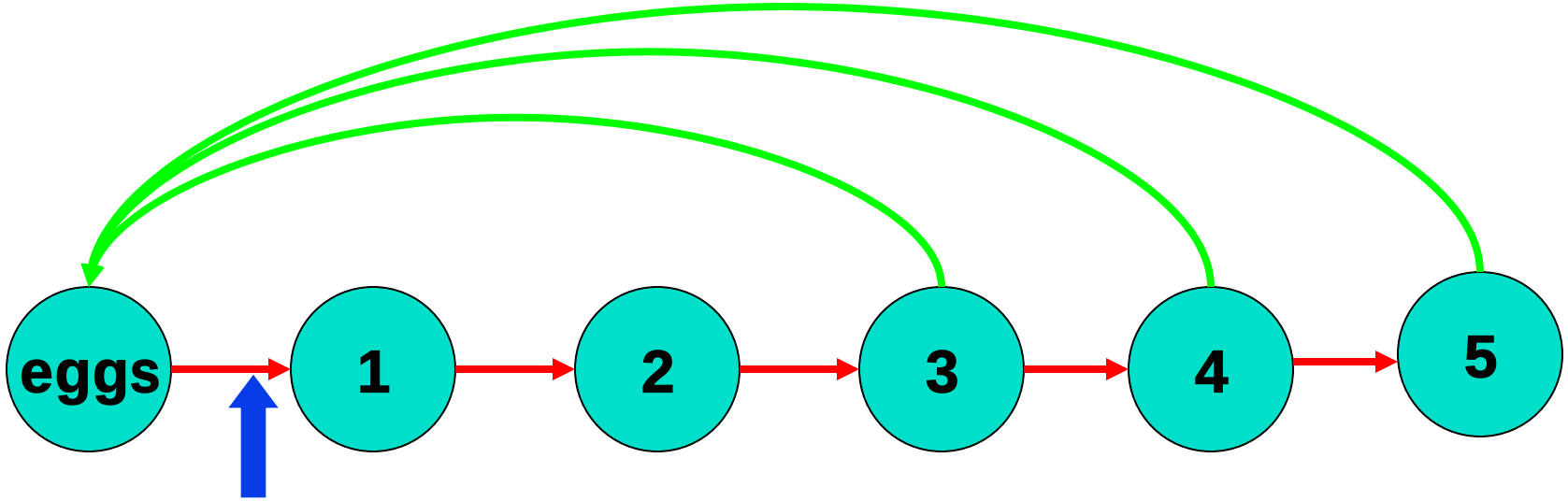

Chinook
10-yr projection
147 series
269 segments
Chinook
20-yr projection
69 series
103 segments
Steelhead
10-yr projection
42 series
100 segments
Snake R Spr/Sum
10-yr projection
47 series
137 segments
Expected vs. Observed Fraction
1.0
0.8
0.6
0.4
0.2
0.0
10.0
2.0
0.5
0.1
Population Size Threshold (x)
D-H
Standard
Observed

#2 Parameter estimation

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

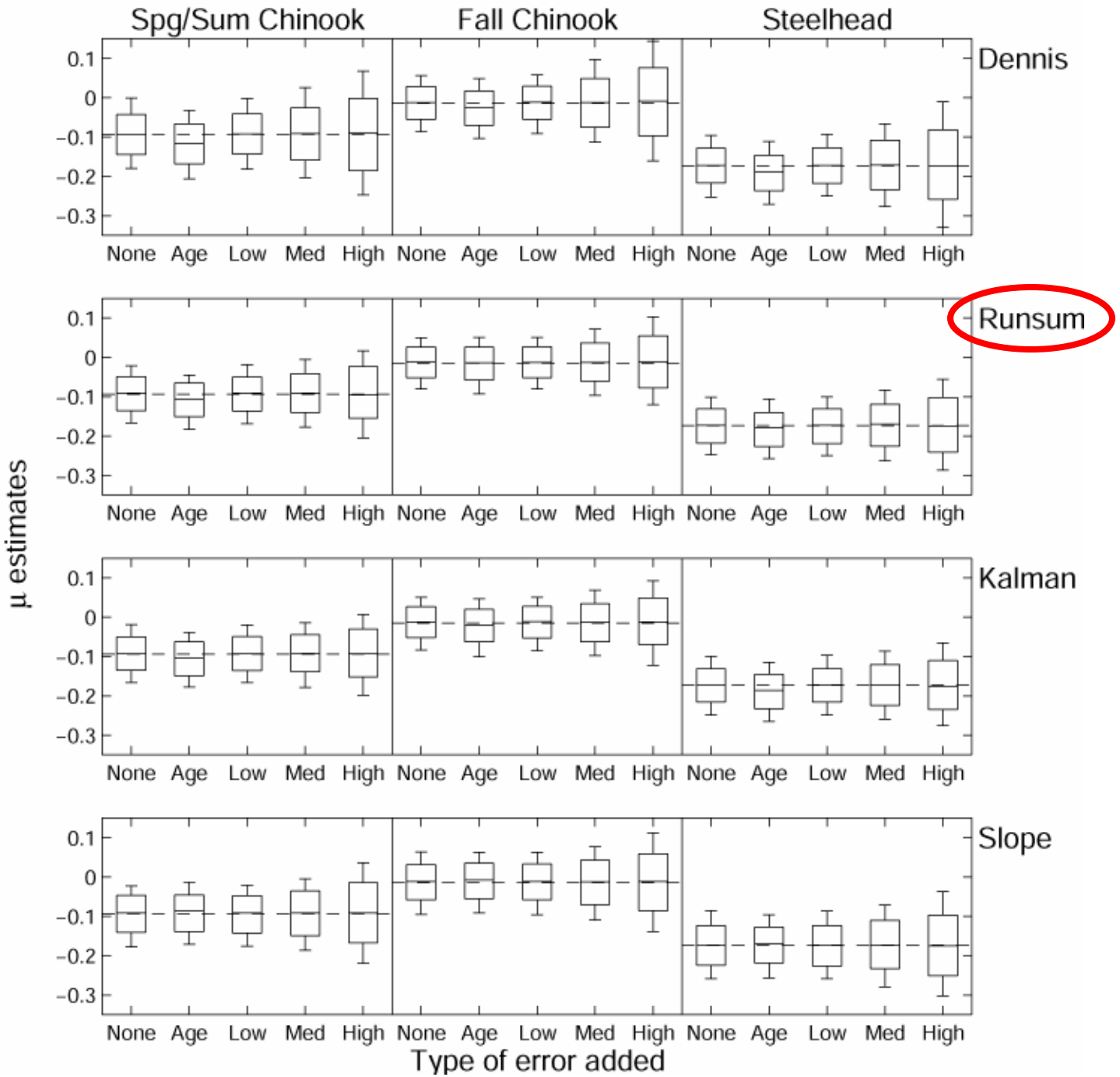
- Dennis methods (assume no non-process error)
- Runsum (used in the Biop)
- Heyde-Cohen (not based on DA)
- State-space approaches using Kalman filters
- Slope methods (used in Biop)

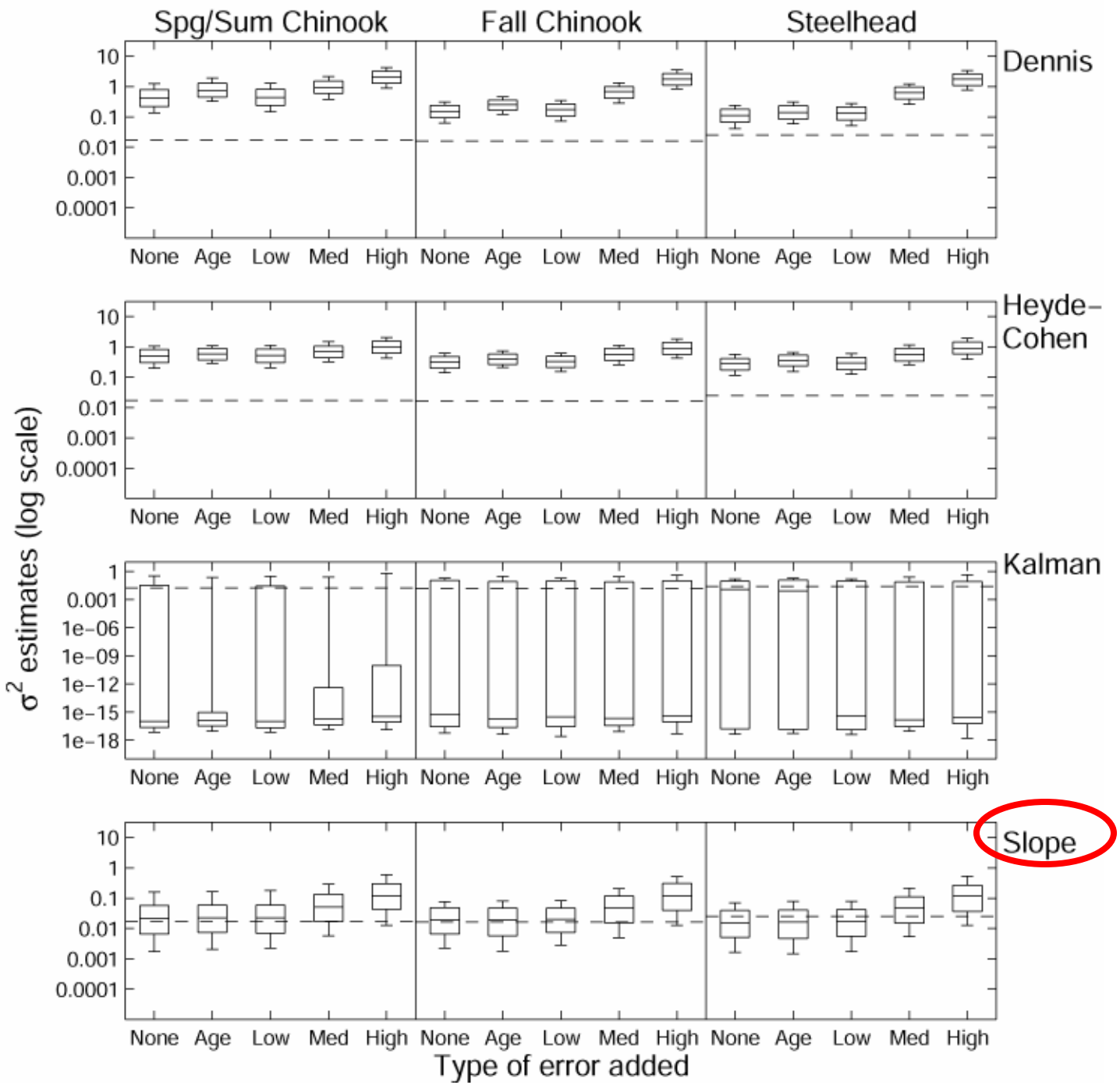
Testing parameterization methods with models



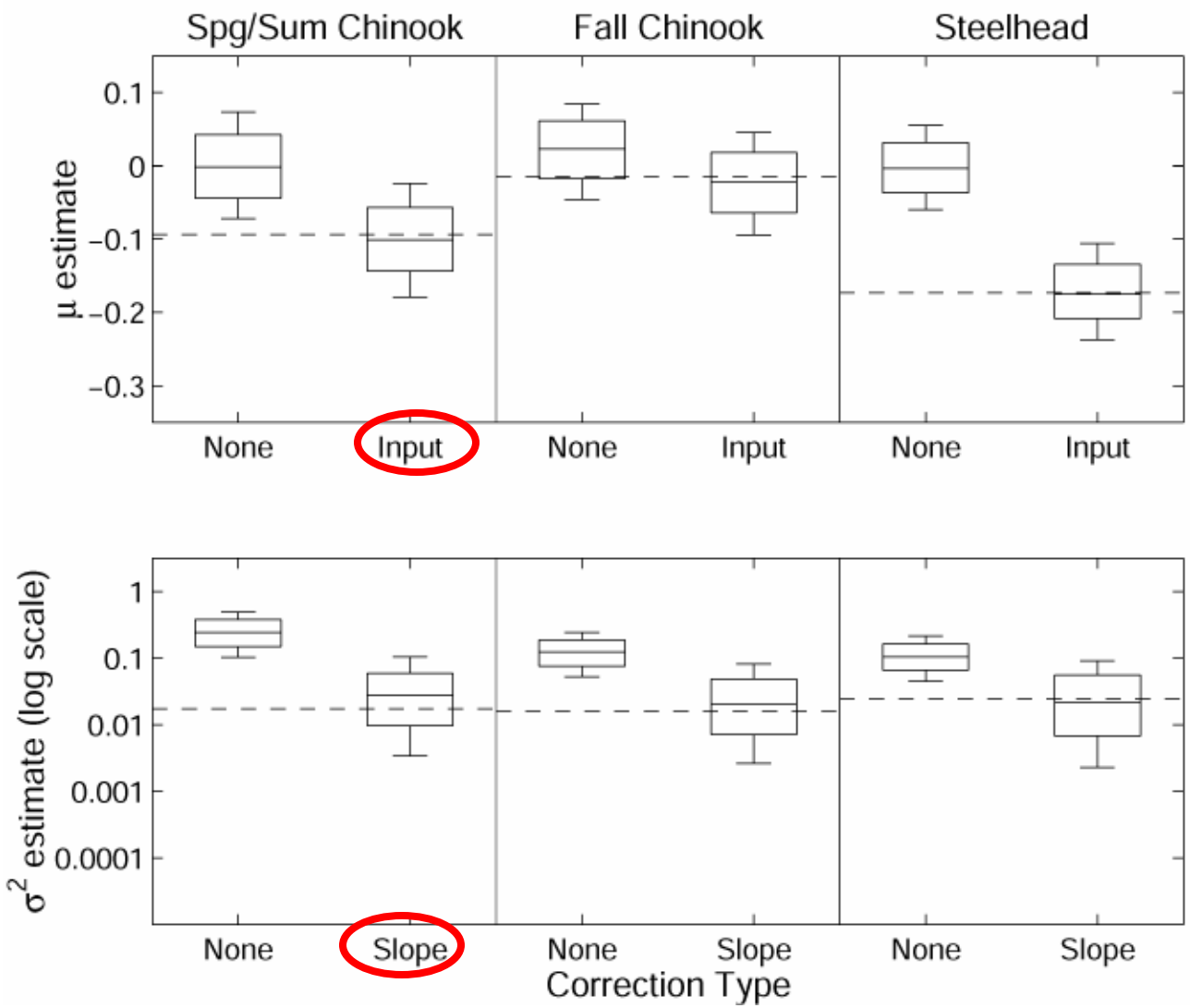
Density-dependence in egg-to-parr survival

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

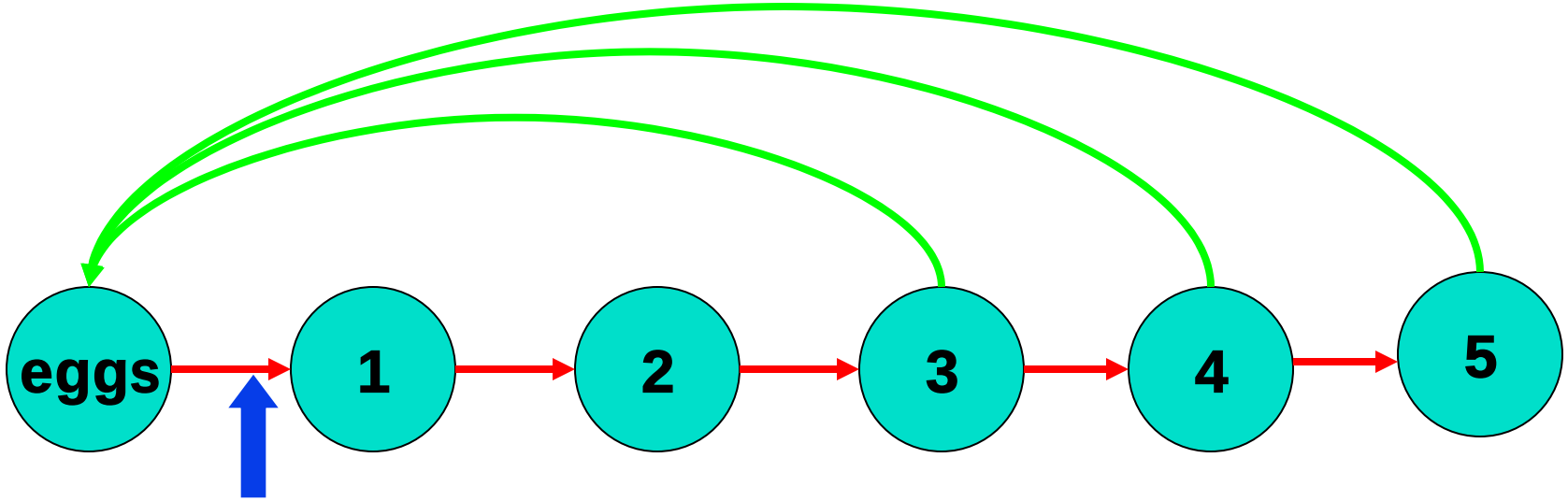

Spg/Sum Chinook
Fall Chinook
Steelhead
Dennis
Runsum
Kalman
Slope
μ estimates
0.1
0
−0.1
−0.2
−0.3
None
Age
Low
Med
High
Type of error added


Spg/Sum Chinook
Fall Chinook
Steelhead
Dennis
Heyde–
Cohen
Kalman
Slope
σ2 estimates (log scale)
10
1
0.1
0.01
0.001
0.0001
1
0.001
1e−06
1e−09
1e−12
1e−15
1e−18
None
Age
Low
Med
High
Type of error added

Hatchery correction



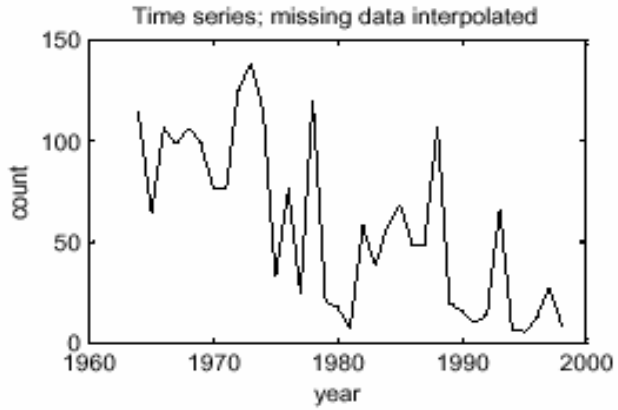
#3 Expressing the uncertainty associated with estimates



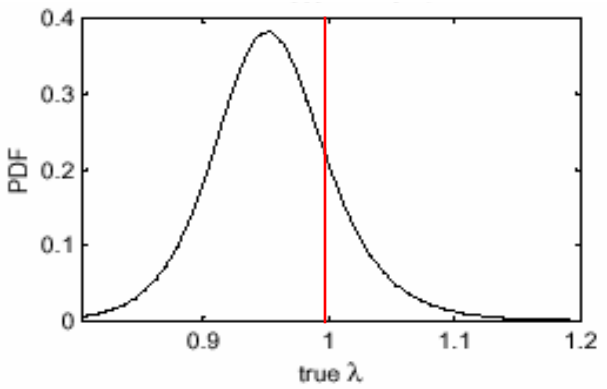
Density-dependence in egg-to-parr survival

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

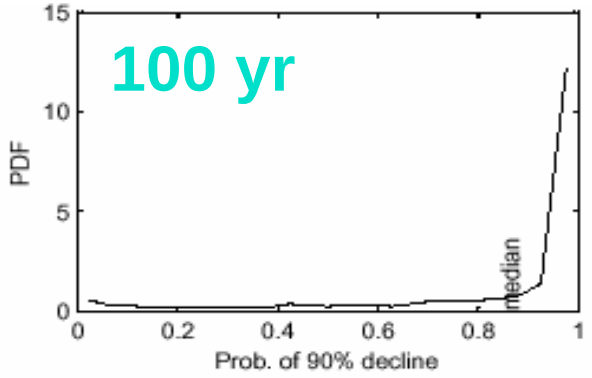
Lostine River 1964-1998

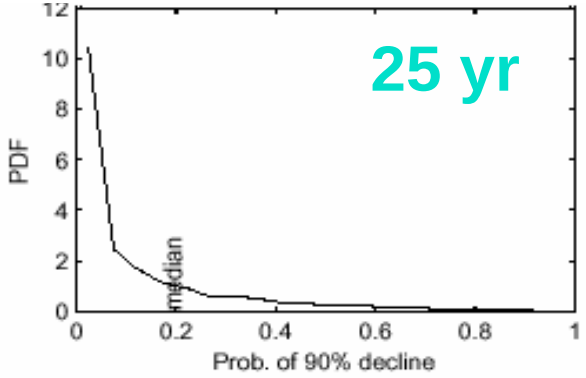


support for different λ's

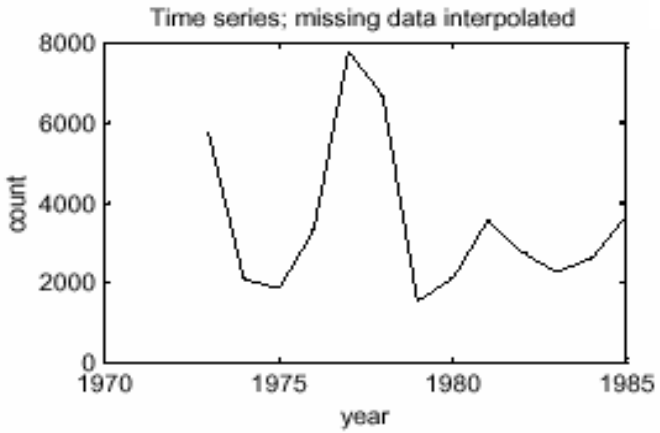


support for different probs of 90% decline

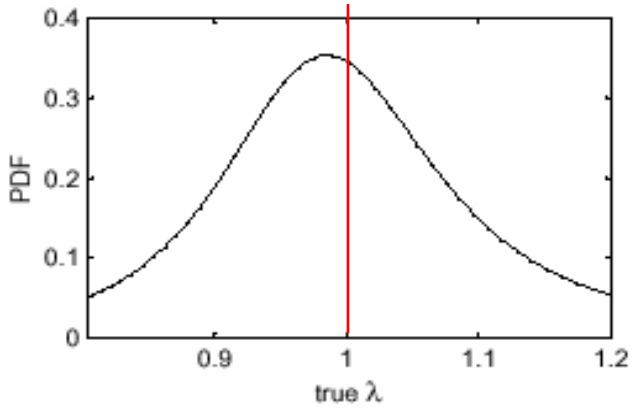




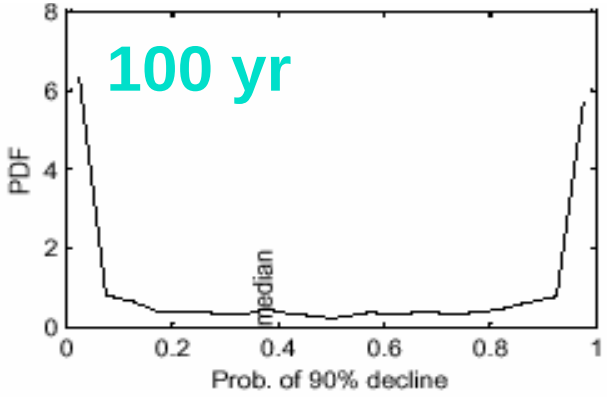
Clearwater River 1973-1985

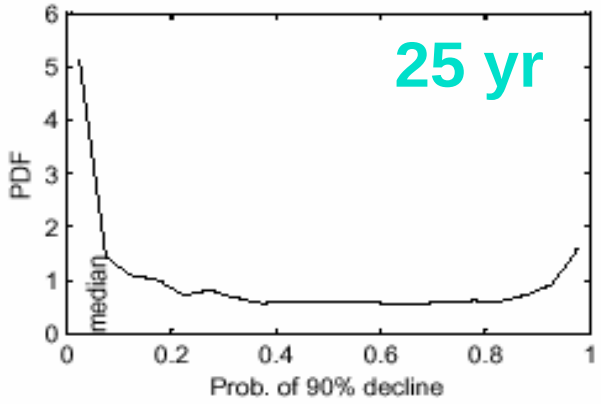


support for different λ's

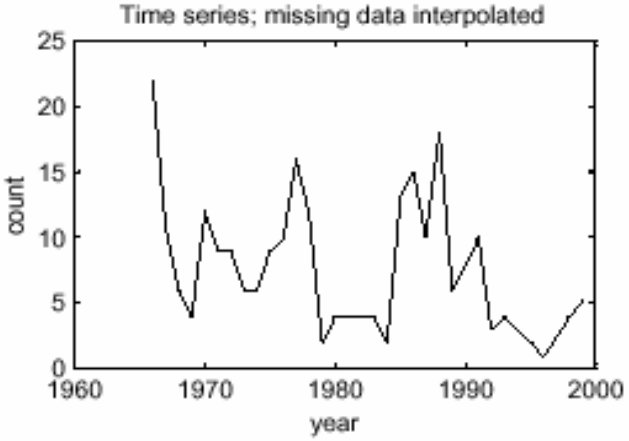


support for different probs of 90% decline

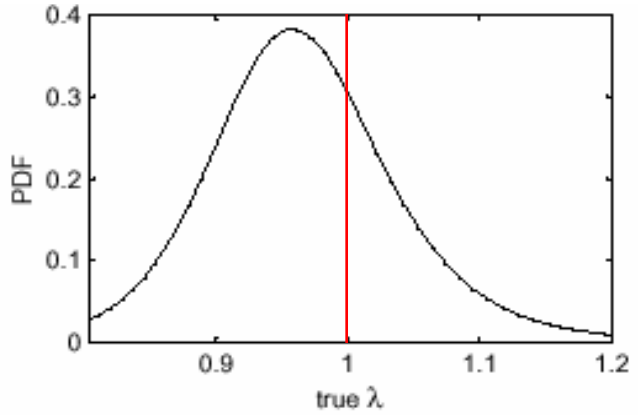




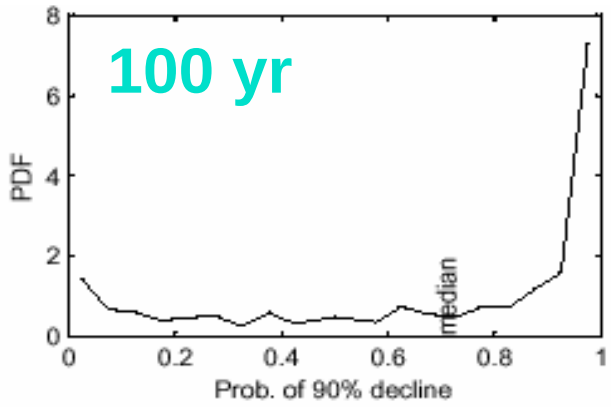
Camp Creek 1966-1999

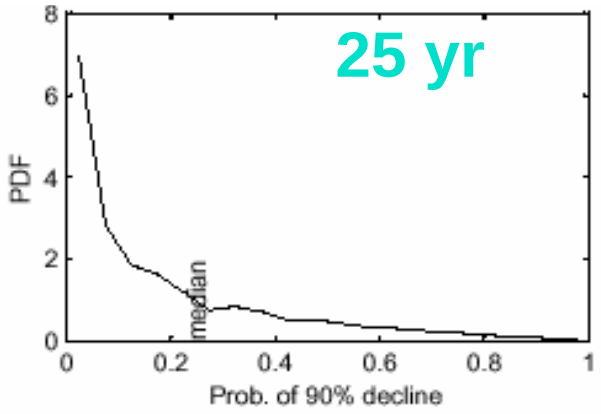


support for different λ's



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