Is interbreeding of wild and artificially propagated animals prevented by divergent life history?

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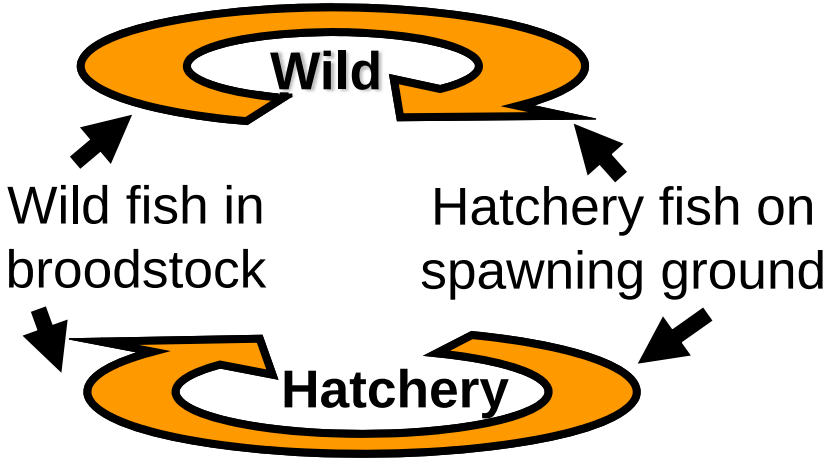
Problems with hatchery supplementation

- Disease
- Overharvest of wild fish
- Behavioral and ecological
- Genetic

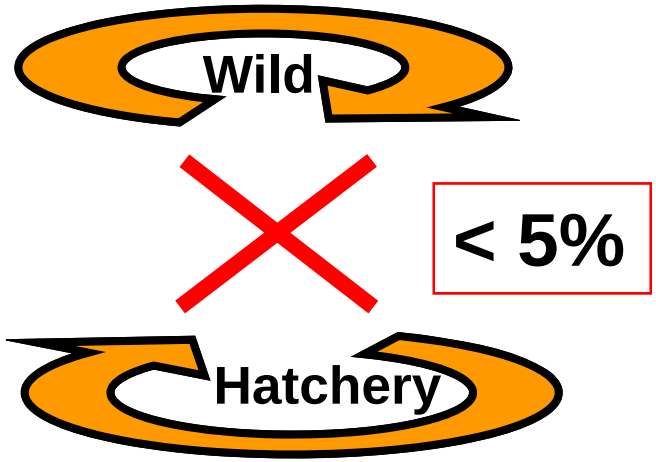
Naish *et al*. 2007 Advances in Marine Biology

Methods to minimize or eliminate risks

- Use one of two approaches to broodstock management:



Hatchery fish are integrated with wild fish



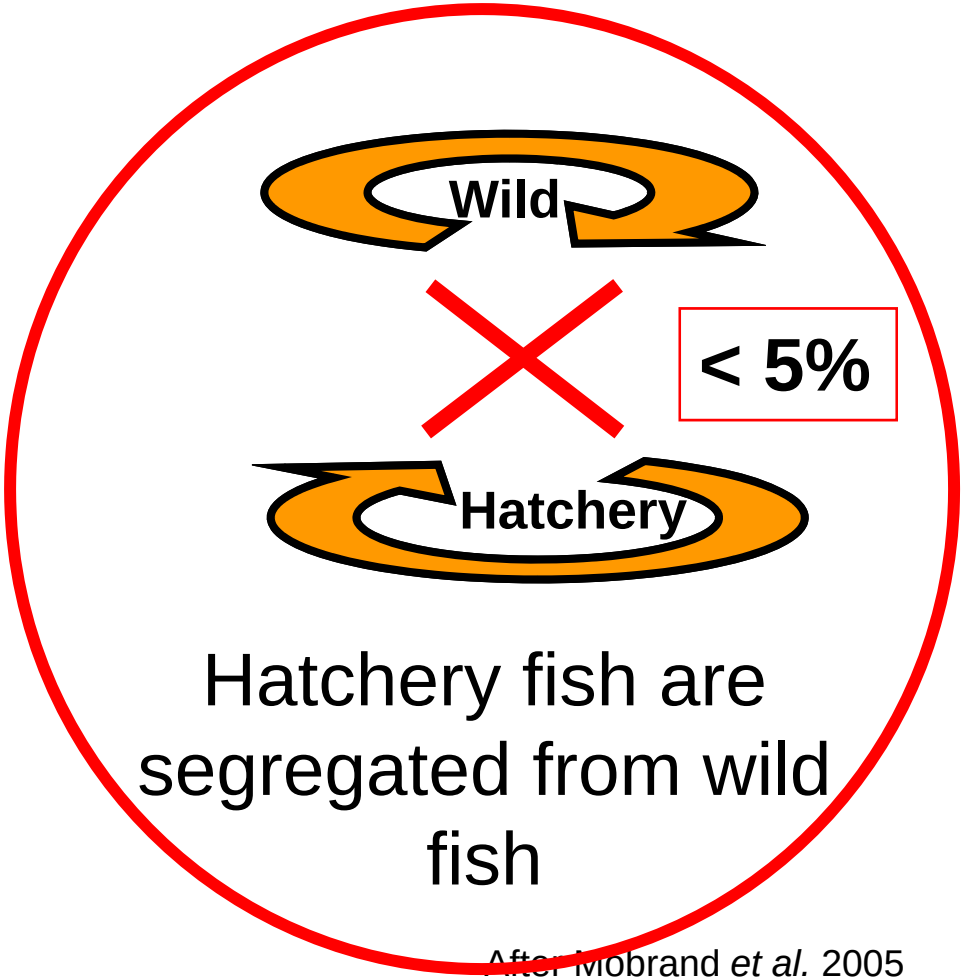
Hatchery fish are segregated from wild fish

After Mobrand *et al.* 2005

Methods to minimize or eliminate risks

- Use artificial selection to increase separation of the populations

Lorenzen *et al.* 2010



After Mobrand *et al.* 2005

Main aims of the study

- Determine whether segregation based on life history is effective
  - Examine temporal trends in relative proportions of **wild** fish
  - Estimate proportions of **hatchery**, **wild** and **hybrid** fish
  - Evaluate explanatory variables/isolating mechanism

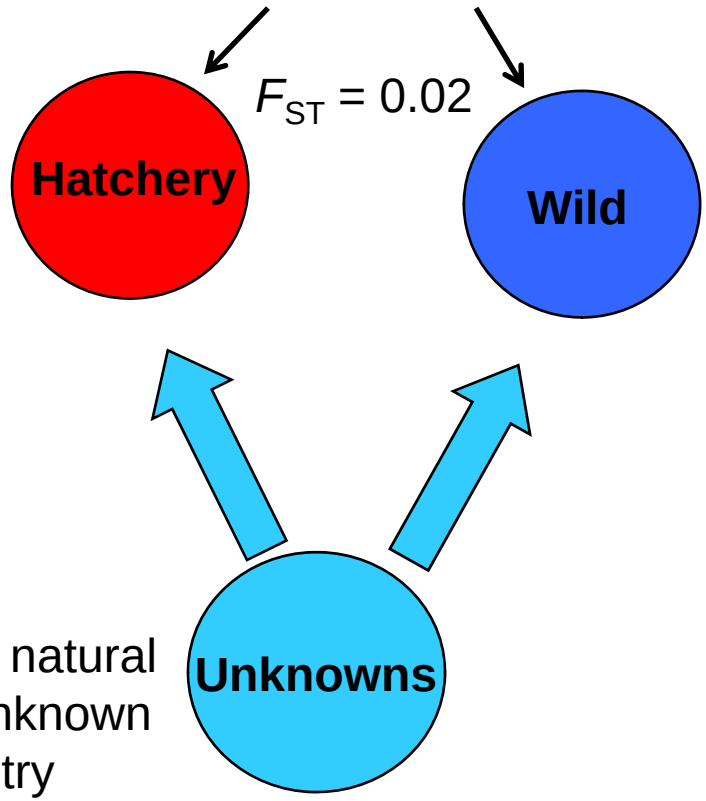
- New hatchery steelhead propagation program starting 1996
  - Sampled fish since 1996
- Weir to facilitate sampling hatchery-produced and wild fish

Genetic and statistical methods

- Two methods of genetic assignment
  - Mixture proportions via individual assignment (GENECLASS2)
  - Admixture proportions (STRUCTURE)

Baseline collections:

Clipped and unclipped adults from 1996, 1997, and 1998

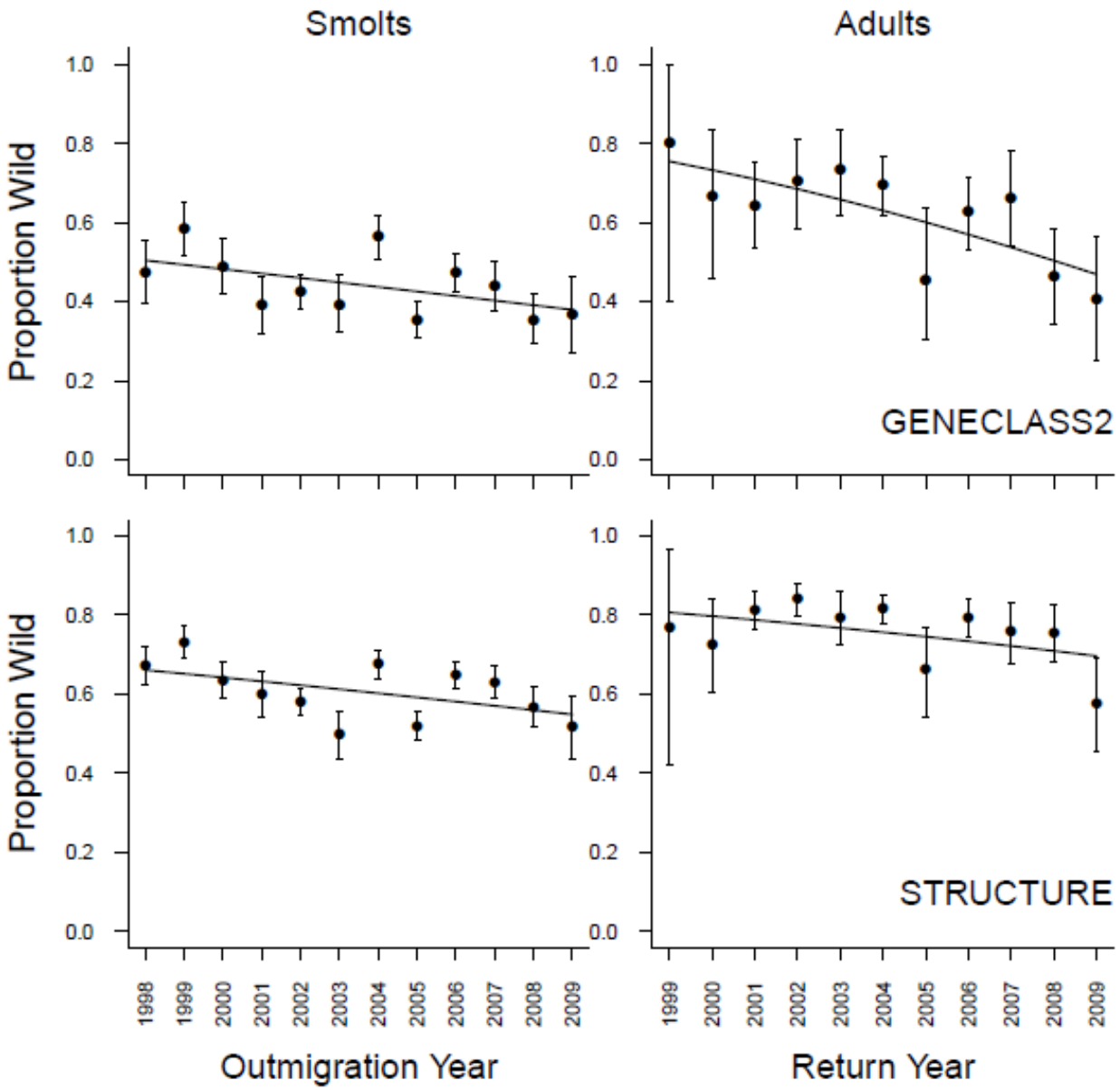


Unclipped, natural origin of unknown ancestry

Piry *et al*. 2004. J. Heredity

Falush *et al.* 2003. Genetics

Hauser *et al*. 2006. Mol. Ecol.

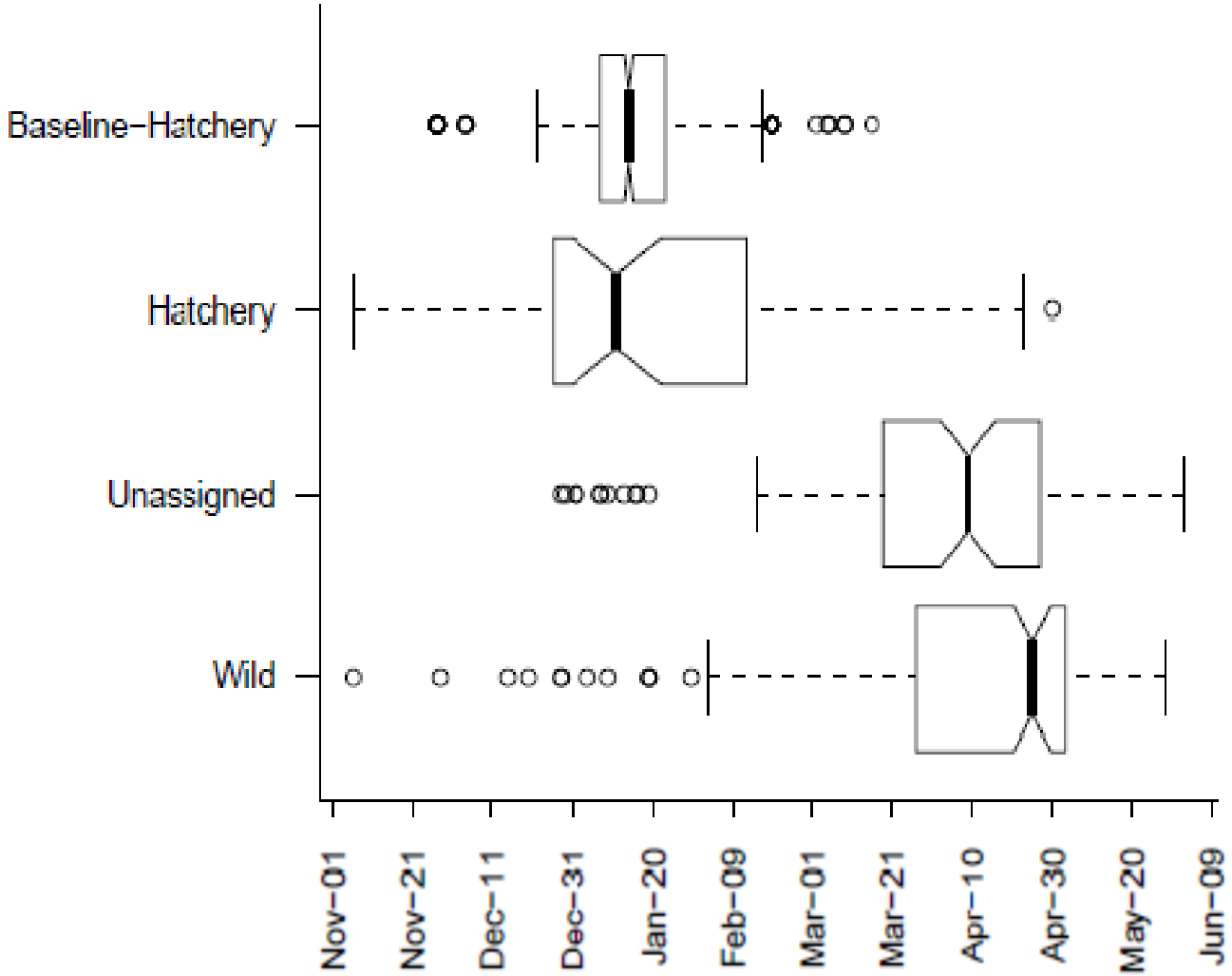


Proportion of collections genetically identified as **wild ancestry declines over time**

Individual assignment criteria

- From GENECLASS2 with confident assignment
  - Decision criteria
    - Prob. of pure H or W > 0.95
    - Results in
    - Wild
    - Hatchery
    - “unassigned”

Significant overlap in adult migration timing



Individual assignment criteria

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    - Results in
      - Wild
      - Hatchery
      - **“unassigned”**

Who are these “unassigned” individuals?

Are they hatchery/wild hybrids?

Just assignment errors?

Estimate assignment test error rates

- From baseline collections simulated100,000 offspring genotypes each of
  - Pure wild
  - Pure hatchery
  - F1 hybrid
- Run them through GENECLASS2

Using HYBRIDLAB, Nielsen *et al*. 2006. Molecular Ecology Notes.

Individual assignment error rates

		True ancestry (simulations)		
		Hatchery	**F1 hybrid**	**Wild**
Estimated ancestry (GENECLASS2)	Hatchery	0.942	0.372	0.007
	Unassigned	0.056	0.411	0.126
	Wild	0.001	0.216	0.868

From these error rates and given some assumptions we can calculate the estimated proportions of **hatchery, wild and hybrid** individuals in our collections

Solve for corrected proportions

Obs(hatchery) = 0.942x + 0.007y + 0.372z

Obs(wild) = 0.001x + 0.868y + 0.216z

Assignment test error rates

Obs(unassigned) = 0.056x + 0.126y + 0.411z

Obs(hatchery)
Obs(wild)
Obs(unassigned)
} Observed proportions

Unknowns {
x = proportion hatchery
y = proportion wild
z = proportion **hybrid**

Solve for corrected proportions

$$Obs(hatchery) = 0.942x + 0.007y + 0.372z$$

$$Obs(wild) = 0.001x + 0.868y + 0.216z$$

$$Obs(unassigned) = 0.056x + 0.126y + 0.411z$$

Assignment test error rates

Obs(hatchery) = 0.198
Obs(wild) = 0.475
Obs(unassigned) = 0.327

Example observed data: 1998 smolt collection

Solve in R using matrix math for each yearly collection, adult and smolt

Critical assumption – only hatchery, wild, or hybrid individuals sampled

- No strays
  - Shouldn't be very many of these since steelhead are good 'homers'
- No rainbow trout
  - No evidence of a rainbow trout population
- No cutthroat
  - Genetically identified and booted out
- No unclipped hatchery-produced fish (cheaters)
  - Genetically identified (parentage) and booted out

Estimates of wild, hatchery, and hybrid proportions – smolt collections

	Smolt collections estimated proportions		
Sample year	Hatchery	F1 Hybrid	Wild
1998	-0.066	0.690	0.376
1999	0.026	0.401	0.573
2000	-0.043	0.637	0.406
2001	0.020	0.704	0.276
2002	0.149	0.480	0.371
2003	0.269	0.369	0.362
2004	0.022	0.439	0.539
2005	0.237	0.477	0.286
2006	0.051	0.540	0.409
2007	0.021	0.631	0.348
2008	0.017	0.763	0.220
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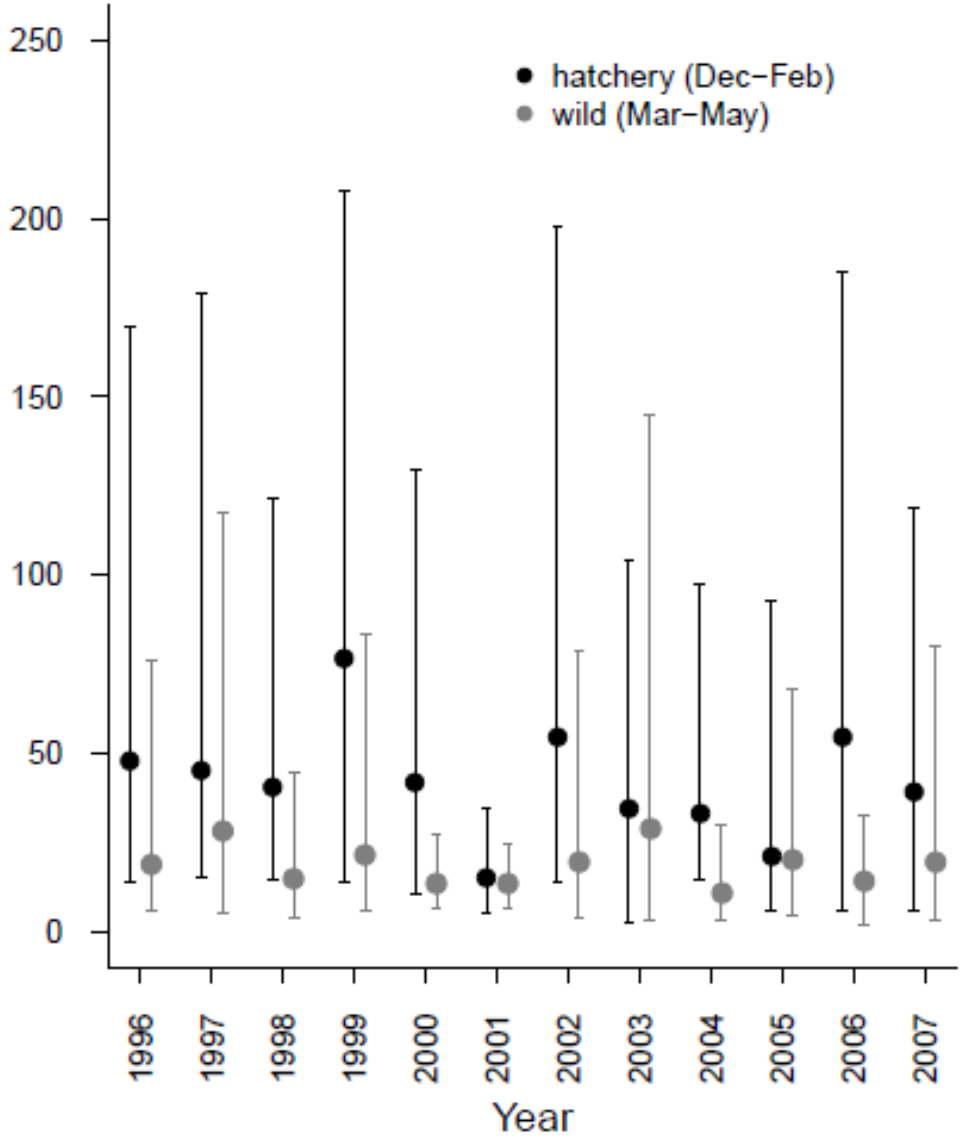
Evaluate possible explanatory variables/isolating mechanisms

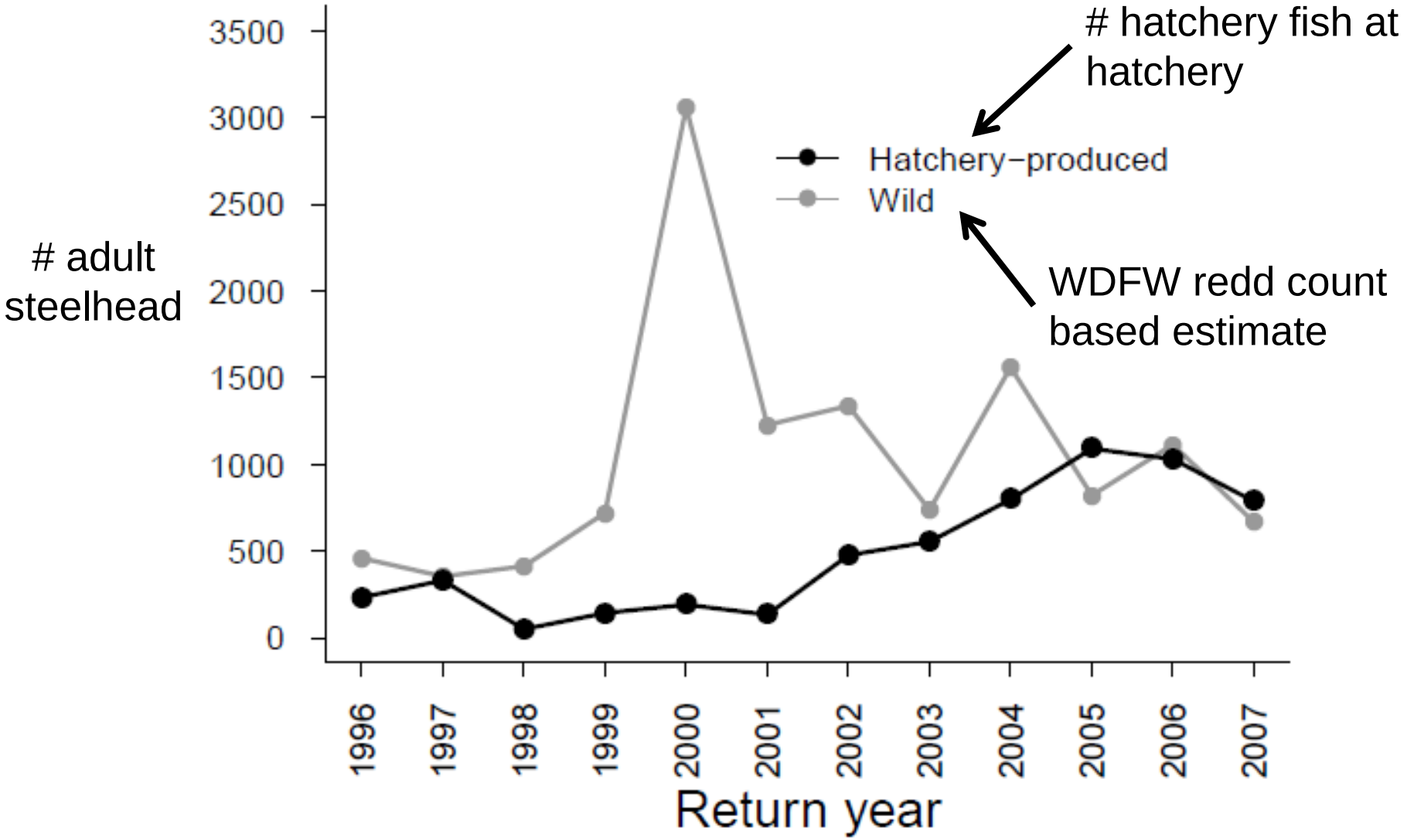
- River discharge during hatchery spawning (Dec – Feb)
  - Possible isolating mechanism?
    - USGS Willapa River stream gauge data
- Number of hatchery-produced adults on the spawning grounds
  - Clipped fish counts at the hatchery
- Number of wild fish on the spawning grounds
  - WDFW SaSI data for entire Willapa River

Willapa River discharge

Willapa River mean daily discharge (m^3s^{-1})



Escapement estimates

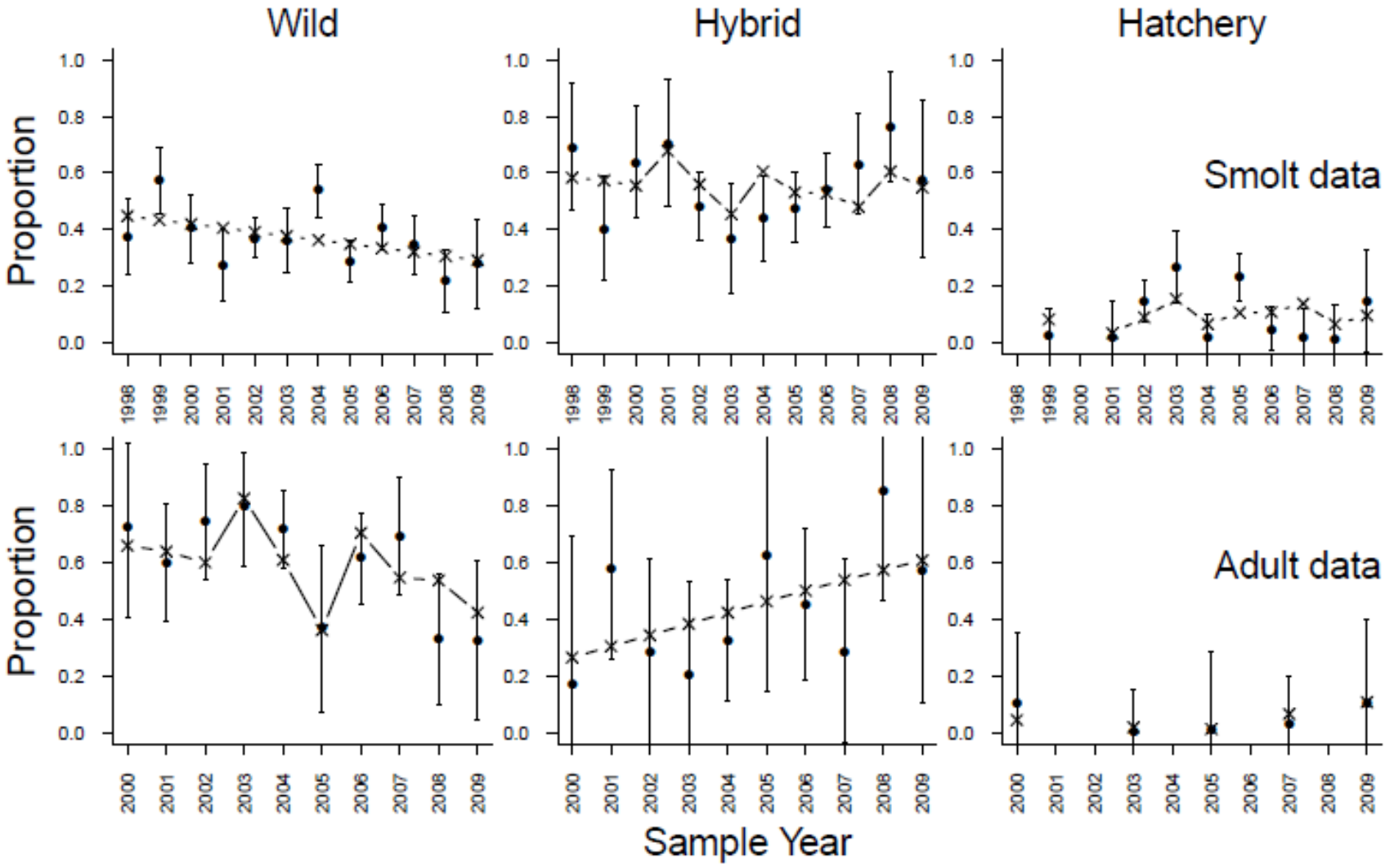


Evaluate covariates – methods

- Forward model selection analysis
  - Add covariate to statistical model (also includes a temporal variable)
  - Evaluate using information theoretic criteria (AIC_c)

"Best fit" models explaining hatchery, wild, and hybrid proportions

-sample year **-discharge** **-discharge**



-discharge **-sample year** **-proportion hatchery**

Summary

- Wild fish declining over time
- Decline may be caused by
  - Hybridization likely due to
  - A constant influx of hatchery-produced adults and
  - Variable environmental conditions
- Discharge likely negatively affects early spawner reproductive success
  - But not an effective segregating mechanism
- Divergent migration/spawning timing not an effective segregating mechanism

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