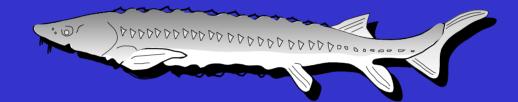
Benefit-Risk Analysis of White Sturgeon in the Lower Snake River





A DECEMBER OF A

Molly Webb Selina Heppell

Kevin Kappenman Rishi Sharma Shawn Narum

Work Plan Phase 1 - acquisition of data and lit. review

Phase 2 - data compilation for BRA

Phase 3 - Benefit-Risk Analysis

Phase 4 - write-up + dissemination of results Timeline = 2 weeks/Phase

Phase 1 (acquisition of data and lit. review)

- Existing data
- Format of existing data
- Data gaps

Affects: Models to be used Appropriate metrics for model comparison

Phase 2 (data compilation for BRA)

 Data formatting and organization for each model

Phase 3 Benefit-Risk Analysis

Key life history characteristics important in model choice and analysis

- Late age at first maturity
- Pulse recruitment
- Long and variable spawning periodicity
- Shifting carrying capacity

Biomass Dynamic (Logistic Growth) Model

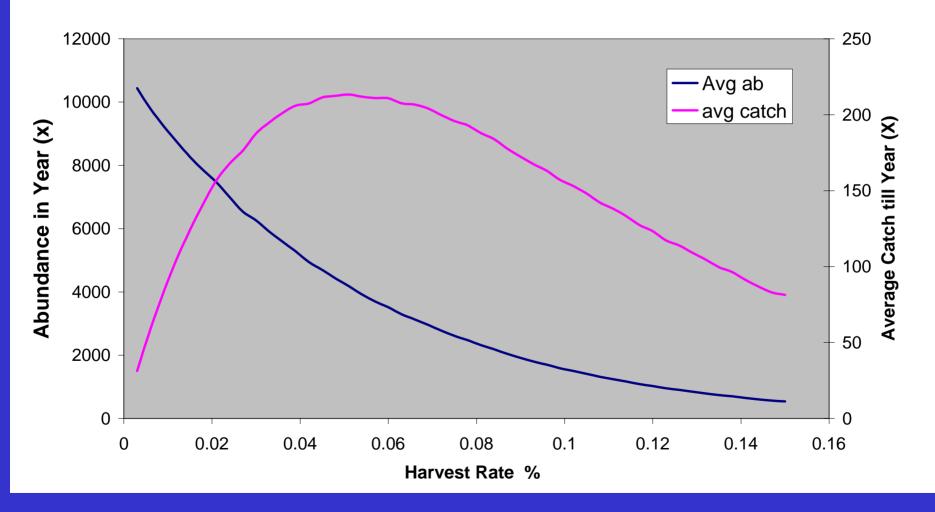
$$N_{t+1} = \left(N_t + rN_t\left(1 - \frac{N_t}{K}\right)\right) \times \left(1 - \mu\right)$$

Where we assume a stable age distribution, N is the population size at time (t), r is the intrinsic growth rate of the population, K is the carrying capacity of the population at virgin biomass and μ is the harvest rate.

Assumptions

- 1) It is a closed population
- 2) Constant r, which doesn't change over time
- 3) All individuals in the population are assumed equal and reproduce at each and every time step

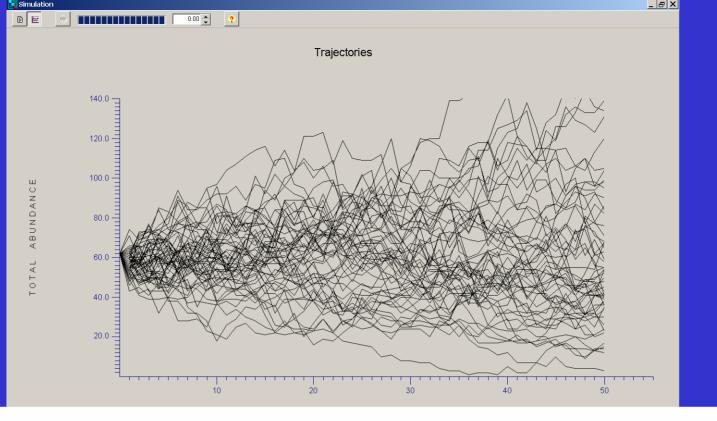
Based on data and biomass estimates we can project things like population size in Year(x) (PVA) based on harvest rate assumptions with multiple simulations



Population Viability Analysis on Age Structured Models

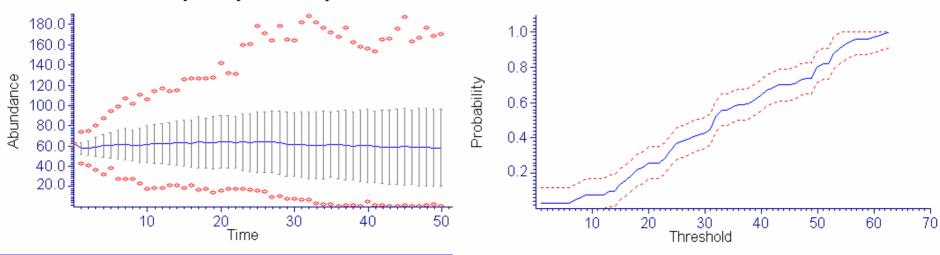
Similar to the previous slide, we can project population trajectories based on the following:

- Recruitment to age 2 (with uncertainty), assuming age 2 is the first age that can be estimated
- Age structure of the population (known)
- Size selectivity for fishery harvest (known)
- Natural mortality by age (known)
- Fishing mortality on those ages, either directly known or as a function of catchability and effort (with uncertainty)



Trajectory summary

Extinction/Decline



Population Viability Analysis from time series of abundance or CPUE

Dennis model – a stochastic projection of exponential growth (Dennis et al. 1991)

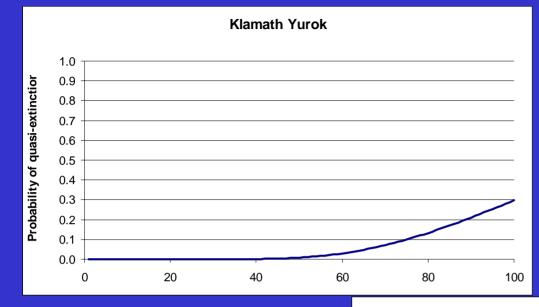
$$N_{t+1} = N_t e^{\mu + \sigma Z_2}$$

where N_t is the population size at time t, μ is rate of increase or decrease in the population, σ^2 is environmentally induced variance and Z_t is a standard normal deviate. The probability that a population will reach size q within some number of years t can be estimated from a diffusion approximation where:

$$\mu = mean\left(\ln\left(\frac{N_{t+1}}{N_t}\right)\right)$$

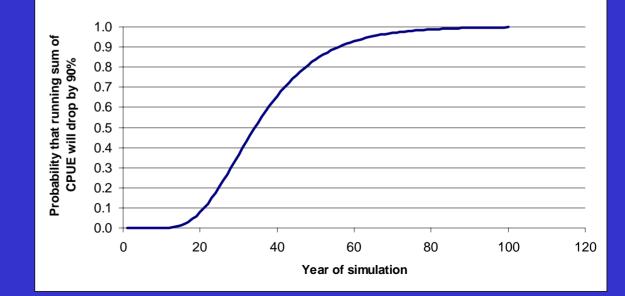
$$\sigma^2 = \operatorname{var}\left(\ln\left(\frac{N_{t+1}}{N_t}\right)\right)$$

Green sturgeon time series analyses



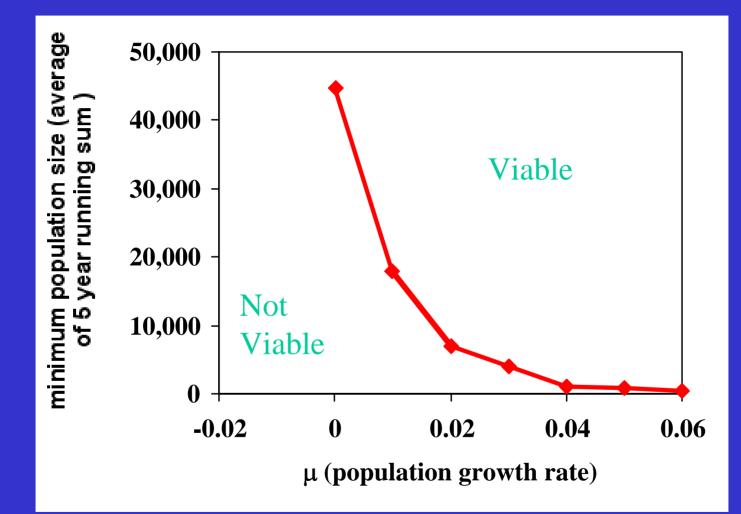
Catch or population estimate time series

CPUE time series



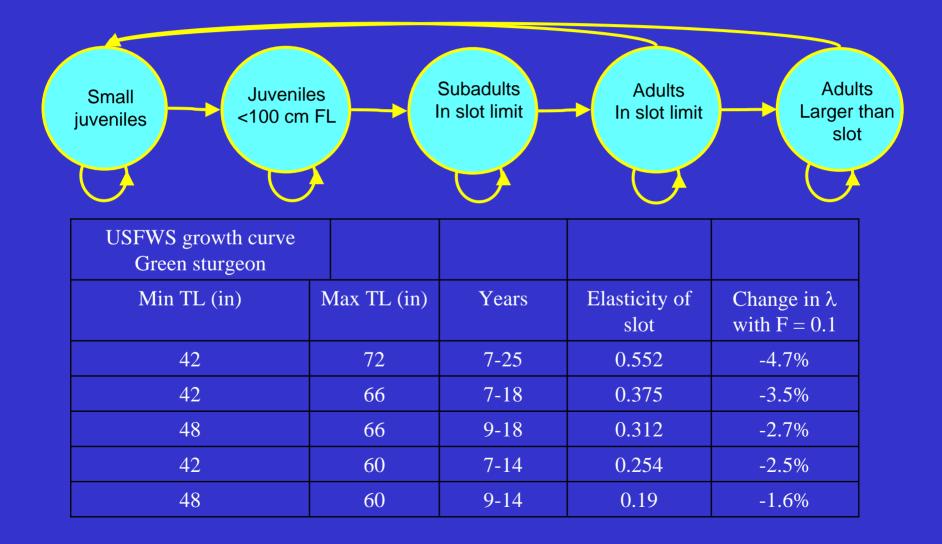
WA coast trawl

Example viability criteria output from DA model

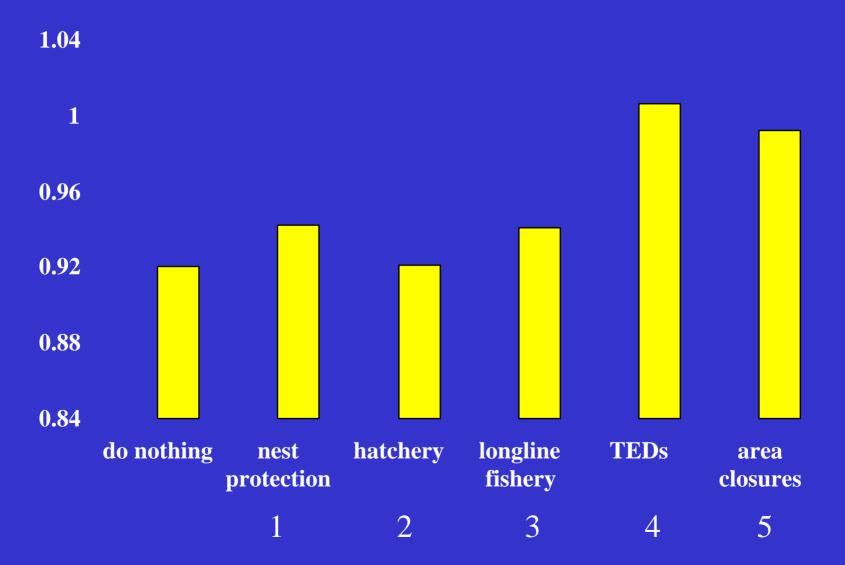


Viable = probability of extinction in x years is less than y% Extinction = predetermined threshold

Age-Structured Sensitivity Analyses

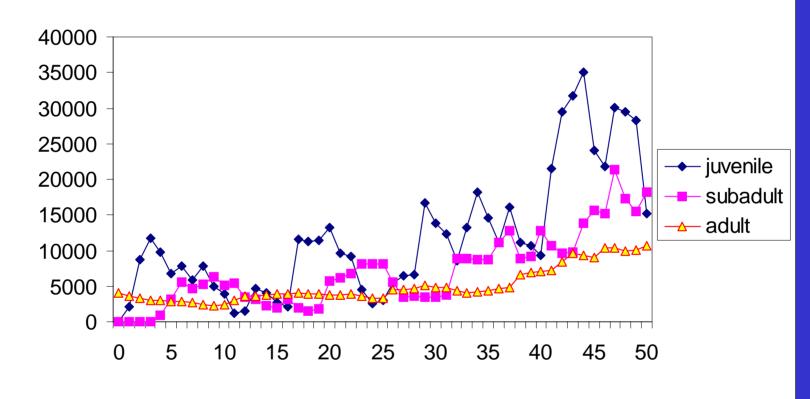


Life cycle model results for Kemp's ridley sea turtle: expected λ for each management option



Age Structured Simulations

Stochastic population



Use many replicate simulations to look at variance in biomass and potential catch...

Biggest Bang for the Buck

If the approximate cost of each management scenario can be estimated, rank options according to:

$$benefit / cost = \frac{\Delta \lambda, biomass, or other model result}{\$}$$

Genetic Variation Analyses Review genetic variation in white sturgeon (Anders et al. 2002; Brown et al. 1992)

- LG mtDNA haplotype/nucleotide diversity
- LG mtDNA heteroplasmy distribution
- Genetic variation relative to other populations and species

Review genetics studies of other sturgeon spp. (Ludwig et al. 2000; Campton et al. 2000)

Review other sturgeon conservation programs (e.g. Kootenai River - Duke et al. 1999)

Conserving Genetic Variability

Recommendations for broodstock selection

- Genotype collections for diverse representation
- Rare haplotypes/alleles

Genetic Monitoring & Evaluation program

- Genetic marker choice
- Estimate effective population size (pre & post supplementation)
- Calculate population genetic variability (pre & post supplementation)

Comparing the Models and Ranking Alternative Mitigation Plans

- Each model includes assumptions and uncertainty
 - Most results will need to be compared qualitatively, rather than quantitatively
- We will use one or more of the models proposed here provide an assessment of each management alternative. The assessment will include:
 - Potential risks and benefits
 - Critical uncertainties
 - Recommendations for further research
- We will attempt to focus on one or more "common currencies" to allow an objective comparison of each option
 - Population growth/recovery rate
 - Biomass of different age or size classes
 - Productivity, recruits per spawner
 - Allowable harvest?

Phase 4 (write-up + dissemination of results)

- Report to Nez Perce Tribe
- Presentation to BRAT
- Publication in peer-reviewed journal