Steelhead Hatchery – Wild Introgression in Puget Sound, WA

Kenneth I. Warheit

WDFW, Olympia WA

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Goal: document H-W introgression (gene flow) for steelhead in Puget Sound

- Logic and terminology
- Methods
- Results

. . . and I'm going to talk fast.

Reminder:

Two types of Hatcheries

- Integrated
  - Hatchery and wild populations managed as a single population
- Segregated
  - Hatchery and wild populations managed as two separate populations
  - Steelhead in Washington
    - Chambers Creek (early winter). Origin = mostly PS
    - Skamania (early summer). Origin = Lower Columbia
  - Domesticated
  - Goal: No (or minimal) gene flow from hatchery to wild

Gene Flow

- Gene flow is the rate at which genes from a hatchery population are incorporated into a wild population.
- Occurs when hatchery fish escape and spawn in wild at same time/space as wild fish

Gene Flow

- Implications: If fitness of hatchery fish spawning in the wild is less than that of wild fish, hatchery-wild introgression can lower fitness of wild fish

- What does that mean?
  - If hatchery fish spawn with wild fish their offspring are less fit than offspring from two wild parents
  - Lowers productivity of wild populations

- What's the evidence for lower fitness of hatchery-origin fish spawning in the wild?

Relative Reproductive Success

Non-native, segregated hatchery programs
Steelhead

Population	Hatchery	Wild	Segment	Sex	RRS (Max)*
Kalama R	Summer (Skamania)	Summer	Lifetime	FM	0.13
Forks Creek	Winter (Chambers)	Winter	Lifetime	FM	0.11
Forks Creek	Winter (Chambers)	Winter	Adult-to-smolt	FM	0.07
Hood R	Winter (Big Creek)	Winter (?)	Lifetime	F	0.06
				M	0.11
Hood R	Summer (Skamania)	Summer (?)	Lifetime	F	0.35
				M	0.37

* Hatchery compared to Wild

From Araki et al. 2008. Ecological Applications

Evolutionary Applications
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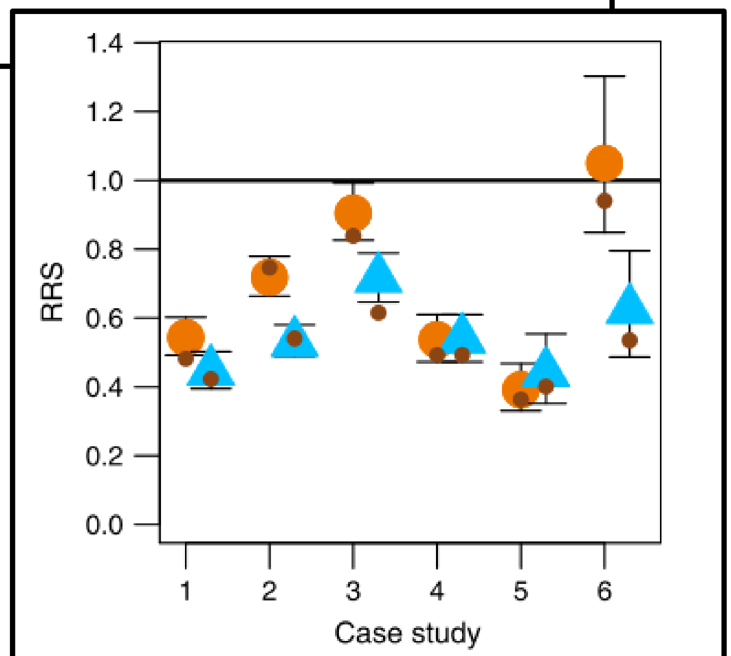
REVIEWS AND SYNTHESIS

On the reproductive success of early-generation hatchery fish in the wild

Mark R. Christie,[1,2] Michael J. Ford[3] and Michael S. Blouin[1]

> "Combining 51 estimates from six studies on four salmon species, we found that (i) early-generation hatchery fish averaged only half the reproductive success of their wild-origin counterparts when spawning in the wild, (ii) the reduction in reproductive success was more severe for males than for females, and (iii) all species showed reduced fitness due to hatchery rearing."

1. Spring Chinook – Wenatchee River
2. Coho – Umpqua River
3. Steelhead – Hood River
4. Atlantic Salmon – Malbaie
5. Steelhead – L. Sheep Creek
6. Spring Chinook – Johnson Creek



Ok, where are we now . . .

1. Segregated hatchery programs. Keep hatchery and wild populations separate
2. Puget Sound: two different steelhead segregated programs
3. Gene flow: hatchery fish spawning naturally may lower RS / fitness of wild fish
4. How do you measure gene flow?

Measuring Gene Flow

- pHOS
  - Proportion hatchery-origin spawners
  - Percentage of spawners that are hatchery-origin
  - Count
  - Hatchery-origin fish defined as those fish without adipose fin

pHOS

Parental Population

Estimate hatchery/wild contribution into

F1 Generation

Measuring Gene Flow

- pHOS
  - **P**roportion **H**atchery-**O**rigin **S**pawners
  - Percentage of spawners that are hatchery-origin
  - Count
- PEHC
  - **P**roportion **E**ffective **H**atchery **C**ontribution
  - The proportion of the parental population that is of hatchery-origin
  - Requires and estimate of proportion of:
    HH, HW, WW in parental populations

PEHC

Parental Population

↑

Estimate composition of parental population

↑

F1 Generation

Proportion of parental population composed of hatchery-origin fish

$$PEHC = \frac{(2 \times HH) + (1 \times HW) + (0 \times WW)}{2}$$

$$PEHC = HH + (0.5 \times HW)$$

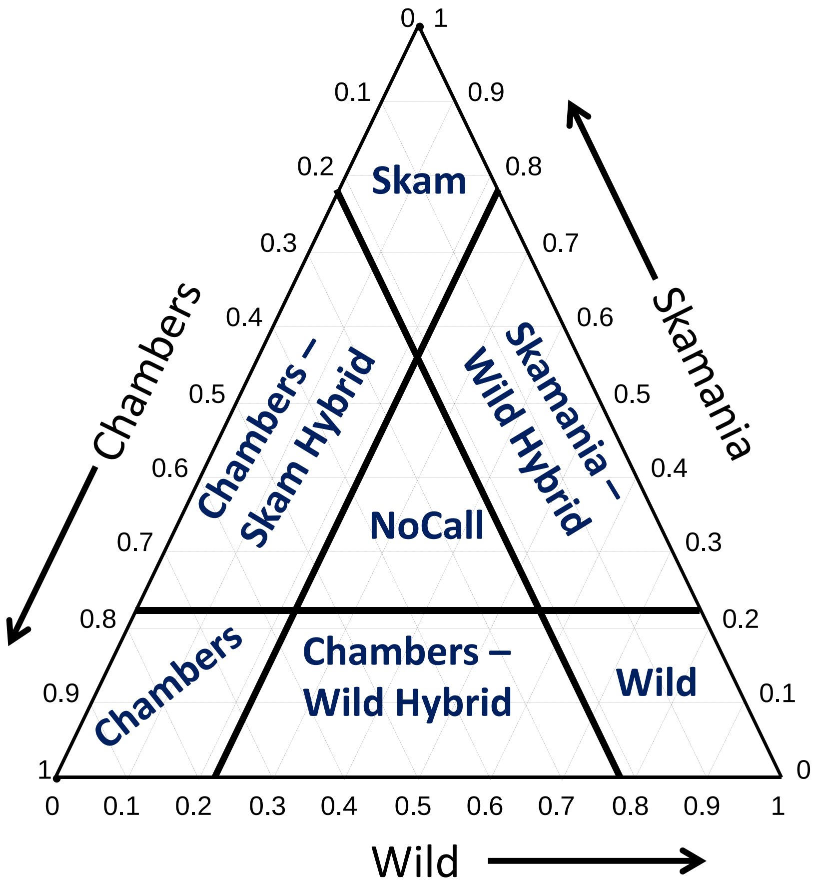
HH = proportion of pop with two hatchery-origin parents
HW = proportion of pop with one hatchery origin parent (a hybrid)
WW= proportion of pop with two wild parents

PEHC
Estimating Proportions

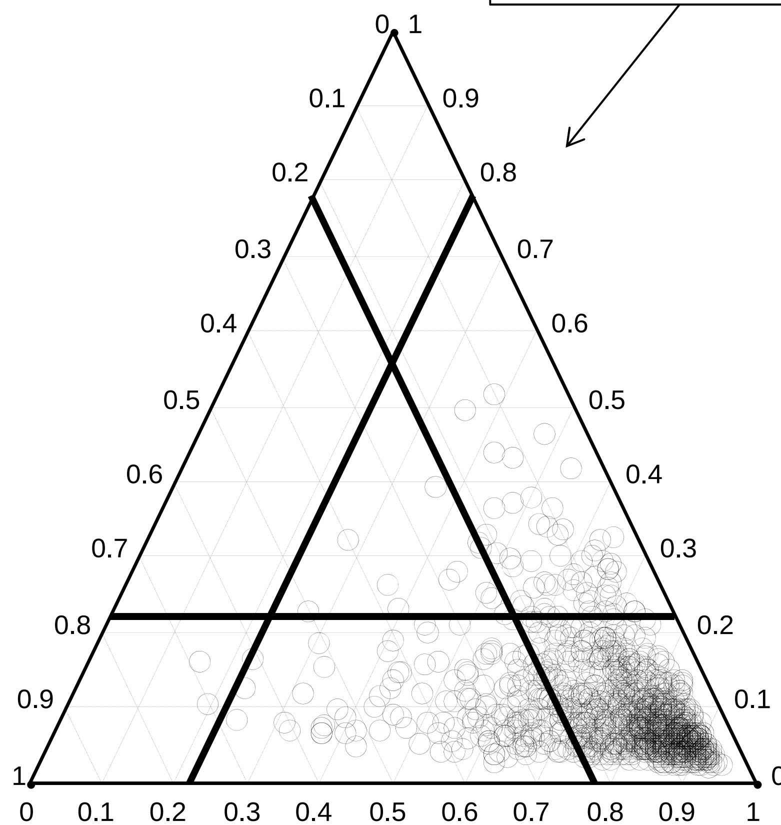
- Genetic data
  - Genetic markers: fixed difference between H and W
  - Pedigree
  - Inferential statistics to estimate HH, HW, WW
    - Difficult when hatchery and wild populations are closely related and share common alleles

Determining Parental Proportions
(HH, HW, WW)

- Two hatchery, one wild population
- Program STRUCTURE
- For each individual – estimates admixture
- K=3

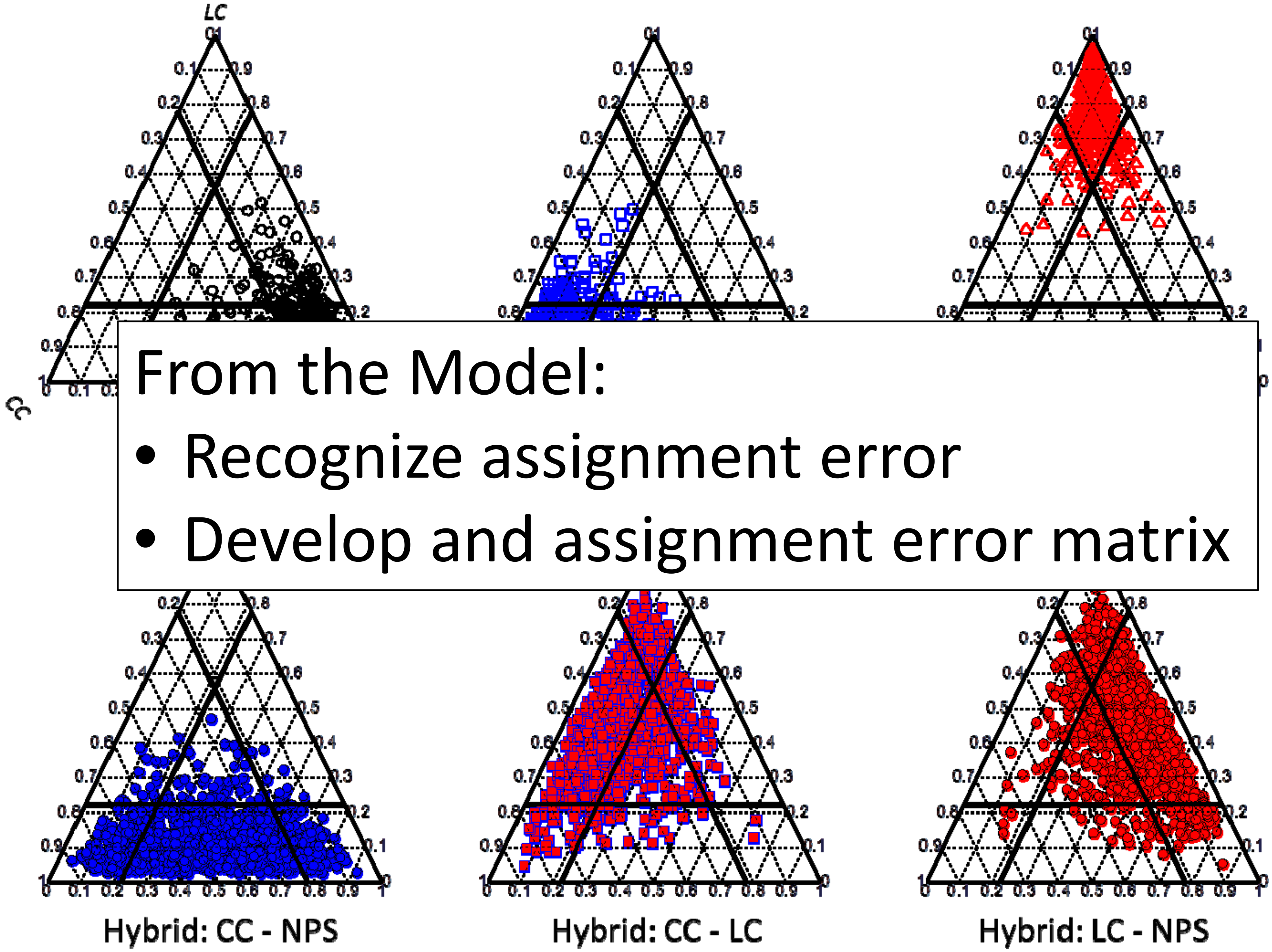


Model:
Pure Chambers
Pure Skamania
Pure Wild Winter



100% Wild Individuals

Complete Model



From the Model:

- Recognize assignment error
- Develop and assignment error matrix

Tools (so far) for measuring gene flow

- Estimate relative proportions using program STRUCTURE
  - Seven categories
- Assignment error matrix (AEM)

Estimating PEHC

- Genetic data
  - Genetic markers: fixed difference between H and W
  - Pedigrees
  - Inferential statistics to estimate HH, HW, WW
    - Difficult when hatchery and wild populations are closely related and share common alleles
- Unbiased estimator
  - Adjust STRUCTURE results using:
    - Method: Knapp and Warheit
- Green, Snohomish, Stillaguamish, Skagit, Nooksack

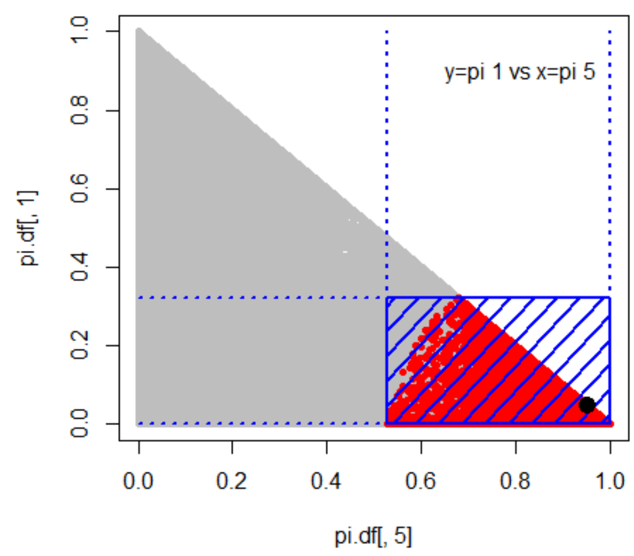
Adjusting STRUCTURE results

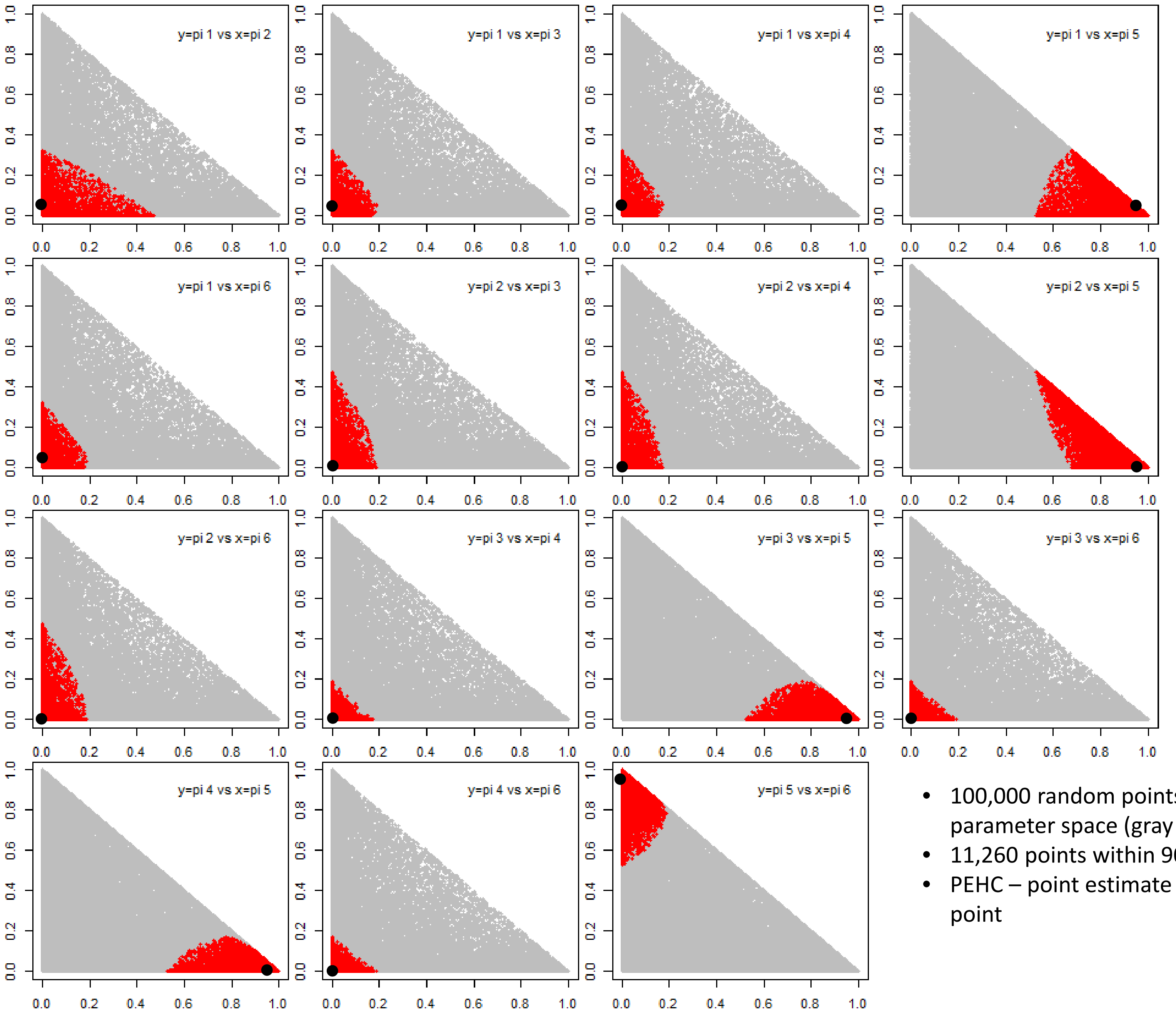
(Knapp and Warheit, ms)

- **y** = the vector of the 7 assigned counts from *STRUCTURE*
- ψ = matrix of Pr(Assigned = *i* | Source = *j*). "Assignment error matrix" from model (previous slide)
- π = the vector of the 6 *adjusted* proportions (multinomial distribution)
- Maximize likelihood = point estimate for π
- 90% CI (confidence hyper-volume) = log-likelihood ratio test.

  X^2 distribution with df = 5; α = 0.10

$$\ln L\left(\boldsymbol{\pi} \middle| \boldsymbol{\psi}, \mathbf{y}\right) = \sum_{i=1}^{7} \left\{ \ln \left(\left[\sum_{j=1}^{6} \left(\psi_{i|j} \pi_j \right) \right]^{y_i} \right) \right\}$$





- 100,000 random points within parameter space (gray + red)
- 11,260 points within 90% CI (red)
- PEHC – point estimate = black point

Group	π	point estimates	90% bounds	
			lower	upper
EWH	π_1	0.04744	0.00000	0.32316
EWH-Wild	π_2	0.00000	0.00000	0.47301
ESH-Wild	π_3	0.00000	0.00000	0.18721
ESH	π_4	0.00000	0.00000	0.17280
Wild	π_5	0.95257	0.52699	1.00000
EWH-ESH	π_6	0.00000	0.00000	0.18722
$PEHC_{winter}$		0.04744	0.00000	0.32316
$PEHC_{summer}$		0.00000	0.00000	0.17280

Measuring Gene Flow

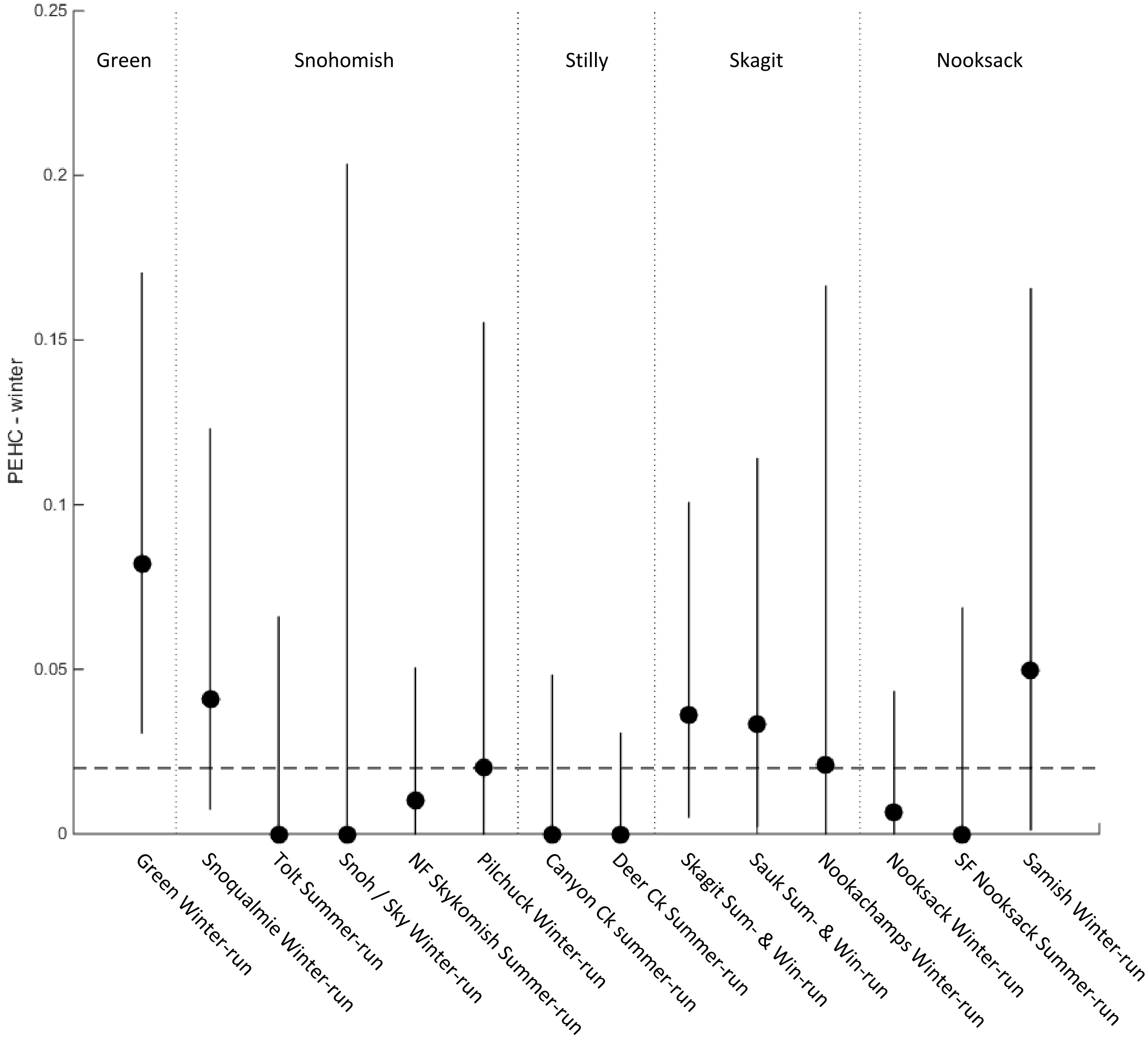
Segregated		Integrated		
			Fitness Factor	
pHOS	Fitness Factor	PNI	pHOS=10%	pHOS=30%
2%	0.85	0.77	0.92	0.91
3%	0.76	0.75	0.91	0.9
4%	0.68	0.71	0.89	0.87
5%	0.62	0.67	0.86	0.83
6%	0.57	0.60	0.81	0.77
10%	0.20	0.50	0.74	0.67

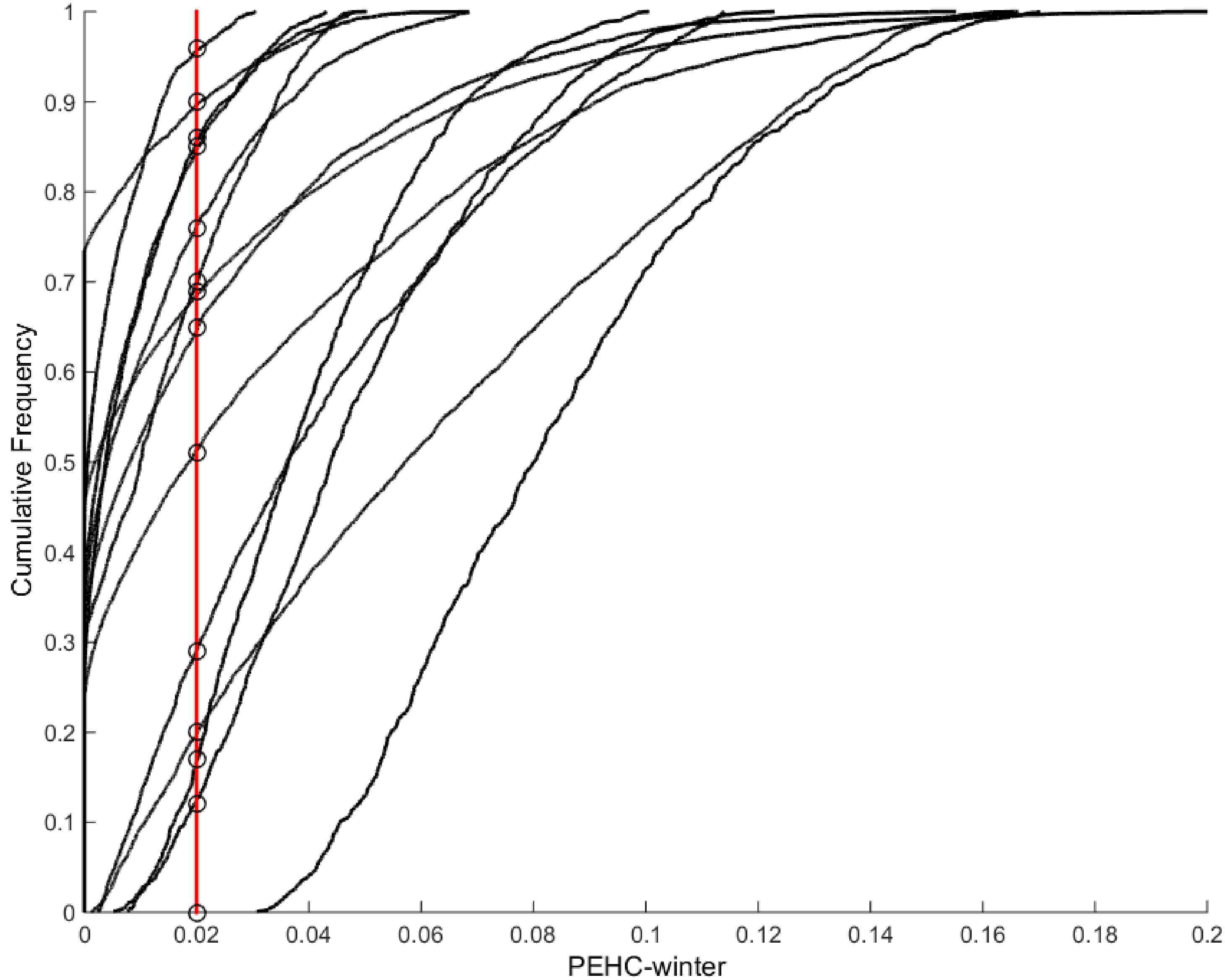
HSRG 2014

- WDFW: PEHC <= 2% for steelhead segregated programs

PEHC – winter

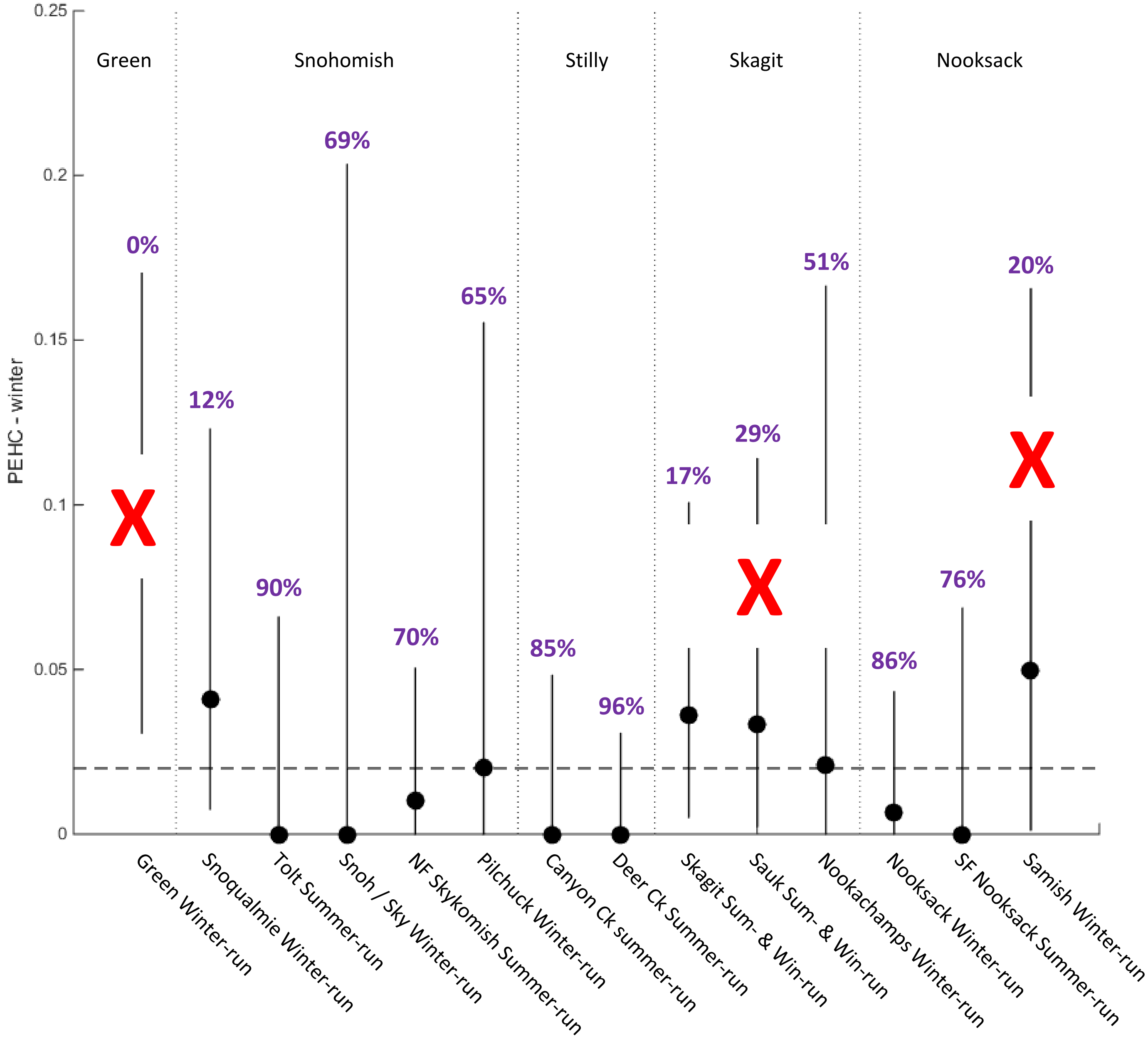
Demographically independent populations (DIPs)




Cumulative Frequency
PEHC-winter
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.02
0.04
0.06
0.08
0.1
0.12
0.14
0.16
0.18
0.2

PEHC – winter

Demographically independent populations (DIPs)



Summary

- PEHC – summary of gene flow
- Use STRUCTURE for initial proportions
- Adjust STRUCTURE proportions using AEM and Knapp and Warheit method
- Estimates of H-W gene flow for many steelhead DIPs in Puget Sound
- Some systems with little gene flow, other systems with higher gene flow

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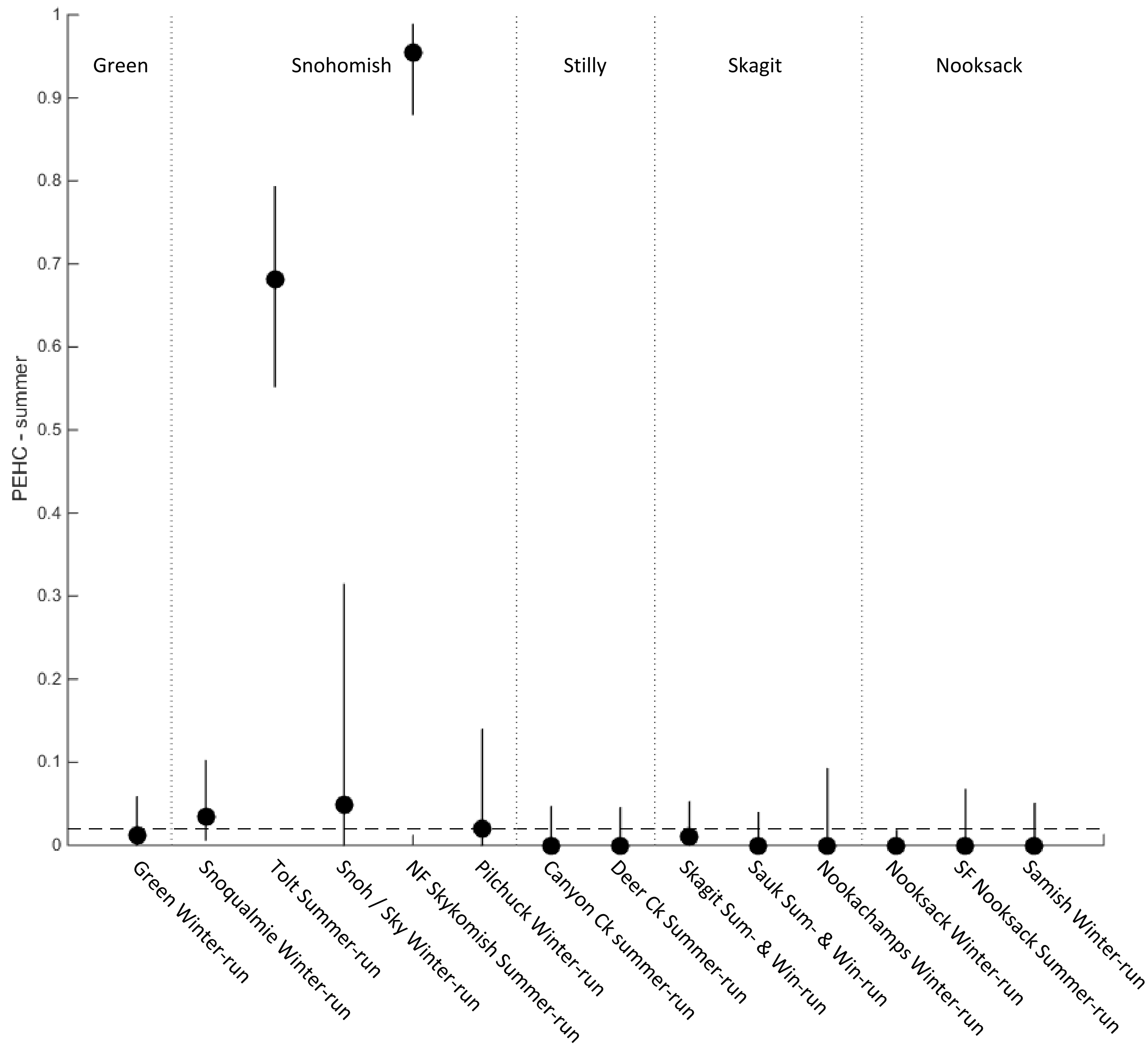
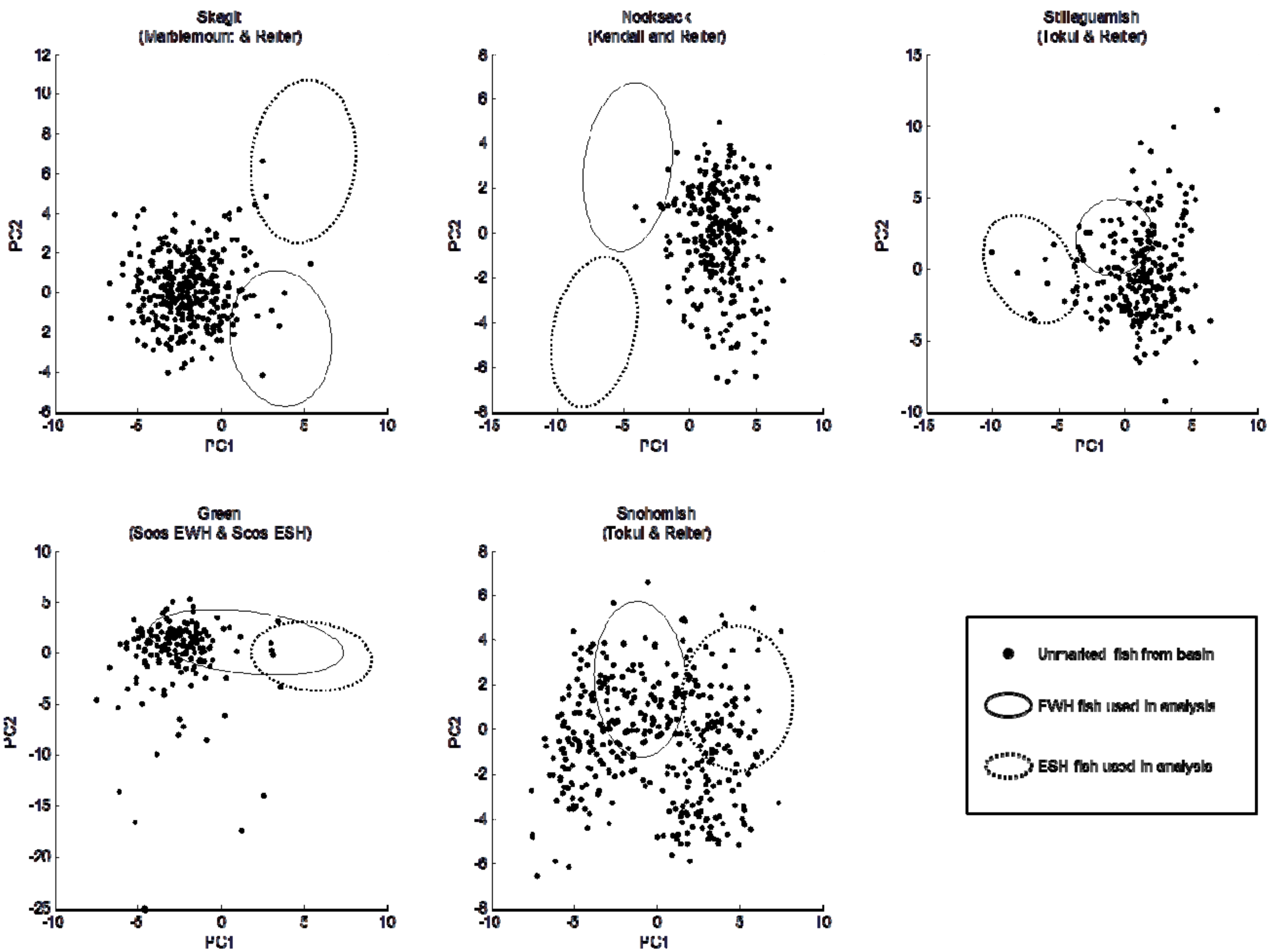
PEHC – summer

Demographically independent populations (DIPs)





Skagit
(Marblemount & Reiter)
Nooksack
(Kendall and Reiter)
Stillaguamish
(Tokul & Reiter)
Green
(Soos EWH & Soos ESH)
Snohomish
(Tokul & Reiter)
PC1
PC2
Unmarked fish from basin
FWH fish used in analysis
ESH fish used in analysis

Last Word – sample size & error

- Lots of moving parts:
  - Two hatcheries, Small sample sizes, Genotyping, Assignments: hybrids & pure, Adjustments
  - All of this contributes to error
- Assume: one hatchery, one wild, no hybrids (assignment =HH or WW), no error
  - Binomial sampling
  - What's the probability of calculating PEHC = 0 (i.e., sampling NO hatchery-lineage fish)?

True PEHC	Sample Size						
	25	50	100	200	300	400	500
0.005	0.88	0.78	0.61	0.37	0.22	0.13	0.08
0.010	0.78	0.61	0.37	0.13	0.05	0.02	0.01
0.020	0.60	0.36	0.13	0.02	0.00	0.00	0.00
0.050	0.28	0.08	0.01	0.00	0.00	0.00	0.00
0.100	0.07	0.01	0.00	0.00	0.00	0.00	0.00
0.250	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.500	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Hatchery Domestication

"Domestication . . . is the cultivating or taming of a population of organisms in order to accentuate traits that are desirable to the cultivator or tamer."

Wikipedia

- Early maturation
- Rapid juvenile development
- Early spawn timing – segregated from wild spawning