

Genetic Monitoring of Grizzly Bears in the Greater Yellowstone Ecosystem



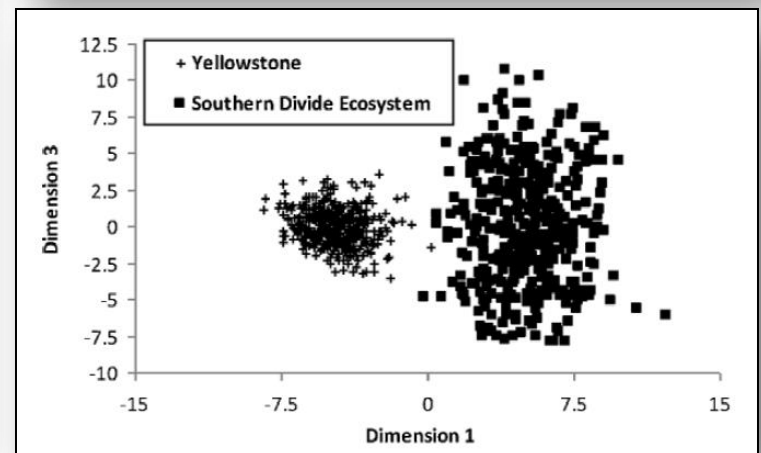
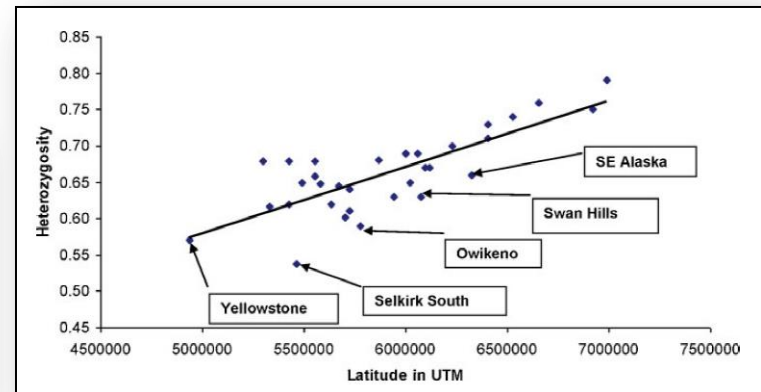
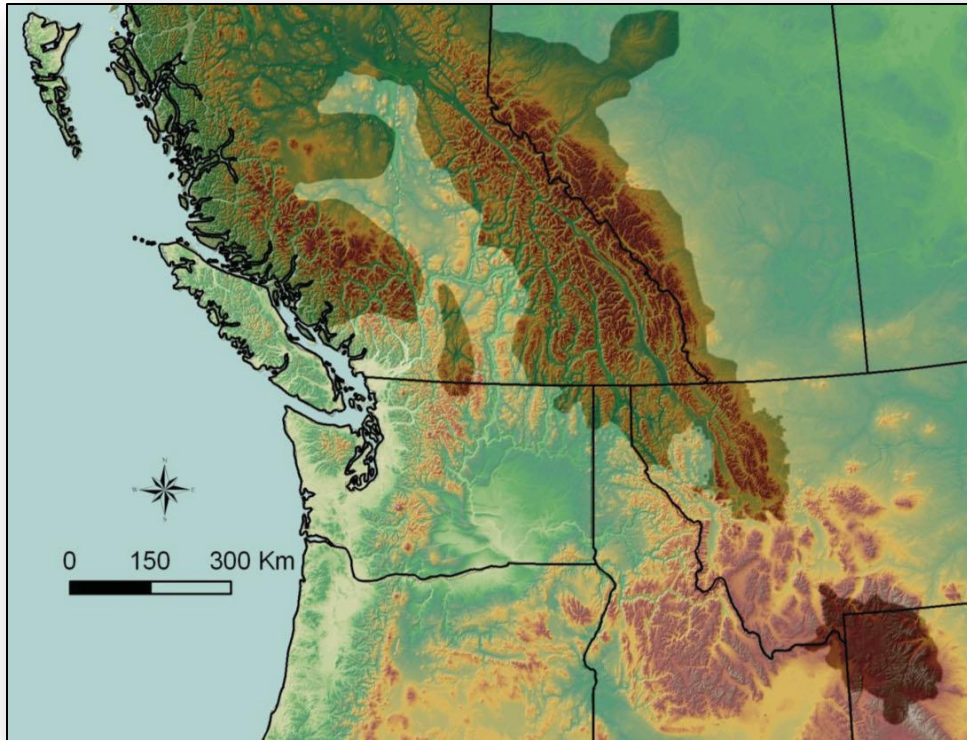
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Photo: Steve Ard

Genetics of Yellowstone grizzly bears

- Yellowstone population isolated for over 100 years
- Low genetic diversity compared with other populations
- Loss of genetic diversity inevitable



What is effective population size (N_e)?

- Technical definition: size of an “ideal” population having the genetic properties of the studied population
- Related to the number of individuals contributing genes to the next generation (i.e., breeders in a generation interval)
- Effective population size < census population size (in most cases)
- N_e is affected by demographics of population
 - Large variation in number of offspring among individuals
 - Overlapping generations
 - Unequal males to females contributing to reproduction
 - Fluctuations in population size

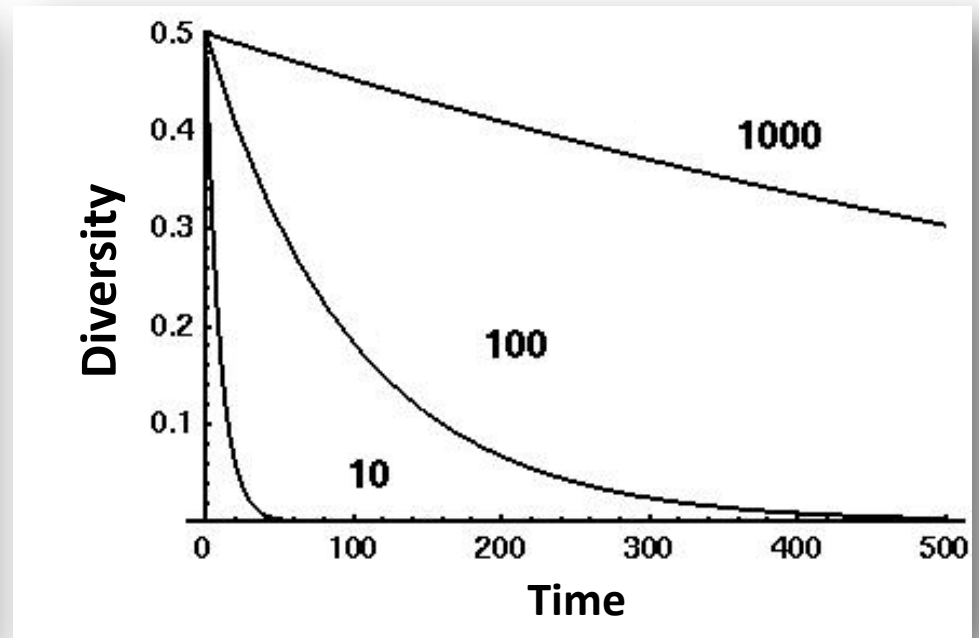
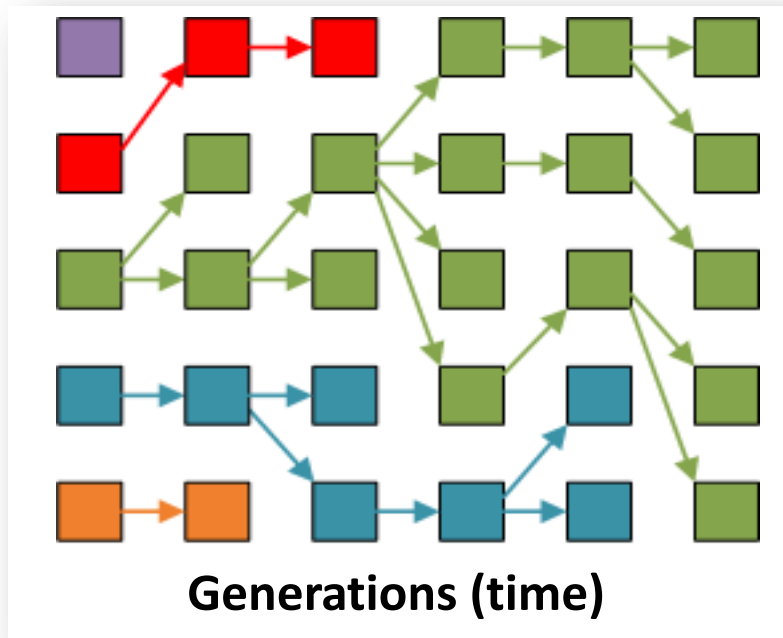
Why is effective population size important?

- Incorporates information about demographics of population
- Reflects population's breeding potential
- Indicator of future evolutionary potential and long-term viability
- Determines the rate at which diversity will be lost

Rate of genetic diversity loss related to population size

Genetic Drift: loss of diversity over time

Rate dependent on effective population size



Multiple estimates of effective population size for monitoring a long-lived vertebrate: an application to Yellowstone grizzly bears

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Abstract

Effective population size (N_e) is a key parameter for monitoring the genetic health of threatened populations because it reflects a population's evolutionary potential and risk of extinction due to genetic stochasticity. However, its application to wildlife monitoring has been limited because it is difficult to measure in natural populations. The isolated and well-studied population of grizzly bears (*Ursus arctos*) in the Greater Yellowstone Ecosystem provides a rare opportunity to examine the usefulness of different methods for monitoring. We genotyped 729 Yellowstone grizzly bears using 20 single-sample estimators to examine contemporary breeders (N_b) and N_e during

Definitions

Effective population size (N_e):

Number of individuals contributing genes to next generation

Effective number of breeders (N_b):

Number of breeding individuals contributing to a cohort
(3-year cohort for grizzly bears)

Generation interval (GI):

Average age of parents producing cubs in a single year

Inbreeding rate:

Probability of inheriting two identical genes from common ancestor

Objectives

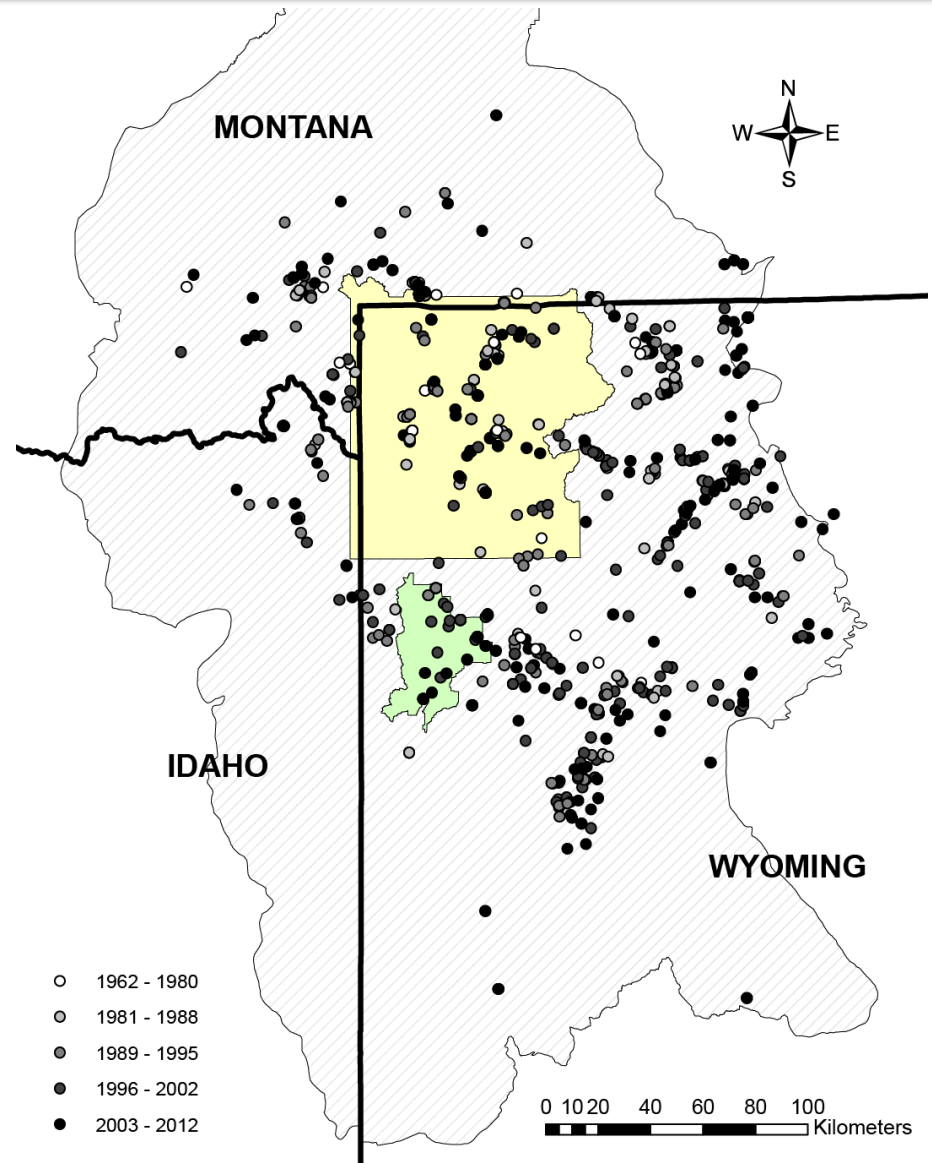
1. Examine change in genetic diversity and trends in N_b and N_e in Yellowstone grizzly bears since the 1980s
2. Compare results across multiple estimators
3. Compare these trends to estimated trend in census population size

Sampling

Data:

Sex, birth year, death year or last known year, multi-locus genotypes (20 loci)

Reconstructed cohort and population samples over time



Estimating grizzly bear effective population size (N_e), number of breeders (N_b), and generation interval (GI)

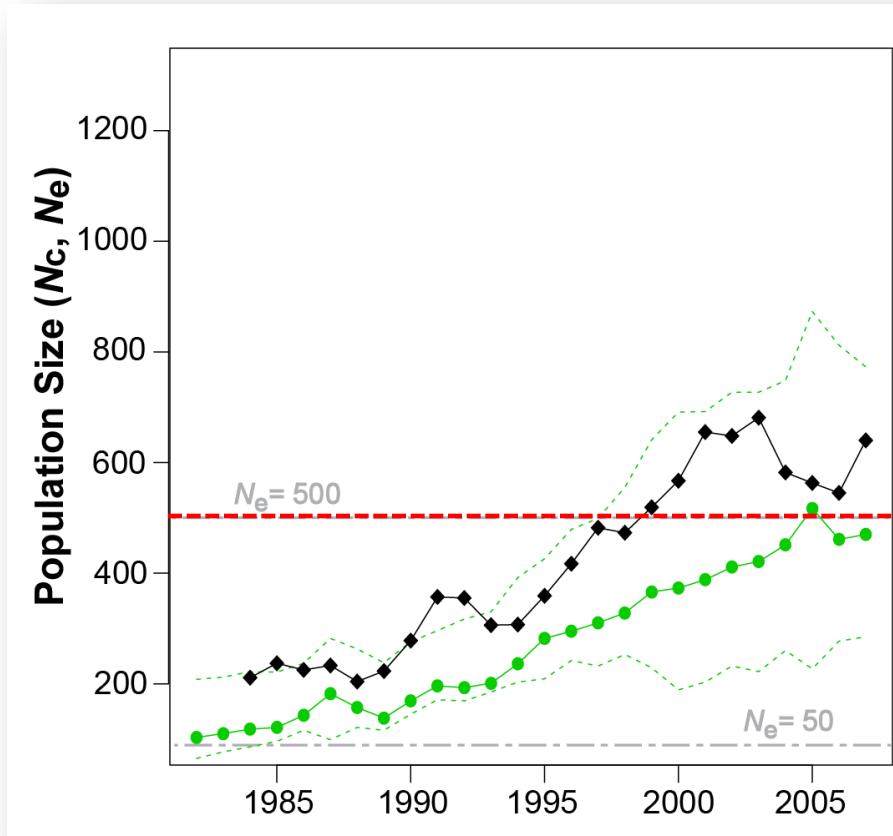
Single-sample estimators:

1. Estimator by parentage assignment (EPA) — N_e , GI
 2. Linkage disequilibrium (LD)
 3. Sibship assignment (SA)
- 
- N_b

Multi-sample N_e estimators:

1. Variance N_e
 2. Inbreeding N_e
- 
- Based on change in diversity between 2 time points

Increase in size of effective population, 1982 - 2007

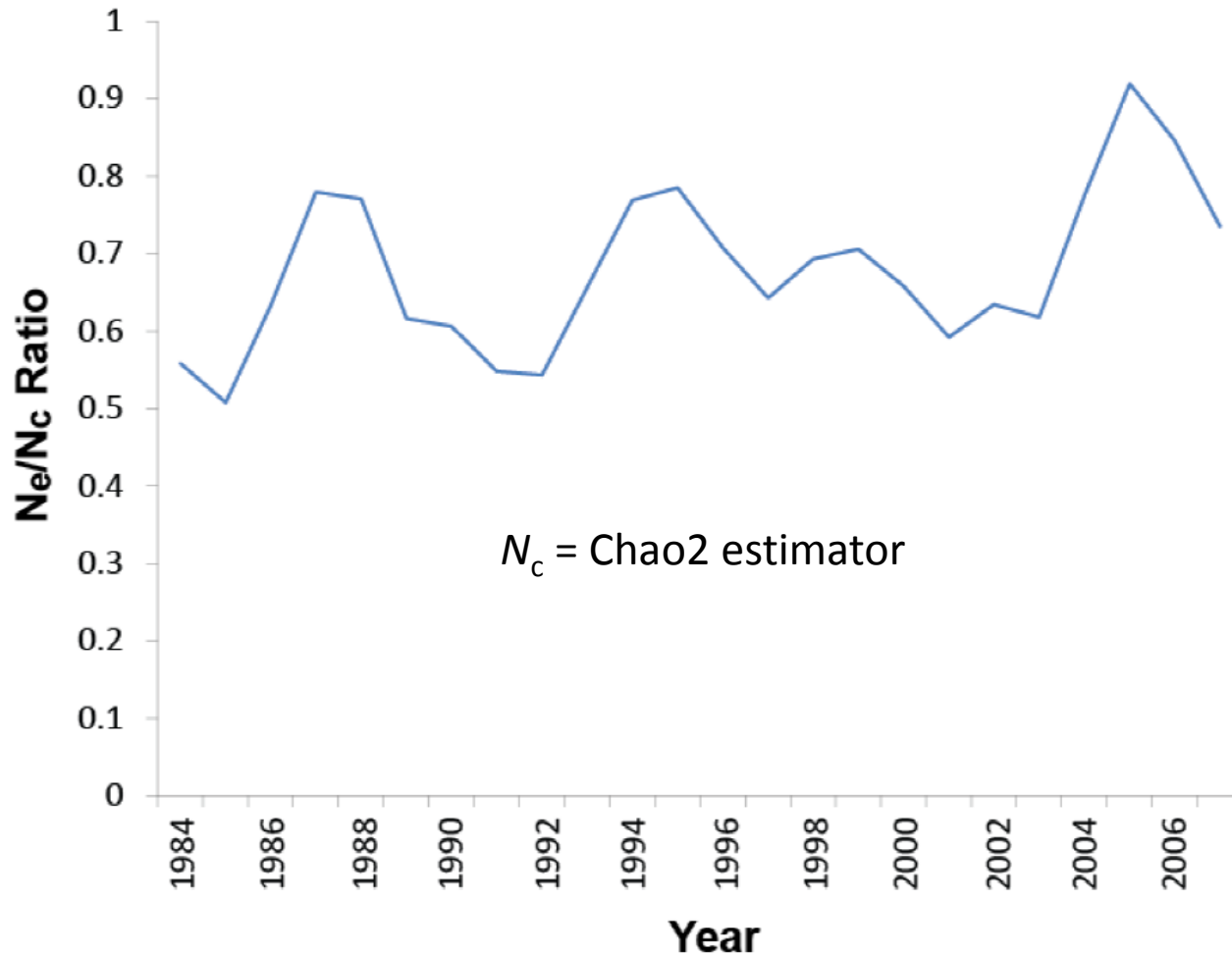


4-fold increase in N_e

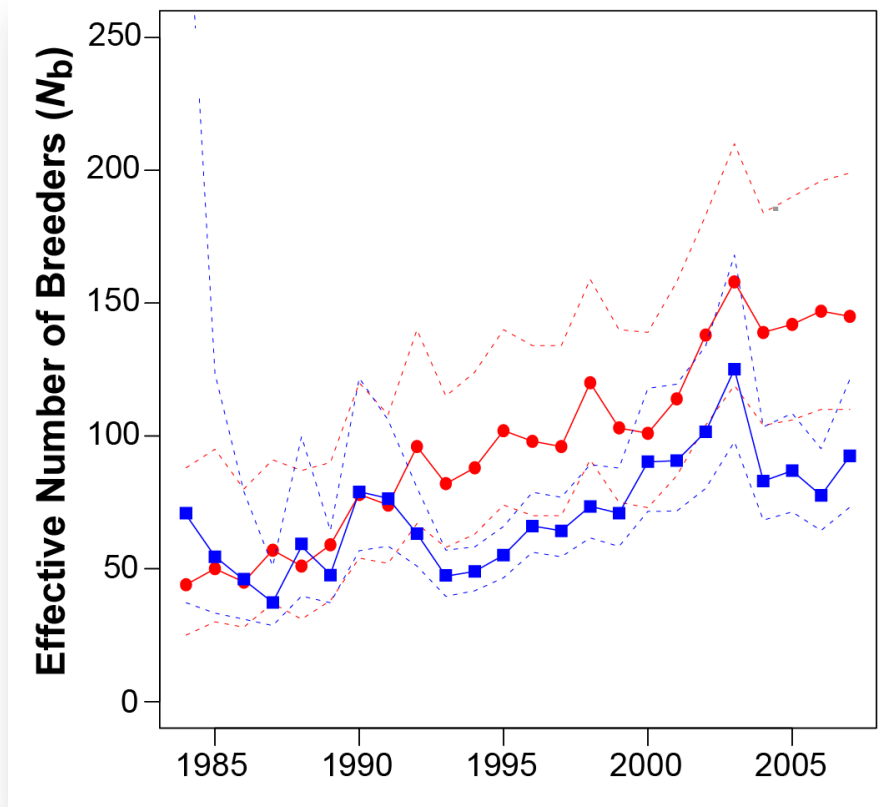
Approaching 500 criterion
for long-term viability
(Franklin 1980)

Corresponds with increase in
estimated **census population
size, N_c** (Chao2 estimator)

Relatively stable ratio of effective to census population size

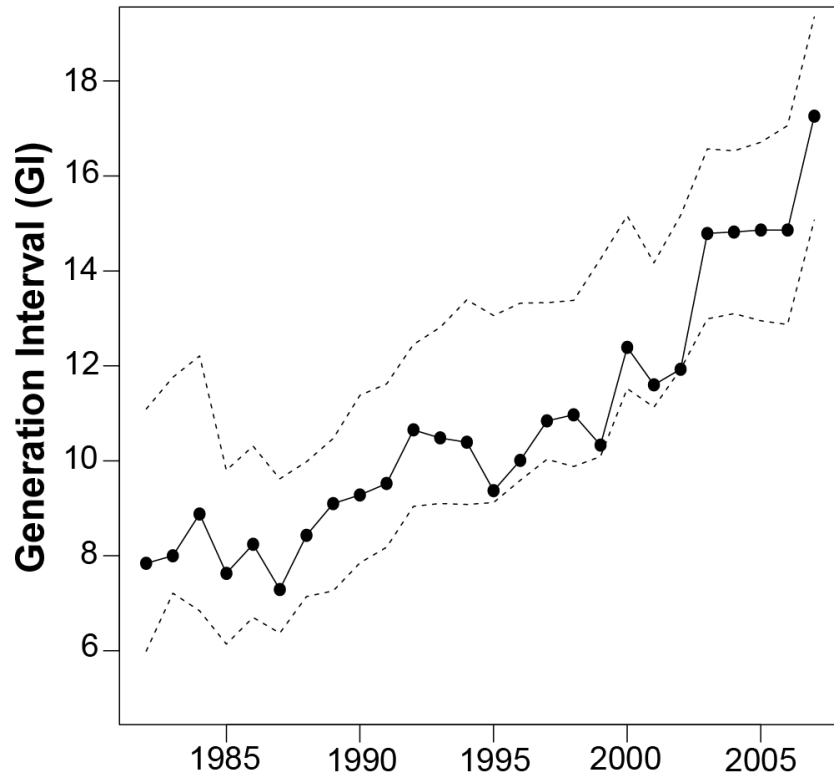


Increase in number of breeding adults, 1984 - 2007



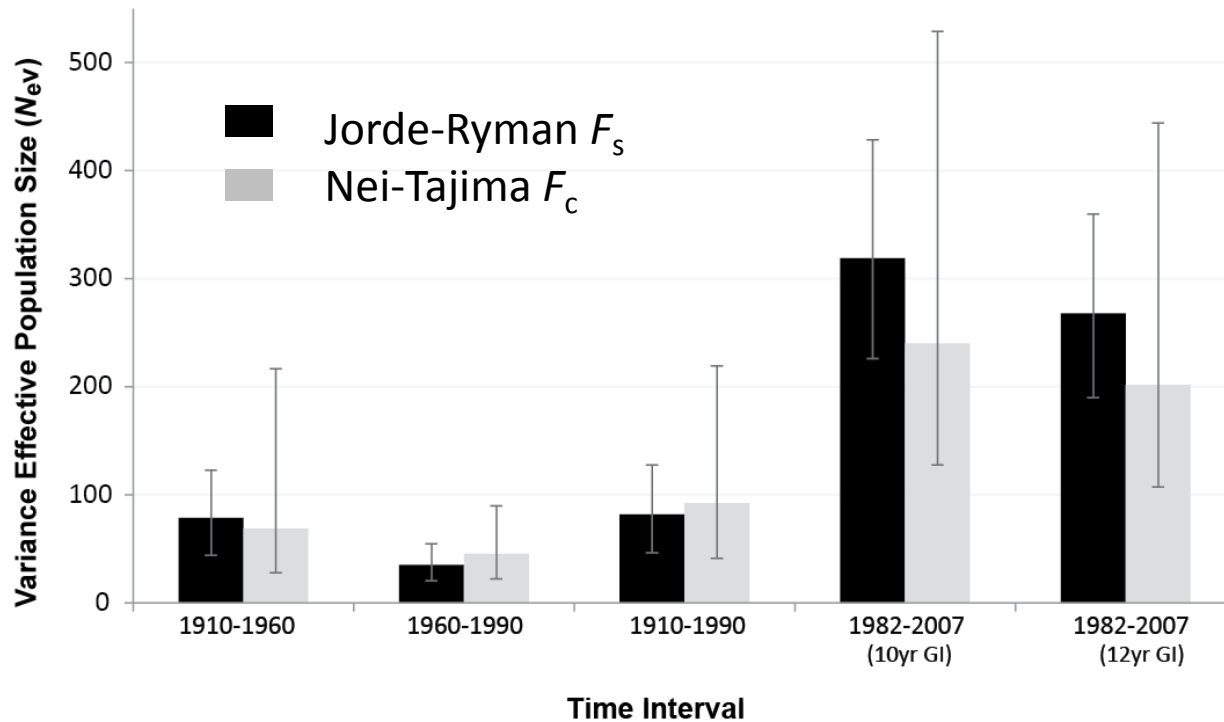
Increase in N_b using two methods: **LD**, **SA**

Increase in generation interval, 1982-2007



Increase in **Generation Interval** from
~8 to 14 years

Increase in effective population size from historic levels

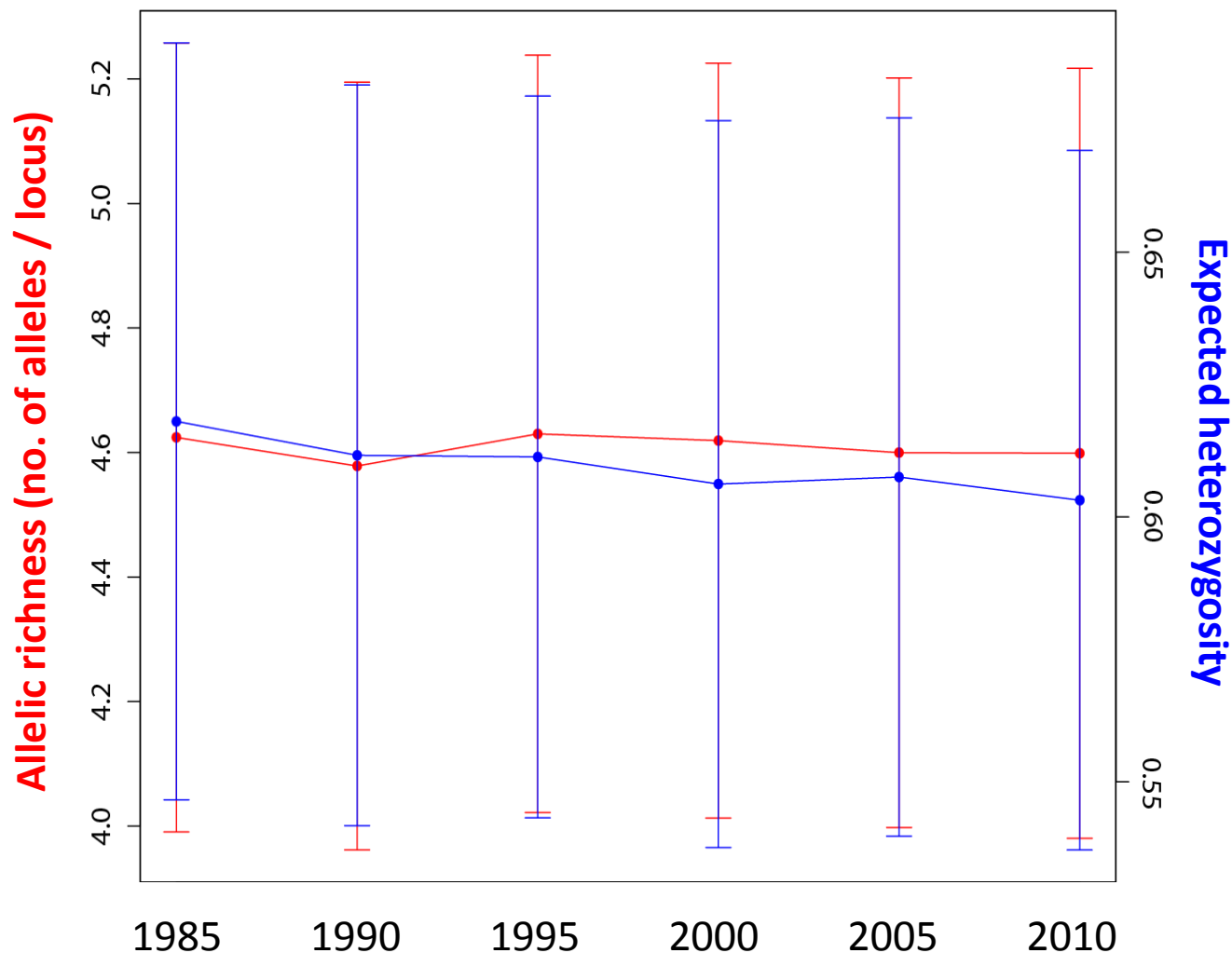


~80 during 1910–1960

~280 during 1980–2007

Genetic data from museum specimens (1910s, 1960s): Miller and Waits (2003)

Stable genetic diversity from 1985 to 2010



Little to no loss of genetic diversity (1985 and 2010 not statistically different)

Rate of inbreeding from 1985 to 2010 = 0.2%

Summary

- N_e in the Yellowstone grizzly bear population has increase 4-fold since the 1980s
- Temporal estimators show similar increase from historical time (1910–1960)
- Number of breeders has also increased
- Generation interval increased from 8 to 14 years
- Genetic diversity has remained stable
- Low rate of inbreeding (0.2% during 1985–2010)

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