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 $p_c$.
    - 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

\[
p' - \hat{p} = p' - p_c = (1 - m)p + m p_c - p_c = (1 - m)(p - p_c)
\]

\[
= (1 - m)(p - \hat{p})
\]

– Conclusions

(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 $\infty$-sized “migrant pool” to which all islands contribute gametes.

- 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, $f_{t+1} = f_t = \hat{f} \approx \frac{1}{1 + 4N m_T}$

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

- If $4Nm_T < 1$: Local homozygosity is substantial
  - drift dominates migration

- If $4Nm_T > 1$: Local diversity (heterozygosity) is substantial
  - migration dominates drift

Note 1

- $4Nm_T > 1$ same as $2Nm_T > 1/2$
⇒ 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: $\bar{H}_S = \text{Avg}(H_{S,i}) \Rightarrow 1 - \hat{f}$, since $\hat{f}$ is the average local homozygosity and there is no additional inbreeding

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

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

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

$$\bar{N}m_T = \frac{4}{4} \frac{1 - F_{ST}}{F_{ST}}$$

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