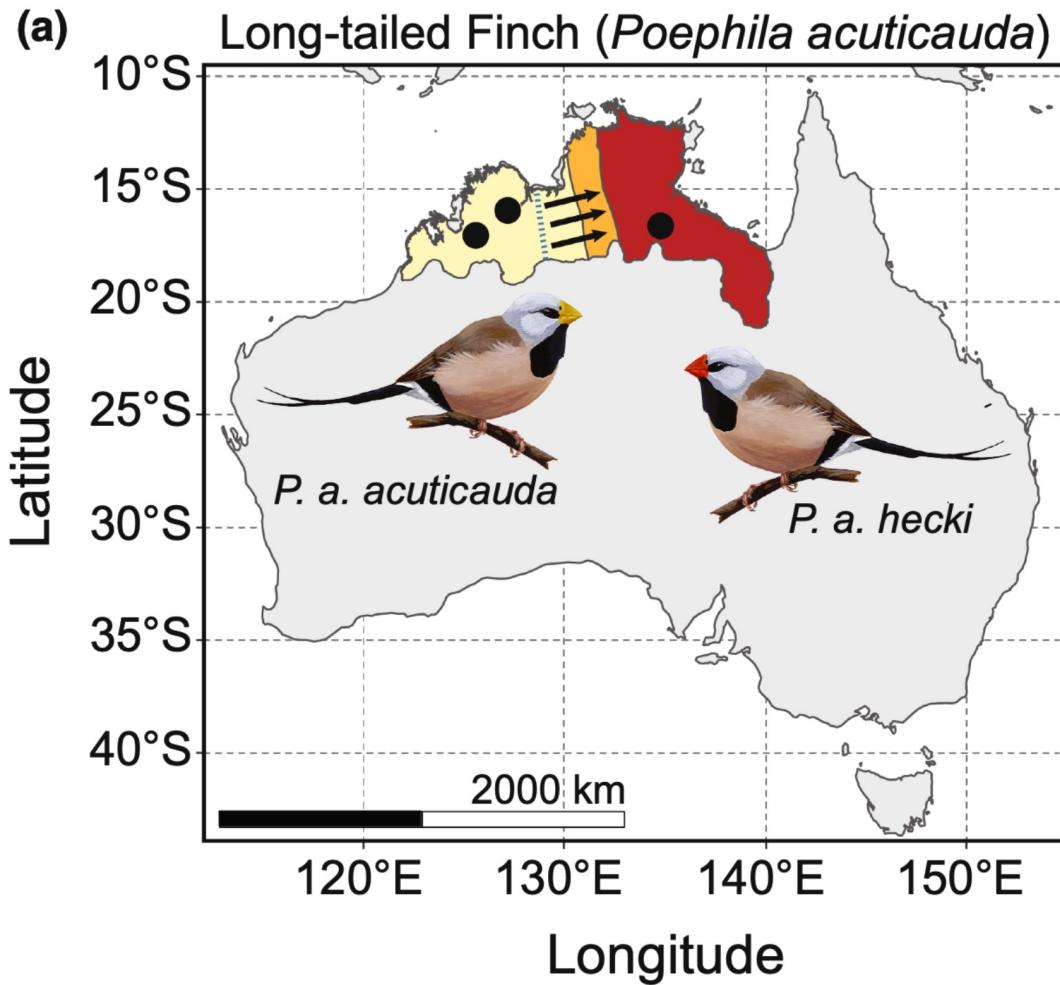


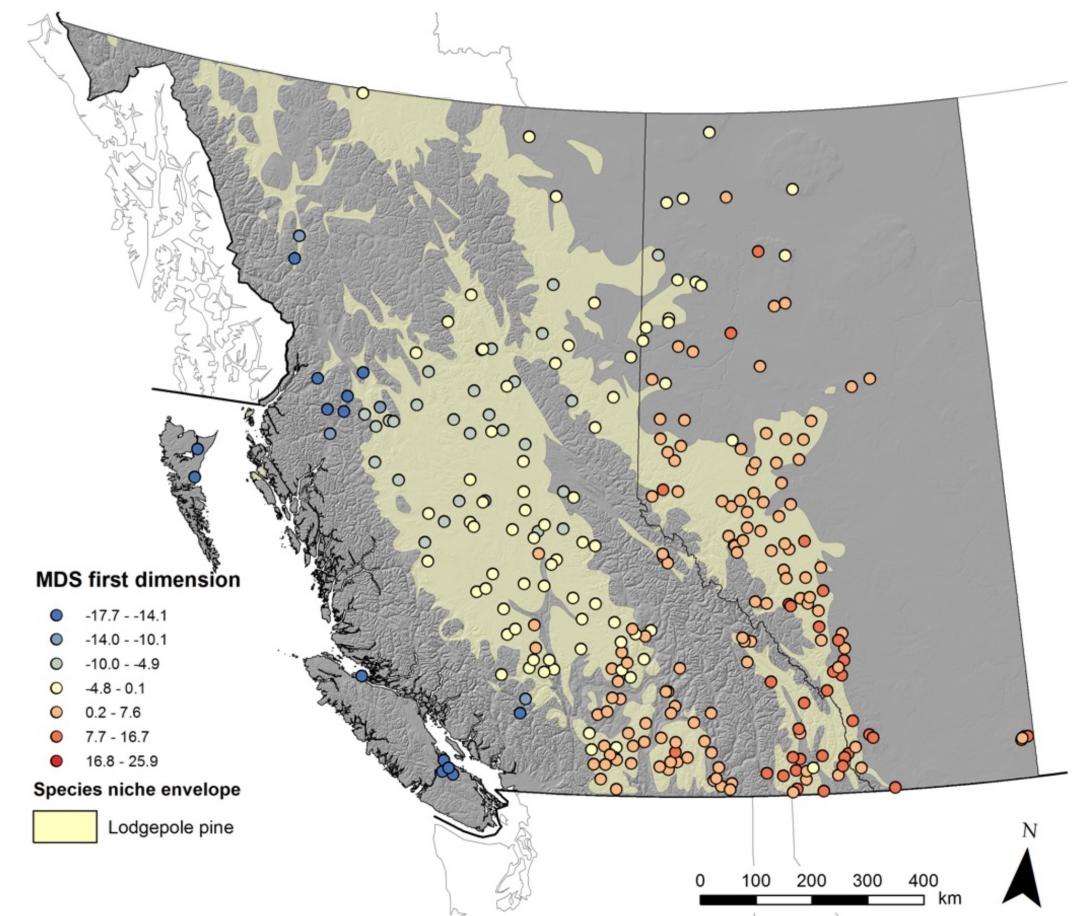
Evolution across space

Fundamentals of Evolution Fall 2023

Traits vary across space



McDiarmid et al. 2023

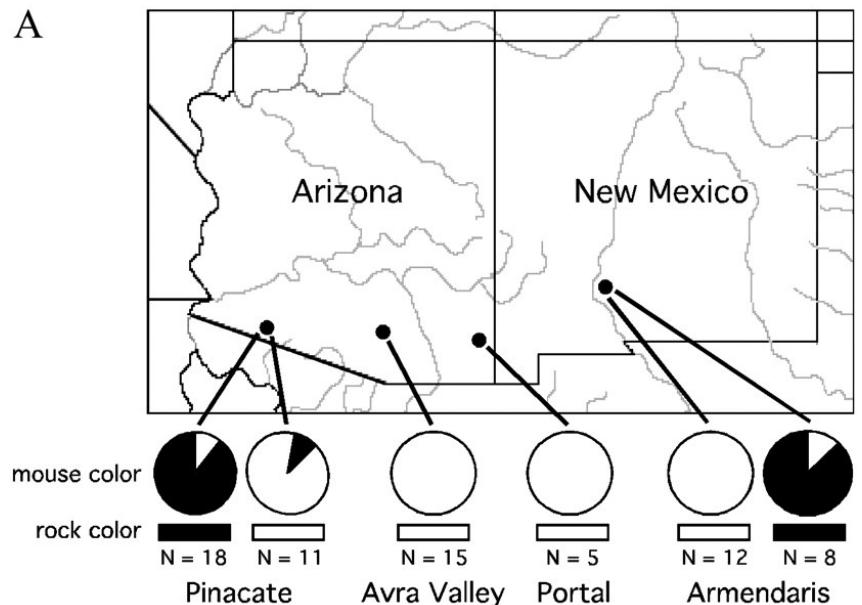


Yeaman et al. 2016

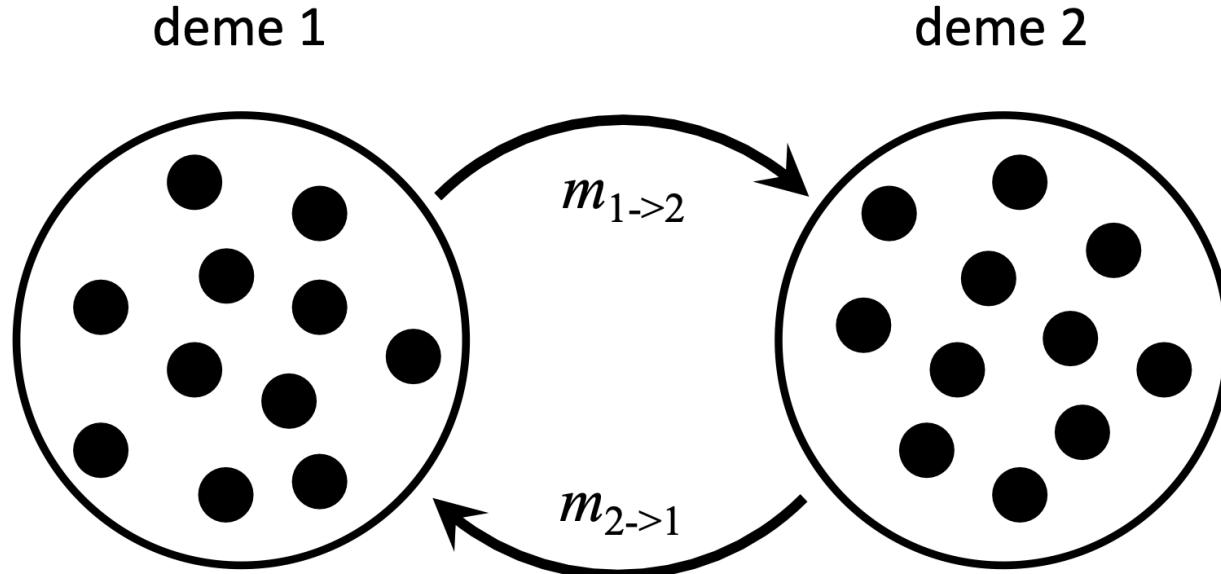
Spatial variation can be adaptive

Phenotype frequency matches
substrate prevalence in
Chaetodipus intermedius

(Nachman et al. 2003)



Spatial variation can be neutral



(adapted from Messer 2022)

vocabulary:

deme = population subdivision

panmictic = a randomly mating population

How is spatial variation measured?

$$H = \Pr(\text{different by state})$$

seq1: CGTAGCAA
seq2: CGTAACAA

5th position is
diff by state

spatial variation is a function of heterozygosity

How is spatial variation measured?

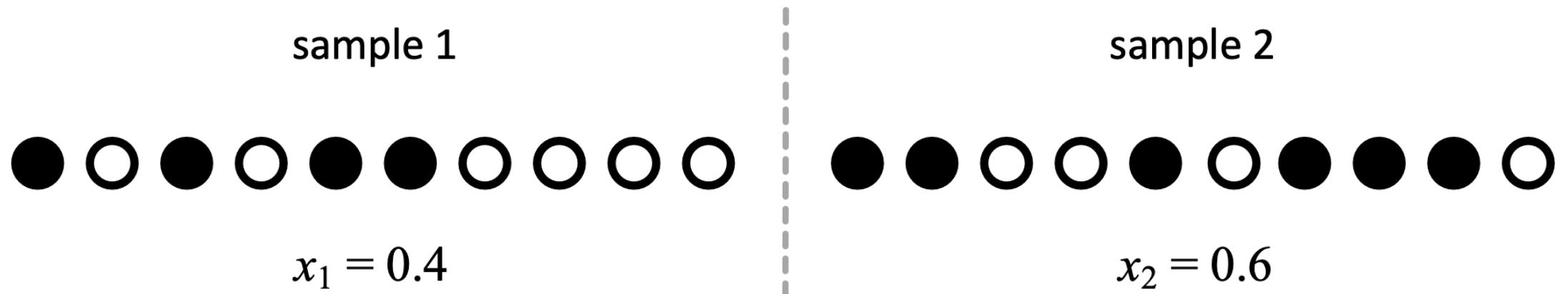
$$H = \text{Pr}(\text{different by state})$$

$$H = 4N_e\mu$$

spatial variation is a function of heterozygosity

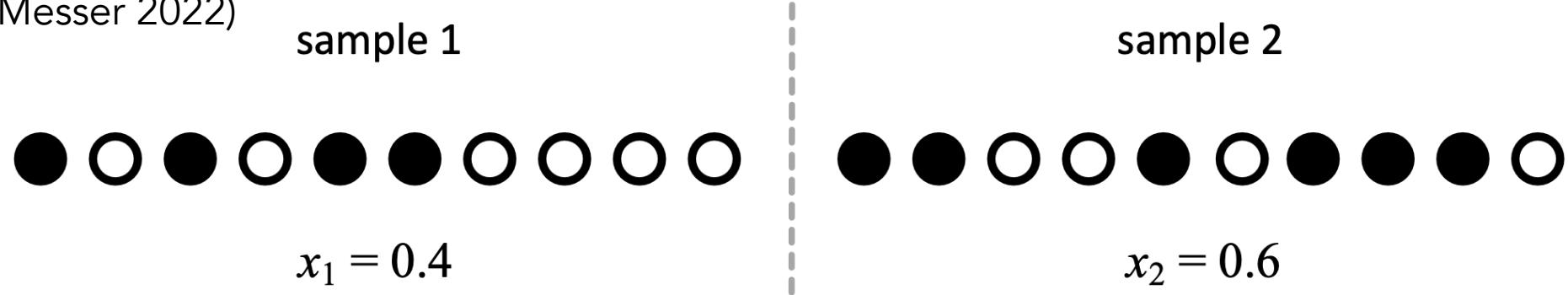
How is spatial variation measured?

(adapted from Messer 2022)



How is spatial variation measured?

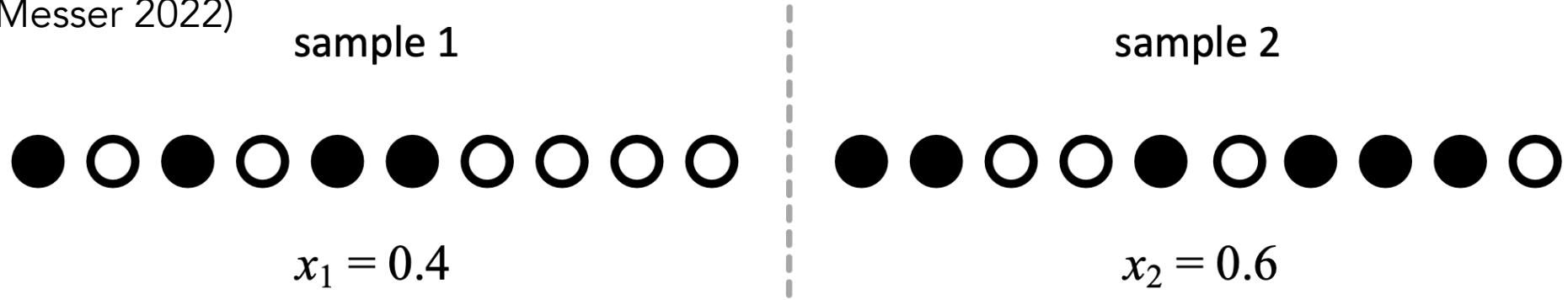
(adapted from Messer 2022)



H_S = heterozygosity within sample

How is spatial variation measured?

(adapted from Messer 2022)

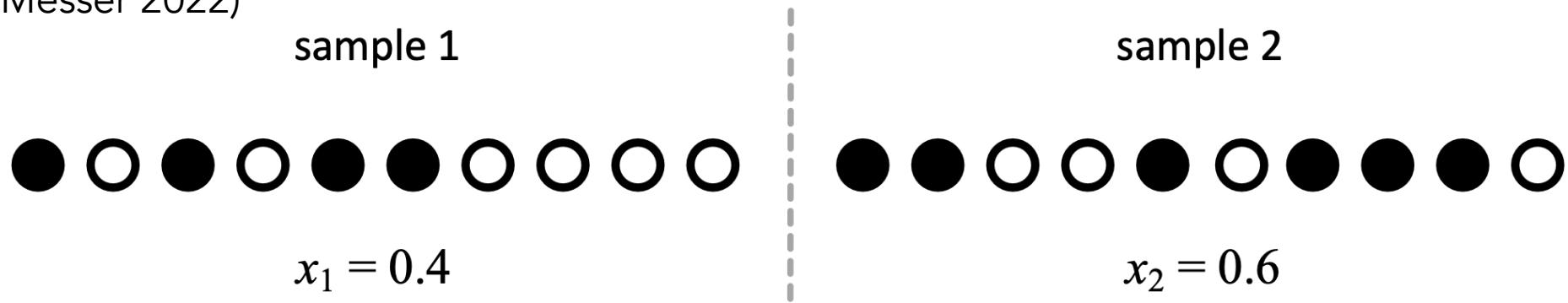


H_S = heterozygosity within sample

H_T = heterozygosity of pooled sample

How is spatial variation measured?

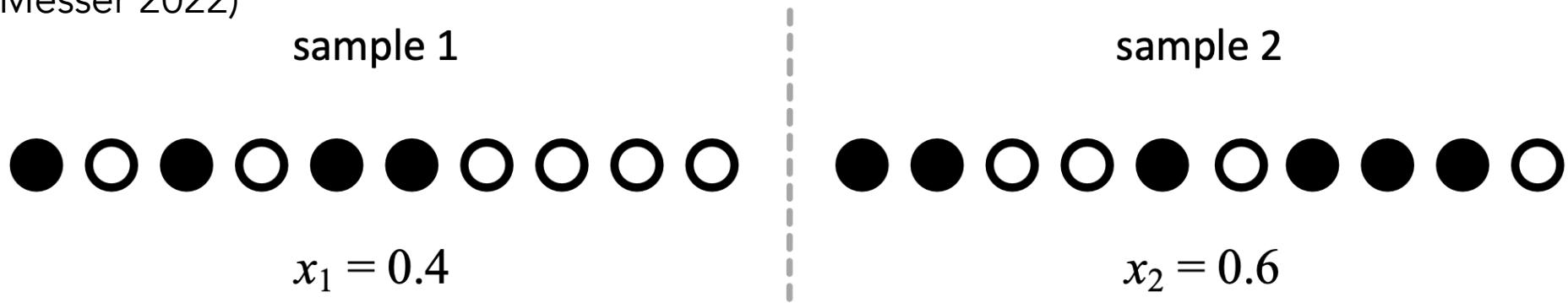
(adapted from Messer 2022)



$$H_S = \frac{1}{n} \sum_{i=1}^n 2x_i(1 - x_i)$$

How is spatial variation measured?

(adapted from Messer 2022)



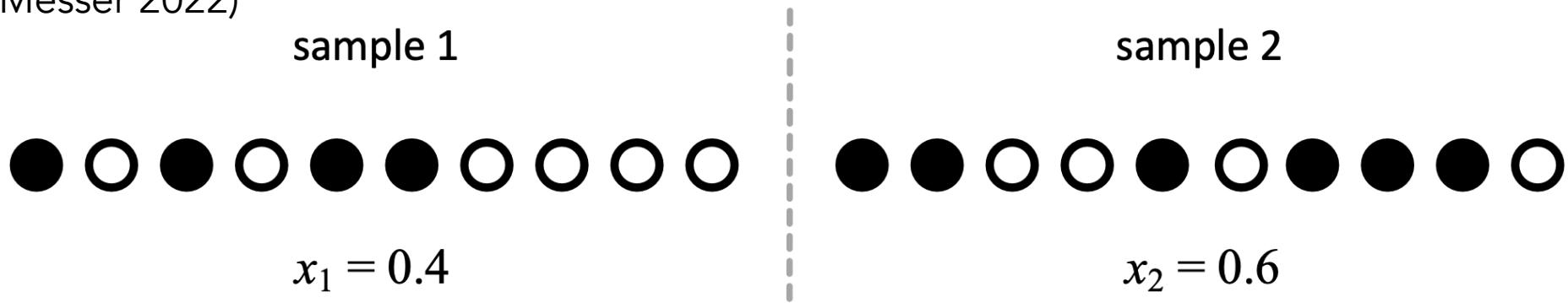
$$H_S = \frac{1}{n} \sum_{i=1}^n 2x_i(1 - x_i)$$

$$\bar{x} = \frac{1}{n} \sum_{i=1}^n x_i$$

$$H_T = 2\bar{x}(1 - \bar{x})$$

How is spatial variation measured?

(adapted from Messer 2022)



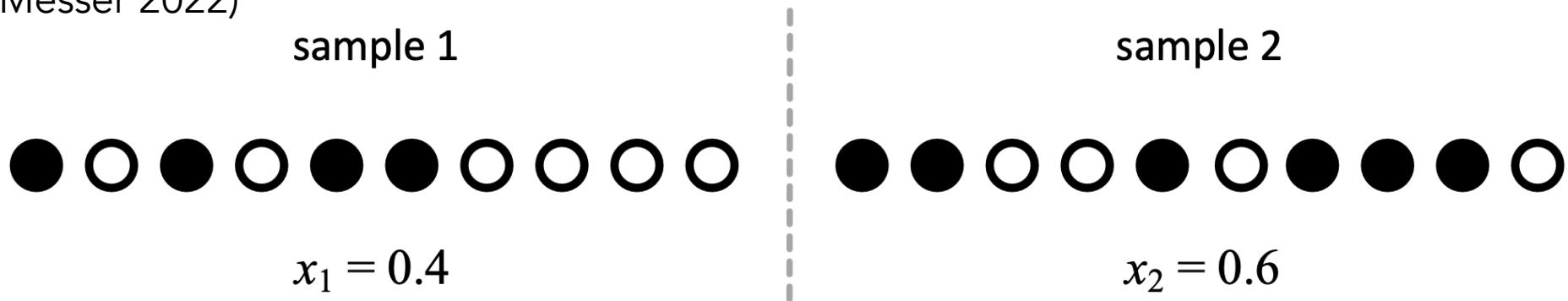
$$H_S = \frac{1}{n} \sum_{i=1}^n 2x_i(1 - x_i)$$

$$F_{ST} = \frac{H_T - H_S}{H_T}$$

$$H_T = 2\bar{x}(1 - \bar{x})$$

How is spatial variation measured?

(adapted from Messer 2022)



$$H_S = \frac{1}{n} \sum_{i=1}^n 2x_i(1 - x_i)$$

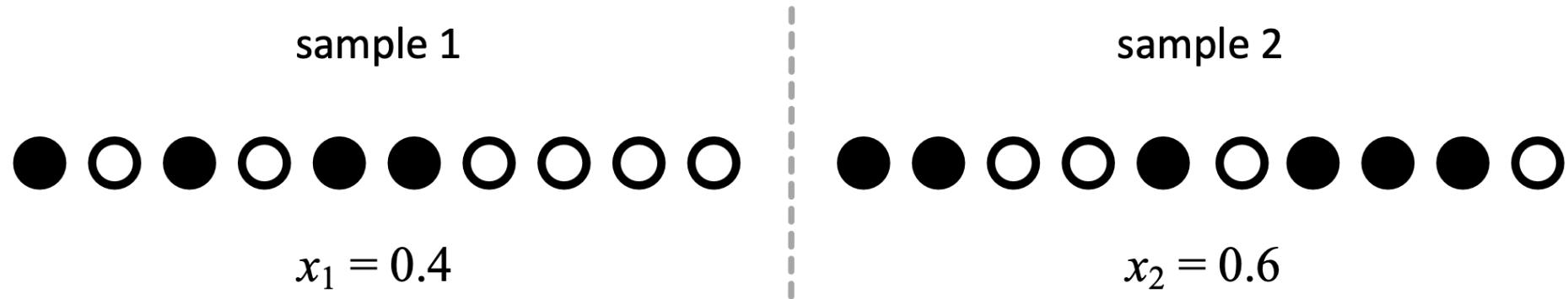
$$H_T = 2\bar{x}(1 - \bar{x})$$

$$F_{ST} = \frac{H_T - H_S}{H_T}$$

$$F_{ST} = \frac{\pi_{\text{between}} - \pi_{\text{within}}}{\pi_{\text{between}}}$$

How is spatial variation measured?

(adapted from Messer 2022)



$$F_{ST} = \frac{H_T - H_S}{H_T} = \frac{0.5 - 0.48}{0.5} = 0.04.$$

(adapted from Messer 2022)

Behavior of F_{ST}

$$F_{ST} = \begin{cases} 0 & x_1 = x_2 \\ > 0 & x_1 \neq x_2 \\ 1 & \text{each sample fixed for different allele} \end{cases}$$

With any subdivision F_{ST} is > 0 , “Wahlund Effect”

Low F_{ST} implies low subdivision

High F_{ST} implies high subdivision

F_{ST} at a single biallelic (A or a) locus in two demes

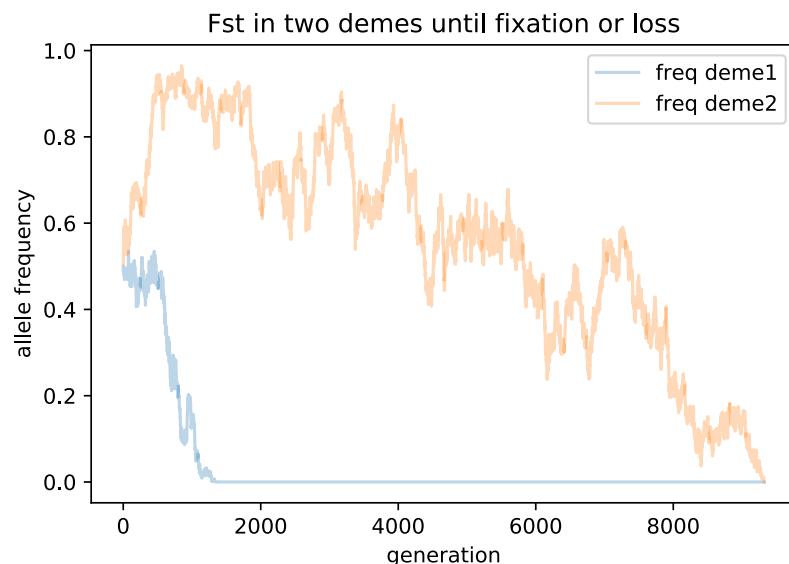
$N_1 = 3000; N_2 = 3000$

$p_{initial} = 0.5$

F_{ST} at a single biallelic (A or a) locus in two demes

$N_1 = 3000; N_2 = 3000$

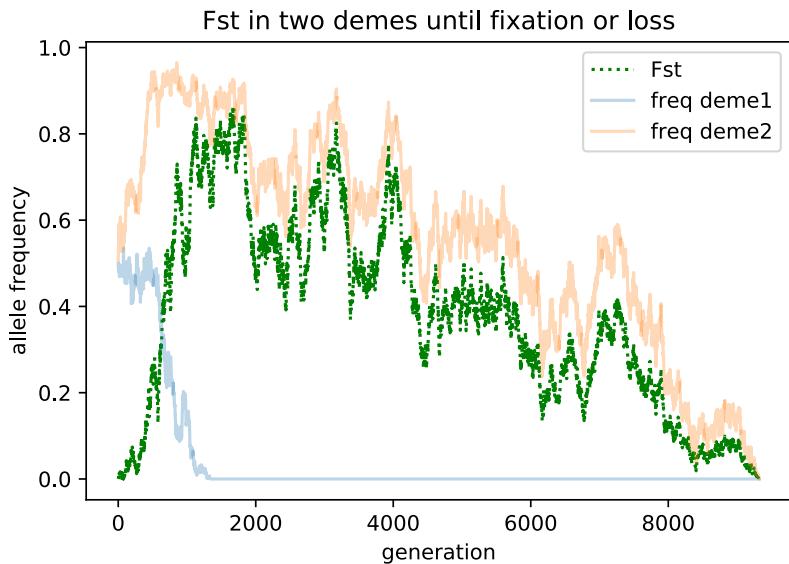
$p_{initial} = 0.5$



F_{ST} at a single biallelic (A or a) locus in two demes

$N_1 = 3000; N_2 = 3000$

$p_{initial} = 0.5$



A lost in deme 1

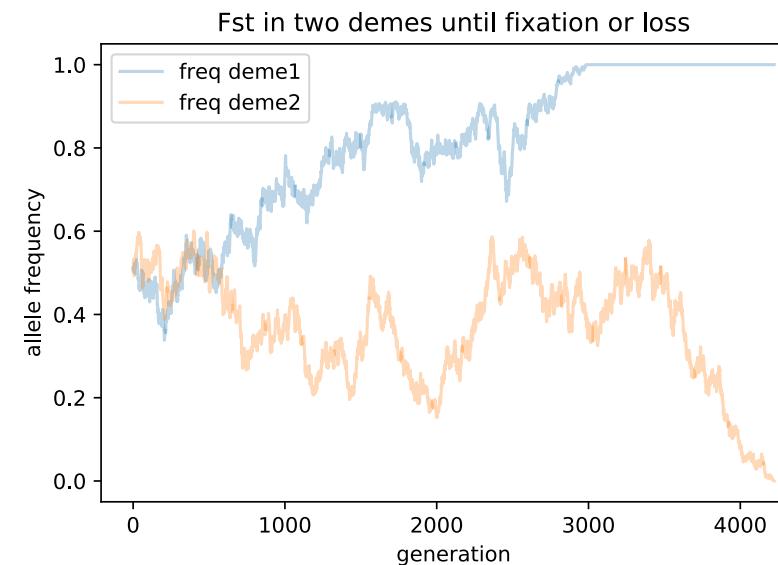
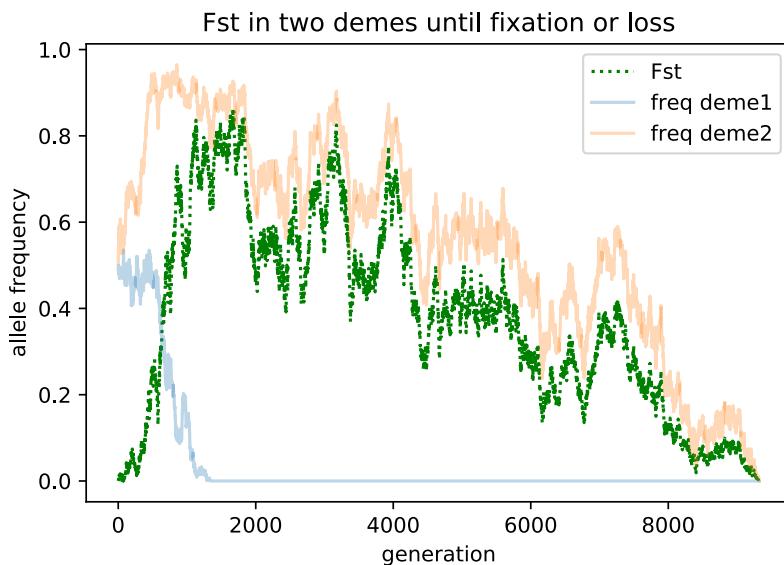
A lost in deme 2

$$F_{ST} = 0$$

F_{ST} at a single biallelic (A or a) locus in two demes

$N_1 = 3000; N_2 = 3000$

$p_{initial} = 0.5$



A lost in deme 1

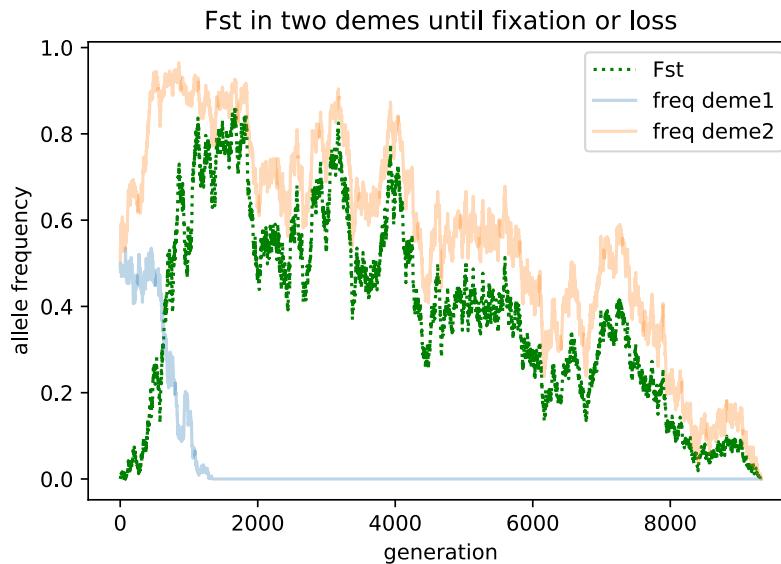
A lost in deme 2

$$F_{ST} = 0$$

F_{ST} at a single biallelic (A or a) locus in two demes

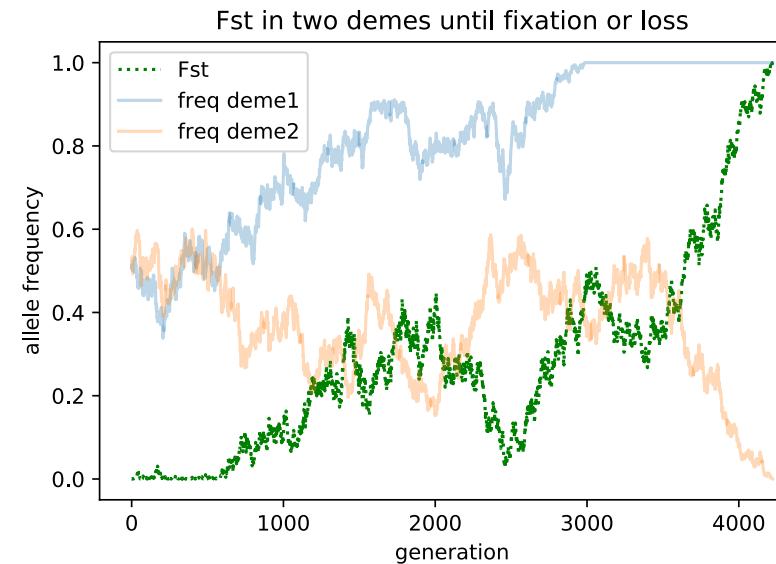
$N_1 = 3000; N_2 = 3000$

$p_{initial} = 0.5$



A lost in deme 1
A lost in deme 2

$$F_{ST} = 0$$



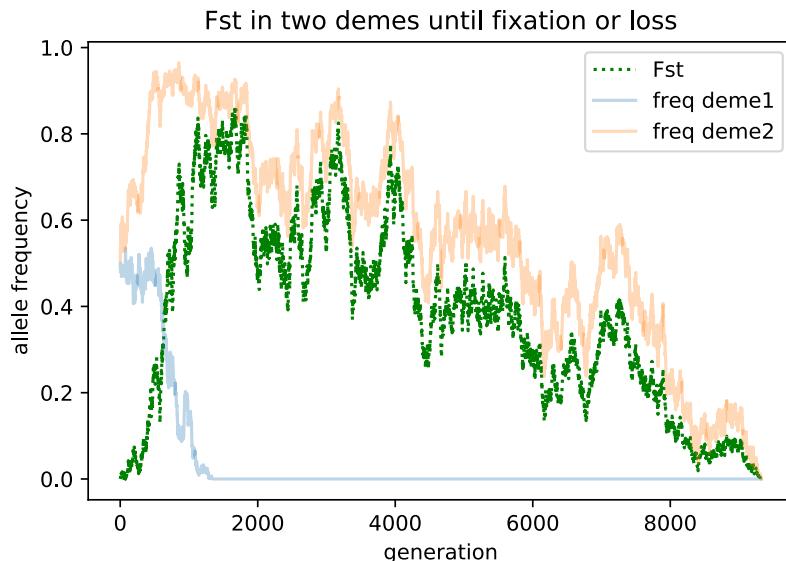
A fixed in deme 1
A lost in deme 2

$$F_{ST} = 1$$

F_{ST} at a single biallelic (A or a) locus in two demes

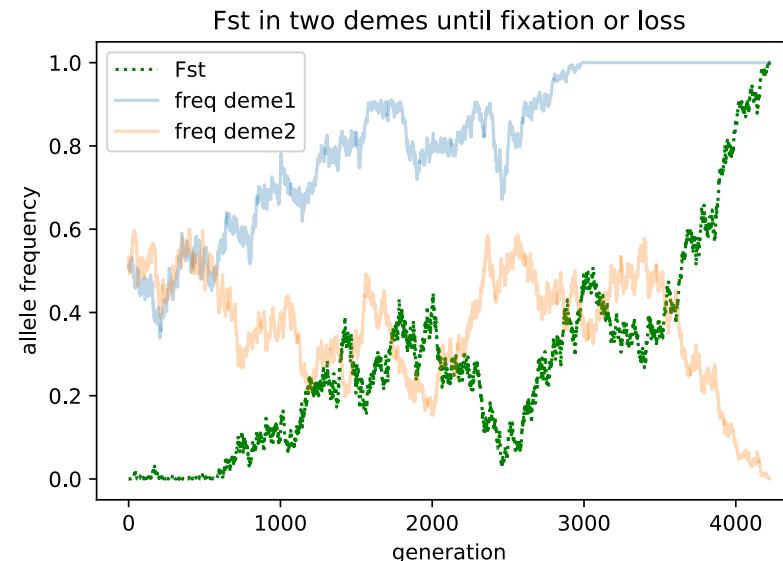
$N_1 = 3000; N_2 = 3000$

$p_{initial} = 0.5$



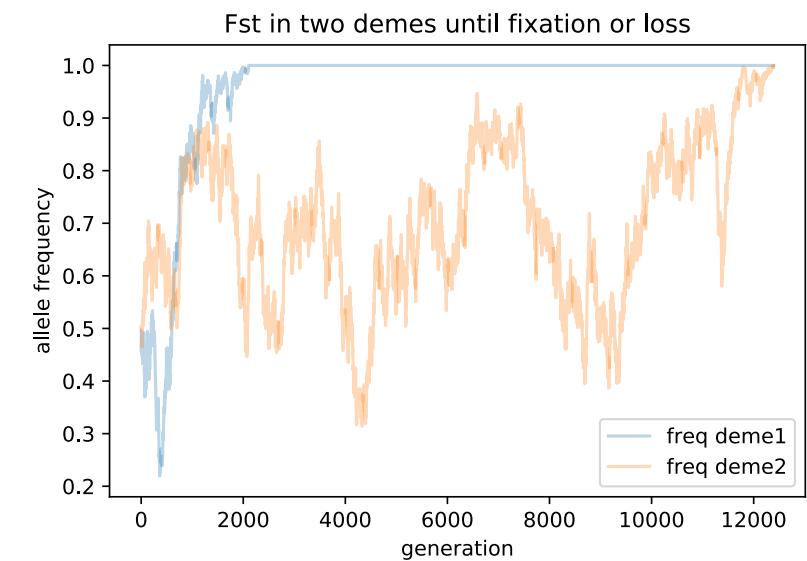
A lost in deme 1
A lost in deme 2

$$F_{ST} = 0$$



A fixed in deme 1
A lost in deme 2

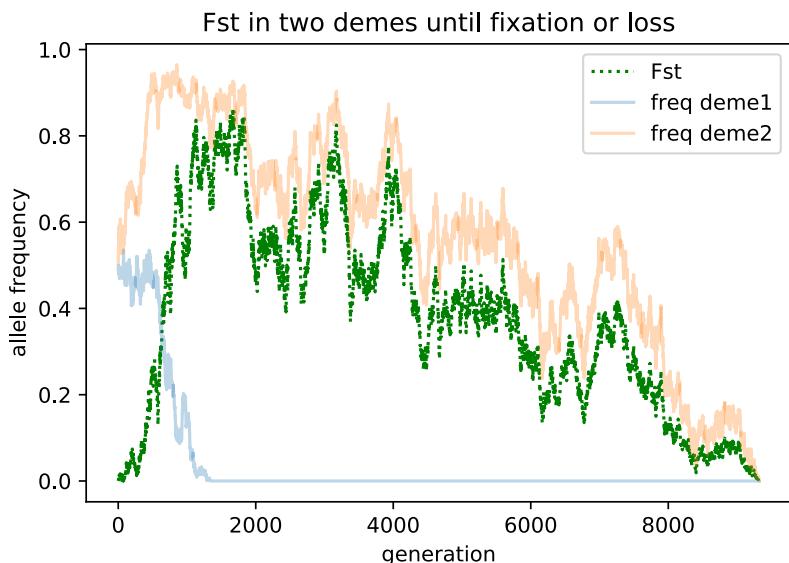
$$F_{ST} = 1$$



F_{ST} at a single biallelic (A or a) locus in two demes

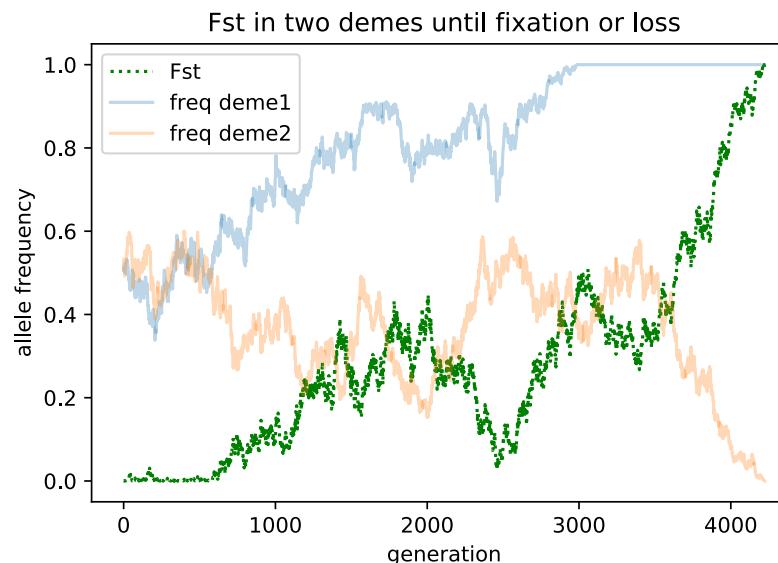
$N_1 = 3000; N_2 = 3000$

$p_{initial} = 0.5$



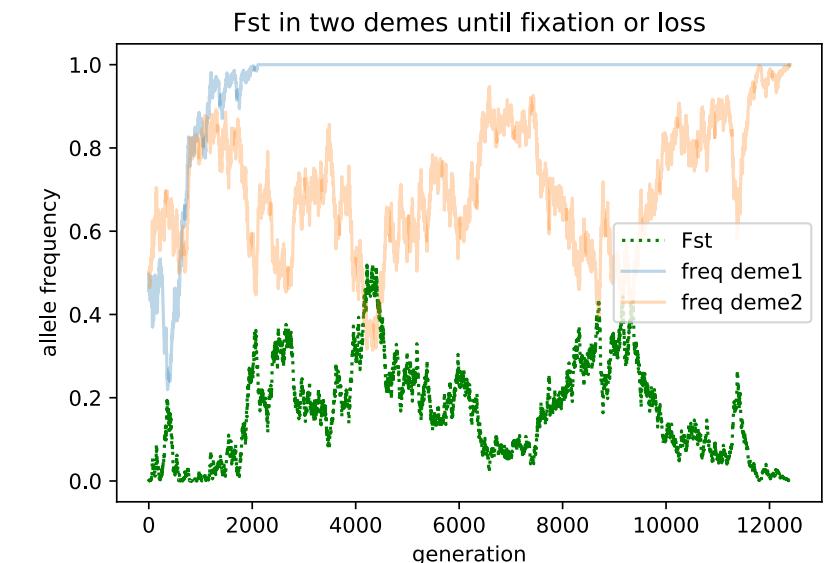
A lost in deme 1
A lost in deme 2

$$F_{ST} = 0$$



A fixed in deme 1
A lost in deme 2

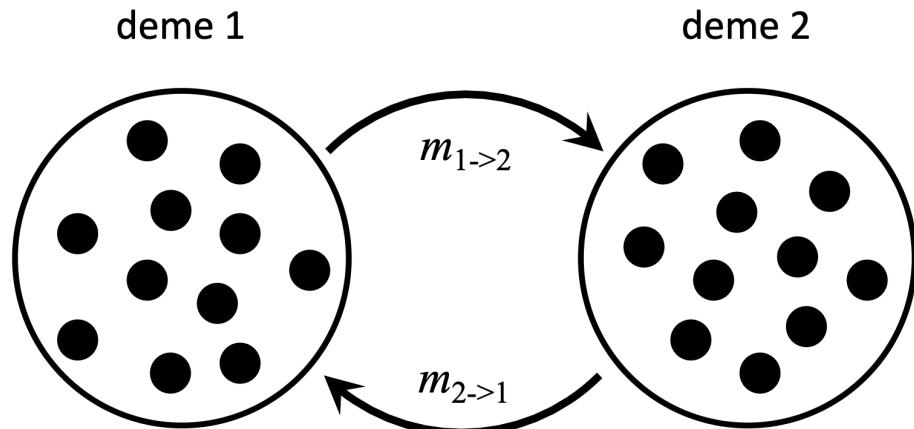
$$F_{ST} = 1$$



A fixed in deme 1
A fixed in deme 2

$$F_{ST} = 0$$

We know from HWE that allele frequencies don't change without selection, mutation, migration, or genetic drift



neutral or adaptive?

Processes other than genetic variation can lead to spatial variation in phenotype

Processes other than genetic variation can lead to spatial variation in phenotype



Locale A
small plants

Processes other than genetic variation can lead to spatial variation in phenotype



Locale A
small plants



Locale B (Locale B != Locale A)
big plants

Processes other than genetic variation can lead to spatial variation in phenotype



Locale A
small plants



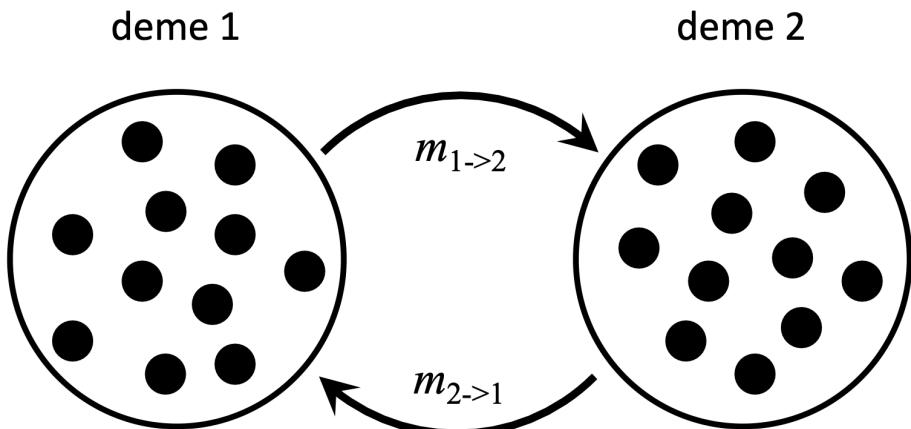
Locale B (Locale B != Locale A)
big plants



Common Garden
same phenotype

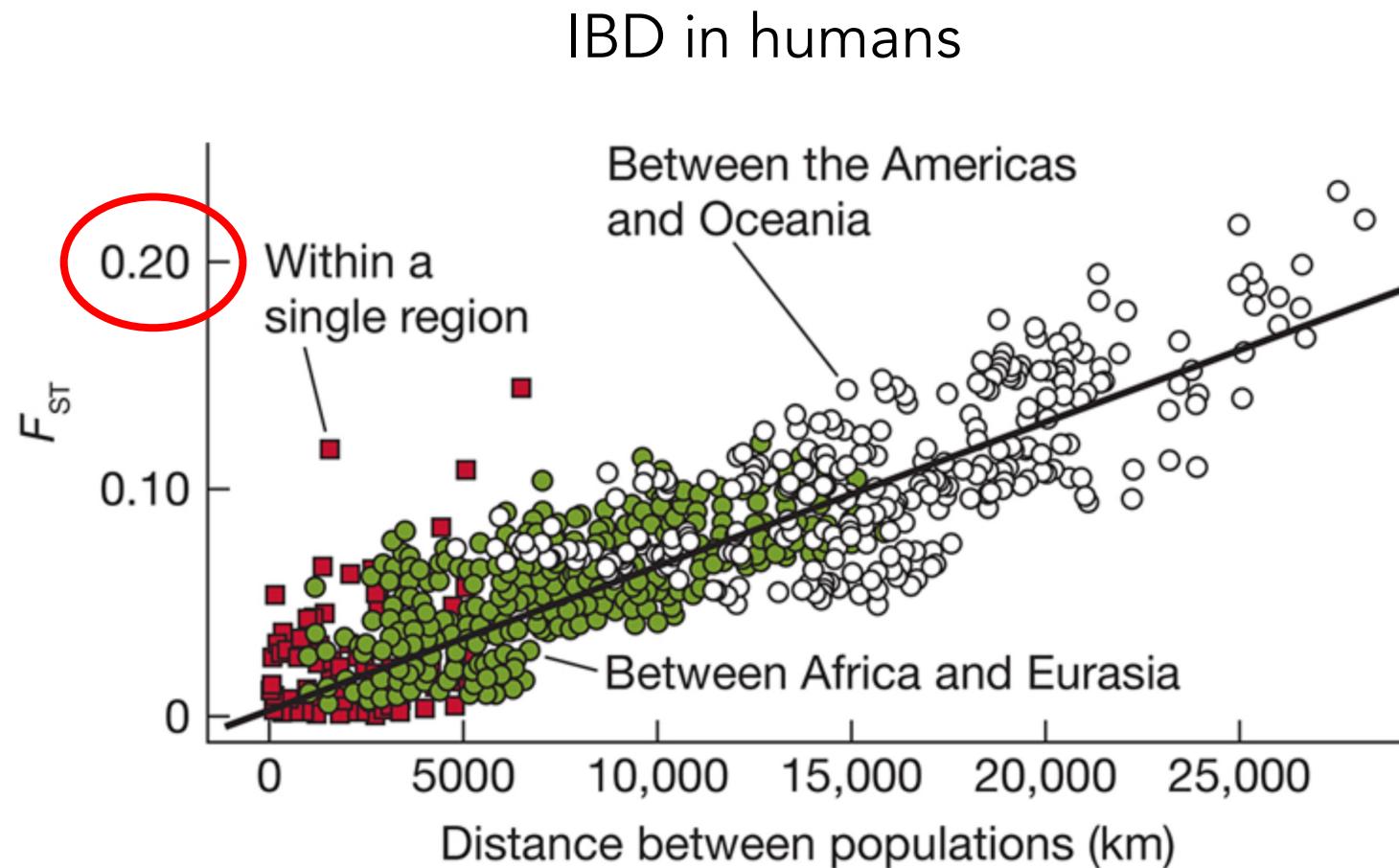
phenotypic plasticity

Local adaptation?



Given trait is not plastic, has variation arisen through drift or selection?

Isolation-by-distance is expected under neutrality with limited dispersal



Dispersal



Dispersal creates gene flow between populations, i.e. mixing of alleles between population subdivisions
(dispersal is also called migration)
(gene flow is also called admixture or introgression)

Dispersal is quantified with migration rate (m) with units [$n/\text{generation}$]

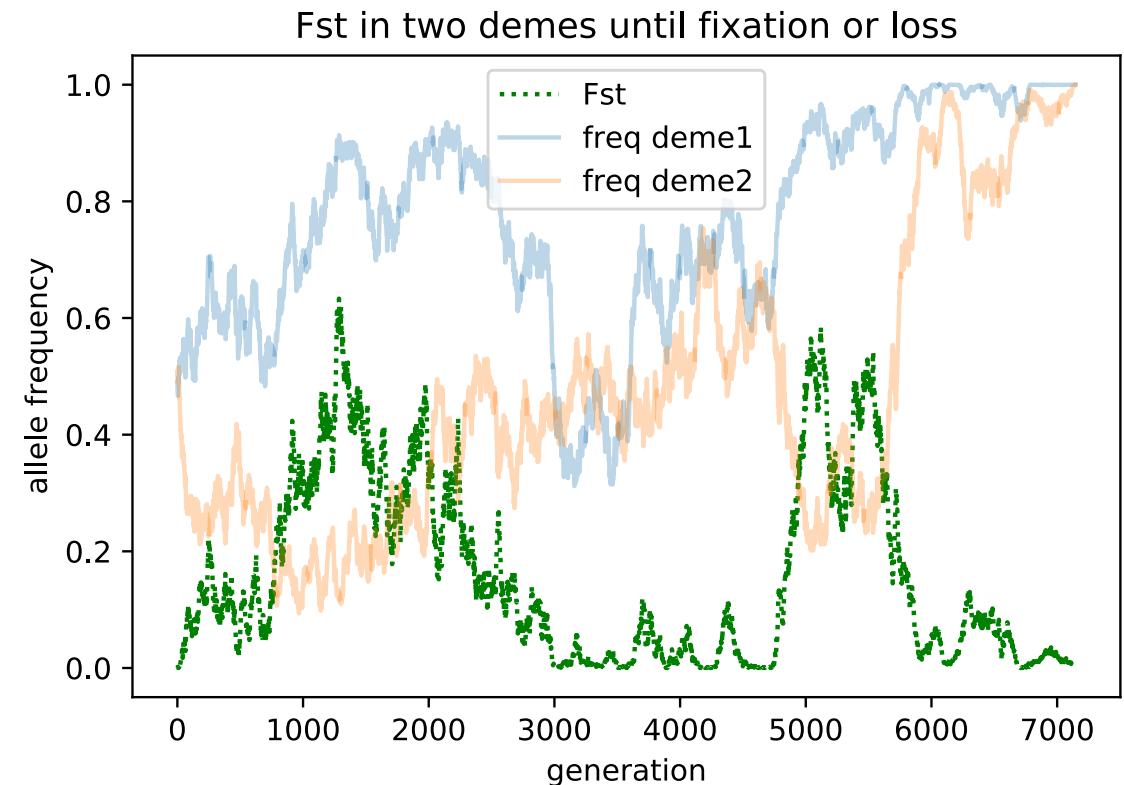
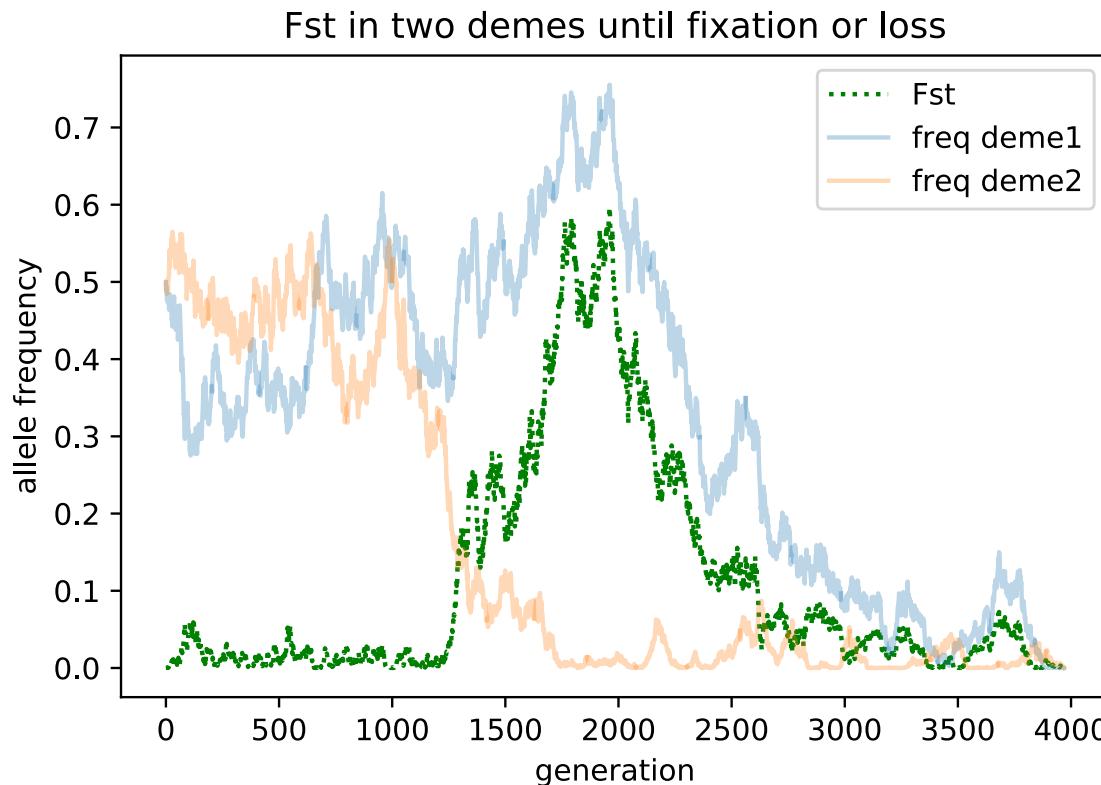
n can be...
individuals
allele counts
allele frequencies

F_{ST} under migration

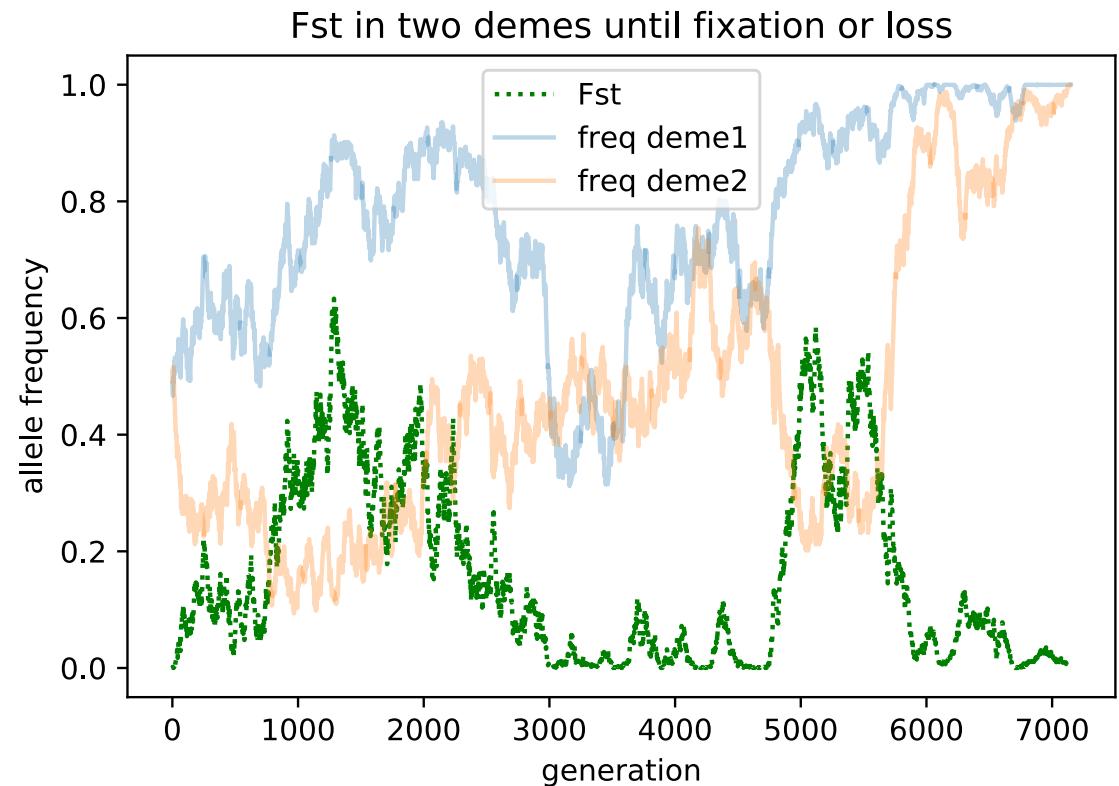
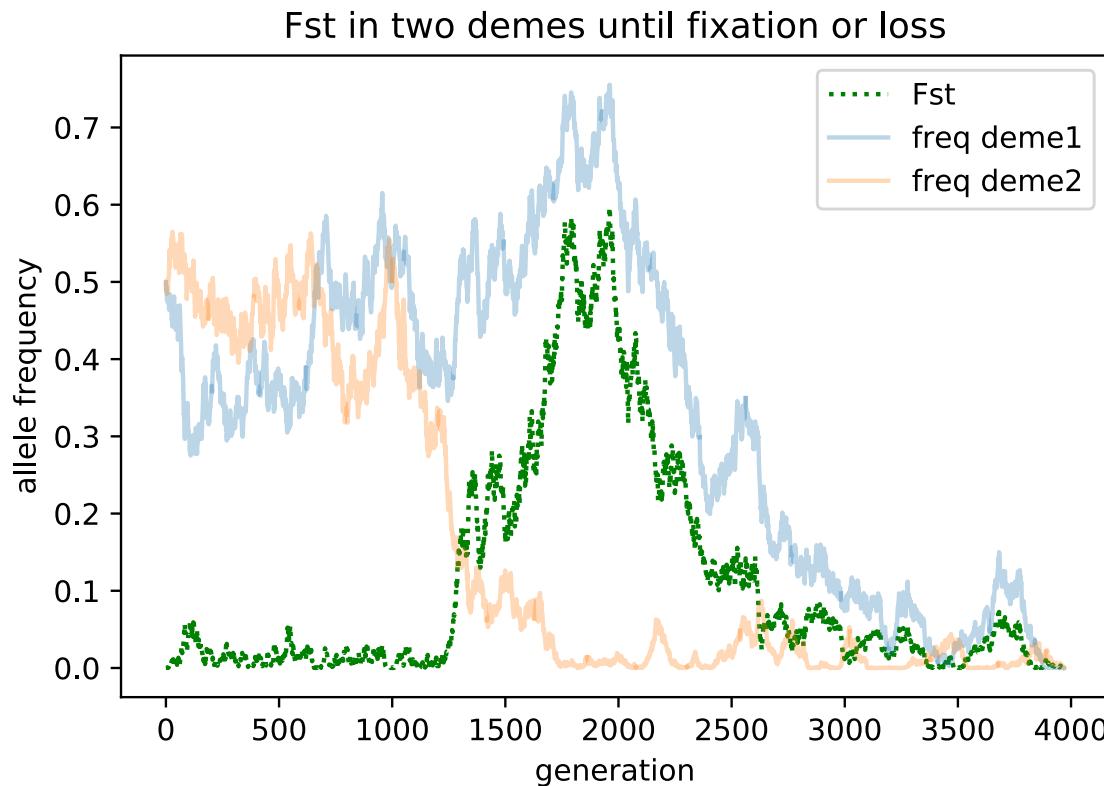
$N_1 = 3000; N_2 = 3000$

$m = 1$ individuals/gen

$p_{initial} = 0.5$



with any migration alleles will become either fixed or lost in both populations

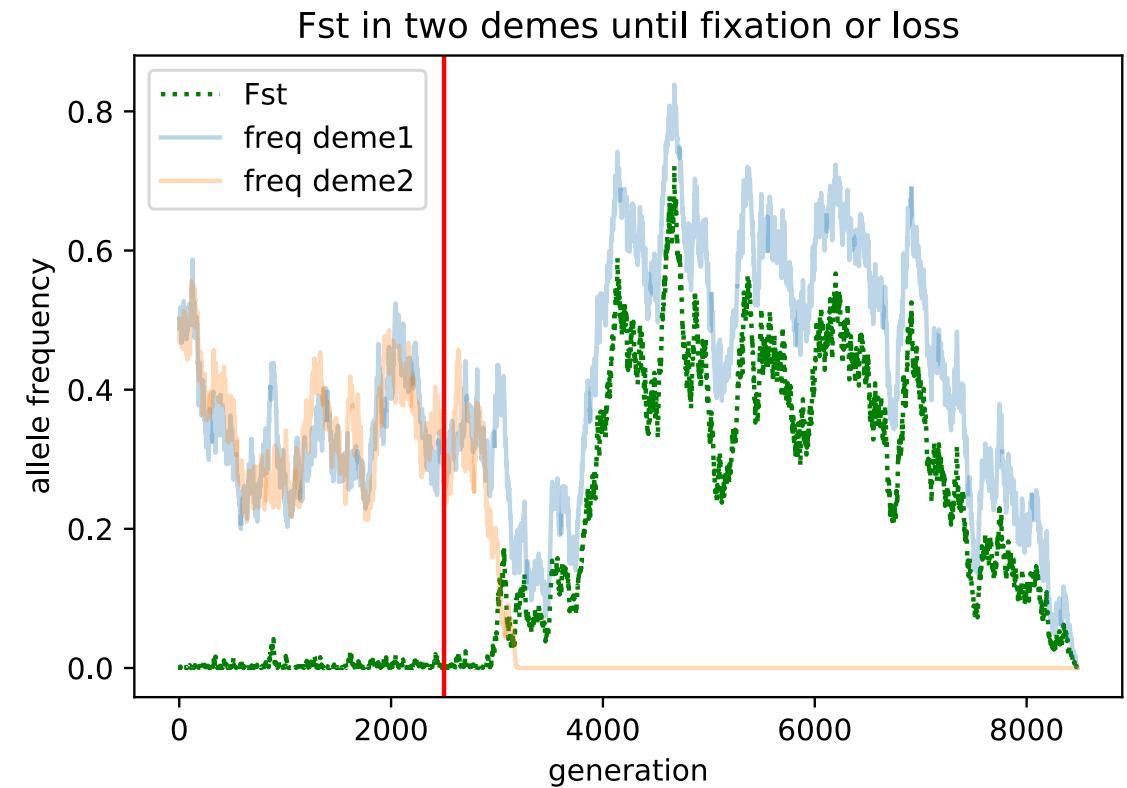
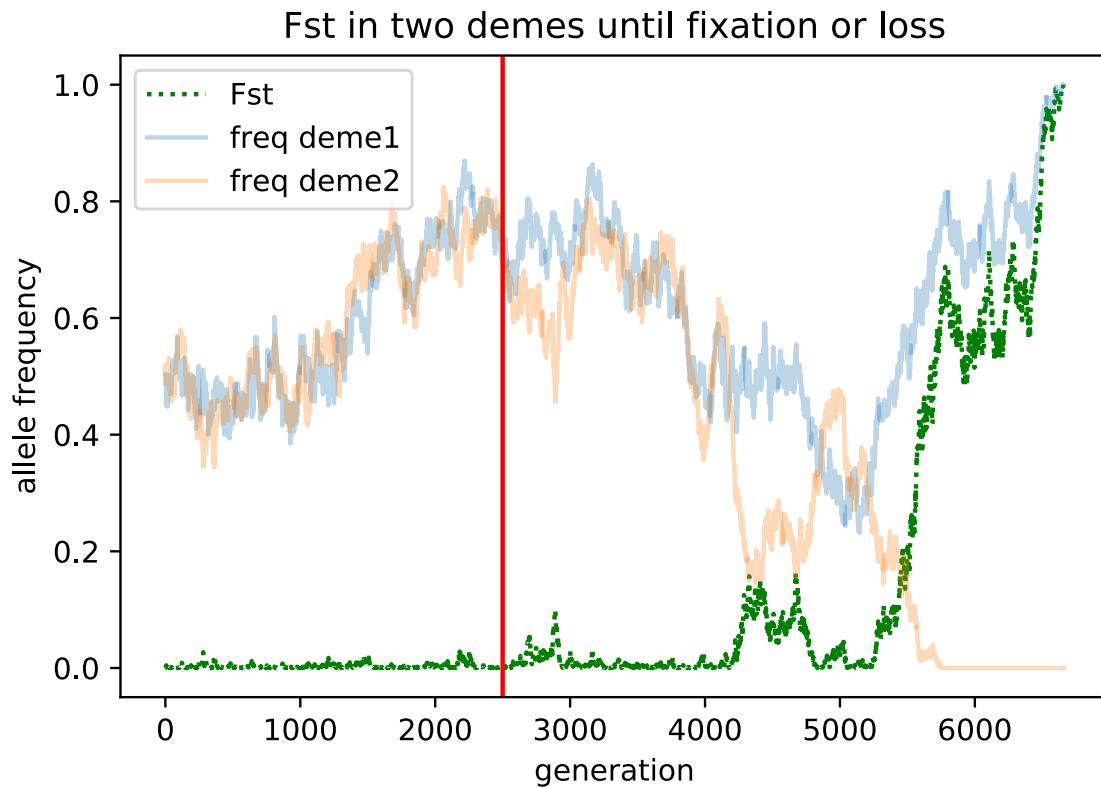


limiting migration allows allele trajectories to diverge

$$N_1 = 3000; N_2 = 3000$$

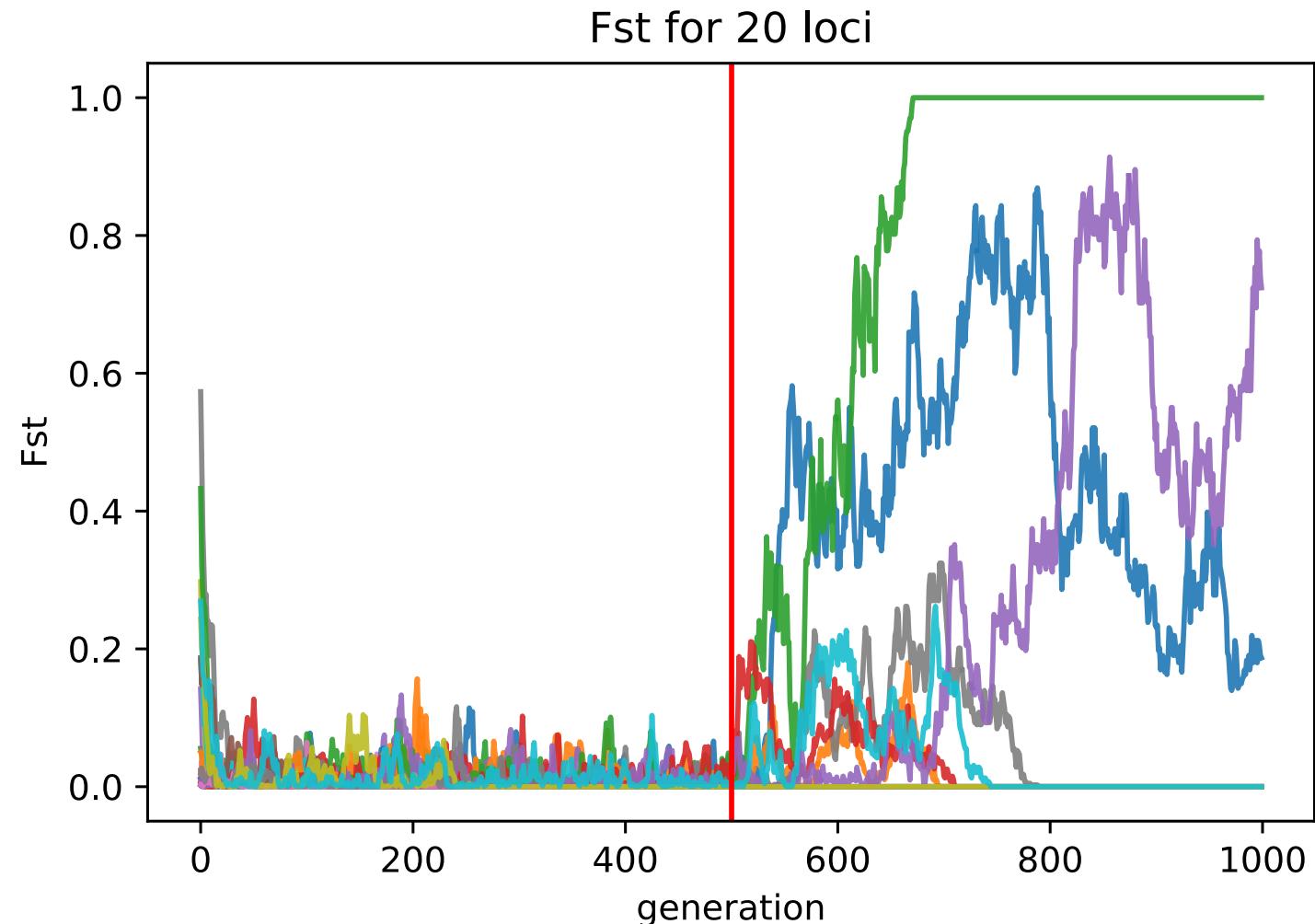
$m = 40$ individuals/gen, stops at generation 2500

$$p_{initial} = 0.5$$



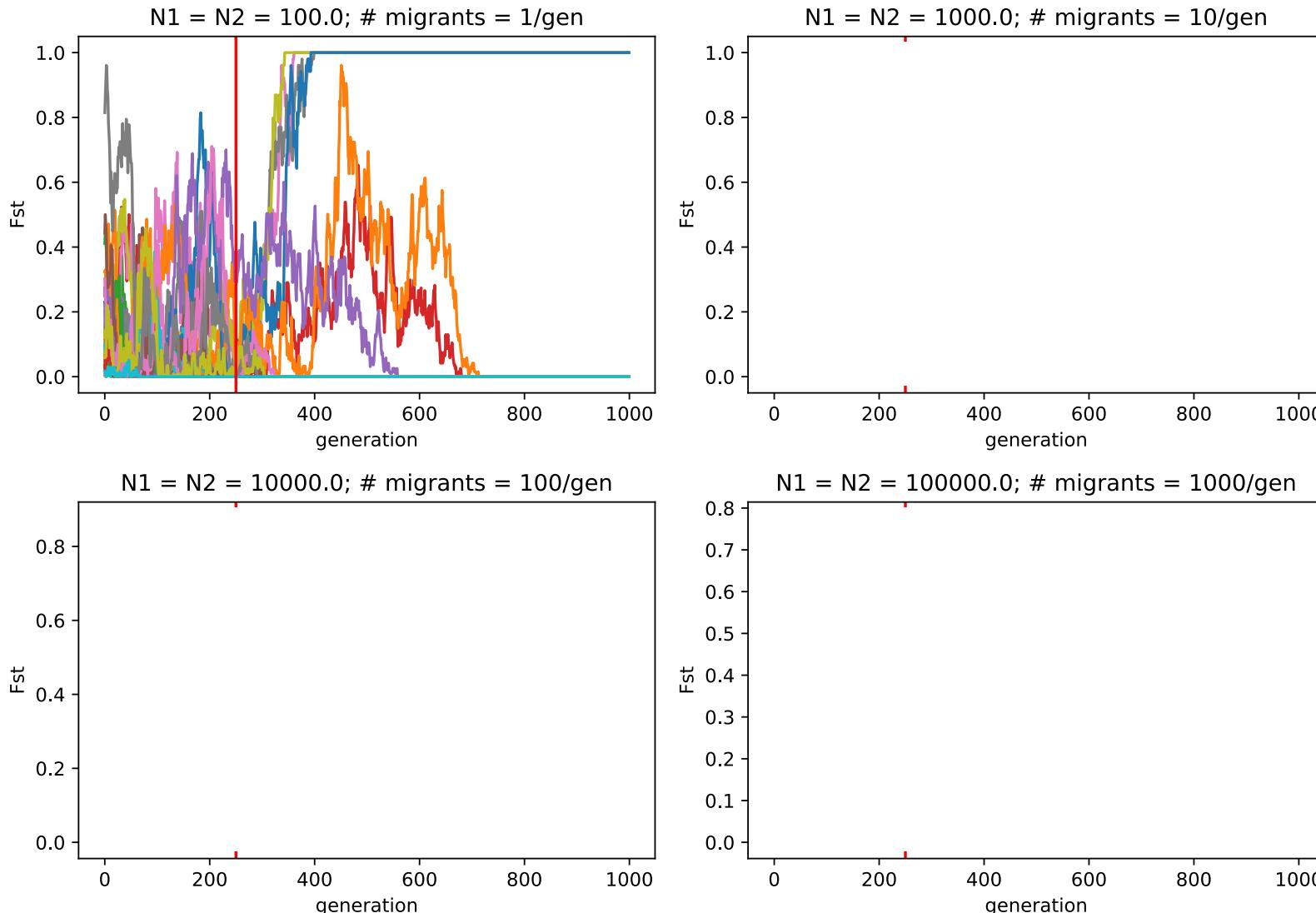
F_{ST} for multiple loci (a neutrally evolving gene)

a 20 bp locus in two demes ($N_1 = 200$; $N_2 = 200$), $p_{initial}$ = random
10 ind. migrants/gen, migration stops at gen = 500



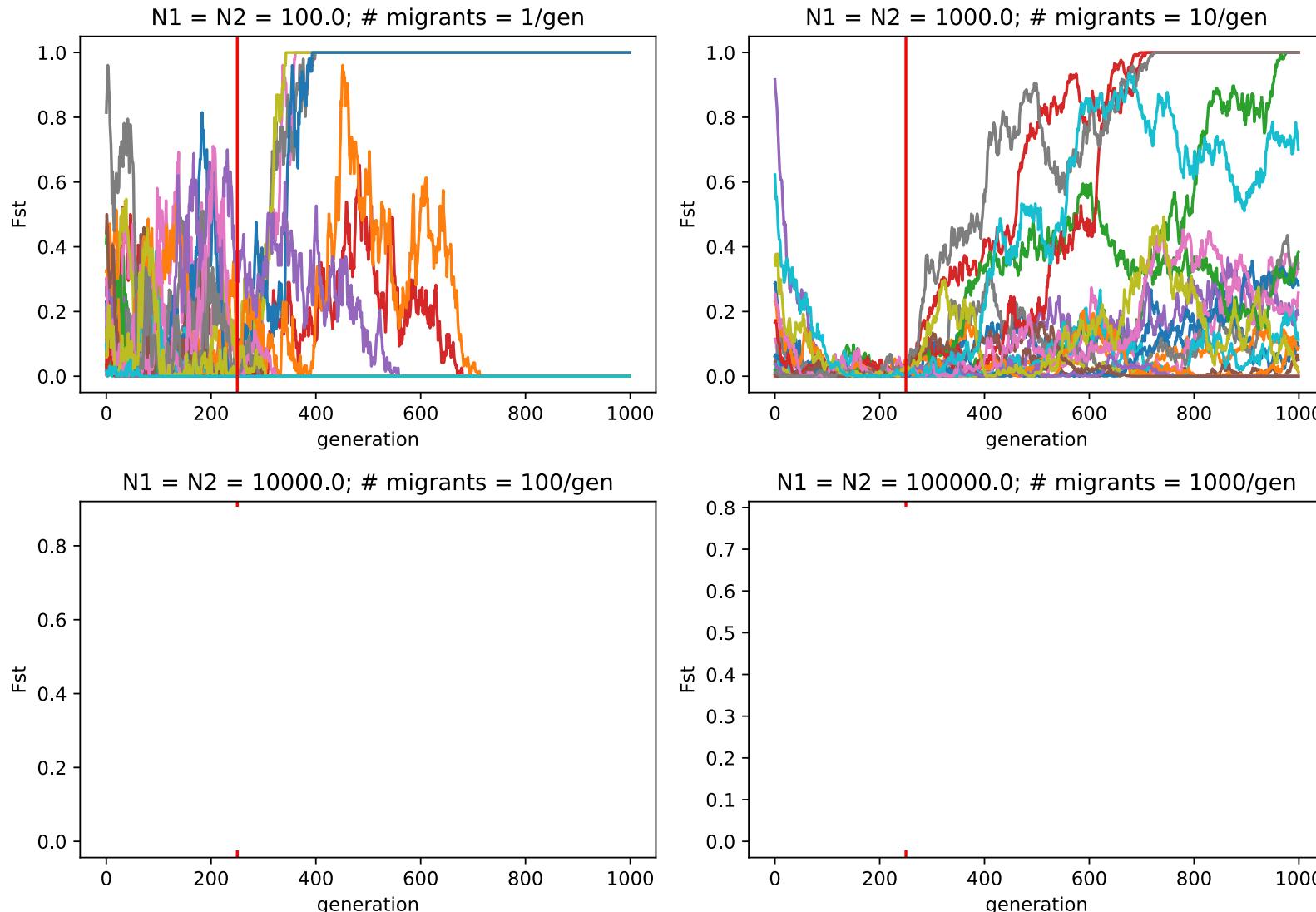
F_{ST} , drift, and migration

a 20 bp locus in two demes, $p_{initial}$ = random, 1% ind. migrants/gen, migration stops at gen = 250



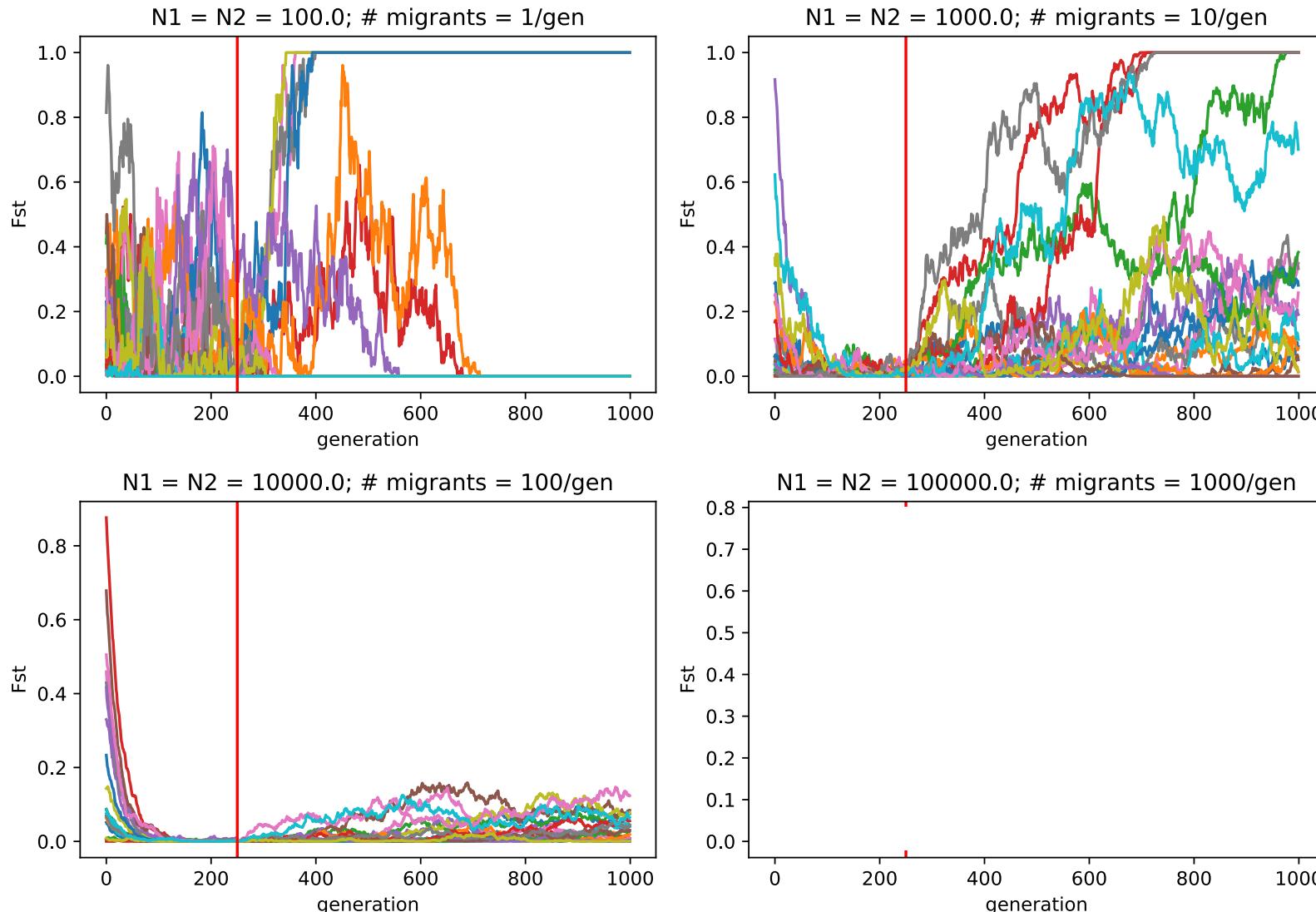
F_{ST} , drift, and migration

a 20 bp locus in two demes, $p_{initial}$ = random, 1% ind. migrants/gen, migration stops at gen = 250



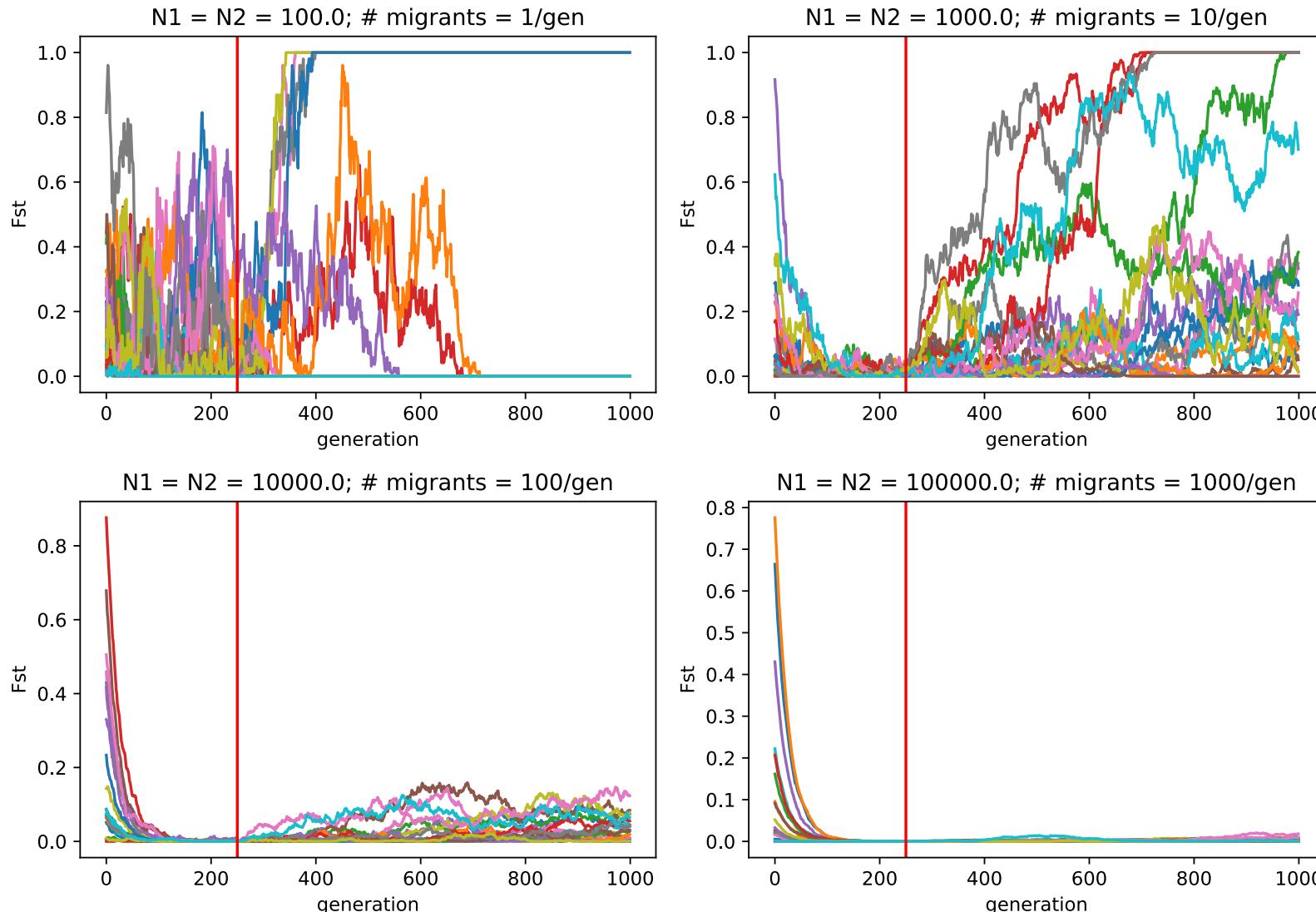
F_{ST} , drift, and migration

a 20 bp locus in two demes, $p_{initial}$ = random, 1% ind. migrants/gen, migration stops at gen = 250



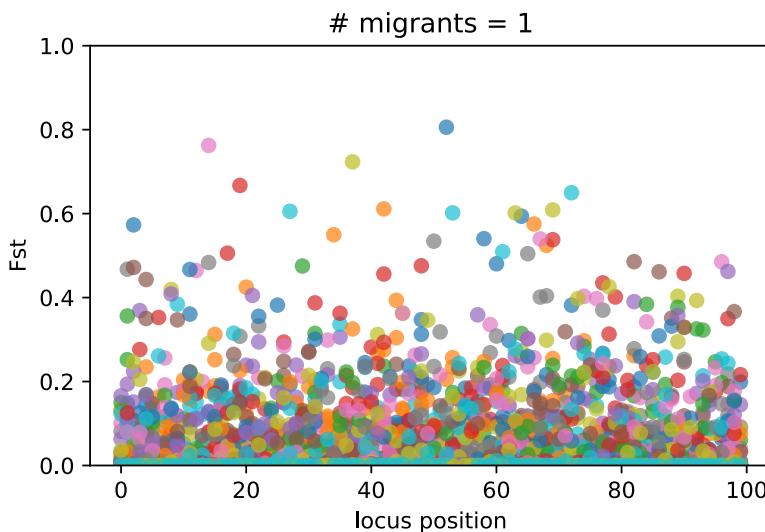
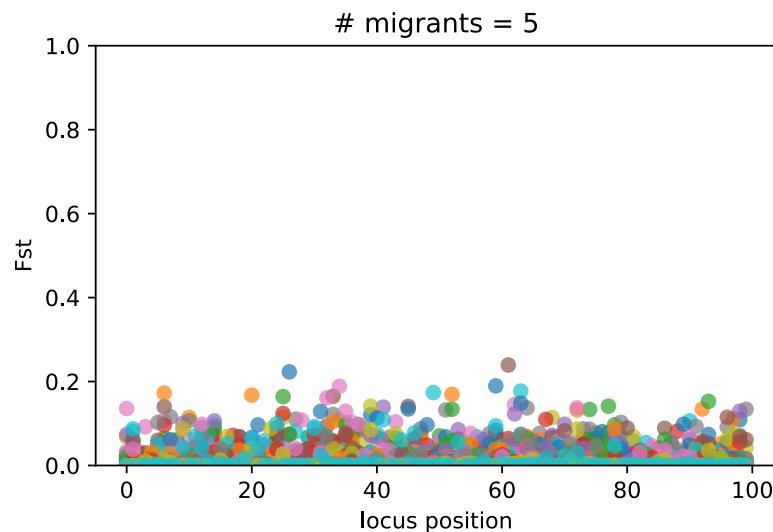
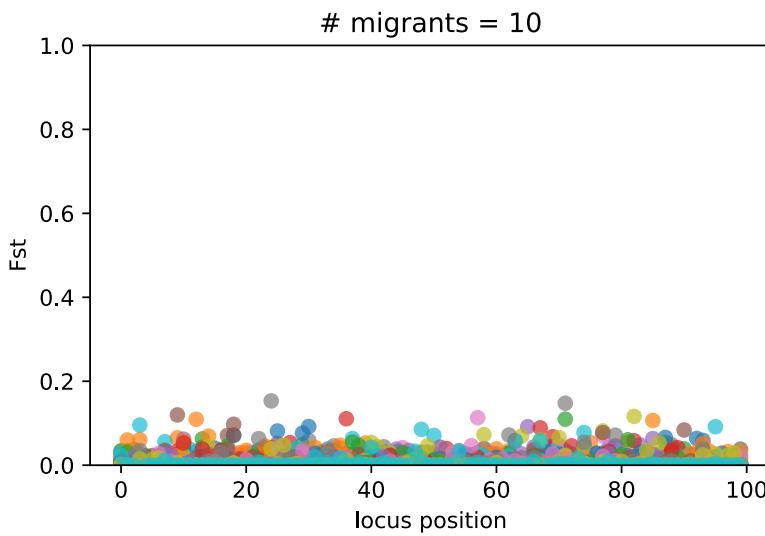
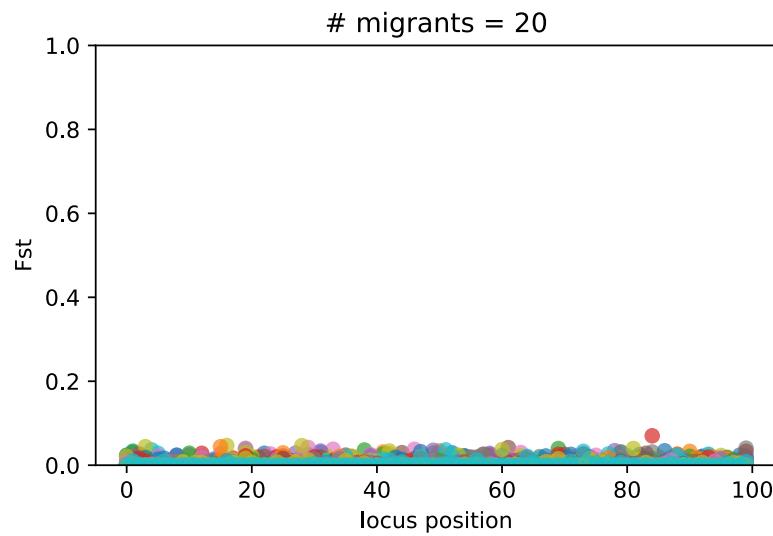
F_{ST} , drift, and migration

a 20 bp locus in two demes, $p_{initial}$ = random, 1% ind. migrants/gen, migration stops at gen = 250

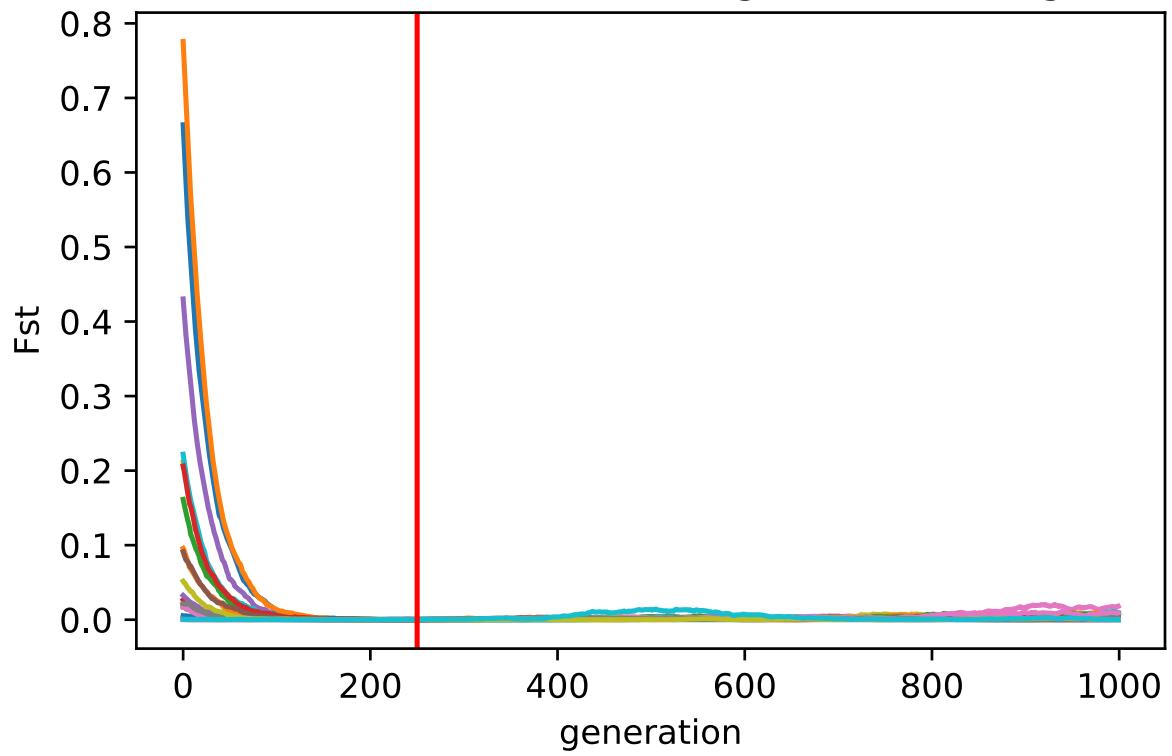


F_{ST} , drift, and migration (50 simulations)

a 100 bp locus in two demes at 1000th generation, $N_1 = N_2 = 1000$, $p_{initial} = 0.9$, constant migration

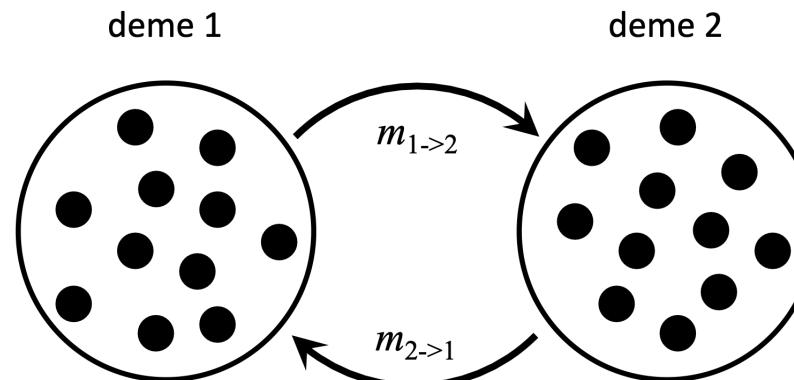
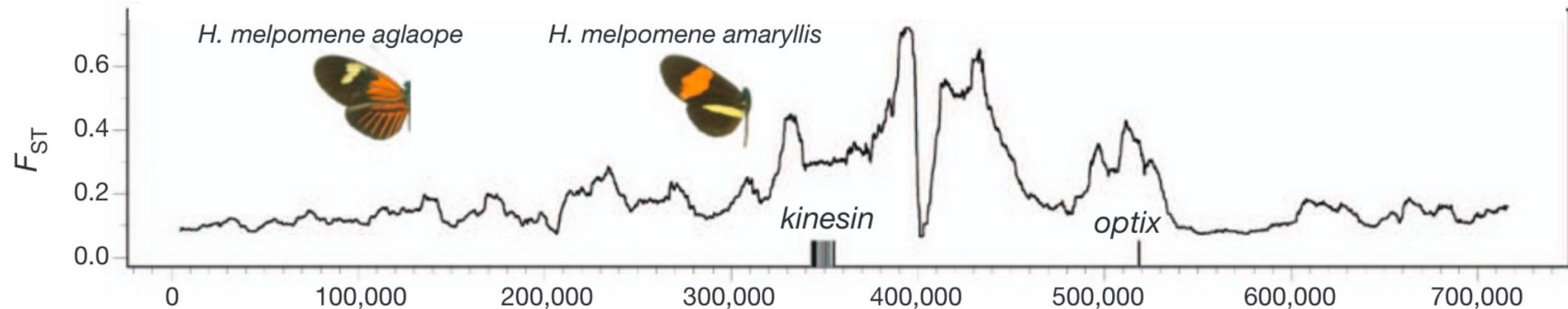


$N1 = N2 = 100000.0$; # migrants = 1000/gen

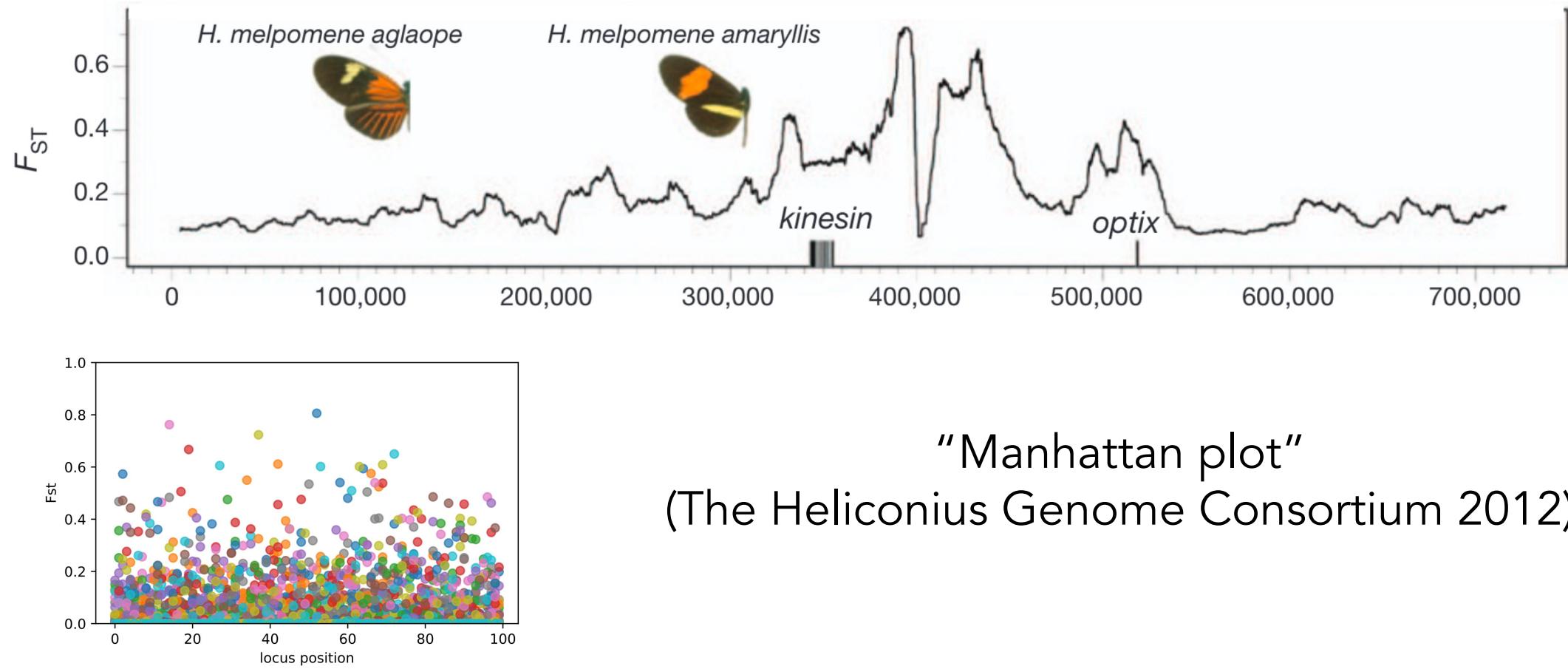


Even *tiny* levels of
gene flow reduce
("swamp") F_{ST}

Gene flow acts on the genome equally, selection does not

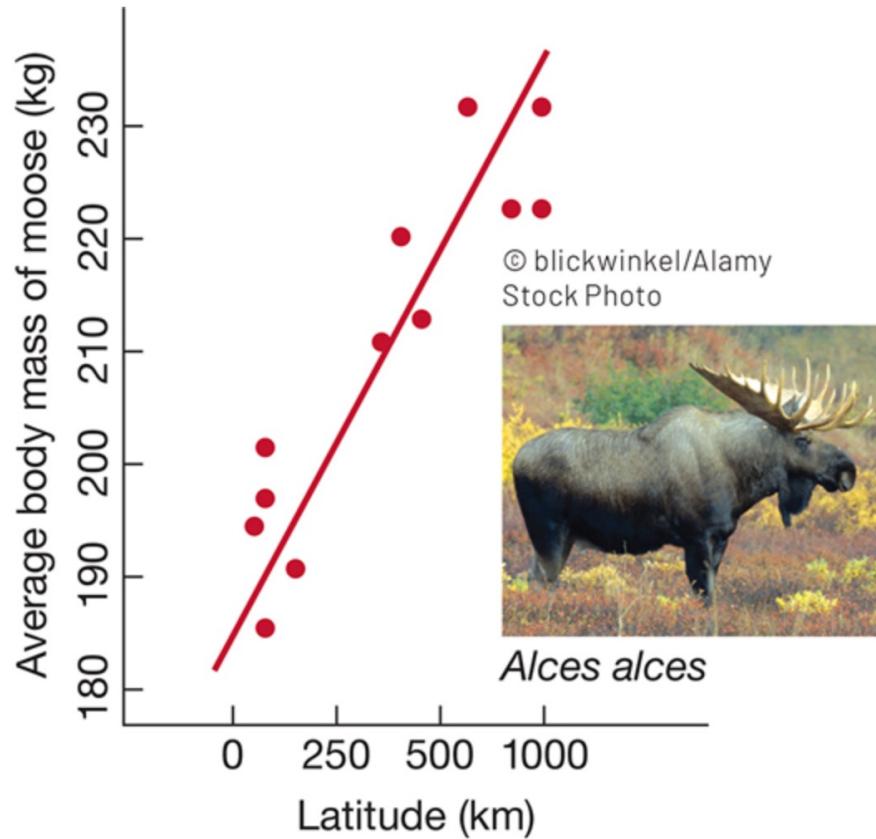


Gene flow acts on the genome equally, selection does not



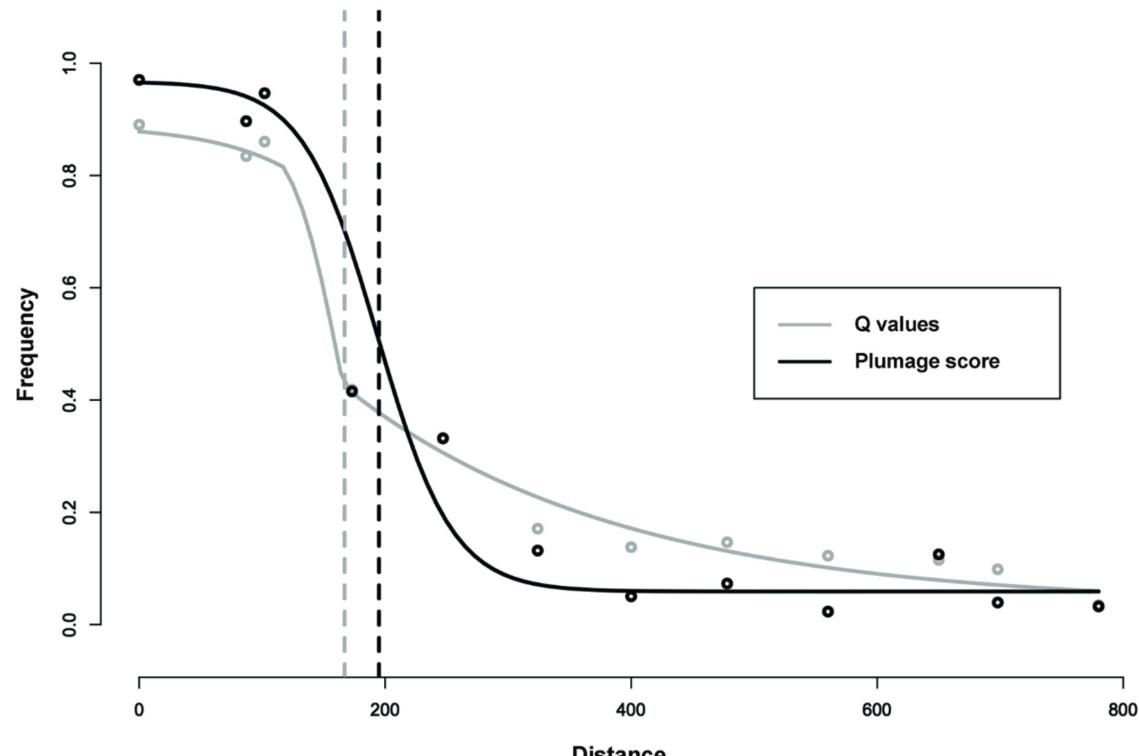
Classic clines—Bergmann's Rule

Also see Allen's Rule, Gloger's Rule, etc.



Allele clines

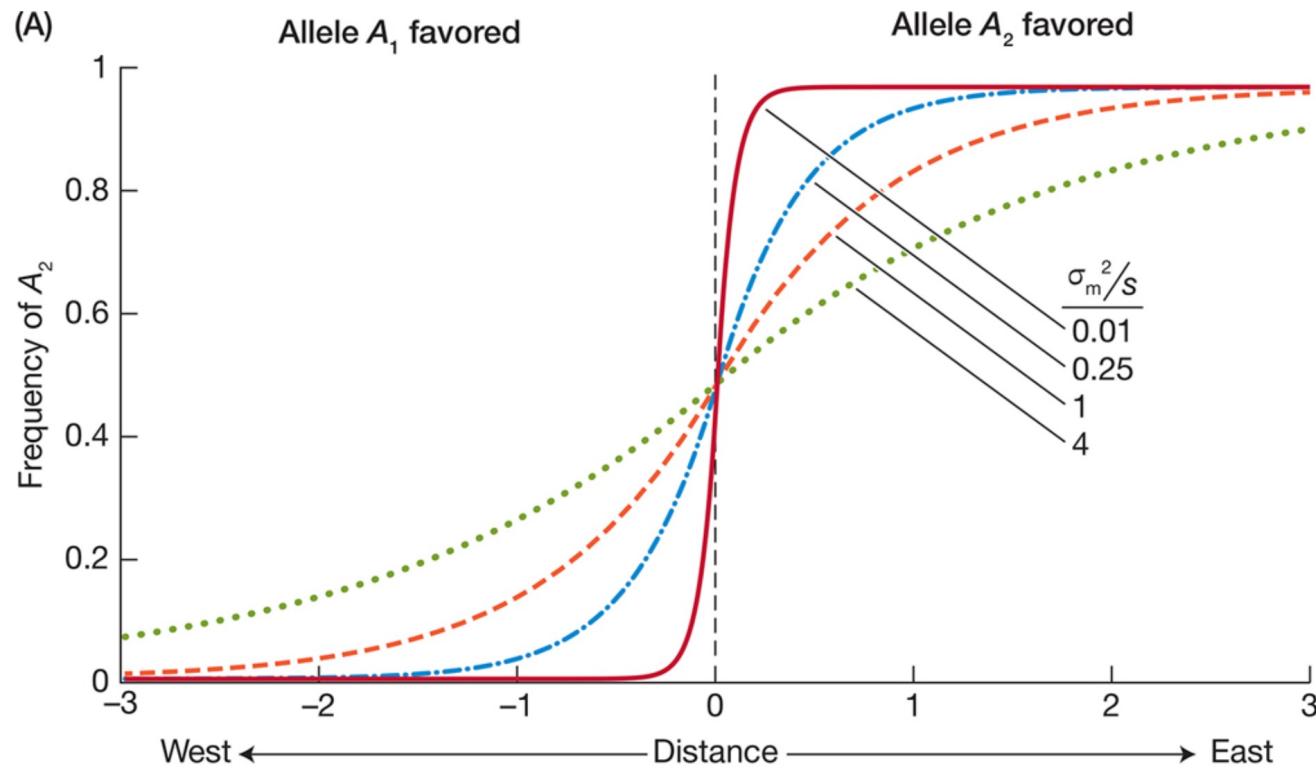
More possible evidence of adaptation



(Walsh et al. 2020)

Allele clines

More possible evidence of adaptation



Allele clines vary with...

- selection strength
- migration variance
- any variables that impact the above

Evolution of range expansion and dispersal

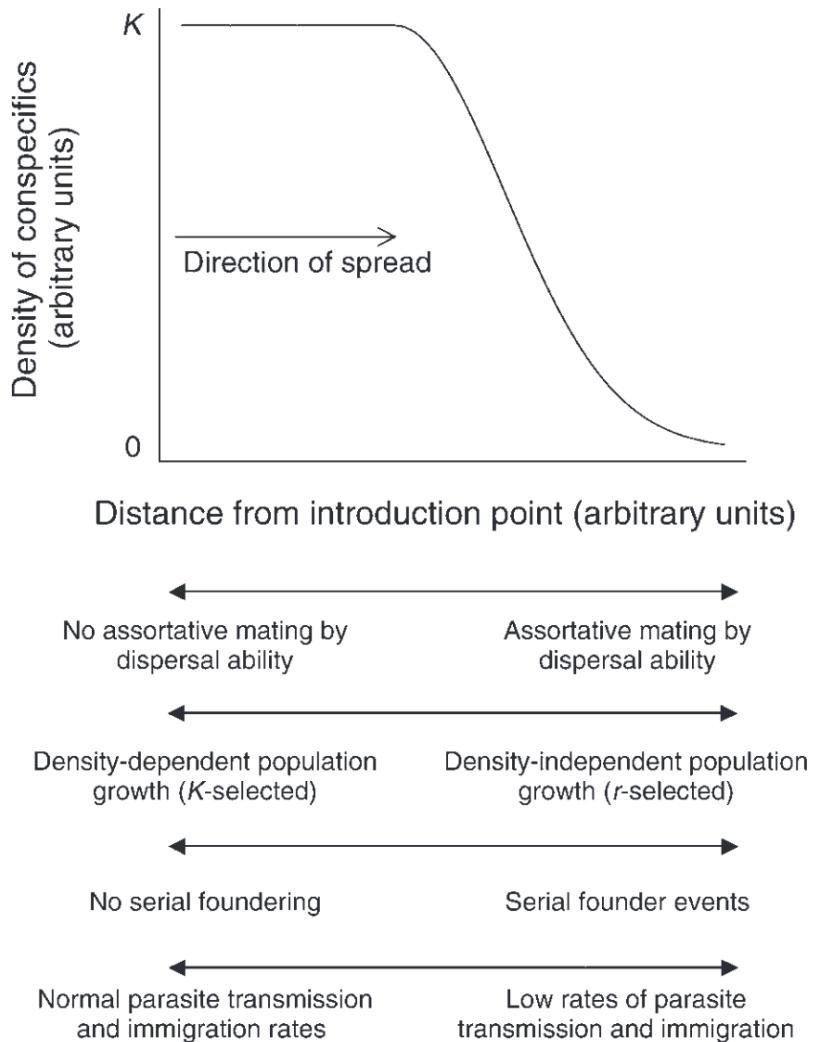
Why disperse?

Evolution of range expansion and dispersal

Why disperse?

- habitat volatility
 - competition
 - inbreeding

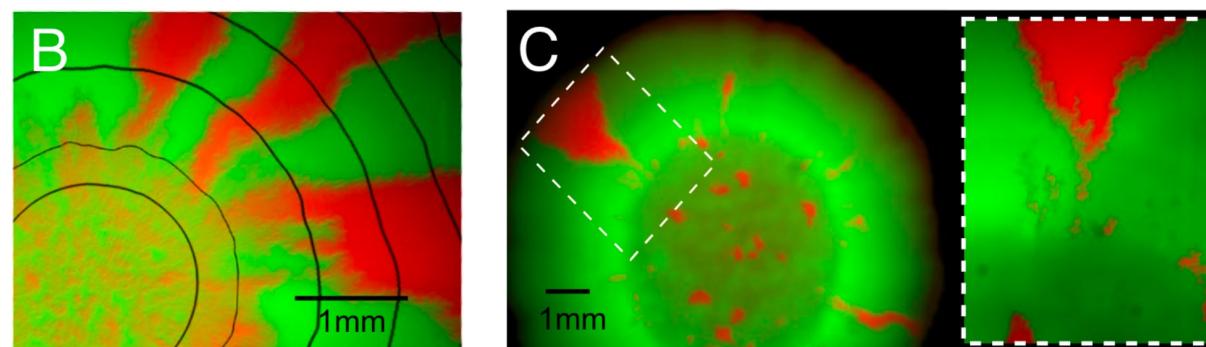
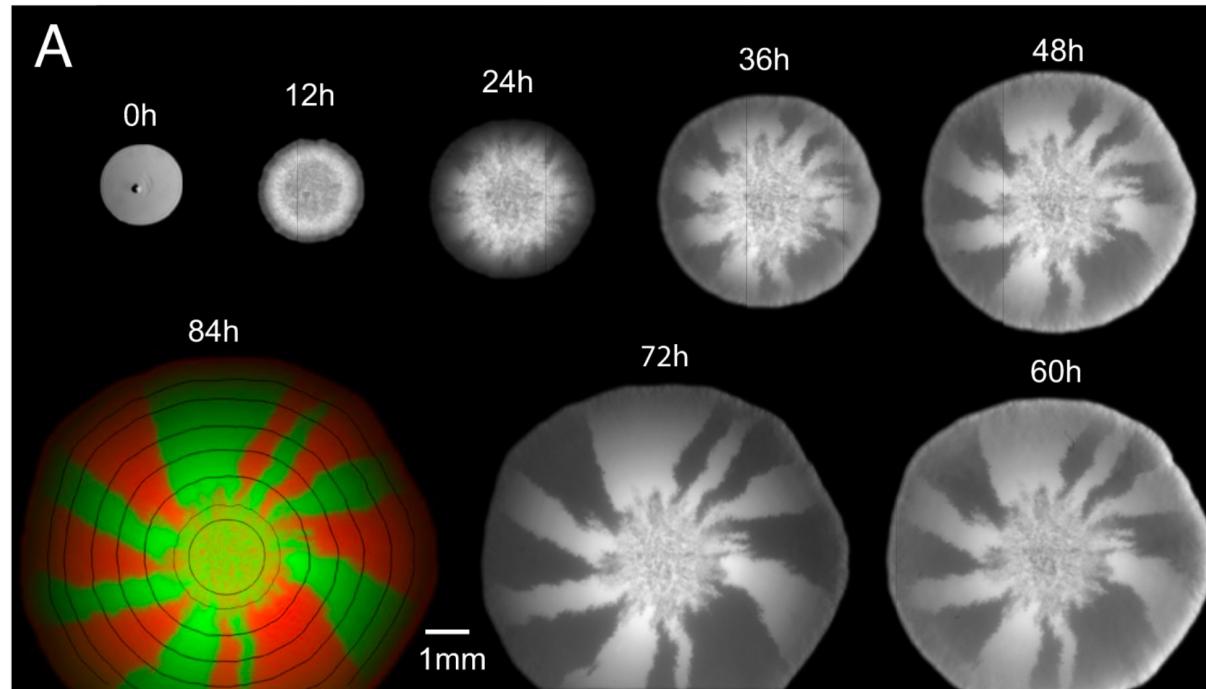
Dispersal may create runaway selection



(Phillips et al. 2010)

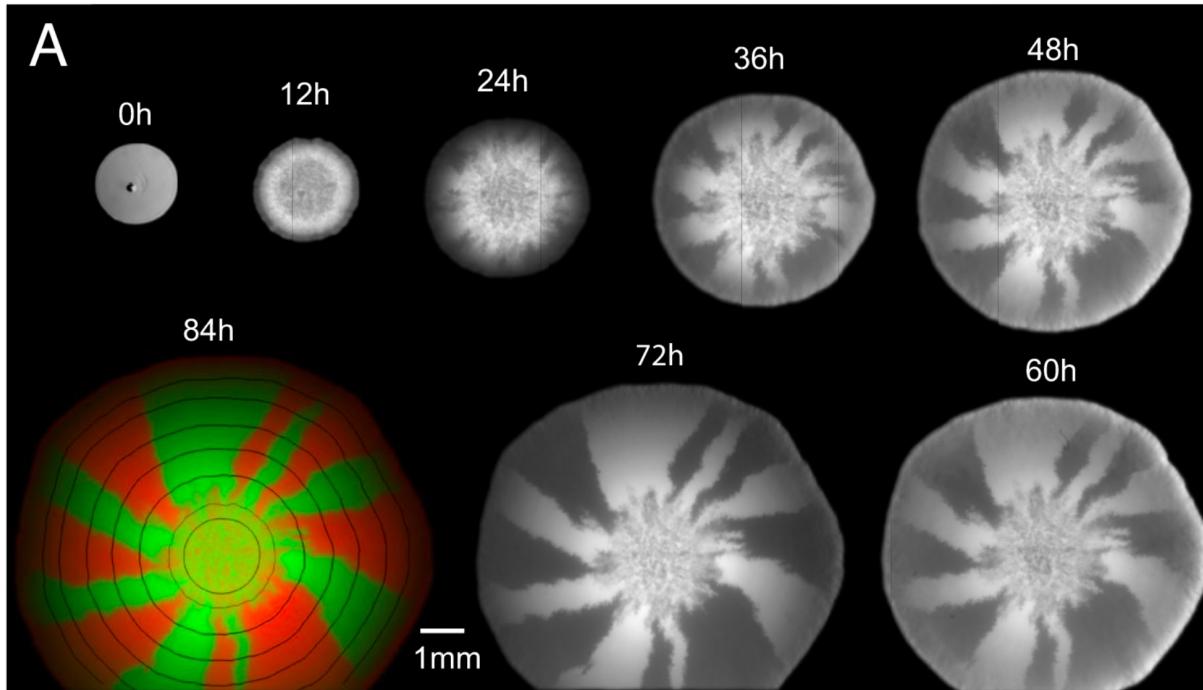
Dispersal without selection

(Hallatschek et al. 2007)

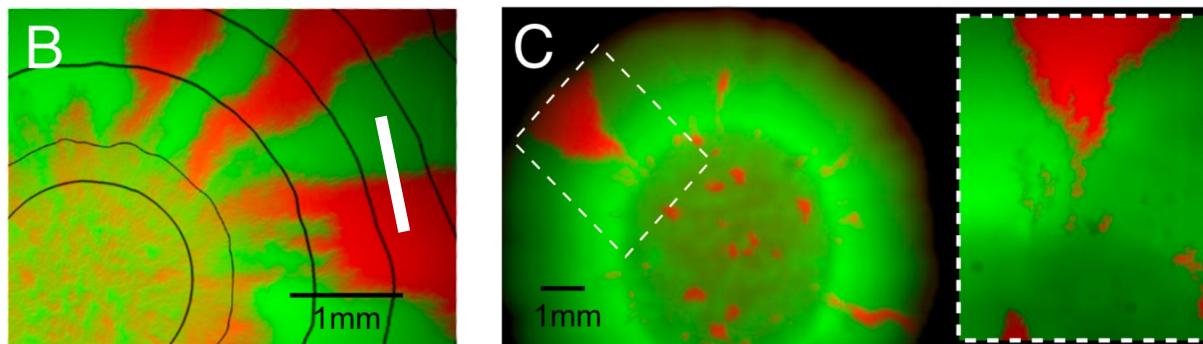


Dispersal without selection

(Hallatschek et al. 2007)

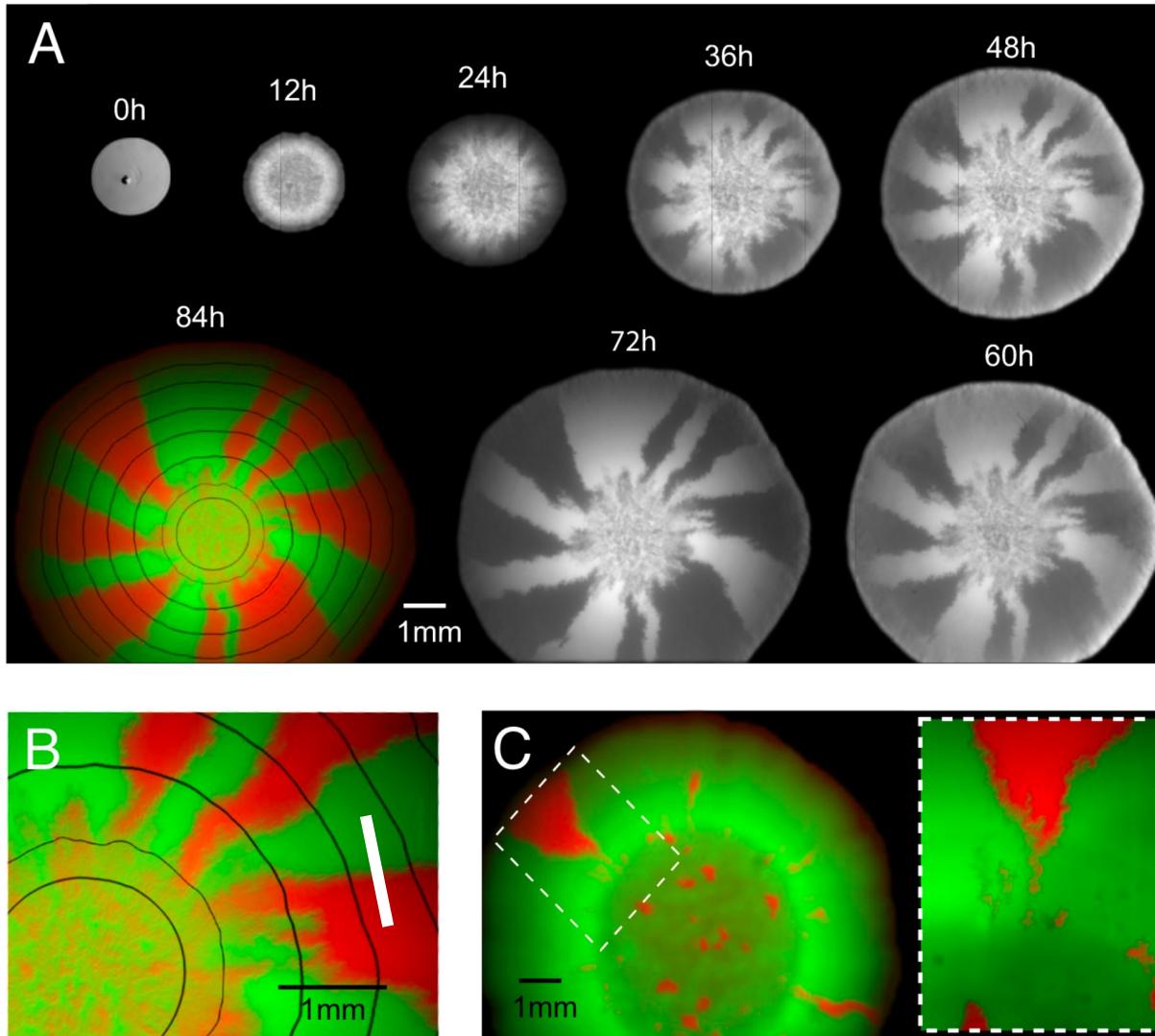


Alleles may “surf” the range frontier thanks to drift

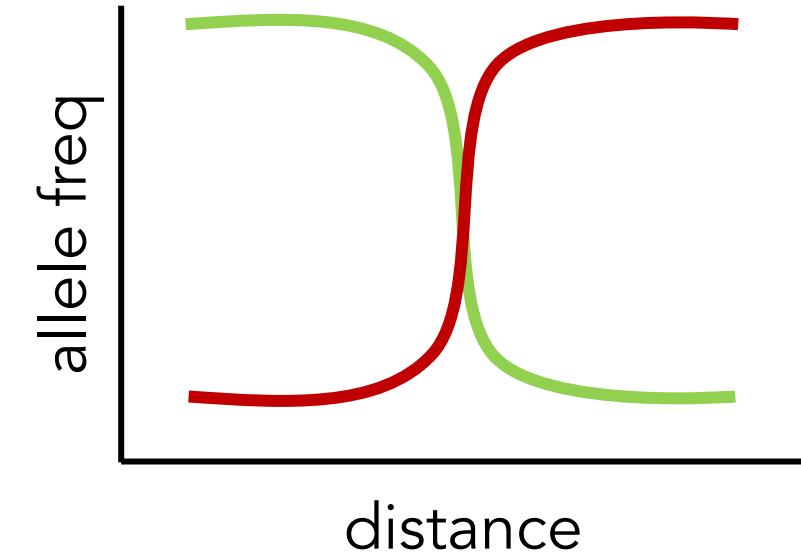


Dispersal without selection

(Hallatschek et al. 2007)



Alleles may “surf” the range frontier thanks to drift



surfing can look like selection

Consequences of range dispersal/range expansion

Selection is weaker in
small populations

Purifying selection
eliminates deleterious
alleles less efficiently

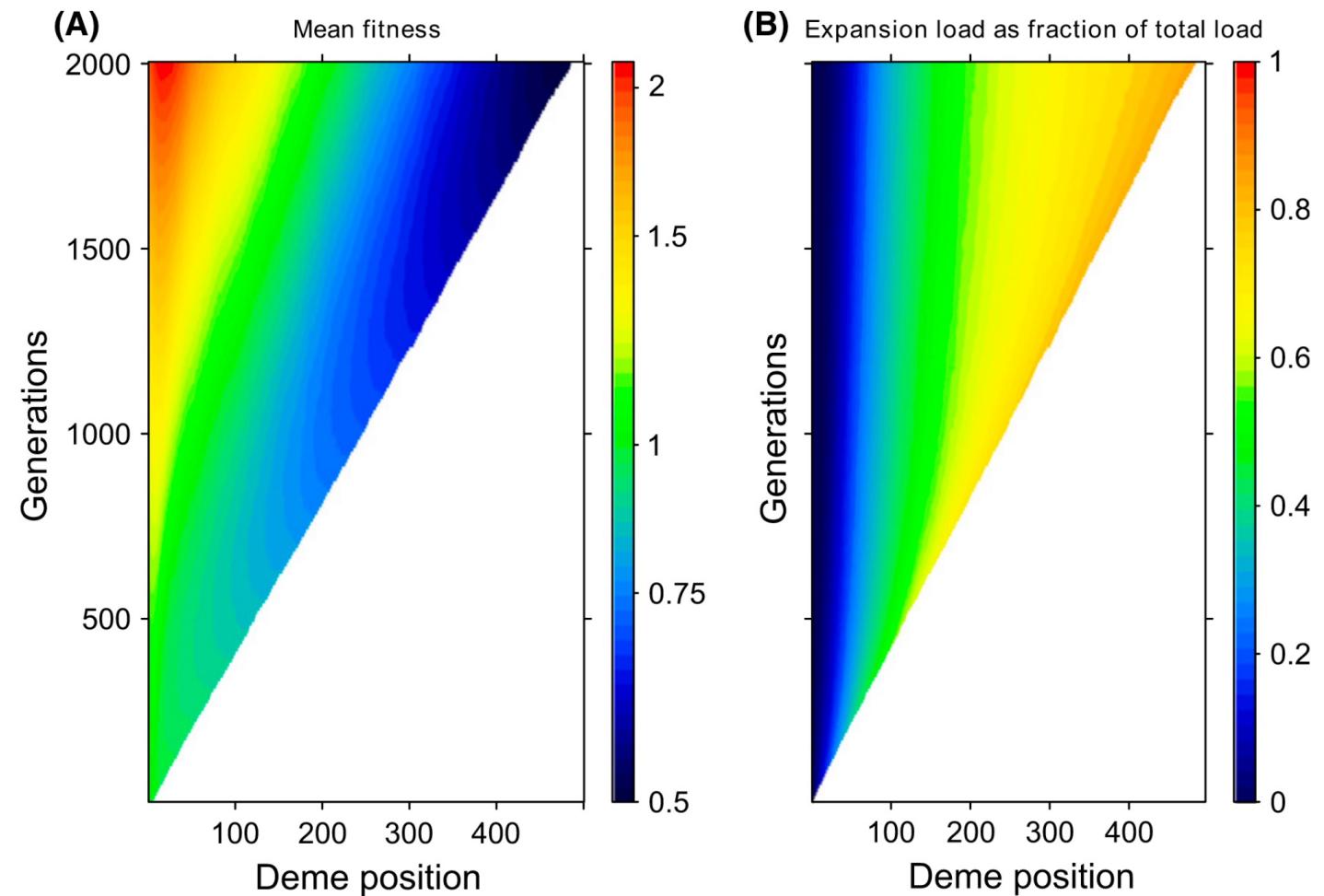
"Genetic load"

Consequences of range dispersal/range expansion

Selection is weaker in small populations

Purifying selection eliminates deleterious alleles less efficiently

"Genetic load"



(Peischl et al. 2013)

Evolution of range expansion and dispersal

Range determinants?

- genetic variation
- gene swamping
- expansion load
- ecological interactions
- climate change

Paper discussion



The Auk
Ornithological Advances

AmericanOrnithology.org

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DOI: 10.1093/auk/ukaa044

RESEARCH ARTICLE

Genomic and plumage variation across the controversial Baltimore and Bullock's oriole hybrid zone

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³ Cornell University Museum of Vertebrates, Cornell Laboratory of Ornithology, Cornell University, Ithaca, New York, USA

*These authors have contributed equally to the manuscript and are joint first authors.

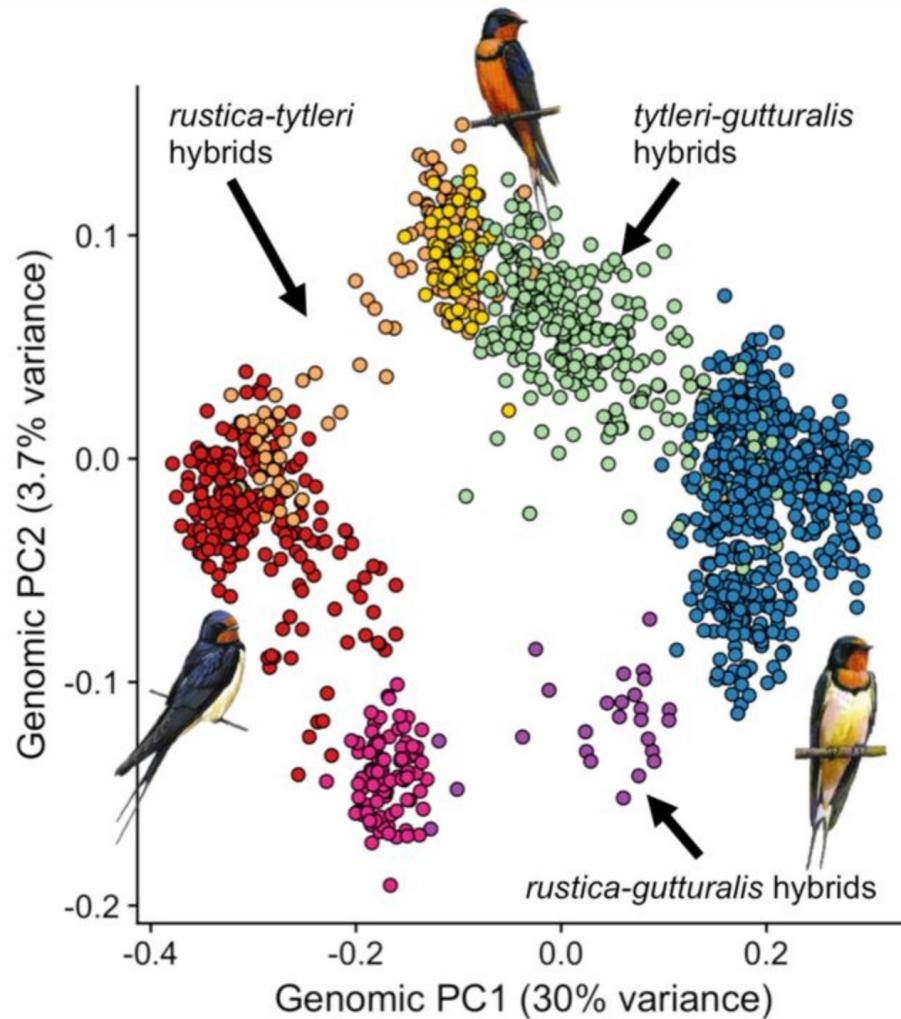
#Corresponding author:jennifer.walsh.emond@gmail.com

Submission Date: January 25, 2020; Editorial Acceptance Date: June 5, 2020; Published: August 1, 2020

Data visualization of population structure—PCA

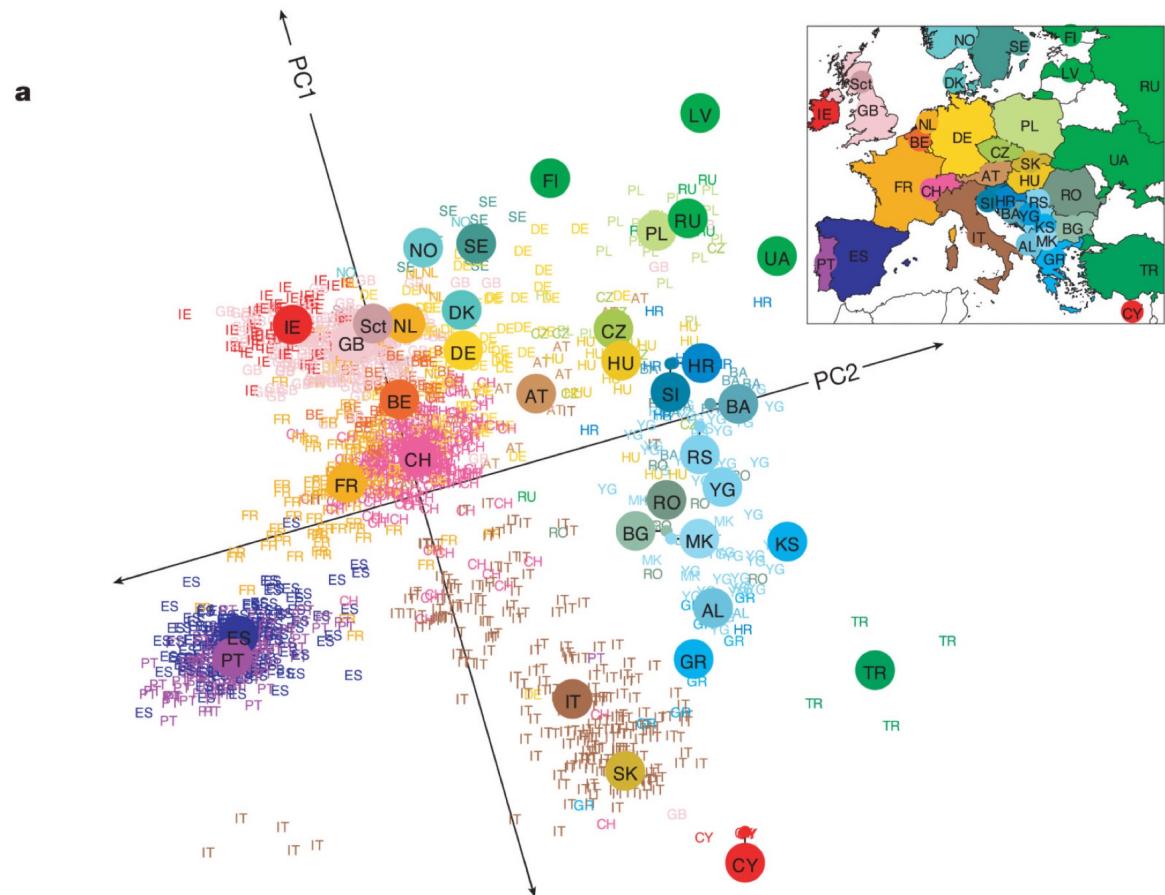
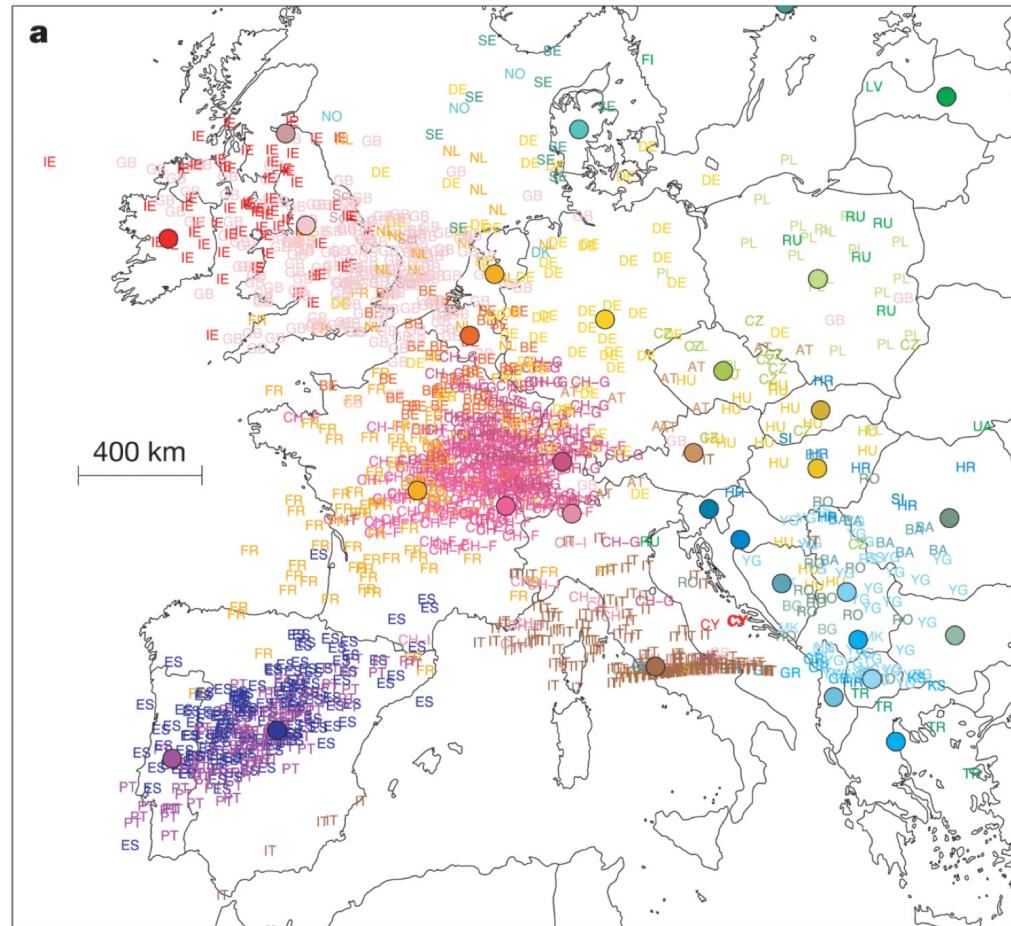
Popular “dimensionality reduction” technique outside of biology

Reduces dimensions of data to the two that capture the most variation (PC1 and PC2)



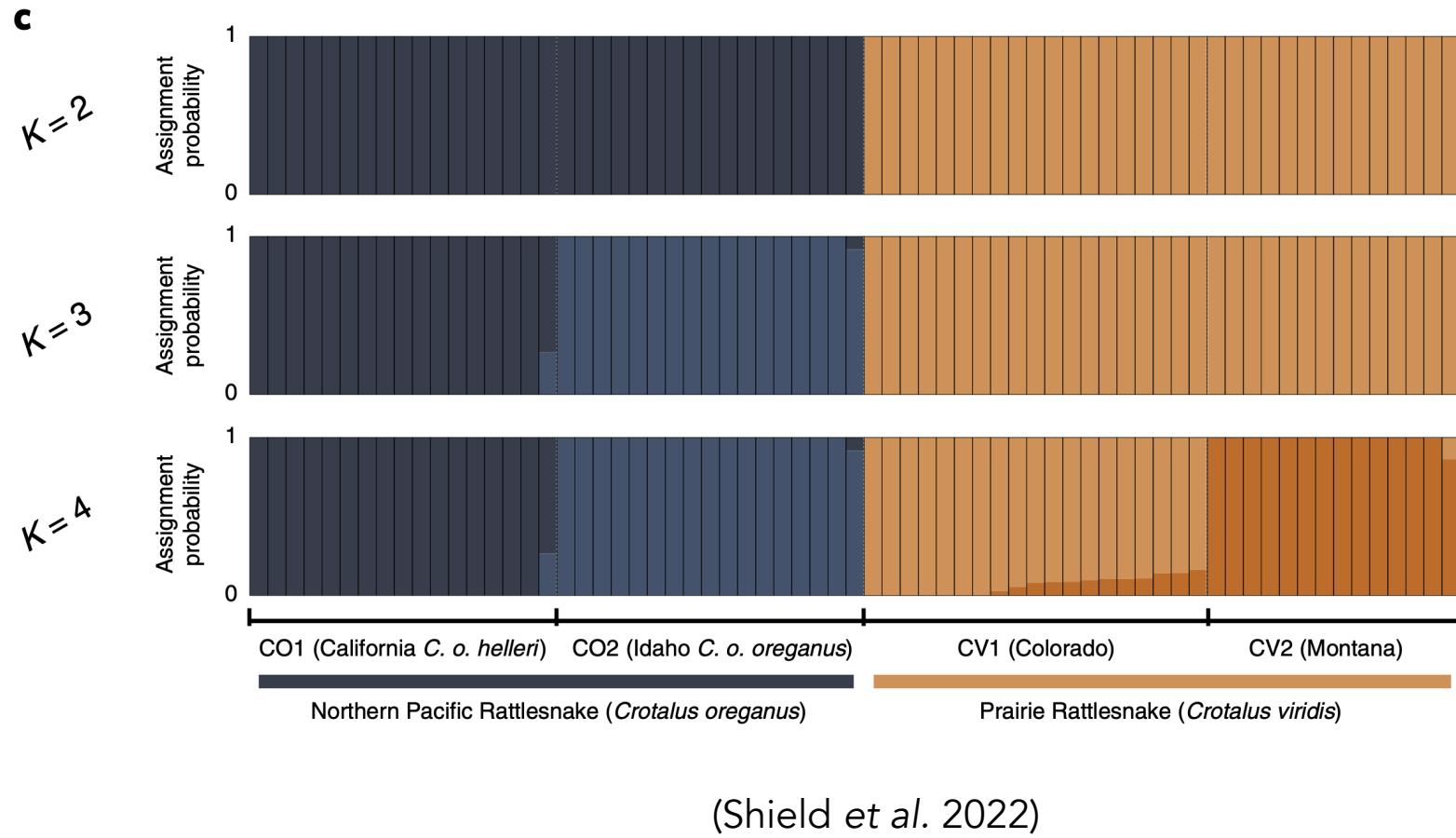
(Scordato et al. 2019)

Data visualization of population structure—PCA



(Novembre et al. 2008)

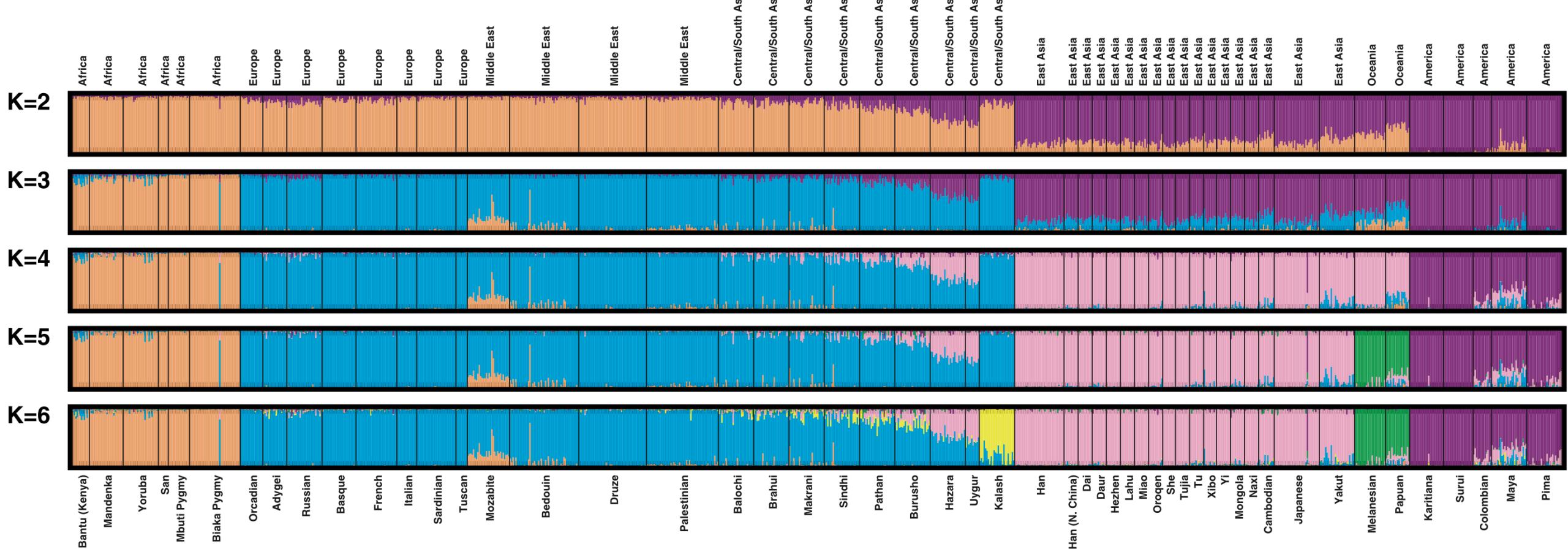
Data visualization of population structure—STRUCTURE



Clustering algorithm

Will bin individual ancestry according to K clusters across sample

Data visualization of population structure— STRUCTURE



(Rosenberg et al. 2002)

Quiz question 4

Question 4

-- / 1 pts

In Walsh *et al.* 2020, the authors use a hybrid index and interspecific heterozygosity to quantify admixture. What is the expected value for both in an F1 hybrid arising from two pure parental types. One pure Bullock's Oriole and one pure Baltimore Oriole.

Expected hybrid index =
Interspecific heterozygosity =

Quiz question 4

Question 4

-- / 1 pts

In Walsh *et al.* 2020, the authors use a hybrid index and interspecific heterozygosity to quantify admixture. What is the expected value for both in an F1 hybrid arising from two pure parental types. One pure Bullock's Oriole and one pure Baltimore Oriole.

Expected hybrid index = 50%

Interspecific heterozygosity =

Quiz question 4

Question 4

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/ 1 pts

In Walsh *et al.* 2020, the authors use a hybrid index and interspecific heterozygosity to quantify admixture. What is the expected value for both in an F1 hybrid arising from two pure parental types. One pure Bullock's Oriole and one pure Baltimore Oriole.

Expected hybrid index = 50%

Interspecific heterozygosity = 100%

Paper discussion



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RESEARCH ARTICLE

Genomic and plumage variation across the controversial Baltimore and Bullock's oriole hybrid zone

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