A model linking ocean survival to smolt length

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Motivation

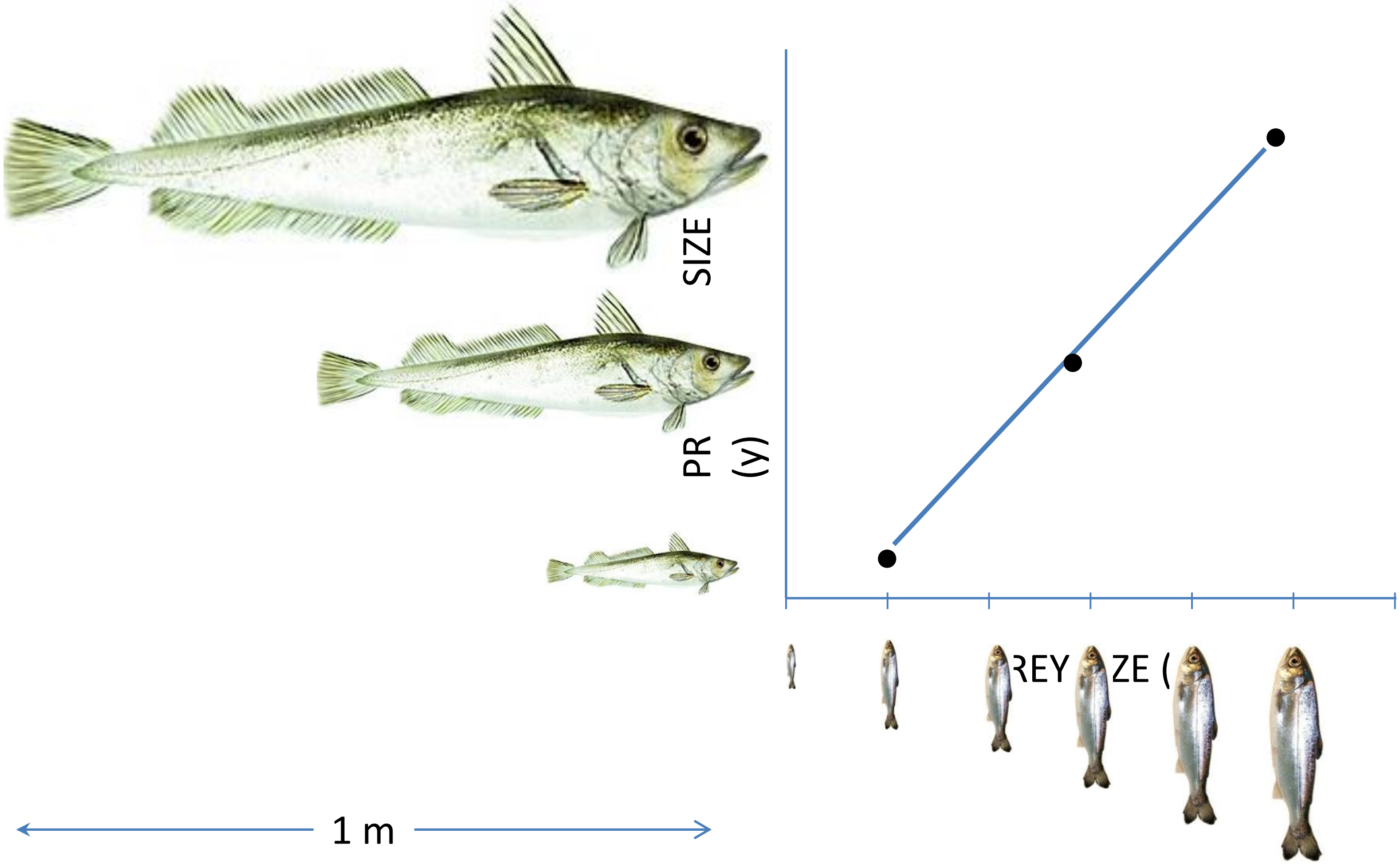
- Fish mortality in juvenile freshwater stages and during the first year in the ocean is important in controlling the number of adult salmon that return to spawn

- Numerous studies indicate that during these early life stages fish size is an important determinant of recruitment to adult stage

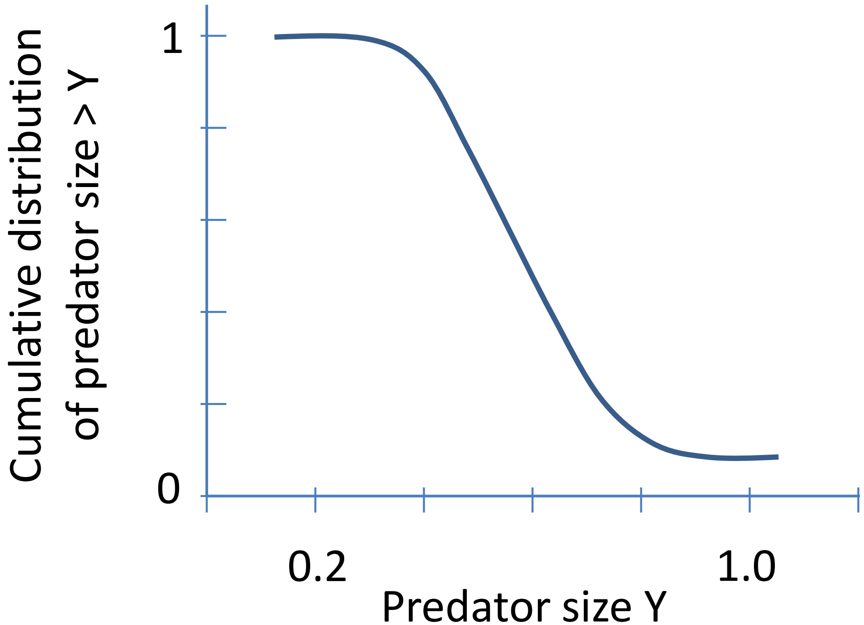
Outline

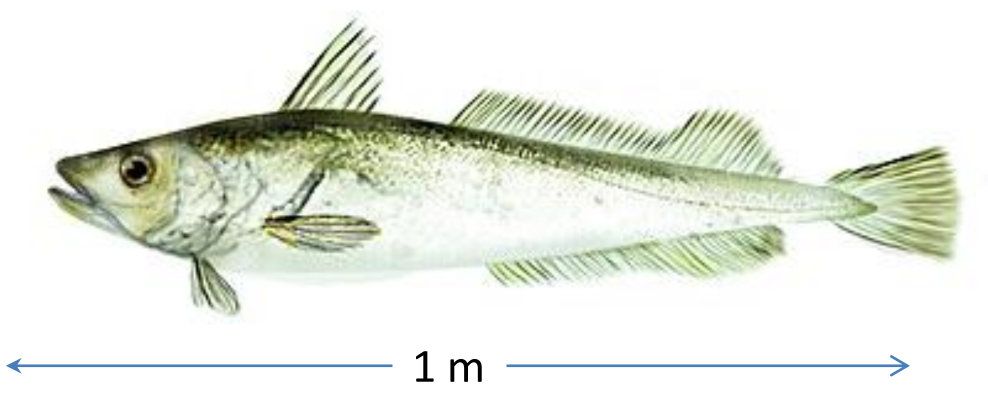
- Theory of gape-limited predation in pictures
- Theory of gape-limited predation in equations
- Fitting data
- Freshwater survival results
- Ocean survival results
- Conclusions

Gape limitation of predator
Pacific Hake consuming Salmon

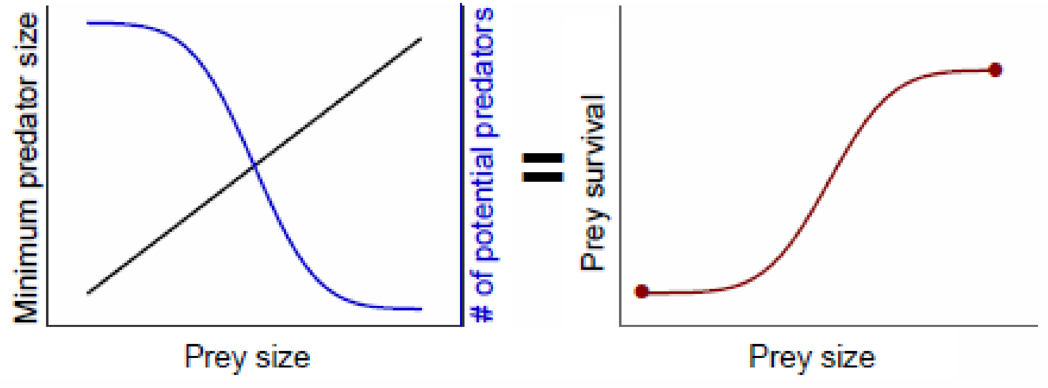


Predator size distribution





Combine the two functions to get prey survival as function of prey size



Model

Prey Mortality

$$\frac{dN_x}{dt} = -c_1 N_x - c_2 N_x P_x$$

Mortality rate = size independent part + size dependent part

N_x = number of prey at size x

P_x = number of predators able to eat prey of size x or smaller

c_1 , c_2 =constants

Number of prey of size *x* alive at time *t*

$$N_x(t) = N_x(0)\exp\left[-(c_1 + c_2 P_x)t\right]$$

P_x = number of predators able to eat prey of size *x* or smaller

N_x (0) = starting number of prey of size x at time 0

N_x (t) = number of prey at size x alive at t

Simplifying survival

$$S_x = \frac{N_x(T)}{N_x(0)} = c_3 \exp(-c_4 P_x)$$

Use a Taylor expansion of the exponential function

$$e^{-y} = 1 - y + \frac{y^2}{2!} - \frac{y^3}{3!} + \cdots$$

Remove higher order terms

$$S_x \approx k_0 + k_1 \;\; 1 - P_x$$

k_0 = base survival independent of size
k_1 = maximum improvement in survival from size

Prey survival as function of predator population size distribution

Assume size distribution of predator is normally distributed then

$$P_x = 1 - \Phi\left(\frac{x - x_c}{\sigma}\right)$$

X_c = prey size susceptible to 50% of predators
σ = SD of susceptibility curve

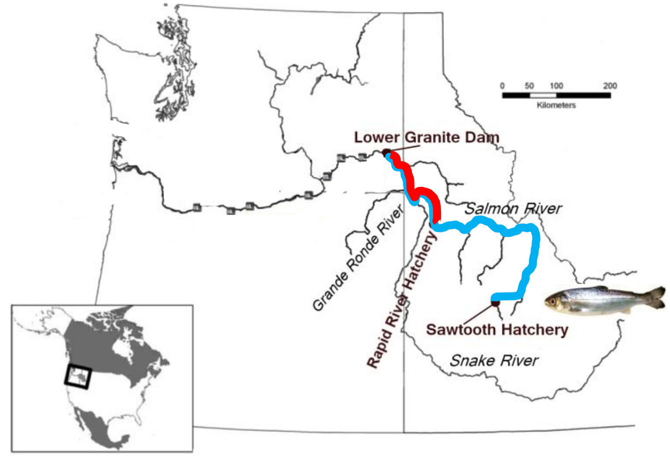
$$S_x \approx k_0 + k_1 \Phi\left(\frac{x - x_c}{\sigma}\right)$$

Assume all parameters are constant within a year

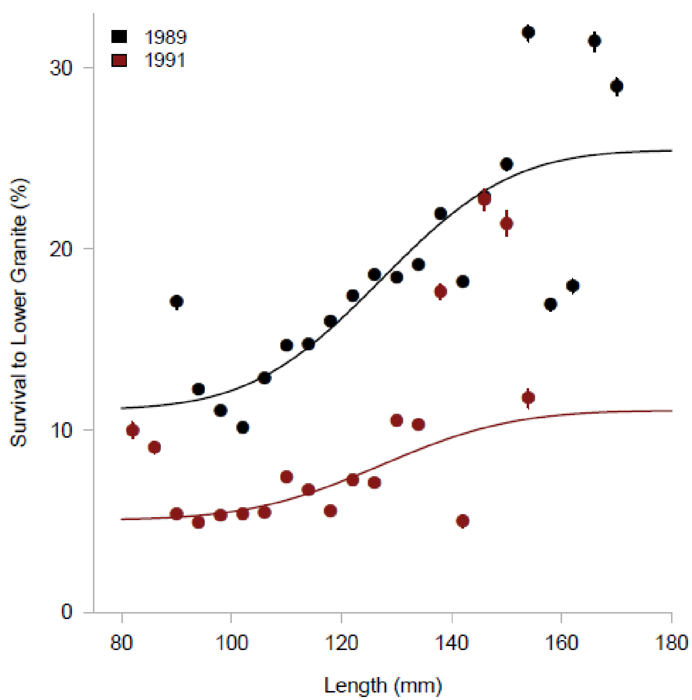
Fitting data

- Data – individual binary survival from PIT tagged fish
- Method – maximum likelihood
- Package – mle2 function in bbmle package in R

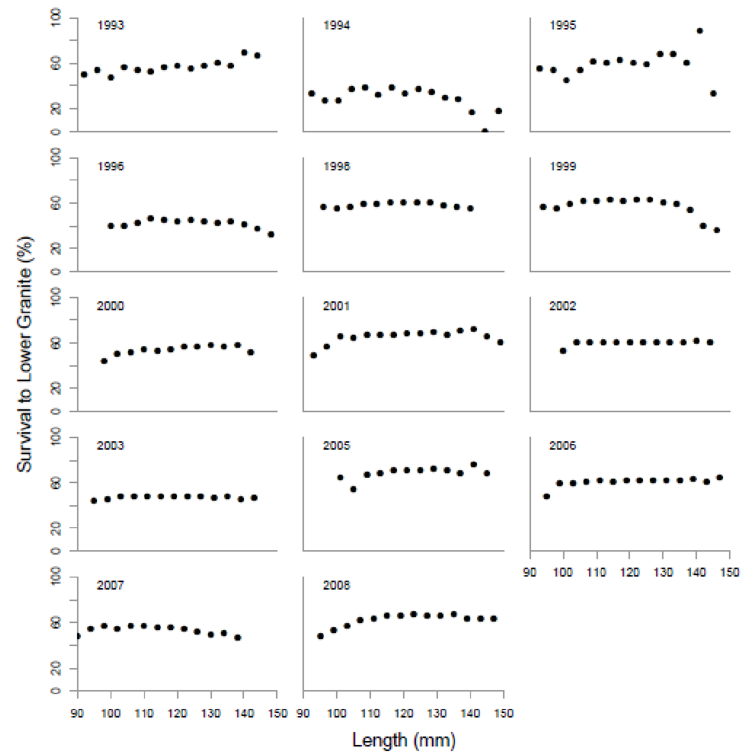
Freshwater survival results



Sawtooth Hatchery
Exhibited strong length effect

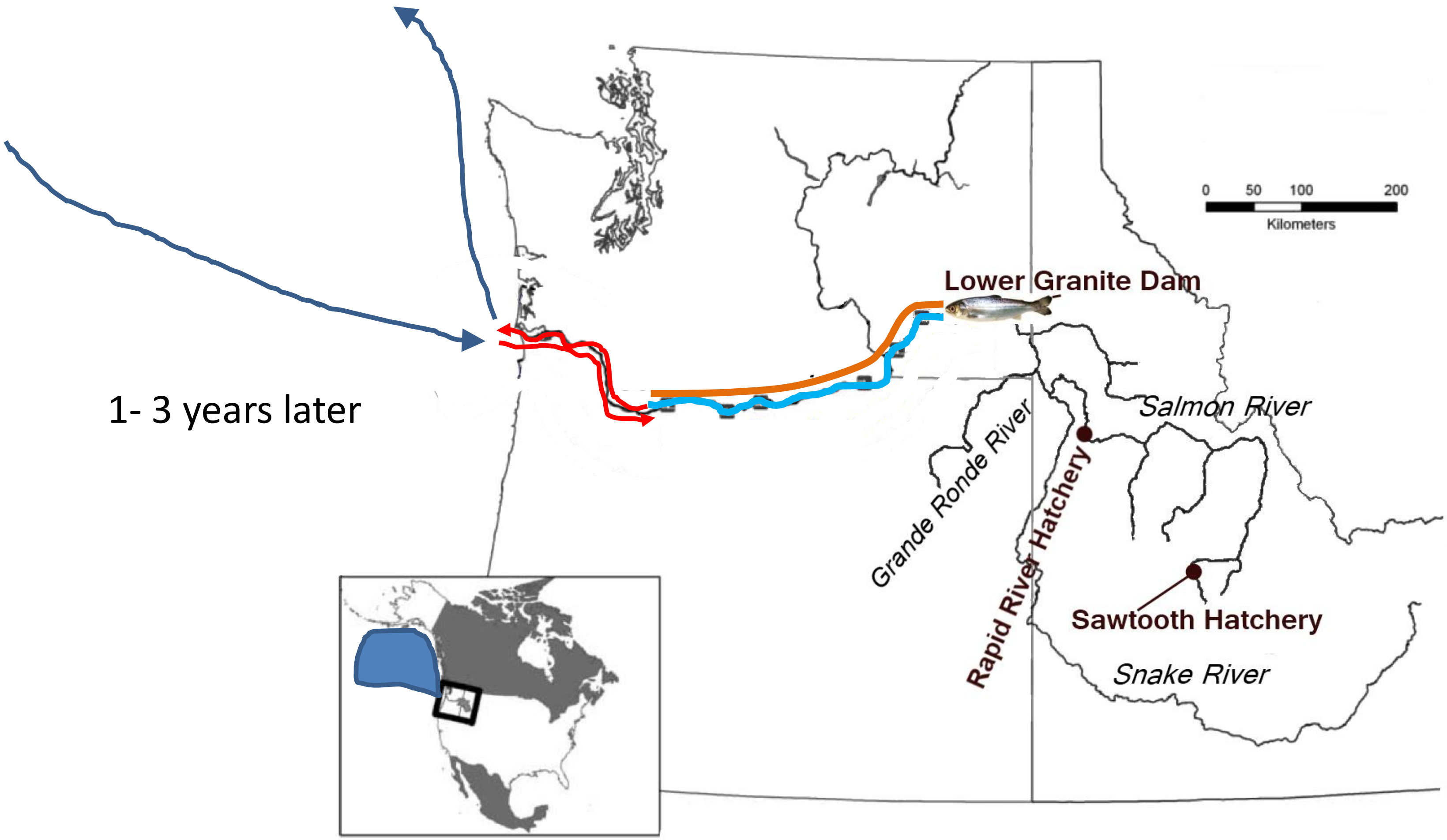


Rapid River Hatchery
Exhibited weal length effect

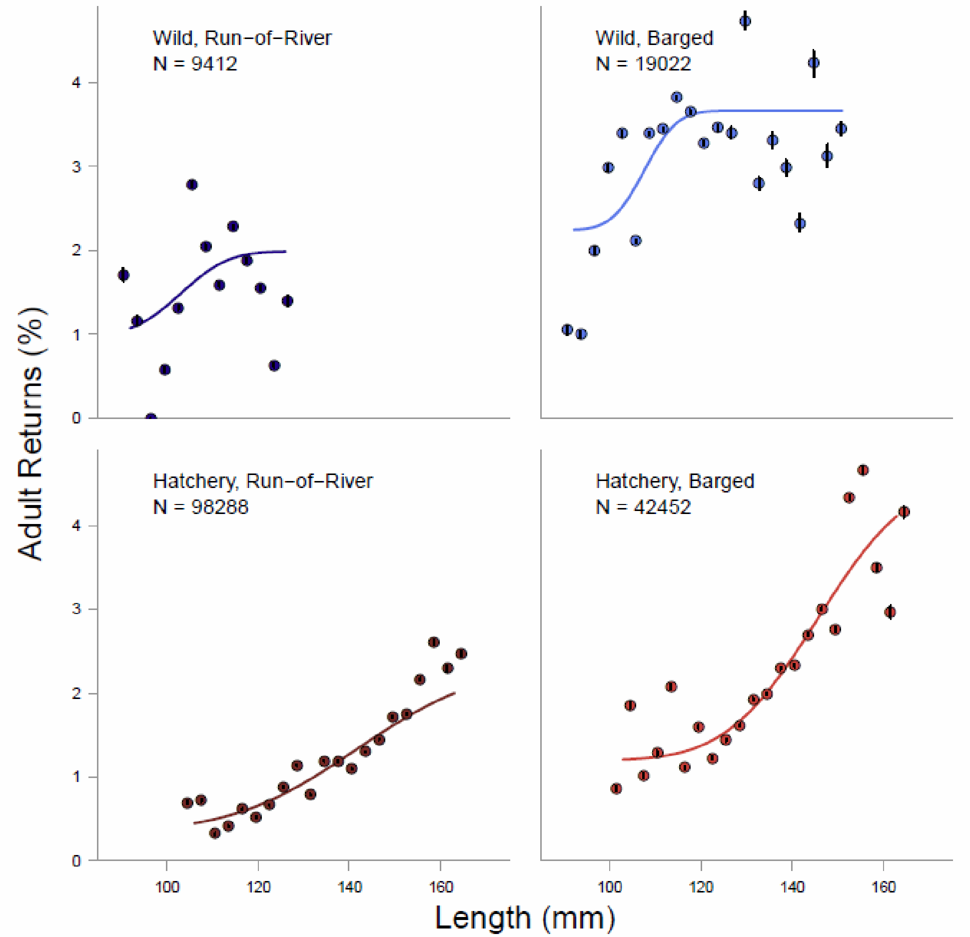


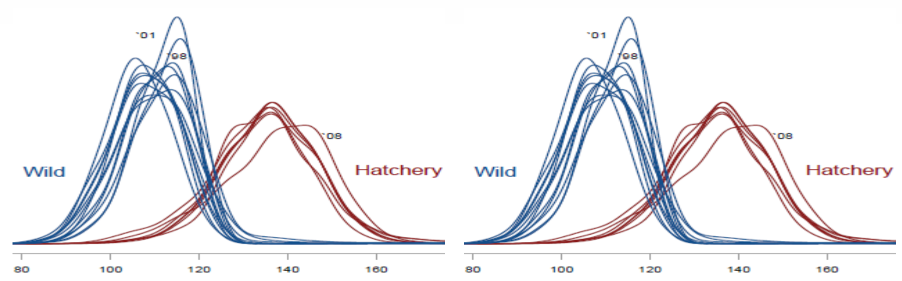
Ocean survival results

1- 3 years later



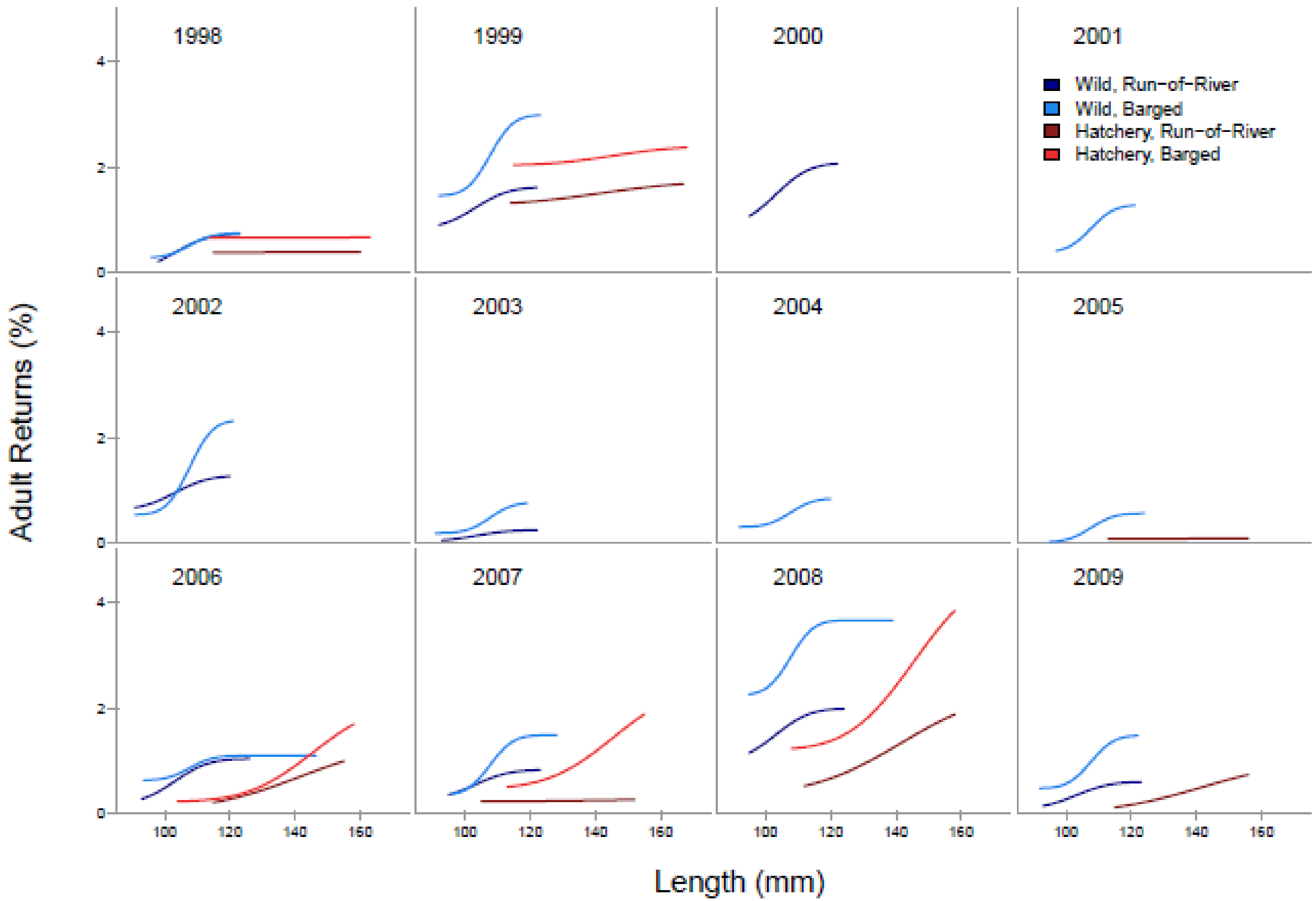
Model fit Juvenile migration year 2008 Barged and RoR fish





The model predictions are shown with data points (binned by length in 3 mm intervals).

Ocean survival all years



Summary of Ocean survival

			l_c			σ_c			
Type	Transport	Mean length (mm)	$\hat{l}_c$	Lower 95% CI	Upper 95% CI	$\hat{\sigma}_c$	Lower 95% CI	Upper 95% CI	ΔAIC
Wild	Barge	110.5	107.6	106.3	109.0	5.6	4.2	7.6	−30
Wild	Run-of-river	109.1	103.1	101.0	105.2	8.2	5.9	11.5	−5
Hatchery	Barge	136.2	145.5	141.0	150.2	15.7	12.6	19.6	−37
Hatchery	Run-of-river	135.6	141.6	138.0	145.3	21.4	18.3	24.9	15

Mean wild fish length is large than mean predator gape

Mean hatchery fish length is smaller than mean predator gape

Hatchery fish susceptible to more predators than wild fish

Take Home Messages

Hatchery and wild fish appear to be susceptible to different predators

Size-selective survival varies by a factor of 5 within a stock

To understand salmon recruitment we need to understand the ecology of fish size