

YNP PVA model

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Historic Genetic Data

Halbert et al. 2012 estimated allele frequencies from 661 Yellowstone bison during 1997-2003. Most samples (about 600) were collected during winter outmigrations. 46 loci evaluated with 224 alleles detected and allele frequencies ranging from <1% to

```
## # A tibble: 46 x 2
##   loc      n
##   <chr>  <int>
## 1 AGLA232    6
## 2 BL1036    4
## 3 BM1225    5
## 4 BM1706    5
## 5 BM17132   5
## 6 BM1824    6
## 7 BM1862    5
## 8 BM188     7
## 9 BM1905    3
## 10 BM2113   4
## # i 36 more rows
```

Current Genetic Data

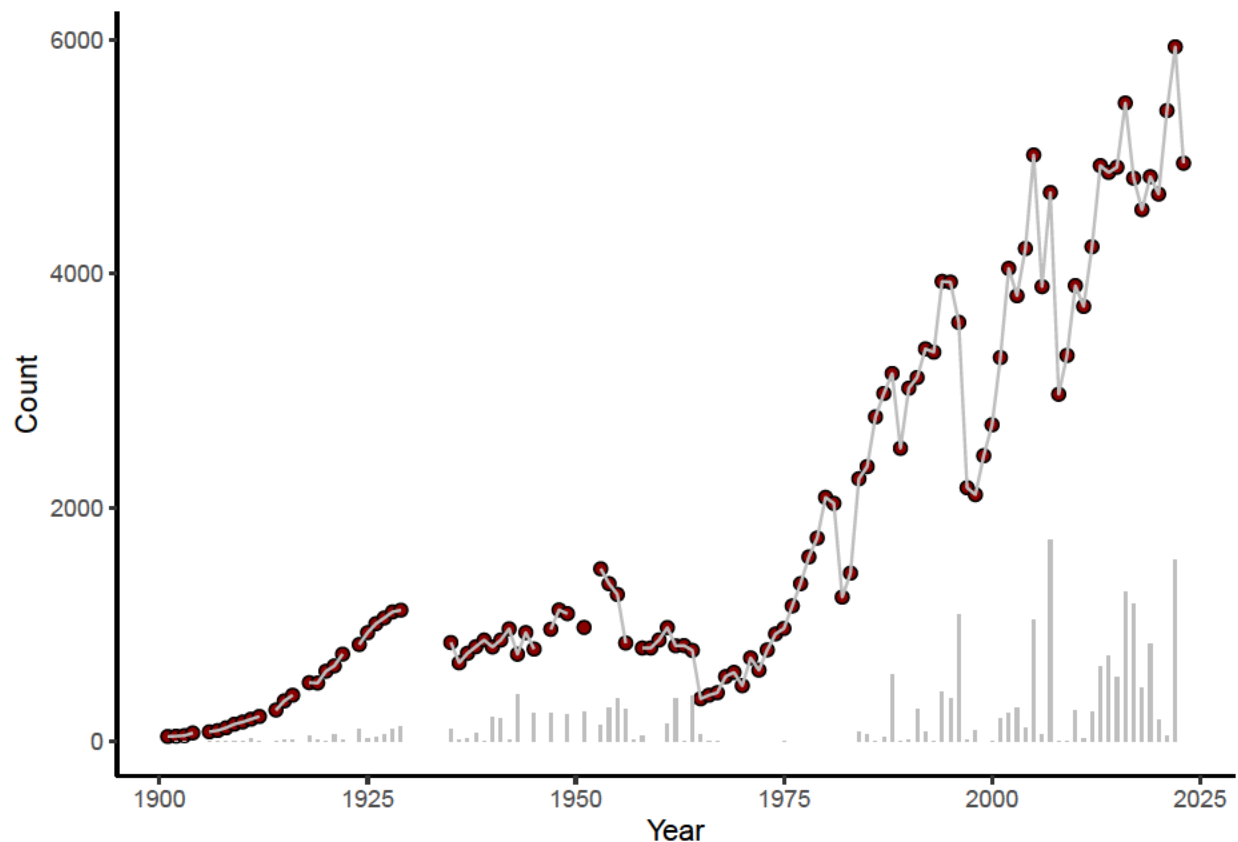
Genetic data were collected during 2018 and 2020 by selecting juvenile animals that migrated out of the north boundary and were entered in the quarantine program. During 2022, data were also collected during the summer breeding season from all age and sex classes. Additional data from summer 2023 (n=100) and winter 2022 (n=282) are currently being evaluated.

```
## /// GENIND OBJECT ///////////
##
## // 221 individuals; 52 loci; 256 alleles; size: 290.2 Kb
##
## // Basic content
## @tab: 221 x 256 matrix of allele counts
## @loc.n.all: number of alleles per locus (range: 3-11)
## @loc.fac: locus factor for the 256 columns of @tab
## @all.names: list of allele names for each locus
## @ploidy: ploidy of each individual (range: 2-2)
## @type: codom
```

```
## @call: .local(x = x, i = i, j = j, drop = drop)
##
## // Optional content
## @pop: population of each individual (group size range: 98-123)
```

Population Counts and Removals

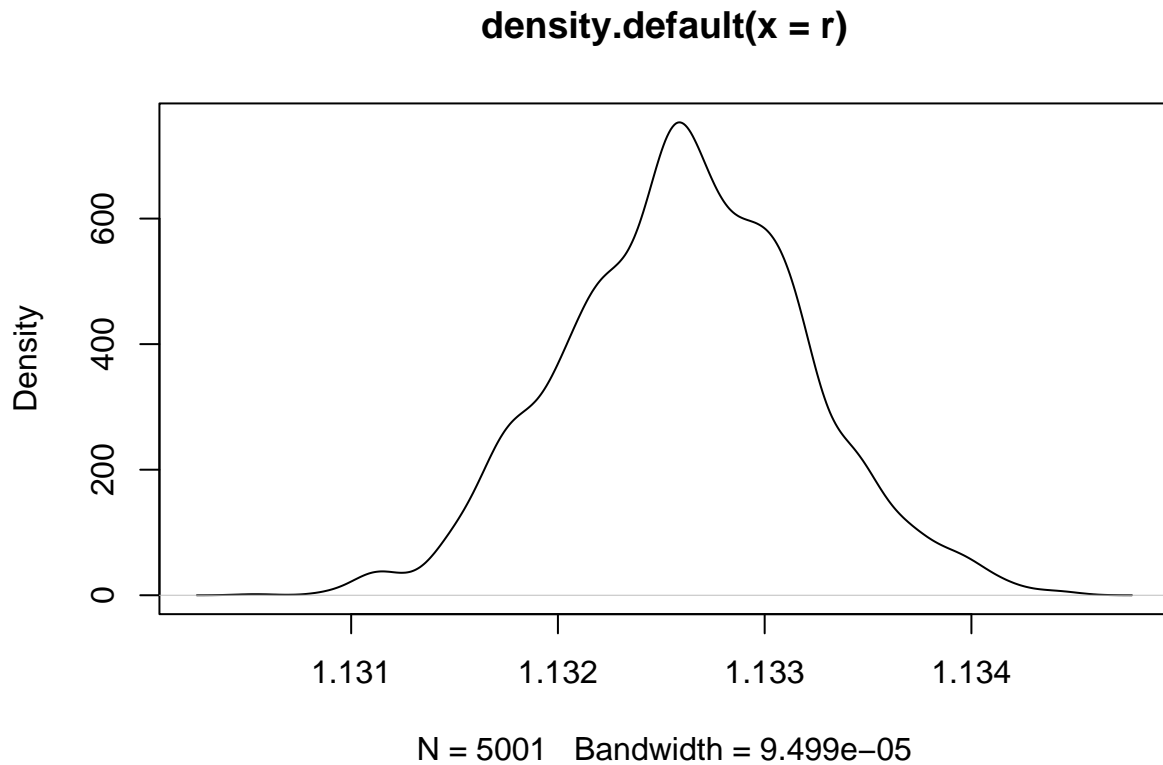
The population increased above 3,000 animals by the late 1990s. Recurrent culls slowed growth since stabilizing the population roughly between 3000 and 5000 bison since 2000. Culls indicated by bars on the figure. Culls repeated removed more than 1,000 animals. Culls were animals that moved out of the park and were shot or rounded up and sent to slaughter. More recently a subset of animals planned for slaughter have been entered in a live transfer program.



Parameters

r

Estimate r using a discrete time model, $y[t+1] = r * (y[t] - h[t]) + \text{epsilon}$. The growth rate is adjusted for removals. $y[t]$ is the summer count that occurs after the breeding season. $h[t]$ are removals that are known and occur during winter (Dec-Mar). Removals include harvests and culls, i.e. round up and slaughter or transfer from the population. Population growth rate estimated from count data is 13% annually. The object 'r' is an estimate of the discrete growth rate using monte carlo integration.



```
## [1] 1.132616
```

```
## [1] 0.0005797594
```

Vital Rates

Survival

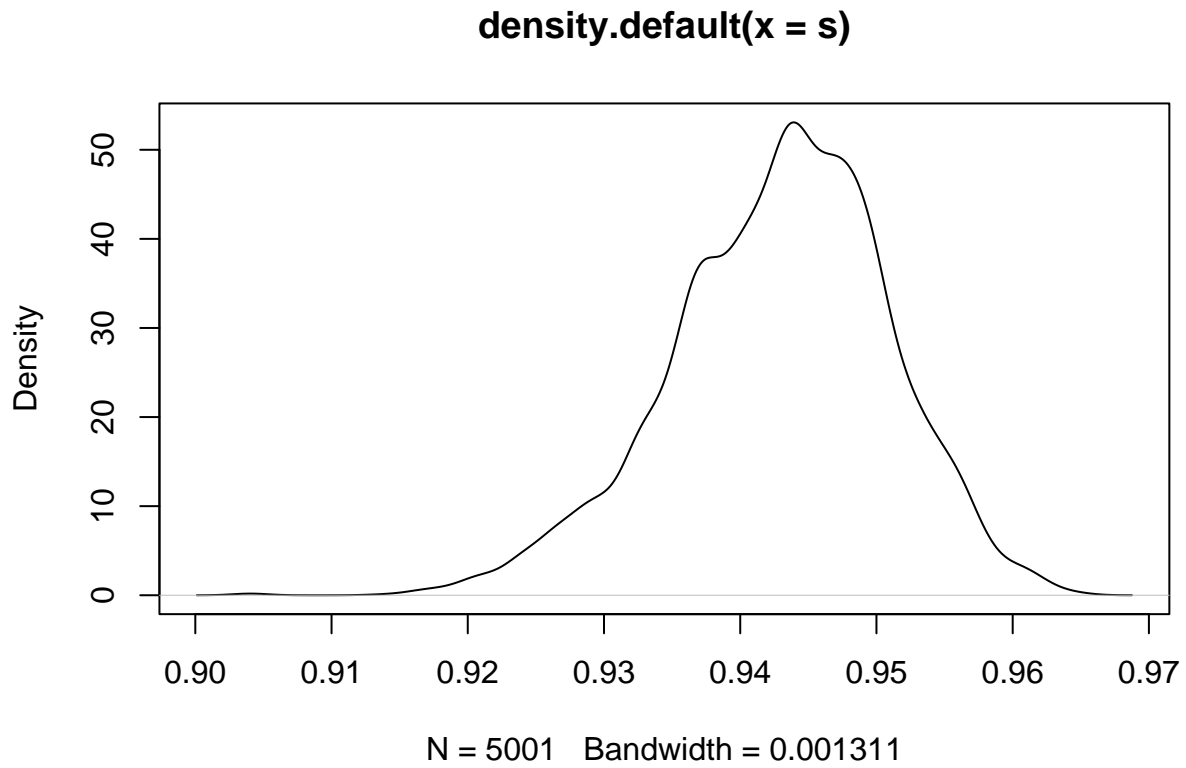
Adult female constant survival

Adult female survival estimated from radio collar data fit to a survival models with constant lifetime hazard.

Annual survival around 0.94. The object `s` is an estimate of annual survival using monte carlo integration. The `sd` is very small given the sample size.

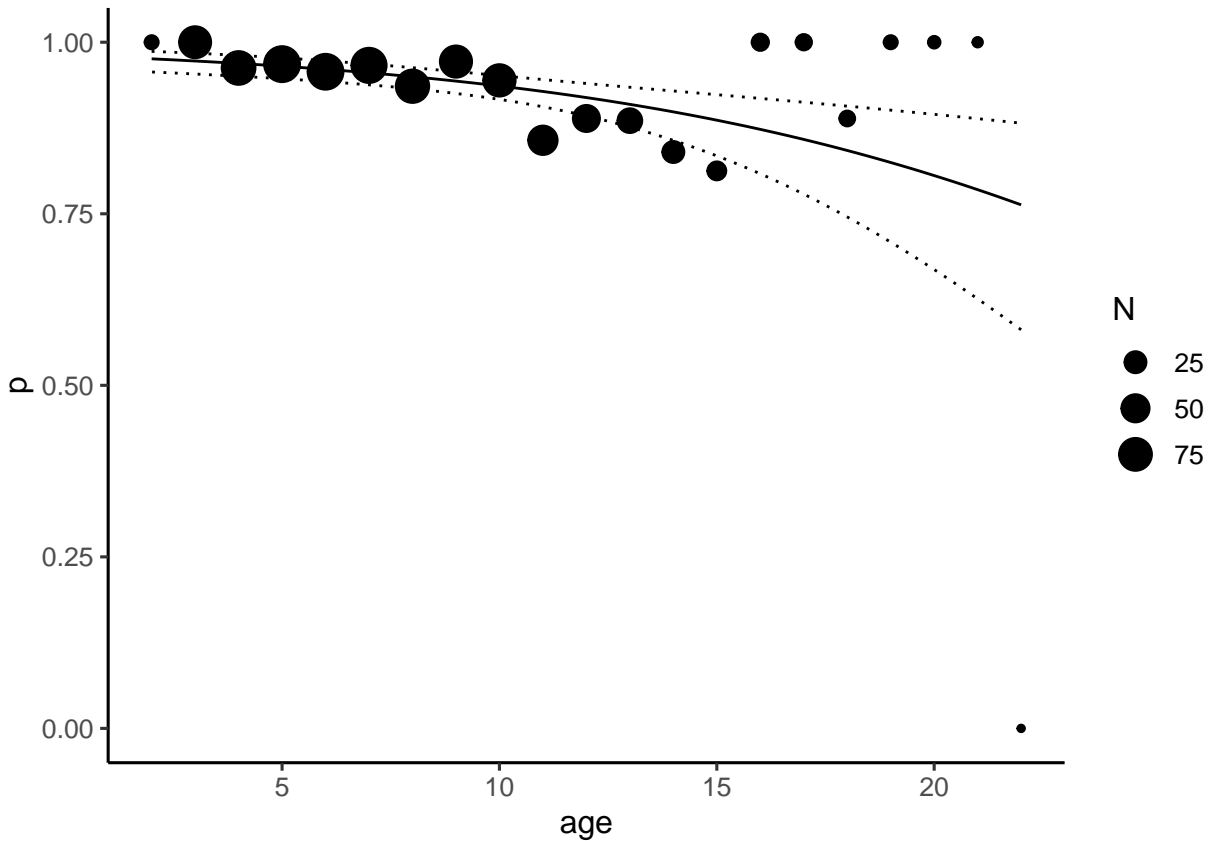
```
## [1] 0.9428666
```

```
## [1] 0.008002481
```



Adult female age-specific survival

Age effects on survival. Age-specific information was recorded on a subset of individuals. Annual survival probability decreased with age based on treating y as a binomial random variable with survival probability given by a linear combination of age.



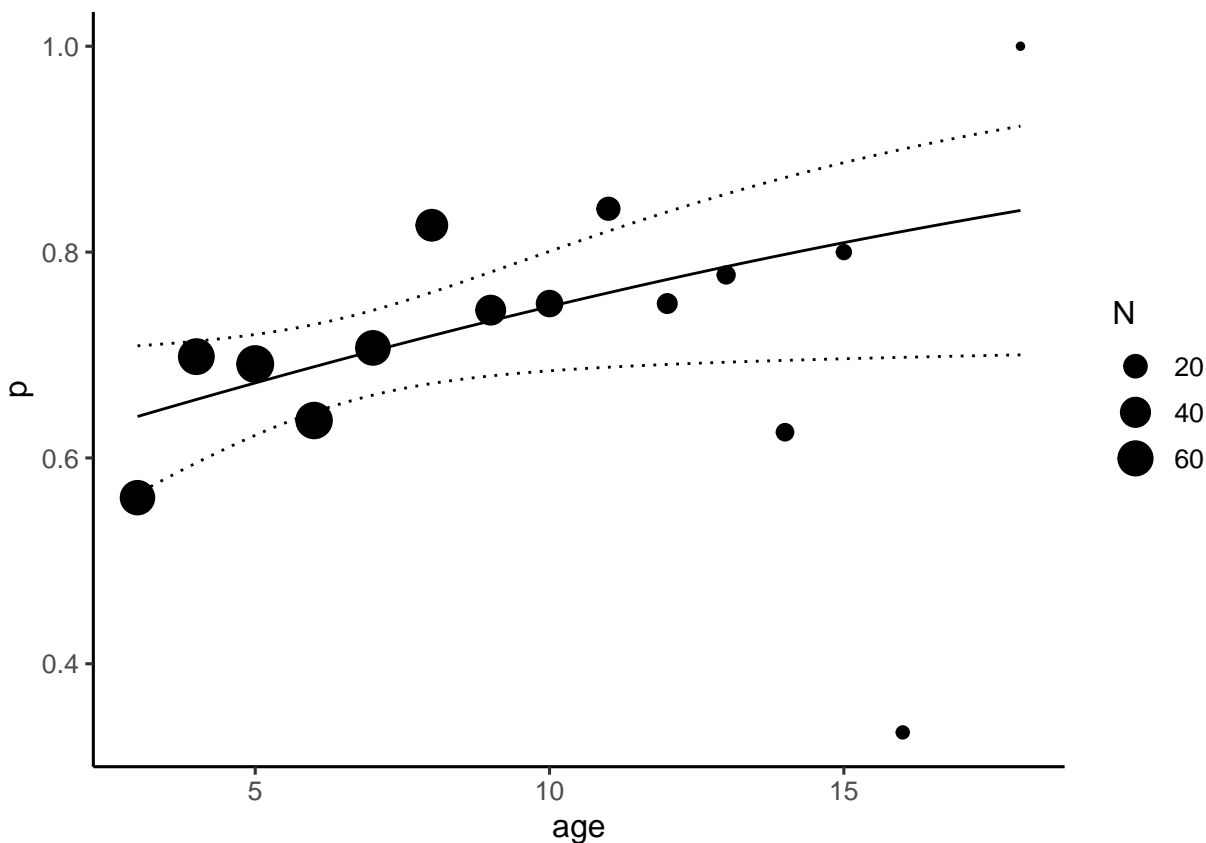
Age specific survival for females declined from age 1 to age 20. The object s.age are survival estimates with each row corresponding to an age. Estimates generated using Monte Carlo integration.

```
## [1] 0.9783530 0.9756733 0.9726416 0.9692111 0.9653294 0.9609376 0.9559704
## [8] 0.9503553 0.9440131 0.9368573 0.9287950 0.9197281 0.9095545 0.8981706
## [15] 0.8854750 0.8713724 0.8557790 0.8386283 0.8198778 0.7995149

## [1] 0.007032184 0.007135802 0.007202208 0.007230530 0.007227009 0.007211158
## [7] 0.007225271 0.007346506 0.007695496 0.008428038 0.009701942 0.011639757
## [13] 0.014319412 0.017790374 0.022090238 0.027249910 0.033289833 0.040212217
## [19] 0.047992626 0.056572938
```

Fertility

Age effects on fertility. Age of first reproduction is 3. Age-specific fertility increased with age, likely owing to brucellosis exposure, and likely declined in older ages. Fertility probability decreased with age based on treating y as a binomial random variable with fertility probability given by a linear combination of age.



The object `fert` are fertility estimates with each row corresponding to an age. Estimates generated using Monte Carlo integration. Age of first reproduction assumed as 3.

```
## [1] NA NA 0.5891849 0.6382104 0.6779992 0.7091155 0.7325248
## [8] 0.7491808 0.7598191 0.7648762 0.7644651 0.7583754 0.7460991 0.7269123
## [15] 0.7000739 0.6651873 0.6226651 0.5740498 0.5218934 0.4691732

## [1] NA NA 0.04688989 0.03143621 0.02420338 0.02347058
## [7] 0.02494316 0.02624917 0.02710304 0.02828564 0.03125931 0.03775848
## [13] 0.04915172 0.06621317 0.08921605 0.11770804 0.15008880 0.18361821
## [19] 0.21515964 0.24220932
```

Other Vitals

Calf survival

Estimated from a integrated population model for Yellowstone bison with mean 0.80 and sd

Fetal Sex ratio

Estimated from a integrated population model for Yellowstone bison with mean 47% of calves are female

Male survival

Estimated as similar to female survival from an integrated population model for Yellowstone bison