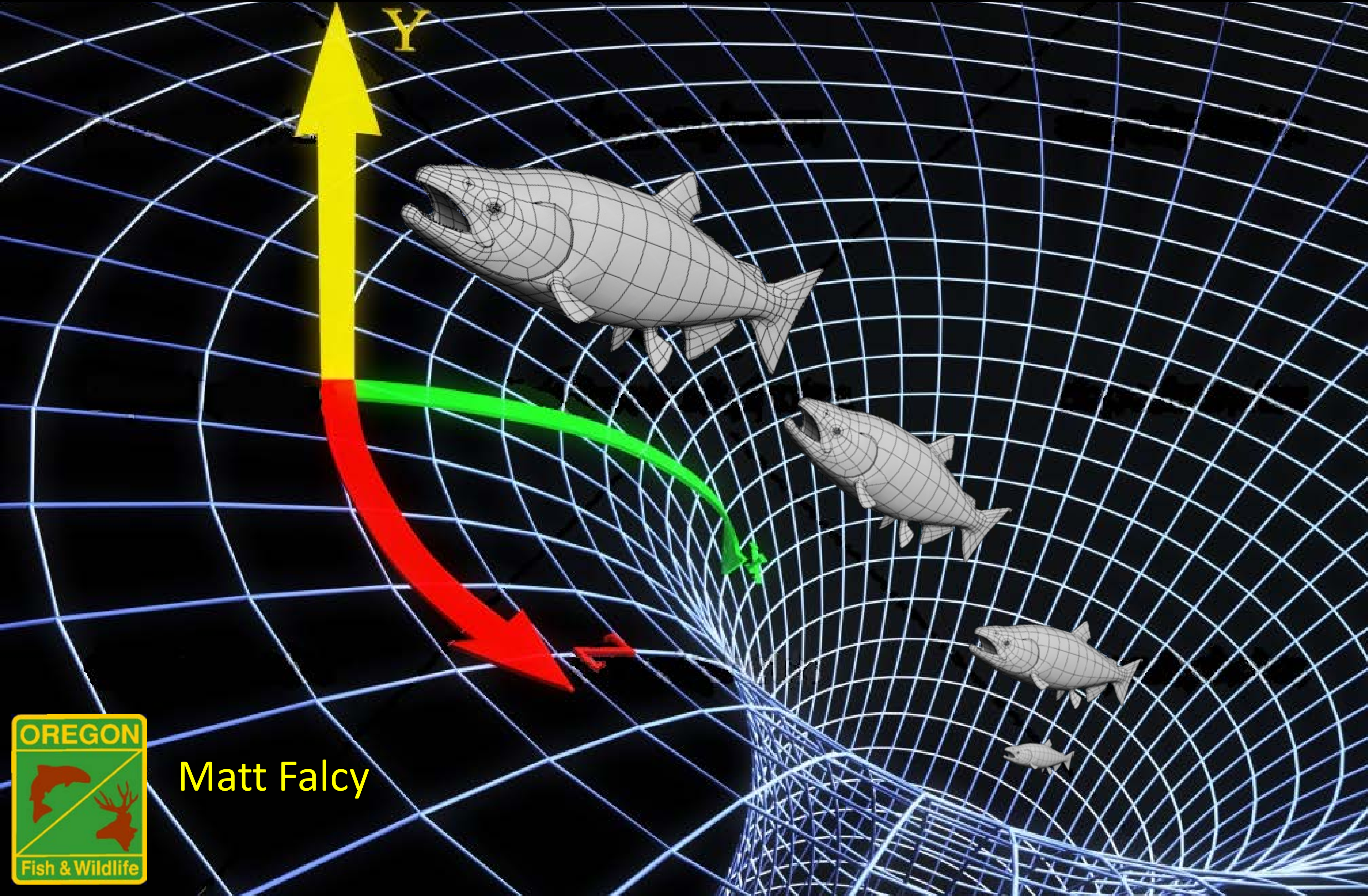
Combining genetics and demographics in a viability model of hatchery-wild systems subject to environmental change



Matt Falcy

OREGON Fish & Wildlife

Objective and Methods

Objective

Explore effects of pHOS, pNOB, and wild broodstock take (“mining”) on population persistence.

Methods

I. Analytical model (genetic)

- Relative fitness is response
- Explore sensitivity to selection parameters

II. Individual-based model (genetic & demographic)

- Population viability is response
- Environmental change
- Explore effect of “mining” wild fish

I. Analytical Model- Quantitative Genetics

Selection in Captivity during Supportive Breeding May Reduce Fitness in the Wild

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Abstract: *I used a quantitative genetic model to explore the effects of selection on the fitness of a wild population subject to supportive breeding. Supportive breeding is the boosting of a wild population's size by breeding part of the population in captivity and releasing the captive progeny back into the wild. The model as-*

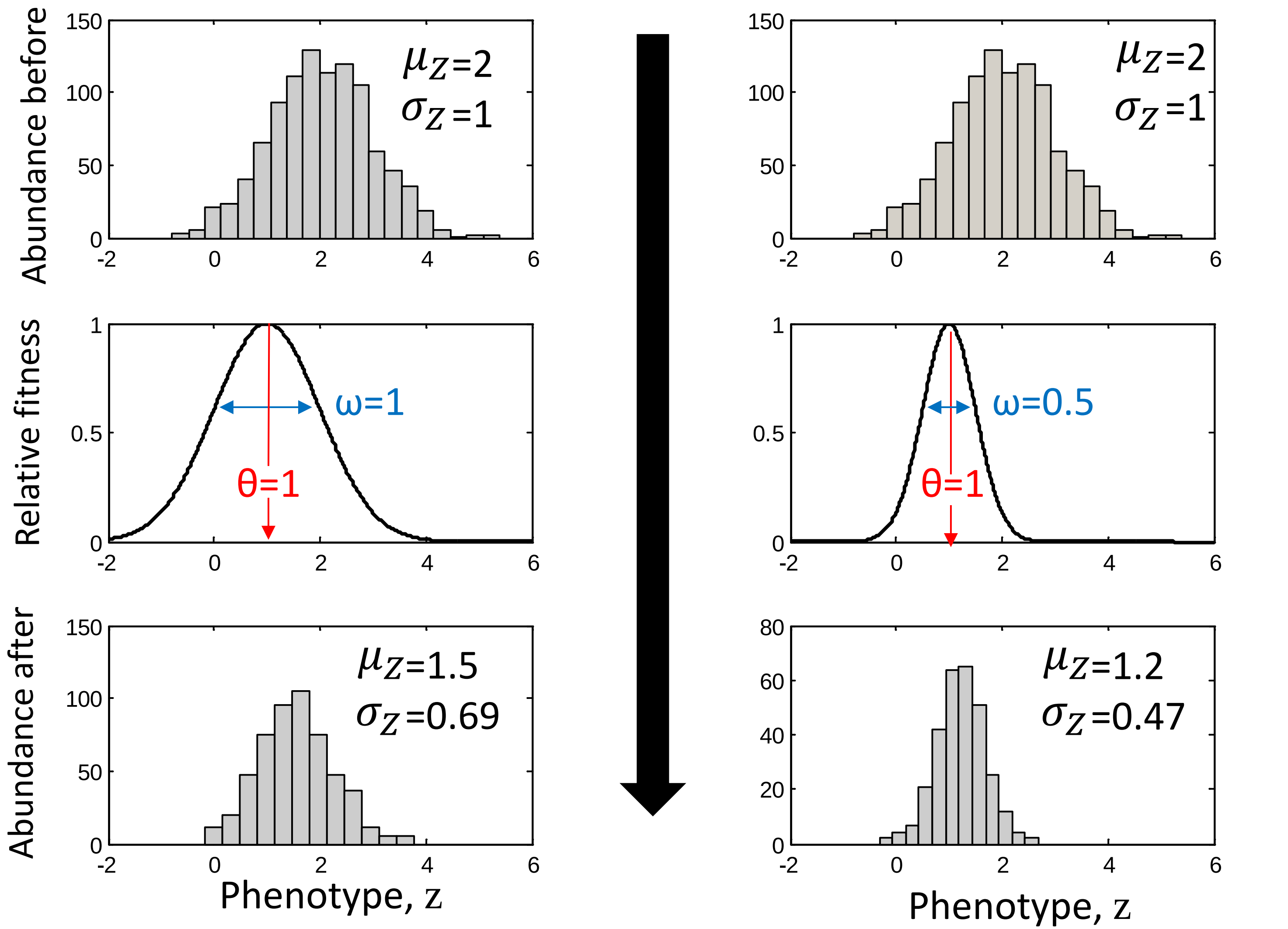
White Paper No. 1[1]

Predicted Fitness Effects of Interbreeding between Hatchery and Natural Populations of Pacific Salmon and Steelhead

1 Introduction

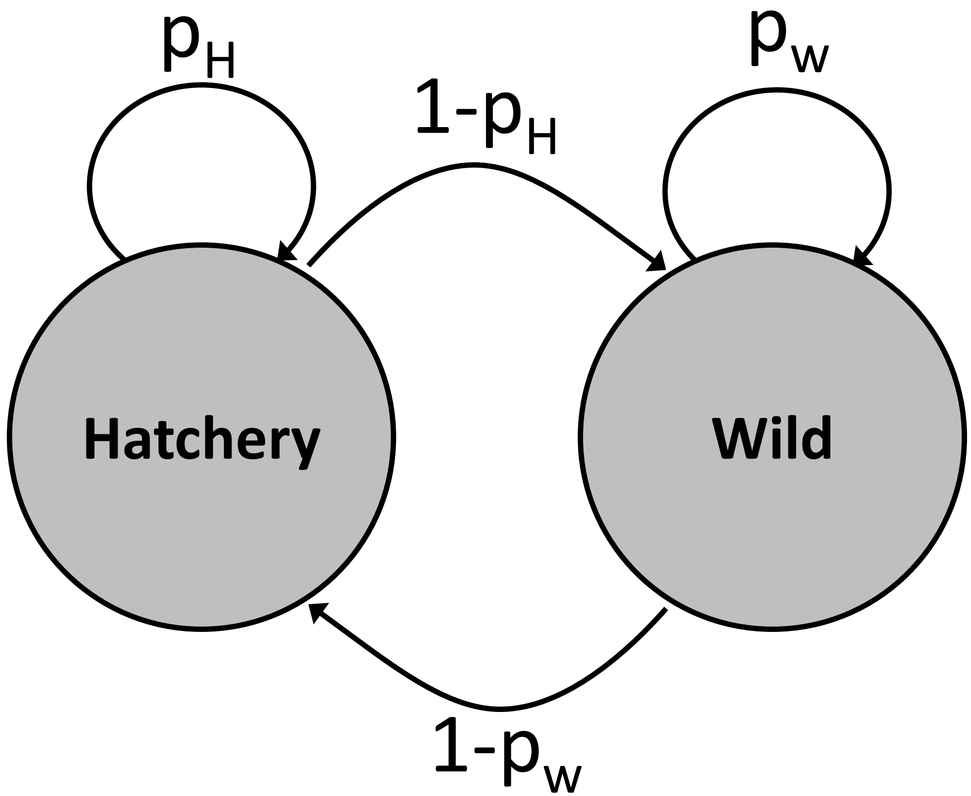
The propagation of Pacific salmon and steelhead (*Oncorhynchus* spp.[2]) in hatcheries has raised concerns for more than 30 years regarding the long-term genetic effects of hatchery-origin fish on the mean fitness of natural populations (Reisenbichler and

Selection on a Quantitative Character



$\mu_Z' = \mu_Z + \left[\frac{\mu_Z\omega^2+\theta\sigma_Z^2}{\omega^2+\sigma_Z^2} - \mu_Z\right] h^2 = 1.5$	$\mu_Z' = \mu_Z + \left[\frac{\mu_Z\omega^2+\theta\sigma_Z^2}{\omega^2+\sigma_Z^2} - \mu_Z\right] h^2 = 1.2$

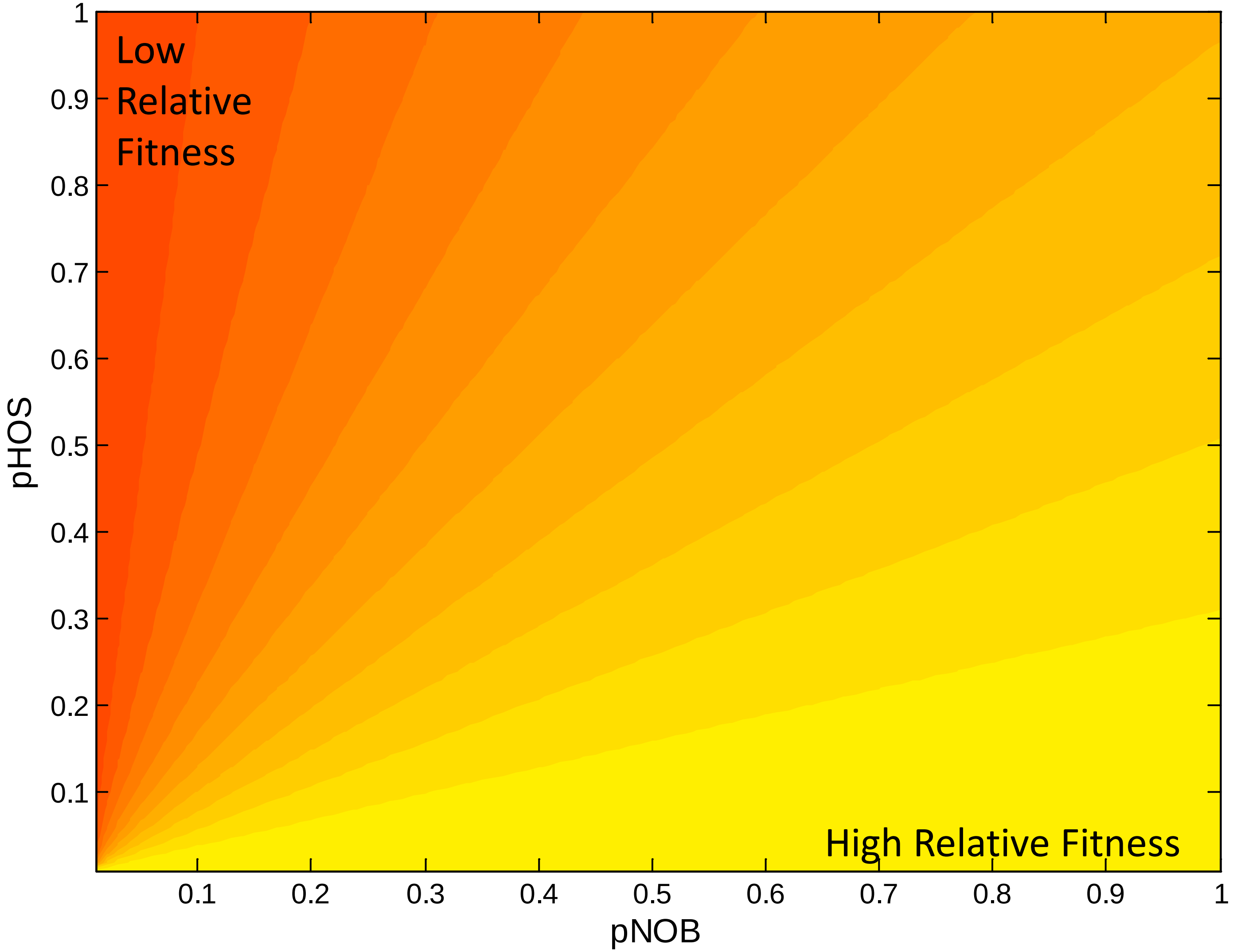
Selection on a Quantitative Character



$$\hat{z}_W = \frac{\sigma^2\Big(\big(1+p_H(h^2-1)\big)\theta_W + (h^2-1)(p_W-1)\theta_H\Big) + \theta_H(\omega_W^2 - \omega_W^2 p_W) - \theta_W\omega_H^2(p_H-1)}{\sigma^2(2-p_W-p_H+h^2(p_W+p_H-1)) + \omega_W^2(1-p_W) + \omega_H^2(1-p_H)}$$

$$\widehat{W} = e^{\left[\frac{-(\hat{z}-\theta)^2}{2(\omega^2+\sigma^2)}\right]}$$

Selection on a Quantitative Character

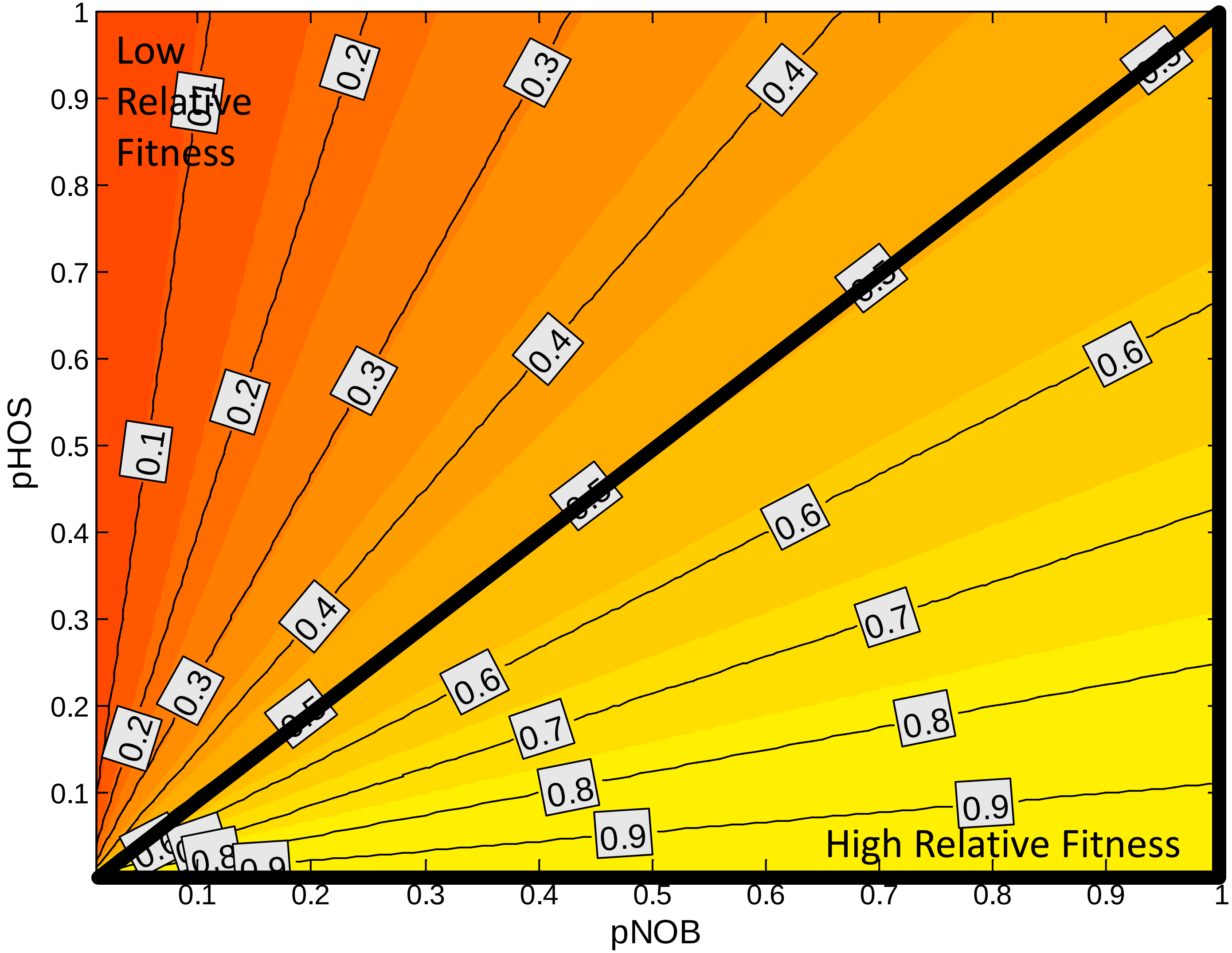


Weak selection

$\omega^2 \gg \sigma^2$

Selection on a Quantitative Character

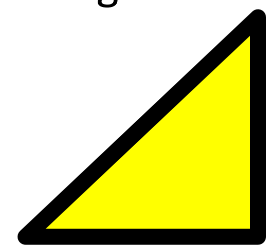
$$PNI_{Approx} = \frac{pNOB}{pNOB + pHOS}$$



Weak selection

$\omega^2 \gg \sigma^2$

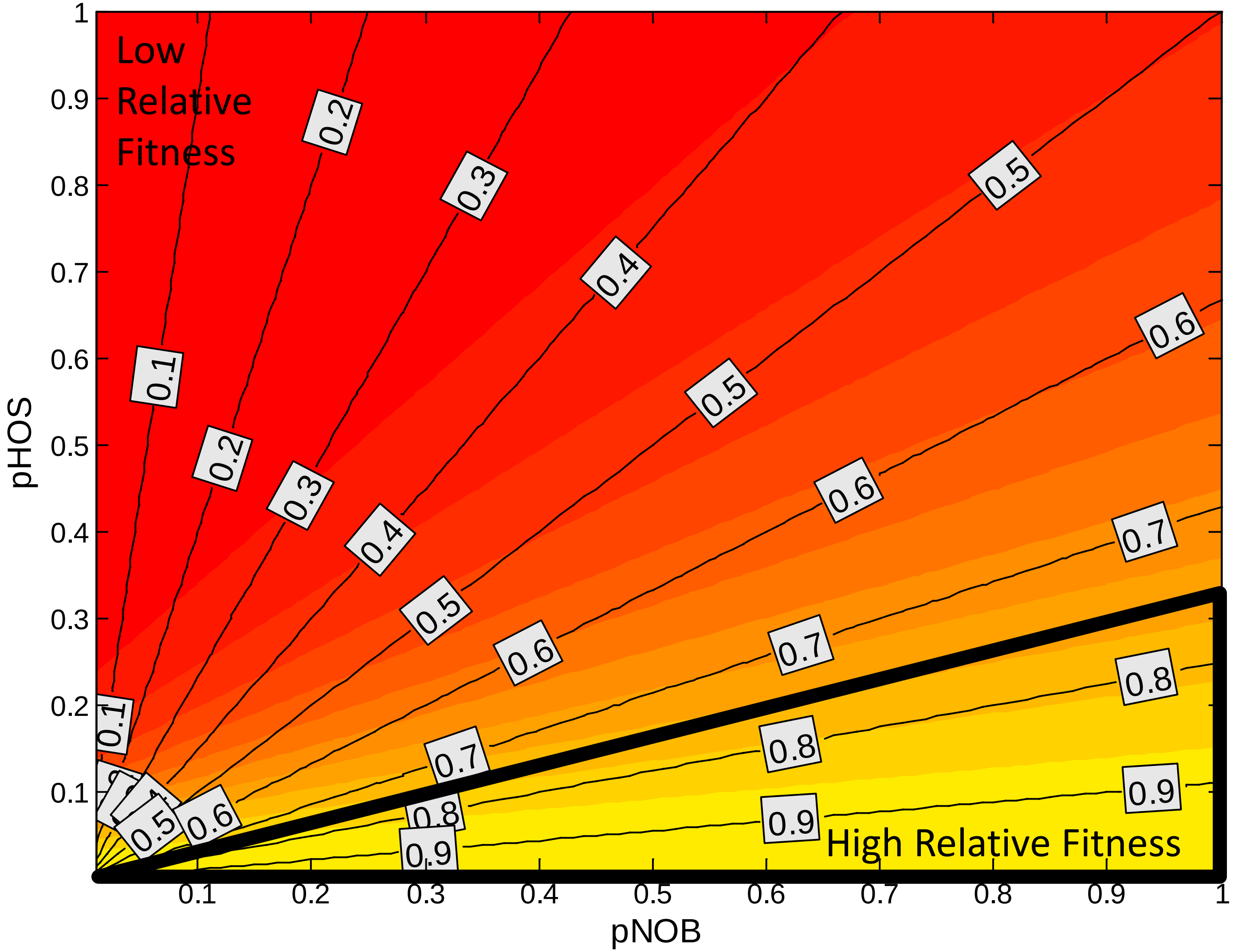
“Golden triangle of genetic goodness”



PNI>0.5

Selection on a Quantitative Character

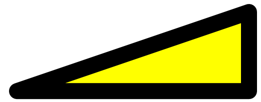
$$PNI_{Approx} = \frac{pNOB}{pNOB + pHOS}$$



Stronger selection

$\omega^2 > \sigma^2$

“Golden triangle of genetic goodness”



PNI>0.75

II. Individual-based Model of Niche Evolution

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The phenomenology of niche evolution via quantitative traits in a 'black-hole' sink

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Previous studies of adaptive evolution in sink habitats (in which isolated populations of a species cannot persist deterministically) have highlighted the importance of demographic constraints in slowing such evolution, and of immigration in facilitating adaptation. These studies have relied upon either single-locus

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Temporal Variation Can Facilitate Niche Evolution in Harsh Sink Environments

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A classic problem in evolutionary biology is to understand the factors that govern the tempo of evolutionary change (Simpson 1944). Many controversies have swirled around

II. Individual-based Model of Niche Evolution

	Parent ♀	
Locus1	0.066	0.272
Locus2	0.136	-0.001
.	.	.
.	.	.
.	.	.
Locus10	0.024	-0.271

	Parent ♂	
Locus1	0.159	-0.338
Locus2	0.082	0.082
.	.	.
.	.	.
.	.	.
Locus10	-0.271	-0.125

	Offspring	
Locus1	0.272	-0.338
Locus2	0.136	0.082
.	.	.
.	.	.
.	.	.
Locus10	-0.271	-0.271

Individual’s phenotype is sum of allelic values + *Normal*(0,1)

II. Individual-based Model of Niche Evolution

Model attributes

- Allows selection-mutation-drift balance
- Relaxes assumption of constant heritability ($h^2 = \frac{V_A}{V_A+V_E}$)
- Relaxes assumption of constant phenotypic variance
- Demographic stochasticity

Reproducible Result

218 R. D. Holt and others *Punctuated niche evolution* **Proceeding of the Royal Society B**

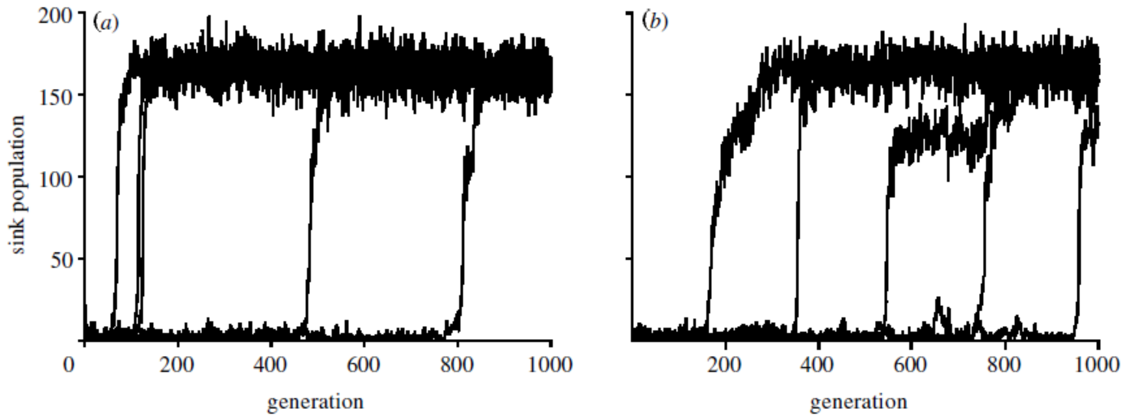
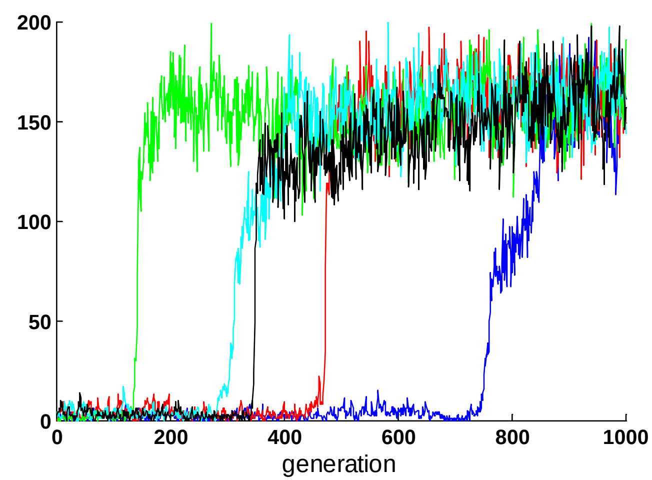


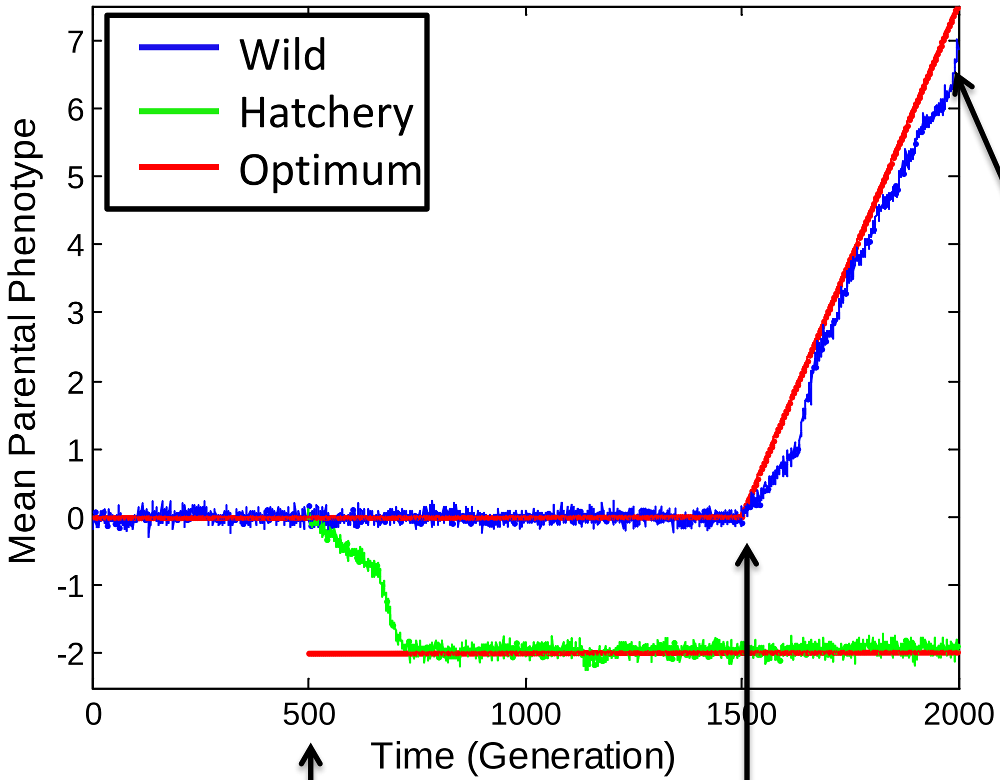
Figure 2. Characteristic examples of population dynamics for species adapting to sink habitats. For the five examples shown on each panel, $K = 64$, $2B = 8$, $n\mu = 0.01$, $n = 10$, $\alpha^2 = 0.05$, $I = 4$, $\omega^2 = 1$, $\theta_{\text{source}} = 0$, and $\theta_{\text{sink}} = 2.8$. The population sizes shown are numbers of adults, after selection and before immigration. (*a*) With sink mutation; (*b*) same as (*a*) except with no sink mutation.

My re-creation



Simulation Result

pHOS=0
pNOB=0

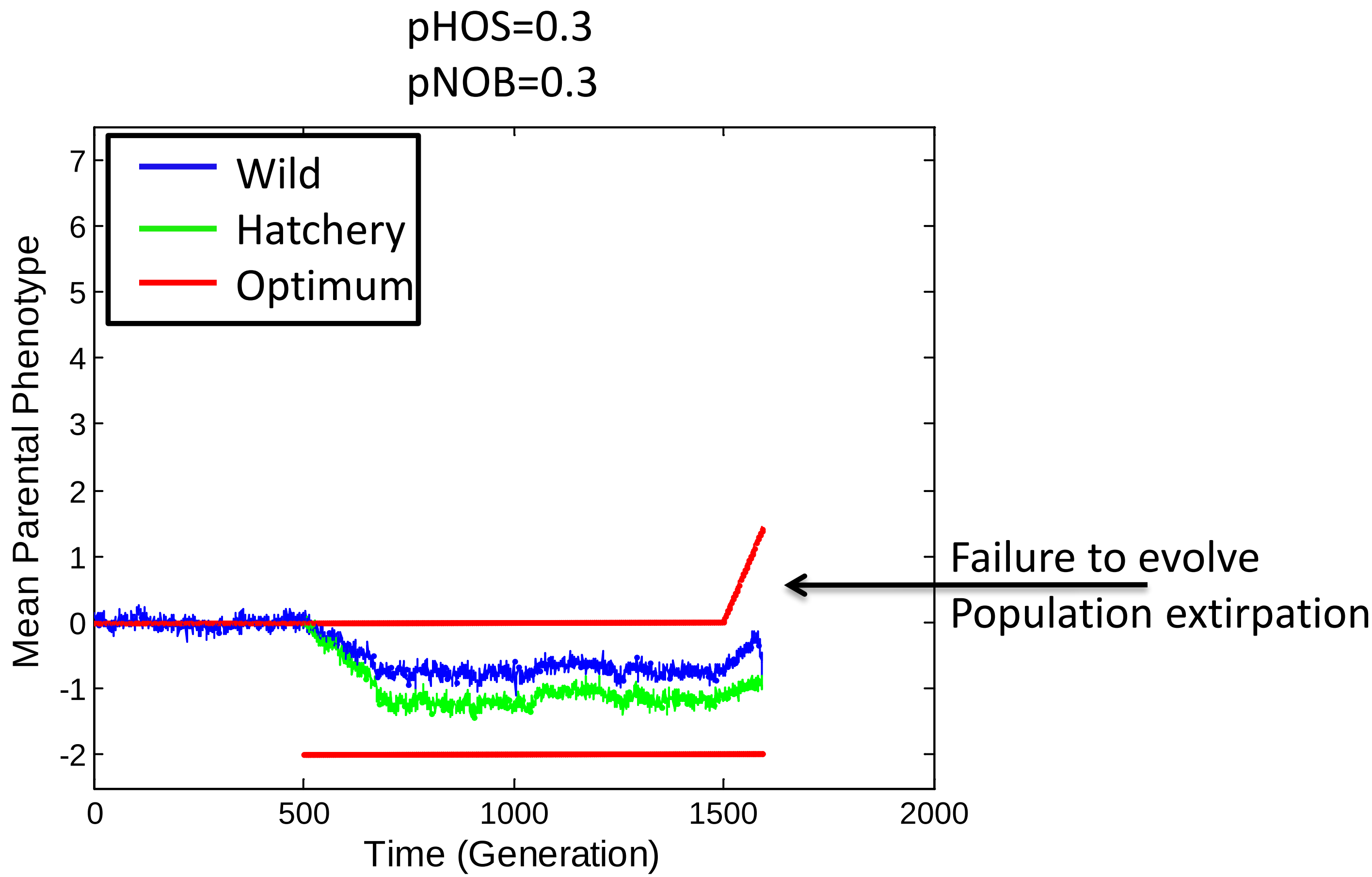


Wild fish adapt and persist

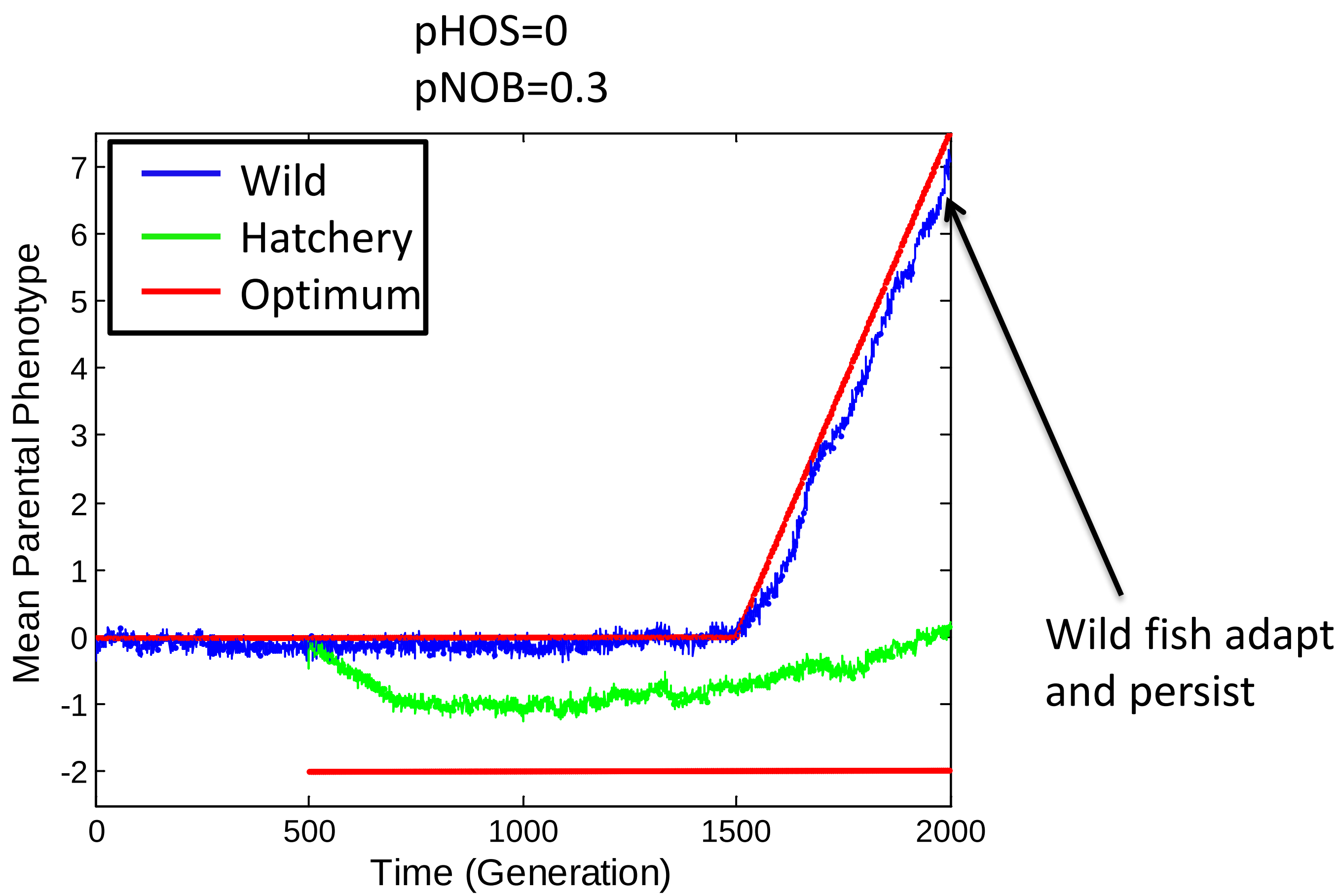
Initiate hatchery program

Optimum phenotype of wild fish begins to change

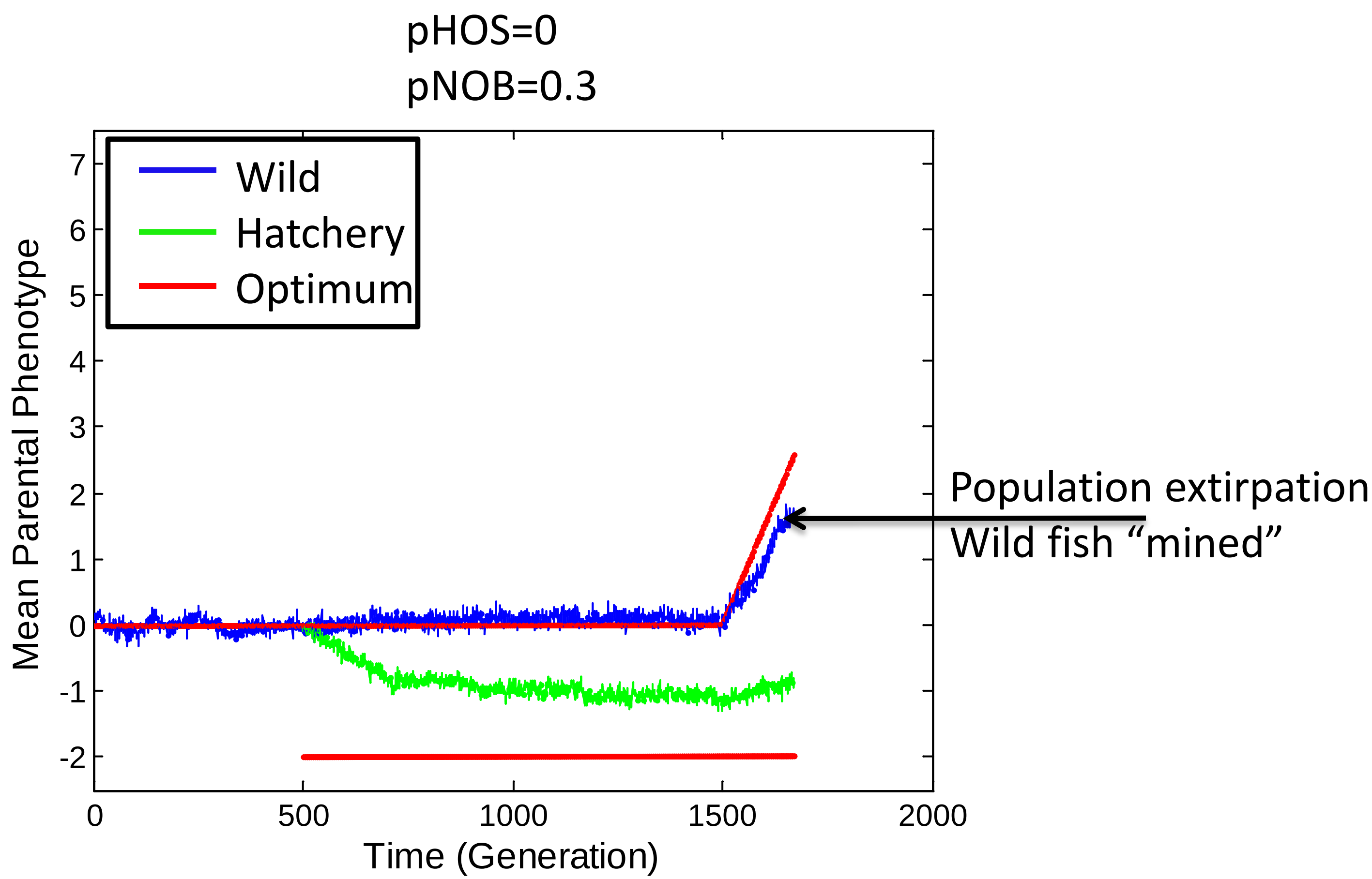
Simulation Result



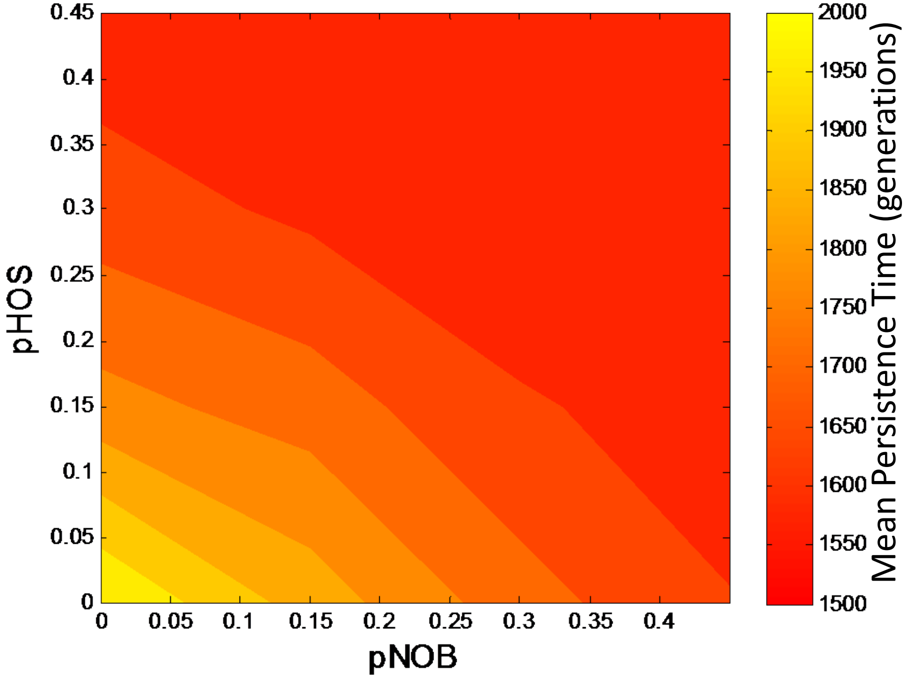
Simulation Result



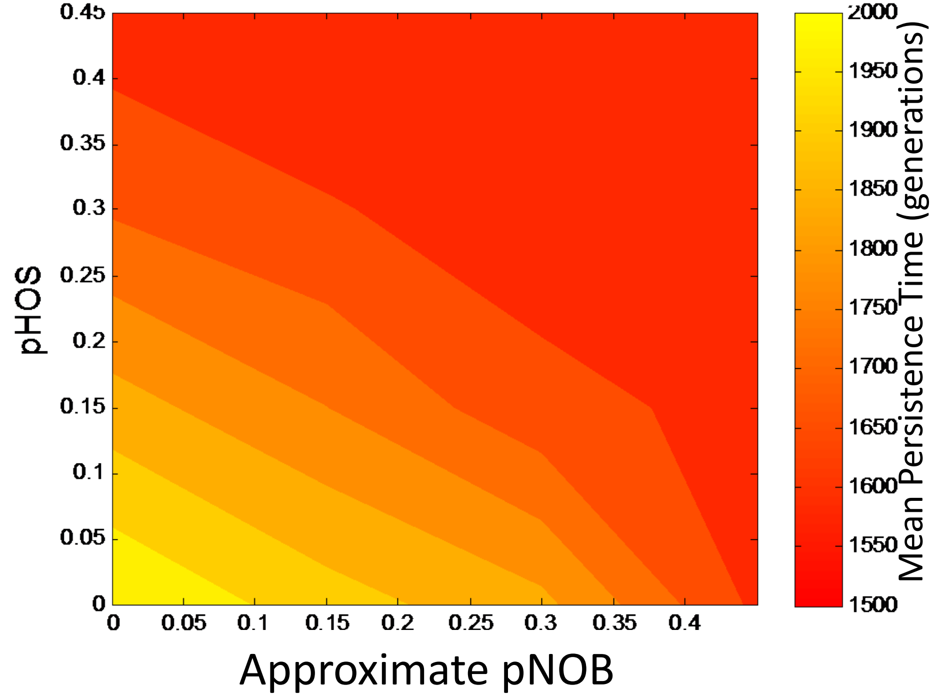
Simulation Result



Simulation Results



Do not take broodstock if N_{wild} < 20



Concluding Remarks

- pHOS and pNOB are measurable and partially controllable
- Analytical and individual-based models can paint different pictures
- Some optimal combination of pHOS, pNOB and "mining rule" must exist in theory
- Individual-based model offers useful realism, but parameterization still problematic
- Value of empirical research on model assumptions?
    i) How different are fitness functions in hatchery and wild?
    ii) Recent finding of rapid adaptation
    iii) Basket and Waples (2012): timing of selection vs. density dependence

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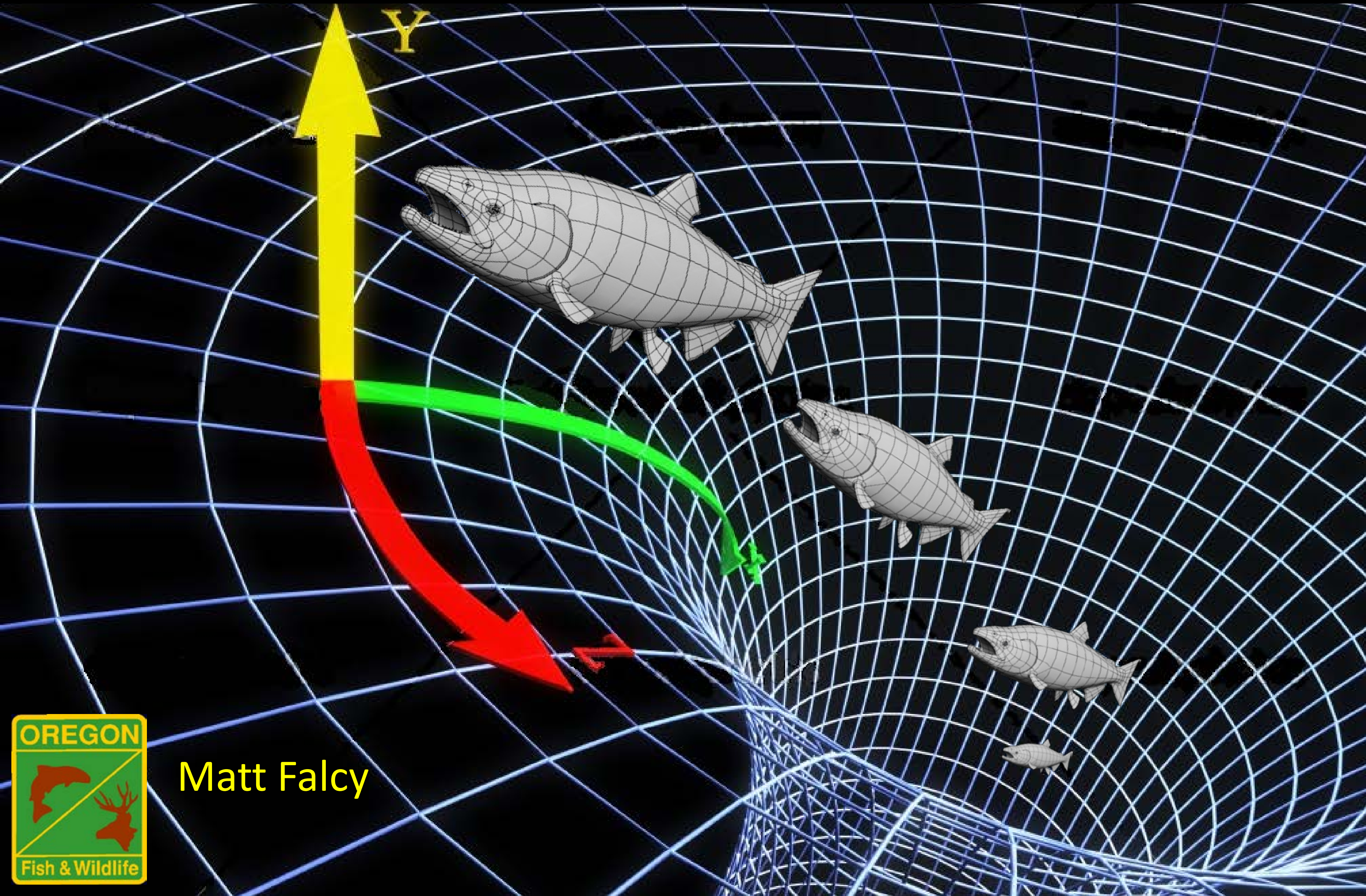

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