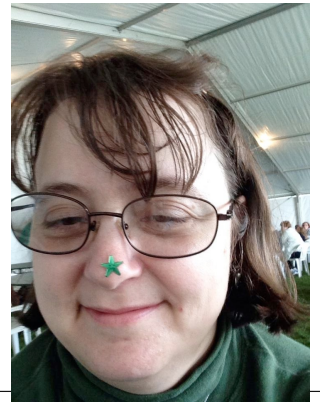
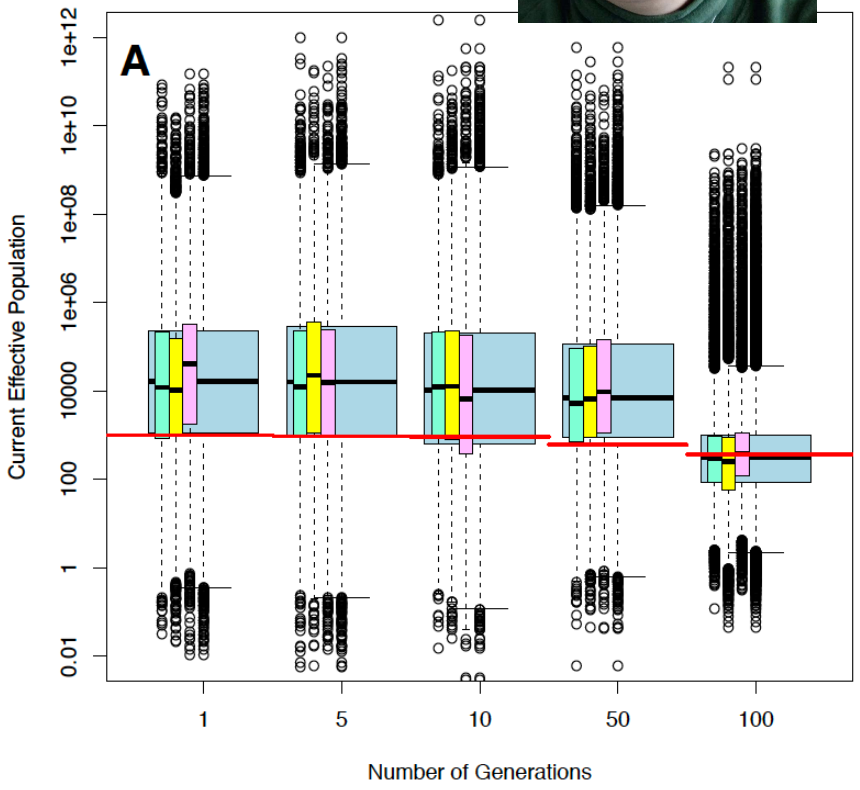
How Many Bats Are There?
And Other Problems in Conservation Genetics

Amy Russell (she/her)
Professor of Biology
Grand Valley State University

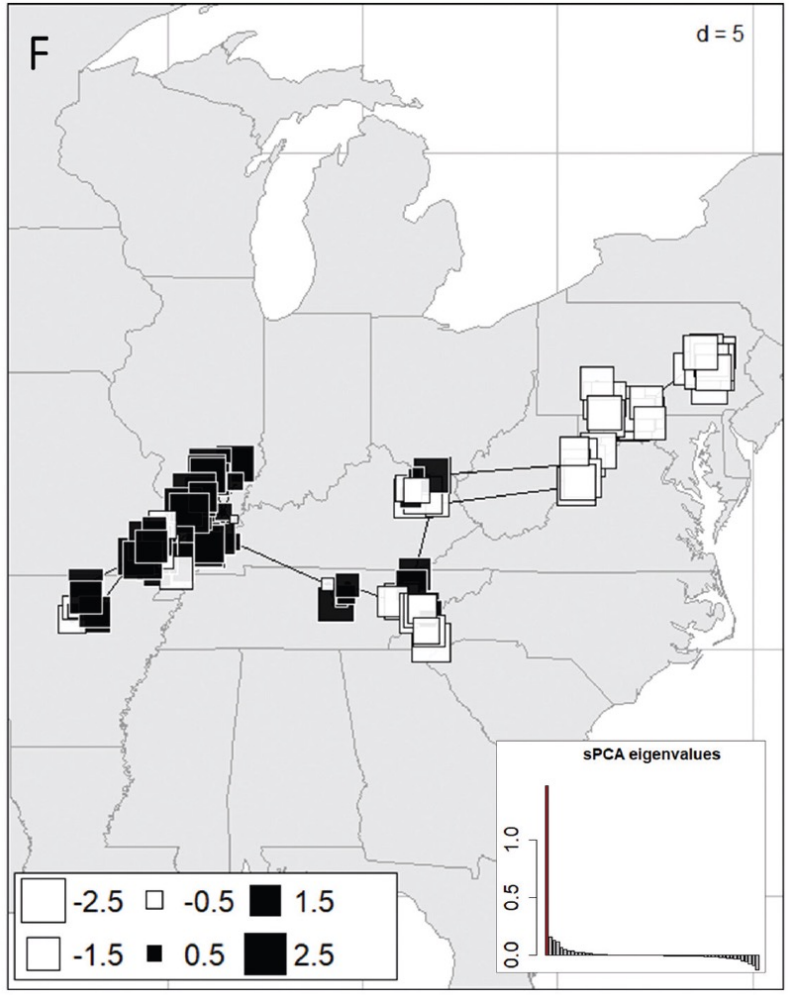
Grand Valley State University



(Jones *et al.* 2022)



(Munster *et al.* in prep)



(Martin *et al.* 2022)

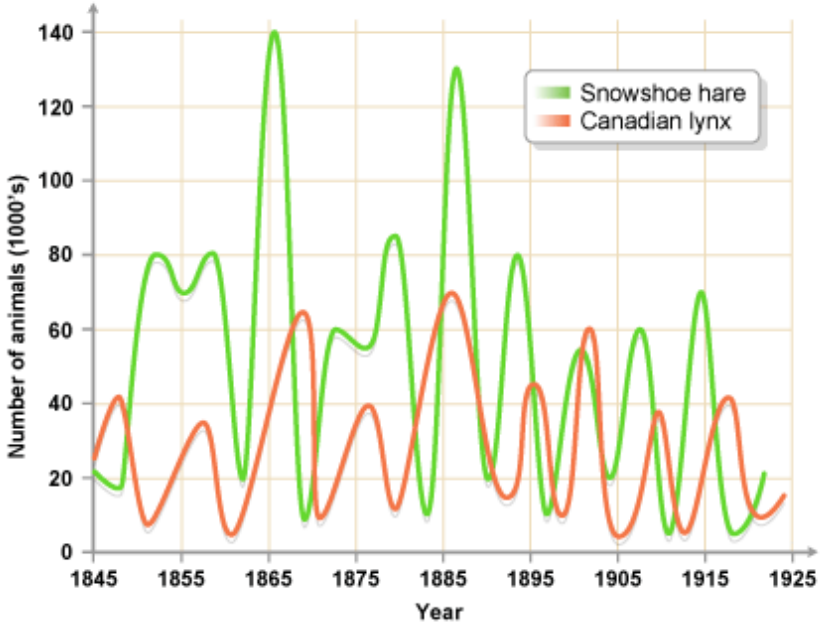
Outline

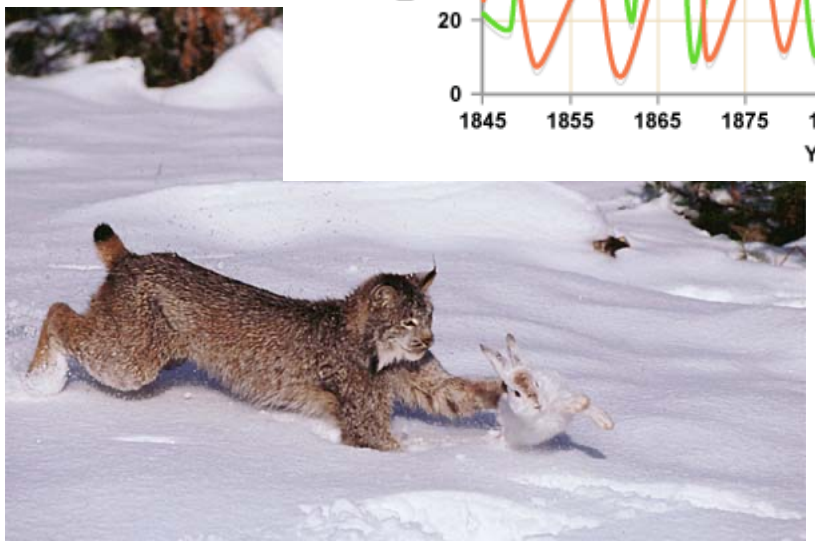
Why use genetics in conservation?

Census vs. effective population size (N_c vs. N_e)

How to estimate N_e?

Why use genetics in conservation?



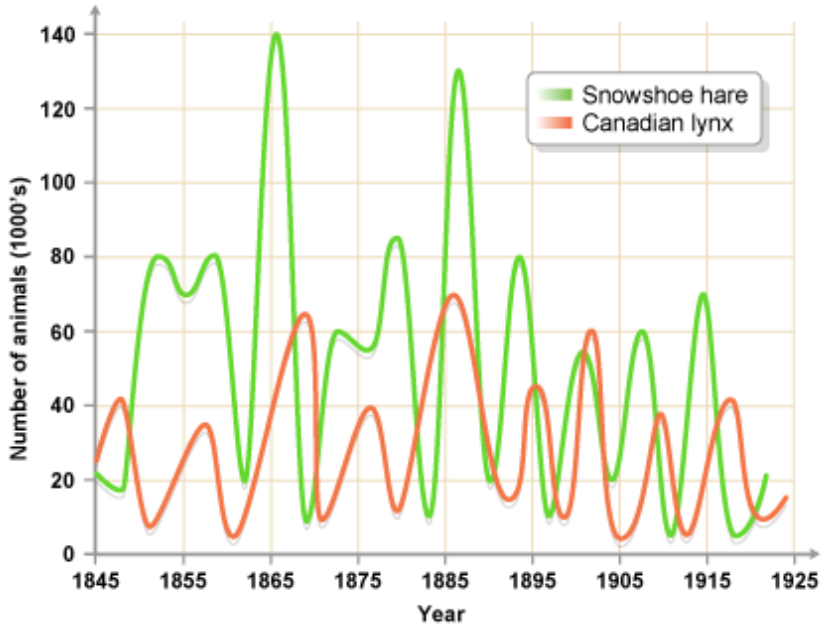


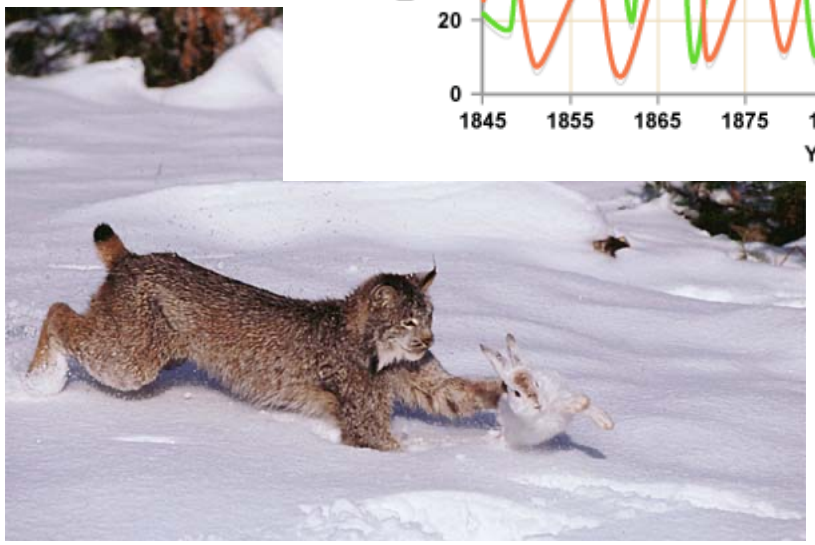
Goal of conservation to preserve sustainable populations

Need to know:

- How many individuals in a population?
- Is population size changing over time?
- What are the geographical limits of a population?

Why use genetics in conservation?





Goal of conservation to preserve sustainable populations

Need to know:

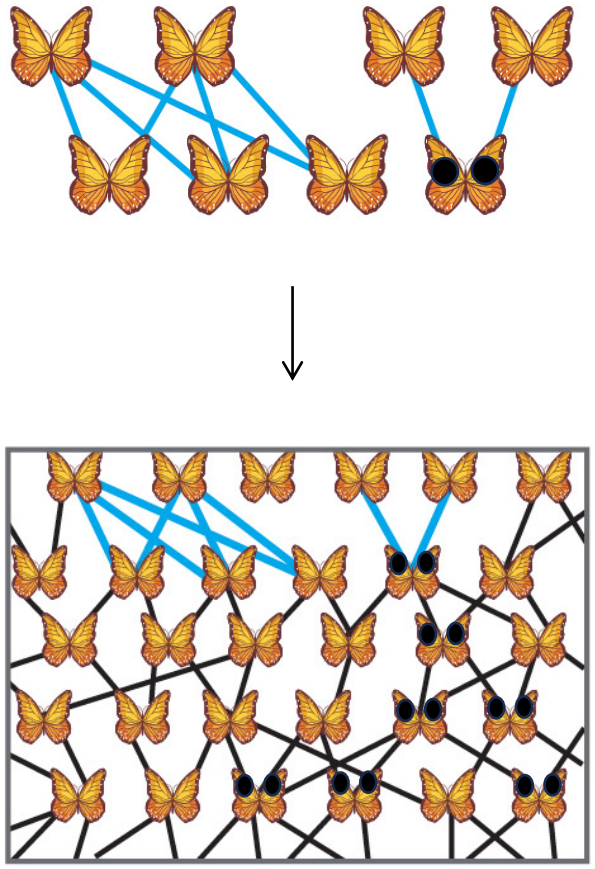
- How many individuals in a population?
- Is population size changing over time?
- What are the geographical limits of a population?

Genetic data can help to answer these questions!

Bats are difficult to count!

- Active at night
- Overwhelming numbers
- Difficult to locate
- Very mobile
- Lack of historical data

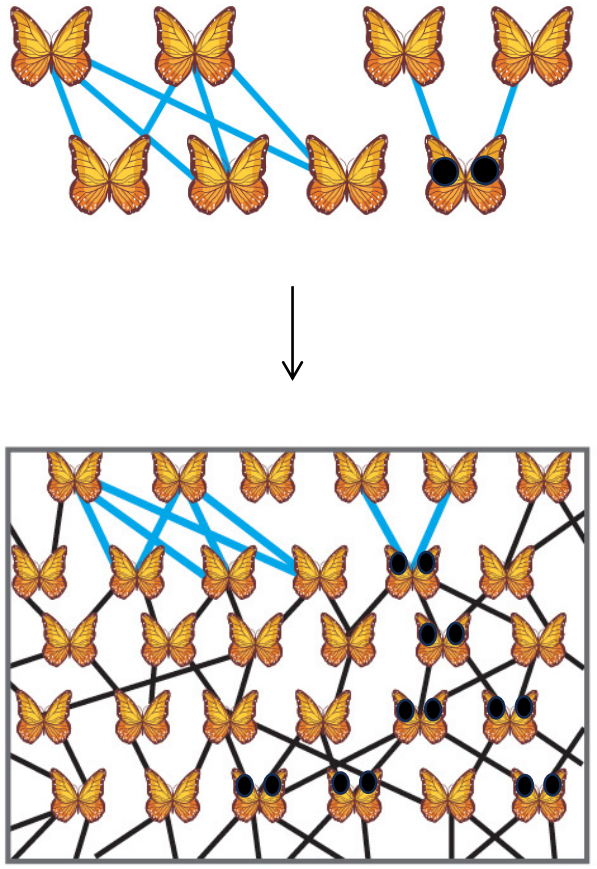
Why use genetics in conservation?



Theory tells us how population size influences genetic measurements

- Amount of genetic diversity
- Shapes of genealogical trees
- Associations among loci

Why use genetics in conservation?



Theory tells us how population size influences genetic measurements

- Amount of genetic diversity
- Shapes of genealogical trees
- Associations among loci

So we can use genetic measurements from real populations to estimate population size!

Census vs. effective population size (N_c vs. N_e)

How large are bat populations?

Census population size (N_c) is the number of adults in a population

Census vs. effective population size (N_c vs. N_e)

How large are bat populations?

Census population size (N_c) is the number of adults in a population

Effective population size (N_e) is the size of an ideal population that experiences genetic drift at the same rate as the observed population

Census vs. effective population size (N_c vs. N_e)

How large are bat populations?

Census population size (N_c) is the number of adults in a population

=> What we want to know

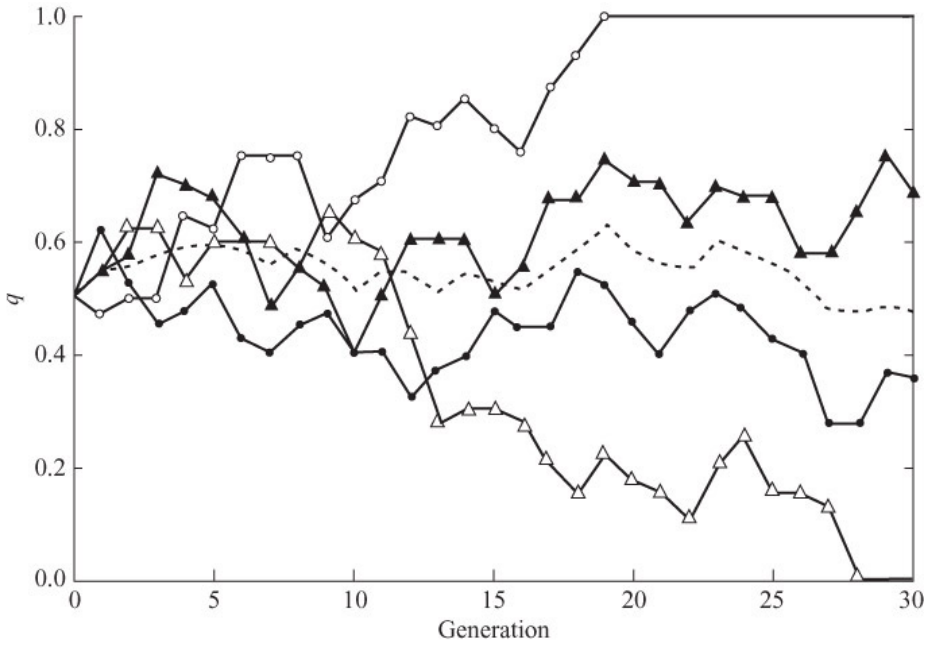
Effective population size (N_e) is the size of an ideal population that experiences genetic drift at the same rate as the observed population

=> What we can measure

Census vs. effective population size (N_c vs. N_e)

Effective population size (N_e) is the size of an ideal population that experiences genetic drift at the same rate as the observed population

Random sampling of alleles from generation to generation



Census vs. effective population size (N_c vs. N_e)

Effective population size (N_e) is the size of an ideal population that experiences genetic drift at the same rate as the observed population

Wright-Fisher population

- Diploid, hermaphroditic, selfing possible
- Equal sex ratio
- Constant size over time
- Poisson distribution of family size

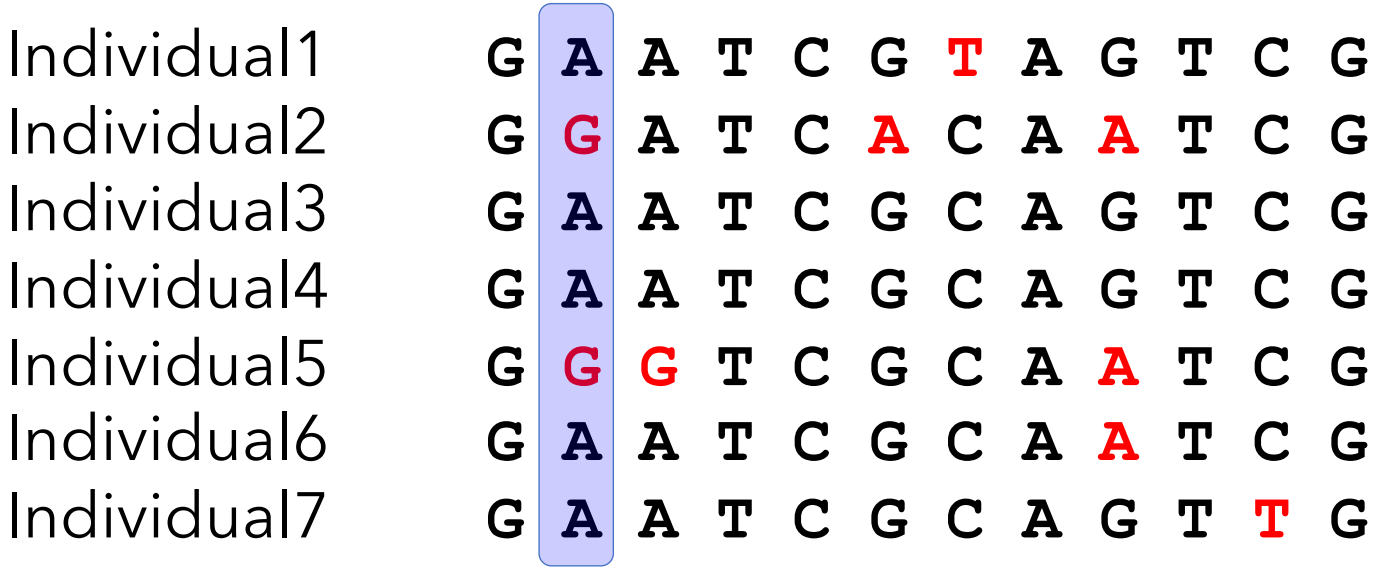
How to estimate N_e?

What type of data are we using?

How to estimate N_e?

What type of data are we using?

SNP data
- Direct sequencing
- Reduced representation SNP data
- Whole genome sequences



How to estimate N_e?

What type of data are we using?

Allelic data
- Microsatellites

```
5′-AGCCTCTCTCTCTCTCTCTCCAGGTA-3′
3′-TCGGAGAGAGAGAGAGAGAGGTCCAT-5′
```
Allele 1: 8 repeats, 26 bp

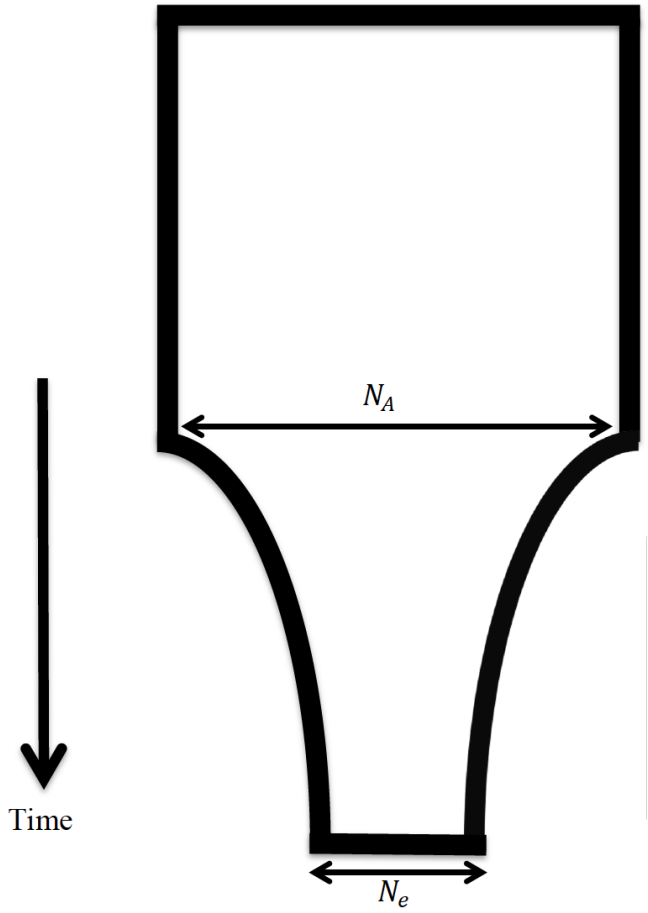
```
5′-AGCCTCTCTCTCTCTCCAGGTA-3′
3′-TCGGAGAGAGAGAGAGGTCCAT-5′
```
Allele 2: 6 repeats, 22 bp

```
5′-AGCCTCTCTCTCTCTCTCTCTCCAGGTA-3′
3′-TCGGAGAGAGAGAGAGAGAGAGGTCCAT-5′
```
Allele 3: 9 repeats, 28 bp

How to estimate N_e?

What type of N_e are we estimating?

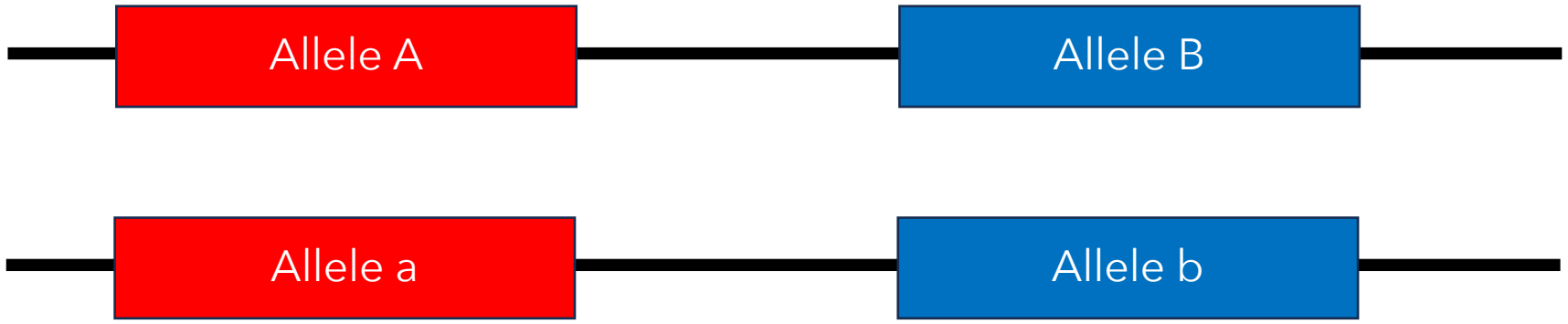
- Contemporary N_e – What is the effective population size now?
- Evolutionary N_e – What was the effective population size at some time in the past?
- N_e trajectory – Is N_e increasing, decreasing, or staying the same?



Munster 2015

How to estimate **contemporary** N_e?

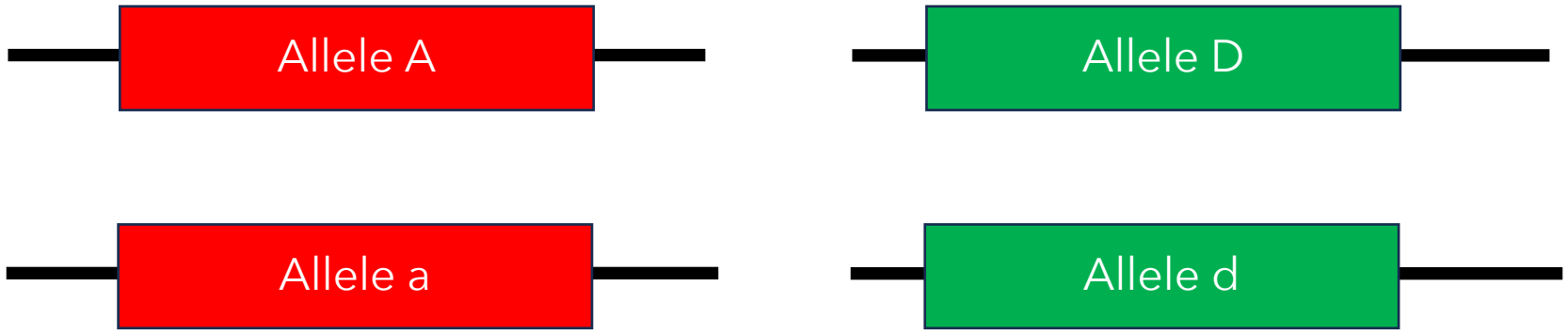
Contemporary N_e: Linkage Disequilibrium (Waples)



Physical linkage → Alleles A and B tend to be inherited together.
Alleles a and b tend to be inherited together.

How to estimate **contemporary** N_e?

Contemporary N_e: Linkage Disequilibrium (Waples)

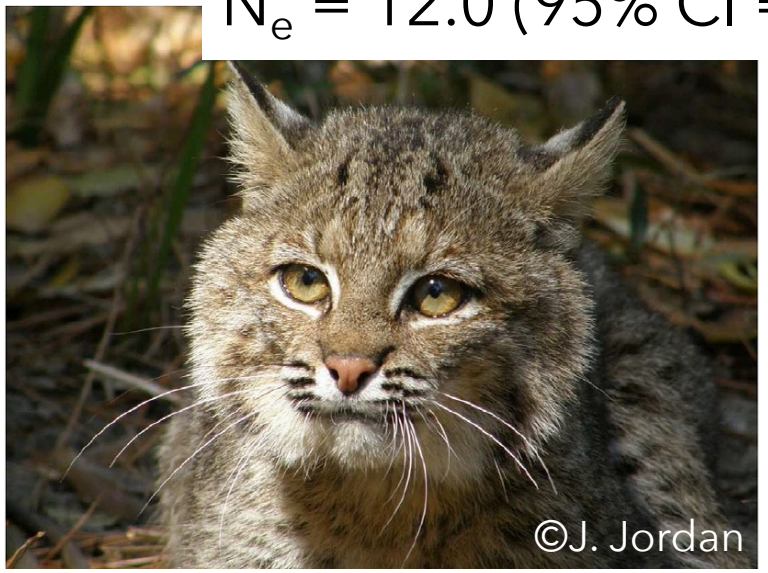


Statistical linkage → In a small population, alleles A and D may tend to be associated if they were found together in an ancestor.

How to estimate **contemporary** N_e?

LD method is accurate and precise for $N_e < 1000$

Kiawah Island
N_e = 21.7 (95% CI = 16.4, 37.8)
Cumberland Island
N_e = 12.0 (95% CI = 9.4, 15.2)



(Miller Butterworth *et al.* 2021)

Accurate – How often does CI include true N_e

	P_{crit}	Parametric	Jackknife
$S = 50$	0.1	91.4	94.0
	0.05	89.0	91.5
	0.02	90.3	90.7
	0.01	88.5	88.5
$S = 200$	0.1	87.2	92.1
	0.05	86.5	91.9
	0.02	86.4	90.6
	0.01	84.1	86.9

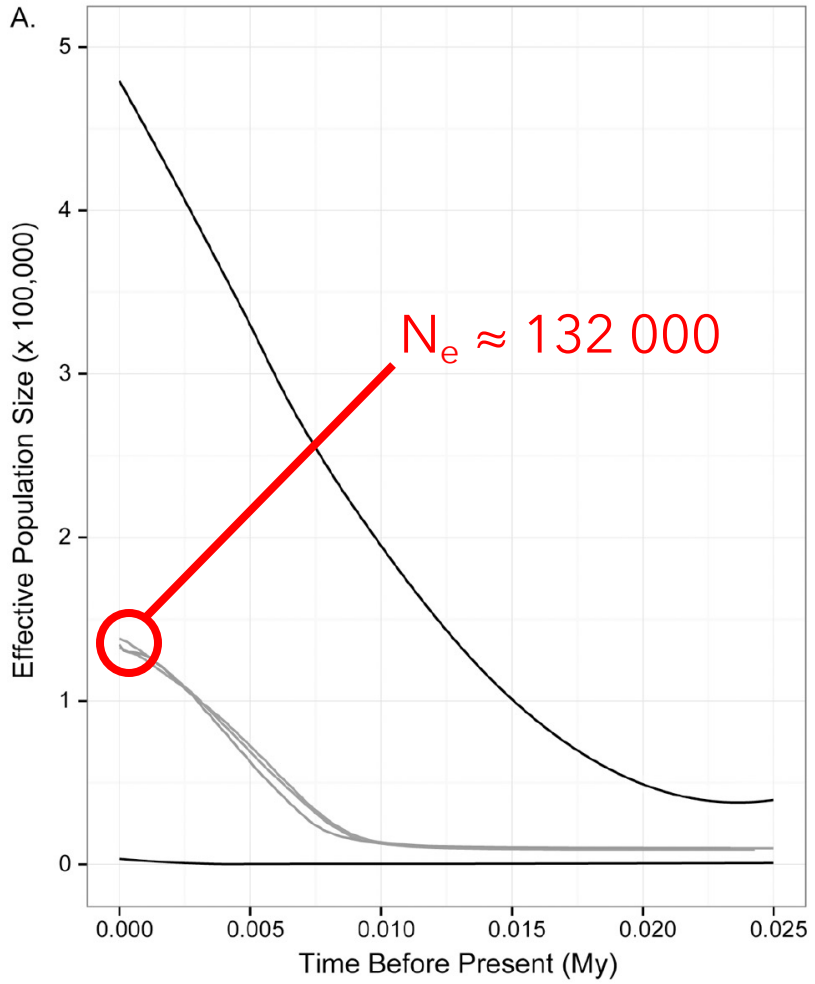
(Waples & Do 2008)

How to estimate **contemporary** N_e?

LD method is imprecise for $N_e > 1000$

Hawaiian hoary bats
$N_e = 2953.5$ (95% CI = 119.4, ∞)

(Russell unpub.)

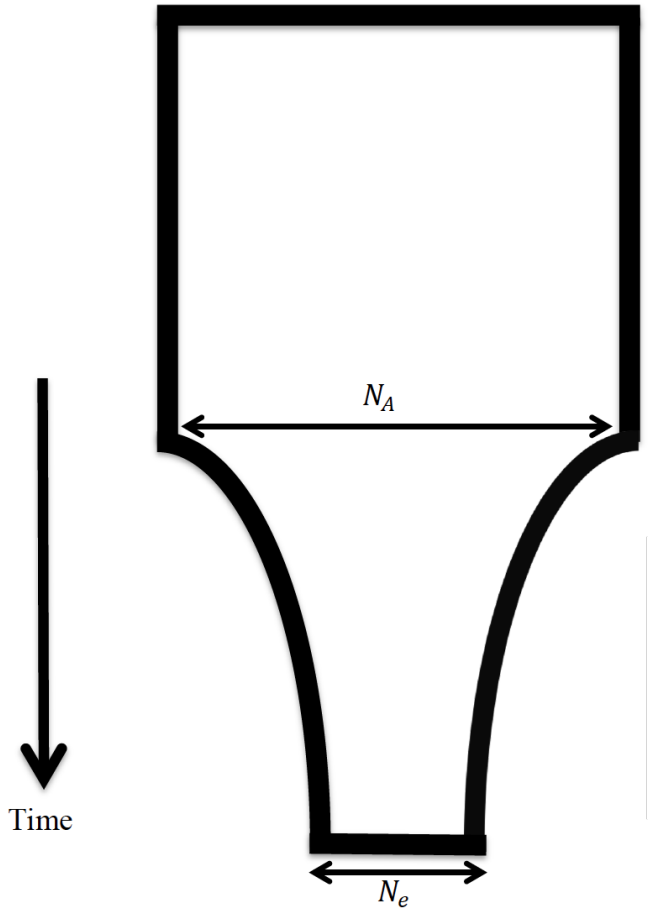


(Russell *et al.* 2015)

How to estimate N_e?

What type of N_e are we estimating?

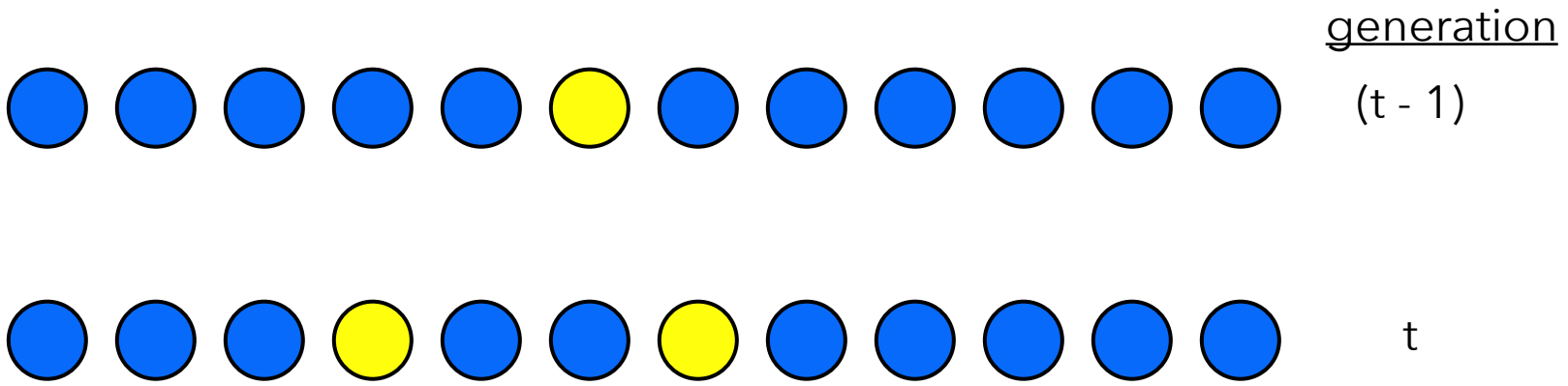
- Contemporary N_e – What is the effective population size now?
- Evolutionary N_e – What was the effective population size at some time in the past?
- N_e trajectory – Is N_e increasing, decreasing, or staying the same?



Munster 2015

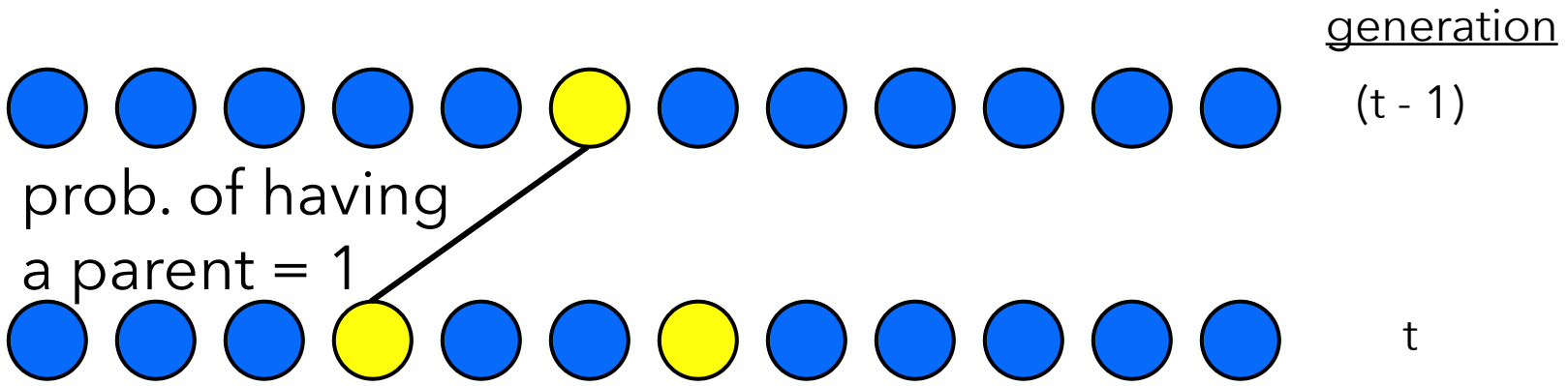
How to estimate **evolutionary** N_e?

Evolutionary N_e – Coalescent methods



How to estimate **evolutionary** N_e?

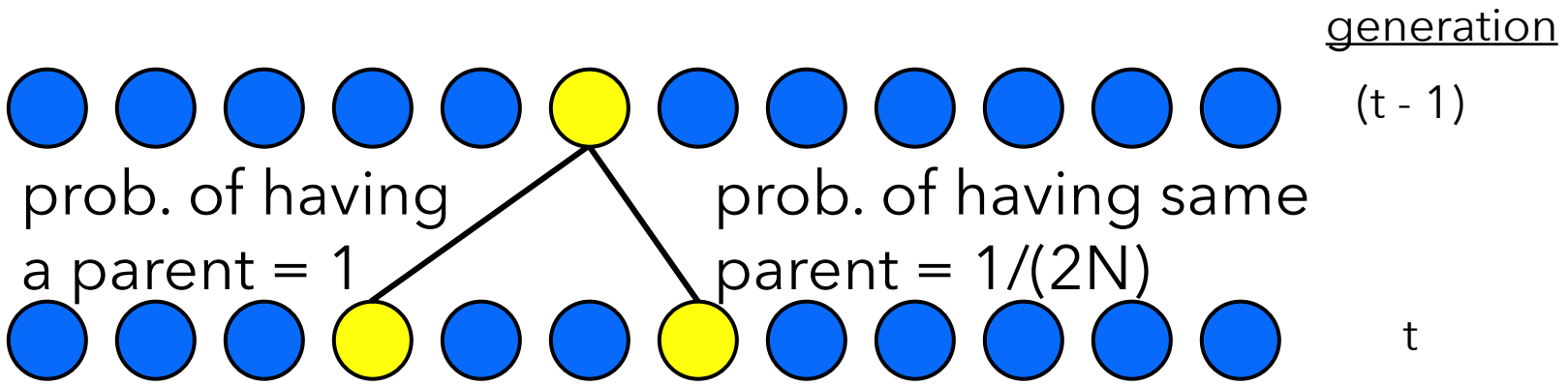
Evolutionary N_e – Coalescent methods



How to estimate **evolutionary** N_e?

Evolutionary N_e – Coalescent methods

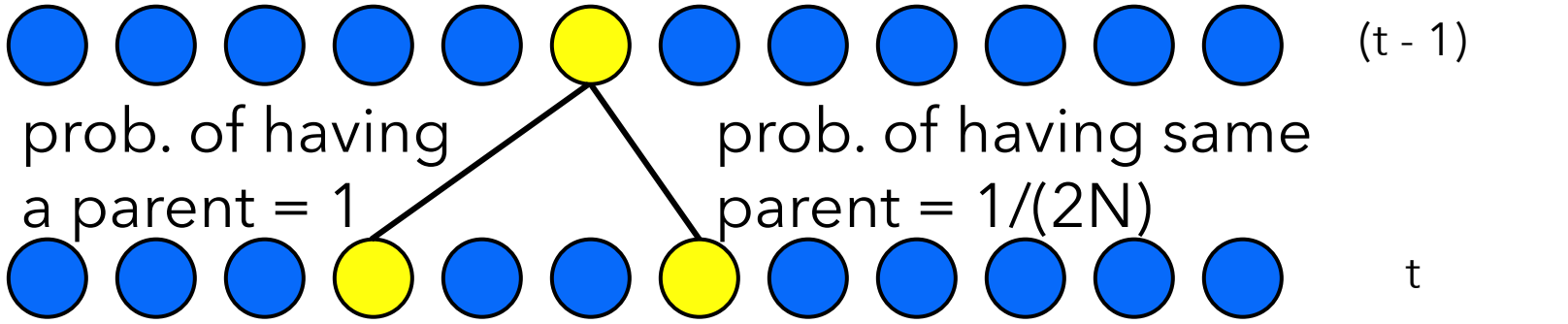
In any generation, the probability of two alleles coalescing is 1/(2N), where N is the population size

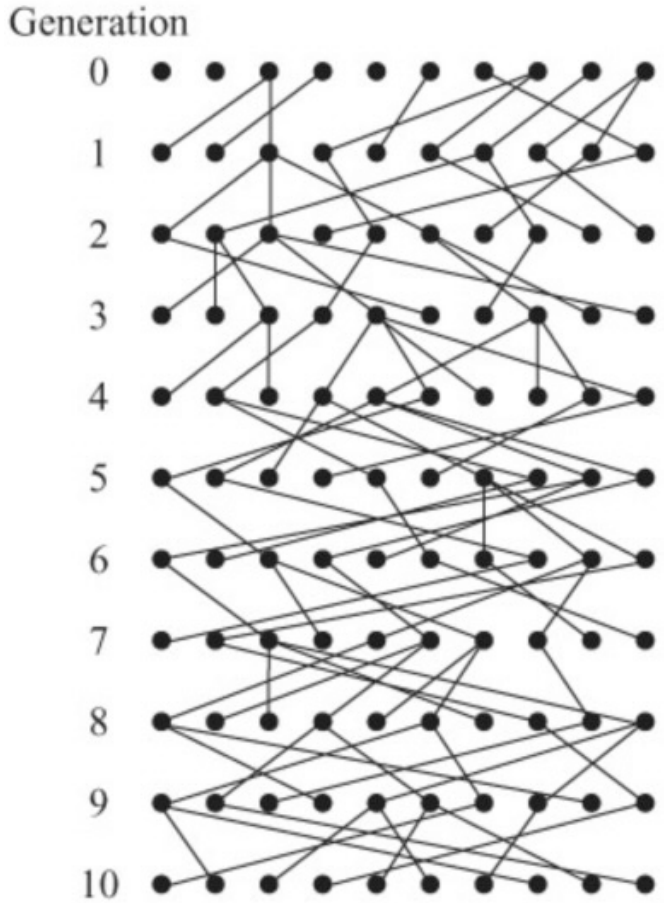


How to estimate **evolutionary** N_e?

Evolutionary N_e – Coalescent methods

In any generation, the probability of two alleles coalescing is 1/(2N), where N is the population size

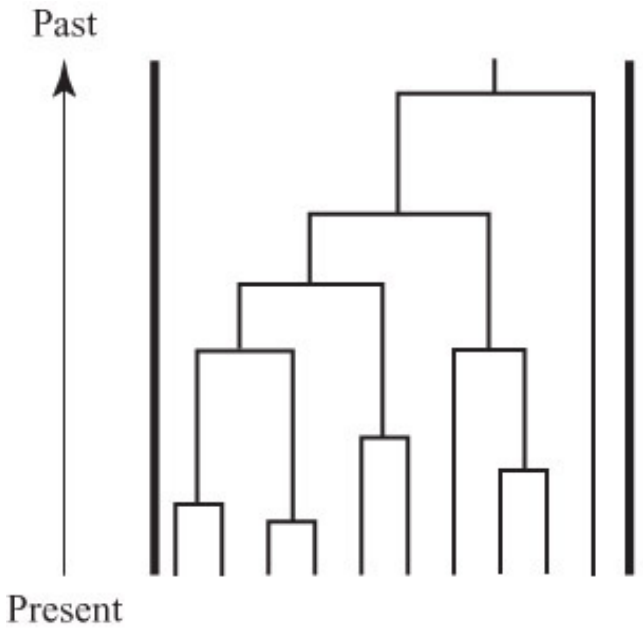




Expected time to coalescence is a function of N_e

How to estimate **evolutionary** N_e?

Evolutionary N_e – Coalescent methods

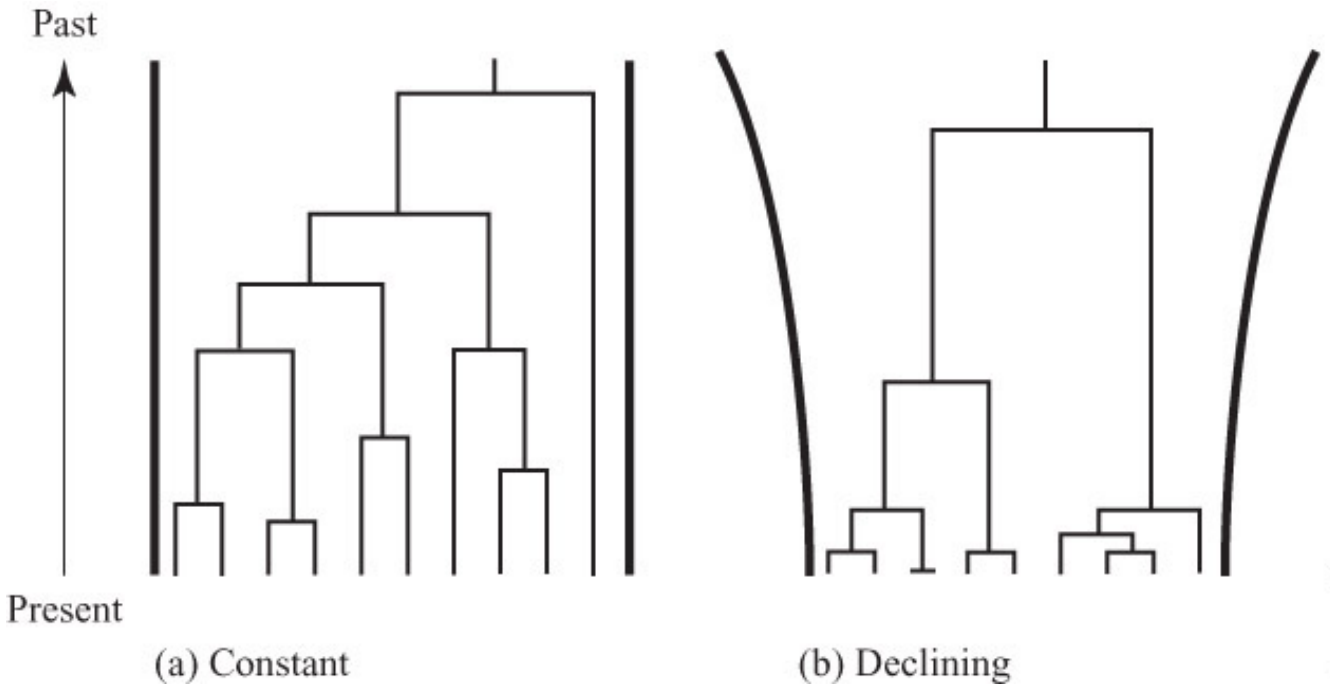


(a) Constant

Expected time to coalescence is a function of N_e

How to estimate **evolutionary** N_e?

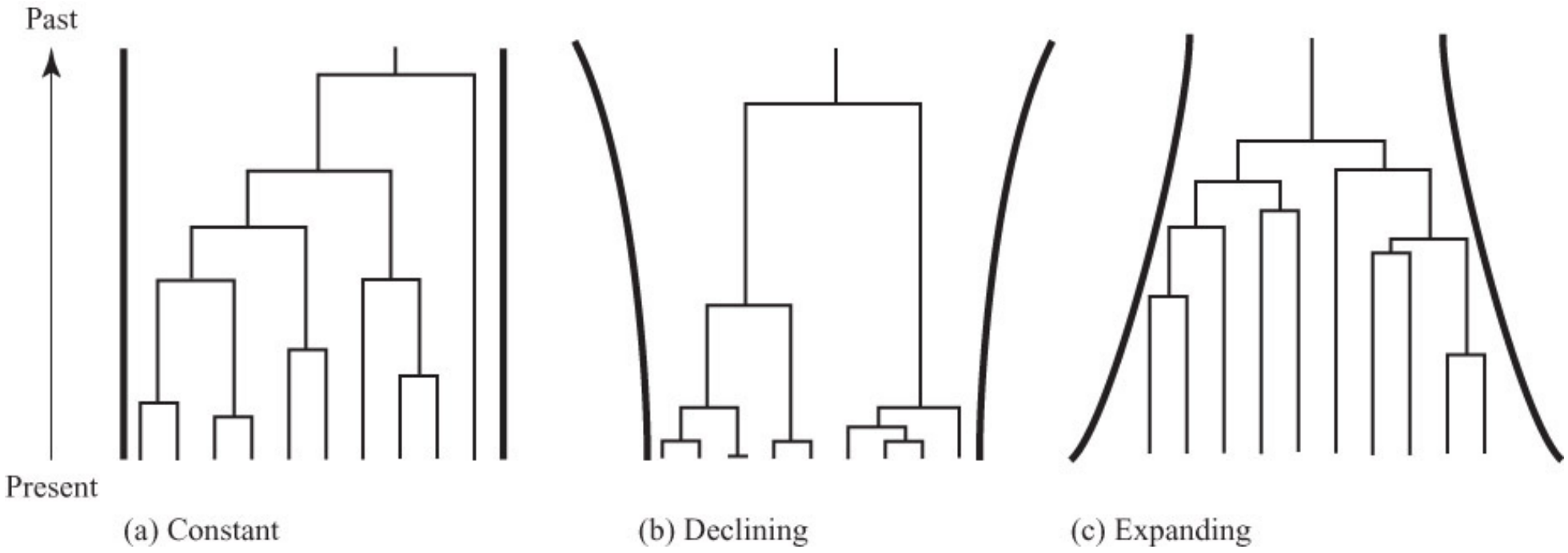
Evolutionary N_e – Coalescent methods



Expected time to coalescence is a function of N_e

How to estimate **evolutionary** N_e?

Evolutionary N_e – Coalescent methods



Expected time to coalescence is a function of N_e

How to estimate **evolutionary** N_e?

Evolutionary N_e – Coalescent methods

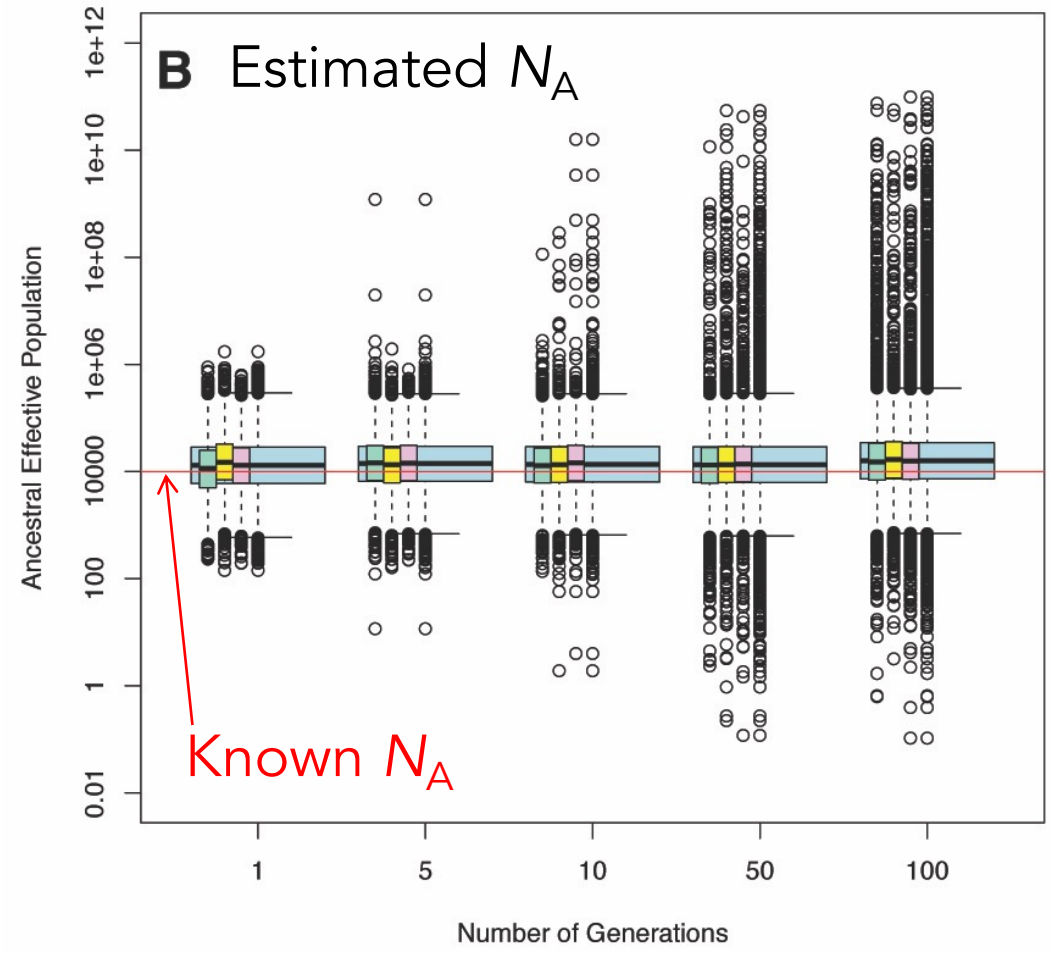
©M. Durham

©M. Tuttle

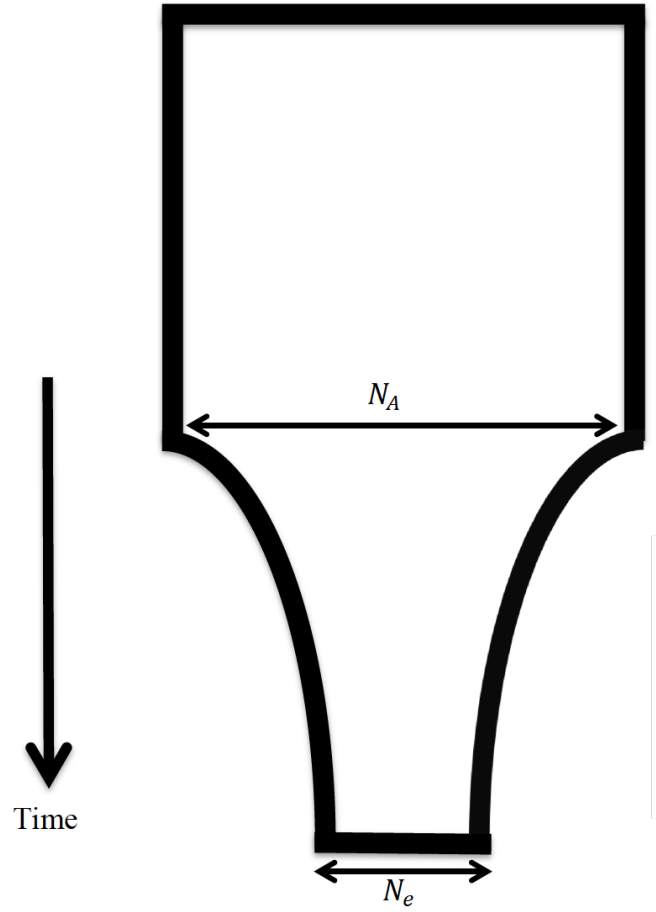
©J. MacGregor

Sovic *et al.* 2016

How to estimate **evolutionary** N_e?



Munster 2015



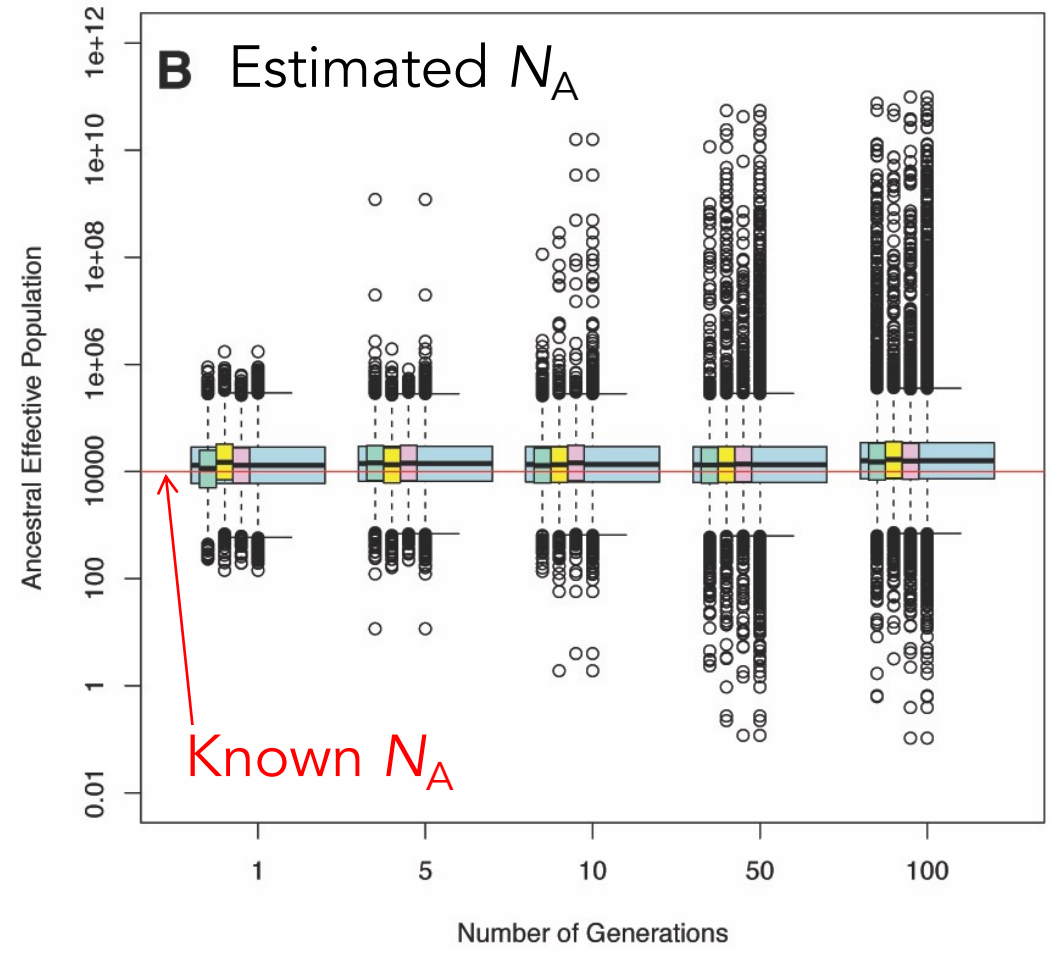
n = 50

10 microsatellite loci

N_A = 10,000

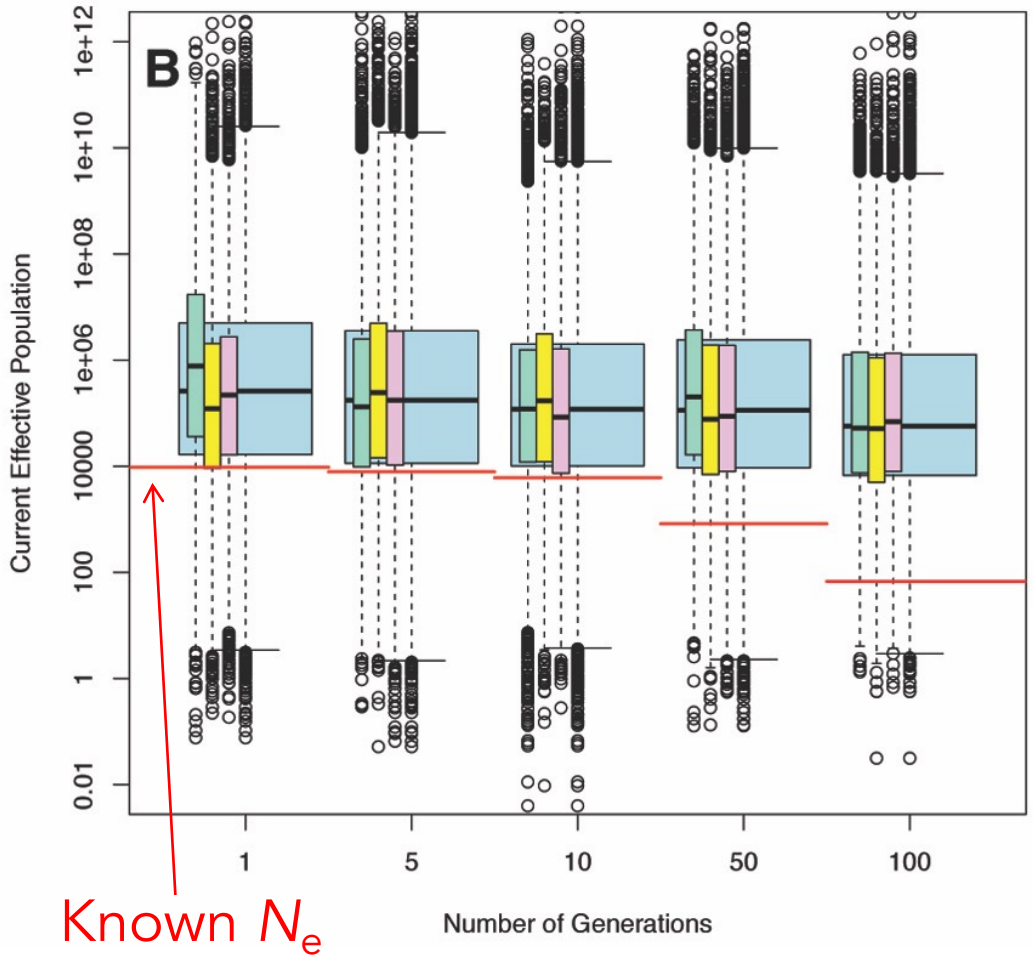
How to estimate **evolutionary** N_e?

Weak power to address current conservation threats



Munster 2015

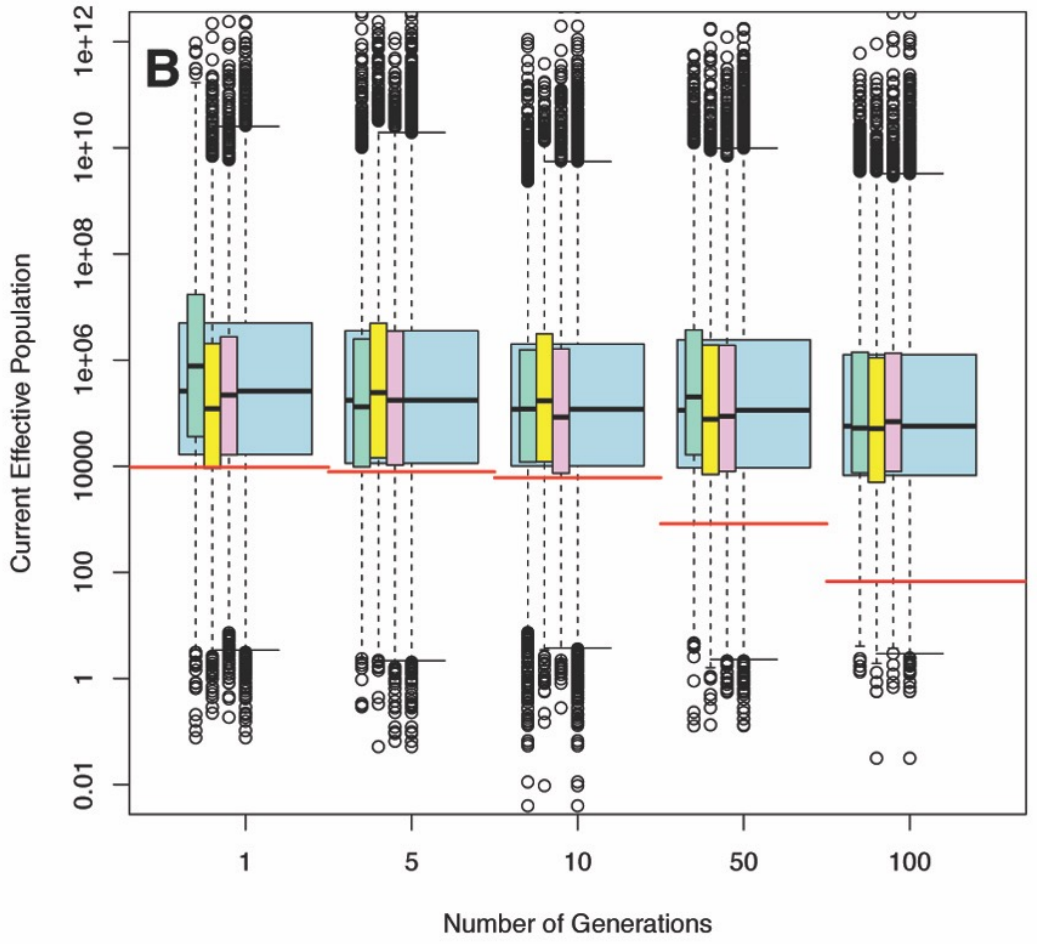
Estimated contemporary N_e



How to estimate N_e?

Be cautious in interpreting N_e

- Conservation interest is in N_c, not N_e
- Often $N_c > N_e$, but not always!
- N_e can indicate evolutionary potential
- N_e as monitoring proxy of N_c?
- Consider the error in estimates



Thank you for listening!

N_e working group (NeWG)

- Francisca Cunha Almeida
- Balaji Chattopadhyay
- Elise Lauterbur
- Amy Russell (russelam@gvsu.edu)