

Estimating Population Size

Census population size (N_c):

- Sufficient power in most populations with ~12 microsatellite DNA loci or ~250 SNPs
- Paper by Per Palsboll in 1999 considered the potential (*Biol. J. Linn. Soc.*, 68: 3-22)

TABLE 1. Comparison of genetic to conventional tagging methods

Tagging technique	Characteristics							
	Universal	Remote marking	Non-invasive	Assessment of random match	Permanency	Automated matching	Error finding	Additional information ^b
Genetic	+ / -	+ / -	+ / -	+	+	+	+	+
Natural markings	-	+	+	+ / - ^a	+ / -	+ / -	+	+
Human tags	-	+ / -	-	+ / - ^a	+ / -	+	+	-

Notes: + = possible, - = not possible, + / - = possible in some instances, but not all. ^aIf double marked.

^bAdditional information in the tag itself, i.e. no additional measurements when tagging.

Effective population size (N_e):

- The size of an idealised population that shows the same rate of loss of diversity as the real population
- The evolutionarily significant number that reflects the rate at which diversity will be lost – affected by number of effective breeders, demographic history, etc.
- Meta-analysis suggested a ratio of $N_e/N_c = \sim 0.11$, though variation was great
- Some of the lowest values proposed for species that have ‘sweepstakes breeding’ – high variance between the size of families – e.g. some marine fish
- Bottleneck can greatly reduce N_e/N_c – e.g. northern elephant seal: $N_e = 100$, $N_c = 220,000$ ($N_e/N_c = 0.00045$) [N_e was $\sim 30,000$ during Eemian]

Estimating N_e based on Linkage Disequilibrium (LD):

- Estimate is for contemporary or recent N_e
- Assumption – loci included in the analysis are not physically linked in the genome
- Relevant measure of LD is associated with genetic drift (Hill 1981)
- Smaller N_e means more genetic drift, which by chance generates associations between alleles at different loci. This **LD happens at a rate that is inversely proportional to N_e** (hence it's use for estimating N_e)
- Large numbers of loci means precision, but also potential bias through physical linkage – this can be corrected (Waples et al. 2016)
- Studies show that the estimate is essentially independent of selection (Novo et al. 2021)

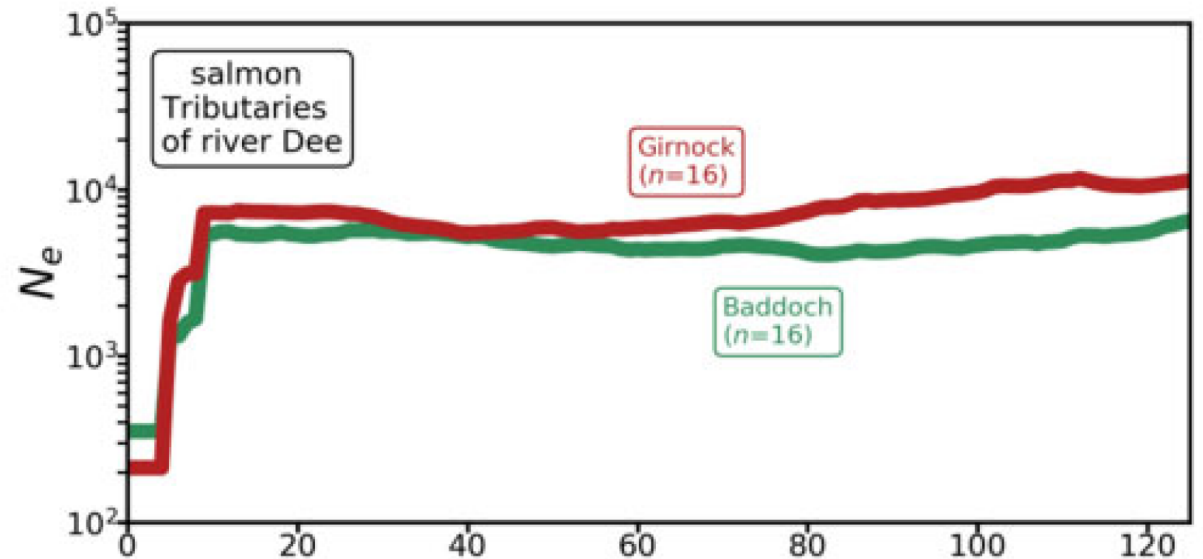
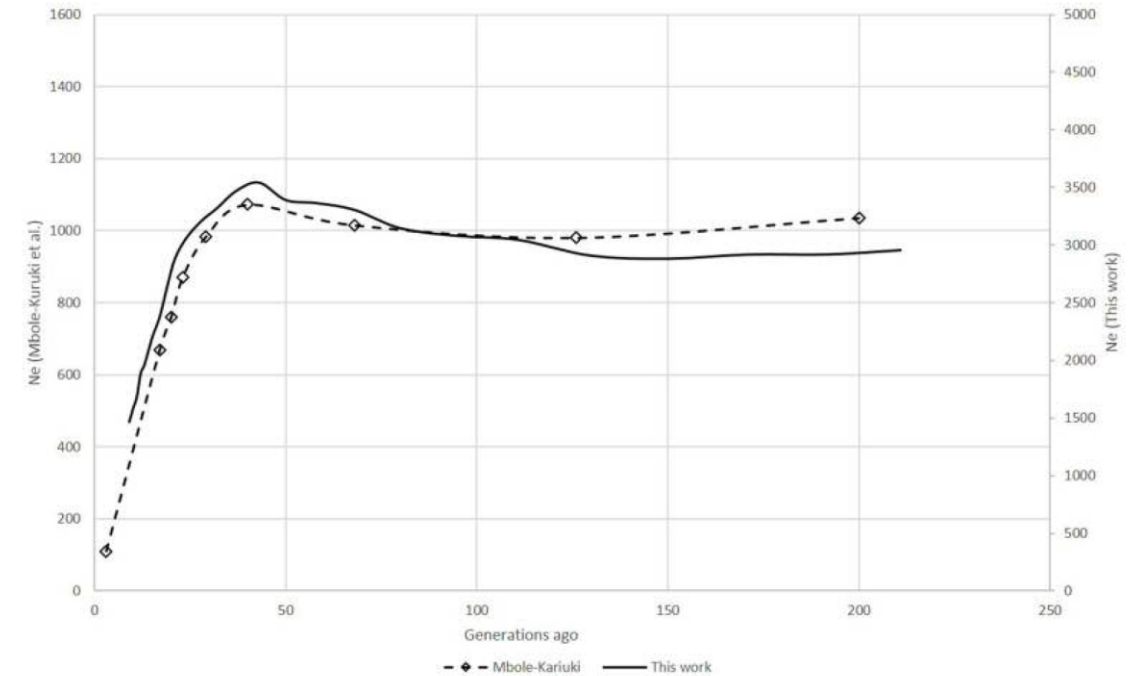
Couple of useful methods using SNP data:

Both use information on the rate and extent of LD to estimate N_t (N_e t generations in the past), with resolution back ~100-200 generations.

SNeP – Barbato et al. (2015) SNeP: a tool to estimate trends in recent effective population size trajectories using genome-wide SNP data. *Front. Genet.* 6:109.

GONE – Santiago et al. (2020) Recent Demographic History Inferred by High-Resolution Analysis of Linkage Disequilibrium. *Mol. Biol. Evol.* 37(12):3642–3653

Note – coalescent methods, such as STAIRWAY plots (based on AFS; Liu & Fu 2015) are also possible, but the timeframe giving good resolution is older (10K-200K years)



Genetic Management Units

Management Unit, ASCOBANS (2009):

“A group of individuals for which there are different lines of complementary evidence suggesting reduced exchange (migration / dispersal) rates over an extended period (low tens of years)”

Early definition based on genetics (Moritz 1994):

“MUs are therefore recognized as populations with significant divergence of allele frequencies at nuclear or mitochondrial loci, regardless of the phylogenetic distinctiveness of the alleles.”

(Very) brief history of defining conservation units using genetics:

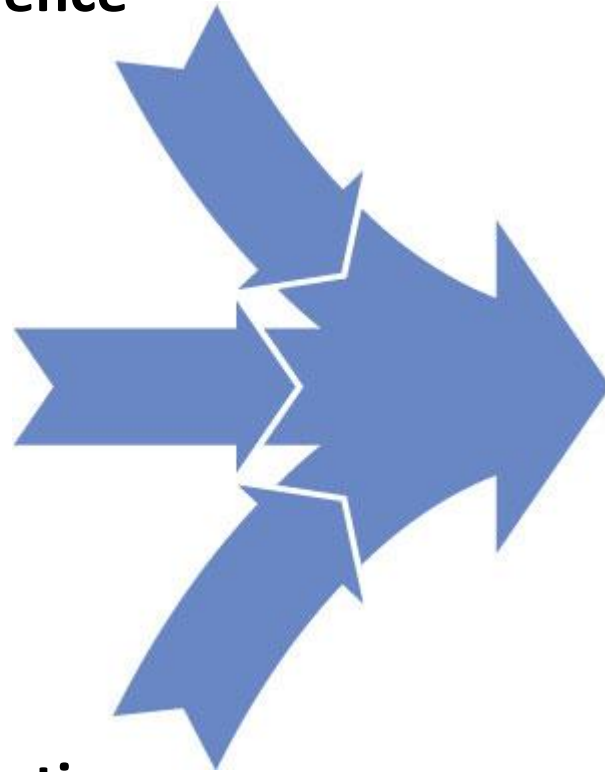
- Evolutionarily significant unit (**ESU**) defined at a meeting of the American Association of Zoological Parks and Aquariums while discussing the 'sub-species problem'. Based on concordant evidence from e.g. morphology and genetics (Ryder 1986).
- Tied to ESA 'distinct population segments' in 1991, proposing that an ESU should 1) be substantially reproductively isolated from other conspecific population units, and 2) represent an important component in the evolutionary legacy of the species. (Waples 1991).
- Focus on isolation and propose binary tools for deciding on conservation units, either ESU or **MU** (Moritz 1994)
- Emphasis on importance of both isolation and adaptation, and institution of a method based on ecological and genetic 'exchangeability' that allowed for characterisation of small and large difference (Crandall et al 2000).

Consensus:

Molecular genetic evidence

Whole species context

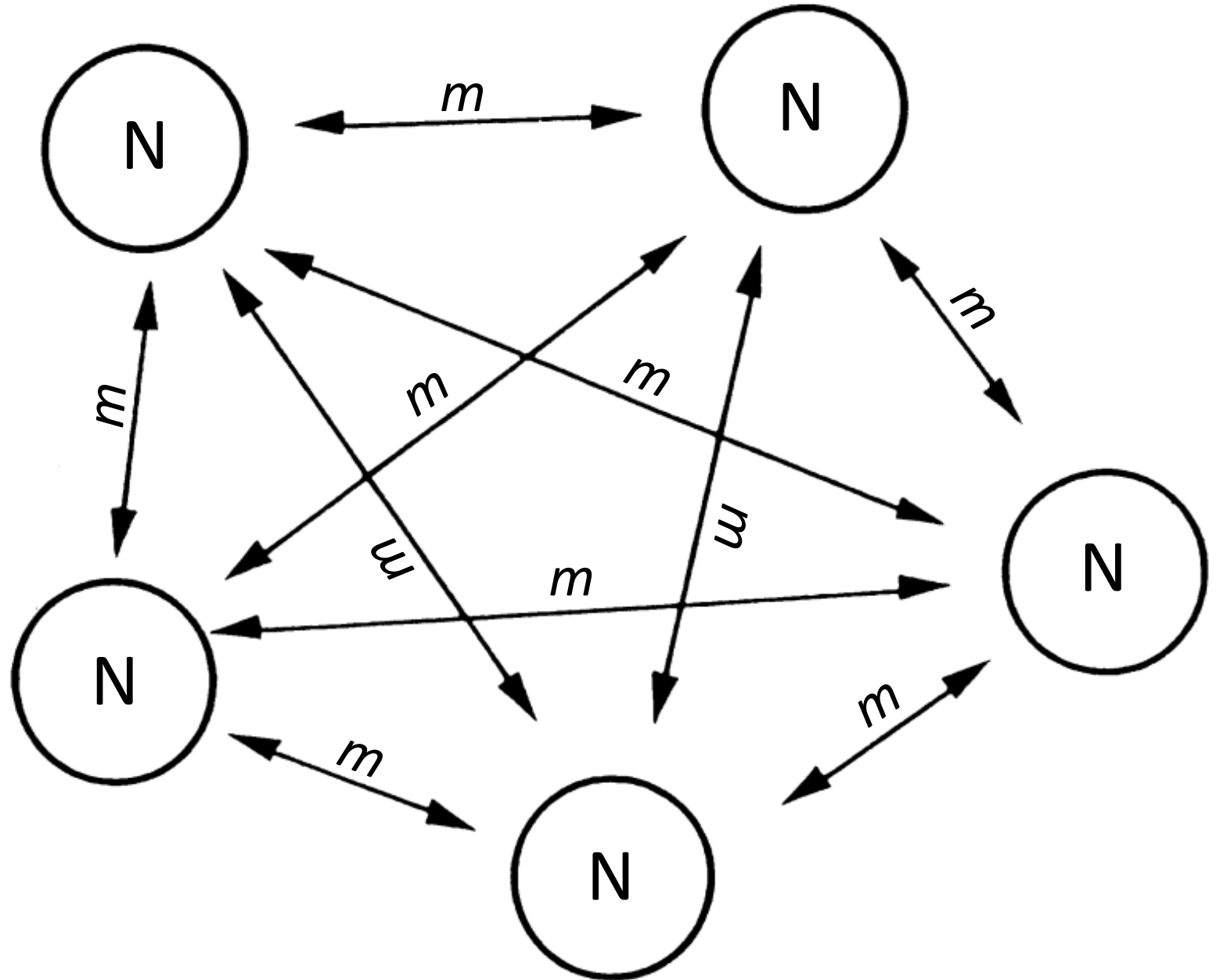
Phenotypic (adaptive) variation



Assign ESU as appropriate/ needed

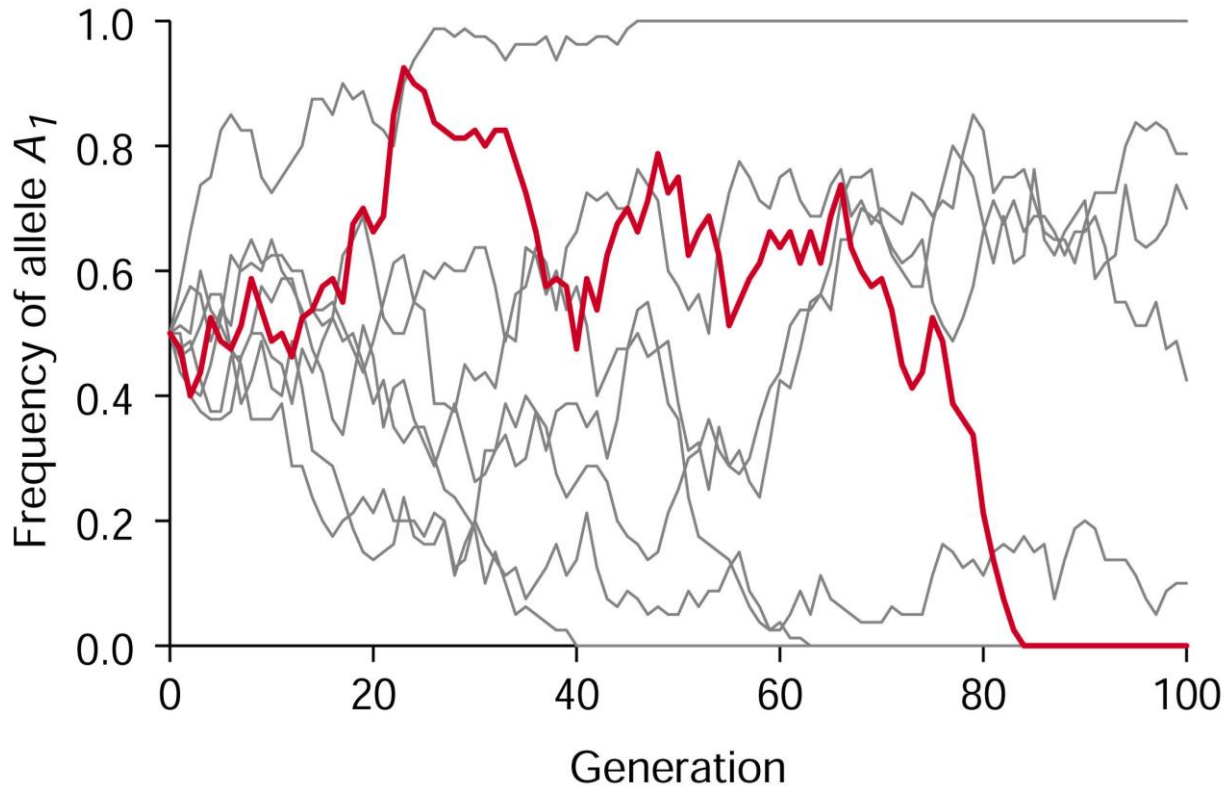
Sewell Wright's Island Model:

- Equal population size and rates of movement between them
- At equilibrium, one migrant per generation can cause panmixia
- Real populations aren't like this, but high migration leads to panmixia (depending on N_e , relative rates, etc.)
- Empirical data gives a sense of migration rates since isolation, especially using Isolation with Migrations models (see Hey & Nielsen 2004)

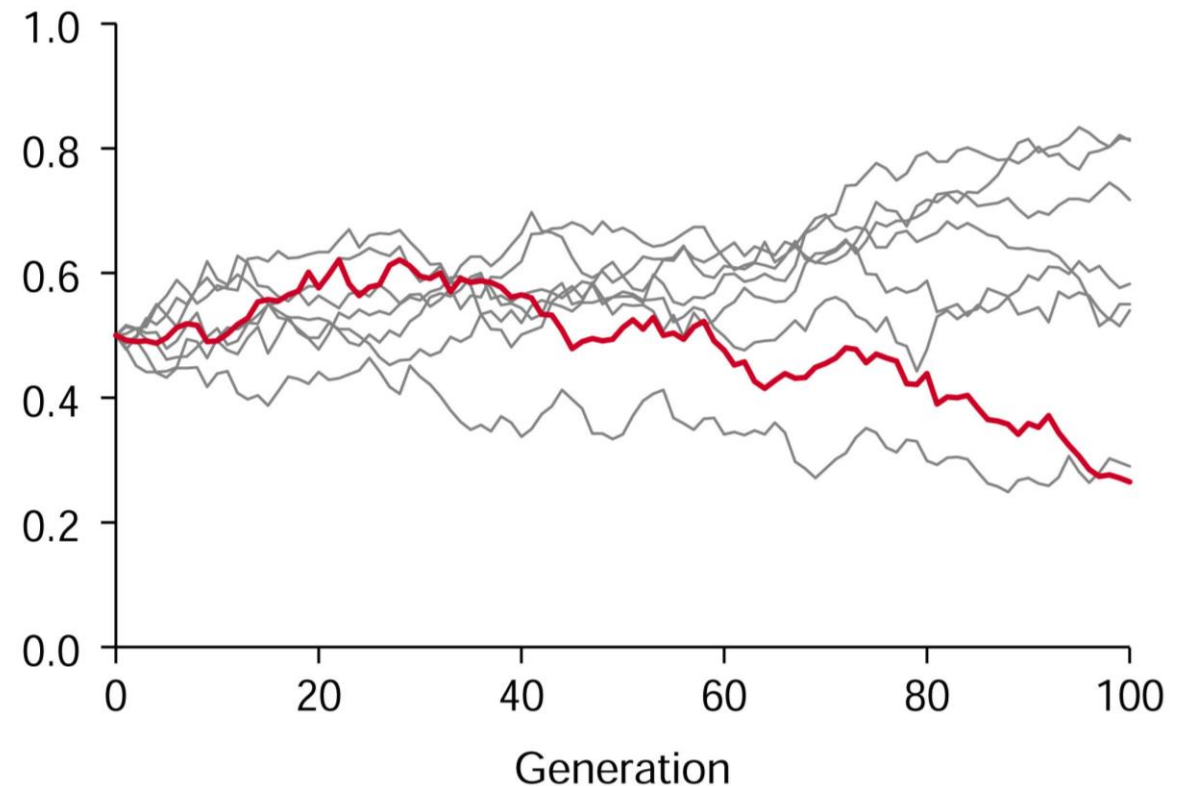


After full isolation ($m = 0$), populations diverge, but the rate depends on N_e (drift), mutation rate, generation time and local adaptation. The rate of drift is approximated by $1/2N_e$; selection is relatively weak when drift is strong and strong when drift is weak.

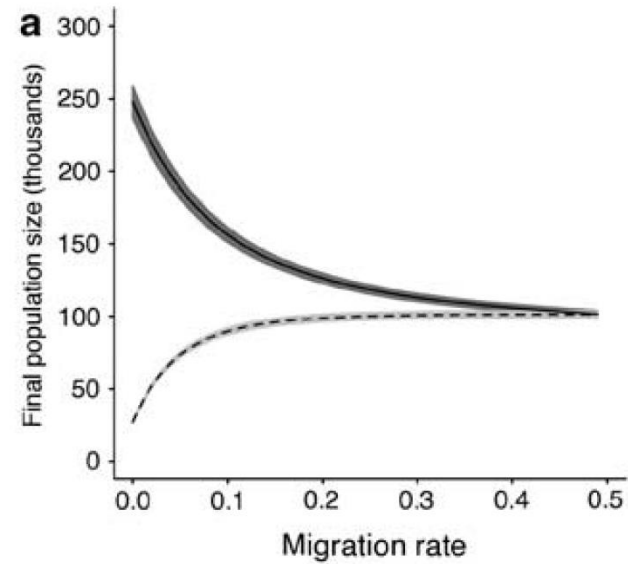
$N_e = 40$



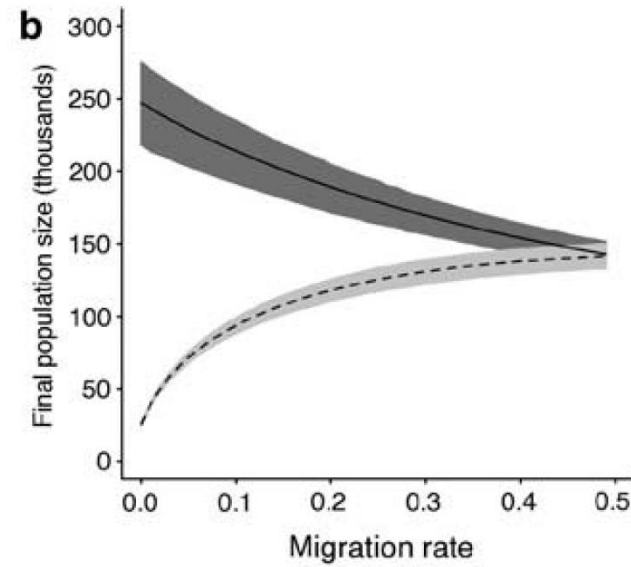
$N_e = 400$



$r=0.1, h_B=0.16$



$r=0.5, h_B=0.38$



$r=0.9, h_B=0.56$

