MIGRATION

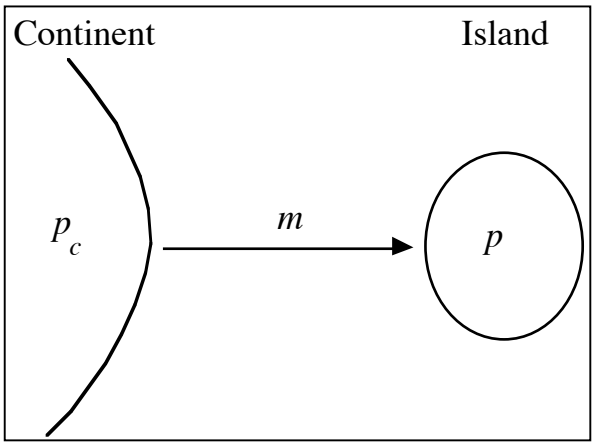
READING: Nielsen & Slatkin pp. 63-70.

ROLES OF MIGRATION IN EVOLUTION

- Introduces novel genetic variation into populations.
- Tends to homogenize gene frequencies in different populations.
- Sets the spatial scale for evolution.
- Opposes local adaptation.
- Migration with an evolutionary impact: Gene Flow
  - Migration introduces *individuals* and *genotypes* ("dispersal").
  - Migrants have no effect on evolution unless their genes are incorporated into a population.

- **A One-Island Model**
  - The simplest model of migration.
  - Two alleles *A* and *a*. Let p = frequency of *A* on island.
  - A fraction m of the island gene pool emigrates from the continent where the frequency of *A* is p_c.

    $\Rightarrow$ A fraction $(1-m)$ of alleles on the island originated on the island.



  - The continent is too vast to be influenced by migration from the island $\Rightarrow$ p_c is constant.
  - Then the frequency of *A* on the island changes according to $p' = (1-m)p + mp_c$.

– At equilibrium, set $p' = p$.

• Solving for p gives $\hat{p} = p_c$

– Rate of approach to equilibrium:

• Rewrite evolutionary equation as

$$p' - \hat{p} = p' - p_c = (1-m)p + mp_c - p_c = (1-m)(p - p_c)$$
$$= (1-m)(p - \hat{p})$$

– <u>Conclusions</u>

(1) At equilibrium, both populations have the same allele frequencies.

(2) Rate of approach to equilibrium ($\hat{p} = p_c$) is determined by the migration rate m.

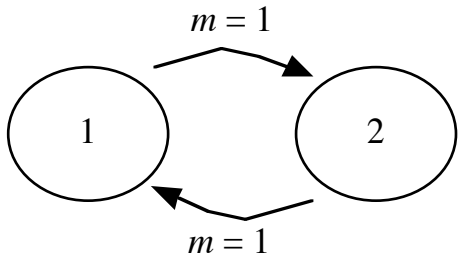
• General Models of Migration

– Same conclusions as one-island model hold.

– Exceptions, however, do exist

• For example, consider two populations with different allele frequencies that switch locations each generation.

• The populations will obviously never homogenize (because there's no real exchange of genes).



– Remark: Have implicitly assumed gene frequencies differ in different locations.

– How could this be?
– "History."
– Genetic drift.
– Selection favors different alleles in different locations.

MIGRATION AND DRIFT

• Migration introduces novel genetic variation into local populations.

• Drift removes local genetic variation.

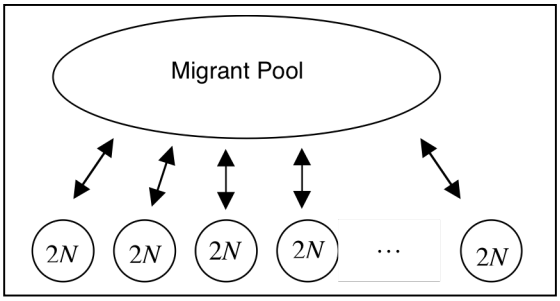
Which for dominates?

One answer…

• **Wright's "Island Model"**

• Consider a large number of "islands" each with a population of size N ($2N$ alleles per locus)

• Each generation, every island exchanges a fraction m_T of its gametes with a ∞-sized "migrant pool" to which all islands contribute gamates.



• Assume infinite-alleles model.

• Let f_t = Pr(pair or randomly drawn gametes on a typical island are IBD in generation t) = average within-island homozygosity

• By the same logic used when studying mutation-drift balance:

$$f_{t+1} = (1 - m_T)^2 \left[\frac{1}{2N} + (1 - \frac{1}{2N}) f_t\right]$$

• At equilibrium, $f_{t+1} = f_t = \hat{f} \approx \frac{1}{1+4Nm_T}$

– expression resembles that describing diversity maintained by mutation & drift, with $\theta = 4Nu$ replaced by $4Nm_T$.

• <u>If $4Nm_T < 1$</u>: Local homozygosity is substantial
– drift dominates migration

• <u>If $4Nm_T > 1$</u>: Local diversity (heterozygosity) is substantial
– migration dominates drift

Note 1

– $4Nm_T > 1$ same as $2Nm_T > 1/2$

$\Rightarrow$ Migration dominates drift if at least *one migrant gamete is exchanged every other generation!*

– Conclusion is independent of m_T, the rate of gene flow. (Why?)

Note 2

– Recall from discussion of F statistics: $\overline{H}_S = \underset{i}{\text{Avg}}\left(H_{S,i}\right) \approx 1 - \hat{f}$, since $\hat{f}$ is the average local homozygosity and there is no additional inbreeding

– Also, $H_T = 1 -$ Pr(pair of randomly chosen gametes from entire population are IBD) $= 1 - 0 = 1$

$\Rightarrow F_{ST} = \frac{H_T - \overline{H}_S}{H_T} = \frac{1-(1-\hat{f})}{1} = \hat{f} = \frac{1}{1+4Nm_T}$.

– Suggests way to estimate rate of migration from F_{ST}:

$\widehat{Nm_T} = \frac{1}{4}\frac{1-F_{ST}}{F_{ST}}$.

– Careful: estimate requires lots of assumptions (island model, equilibrium, etc.) to be valid.