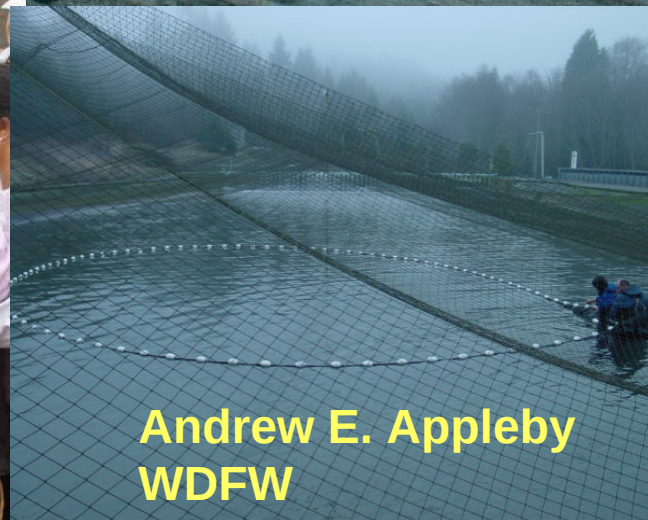
Hatchery Reform Implementation: All-H Hatchery Analyzer (AHA)



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What is the All-H Hatchery Analyzer, really?

- Gene Flow Calculator.
- Currency is adult spawning fish (wild and hatchery).
- Allows you to calculate the amount and direction of gene flow (to and from wild/hatchery).

Why is Gene Flow Important?

- Important if you want the natural environment to drive the fitness of the population as a whole (hatchery and wild).

- Ultimately, this allows fish spawning naturally to be as productive as possible.

Two types of hatchery programs

1. Genetically *Segregated* Broodstocks

2. Genetically *Integrated* Broodstocks

AHA can be used to evaluate either type.

Key Points: Integrated/Segregated

- Must be able to ID hatchery- and natural-origin fish in broodstock and on spawning grounds
- Program sizes must be matched to productivity and capacity of natural environment
- Must be able to control numbers of hatchery fish spawning naturally
- Both strategies represent trade-offs

Support Tool – All H Analyzer

- Ecosystem perspective promotes improved performance:
  - HSRG, WDFW, and tribal scientists developed decision support tool
  - It integrates habitat, harvest, and hatchery information

Thoughts on Using AHA

- Does not absolutely define effects of actions
- Provides hypotheses for interaction of Hs and population
- RM&E required to test hypotheses and adjust actions
- Helps think through integrated all-H strategy, but not an “answer machine”

Population Parameters

- *HOS* = hatchery-origin adults spawning in the wild
- *NOB* = natural-origin adults in hatchery broodstock
- *pHOS* = proportion of natural spawners composed of hatchery-origin adults
- *pNOB* = proportion of hatchery broodstock composed of natural origin adults

Subbasin	*Species*	*Stock Name*		
MyBasin	Chinook	MyChinook	Current	
Habitat:	Productivity | Capacity		2.0	4,000
Harvest:	Harvest Rate [Wild | Hatchery]		0.2	0.2
Primary Hatchery Program	Broodstock Composition:		pNOB	pHOS
		Goal	0%	50%
		Realized	0%	62%
	[Broodstock | Smolt Release]		300	504,900
	HOR Destination [Hat | River]		90%	10%
	[Recruits/Spawner | Fitness?]		10.4	y

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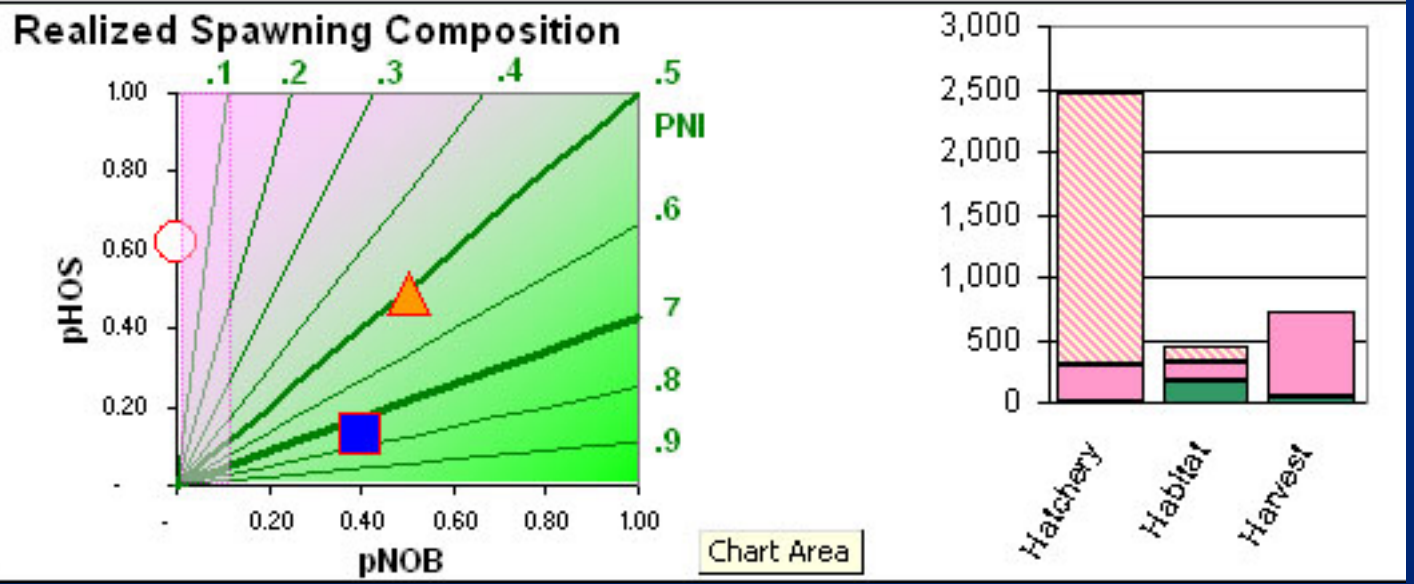
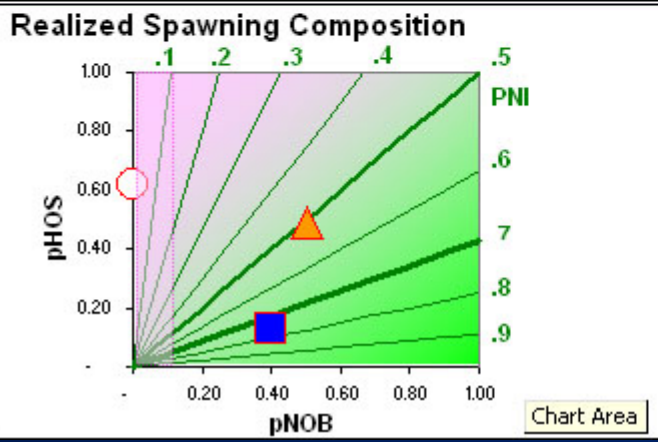
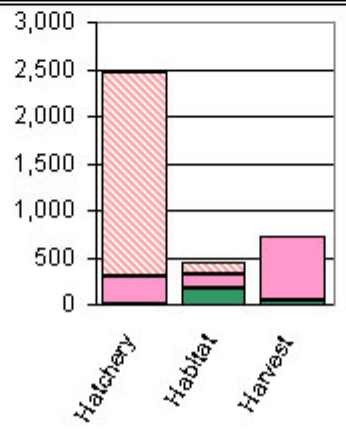
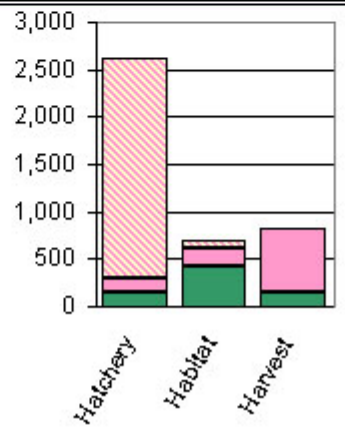
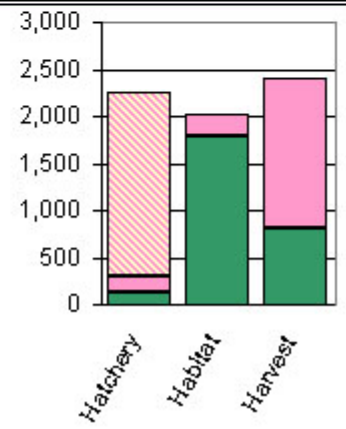


Subbasin	Species	Stock Name	Current		Short Term		Long Term	
MyBasin	Chinook	MyChinook						
Habitat:	Productivity | Capacity		2.0	4,000	2.0	4,000	3.0	5,000
Harvest:	Harvest Rate [Wild | Hatchery]		0.2	0.2	0.2	0.2	0.3	0.4
Primary Hatchery Program	Broodstock Composition:		pNOB	pHOS	pNOB	pHOS	pNOB	pHOS
		Goal	0%	50%	50%	40%	40%	90%
		Realized	0%	62%	50%	47%	40%	13%
	[Broodstock | Smolt Release]		300	504,900	300	503,118	300	503,118
	HOR Destination [Hat | River]		90%	10%	90%	10%	90%	10%
	[Recruits/Spawner | Fitness?]		10.4	y	10.4	y	12.0	y









All H-Analyzer Key Conclusions:

1) Healthy habitat is key to sustaining salmon populations.
2) Marking of fish produced from hatcheries is essential to effectively operate and monitor hatchery programs.
3) Mark-selective fisheries may be required to maximize economic and conservation benefits.
4) Improving hatchery programs will require additional operating and capital funds.

Why Use the All-H Analyzer?

- Uses NOAA approved Watershed/Subbasin plans (Habitat), FMEPs (Harvest), and HGMPs (Hatchery) as data sources.
- Identifies how all the “H”s interact to affect natural populations genetically in a transparent, scientifically defensible manner.
- Helps layout a series of strategies that can move us toward recovery and monitor our progress.

Where is the AHA model being used?

- Staff have done simulations on hatchery programs in Puget Sound, Coast and Col. River.
- Efforts have focused on chinook programs in Puget Sound and lower Col. Ri. coho, but many other programs around the state have been analyzed. Some steelhead programs analyzed as well.
- Currently working with co-managers to develop operational plans; fall of 2005, fall 2006.
- Available operational plans included in HGMPs submitted to NOAA in June 2005.